Title

The Description, Prediction and Misprediction of Protein Function

Author

Schnoes, Alexandra Maria

Publication Date

2008

The Description, Prediction and Misprediction of Protein Fucntion

by

Alexandra Maria Schnoes

DISSERTATION

Submitted in partial satisfaction of the requirements for the degree of

DOCTOR OF PHILOSOPHY

in

Biophysics

in the

GRADUATE DIVISION

of the

UNIVERSITY OF CALIFORNIA, SAN FRANCISCO

[redacted]

To my parents,
without whom none of this would have been possible.

Always, my love.

Acknowledgements

There will never be enough space for me to adequately thank everyone who has aided and abetted me along this involved process known as graduate school, though I make the feeble attempt here. In reality, I give thanks for all my experiences over these past years as I have learned more than I ever thought possible and I cannot imagine being who I am today without them.

Without question I wish to acknowledge and thank my advisor Patsy Babbitt. Over the years she has shown tremendous support and consistent confidence in my abilities. I feel exceedingly lucky to have been part of this lab and I have such gratitude for the collegial environment she has encouraged and fostered. My lab mates have also been a true pleasure to work with (and be friends with!). They have been supportive, critical, interested and engaged. Thank you to all! I would like to especially mention Ranyee, Elaine, Margy and Shoshana for many critical readings of my work and for always useful advice, Scott for his tremendous work on the SFLD and Sunil, Ben, Mark, Courtney and Corey for their critical thinking and generously shared knowledge.

Many thanks also go to my committee, Andrej Sali, Tanja Kortemme and Brian Shoichet. They have always been available to me and supportive and I have greatly appreciated the chance to be able to work with them and receive their advice. Much gratitude also goes to Tanja for sharing her lab with me and acting often as a second mentor. It has meant quite a lot to me. I would also like to thank Fred Cohen and his lab for being my first home here at UCSF. Last but not least, I would also like to mention Julie Ransom and Rebecca Brown, Biophysics Coordinators extraordinaire. You two made navigating UCSF seem easy.

I don’t where I’d be without my peer mentor group, so KF, GC, KH, CA, CB, DF, FYL, and CO thanks for everything. The same goes to EI. I’d also like to thank the wonderful people at the Office of Student Life. Maureen, JoAnn, Eric, and Bill, you often made the OSL feel like a home away from home. To Angela and the QG crew, it’s been a lot of years and a lot of fun. As for my friends and family, I barely know where to begin. Sarah and Ranjani, thank you for being my tireless cheering squad, you are amazing. Cynthia, Paula, Michelle, Chris and Ab (and the rest of the GSA crew), my friends from way back (Steffi, Cindy, Joce, Alice, Juneko, Miriam and Paige) and my numerous fabulous roommates over the years (including my über-fabulous current roommate Weisen) thank you for just being you. And to my family, especially my parents, thank you, thank you, thank you (ad infinitum).

Most of Chapter 2 derives from a manuscript *in preparation*. The co-author Patricia C. Babbitt directed and supervised the research that is described both in this chapter and the remainder of the thesis. The co-author Igor Dodevski performed initial work into the misannotation analysis detailed in Chapter 2. The co-author Shoshana Brown provided Python code in addition to project advice and expert knowledge of the Structure Function Linkage Database and the functions listed therein. The data discussed in section 2.4.1 is part of another manuscript *in preparation* in collaboration with John Gerlt's laboratory at the University of Illinois, Urbana-Champaign. Except for this short section, the research described in Chapter 2 (and the remainder of the thesis) was essentially all conducted by Alexandra M. Schnoes. The work presented in this thesis is comparable to work for a standard thesis awarded by the University of California San Francisco.

Patricia C. Babbitt
Professor of Biopharmaceutical Sciences

Abstract

The Description, Prediction and Misprediction of Protein Function

Alexandra M. Schnoes

Understanding protein function is a key biological question that is the focus of much current research. This question has become increasingly complicated in the post-genomic era with the influx of millions of new sequences. We are no longer able to experimentally characterize even a small fraction of these protein sequences, however this sequence data is a treasure trove of new biologically important information. Currently most sequences are annotated with protein functions predicted through computational methodologies. Computational prediction poses a number of issues, however. The concept of 'protein function' is nebulous in practice and can be defined innumerable different ways depending on the context. Methods for computational prediction all contain some level of inherent error leading to an unknown level of functional misannotation in sequence databases. The common practice of annotating functions through the process of annotation transfer (the transfer of an annotation from a 'known' sequence to an 'unknown' sequence typically determined by sequence similarity) is potentially compounding the misannotation problem via the inclusion of new errors and the propagation of errors already in the sequence databases. The thesis work here presented provides an in depth analysis of the issue of protein misannotation. The levels of misannotation for 37 different enzyme families are examined in four public sequence databases (GenBank NR, UniProtKB/TrEMBL, KEGG and UniProtKB/Swiss-Prot) and shown to be significantly high. The types of misannotations found are detailed to provide some insight into the possible causes. Additionally, the directional trend in misannotation over time is determined to be increasing. In conclusion, methodologies to ameliorate the misannotation problem are discussed and several proposals to quickly find new misannotations and communicate these findings to the scientific community are made.

Table of Contents

List of Tables

List of Figures

Chapter 1.
Introduction

1.1. Protein function

1.1.1. What does ‘protein function’ mean?

Although much effort is expended by both computational and experimental scientists to predict and characterize protein function, the actual term ‘protein function’ is inherently nebulous. What is meant by ‘protein function’ depends entirely upon the context in which it is used. Protein function can mean biological role, enzymatic activity, metabolic context, a combination of the above or something else entirely. Figure 1-1 gives a short list of the possible definitions of ‘protein function’. As evidenced by this list, the boundaries that define ‘protein function’ are broad and ill defined. This does not change the fact, however, that the understanding of protein function, in whatever its forms, is a key biological problem and that communicating effectively about protein function is important in scientific discourse.

Protein Function

- Biological role
- Enzymatic activity
- Protein localization
- Protein interactions
- Protein expression
- Temporal activity
- Post-translational modifications
- Structural domain
- Sequence motif
- Structural motif
- Binding sites
- Functionally important residues
- Genomic context
- Metabolic pathway

Figure 1-1. A short list of potential definitions of protein functions.

1.1.2. The description of function

With the diversity of potential functions, effectively describing function in a concrete manor can be challenging. Each different type of function requires its own, sometimes very specialized, vocabulary. Often the words used to describe the function can be nebulous themselves. For example, the term ‘interaction’ can be used to indicate a binding event between proteins or instead an enzymatic event. Only context and explanation can make the term clear. Therefore the theoretical problem of how to appropriately convey ‘protein function’ is inherently complex.

The problem of protein function description is also a practical one. Ideally, every discovery about protein function (whatever the specific type of protein function) would be input into some kind of publicly available data repository. The information about protein function would be translated into a format that is appropriate for computational storage and retrieval. In theory whatever format would be chosen would be concrete (i.e. interpretable in only one way), encapsulate all necessary information and be identifiable with other proteins of the same function. In addition, the function would be easily parsable by computational means.

In reality, however, protein function annotation has been primarily an ad hoc affair [1]. In the large primary sequence databases like GenBank and TrEMBL [2-4] function description is determined entirely by the sequence submitter. There have been a number of problems with this approach. Because there is no defined vocabulary for ‘protein function’, proteins with the same function can be described differently depending on the annotator. This problem often starts with gene names, which have been shown to be ambiguous and often confusingly named [1, 5, 6]. In addition, functional modifiers, such as ‘probable’, ‘similar-to’, ‘-like’, ‘hypothetical’ etc., can make the interpretation of any function definition problematic as these terms do not have an agreed upon definition [7]. Annotators also often utilize general classification tools like Pfam [8] or InterProScan [9] but fail to acknowledge the sources.

There have been a number of approaches used to deal with the complicated issue of annotating protein function. A common approach, utilized by Swiss-Prot [3] is the addition of multiple sources of function information on a sequence’s information page. This approach can be very useful for manual examination but can be very difficult to compute upon. Another approach is that of using ontologies. Ontologies attempt to classify information into defined relationships and typically use defined vocabularies. A common ontology in the biological science is the Gene Ontology (GO) [10]. GO has been used in the annotations of several model organisms (including yeast [11]) and Swiss-Prot has started including GO terms on its sequence pages. Currently however, no single ontology is universally accepted and no ontology yet created fully encapsulates the complexities of protein function.

For enzymatic proteins the Enzyme Commission (E.C) numbering system is often used and, when all four E.C. numbers are used, can allow for a concrete description of enzymatic function. However not all enzymes have E.C. numbers assigned and the simplicity of the E.C. system is not always sufficient to convey the appropriate enzymatic detail [12]. A more extensive way to describe protein function is found in the Structure-Function Linkage Database (SFLD) [13, 14] and the Catalytic Site Atlas (CSA) [15]. Both of these resources connect an enzyme's function to structure and sequence. The CSA focuses primarily on connecting enzyme function to functionally important residues and gives tools to examine new sequences using this information. The SFLD also delineates functionally important residues but also has a significant focus on putting each sequence (and each function) in a hierarchical sequence/structure superfamily context that allows for additional inferences. However, because both databases involve significant manual curation, the families and functions covered in each databases are limited.

1.2. Protein function annotation error

1.2.1. The fundamentals of annotation error

The manner in which protein function is described in a sequence's annotation is intimately tied to the issue of protein function prediction error. The primary method of protein function annotation is annotation transfer, in which the annotation of one sequence is transferred to another based upon some level of sequence similarity [16-18]. The frequent use of annotation transfer means that, whatever the definition of protein function used in the original annotation, it is now being assigned to sequences that may or may not be appropriately 'similar' to the original (similarity is entirely decided by the individual annotator). The sequence similarity at which to transfer annotations is a significant issue. Given the propensity of using annotation transfer as a function prediction method, this issue has engendered a certain amount of investigation [19-23]. While the goal has been to determine one sequence similarity threshold at which it would be safe to transfer all annotations, the most recent and thorough investigation [24] has indicated that a single threshold does not exist. In fact, thresholds need to be determined for each protein family. Currently, however, no such global threshold set has been developed for the protein universe. This translates to individual annotators or annotating institutions making their own decisions about similarity thresholds leading to varying quality in the implementation of annotation transfer.

The current variability in function definitions and metrics for annotation transfer has lead to another significant issue: annotation error propagation. Even before the success of whole-genome sequencing, there was concern that the errors that were already present in the public sequence databases were being propagated to new sequences [25, 26]. Additionally, instances of error propagation were described in the literature [7, 27, 28]. Recent theoretical models of error propagation have also shown that given a significant enough level of database error, error propagation can seriously degrade the quality of the database [29, 30]. In this way, annotation error affects not only the misannotated sequence but also potentially numerous others.

1.2.2. Finding misannotation

Given the size and scope of the available protein sequences, in addition to the multitude of ways to specify function, it has been difficult to quantify the exact level of misannotation in protein sequence databases. In fact most misannotation studies do not specifically examine the issue annotation error within the context of the public sequence databases. An early study by Brenner examined the level of misannotation present in the small genome *Mycoplasma genitalium* (by comparing annotations from three different groups) and found that function annotation was at minimum 8% [31]. Devos and Valencia expanded upon this study by examining three small genomes and investigating different definitions of function [32]. The levels of misannotation found ranged from 4% to 40% for the 1,228 sequences they examined. Greene and Karp examined the issue of using E.C. numbers as functional annotations, specifically when the full E.C. number is not assigned. They found that almost 7% of the *E. coli* genes in the pathway database KEGG had incorrect partial E.C. numbers. A recent paper modeling the level of misannotation in GO [33] predicted that up to 49% of computationally annotated sequences were misannotated.

1.3. Dissertation overview

What has been missing from the above investigations is an examination of the large sequence databases themselves. These sequence databases (e.g. GenBank NR, TrEMBL, Swiss-Prot and KEGG) are daily used by the scientific community and often assumed to be correct. However, no one has yet investigated the extent to which the already enumerated problems have affected the annotations available in these databases. The goal of this thesis is to examine the issue of misannotation in public databases, focusing on the level of misannotation, the types of misannotation, and the mechanisms by which misannotation can be addressed. Chapter 2 focuses primarily on examining misannotation in several public databases for a set of proteins for which the function is now experimentally known. Chapter 3 describes an additional approach to investigating misannotation that examines the contribution of other sources of annotation error: annotations that are partially correct or completely mislabeled. This work is a tangential analysis to the core thesis work that is presented in Chapter 2. Chapter 4 is the concluding chapter and discusses several proposed analysis directions that could address the problem of annotation error and the chapter summarizes the findings in this thesis.

Chapter 2.
Annotation Error in Public Databases: Misannotation of Molecular Function in Enzyme Superfamilies

2.1. Abstract

2.1.1. Background

Due to the rapid release of new data generated from genome sequencing projects, the majority of protein sequences in public databases have not been experimentally characterized; rather, sequences are annotated using computational analysis. As such, the level of misannotation in large public databases is currently unknown. Moreover, the types of misannotation that exist have not been analyzed in depth.

2.1.2. Results

We have investigated the error in the annotation of molecular function in four public protein sequence databases (UniProtKB/Swiss-Prot, GenBank NR,

UniProtKB/TrEMBL, and KEGG)) for a model set of 37 enzyme families for which extensive experimental information is available. These families come from six different superfamilies (enolase, haloacid dehalogenase, vicinal oxygen chelate, terpene cyclase, amidohydrolase and crotonase) representing five fold classes and enzymatic functions spanning all six major classes of the E.C. system. The manually curated database Swiss-Prot shows the lowest levels of annotation error (close to 0% for most families); the two other protein sequence databases (GenBank NR and TrEMBL) and the KEGG pathways database exhibit similar and surprisingly high levels of misannotation that average 5%-63% across the six superfamilies studied. For ten of the 37 families examined, the level of misannotation in one of more of these databases is >80%. Examination of the NR database over time shows that misannotation has increased from 1993 to 2005. The types of misannotation fall into several categories, most associated with "overprediction" of molecular function, e.g., assignment of a specific substrate or reaction when evidence from sequence or structural comparisons supports annotation only at the more general level represented by assignment to a superfamily.

2.1.3. Conclusions

These results suggest that misannotation in enzyme superfamilies may be a larger problem than has been recognized. Moreover, the problem appears to be worsening over time and shows propagation of annotation errors into at least one important secondary database, the KEGG pathways database. Strategies are discussed for addressing some of the systematic problems contributing to these high levels of misannotation, including database evidence codes, use of ontologies and an adjusted approach to annotation.

2.2. Background

The daily addition of new genomes into public sequence databases allows for rapid access to sequences from more than a quarter million named species [2], an accumulation of genomic and proteomic sequence information that is astounding in both its scale and breadth. While these data hold enormous potential for biological and medical discovery, as evidenced by the many “omics” fields that have emerged, experimental characterization has been performed on only a tiny fraction of the available sequences. Moreover, current technology, including high-throughput techniques, can be applied to at most a few thousand genes or proteins at a time. As a result, computational methods are required to predict the molecular functions of the millions of protein sequences that have not and cannot be characterized experimentally. Already, the majority of sequences found in public databases have been annotated using computational prediction alone, raising the issue of annotation accuracy and database quality [25, 26].

Driven by concerns that some proportion of these proteins had been functionally misannotated, the accuracy of predicted functions was a topic of inquiry even before the availability of many whole-genome sequences. Two important papers examining genome annotation error [31, 32], in one and three small genomes respectively, predicted that at least 8% of molecular function annotations were incorrect. Depending on the definition of function used, Devos and Valencia further suggested that misannotation levels could be as high as

40%. These findings were corroborated anecdotally by published examples of annotation error [27, 34-36]. An additional concern was that the misannotation problem would continue to be compounded by error propagation from annotation transfer [25]. Models of error propagation have since shown that given sufficient initial error in a database, error propagation can significantly degrade the quality of the annotations it contains [29, 30] and some examples of error propagation have already been noted [7, 28]. A recent paper modeled the annotation error for annotations in the Gene Ontology database and estimated that up to 49% of computationally annotated sequences could be misannotated [33]. Although sequence misannotation in commonly used public sequence databases is now becoming of great concern [37, 38] no one has yet performed an in depth analysis into the prevalence of annotation error in these databases.

Concomitant with the growth of sequence data, annotation strategies have become more sophisticated, benefiting especially from the use of multiple orthogonal methods to improve prediction accuracy. These include methods that take advantage of co-localization of functionally linked genes [39-42], homology-based annotation transfer using phylogenetic and phylogenomic information [43-45], and experimental proteomics approaches such as mass spectrometry [46]. Using the massive influx of genomics data now available, important resources have been developed that can be expected to improve computational annotation, including databases of motifs [15, 47, 48], ortholog sets [49, 50],[49, 50] sequence profiles [8, 51] and structure-based comparisons [52-55]. In addition, multidisciplinary efforts have focused on accurate annotation for the most important model organisms, including *E. coli*, yeast, mouse and human [11, 56-58]. Given this substantial body of work, we might expect that the problem of misannotation has diminished. However, the most common approach in use today continues to be the assignment of molecular function from homology followed by annotation transfer [16-18]. Thus, a fresh look at the misannotation problem is timely, particularly for primary public databases containing the broadest set of available sequence data.

In this work, we have performed the first investigation into the prevalence of annotation error in several large public protein databases in common use today. The large primary sequence databases GenBank NR (NR) [2, 4], and UniProtKB/TrEMBL (TrEMBL) [3], which contain sequences primarily annotated using automated methods, were examined. Sequences associated with the Kyoto Encyclopedia of Genes and Genomes (KEGG) [59], a database of metabolic pathways, were also examined to obtain a preliminary picture of the degree to which misannotation has been propagated to secondary databases. Finally, we examined the manually curated primary database UniProtKB/Swiss-Prot (Swiss-Prot) [3], is often used in computational analyses as a gold standard.

The analysis examines the level of misannotation for 37 enzyme families (Figure 2-1). Enzymes were chosen for analysis because they typically have concrete, precise definitions of molecular function compared to many other classes of proteins. Annotation error in the NR, TrEMBL, KEGG, and Swiss-Prot databases was determined using, as a gold standard, highly curated and experimentally well-characterized enzyme families from the Structure-Function

Linkage Database (SFLD) [13, 14, 60]. The families that were analyzed come from six different superfamilies (enolase, haloacid dehalogenase [HAD], vicinal oxygen chelate [VOC], terpene cyclase, amidohydrolase [AH] and crotonase) representing five fold classes and enzymatic functions spanning all six major classes of the E.C. system. Superfamilies from the SFLD have already been described as a Gold Standard for use as a functional benchmark [60]. The set of enzymes used here are a subset of families from that set plus families from the terpene cyclase superfamily, added to the SFLD after the publication of the Gold Standard set. In the SFLD, a superfamily is defined as a set of homologous proteins in which conserved sequence or structural characteristics can be associated with conserved functional characteristic. A family is defined as a set of homologous proteins within a superfamily that perform an identical function by the same mechanism.

Superfamily	Family	E.C. No.	Family Color	Number of Sequences Analyzed			
				Database			
				NR	TrEMBL	KEGG	Swiss-Prot
Enolase[1]	Enolase[1]	4.2.1.11	●	666	353	365	284
	Galactonate dehydratase	4.2.1.6	●	38	14	21	1
	Mandelate racemase	5.1.2.2	●	57	23	31	1
	Glucarate dehydratase	4.2.1.40	●	145	44	47	5
	Methylaspartate ammonia-lyase	4.3.1.2	●	52	20	16	1
	Ortho-succinyl benzoate synthase	—	●	66	28	29	13
	Dipeptide epimerase	—	●	2	1	0	0
	Chloromuconate cycloisomerase	5.5.1.7	●	86	33	23	6
	Muconate cycloisomerase	5.5.1.1	●	158	61	35	4
	L-fuconate dehydratase	4.2.1.68	●	1	0	0	0
Crotonase	Dodecenoyl-CoA delta-isomerase (mitochondrial)	5.3.3.8	●	11	8	17	4
	Delta(3,5)-delta(2,4)-dienoyl-CoA isomerase	—	●	10	1	1	4
	Methylmalonyl-CoA decarboxylase	4.1.1.41	●	7	0	1	1
	3-Hydroxyisobutyryl-CoA hydrolase	3.1.2.4	●	53	21	9	0
	4-Chlorobenzoate dehalogenase	3.8.1.7	●	14	7	0	0
	1,4-Dihydroxy-2-napthoyl-CoA synthase	—	●	0	0	0	0
Vicinal Oxygen Chelate (VOC)	Methylmalonyl-CoA epimerase	5.1.99.1	●	22	16	12	2
	4-Hydroxyphenylpyruvate dioxygenase	1.13.11.27	●	182	141	110	26
	FosA	2.5.1.18	●	26	4	4	2
	Glyoxalase I	4.4.1.5	●	348	336	352	24
Terpene Cyclase	5-Epi-aristolochene synthase	—	●	11	5	0	0
	Bornyl diphosphate synthase	5.5.1.8	●	15	0	0	1
	Pentalenene synthase	4.2.3.7	●	7	2	2	1
	Squalene-hopene synthase	5.4.99.17	●	62	55	31	4
	Trichodiene synthase	4.2.3.6	●	72	13	0	17
	Aristolochene synthase	4.2.3.9	●	3	1	0	1
Haloacid Dehalogenase (HAD)	Deoxy-D-mannose-octulosonate 8-phosphate phosphatase	3.1.3.45	●	81	32	87	8
	Phosphonoacetaldehyde hydrolase	3.11.1.1	●	28	27	22	0
	2-Haloacid dehalogenase	3.8.1.2	●	134	86	74	9
	Beta-phosphoglucomutase	5.4.2.6	●	50	43	53	3
Amidohydrolase (AH)	Cytosine deaminase	3.5.4.1	●	82	62	75	1
	Adenosine deaminase	3.5.4.4	●	238	142	136	50
	N-acyl-D-amino-acid deacyclase	3.5.1.81	●	80	58	28	3
	L-hydantoinase	3.5.2.2	●	4	2	0	1
	D-hydantoinase	3.5.2.2	●	46	34	10	0
	Urease	3.5.1.5	●	267	168	112	39
	Isoaspartyl dipeptidase	—	●	26	25	19	1
	Total No. Sequences			3150	1866	1722	517

[1] Enolase is both the name of the superfamily and the name of one of its member families.

Figure 2-1. Enzyme superfamilies and their constituent functional families examined in this analysis

Enzyme Nomenclature Commission (E.C.) numbers are included where available. Dashes (—) are used for those families for which a full E.C. number has yet to be assigned. Each family is designated by a specific color and these mappings are also used in Figure 2-3, Figure 2-7and Appendix B. The number of sequences in each family that were analyzed from each database is listed; the total number of sequences analyzed from each database is also given.

Our analysis of this gold standard set of 37 families show similar and surprisingly high levels of misannotation across all of the databases evaluated except for Swiss-Prot. We also investigated the change in levels of misannotation for these families in the GenBank NR database over the period 1993-2005 and found that despite the current availability of well-curated genomes, sophisticated tools and numerous resources for functional inference, the levels of misannotation have risen dramatically over this time period. As a corollary to this analysis, we examined whether evidence of error propagation could be identified among the misannotated sequences that were found in the NR database. Finally, we classified the misannotations found, providing an initial view of the most prevalent types of errors and allowing us to propose strategies for addressing some of the systematic problems that contribute to them.

2.3. Results

Our misannotation analysis examines the question: Given a sequence annotated to a specific enzymatic function, is the annotation correct? These functions come from six different superfamilies (enolase, HAD, VOC, terpene cyclase, AH and crotonase) representing five fold classes and spanning all six major classes of the E.C. system. A total of 7266 sequences annotated to one of 37 SFLD gold standard families (Figure 2-1) were retrieved from the NR, TrEMBL, KEGG and Swiss-Prot databases and analyzed by the multi-step process described in Figure 2-2.

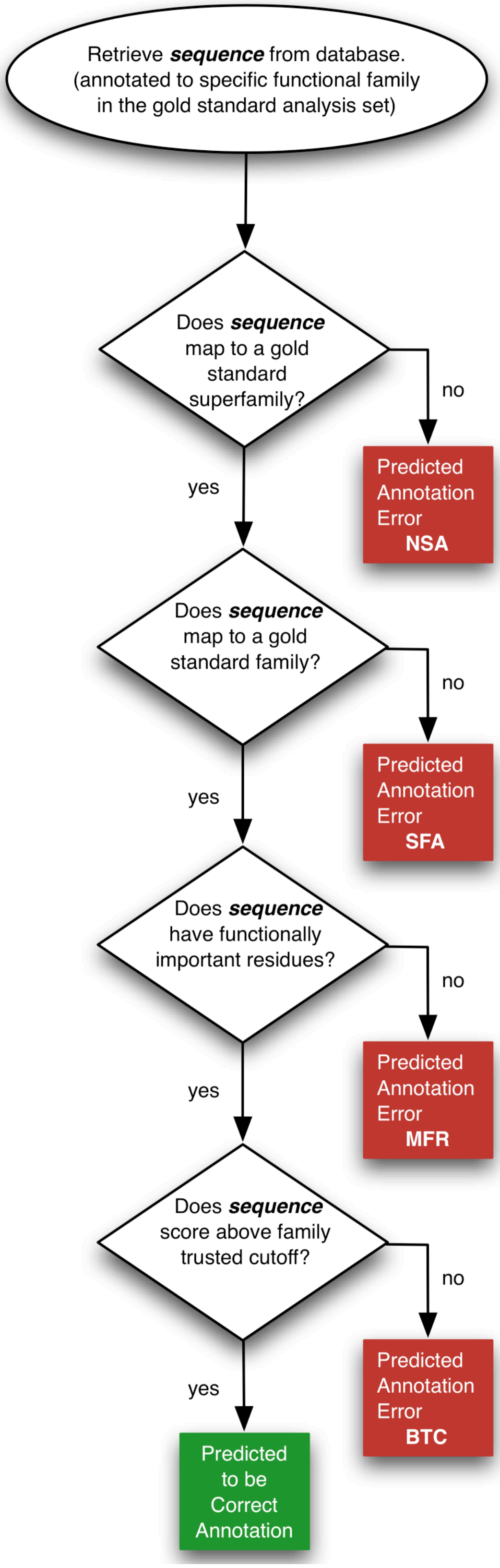

Retrieve *sequence* from database.
(annotated to specific functional family
in the gold standard analysis set)
Does *sequence* map to a gold standard superfamily?
no
Predicted Annotation Error **NSA**
yes
Does *sequence* map to a gold standard family?
no
Predicted Annotation Error **SFA**
yes
Does *sequence* have functionally important residues?
no
Predicted Annotation Error **MFR**
yes
Does *sequence* score above family trusted cutoff?
no
Predicted Annotation Error **BTC**
yes
Predicted to be Correct Annotation

Figure 2-2. The misannotation analysis flow chart
The analysis starts with the selection of a sequence from one of the four databases investigated, annotated to a specific enzymatic function in the gold standard analysis set. Using automated tools from the SFLD, each sequence in the analysis set is first examined for sequence similarity to the gold standard superfamilies using manually curated HMMs for each of the gold standard superfamilies and families. If a sequence does not score against any superfamily HMM, it is predicted to be misannotated and labeled with the misannotation code 'No Superfamily Association' (NSA). A sequence that passes this first step is then tested against the HMM for the family to which the sequence is annotated. If the sequence fails to score against the family HMM it is predicted to be misannotated and labeled with the misannotation code 'SuperFamily Association only' (SFA). Sequences passing this step are then checked for the presence/absence of required functionally important residues as defined by the SFLD. If the necessary residues are deleted or mutated, the sequence is predicted to be misannotated and is labeled with the misannotation code 'Missing Functionally important Residue(s)' (MFR). A sequence that passes these steps but does not score above the HMM score that defines membership to a functional family (see Methods for details), is predicted to be misannotated and labeled with the misannotation code 'Below Trusted Cutoff' (BTC). Only if a sequence passes all four analysis steps, is it predicted to be correctly annotated.

As shown in Figure 2-3, misannotation was found in all six superfamilies examined (Table 2-1 provides tabulated values associated with Figure 2-3). The average levels of misannotation varied greatly between the superfamilies but were remarkably high for four of the six superfamilies (enolase, VOC, HAD, AH) in the three automated curation databases (NR, TrEMBL and KEGG). The average percent misannotation over the superfamily ranged from a little under 25% in the enolase superfamily to over 60% in the HAD superfamily (Figure 2-3 A, C, E, F). In the crotonase superfamily, the average percent misannotation over the superfamily was also found to be greater than 20% in the TrEMBL and KEGG databases (Figure 2-3 B). Additionally, within a superfamily the results for the NR, TrEMBL and KEGG databases were nearly identical (Figure 2-3 A, C-F). For example, in the enolase superfamily (Figure 2-3 A) the average percent misannotations in the NR, TrEMBL and KEGG databases were 24%, 22%, and 22%, respectively. The crotonase superfamily (Figure 2-3 B) was the outlier, showing increasing levels of misannotation across the databases, (NR [12%] < TrEMBL [32%] < KEGG [46%]).

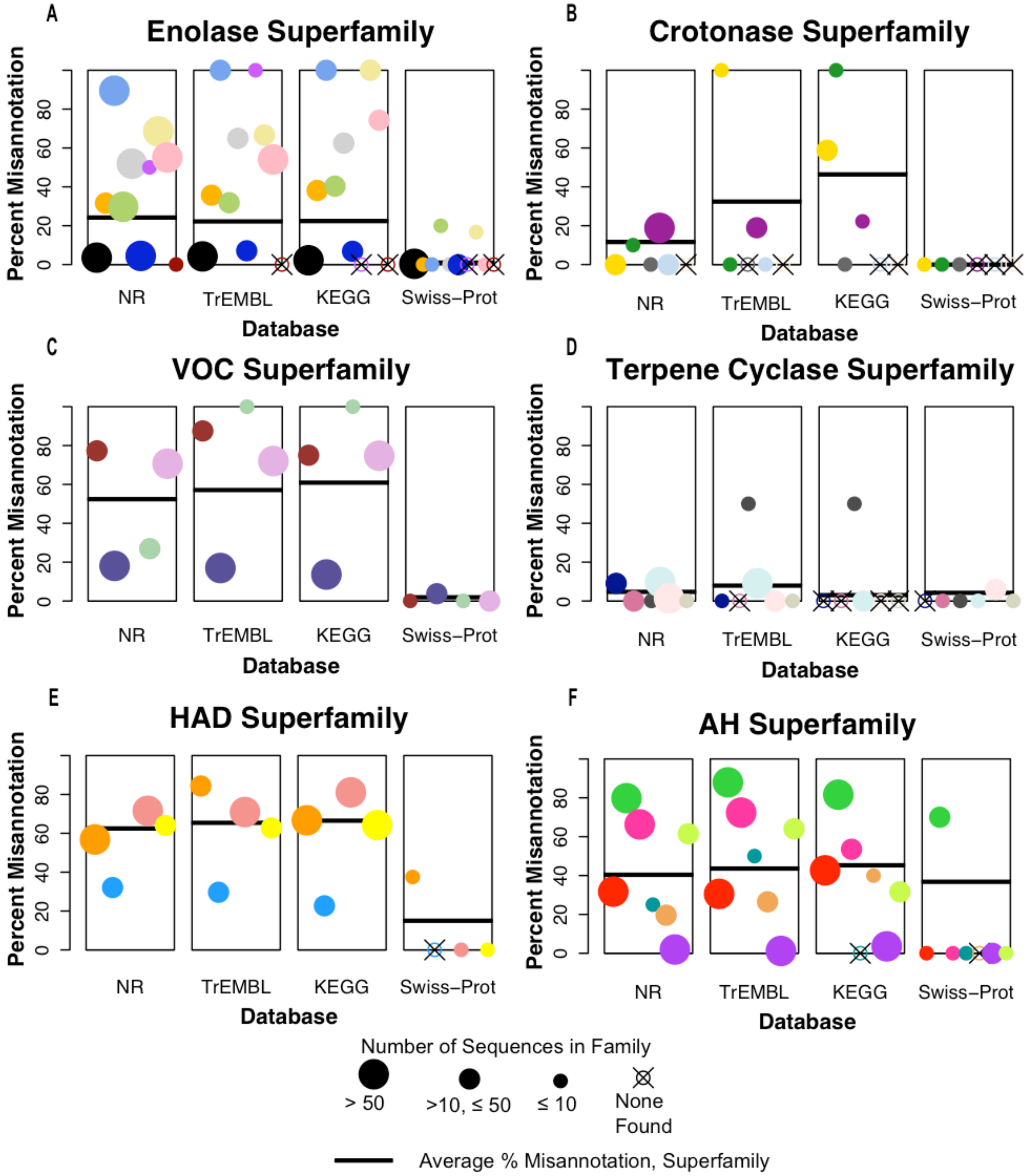


Figure 2-3. Percent misannotation in six enzyme superfamilies over the four databases analyzed in this study

The results are organized by superfamily; Panel A: enolase, B: crotonase, C: vicinal oxygen chelate, D: terpene cyclase, E: haloacid dehalogenase and F: amidohydrolase. Each panel depicts the percent misannotation for the superfamily in four plots, corresponding to the NR, TrEMBL, KEGG, and Swiss-Prot databases, respectively. In each plot, a black bar denotes the average percent misannotation for that superfamily in that database. The percent misannotation for each family within the superfamily is given by a colored circle. The size of the circle provides an estimate of the number of sequences retrieved for that family (scaling in legend). An X through an open circle means that no sequences annotated with that function were retrieved from that database. The order of the families depicted for each superfamily is arbitrary but is consistent through all four plots. The colors of the family circles correspond to the colors given in Figure 2-1, which provide a mapping between a family's color and its function.

Table 2-1. Percent misannotation for each family in the NR, TrEMBL, KEGG and Swiss-Prot databases.

Superfamily	Family	NR % Mis.			TrEMBL % Mis.	KEGG % Mis.	Swiss-Prot % Mis
		Thresh.[a]			Thresh.	Thresh.	Thresh.
		TC[b]	NC[c]	LC[d]	TC	TC	TC
Enolase							
	Enolase	4	3	3	4	2	0.4
	Galactonate dehydratase	32	26	26	36	38	0
	Mandelate racemase	90	90	68	100	100	0
	Glucarate dehydratase	30	26	10	32	40	20
	Methyl aspartate ammonia-lyase	52	27	0	65	63	0
	Ortho-succinyl benzoate synthase	5	5	5	7	7	0
	Dipeptide epimerase	50	50	50	100	0	0
	Chloromuconate cycloisomerase	69	69	69	67	100	17
	Muconate cycloisomerase	55	52	52	54	74	0
	L-fuconate dehydratase	0	0	0	0	0	0
	Superfamily Avg. % Misannot.	24	22	18	22	22	1
Crotonase							
	Dodecenoyl-CoA delta-isomerase (mitochondrial)	0	0	0	100	59	0
	Delta(3,5)-delta(2,4)-dienoyl-CoA isomerase	10	10	10	0	100	0
	Methylmalonyl-CoA decarboxylase	0	0	0	0	0	0
	3-Hydroxyisobutyryl-CoA hydrolase	19	13	6	19	22	0
	4-Chlorobenzoate dehalogenase	0	0	0	0	0	0
	1,4-Dihydroxy-2-napthoyl-CoA synthase	0	0	0	0	0	0
	Superfamily Avg. % Misannot.	12	8	4	32	46	0
VOC							

	Methylmalonyl-CoA epimerase	77	55	0	88	75	0
	4-Hydroxyphenylpyruvate dioxygenase	18	9	8	17	14	4
	FosA	27	27	27	100	100	0
	Glyoxalase I	71	60	42	72	75	0
	Superfamily Avg. % Misannot.	52	42	29	57	61	2
Terpene Cyclase							
	5-Epi-aristolochene synthase	9	9	9	0	0	0
	Bornyl diphosphate synthase	0	0	0	0	0	0
	Pentalenene synthase	0	0	0	50	50	0
	Squalene-hopene synthase	10	5	5	9	0	0
	Trichodiene synthase	1	1	0	0	0	6
	Aristolochene synthase	0	0	0	0	0	0
	Superfamily Avg. % Misannot.	5	2	2	8	3	4
HAD							
	Deoxy-D-mannose-octulosonate 8-phosphate phosphatase	57	7	3	84	67	38
	Phosphonoacetaldehyde hydrolase	32	11	4	30	23	0
	2-Haloacid dehalogenase	72	60	44	71	81	0
	Beta-phosphoglucomutase	64	50	38	63	64	0
	Superfamily Avg. % Misannot.	63	39	28	65	67	15
AH							
	Cytosine deaminase	32	32	32	31	43	0
	Adenosine deaminase	80	77	31	88	82	70
	N-acyl-d-amino-acid deacylase	66	48	23	72	54	0
	L-Hydantoinase	25	25	25	50	0	0
	D-Hydantoinase	20	9	9	27	40	0
	Urease	2	2	2	1	4	0
	Isoaspartyl dipeptidase	62	62	8	64	32	0
	Superfamily Avg. % Misannot.	40	37	18	44	45	37

[a] Misannotation HMM analysis thresholds

[b] Trusted Cutoff

[c] Noise Cutoff

[d] Lenient Cutoff

In contrast to the misannotation noted above, the families in the terpene cyclase superfamily (Figure 2-3 D) were consistently the best annotated with relatively low but still significant levels of misannotation in all four of the databases: NR (5%), TrEMBL (8%), KEGG (3%), and Swiss-Prot (4%). Additionally, across the entire test set, Swiss-Prot was uniformly the best-annotated database showing an average percent misannotation level of 0% (or very nearly 0%) for four of the superfamilies (Figure 2-3 A-D). In all cases there was a clear decrease in the level of misannotation found in the manually curated Swiss-Prot as compared to the automatically curated databases.

Most families displayed consistent levels of misannotation across the NR, TrEMBL and KEGG databases. For instance, the average percent misannotation in the 4-hydroxyphenylpyruvate dioxygenase family (Figure 2-3 C, purple-blue dot) was 18%, 17% and 14% in NR, TrEMBL and KEGG, respectively. This trend is was not surprising given that after the analysis had been completed it was determined that many sequences within the databases were identical to one another and were annotated with identical functional annotations (data not shown).

We found large differences in the misannotation among the entire set of families in each superfamily. For example, in the enolase superfamily (Figure 2-3 A), the family percent misannotation in NR ranged from a minimum of 0% (red dot, fuconate dehydratase family) to a maximum of 90% (light blue dot, mandelate racemase family). As before, this trend is most visible in the more automated databases (NR, TrEMBL and KEGG) and not in the highly curated Swiss-Prot.

The accuracy of our results was verified by several orthogonal protocols. We searched the literature for experimental results that contradicted our misannotation predictions and found such evidence for only six sequences (out of 1155). Another test of our method was a blinded analysis of proteins that had been newly experimentally characterized subsequent to our initial analysis. Out of 27 newly characterized sequences, 26 were correctly classified. We also examined whether any annotation corrections had been made to the sequences that we had predicted to be misannotated. Of a random sampling of 111 of the 1112 sequences in the NR database found to be misannotated by our analysis, we found 96% of the sequences had unchanged functional annotations.

2.3.1. Effect of threshold stringency on misannotation levels.

To determine whether the relatively stringent similarity threshold (Trusted Cutoff [TC]) in the final step of the analysis protocol (Figure 2-2), had inflated the levels of misannotation reported in Figure 2-3, we modeled what would happen to the levels of misannotation for the NR database when less stringent thresholds were used. Two new thresholds for each family were defined, a Noise Cutoff and Lenient Cutoff, and each sequence was re-analyzed using these thresholds (see methods and Figure 2-4 for extended definitions). The average levels of percent misannotation did not dramatically change using the less stringent NC cutoff (Figure 2-5). Averaged across each superfamily, the change in misannotation levels determined using the Noise Cutoffs is 4 % except in the HAD superfamily which shows a change of 24 % (although the resulting level of misannotation is still quite high at 39%). As expected, the results from the analysis using the Lenient Cutoff showed a larger difference. On average, the difference in misannotation from the TC to the LC across all six superfamilies using these cutoffs was 16 %. A change of this magnitude was not surprising considering that the lenient threshold was placed well within the noise of the data and included sequences that were known to be members of different families. Moreover, even when using the Lenient Cutoff, significant levels of misannotation remain in each superfamily.

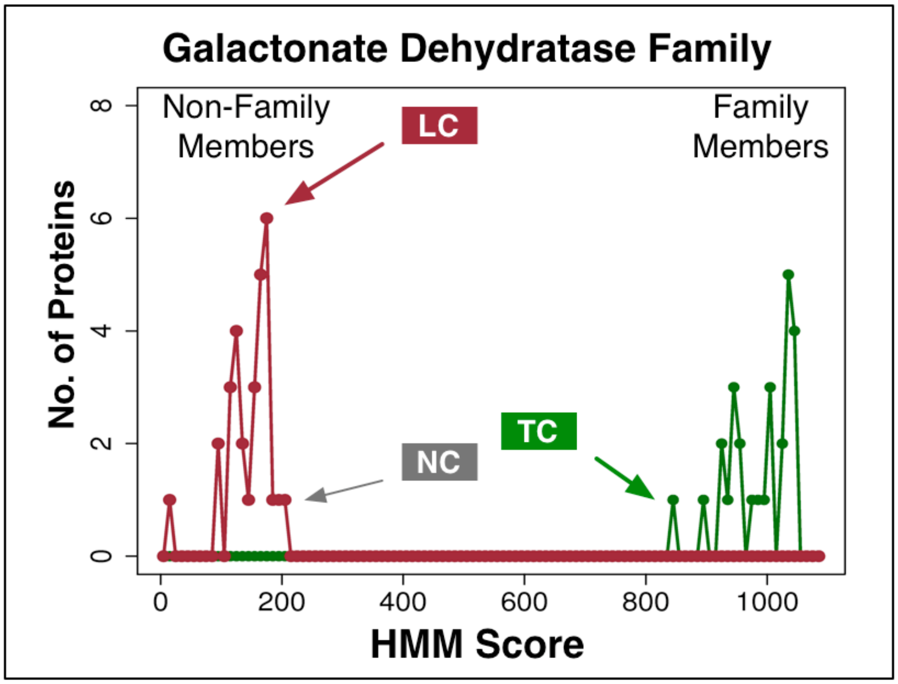


Figure 2-4. The three analysis thresholds used in the misannotation analysis.
This example for the galactonate dehydratase family (enolase superfamily) illustrates how the three score thresholds were defined for each of the 37 families evaluated in this study. The Trusted Cutoff (TC) (used for the main misannotation analysis) was defined as the lowest score at which a family member scores against the family HMM. The Noise Cutoff (NC) threshold was defined as the highest score at which a non-family member scores against the family HMM. The Lenient Cutoff (LC) threshold includes some false positives along with the true family members, yielding a false positive rate of 5%. Using this artificial family set, the LC threshold for each family was defined as the lowest score at which one of the non-family sequences scored.

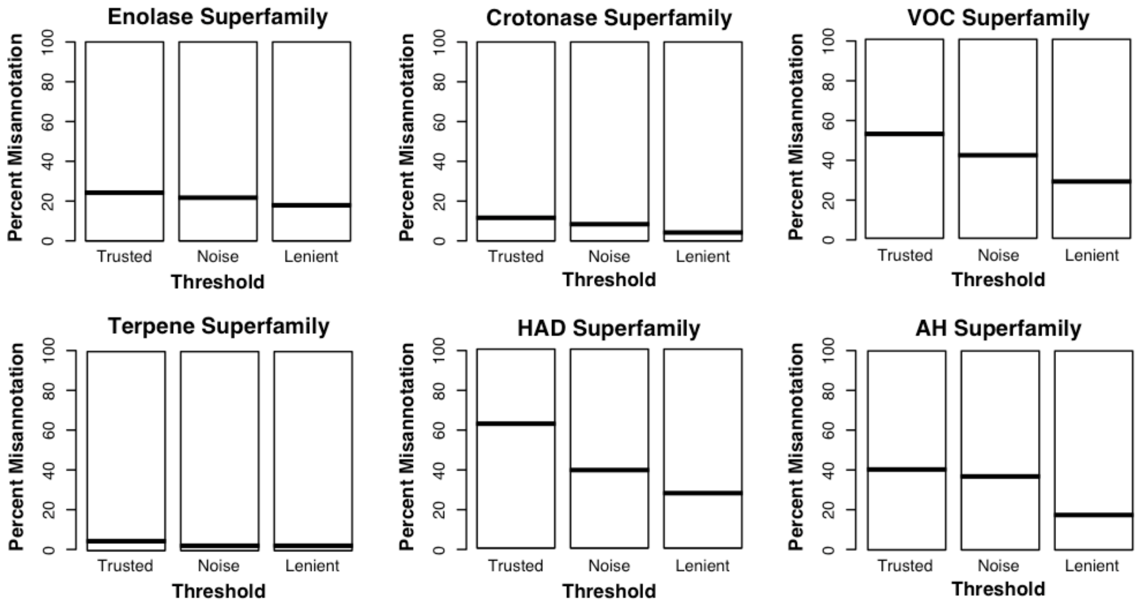


Figure 2-5. Average percent misannotation in the NR database across families in each superfamily using different thresholds
The Trusted Cutoff, used for the main misannotation analysis (see methods), is the most stringent of the cutoffs. The Noise Cutoff and the Lenient Cutoff represent progressively less stringent thresholds. The black bar in each plot depicts the average percent misannotation over each superfamily at these thresholds.

2.3.2. Misannotation over time.

Expecting that improved methods for annotation of genomic sequence would result in higher accuracy annotation over time, we investigated whether the level of misannotation we observed had improved over the period 1993-2005. Analyzing sequences in the NR database, the original sequence submission dates were retrieved from the NR and binned into groups based upon their submission date and misannotation assignment (“correct” or “incorrect”) according to our protocol. As shown in Figure 2-6, for the 37 families investigated in this study, misannotation has increased over this twelve-year period: essentially no misannotated sequences were submitted in 1993, while in 2005 approximately 40% of the sequences submitted to NR were misannotated. Not only are more misannotated sequences deposited in later years, they represent an increasing fraction (black line) of the total depositions annotated to the 37 families. This suggests that the rising level of misannotation is not simply due to the submission of increasingly greater numbers of sequences over this time period.

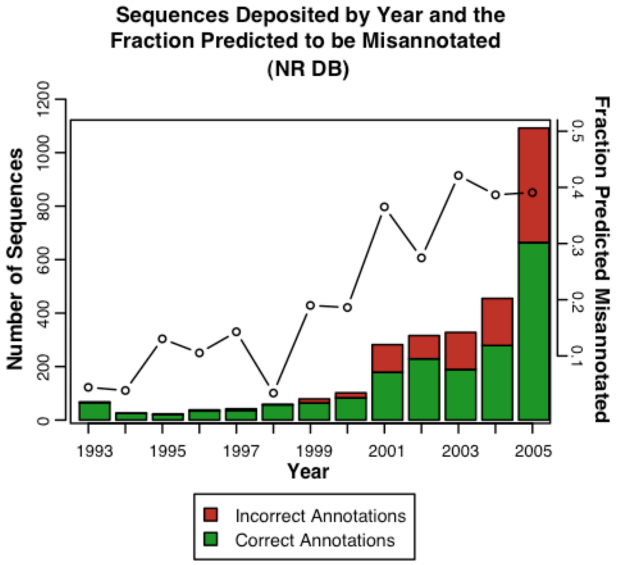


Figure 2-6. The change in misannotation over time in the NR database for the 37 families investigated
Sequences are plotted by the year when they were originally deposited in the database (x-axis). The number of sequences (left y-axis, bar graph) found to be correctly annotated is shown in green. The number of sequences found to be misannotated by our analysis is shown in red. The fraction (right y-axis, line plot) of misannotated superfamily sequences deposited each year into the NR database is given by the open nodes, connected by the black line to aid in visualizing the overall trend. This fraction represents the number of sequences in the 37 test families predicted to be misannotated divided by the total number of sequences deposited each year from the test set, i.e. the sum of the sequences depicted in the red and green bars for each year.

2.3.3. Misannotation in relation to sequence similarity.

Mindful of earlier studies suggesting error propagation as a cause of misannotation [7, 28-30], we were interested in determining to what extent a sequence-based relationship between the misannotated sequences could account for our results. To address this issue, we determined whether misannotated sequences clustered together by sequence similarity and the extent to which they showed similarity to correctly annotated sequences. An all-by-all BLAST [61] was performed on all the sequences analyzed from the 37 -family test set in the NR database and the results were visualized as a network [62] (Figure 2-7). In the majority of families, misannotated sequences either clustered with one another or were completely unconnected to the other sequences. This result could indicate that error propagation had indeed occurred by annotation transfer from one incorrectly labeled sequence to another (possible examples are highlighted with arrows in Figure 2-7). Investigation of this issue by examining propagation of these errors over time (1993-2005) provided further support for this result (Appendix B). This hypothesis cannot be confirmed, however, as the records available from the NR database are insufficient to determine how annotations were propagated based on sequence similarity.

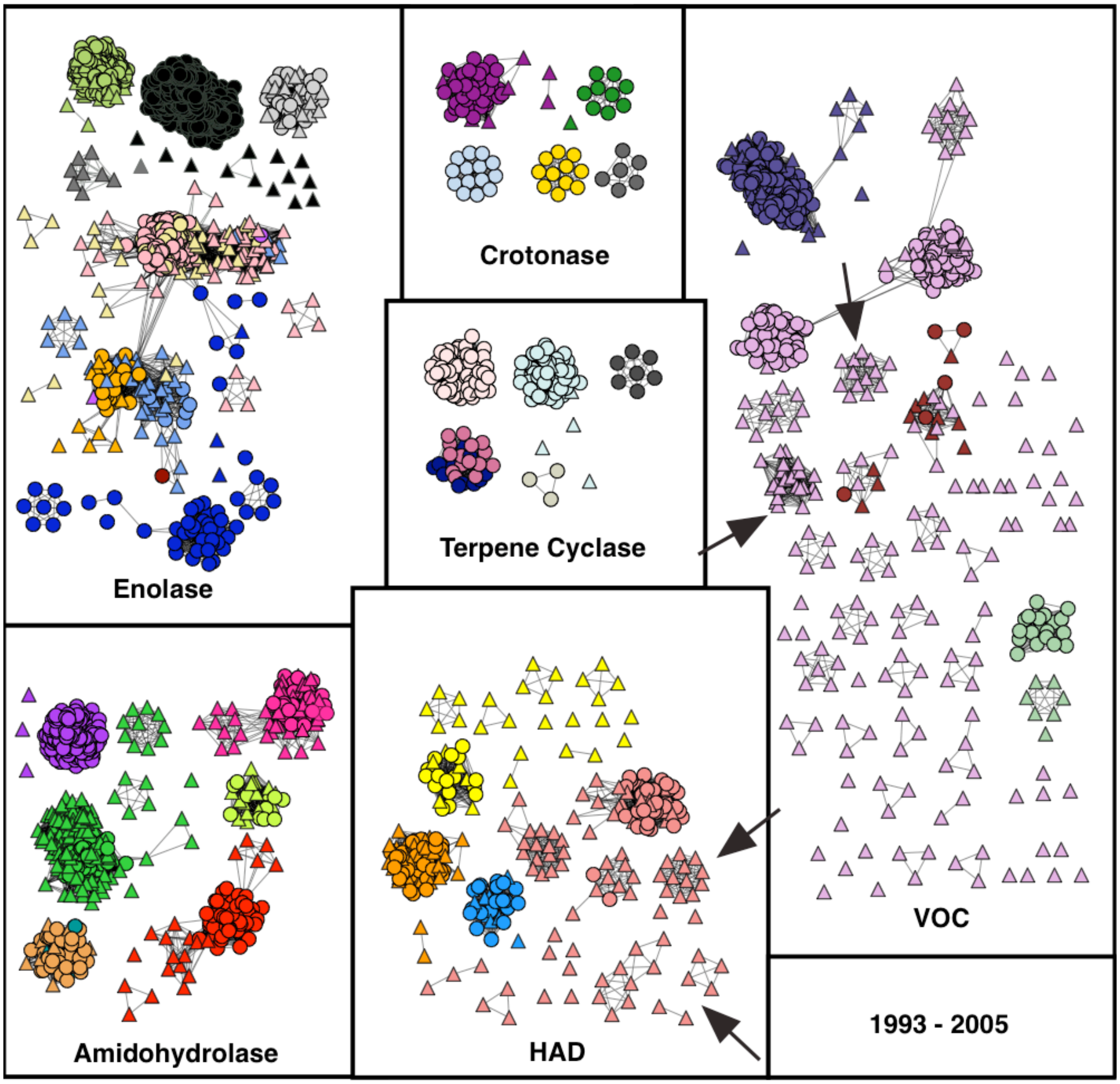


Figure 2-7. Sequence similarity clustering of correctly annotated and misannotated sequences deposited into the NR database (1993-2005)

The similarity network shows sequences from analysis families arranged by superfamily and colored as in Figure 2-1. The network was generated from an all-by-all BLAST analysis where all results that had BLAST E-value scores of $1x10^{-30}$ or lower were retained. Nodes represent sequences. Any two nodes are connected if at least one node found the other with a BLAST E-value less than or equal to $1x10^{-30}$. The network visualization was created with Cytoscape v2.6.1. The distance between any two connected nodes is roughly inversely proportional to the strength of the E-value between them (force-directed layout). The shapes of the nodes indicate annotation status: circles depict correctly annotated sequences and triangles depict incorrectly annotated sequences. Black arrows indicate examples in the haloacid dehalogenase family (HAD) and glyoxalase I family (VOC) which both display potential evidence of error propagation.

2.3.4. Types of misannotation.

Each misannotated sequence was labeled with an individual, mutually exclusive code describing the type of annotation error found by the analysis (Figure 2-2). Figure 2-8 shows the distribution of the four types of misannotation found (NR database). The two misannotation codes ‘Below Trusted Cutoff’ (BTC) and ‘Superfamily Association only’ (SFA) describe cases of overprediction, in which proteins have been annotated to functions that are more specific than the available evidence supports. SFA describes cases in which sequences do not score against the specific family HMM but instead score only against HMM(s) that capture similarities across all families in a superfamily. BTC describes cases in which sequences are found to score against both a superfamily and a specific family HMM and contain the necessary functionally important residues, yet fail to score above the Trusted Cutoff threshold. Often, this designation refers to a sequence that should have been assigned to a different but similar family (determined by the sequence scoring better against another family HMM). The majority of misannotations in the NR database were found to be overpredictions (85%, SFA + BTC). The remaining 15% of misannotations can be associated with two other misannotation codes, ‘No Superfamily Association’ (NSA) and ‘Missing Functionally important Residue(s)’ (MFR). These codes describe cases in which a sequence cannot be associated with the superfamily (NSA), or does not have the necessary functional residues, even though it scores against the family HMM (MFR) [63].

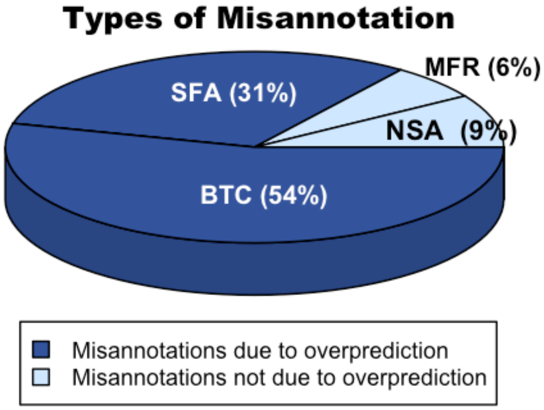


Figure 2-8. Distribution of major types of misannotation found in the NR database. Classification of misannotated sequences: 'No Superfamily Association' (NSA); 'Missing Functionally important Residue(s)' (MFR) 'Superfamily Association only' (SFA) 'Below Trusted Cutoff' (BTC), as defined in Figure 2-2 and methods. The codes can be grouped into two sets that specify whether the misannotation is associated with overprediction or to other types of errors (e.g., missing a required residue).

2.3.5. Examples.

Examples of some misannotations from the NR database associated with these misannotation codes are provided in Table 2-2. An example of an NSA misannotation is gi 505585, which had been annotated to the glyoxalase I function (VOC superfamily) in the soybean. This sequence did not score against any SFLD HMMs. In addition, when searched against the Pfam database [8], the sequence had significant matches only against the glutathione S-transferase N- and C-terminal domain models and did not score against any glyoxalase related models. With a literature search it was determined that the glyoxalase I gene in soybean had been characterized. In fact, in the same paper that characterized the soybean glyoxalase I gene, this sequence (gi 505585) had been characterized as a glutathione S-transferase [36], confirming our prediction that gi 505585 is misannotated. It should also be noted that this sequence corresponds to a Swiss-Prot sequence P46417 that also bears the same incorrect annotation. As a side note, the actual glyoxalase I sequence from soybean that had been characterized in the Skipsey et al. paper was appropriately classified by our analysis as correctly annotated.

Table 2-2. Examples of predicted misannotations in the NR database.

Misann. Type	Example	Description
NSA	**gi**: 48861106 **annotation**: COG1657: Squalene cyclase' **superfamily**: terpene cyclase	This sequence does not score against any HMMs in the entire SFLD. Using Interpro [9, 51],sequence maps to the carbohydrate binding superfamily and the galactose-binding like superfamily. Sequence does not map to any squalene cyclase motifs[64] or known models.
	gi: 505585 **annotation**: 'lactoylglutathione lyase'[a] **superfamily**: VOC	This sequence does not score against any HMMs in the entire SFLD. Sequence has significant matches against the Glutathione S-transferase N- and C-terminal domain Pfam-A models. Sequence was characterized and found to be a glutathione S-transferase and not a glyoxalase[36].
SFA	**gi**: 17987990 **annotation**: 'MANDELATE RACEMASE' **superfamily**: enolase	Sequence does not score against the mandelate racemase family HMM. It does score significantly well against the family HMM and contains the necessary residues for the fuconate dehydratase function.
	gi: 52628216 **annotation**: '3-hydroxyisobutyryl Coenyzme A hydrolase' **superfamily**: crotonase	Sequence does not score against the 3-hydroxyisobutyryl CoA hydrolase HMM but does score against six other family HMMs in the crotonase superfamily.
MFR	**gi**: 17983363 **annotation**: '2-HALOALKANOIC ACID DEHALOGENASE I' **superfamily**: HAD	Aspartate 180 that is necessary for the hydrolysis of the ester intermediate is mutated to an arginine. Mutational work by Kurihara et al.[65].indicates that this mutation would deactivate the enzyme. .
	gi: 71915096 **annotation**: 'n-acylamino acid racemase : O-succinylbenzoate-CoA synthase' **superfamily**: enolase	Sequence has a mutation of the lysine 166 base to a histidine among several other mutations to canonical OSBS/NSAAR motifs. Glasner et al. [66] discusses this sequence and its genomic context and why it appears to be a new function in the enolase superfamily.
BTC	**gi**: 16082480 **annotation**: 'Galactonate dehydratase' **superfamily**: enolase	Sequence hits the galactonate dehydratase family HMM (bit score: 126.6) but its score is well below the analysis cutoff for the family (cutoff: 843.6). Sequence does score significantly against the gluconate dehydratase[b] family HMM.

	gi: 56604528 **annotation**: ‘adenosine deaminase’ **superfamily**: AH	Sequence hits the adenosine deaminase family HMM (bit score: 9.7) but its score is well below the defined cutoff for the family (cutoff: 645.9). Sequence does score significantly against an AH superfamily HMM for sequences of unknown function.

[a] Synonym for glyoxalase I family function

An example of an SFA misannotation is gi 17987990, annotated to the mandelate racemase function in the enolase superfamily. This sequence did not score against the mandelate racemase family HMM, but it did score against other enolase superfamily HMMs. In particular, it scored above the Trusted Cutoff for the fuconate dehydratase family and contained all the necessary functional residues for that function. As such, we predict that the correct function for this sequence is fuconate dehydratase. It should be noted that at least eleven other sequences in NR score against this sequence with a BLAST E-value of better than or equal to $1x10^{-150}$ and are annotated with the same ‘mandelate racemase’ annotation, potentially indicating a case of error propagation in the database.

The sequence gi: 71915096 is an example of an MFR misannotation from the enolase superfamily. Although it was labeled to the *o*-succinylbenzoate-CoA synthase (OSBS) function and scored against the HMM for this family, one of the main catalytic amino acids for this function had been mutated. The base of the enzymatic reaction, lysine 166, had been mutated to a histidine. Further investigation of this sequence revealed that this sequence also contained a number of other mutations in OSBS/NSAAR motifs [66]. Glasner et al. discuss this sequence in much greater depth and enumerate the reasons (including genetic context) why this sequence is likely a new function in the enolase superfamily.

A BTC example is gi 16082480. This sequence was annotated to the galactonate dehydratase family in the enolase superfamily. Though the sequence scores against the galactonate dehydratase family HMM at a bit score of 126.6, the sequence falls well below the Trusted Cutoff of 843.6. Additionally, the sequence scores significantly against the gluconate dehydratase family (E-value 6.10E-153). Though the gluconate dehydratase family was not part of the misannotation analysis because not enough public information was available in the SFLD at the time to perform the analysis or determine a family threshold, our current understanding allows predicting that gi 16082480 is a gluconate dehydratase rather than a galactonate hydratase.

2.4. Discussion

Using a well-curated set of structurally and chemically diverse enzyme families as a test set, we have found that misannotation remains a serious problem, specifically in three public sequences databases that are mostly curated using automated methods (NR, TrEMBL and KEGG, Figure 2-3). Our manual examination of the annotations of over seven thousand sequences found that over a quarter of the enzyme families examined had levels of misannotation at or above 80% and five out of the six superfamilies examined displayed over 20% average misannotation in at least one database. The results for the primary sequence databases (NR, TrEMBL) and the secondary database (KEGG) were typically very similar. Because KEGG is a secondary database that sources its sequence information from databases like NR and TrEMBL, it would appear that KEGG's annotation errors are a direct result of error propagation from primary databases. These findings have significant implications for any database that uses primary sequence data without some degree of functional checking. Only the manually curated database, Swiss-Prot, consistently exhibited low levels of misannotation. This is a reassuring result, as many computational studies have used Swiss-Prot as a gold standard set. Our results also highlight the necessity of building and supporting manually curated databases that rely heavily (or exclusively) on experimental evidence. The main drawback to manual curation is the difficulty of keeping pace with new functional data. However, given the considerable difference in quality between manually and automatically curated databases, additional focus and resources should be devoted to manual curation. As an aid, the scientific community might consider requiring the submission of all experimentally characterized sequences to a centralized source (such as Swiss-Prot) at the time of publication so that the manually annotated databases can be larger and more current.

In examining not only four separate databases, but also sequences at the enzymatic family and superfamily level, we have greatly expanded upon previous investigations into annotation error. An interesting trend observed in the data was the high variability in the level of misannotation between families. While some families displayed significant misannotation (e.g. adenosine deaminase, AH superfamily), other families were very well behaved (e.g. bornyl diphosphate synthase, terpene cyclase superfamily). This trend holds true also at the level of the superfamily. The six superfamilies analyzed were found to have different average levels of misannotation, from low (5%, terpene cyclase superfamily) to significantly high (63%, HAD superfamily). Given this variation, it is not possible to predict *a priori* the exact misannotation level of any new function or superfamily and it underscores the difficulty of making general annotation rules. These results are very much in keeping with previous work that showed that the criteria for functional annotation transfer are family-specific [24]. In addition, because of the structural and chemical diversity of the analysis set and the fact that many other enzymatic systems display complicated sequence-structure-function relationships [67-69], similar patterns and levels of misannotation likely exist for a variety of additional enzyme families.

2.4.1. Unexpected consequence of the misannotation analysis

The advantages of the misannotation analysis as we have framed it is that it is based upon experimental information and expert knowledge. However, one noticeable drawback is that this analysis is most accurate at evaluating cases that resemble what has already been seen. Given the results of the analysis control tests (examining every sequence predicted to be ‘incorrect’ in Swiss-Prot and NR and assessing newly characterized sequences), we find that this does not appear to be a prevalent problem. However, one instance where our prediction failed, however, has lead to an interesting discovery relating to the muconate lactonizing enzyme (MLE I) family in the enolase superfamily.

While examining every sequence that had been labeled ‘incorrect’ in the NR database, we discovered that gi 42627730 had been experimentally characterized as an MLE I [70]. This was a surprise as our methodology, in addition to unpublished work (Glasner and Brown, personal communication), showed that this sequence belonged to a group of sequences that had not been expected to perform the MLE I function. It had been proposed that this group might in fact perform a new, as yet uncharacterized function. An evolutionary tree built by Glasner clearly showed that this unknown group was evolutionarily distinct and was also separated from the original ('old') MLE I group by another sequence group of unknown function. With the discovery by Murakami et al. that gi 42627730 was clearly and MLE I, the sequence group it belonged to was designated as the 'new' MLE group. The sequence group that separated the 'old' MLE group from the 'new' MLE group was designated as the MLE related sequences (or 'unknown' group).

Our collaborators in the Gerlt lab crystallized and experimentally characterized a *Mycobacterium smegmatis* protein sequence (gi:118470554) from the 'new' MLE group [71]. Unexpectedly, although the sequence contained all of the canonical functional residues in their usual positions, and the overall reaction was identical to the 'old' MLE I reaction, the reaction mechanism of the 'new' MLE I was found to proceed in a different manner. The 'old' MLE I proteins perform syn-cycloisomerization whereas the 'new' MLE I proteins perform ant-cycloisomerization.

Because the 'old' and 'new' MLE I proteins were distinct evolutionary groups and separated by another distinct sequence group this brought into question whether the two MLE I sequence groups had evolved their functionalities separately (i.e. a case of functional convergence). We investigated this question by examining the genomic operon context of the ‘new’, ‘old’ and ‘unknown’ MLE sequences groups. All sequences from the three MLE groups were used to query the Microbes Online database [72] and all proteins that mapped to the operons of each query sequence were retrieved. The full operons (including the sequences from the MLE groups) were visualized in a sequence similarity network (Figure 2-9). Nearly all of the sequences from the ‘old’ and ‘new’ MLE operons map closely to one-another. However, only the sequences in the ‘unknown’ operons that were MLE-like showed any connections to ‘old’ or ‘new’ sequences. All other ‘unknown’ operon sequences connected only to other ‘unknown’ operon sequences or were singletons.

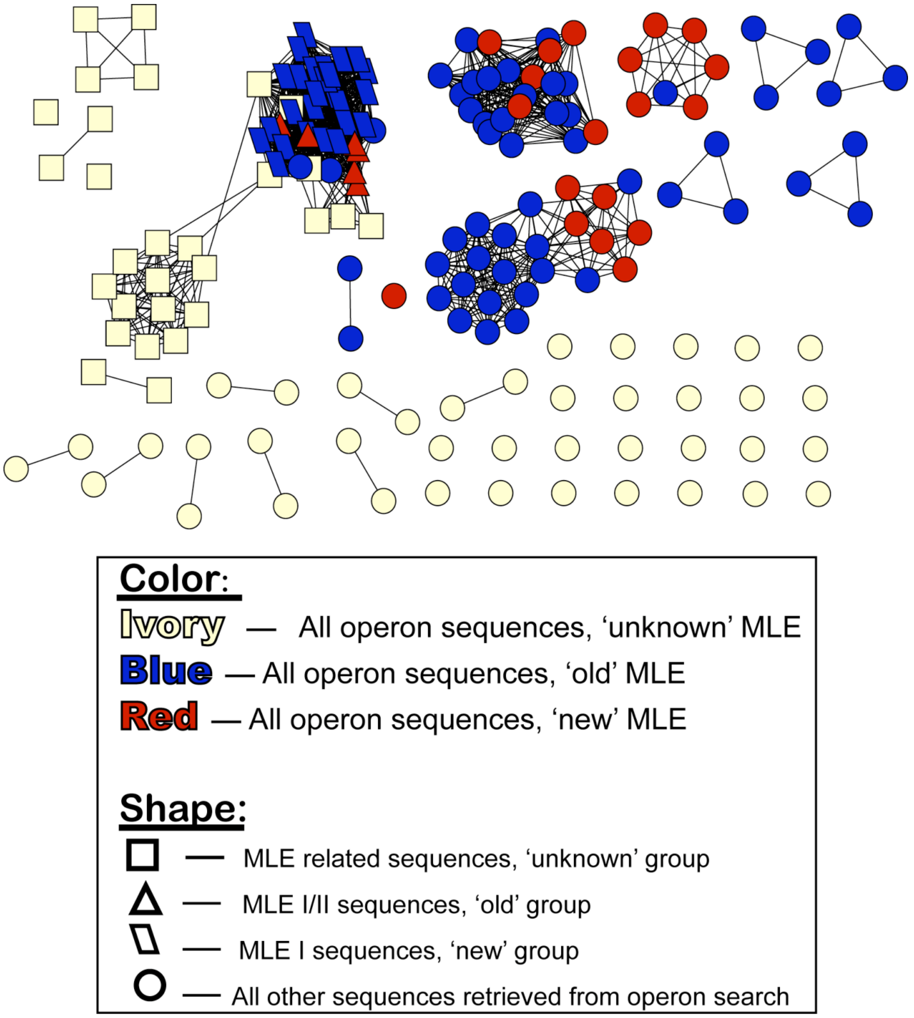


Figure 2-9. Comparing operon context for three MLE sequence groups.
The sequence network is based upon sequence similarity (BLAST). Nodes in the network represent proteins and represent sequences from three different MLE sequence groups and the sequences from their respective operons. Two nodes are connected if at least one of the nodes finds the other with a BLAST E-value less than or equal to 1E-30. Nodes are colored based upon what sequence group they belong to. The shape of the nodes indicates whether the sequences are from an MLE group or whether they are the sequences retrieved from the operon search. The distance between any two nodes is an indication of the strength of their sequence similarity (force-directed layout).

Because the 'unknown' MLE group separates the 'new' and 'old' MLE groups on the evolutionary tree and the 'unknown' group appears to have completely different operon context than the 'old' and 'new' MLEs, we have initial evidence that perhaps the 'old' and 'new' MLE groups were evolved separately. However, at this time it is not possible to separate this hypothesis from the contradicting hypothesis that perhaps the ‘new’, ‘old’ and ‘unknown’ groups are simply divergent groups from one initial MLE I functional group. Without a more extensive examination of the evolutionary history of these enzymes, perhaps coupled with experimental characterization of ancestral sequences it is not possible to distinguish between the divergent and convergent hypotheses.

2.4.2. Intrinsic problems for databases

The level of misannotation in public databases is increasing rapidly (Figure 2-6). Our visualization of misannotation in relation to sequence similarity provides strong evidence that error propagation (via annotation transfer) is a common source of annotation error (Figure 2-7, Appendix B). Given the continued use of annotation transfer as the functional prediction method of choice [16-18]and the high levels of misannotation predicted by our analysis, this trend is likely to continue.

Another annotation issue is the use of source information without reference. Often information from sites such as Pfam [8], or InterPro [9] are utilized for annotation without any reference to the original source. Annotating without reference in this manner can be problematic. Firstly, the original source information might not actually refer to a functional annotation. It may, in fact, only refer to a structural domain group or a broad sequence group. Frequently, however, the designation of ‘domain’ or ‘superfamily’ is not included in the final annotation, which will then lead the reader to conclude it is a functional definition. For example, the annotation ‘Mandelate racemase/muconate lactonizing enzyme’ is frequently used to annotate members of the enolase superfamily. While this annotation appears to be describing a multifunctional enzyme that performs both racemization and lactonization, in reality it is the descriptor of the N- and C-terminal Pfam-A models of the same name (PF01188 and PF02746) that describe a broad range of enolase superfamily functions [60]. Additionally, at no time was Pfam referenced as the source of the annotation. Because we were aware of the Pfam models and their designations we removed all these sequences from our analysis, but anyone not as familiar with the enolase superfamily might have been led astray.

It should also be noted that this practice of using unreferenced information for annotations is additionally questionable because it denies these sources their due acknowledgment. Additionally, it makes it impossible to propagate corrections either from the source of the annotation or from the annotation recipient back to its source when corrections are needed. The issue of information propagation is a significant one. Not only did we find suggestive evidence of error propagation (Appendix B), the example of the misannotated glyoxalase I sequence (Table 2-2) underscores how difficult it is to propagate new information through a database to sequences and annotations that are already there. Although gi 505585 had been shown to be a glutathione S-transferase (and not a glyoxalase I) in 2000, the old annotation in NR and in Swiss-Prot still persists. Another interesting case of this sort of misannotation is that of the 1,4-dihydroxy-2-napthoyl-CoA synthase family (crotonase superfamily). Originally, it was believed that the MenB gene in the Vitamin K_2 biosynthetic pathway performed the full synthesis of *o*-succinylbenzoyl-CoA to

1,4-dihydroxy-2-napthoate. However, it was discovered that many (if not most) MenB proteins in fact only catalyze the reaction of *o*-succinylbenzoyl-CoA to 1,4-dihydroxy-2-napthoyl-CoA [73, 74] and another enzyme (gene yfbB) converts 1,4-dihydroxy-2-napthoyl-CoA to 1,4-dihydroxy-2-napthoate. Although these discoveries were made in 2001, no sequences in the four analyzed databases were labeled with the new 1,4-dihydroxy-2-napthoyl-CoA synthase function (though there were many sequences that mapped to this function by sequence). Because no sequences were so labeled, this type of misannotation did not add to the level of misannotation calculated by our analysis. However, this example underscores the serious difficulty of reannotating sequences with a corrected function.

2.4.3. Addressing the issue of misannotation.

A way to address the issue of annotation error in both manually curated and automatically curated databases is to incorporate the use of evidence codes in databases. In this work we used evidence codes to label the type of misannotations found. Evidence codes can also be used to label other kinds of data, such as sources of functional annotations. A few databases, like the SFLD and Swiss-Prot have added evidence codes to all or some of their data and evidence codes are integral to the Gene Ontology [10]. Evidence codes are useful not only because they convey important information simply and clearly but also because they facilitate automatic analyses. For example, to find all sequences that have been experimentally characterized in a database (e.g. in GO), one could simply filter the database by the evidence code “Inferred from

Direct Assay" (IDA) and quickly retrieve the sequences of interest. Evidence codes require little effort to add to an annotation, although the addition of this information to a database might require some readjustment to the database schema and access depending on how such codes would be implemented.

Ontologies also facilitate annotation. An ontology is a regularized set of objects and relationships between the objects that attempts to describe complex systems concretely and in a regularized fashion. The concept of function is inherently complex and can mean anything from chemical activity to metabolic context to organismal phenotype to something else entirely. This complexity can give rise to confusing or imprecise annotations when there is no universally accepted vocabulary to describe function. The utility of an ontology is that it enforces a clear structure upon the data and aids in clear communication. Because 'function' is so complex, no ontology yet exists that can completely encapsulate biological reality. However, giving functional information a framework for organization and propagation can help in minimizing unintended interpretations of annotations or misguided annotation transfers. The Open Biological Ontology is a commonly used ontology that contains the Gene Ontology (GO). GO is already being incorporated into databases such as Swiss-Prot and the Protein Data Bank, and the SFLD has its own ontology. While it might take considerable work to adjust a database to conform to an ontology, the resulting clarification of the internal data makes such a goal worthwhile.

While we have just detailed several operational ideas to improve database quality and utility, there is also the theoretical question of how to annotate sequences. In our analysis we found that the majority of misannotated sequences were annotated to families even though their scores against the family HMMs fell far below the family Trusted Cutoffs. Many sequences were annotated to functions with comparatively scant sequence similarity. Because this happened so frequently (Figure 2-8) it is clear that function overprediction is a common source of misannotation. Given these findings, we suggest a more measured approach to annotation in which function is only annotated to the level at which there is strong evidence. We term this annotating to the appropriate functional granularity. Therefore, when there is only enough evidence to clearly place a sequence in a superfamily but not in a functional family, the sequence should only be annotated to the granularity of the superfamily. While this might functionally underpredict some sequences, it prevents any problem of annotation error propagation as the information in the annotation might be general but it would be correct. This is especially crucial as our findings indicate that error propagation both within a single database (Appendix B) and between databases (e.g. error propagation from primary to secondary databases) is a prevalent problem.

2.5. Conclusions

Misannotation is a serious problem affecting at least three major sequence databases. Error propagation and the increase of annotation errors over time appear to be significant issues. While we looked at a set of six protein enzyme superfamilies, it is not unreasonable to suspect that the level of misannotation for all protein enzymes (and perhaps all proteins) is also significant enough to warrant concern. We stress, however, that as this is a computational investigation, we can only provide an estimate of the true level of misannotation. We have briefly discussed ideas for improving the annotation process but, given the scope of the problem, progress can only be made from community-wide engagement. This is why we are developing a Misannotation Resource to which the community can submit cases of confirmed or suspected misannotation, so that the issue of functional misannotation can begin to be addressed. The critical next steps are the development of speedy large-scale methods to check and reannotate functional annotations in public databases and the continued support of these databases to re-organize and adjust as necessary to address the growing problem of annotation error.

2.6. Methods

2.6.1. Selection off functions to investigate for misannotation

The functions analyzed in this investigation were all selected from the Structure-Function Linkage database (SFLD) [13]. The families analyzed met three criteria: each family had at least one x-ray crystal structure associated with it, catalytic residues needed for enzymatic function were identified, and suitable curated hidden Markov models [75] and alignments were available. Additionally, for the purposes of this text, the terms ‘function’ and ‘family’ are used as synonyms.

The version of the SFLD used was from August 11, 2005. Six superfamilies were analyzed in the analysis, covering five different structural folds and 37 different functions (Figure 2-1): enolase superfamily (10 families), crotonase superfamily (6 families), vicinal oxygen chelate superfamily (4 families), terpene cyclase superfamily (6 families), haloacid dehalogenase superfamily (4 families) and amidohydrolase superfamily (7 families).

2.6.2. Protein sequence data

Four public databases were analyzed for misannotation: the GenBank Non-redundant (NR) database [2], the UniProtKB/TrEMBL and UniProtKB/Swiss-Prot databases [3] and the protein database of the Kyoto Encyclopedia of Genes and Genomes (KEGG) [59]. The protein sequences from these four databases were downloaded on February 17, 2006 in FASTA-formatted files. The NCBI program formatdb [76] was used to create BLAST databases out of the FASTA files. Additionally, the protein sequences from the Gene Ontology (GO) database [10] were downloaded on the same day.

2.6.3. Thresholds to determine family (functional) membership

In order to differentiate family members from non-family members, HMM bit-score thresholds were determined for each family examined in the misannotation analysis (Appendix A). All sequences in the SFLD assigned to families and all sequences in GO that were marked with the evidence code “Inferred from Direct Assay” (IDA) were scored against all SFLD hidden Markov models using the HMMER program hmmpfam using an E-value cutoff of 100 (14,902 sequences scored). The resulting scores of every sequence relative to every HMM were then compiled and labeled according to whether they the sequences functionally belonged to the family that they scored against. The Trusted Cutoff (TC) was defined as the HMM score of the lowest -scoring family member (Figure 2-4) against the appropriate family HMM. The Trusted Cutoff was the threshold at which the misannotation analysis was performed.

Two additional thresholds were defined in order to model the change in predicted misannotation as a function of threshold: Noise Cutoff (NC) and Lenient Cutoff (NC). The NC is the HMM score of the highest -scoring non-family member (Figure 2-4) against a given family HMM. The LC is a permissive threshold that is chosen by adding erroneous data. The score threshold is lowered from the Noise Cutoff to a score at which 5% of the total sequences encompassed by that threshold are non-family members. The designation of the TC and NC thresholds is very similar to the process used by Pfam [8, 77].

There were several cases in which no non-family members scored against certain family HMMs. For these cases the LC was defined as a score of 40, which in our models, roughly corresponds to an E-value of $1x10^{-10}$. An E-value of $1x10^{-10}$ is often used as a lower bound threshold for displaying homology [75]. The NC was then defined as the midpoint between the TC and the LC.

In one instance, the glucarate dehydratase family (enolase superfamily), scores for non-family members and family members overlapped. In this case, the Trusted Cutoff was defined as the lowest-scoring family member that scored above all non-family members. The Noise Cutoff was defined as the score at which the first non-family member scored. The Lenient Cutoff was then defined as the lower of either the lowest-scoring family member or the lowest-scoring non-family member that had been included in the set to create 5% error. For this family, the lowest score (and therefore the LC) was a family member.

2.6.3.1. Modeling analysis dependence on thresholds.

In order to determine whether the choice of family thresholds (Trusted Cutoff) were overly influencing the misannotation results, two other thresholds were used to see whether the misannotation analysis results changed dramatically. The other thresholds, the Noise Cutoff and the Lenient Cutoff, were defined as stated previously and the misannotation analysis was performed for each threshold identically to the analysis described below.

2.6.4. Misannotation analysis algorithm

2.6.4.1. Keyword search

The misannotation analysis encompassed several steps (Figure 2-2) and was identical for each database examined and each family analyzed. Keyword search was the first step in the misannotation analysis. For each of the 37 functions analyzed keyword dictionaries were compiled (Appendix F). The dictionaries were created using information available in the SFLD and, when appropriate, the functional information and synonym lists from the Enzyme Commission (EC)[78]. All sequences with annotations matching one or more of the keywords were retrieved from each database (regular expression string matching). This was an automated step using the checkKeywordMisannotation.py code in Appendix B. The annotation of every sequence retrieved was examined by eye and the sequences associated with any spurious annotations were removed. All annotations that did not specify the enzymatic function under analysis were also removed (this included any annotations that only specified gene names). If an enzymatic function and some other function (not associated with its catalytic functionality such as localization or biological role) were listed in the annotation, only the catalytic designation was analyzed. Any annotation that used the words ‘family’, ‘-like’, ‘similar to’, ‘related to’ and ‘homolog’ were not included in the final analysis as it was assumed that these designations did not mean to specify an exact function but rather a group of sequence-related proteins. All descriptors of ‘hypothetical’, ‘probable’, ‘putative’, ‘potential’, ‘predicted’ and ‘likely’ were noted but the descriptors were ignored in the analysis. If an annotation contained both a general description and a specific description (e.g. “(GLYOXALASE I HOMOLOG); lactoylglutathione lyase”) the portion of the annotation that defined a specific function was analyzed. Additionally, all fragments were removed from the analysis. A sequence was considered a fragment if it was too short either at the N or C terminus to contain all functionally important residues. A sequence that appeared to be missing interior portions of sequence was not considered a fragment. Also any sequence that corresponded to a crystal structure was noted and removed if it contained mutations in the functionally important residues. All other crystal structure sequences were analyzed normally.

2.6.4.2. Misannotation prediction and classification

The next steps in the analysis were the determination of the presence of catalytically important residues and the confirmation of the sequence as a family member by virtue of its HMM score. Each of the sequences retrieved by the keyword search were scored against all of the HMMs in the SFLD using the HMMER program hmmpfam (E-value cutoff of 100). Every time a sequence scored against an HMM it was additionally aligned to the HMM. Using a defined database of catalytic residues for each family (SFLD), it was automatically checked if the aligned sequence contained the necessary functionally important residues. Both the scores of the sequences against all HMMs and the presence/absence of catalytic residues were output into a human-readable format.

At this point the analysis became manual. Each functionally annotated sequence was checked by eye to determine whether the sequence was misannotated and, if so, what type of misannotation it exemplified (Figure 2-2). Examining the output scores for each sequence, it was first determined whether the sequence mapped to the appropriate superfamily by scoring against the superfamily HMMs. If the sequence did not score against the appropriate superfamily HMM, it was labeled as misannotated and was classified as ‘No Superfamily Association’ (NSA). If the sequence passed this test, it was then checked whether it mapped to the appropriate family. If the sequence did not score against the family HMM it was labeled as misannotated and classified as ‘Superfamily Associated Only’ (SFA). If the sequence did map to the family HMM it was then checked whether it contained the necessary functionally important residues (residue designations from the SFLD). If the sequence did not contain one or more of the necessary residues due to mutation or addition/deletion the sequence was labeled misannotated and classified as ‘Missing Functionally Important Residue(s)’ (MFR). It should be noted that conservative amino acid substitutions and/or mutations that might still be functional (e.g. still bind to a metal etc.) were acceptable and not labeled as ‘missing’. If the sequence contained all the necessary residues it was passed on to the final test, checking whether it scored at or above the family threshold (Trusted Cutoff) for that family. If the sequence did not score above the threshold it was labeled misannotated and classified as “Below Trusted Cutoff’ (BTC). If the sequence did score above the threshold it was labeled as correctly annotated. In total, over all four databases, 7255 sequences were examined in the misannotation analysis. The raw data is in Appendix K.

2.6.5. Change in misannotation over time.

For each sequence analyzed in the NR database, the original submission date of that sequence was retrieved from NR. The sequences were then binned by submission year and predicted annotation status (Figure 2-6). In order to check that the results were not skewed by the fact that more sequences were being submitted every year to the database, we calculated the fraction of predicted misannotated sequences per year versus the total number of sequences that were deposited that year from our analysis set (misannotated sequences deposited in specific year from analysis set/Total sequences deposited in specific year from analysis set).

2.6.6. Misannotation analysis controls and tests.

2.6.6.1. Examination of every sequence in NR and Swiss-Prot found to be incorrect.

To verify the accuracy of our misannotation analysis results using an alternative to our protocol, we looked for literature that might contradict our misannotation predictions. All sequences from the NR and Swiss-Prot databases found to be misannotated by the analysis were checked to insure that no reference existed that contained experimental characterization of the sequence's catalytic functionality that contradicted our prediction. All of the full NCBI and Swiss-Prot data pages for each sequence labeled incorrect were examined manually and the accompanying references inspected for experimental characterization. In total the references of 1155 sequences were manually examined. Of the 1112 and 43 sequences predicted to be misannotated in NR and Swiss-Prot respectively, only 4 sequences (3 in NR, 1 in Swiss-Prot) could be associated with a publication that contained experimental results that conflicted with our predictions. One additional sequence in NR was found to be incorrectly classified as misannotated based upon an extensive study of genome context and evolutionary relationships [66]. Another sequence was found to be incorrectly classified based upon a collaborator's manuscript in progress (F. Raushel, personal communication). Each of these six contradicting sequences had their annotation predictions corrected and they do not contribute to the final level of misannotation predicted. Additionally, for the six contradicting sequences found, all sequences that were 99% identical to these sequences were also changed to be ‘correct’ and do not contribute to the final misannotation level.

2.6.6.2. Assessment of newly characterized sequences.

Another test of our method was performed by analyzing sequences of proteins that had been newly experimentally characterized. We compiled a list of 27 sequences that had been characterized since the download of our analysis databases (February 2006) and submitted to the NR database. These sequences belong to 4 superfamilies: enolase (7 sequences), crotonase (2 sequences), terpene cyclase (2 sequences), and amidohydrolase (16 sequences). We performed the identical misannotation analysis on these sequences as described above and compared our predictions against their known experimental characterizations. Of these, 26/27 were labeled by our analysis protocol as correctly annotated, consistent with the experimental results. One sequence, a muconate cycloisomerase in the enolase superfamily, scored against the family HMM slightly below the Trusted Cutoff for that family and was therefore incorrectly classified as misannotated. This example shows that threshold choice can have an affect on our misannotation results, although lowering the stringency of the Trusted Cutoff did not dramatically increase the predicted incidence of misannotation.

2.6.6.3. Stability of annotations.

We examined whether any corrections had been made for sequences that we had predicted to be misannotated. Of the 1112 sequences in the NR database found to be misannotated by our analysis, we examined the current annotations of 111 of them (~10%), chosen randomly. These 111 sequences were re-downloaded from the February 2008 NR database and the annotations were manually compared to the annotations from 2006. Of these, 96% of the annotations were unchanged (107 sequences), 3% of the sequences had new functional annotations (3 sequences) and for 1% (1 sequence), there was no longer a functional annotation.

2.6.6.4. Assessment of functional residue designation.

Every sequence that was found by our automated process to be missing one or more functionally important residues was checked manually. The alignment of the sequence to the family HMM alignment was first visually inspected to ensure that there was no obvious misalignment or conservative substitution (all standard amino acid substitutions were accepted). If there was no obvious substitution or simple shift in the alignment that would rectify the mutated amino acid further analysis was performed. Using the alignment program Muscle [79] the mutated sequence was aligned to the set of sequences in the SFLD found in that functional family. In conjunction with an examination of the available literature, the alignments were manually analyzed and a case-by-case decision was made whether to accept the mutation. Any sequences for which the mutation was accepted were passed on to the next (and final) analysis step (threshold step).

2.6.7. Examining the genome context of ‘new’ MLE sequences

All sequences in the SFLD belonging to the ‘new’ and ‘old’ MLE families were downloaded and retrieved. The set of ‘unknown’ MLE sequences was defined and provided by M. Glasner (personal communication). Using an automated program, Microbes Online was queried to return all the sequences identified to be in the operons of the three MLE groups. All sequences retrieved were blasted against each other (all-by-all BLAST). The resulting network was visualized with Cytoscape 2.6.1 with edges filtered to at or below 1E-30. The accession numbers and the operons returned are in Appendix M.

2.6.8. Computation and figures

. The automated portions of the misannotation analysis were all preformed on linux computers. All data plots were produced using the software R v2.6.0 see Appendix G for R code.

2.7. Acknowledgments

The authors would like to thank the other members of the Babbitt lab for critical and insightful feedback on this research. Many thanks to Dr. S. Ojha and Dr. M. Glasner for help with enzymatic mechanisms and functionally important residues and to Dr. S. C.-H. Pegg for his work on the SFLD. Dr. B. Polacco and C. Smith provided invaluable help with R and special thanks go to Dr. R. Chiang and Dr. E. Meng for multiple readings of the manuscript. AMS would also like to thank Dr. T. Kortemme and her lab for a welcome seat at their group meetings and for continued thoughtful commentary on the project. Additionally, AMS would like to thank F. Lauck for python code to query the Microbes Online database.

Chapter 3.
A Second Approach to Finding Annotation Error

3.1. Abstract

3.1.1. Background

A frequent scientific problem in today's post-genomic era is the functional annotation of new uncharacterized sequences. Our work in Chapter 2 has shown that a significant number of the functionally predicted sequences in commonly-used, public databases have been incorrectly labeled to specific protein functions. The misannotation analysis in Chapter 2 focused only on sequences that were annotated to one of 37 enzyme families. Any sequences labeled to other functions (either partially or completely) or labeled generally (not to a specific function) were ignored. However, these omissions potentially leave out interesting knowledge about annotation and misannotation. How often are sequences that should be annotated to a given function annotated as something else? Are general annotations commonly used? How often do annotations contain both correct and incorrect information? The focus of this chapter is to

examine these questions in order to gain a better understanding of annotation trends and annotation error.

3.1.2. Results

Using sequence similarity searches coupled with defined family thresholds we have gathered all sequences belonging to 37 different enzyme families from four public sequence databases (GenBank NR, UniProtKB/TrEMBL, UniProtKB/Swiss-Prot and KEGG). For each of these 37 functions we examined whether the functional annotations retrieved for the sequences corresponded to their assigned functional family. Using this analysis procedure we find that the levels of misannotation in the family groups widely vary. While certain families (e.g. in the enolase and crotonase superfamilies) display high levels of misannotation (over 20%), other families do not contain any sequences with annotation error (e.g. in the terpene cyclase superfamily). We find that in 70% of the families investigated, sequences are often annotated correctly but generally, meaning that a specific function description is not given. In addition we find frequent use of equivocal annotations, in which part of the annotation is correct, but part of the annotation is incorrect. We also determine that the majority of all types of annotation error (incorrect and equivocal annotations) and the use of general annotations appear primarily in the post-genomic era, and they are not simply a result of the addition of more sequences to the databases.

3.1.3. Conclusions

The extremely variable levels of misannotation in the 37 analyzed families indicate the difficulty in predicting which families might display significant misannotation prior to analysis. However, the levels of misannotation found in some of the 37 families displayed significantly less annotation error than found when performing the general misannotation analysis (Chapter 2). Given the fact that the 37 families investigated all have been experimentally characterized it is not immediately clear why certain families evidenced such large levels of incorrect and equivocal annotations while others did not. It is possible that the largess of new genome sequences, the expectation of rapid sequence annotation, the prevalent use of prediction from annotation transfer and the difficulty of updating misannotated sequences in the databases might all contribute in non-systematic ways to the misannotation problem. These findings underscore the idea that using a family context for annotation as opposed to binary annotation transfer can improve annotation accuracy.

3.2. Introduction

The work in Chapter 2 showed that misannotation is a significant issue for public sequence databases. However, this analysis only examined one general kind of annotation error, the error of annotating a sequence incorrectly to a specific function. This analysis ignored any sequences that were not labeled to a specific function (i.e. were annotated with a general, not exact, function description). Additionally, it discarded any sequences that contained both incorrect and correct functional data. That analysis also did not catch any sequences that should have been annotated to one function but were annotated to a function not included in the analysis set. Because of these omissions an additional annotation analysis was devised that would attempt to determine the contribution of annotation errors that occur from the above situations.

We have modeled this question by gathering sequences of known function from several public databases (based upon homology and experimental information) and checked whether the each sequence was annotated correctly. The functions used are the 37 families examined in Chapter 2 and the databases are identical (GenBank NR, UniProt/TrEMBL, UniProt/Swiss-Prot and KEGG [2-4, 59]). The methodology for the annotation analysis is depicted in Figure 3-1. The analysis is a step-wise process to identify sequences that map to a specific function and then ascertain whether they are annotated correctly. NR and TrEMBL are both large public primary databases where most annotations have been automatically assigned through computational function prediction. Swiss-Prot is also a primary sequence database but it is manually curated. KEGG is a secondary database where its protein sequences and annotations are derived from primary sequence databases.

The 37 enzyme families are members of six superfamilies (Table 3-1): amidohydrolase (AH), crotonase, enolase, haloacid dehalogenase (HAD), terpene cyclase and vicinal oxygen chelate (VOC). These families were chosen because of the availability of mechanistic, structural and sequence information for these functions. A hand-curated hidden Markov model (HMM) represents each family and the residues for necessary for enzymatic activity have been identified. This and more extensive information is available from the Structure-Function Linkage Database (SFLD), a manually curated database of enzymatic superfamilies [13, 14, 60].

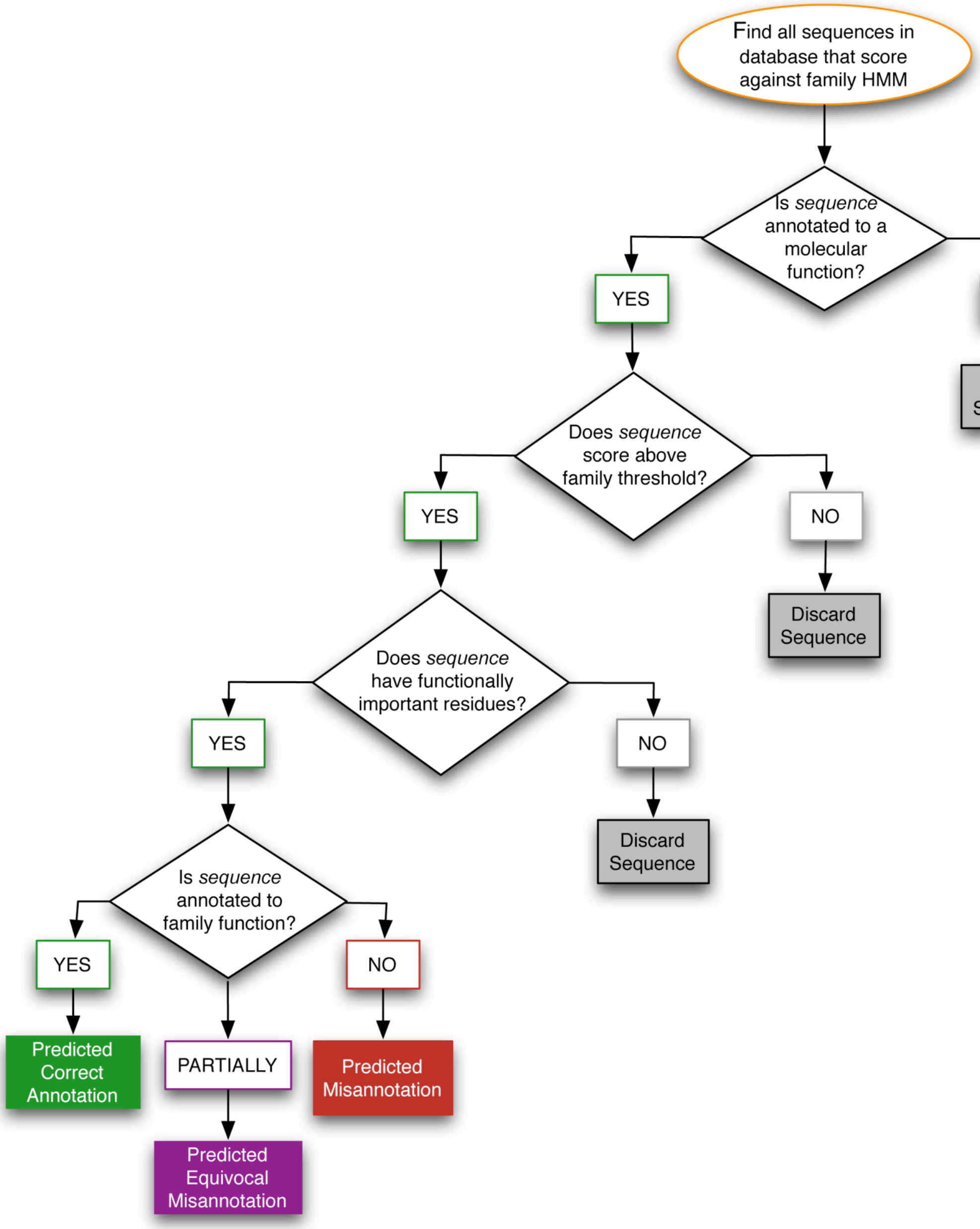


Figure 3-1. Similarity-based annotation analysis flow chart.
The analysis starts by gathering all sequences (by HMM) that belong to one of the 37 functional families. These sequences are taken from one of four sequence databases (NR, TrEMBL, Swiss-Prot or KEGG). Each sequence retrieved proceeds through a stepwise process to determine if it is appropriate to analyze. The first step checks whether the sequence is annotated to a molecular

(enzymatic) function. The second step checks whether the sequence scores above the previously defined family threshold for that function. The third step checks whether the sequence contains the necessary residues to perform the function of the family to which it has been placed. If the sequence passes all of these steps, it is then checked to see whether it is annotated to the correct function. The correct function must either specify the exact function of the enzyme or must be a more general function designation that is accurate. Misannotations can either be completely incorrect annotations, or annotations containing both correct and incorrect information making them equivocal.

For the annotation analysis described in Figure 3-1 the first step is to select sequences from a database that map by sequence similarity to the function under investigation (using the SFLD's HMMs). Only sequences that are annotated to an enzymatic function are analyzed, the remainder are discarded. A sequence is found to belong to a family if it scores against the family HMM well enough to score better than the pre-defined family threshold (see methods). All sequences that pass this threshold are further examined to determine whether they contain the necessary functionally important residues to perform the enzymatic function. Any sequences that do not have one or more of the appropriate residues are discarded. At this point the set of sequences belonging to the function under investigation have been defined.

The annotations of each sequence are then manually checked to determine if they are accurately annotated to the known function. The annotations can be classified into four categories. If the annotation is found to be incorrect, it is labeled as 'incorrect'. If the annotation is found to contain both correct and incorrect function designations it is labeled as 'equivocal'. If the annotation is found to be correct it will either be labeled as 'exact', if it has the specific function definition of the enzymatic activity, or it will be labeled 'general'.

Table 3-1. Number of sequences analyzed per family in the similarity-based misannotation analysis.

Superfamily	Family	E.C. No.	Family Color	Number of Seq. Analyzed			
				Database			
				NR	TrEMBL	KEGG	Swiss-Prot
Enolase[a]	Enolase[a]	4.2.1.11	●[c]	1594	339	364	280
	Galactonate dehydratase	4.2.1.6	●	106	37	26	1
	Mandelate racemase	5.1.2.2	●	7	0	0	1
	Glucarate dehydratase	4.2.1.40	●	131	37	33	4
	Methylaspartate ammonia-lyase	4.3.1.2	●	24	7	6	1
	Ortho-succinyl benzoate synthase	—[b]	●	231	68	85	13
	Dipeptide epimerase	—	●	203	68	61	0
	Chloromuconate cycloisomerase	5.5.1.7	●	31	10	1	5
	Muconate cycloisomerase	5.5.1.1	●	113	37	18	5
	L-fuconate dehydratase	4.2.1.68	●	65	29	14	0
Crotonase	Dodecenoyl-CoA delta-isomerase (mitochondrial)	5.3.3.8	●	26	5	8	3
	Delta(3,5)-delta(2,4)-dienoyl-CoA isomerase	—	●	85	32	25	4
	Methylmalonyl-CoA decarboxylase	4.1.1.41	●	30	4	6	1
	3-Hydroxyisobutyryl-CoA hydrolase	3.1.2.4	●	415	159	113	0
	4-Chlorobenzoate dehalogenase	3.8.1.7	●	14	7	7	0
	1,4-Dihydroxy-2-napthoyl-CoA synthase	—	●	335	122	111	6
Vicinal Oxygen Chelate (VOC)	Methylmalonyl-CoA epimerase	5.1.99.1	●	24	2	6	2
	4-Hydroxyphenylpyruvate dioxygenase	1.13.11.27	●	424	120	95	25
	FosA	2.5.1.18	●	27	0	1	2
	Glyoxalase I	4.4.1.5	●	348	97	91	24
Terpene Cyclase	5-Epi-aristolochene synthase	—	●	10	5	0	1
	Bornyl diphosphate synthase	5.5.1.8	●	15	0	0	1
	Pentalenene synthase	4.2.3.7	●	7	1	1	1
	Squalene-hopene synthase	5.4.99.17	●	196	61	42	4
	Trichodiene synthase	4.2.3.6	●	71	13	0	16
	Aristolochene synthase	4.2.3.9	●	8	1	0	1
Haloacid Dehalogenase (HAD)	Deoxy-D-mannose-octulosonate 8-phosphate phosphatase	3.1.3.45	●	56	15	20	1
	Phosphonoacetaldehyde hydrolase	3.11.1.1	●	76	22	21	0
	2-Haloacid dehalogenase	3.8.1.2	●	111	31	16	10
	Beta-phosphoglucomutase	5.4.2.6	●	77	21	23	3
Amidohydrolase (AH)	Cytosine deaminase	3.5.4.1	●	197	58	51	1
	Adenosine deaminase	3.5.4.4	●	152	19	25	15
	N-acyl-D-amino-acid deacyclase	3.5.1.81	●	68	19	12	3
	L-hydantoinase	3.5.2.2	●	2	1	0	1
	D-hydantoinase	3.5.2.2	●	199	60	37	13
	Urease	3.5.1.5	●	478	174	108	39
	Isoaspartyl dipeptidase	—	●	39	9	13	1
	Total No. Sequences			5995	1690	1440	488

[a] Enolase is both the name of the superfamily and the name of one of its member families.

[b] E.C number not yet assigned.

[c] Family color designation corresponds to that also used in figure 3-2.

3.3. Results

3.3.1. Annotation trends in 37 functional families

The results of the annotation analysis (Figure 3-1) are plotted in Figure 3-2 and tabulated in Table 3-2. The levels of correct, incorrect and equivocal annotation varied widely between the different families. For example in the enolase superfamily in the NR database (Figure 3-1 A), the mandelate racemase family was 100% correct (general annotations of 14%), whereas the galactonate dehydratase family was almost 40% incorrectly annotated with an additional 4% of its sequences annotated equivocally. In general the enolase and crotonase superfamilies exhibited the highest levels of misannotation. Similar to our findings in Chapter 2, the terpene cyclase superfamily (Figure 3-1 D) was particularly well annotated, however, in contrast to Chapter 2, the VOC (Figure 3-1 C) and AH (Figure 3-1 F) superfamilies displayed significantly less misannotation. Thirty-five percent of the families examined exhibited over 20% incorrect/equivocal annotations in at least one database. Seventy percent of the families investigated contained sequences that were correctly, but generally, annotated.

The annotation analysis results in the automated-curation databases (NR, TrEMBL and KEGG) were similar to one another, although variation was evident. For example in the 3-hydroxyisobutyryl-CoA hydrolase family (crotonase superfamily, Figure 3-1 B) the levels of misannotation were 86%, 83% and 89% in the NR, TrEMBL and KEGG databases respectively. However, in the FosA family (VOC superfamily, Figure 3-1 C) the level of misannotation was 19% in the NR database, and 0% (all general annotations) in KEGG (no FosA sequences were found in the TrEMBL database). Similar to the results seen in Chapter 2, the Swiss-Prot database was uniformly well annotated.

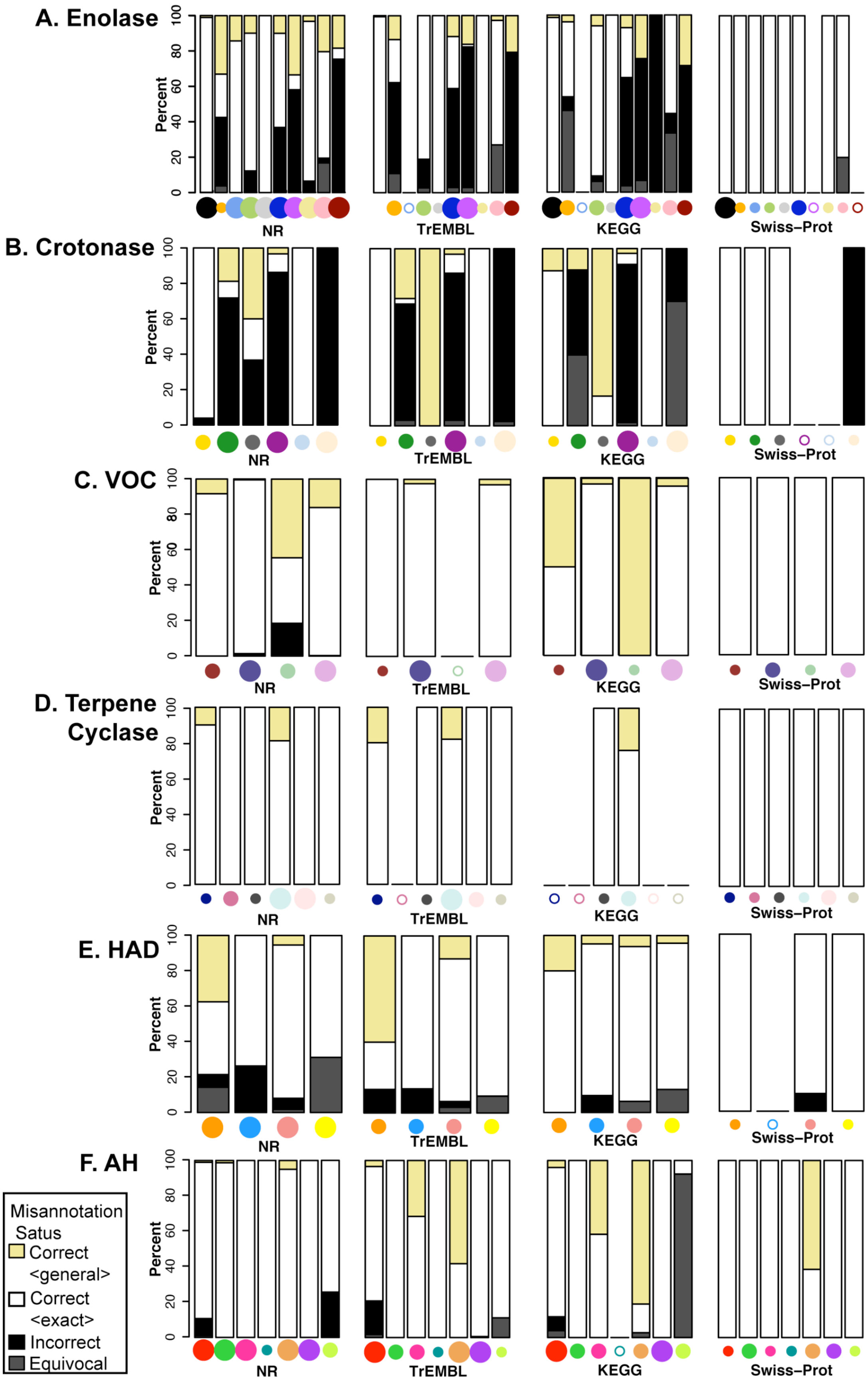

A. Enolase
B. Crotonase
C. VOC
D. Terpene Cyclase
E. HAD
F. AH
Percent
0
20
40
60
80
100
NR
TrEMBL
KEGG
Swiss–Prot
Misannotation Satus
Correct <general>
Correct <exact>
Incorrect
Equivocal

Figure 3-2. Levels of misannotation and correct annotation in six superfamilies (similarity-based analysis).
The results are organized by superfamily; Panel A: enolase, B: crotonase, C: vicinal oxygen chelate, D: terpene cyclase, E: haloacid dehalogenase and F: amidohydrolase superfamily. In each panel, the percent misannotation for each superfamily in each database is depicted. The four plots in each panel correspond to the NR, TrEMBL, KEGG, and Swiss-Prot databases, respectively. Each bar within each plot is a stacked bar plot indicating the percentage of sequences in that family that are correctly, incorrectly or equivocally annotated (yellow, white, black and grey bars respectively). The colors below each stacked bar designated the family as defined in Table 3-1. The size of each circle corresponds to the number of sequences in the family (as defined in Figure 2-3): smallest circle ≤ 10 sequences, medium circle 11-49 sequences, largest circle ≥ 50 sequences. A family with no bar and an empty circle means that no sequences were retrieved from that database in that family. The order of the families depicted for each superfamily is arbitrary but is consistent through all panels.

Table 3-2. The results from the similarity-based misannotation analysis of four databases.

Superfamily	Family	NR				TrEMBL				KEGG				Swiss-Prot			
		Eqv[A]	Mis[B]	Spc[C]	Gen[D]	Eqv	Mis	Spc	Gen	Eqv	Mis	Spc	Gen	Eqv	Mis	Spc	Gen
Enolase	Enolase	0	0	99	1	0	0	99	1	0	0	99	1	0	0	100	0
	Galactonate dehydratase	4	39	25	33	11	51	24	14	46	8	42	4	0	0	100	0
	Mandelate racemase	0	0	86	14	0	0	0	0	0	0	0	0	0	0	100	0
	Glucarate dehydratase	0	12	78	10	3	16	81	0	6	3	85	6	0	0	100	0
	Methyl aspartate ammonia-lyase	0	0	100	0	0	0	100	0	0	0	100	0	0	0	100	0
	OSBS	0	36	53	10	3	56	29	12	4	61	28	7	0	0	100	0
	Dipeptide epimerase	0	58	8	33	3	79	1	16	7	69	0	25	0	0	0	0
	Chloromuconate cycloisomerase	0	6	90	3	0	0	100	0	0	100	0	0	0	0	100	0
	Muconate cycloisomerase	17	3	60	20	27	0	70	3	33	11	56	0	20	0	80	0
	l-Fuconate dehydratase	0	75	6	18	0	79	0	21	0	71	0	29	0	0	0	0
Crotonase	Dodecenoyl-CoA delta-isomerase (mitochondrial)	0	4	96	0	0	0	100	0	0	0	88	13	0	0	100	0
	Delta(3,5)-delta(2,4)-dienoyl-CoA isomerase	0	72	9	19	3	66	3	28	40	48	0	12	0	0	100	0
	Methylmalonyl-CoA decarboxylase	0	37	23	40	0	0	0	100	0	0	17	83	0	0	100	0
	3-Hydroxyisobutyryl-CoA hydrolase	0	86	10	3	3	83	11	3	2	89	6	3	0	0	0	0

A. Percent equivocal annotations
B. Percent misannotated annotations
C. Percent correct annotations, speciific function annotation
D. Percent correct annotations, general function annotation

Table 3-2. The results from the similarity-based misannotation analysis of four databases.

Superfamily	Family	NR				TrEMBL				KEGG				Swiss-Prot			
		Eqv[A]	Mis[B]	Spc[C]	Gen[D]	Eqv	Mis	Spc	Gen	Eqv	Mis	Spc	Gen	Eqv	Mis	Spc	Gen
	4-Chlorobenzoate dehalogenase	0	0	100	0	0	0	100	0	0	0	100	0	0	0	0	0
	1,4-Dihydroxy-2-napthoyl-CoA synthase	0	100	0	0	2	98	0	0	70	30	0	0	0	100	0	0
VOC	Methylmalonyl-CoA epimerase	0	0	92	8	0	0	100	0	0	0	50	50	0	0	100	0
	4-Hydroxyphenylpyruvate dioxygenase	0	1	98	0	0	0	98	3	0	0	97	3	0	0	100	0
	FosA	0	19	37	44	0	0	0	0	0	0	0	100	0	0	100	0
	Glyoxalase I	0	0	84	16	0	0	97	3	0	0	96	4	0	0	100	0
Terpene Cyclase	5-Epi Aristolochene	0	0	90	10	0	0	80	20	0	0	0	0	0	0	100	0
	Bornyl diphosphate	0	0	100	0	0	0	0	0	0	0	0	0	0	0	100	0
	Pentalenene	0	0	100	0	0	0	100	0	0	0	100	0	0	0	100	0
	Squalene-hopene	0	0	81	19	0	0	82	18	0	0	76	24	0	0	100	0
	Trichodiene	0	0	100	0	0	0	100	0	0	0	0	0	0	0	100	0
	Aristolochene	0	0	100	0	0	0	100	0	0	0	0	0	0	0	100	0
HAD	Deoxy-d-mannose-octulosonate 8-phosphate phosphatase	14	7	41	38	0	13	27	60	0	0	80	20	0	0	100	0

A. Percent equivocal annotations
B. Percent misannotated annotations
C. Percent correct annotations, speciific function annotation
D. Percent correct annotations, general function annotation

Table 3-2. The results from the similarity-based misannotation analysis of four databases.

Superfamily	Family	NR				TrEMBL				KEGG				Swiss-Prot			
		Eqv[A]	Mis[B]	Spc[C]	Gen[D]	Eqv	Mis	Spc	Gen	Eqv	Mis	Spc	Gen	Eqv	Mis	Spc	Gen
	Phosphonoacetaldehyde hydrolase	0	26	74	0	0	14	86	0	0	10	86	5	0	0	0	0
	2-Haloacid dehalogenase	2	6	86	5	3	3	81	13	6	0	88	6	0	10	90	0
	Beta-phosphoglucomutase	31	0	69	0	10	0	90	0	13	0	83	4	0	0	100	0
AH	Cytosine deaminase	1	10	88	1	2	19	76	3	4	8	84	4	0	0	100	0
	Adenosine deaminase	0	0	99	1	0	0	100	0	0	0	100	0	0	0	100	0
	n-Acyl-d-amino-acid deacylase	0	0	100	0	0	0	68	32	0	0	58	42	0	0	100	0
	l-Hydantoinase	0	0	100	0	0	0	100	0	0	0	0	0	0	0	100	0
	d-Hydantoinase	0	0	95	5	0	0	42	58	3	0	16	81	0	0	38	62
	Urease	0	0	100	0	0	1	99	0	0	0	100	0	0	0	100	0
	Isoaspartyl dipeptidase	0	26	74	0	11	0	89	0	92	0	8	0	0	0	100	0

A. Percent equivocal annotations
B. Percent misannotated annotations
C. Percent correct annotations, speciific function annotation
D. Percent correct annotations, general function annotation

3.3.2. Annotation results in relation to submission date

We found in Chapter 2 that the majority of misannotation was added to the database in the post-genomic era (after 2000). We performed a similar analysis for the sequences analyzed here (Figure 3-3). As before, we found that concomitant with a large increase in overall sequence depositions to the NR database there was an increase in the number of sequences with incorrect and equivocal annotations. The proportion of sequences that were incorrectly annotated (black line) also increased from year to year, therefore the increase in misannotation was not due simply to an increase in the number of sequences. Similarly, a greater fraction of sequences were annotated to general function annotations and not specific function annotations in the post-genomic years. Again, this increase was not due simply to the increase in database size (data not shown).

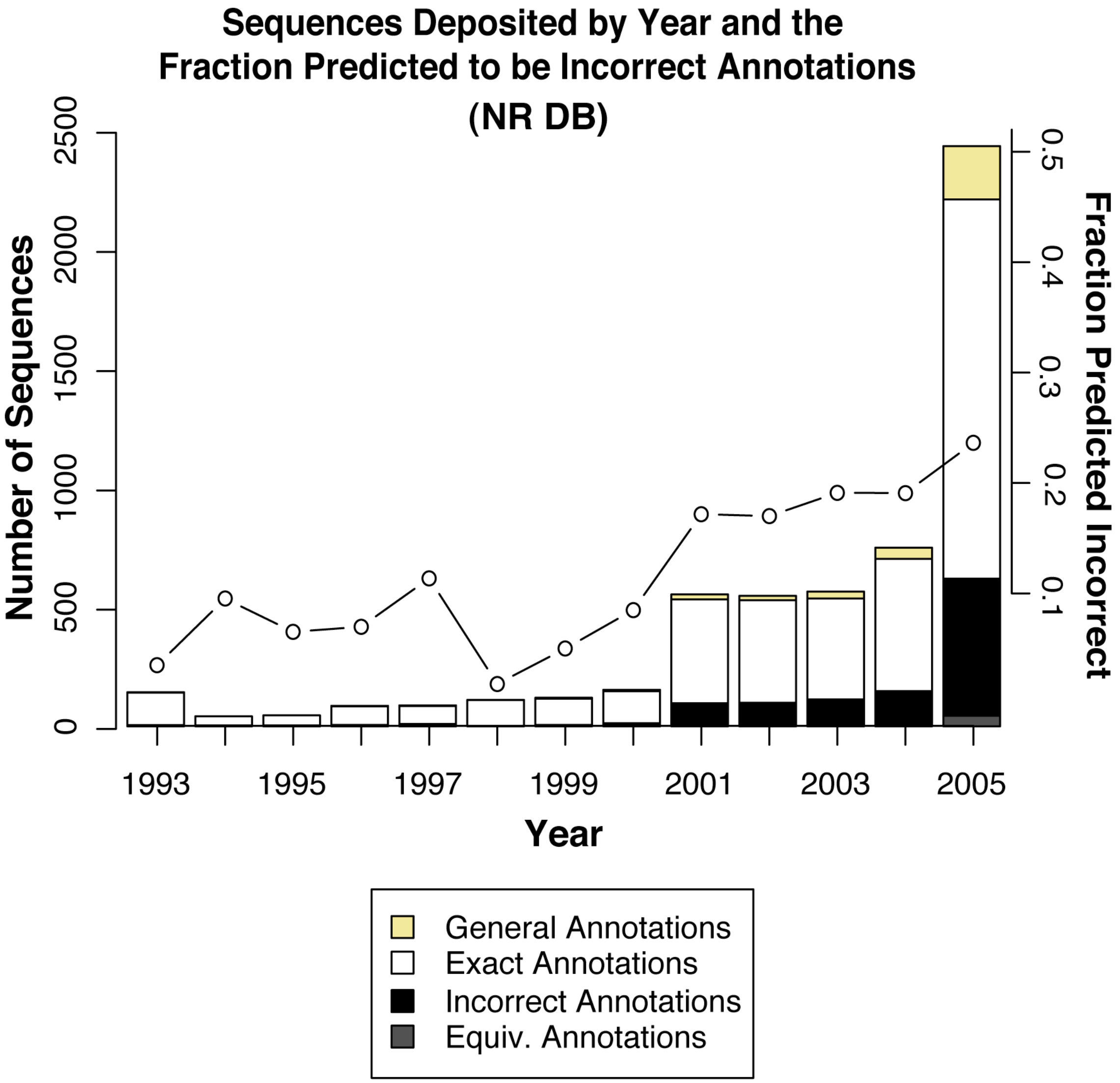


Figure 3-3. Distribution of annotations over time in the NR database.
Sequences are plotted by the year when they were originally deposited in the database (x-axis). The number of sequences (left y-axis, bar graph) found to be correctly annotated for a specific function is shown in white. General, though correct, annotations are shown in yellow. The number of sequences found to be incorrectly annotated by our analysis is shown in black. Any annotations that contained both correct and incorrect information (equivocal) are shown in grey. The fraction (right y-axis, line plot) of incorrect superfamily sequences deposited each year into the NR database is given by the open nodes, connected by the black line to aid in visualizing the overall trend. This fraction represents the number of sequences in the 37 test families predicted to be incorrect divided by the total number of sequences deposited each year from the test set, i.e. the sum of the sequences depicted in the yellow, white, black and grey bars for each year.

3.4. Discussion

Our analysis in Chapter 2, in addition to early investigations into annotation error [31, 32] and anecdotal reports [27, 34-36] have shown that misannotation is a considerable problem in public databases. As an addition to the work in Chapter 2 we have investigated the contribution of other kinds of misannotation to the problem of annotation error. We have investigated this question by examining how many sequences that belong (by sequence similarity) to a functional family are misannotated in four public databases (NR, TrEMBL, KEGG and Swiss-Prot). We worked with 37 families from the SFLD that had been experimentally characterized and utilized in Chapter 2.

The results from our annotation analysis (Figure 3-2) show that the levels of incorrect, equivocal and correct annotation (of both the specific and general types) vary greatly from family to family. It is not possible to *a priori* predict the misannotation level of a new family from a previously known family. This is very similar to what was found in Chapter 2 and to previous reports that stressed the necessity of analyzing and annotating families individually versus a uniform process [24]. However, two superfamilies—enolase and crotonase—exhibited consistently more annotation error that the remaining four superfamilies. Additionally, one superfamily (terpene cyclase) displayed no misannotation, allowing for a coarse-grained prediction of likelihood of misannotation levels for any new families: enolase, crotonase (high), HAD (medium), VOC, AH, terpene cyclase (low). Analogous to the analysis results in Chapter 2, the three large automated-curation databases (NR, TrEMBL, KEGG) exhibited similar annotation trends, showing that error propagation had occurred from primary databases (NR, TrEMBL) to secondary databases (KEGG). Additionally, Swiss-Prot was almost entirely correctly annotated, indicating again the data quality of the manually curated database.

The misannotation analysis in Chapter 2 only examined proteins with specific functional descriptions. In the analysis presented here, all proteins that mapped by sequence and catalytic residues to a function were investigated. This meant that any annotation (as long as it was a description of an enzymatic function) was examined. As a result, in addition to incorrect and correct function descriptions there were two new annotation types: equivocal and general (correct). Equivocal and general annotations only appear to have entered the database in the post-genomic era (Figure 3-3). This correlated with a marked increase of incorrect annotations in the databases. It is interesting to note that the introduction of equivocal and general annotations to the NR database lags that of incorrect annotations. It is possible that the equivocal annotations result from the increased error in the database and the general annotations result from annotators' attempts to minimize error from function overprediction. Given that the annotation histories of sequences are not available, it is not currently possible to examine this hypothesis. However, as we see here in Figure 3-3 and previously in Figure 2-6, the influx of sequences to public databases in the post-genomic era appears to have created a significant annotation problem and eroded database quality. The apparent expansion of the practice of using general annotations (Figure 3-3, year 2005) is encouraging however, as this is a simple way to keep erroneous overpredictions from propagating (one that we discussed in Chapter 2).

Given the levels of misannotation found in Chapter 2 it was notable to see an overall decrease in annotation error in this analysis. However, it is still unclear as to why, when these families are so well characterized and when it was a simple matter to map these sequences to known families, certain families displayed significant levels of misannotation. It is possible that the pressure to quickly annotate an overwhelming numbers of sequences coupled with the prevalent use of annotation transfer and the difficulty of reannotating misannotated sequences (Chapter 2) has created a situation in which even ‘simple’ cases can become difficult. This leads us to conclude that utilizing family context when it is available is exceedingly important (instead of the annotation transfer method which is essentially binary—‘known’ annotation to ‘unknown’ sequence). Databases like the SFLD, were experimental information is aligned with sequence and functional families are well defined, appear to be great aids in filtering out some level of misannotation. This corroborates the opinions of two recent reviews that advocate the abandonment of annotation transfer for annotation methodologies that use functional family context and orthogonal information [16, 17].

3.5. Conclusions

We manually investigated the annotations of nearly ten thousand proteins in 37 different functional families in order to investigate additional sources of misannotation. The misannotation problems uncovered (incorrect and equivocal annotations) are correlated with the large influx of sequences from genomic sequencing projects. The more prevalent use of general annotations is believed to be also a result of this sequence explosion. It should be noted, however, that the family groups gathered by our analysis were stringently structured so as to ensure that each sequence analyzed did belong to the family to which it was assigned. If in reality the families encapsulate sequences that are more sequence diverse, we have found that the levels of misannotation can increase dramatically in some families (data not shown) and the true level of misannotation determined in this analysis might be significantly underestimated.

3.6. Methods

3.6.1. Selection of functions, protein sequence data, thresholds

The selection of functions to investigate and the protein sequence data sources used were identical to that described in Chapter 2 in sections 2.6.1 (Selection off functions to investigate for misannotation), and 2.6.2 (Protein sequence data). The process to determine the family sequence thresholds is covered in section 2.6.3 (Thresholds to determine family (functional) membership).

3.6.2. Similarity-based annotation analysis algorithm

The general process of this analysis follows the flow chart in Figure 3-1. Each of the 37 different families was analyzed in the following manner. The hidden Markov model for the family was used to search each database (NR, Swiss-Prot, TrEMBL, KEGG) for family sequences using the HMMER program hmmsearch [75] with an E-value cutoff of 10^{-10}. The scores and E-values for each hit was parsed from the resulting files and the accession numbers for these hits were used to retrieve the annotation for each sequence from the source database. This was done using the NCBI program fastacmd with the flag '-t' in order to only retrieve the information related to that specific accession number. Each sequence was also aligned to the HMM that found it (using HMMER hmmalign) and it was determined whether the sequence contained the necessary functionally important residues. All of the above steps were performed by a series of two automated python scripts (runHMMSearchSFLD.py Appendix H and filterHomolSearchSFLD.py Appendix I).

The analysis of the results from the above scripts was performed using the TC as the analysis threshold (Appendix A). The annotations of all sequences that fell above the cutoff threshold and contained the necessary residues were manually analyzed. If a sequence did not have an annotation that described an enzymatic function it was discarded. If a sequence's annotation was found to be completely correct or incorrect, it was so marked. If the sequence was correctly annotated (as defined by our analysis) but the annotation contained additional incorrect enzymatic functional designations, the annotation was labeled equivocal. If a sequence was found to be annotated correctly, but not to the level of detail as could be applied, the sequences was marked as general. In total, over the four databases, 9613 sequences were manually examined. The raw data is in Appendix L.

3.6.3. Annotation results in relation to submission date

This analysis was performed identically to that as described in Chapter 2 section 2.6.5 (Change in misannotation over time.). For the plotted line representing the fraction of sequences predicted to be incorrect per year, only the sequences with incorrect annotations were counted (not the equivocal annotations). The results do not significantly change with the addition of the equivocal sequences.

3.6.4. Computation and Figures

The automated portions of the misannotation analysis were all preformed on a 90-node x86 cluster running Fedora Core 4 (nodes had either dual 2.6GHz Xeon or dual 1.5 GHz Athlon processors). The scoring of the protein sequences against all SFLD hidden Markov models to determine family thresholds was performed on single processor x86 machine running Redhat Workgroup 3. All data plots were produced using the software R.

Chapter 4.
Conclusions and Future Directions

4.1. Abstract

Misannotation is a serious problem facing public sequence databases. The results from Chapter 2 showed that the levels of misannotation are more significant and prevalent than previously reported and the annotation analysis in Chapter 3 corroborated these results. Error propagation additionally appears to be common. In every annotation analysis here performed the level of misannotation was found to be increasing over time. There is now a critical need for simple and quick ways to predict misannotations and a mechanism to propagate this information. As a future direction, a rapid misannotation prediction algorithm is described and a Misannotation Resource database for the community is discussed.

4.2. The annotation analyses—summary and thoughts

The research presented in this dissertation has shown that misannotation in public protein sequence databases is a prevalent and serious problem. Unfortunately, it is also difficult to predict what functions will or will not be misannotated as certain families can be almost entirely misannotated while others are perfectly annotated (Figure 2-3, Figure 3-2). The results presented in Chapter 2 provide initial evidence that error propagation is a significant source of the misannotations. Additionally, as evidenced by the levels of misannotation found in the KEGG database, there is a very real problem of error propagation from primary to secondary databases. All of the annotation analyses performed in this thesis (Chapter 2 and Chapter 3) show that misannotation is a problem that is worsening over time. This worsening correlates directly with the massive influx of genome sequencing project proteins into the databases. Without action, the sequence databases that form the core of much experimental and computational work will be riddled with errors.

Not every database exhibited significant misannotation. The manually curated database Swiss-Prot was almost uniformly well annotated. These results clearly show the importance of maintaining manually curated databases. Several other concepts are important considerations for improving database quality. First evidence codes and proper source attribution are critical in order to help the annotation reader know how much confidence to attribute to the annotation. Also important is the implementation and utilization of a standardized vocabulary or ontology to allow for clearer communication of ideas. Lastly, a significant issue is that of annotating to the level appropriate for the functional evidence available. Annotating to the appropriate functional granularity helps insure that misannotations due to functional overpredictions are not as likely.

Fundamentally, the problem of misannotation derives from the fact that identifying misannotations is not a rapid task, further complicated by the fact that reannotation is currently difficult [80] which in turn means that any corrections are long in coming. The analyses described in this thesis required significant manual effort, which is not a tenable option when dealing with entire databases (or even large portions of databases). The next step beyond this work is the design and implementation of algorithms that can quickly and easily find potential misannotations. What is additionally needed is a way to propagate these misannotation predictions to the public. Another future direction step that will be discussed is the design and implementation of a Misannotation Resource database for the public.

4.3. Future work: methods for rapid misannotation prediction

4.3.1. Rapid prediction of misannotated proteins through visualization and simple sequence metrics

When performing the misannotation analysis in Chapter 2, it became apparent that many misannotations that were found fell into distinct patterns in sequence networks. Figure 4-1 is a detailed view of the VOC superfamily misannotation results from Chapter 2. Highlighted on this network in rectangles are the commonly observed types of misannotation groups. We saw that a large proportion of misannotations were either a) singletons, unconnected to other sequences or b) in offshoot groups from a main sequence group. Because of this observation, it became evident that a Misannotation Finder algorithm could be designed that would allow for the rapid prediction of potential misannotations. The goal of this algorithm would not be to determine every misannotation, or even to be stringently accurate. The goal would be to create a ‘suspect list’ of proteins for which one should be cautious when using the annotation. Such a suspect list would alert any scientist to the potential issue of function annotation error without necessarily designating the annotation as definitively incorrect.

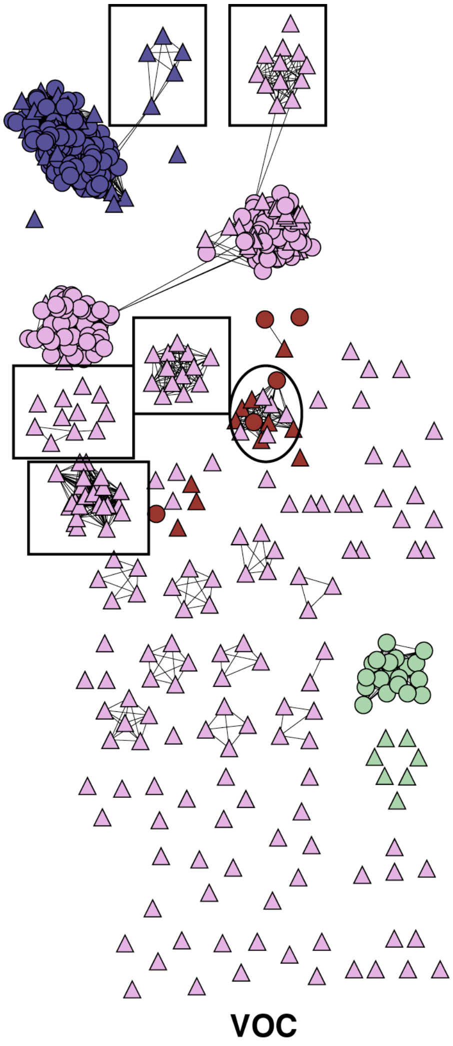


Figure 4-1. Detailed view of the VOC superfamily correct and incorrect annotations. Figure is detail of VOC superfamily from Figure 2-7. Circular nodes are ‘correct’. Triangular nodes are ‘incorrect’. Nodes highlighted by rectangles are examples of misannotation groups that can be identified by the Misannotation Finder algorithm. Nodes highlighted by a circle are examples of where some of the nodes would be classified incorrectly by the Misannotation Finder algorithm.

The description of the process to create a suspect list of potential misannotations is covered in Figure 4-2. As an input one would need a set of known sequences and the set of unknown sequences that need to be analyzed.

The sequence similarities of the input protein group would be calculated (all-by-all BLAST). The protein group would be visualized in a similarity network (Cytoscape) using an appropriate E-value cutoff. It is anticipated that this cutoff would be empirically determined from a training set of sequences. With the 'knowns' labeled in the network, the Misannotation Finder algorithm could be used to manually designate suspect sequences.

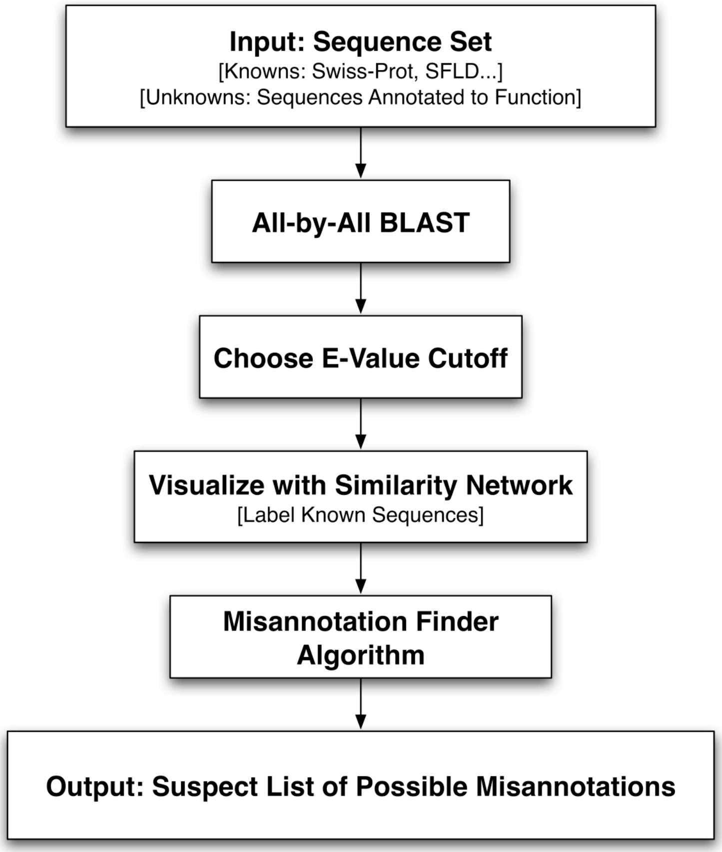


Figure 4-2. Flowchart to generate suspect list of potential misannotations. Starting with an input set of sequences that contain both knowns and unknowns (to be analyzed), the similarity of the sequences to each other are determined using all-by-all BLAST. Using an empirically defined E-value cutoff the sequences are visualized as a similarity network (using Cytoscape). The network is examined manually and the nodes are labeled using the Misannotation Finder algorithm. The output is a list of sequences with possible misannotations.

Misannotation Finder algorithm is detailed in Figure 4-3. The algorithm follows two steps. First all sequence network groups that contain 'known' sequences are examined. Any groups that contain ‘knowns’ of more than one function are ignored because the case is too complex. For any groups that only contain one ‘known’ function all the annotations of the ‘unknowns’ are compared to the ‘known’ and any discrepancies are noted as ‘suspect’. It should be pointed out that this algorithm would fail in cases such as circled in Figure 4-1. Assuming that the red circular nodes are ‘knowns’, all other sequences that would be annotated to this function in this group would be assumed to be correct. However, as can be seen, all the other red nodes in the circled group are triangular, indicating that they are misannotated. The second step in the algorithm is to examine the singleton nodes and any sequence network groups that do not contain any ‘knowns’. In both cases, it is assumed that these sequences are potential misannotations and are labeled ‘suspect’.

The main weaknesses of the Misannotation Finder algorithm are first that all predictions rest on ‘known’ information, essentially guaranteeing misclassification for any new protein that does not conform to what is known, and second that it makes the assumption that sequence similarity is always a valid proxy for functional similarity/dissimilarity. The fundamental power of this algorithm, however, is that it is rapid and simple and strives only to predict *potential* misannotations for the purposes of future investigation. A test set would be used to estimate the extent to which the weaknesses of the algorithm affect the accuracy of the suspect list.

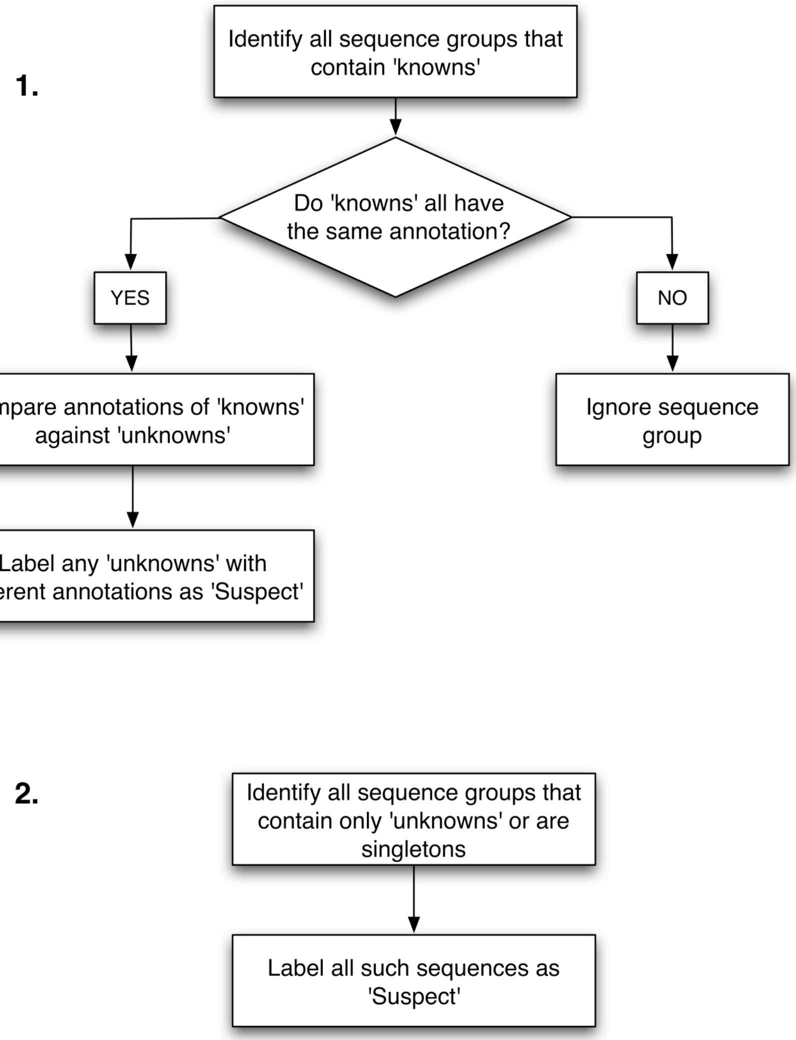


Figure 4-3. Misannotation Finder algorithm flowchart.
Two step algorithm to make a list of sequences that are potentially misannotated.

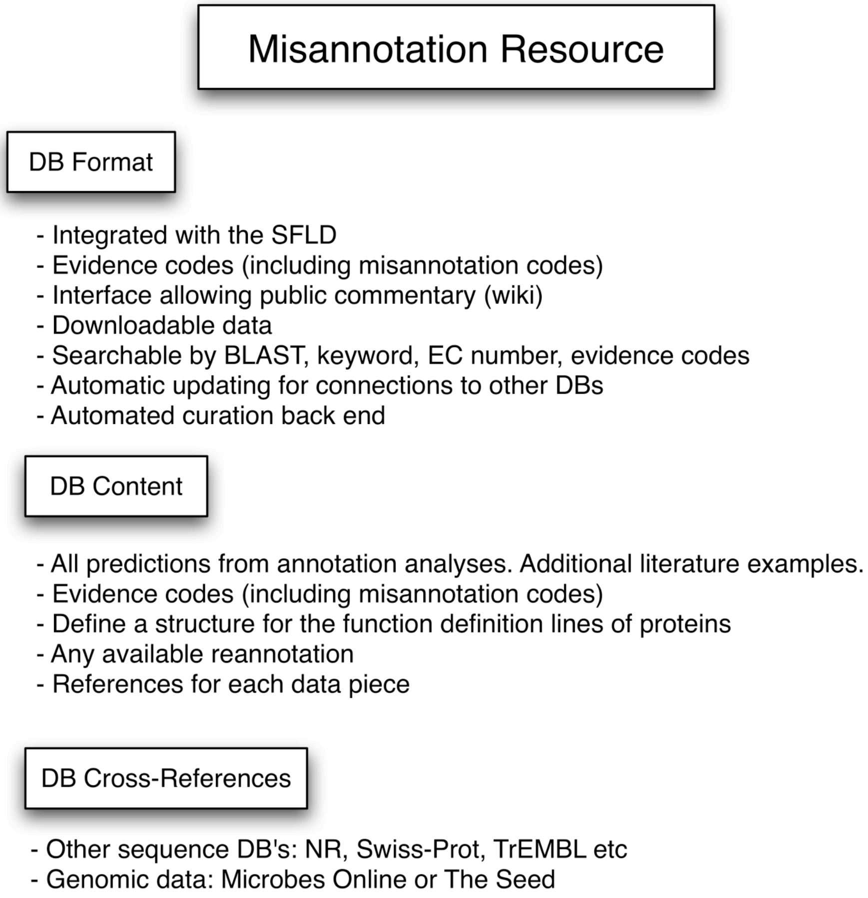
4.3.2. Large-scale misannotation prediction via annotation clustering and automated sequence similarity clustering

While the Misannotation Finder algorithm is a simple way to predict possible misannotations it has a noticeable drawback in that it is not completely automated. The designation of ‘suspect’ proteins requires the visual inspection of a sequence similarity network. Not only does this take a certain amount of time, it limits the scale to which the algorithm can be applied. A possible adjustment to the manual aspect is to automate the designation of sequence groups so that a visual inspection would not be needed to determine separate groups and the placement of ‘knowns’ within those groups. The TRIBE-MCL algorithm [81] has been shown to automatically and successfully group sequences based upon sequence similarities and the coded implementation of the algorithm is available in Biopython. The TRIBE-MCL algorithm could be added to the above procedure in order to remove the necessity of visually examining the sequence similarity networks.

In order to address the issue of scale, another automated aspect could be added to the procedure. Until this point it has been assumed that the input sequences have been restricted to a defined set sequences of particular interest. However, Kunin and Ouzounis published the CLAN algorithm that allowed for the rapid annotation clustering of entire databases [82]. This algorithm could be used to cluster a full database of annotations (such as NR) and then the TRIBE-MCL algorithm could be used to sequence cluster each annotation group. As in the original Misannotation Finder algorithm, ‘knowns’ (e.g. from Swiss-Prot) would be used automatically designate which TRIBE-MCL groups were annotated correctly. In this fashion, a suspect list for an entire database could be derived.

4.4. Future work: a misannotation resource for the scientific community

Another significant issue in relation to misannotation is that even when misannotations are found it is difficult to disseminate or propagate this information. Currently there is no repository for misannotations or potential misannotations. Databases like GenBank, in fact, only allow the original submitters of a sequence to amend anything about the sequence (including the function annotation) even when new experimental evidence from another source contradicts the annotation [37] and currently GenBank is not planning to modify this procedure [80]. What is missing from the scientific community, therefore, is a public resource that lists known and potential protein function misannotations. This Misannotation Resource would be a publicly available database where interested parties could both search and download misannotations but where they could contribute their own misannotations. Figure 4-4 list several characteristics of the proposed Misannotation Resource. While it would be managed as a manually curated database, it would also allow for public commentary with a wiki-like interface similar to several other new protein and genomic sequence databases [83-86]. The Misannotation Resource would be integrated with the SFLD and would operate under the similar guidelines of utilizing evidence codes and noting reference information for each data piece. The database would also be cross-referenced to the main sequence databases (NR, TrEMBL, Swiss-Prot) and to genomic resources (e.g. Microbes Online) where appropriate. Additionally, all downloaded sequences from the Misannotation Resource would contain structured functional definition lines that specify evidence codes and sources of data. The Misannotation Resource database would strive to be the community repository of known and potential annotation error until the time at which the large primary sequence databases have mechanisms in place to update and reannotate erroneous function annotations.



Misannotation Resource

DB Format

- Integrated with the SFLD
- Evidence codes (including misannotation codes)
- Interface allowing public commentary (wiki)
- Downloadable data
- Searchable by BLAST, keyword, EC number, evidence codes
- Automatic updating for connections to other DBs
- Automated curation back end

DB Content

- All predictions from annotation analyses. Additional literature examples.
- Evidence codes (including misannotation codes)
- Define a structure for the function definition lines of proteins
- Any available reannotation
- References for each data piece

DB Cross-References

- Other sequence DB's: NR, Swiss-Prot, TrEMBL etc
- Genomic data: Microbes Online or The Seed

Figure 4-4. Details of the Misannotation Resource.
Initial outline of elements that will be present in the Misannotation Resource Database.

4.5. In Conclusion

Protein function misannotation is a significant problem. Given the prevalence of misannotation the issue has the potential to negatively affect large portions of the scientific community. With this large a scope, efforts need to be quickly undertaken by the community so as to keep the problem from becoming intractable. Substantial research efforts should be geared towards the rapid and large-scale prediction of misannotation and mechanisms to disseminate misannotation information and reannotate erroneous sequences.

References

1. Fundel K, Zimmer R: **Gene and protein nomenclature in public databases**. *BMC bioinformatics* 2006, **7**:372.
2. Benson DA, Karsch-Mizrachi I, Lipman DJ, Ostell J, Wheeler DL: **GenBank**. *Nucleic acids research* 2008, **36**(Database issue):D25-30.
3. UniProt Consortium: **The universal protein resource (UniProt)**. *Nucleic acids research* 2008, **36**(Database issue):D190-195.
4. Wheeler DL, Barrett T, Benson DA, Bryant SH, Canese K, Chetvernin V, Church DM, Dicuccio M, Edgar R, Federhen S *et al*: **Database resources of the National Center for Biotechnology Information**. *Nucleic acids research* 2008, **36**(Database issue):D13-21.
5. Chen L, Liu H, Friedman C: **Gene name ambiguity of eukaryotic nomenclatures**. *Bioinformatics* 2005, **21**(2):248-256.
6. Seringhaus MR, Cayting PD, Gerstein MB: **Uncovering trends in gene naming**. *Genome Biol* 2008, **9**(1):401.
7. Kyrpides NC, Ouzounis CA: **Whole-genome sequence annotation: 'Going wrong with confidence'**. *Molecular microbiology* 1999, **32**(4):886-887.
8. Finn RD, Mistry J, Schuster-Bockler B, Griffiths-Jones S, Hollich V, Lassmann T, Moxon S, Marshall M, Khanna A, Durbin R *et al*: **Pfam: clans, web tools and services**. *Nucleic acids research* 2006, **34**(Database issue):D247-251.
9. Quevillon E, Silventoinen V, Pillai S, Harte N, Mulder N, Apweiler R, Lopez R: **InterProScan: protein domains identifier**. *Nucleic acids research* 2005, **33**(Web Server issue):W116-120.
10. **The Gene Ontology (GO) project in 2006**. *Nucleic acids research* 2006, **34**(Database issue):D322-326.
11. Hong EL, Balakrishnan R, Dong Q, Christie KR, Park J, Binkley G, Costanzo MC, Dwight SS, Engel SR, Fisk DG *et al*: **Gene Ontology annotations at SGD: new data sources and annotation methods**. *Nucleic acids research* 2008, **36**(Database issue):D577-581.
12. Babbitt PC: **Definitions of enzyme function for the structural genomics era**. *Current opinion in chemical biology* 2003, **7**(2):230-237.
13. Pegg SC, Brown S, Ojha S, Huang CC, Ferrin TE, Babbitt PC: **Representing structure-function relationships in mechanistically diverse enzyme superfamilies**. *Pac Symp Biocomput* 2005:358-369.

14. Pegg SC, Brown SD, Ojha S, Seffernick J, Meng EC, Morris JH, Chang PJ, Huang CC, Ferrin TE, Babbitt PC: **Leveraging enzyme structure-function relationships for functional inference and experimental design: the structure-function linkage database**. *Biochemistry* 2006, **45**(8):2545-2555.
15. Porter CT, Bartlett GJ, Thornton JM: **The Catalytic Site Atlas: a resource of catalytic sites and residues identified in enzymes using structural data**. *Nucleic acids research* 2004, **32**(Database issue):D129-133.
16. Frishman D: **Protein annotation at genomic scale: the current status**. *Chemical reviews* 2007, **107**(8):3448-3466.
17. Lee D, Redfern O, Orengo C: **Predicting protein function from sequence and structure**. *Nature reviews* 2007, **8**(12):995-1005.
18. Raes J, Harrington ED, Singh AH, Bork P: **Protein function space: viewing the limits or limited by our view?** *Current opinion in structural biology* 2007, **17**(3):362-369.
19. Devos D, Valencia A: **Practical limits of function prediction**. *Proteins* 2000, **41**(1):98-107.
20. Pawlowski K, Jaroszewski L, Rychlewski L, Godzik A: **Sensitive sequence comparison as protein function predictor**. *Pac Symp Biocomput* 2000:42-53.
21. Rost B, Liu J, Nair R, Wrzeszczynski KO, Ofran Y: **Automatic prediction of protein function**. *Cell Mol Life Sci* 2003, **60**(12):2637-2650.
22. Todd AE, Orengo CA, Thornton JM: **Evolution of function in protein superfamilies, from a structural perspective**. *J Mol Biol* 2001, **307**(4):1113-1143.
23. Wilson CA, Kreychman J, Gerstein M: **Assessing annotation transfer for genomics: quantifying the relations between protein sequence, structure and function through traditional and probabilistic scores**. *J Mol Biol* 2000, **297**(1):233-249.
24. Tian W, Skolnick J: **How well is enzyme function conserved as a function of pairwise sequence identity?** *J Mol Biol* 2003, **333**(4):863-882.
25. Karp PD: **What we do not know about sequence analysis and sequence databases**. *Bioinformatics* 1998, **14**(9):753-754.
26. Bork P, Bairoch A: **Go hunting in sequence databases but watch out for the traps**. *Trends Genet* 1996, **12**(10):425-427.
27. Kyrpides NC, Ouzounis CA: **Errors in genome reviews**. *Science (New York, NY* 1998, **281**(5382):1457.
28. Pallen M, Wren B, Parkhill J: **'Going wrong with confidence': misleading sequence analyses of CiaB and clpX**. *Molecular microbiology* 1999, **34**(1):195.
29. Gilks WR, Audit B, De Angelis D, Tsoka S, Ouzounis CA: **Modeling the percolation of annotation errors in a database of protein sequences**. *Bioinformatics* 2002, **18**(12):1641-1649.

30. Gilks WR, Audit B, de Angelis D, Tsoka S, Ouzounis CA: **Percolation of annotation errors through hierarchically structured protein sequence databases**. *Math Biosci* 2005, **193**(2):223-234.
31. Brenner SE: **Errors in genome annotation**. *Trends Genet* 1999, **15**(4):132-133.
32. Devos D, Valencia A: **Intrinsic errors in genome annotation**. *Trends Genet* 2001, **17**(8):429-431.
33. Jones CE, Brown AL, Baumann U: **Estimating the annotation error rate of curated GO database sequence annotations**. *BMC bioinformatics* 2007, **8**:170.
34. Andorf C, Dobbs D, Honavar V: **Exploring inconsistencies in genome-wide protein function annotations: a machine learning approach**. *BMC bioinformatics* 2007, **8**:284.
35. Naumoff DG, Xu Y, Stalon V, Glansdorff N, Labedan B: **The difficulty of annotating genes: the case of putrescine carbamoyltransferase**. *Microbiology (Reading, England)* 2004, **150**(Pt 12):3908-3911.
36. Skipsey M, Andrews CJ, Townson JK, Jepson I, Edwards R: **Cloning and characterization of glyoxalase I from soybean**. *Archives of biochemistry and biophysics* 2000, **374**(2):261-268.
37. Bidartondo MI: **Preserving accuracy in GenBank**. *Science (New York, NY* 2008, **319**(5870):1616.
38. Hadley C: **Righting the wrongs**. *EMBO reports* 2003, **4**(9):829-831.
39. Dandekar T, Snel B, Huynen M, Bork P: **Conservation of gene order: a fingerprint of proteins that physically interact**. *Trends in biochemical sciences* 1998, **23**(9):324-328.
40. Korbel JO, Jensen LJ, von Mering C, Bork P: **Analysis of genomic context: prediction of functional associations from conserved bidirectionally transcribed gene pairs**. *Nature biotechnology* 2004, **22**(7):911-917.
41. Marcotte EM, Pellegrini M, Ng HL, Rice DW, Yeates TO, Eisenberg D: **Detecting protein function and protein-protein interactions from genome sequences**. *Science (New York, NY* 1999, **285**(5428):751-753.
42. Overbeek R, Fonstein M, D'Souza M, Pusch GD, Maltsev N: **The use of gene clusters to infer functional coupling**. *Proceedings of the National Academy of Sciences of the United States of America* 1999, **96**(6):2896-2901.
43. Pellegrini M, Marcotte EM, Thompson MJ, Eisenberg D, Yeates TO: **Assigning protein functions by comparative genome analysis: protein phylogenetic profiles**. *Proceedings of the National Academy of Sciences of the United States of America* 1999, **96**(8):4285-4288.
44. Brown D, Sjolander K: **Functional classification using phylogenomic inference**. *PLoS computational biology* 2006, **2**(6):e77.
45. Eisen JA: **Phylogenomics: improving functional predictions for uncharacterized genes by evolutionary analysis**. *Genome research* 1998, **8**(3):163-167.

46. Gupta N, Tanner S, Jaitly N, Adkins JN, Lipton M, Edwards R, Romine M, Osterman A, Bafna V, Smith RD *et al*: **Whole proteome analysis of post-translational modifications: applications of mass-spectrometry for proteogenomic annotation**. *Genome research* 2007, **17**(9):1362-1377.
47. Attwood TK, Bradley P, Flower DR, Gaulton A, Maudling N, Mitchell AL, Moulton G, Nordle A, Paine K, Taylor P *et al*: **PRINTS and its automatic supplement, prePRINTS**. *Nucleic acids research* 2003, **31**(1):400-402.
48. Hulo N, Bairoch A, Bulliard V, Cerutti L, De Castro E, Langendijk-Genevaux PS, Pagni M, Sigrist CJ: **The PROSITE database**. *Nucleic acids research* 2006, **34**(Database issue):D227-230.
49. Tatusov RL, Fedorova ND, Jackson JD, Jacobs AR, Kiryutin B, Koonin EV, Krylov DM, Mazumder R, Mekhedov SL, Nikolskaya AN *et al*: **The COG database: an updated version includes eukaryotes**. *BMC bioinformatics* 2003, **4**:41.
50. Chen F, Mackey AJ, Stoeckert CJ, Jr., Roos DS: **OrthoMCL-DB: querying a comprehensive multi-species collection of ortholog groups**. *Nucleic acids research* 2006, **34**(Database issue):D363-368.
51. Mulder NJ, Apweiler R, Attwood TK, Bairoch A, Bateman A, Binns D, Bork P, Buillard V, Cerutti L, Copley R *et al*: **New developments in the InterPro database**. *Nucleic acids research* 2007, **35**(Database issue):D224-228.
52. Polacco BJ, Babbitt PC: **Automated discovery of 3D motifs for protein function annotation**. *Bioinformatics* 2006, **22**(6):723-730.
53. Kristensen DM, Ward RM, Lisewski AM, Erdin S, Chen BY, Fofanov VY, Kimmel M, Kavraki LE, Lichtarge O: **Prediction of enzyme function based on 3D templates of evolutionarily important amino acids**. *BMC bioinformatics* 2008, **9**:17.
54. Binkowski TA, Joachimiak A, Liang J: **Protein surface analysis for function annotation in high-throughput structural genomics pipeline**. *Protein Sci* 2005, **14**(12):2972-2981.
55. Shulman-Peleg A, Nussinov R, Wolfson HJ: **SiteEngines: recognition and comparison of binding sites and protein-protein interfaces**. *Nucleic acids research* 2005, **33**(Web Server issue):W337-341.
56. Bult CJ, Eppig JT, Kadin JA, Richardson JE, Blake JA: **The Mouse Genome Database (MGD): mouse biology and model systems**. *Nucleic acids research* 2008, **36**(Database issue):D724-728.
57. Lander ES, Linton LM, Birren B, Nusbaum C, Zody MC, Baldwin J, Devon K, Dewar K, Doyle M, FitzHugh W *et al*: **Initial sequencing and analysis of the human genome**. *Nature* 2001, **409**(6822):860-921.
58. Riley M, Abe T, Arnaud MB, Berlyn MK, Blattner FR, Chaudhuri RR, Glasner JD, Horiuchi T, Keseler IM, Kosuge T *et al*: **Escherichia coli K-12: a cooperatively developed annotation snapshot--2005**. *Nucleic acids research* 2006, **34**(1):1-9.
59. Kanehisa M, Araki M, Goto S, Hattori M, Hirakawa M, Itoh M, Katayama T, Kawashima S, Okuda S, Tokimatsu T *et al*: **KEGG for linking genomes**

to life and the environment. *Nucleic acids research* 2008, **36**(Database issue):D480-484.

60. Brown SD, Gerlt JA, Seffernick JL, Babbitt PC: **A gold standard set of mechanistically diverse enzyme superfamilies**. *Genome Biol* 2006, **7**(1):R8.
61. Altschul SF, Madden TL, Schaffer AA, Zhang J, Zhang Z, Miller W, Lipman DJ: **Gapped BLAST and PSI-BLAST: a new generation of protein database search programs**. *Nucleic acids research* 1997, **25**(17):3389-3402.
62. Shannon P, Markiel A, Ozier O, Baliga NS, Wang JT, Ramage D, Amin N, Schwikowski B, Ideker T: **Cytoscape: a software environment for integrated models of biomolecular interaction networks**. *Genome research* 2003, **13**(11):2498-2504.
63. George RA, Spriggs RV, Bartlett GJ, Gutteridge A, MacArthur MW, Porter CT, Al-Lazikani B, Thornton JM, Swindells MB: **Effective function annotation through catalytic residue conservation**. *Proceedings of the National Academy of Sciences of the United States of America* 2005, **102**(35):12299-12304.
64. Pearson A, Flood Page SR, Jorgenson TL, Fischer WW, Higgins MB: **Novel hopanoid cyclases from the environment**. *Environmental microbiology* 2007, **9**(9):2175-2188.
65. Kurihara T, Liu JQ, Nardi-Dei V, Koshikawa H, Esaki N, Soda K: **Comprehensive site-directed mutagenesis of L-2-halo acid dehalogenase to probe catalytic amino acid residues**. *Journal of biochemistry* 1995, **117**(6):1317-1322.
66. Glasner ME, Fayazmanesh N, Chiang RA, Sakai A, Jacobson MP, Gerlt JA, Babbitt PC: **Evolution of structure and function in the o-succinylbenzoate synthase/N-acylamino acid racemase family of the enolase superfamily**. *J Mol Biol* 2006, **360**(1):228-250.
67. Babbitt PC, Gerlt JA: **New functions from old scaffolds: how nature reengineers enzymes for new functions**. *Advances in protein chemistry* 2000, **55**:1-28.
68. Gerlt JA, Babbitt PC: **Mechanistically diverse enzyme superfamilies: the importance of chemistry in the evolution of catalysis**. *Current opinion in chemical biology* 1998, **2**(5):607-612.
69. Gerlt JA, Babbitt PC: **Divergent evolution of enzymatic function: mechanistically diverse superfamilies and functionally distinct suprafamilies**. *Annual review of biochemistry* 2001, **70**:209-246.
70. Murakami S, Kohsaka C, Okuno T, Takenaka S, Aoki K: **Purification, characterization, and gene cloning of cis,cis-muconate cycloisomerase from benzamide-assimilating Arthrobacter sp. BA-5-17**. *FEMS microbiology letters* 2004, **231**(1):119-124.
71. Sakai A, Gerlt JA, Coworkers: *in preparation*.
72. Alm EJ, Huang KH, Price MN, Koche RP, Keller K, Dubchak IL, Arkin AP: **The MicrobesOnline Web site for comparative genomics**. *Genome research* 2005, **15**(7):1015-1022.

73. Meganathan R: **Biosynthesis of menaquinone (vitamin K2) and ubiquinone (coenzyme Q): a perspective on enzymatic mechanisms**. *Vitamins and hormones* 2001, **61**:173-218.
74. Truglio JJ, Theis K, Feng Y, Gajda R, Machutta C, Tonge PJ, Kisker C: **Crystal structure of Mycobacterium tuberculosis MenB, a key enzyme in vitamin K2 biosynthesis**. *The Journal of biological chemistry* 2003, **278**(43):42352-42360.
75. **HMMER: biosequence analysis using profile hidden Markov models** [http://hmmer.janelia.org/]
76. **NBCI: BLAST program suite** [ftp://ftp.ncbi.nlm.nih.gov/blast/executables/LATEST/]
77. **Help with Pfam HMM scores** [http://pfam.janelia.org/help]
78. **Recommendations of the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology on the Nomenclature and Classification of Enzymes by the Reactions they Catalyse** [http://www.chem.qmul.ac.uk/iubmb/enzyme/]
79. Edgar RC: **MUSCLE: multiple sequence alignment with high accuracy and high throughput**. *Nucleic acids research* 2004, **32**(5):1792-1797.
80. Pennisi E: **DNA data. Proposal to 'Wikify' GenBank meets stiff resistance**. *Science (New York, NY* 2008, **319**(5870):1598-1599.
81. Enright AJ, Van Dongen S, Ouzounis CA: **An efficient algorithm for large-scale detection of protein families**. *Nucleic acids research* 2002, **30**(7):1575-1584.
82. Kunin V, Ouzounis CA: **Clustering the annotation space of proteins**. *BMC bioinformatics* 2005, **6**:24.
83. Hodis E, Prilusky J, Martz E, Silman I, Moult J, Sussman JL: **Proteopedia - a scientific 'wiki' bridging the rift between three-dimensional structure and function of biomacromolecules**. *Genome Biol* 2008, **9**(8):R121.
84. Hoffmann R: **A wiki for the life sciences where authorship matters**. *Nature genetics* 2008, **40**(9):1047-1051.
85. Huss JW, 3rd, Orozco C, Goodale J, Wu C, Batalov S, Vickers TJ, Valafar F, Su AI: **A gene wiki for community annotation of gene function**. *PLoS biology* 2008, **6**(7):e175.
86. Mons B, Ashburner M, Chichester C, van Mulligen E, Weeber M, den Dunnen J, van Ommen GJ, Musen M, Cockerill M, Hermjakob H *et al*: **Calling on a million minds for community annotation in WikiProteins**. *Genome Biol* 2008, **9**(5):R89.

Appendix A. Misannotation Analysis Thresholds

Table A-1. Thresholds for the annotation analyses.

Superfamily	Family	Threshold		
		TC[a]	NC[b]	LC[c]
Enolase	Enolase	386	213.0	40.0
	Galactonate Dehydratase	843.6	200.9	193.1
	Mandelate Racemase	910.6	475.3	40.0
	Glucarate Dehydratase	1038.4	989.2	861.4
	Methylaspartate Ammonia-lyase	1031	535.5	40.0
	OSBS	99.6	91.3	79
	Dipeptide Epimerase	454.2	113.5	96.9
	Chloromuconate Cycloisomerase	784	566.0	565
	Muconate Cycloisomerase	780.5	504.8	499.8
	L-Fuconate Dehydratase	775.4	407.7	40.0
Crotonase	Dodecenoyl-CoA delta-isomerase (mitochondrial)	522.6	281.3	40.0
	delta(3,5)-delta(2,4)-Dienoyl-CoA isomerase	355.9	91.2	90.4
	Methylmalonyl-CoA decarboxylase	662.5	105	105
	3-Hydroxyisobutyryl-CoA hydrolase	367.9	204.0	40.0
	4-Chlorobenzoate dehalogenase	772.7	79.3	79.3
	1,4-Dihydroxy-2-napthoyl-CoA synthase	341.6	251.8	70.9
VOC	Methylmalonyl-CoA epimerase	269.1	154.6	40.0
	4-Hydroxyphenylpyruvate dioxygenase	430.7	180.1	158.4
	FosA	361.1	90	84.8

	Glyoxalase I	263.9	152.0	40.0
Terpene Cyclase	5-Epi-aristolochene	1445	1320.3	1320.3
	Bornyl Diphosphate Synthase	1549.8	1207.2	763
	Pentalenene Synthase	727.3	383.7	40.0
	Squalene-Hopene Synthase	803.4	421.7	40.0
	Trichodiene Synthase	996.8	518.4	40.0
	Aristolochene Synthase	849.2	444.6	40.0
HAD	Deoxy-d-mannose-octulosonate 8-phosphate phosphatase	295.6	167.8	40.0
	Phosphonoacetaldehyde hydrolase	563.8	301.9	40.0
	2-Haloacid dehalogenase	339.8	189.9	40.0
	beta-Phosphoglucomutase	408.5	224.3	40.0
AH	Cytosine deaminase	774.1	161.1	158
	Adenosine deaminase	645.9	343.0	40
	n-Acyl-d-amino-acid deacylase	1122.1	581.1	40
	l-Hydantoinase	1412.1	183	174
	d-Hydantoinase	635.4	176.7	174.2
	Urease	90.4	65.2	40
	Isoaspartyl dipeptidase	1044.2	542.1	40

[a] Trusted Cutoff
[b] Noise Cutoff
[c] Lenient Cutoff

Appendix B. Snapshots of Misannotation over Time

Figure B - 1. Sequence similarity network: year 1993.

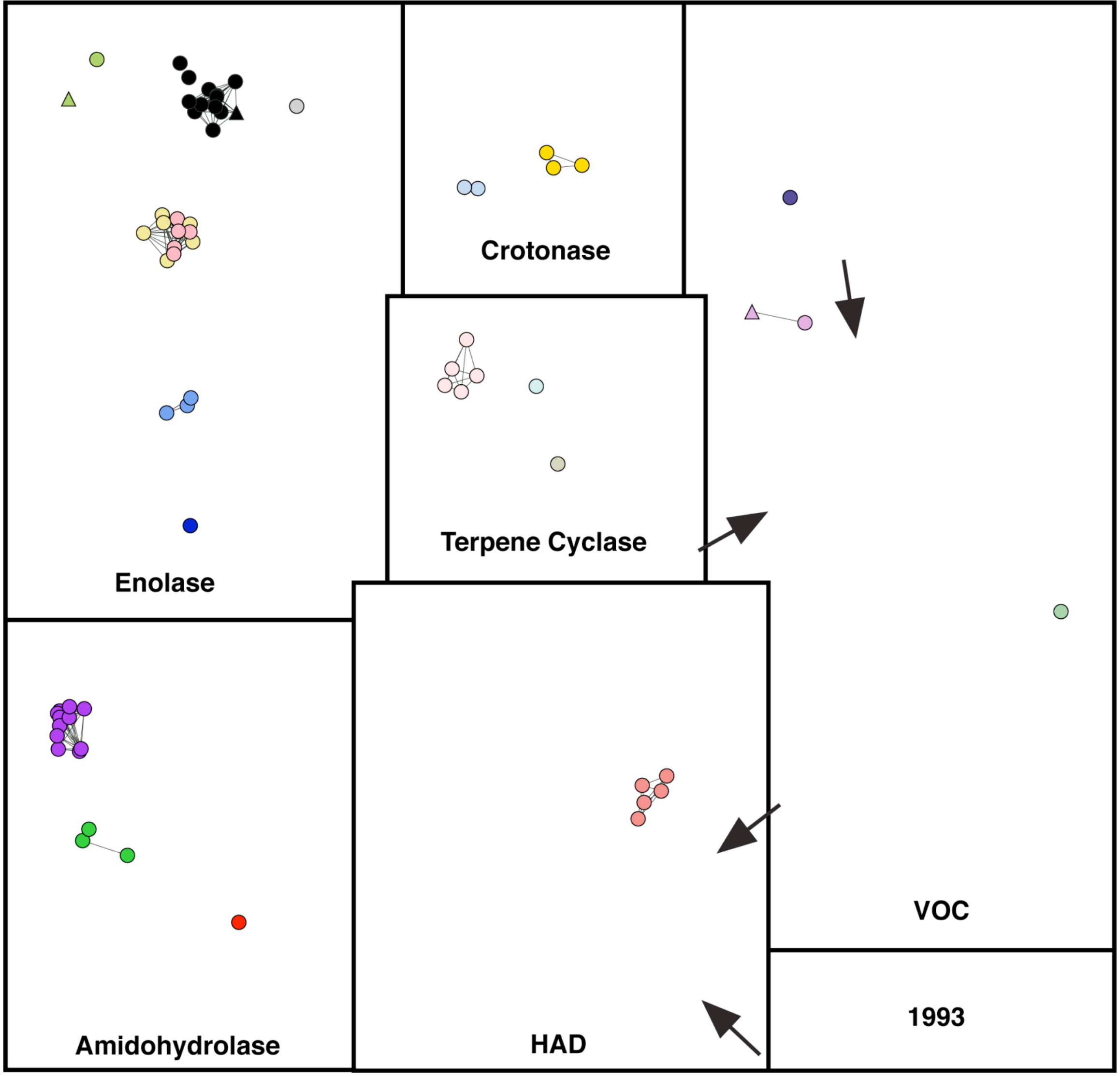


Figure B - 2. Sequence similarity network: years 1993-1994.

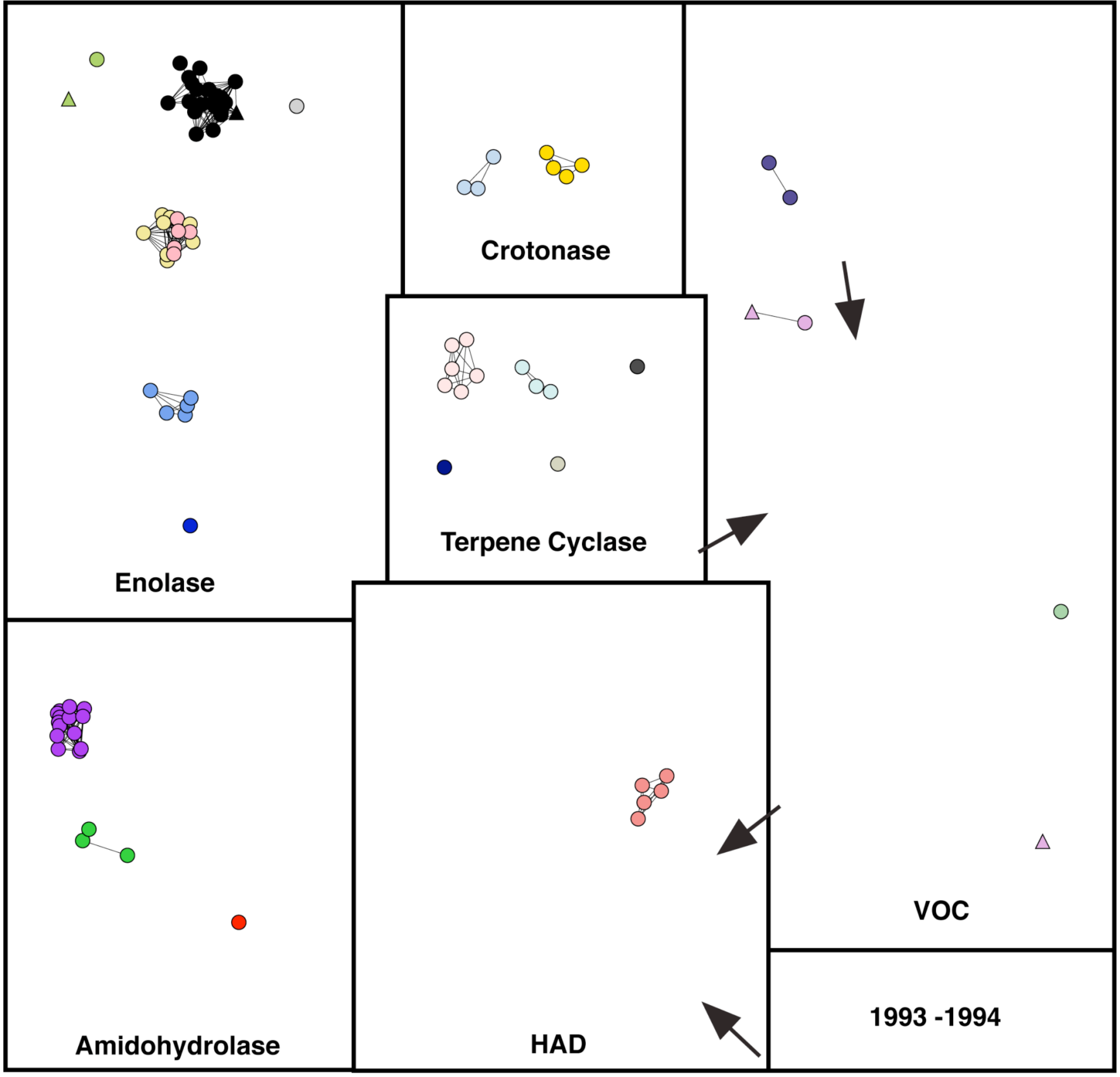


Figure B - 3. Sequence similarity network: years 1993-1995.

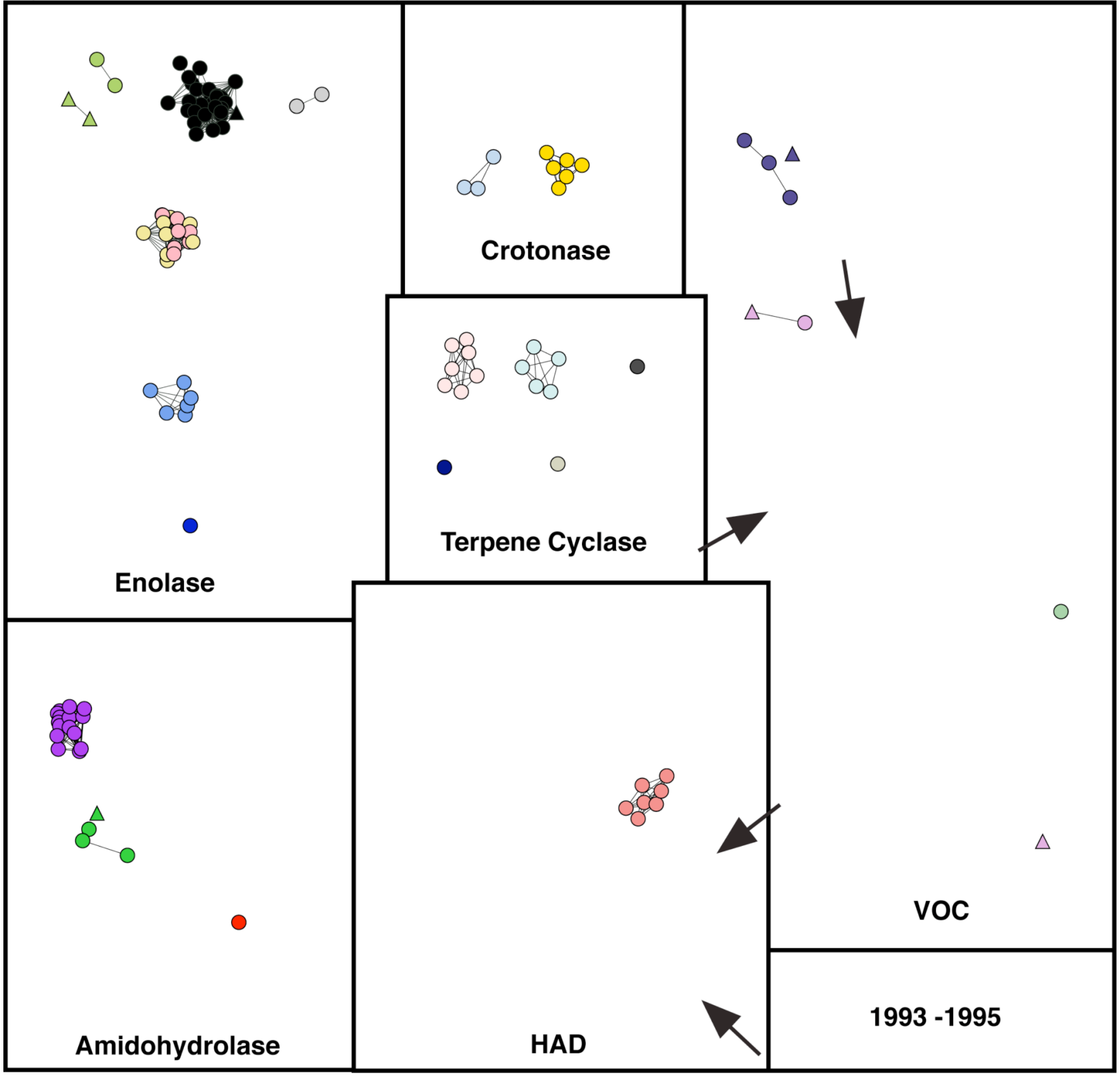


Figure B - 4. Sequence similarity network: years 1993-1996.

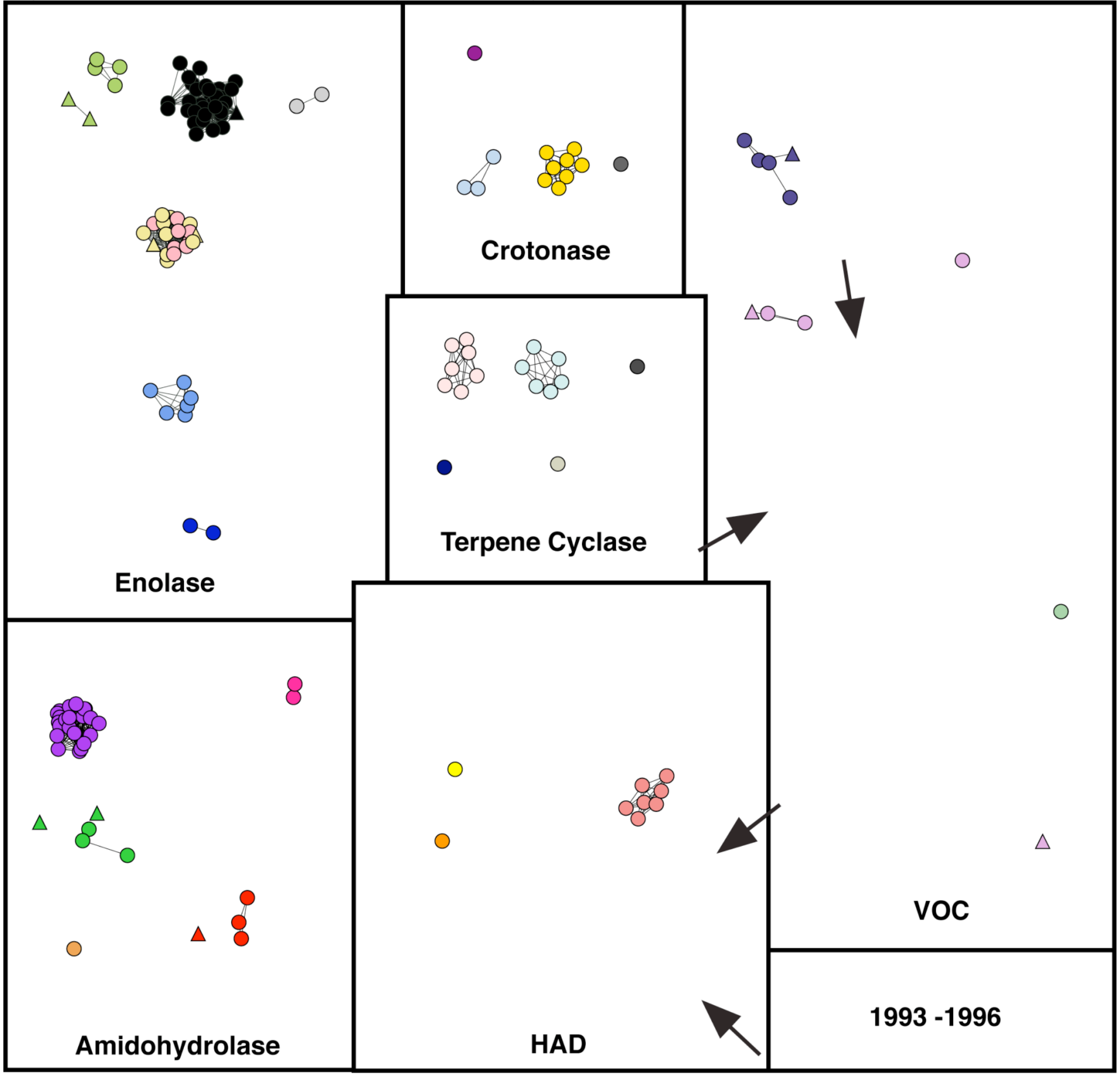


Figure B - 5. Sequence similarity network: years 1993-1997.

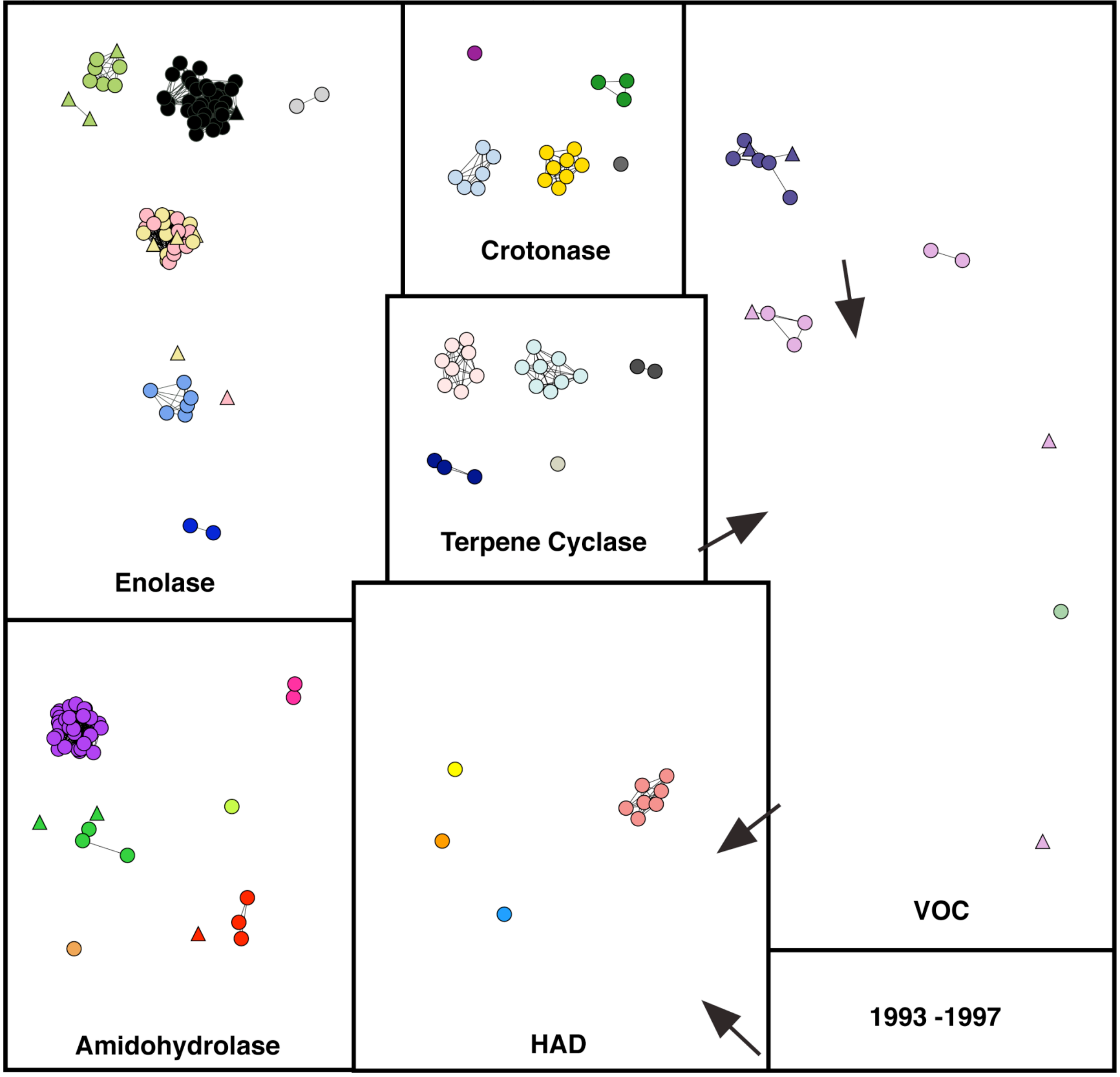


Figure B - 6. Sequence similarity network: years 1993-1998.

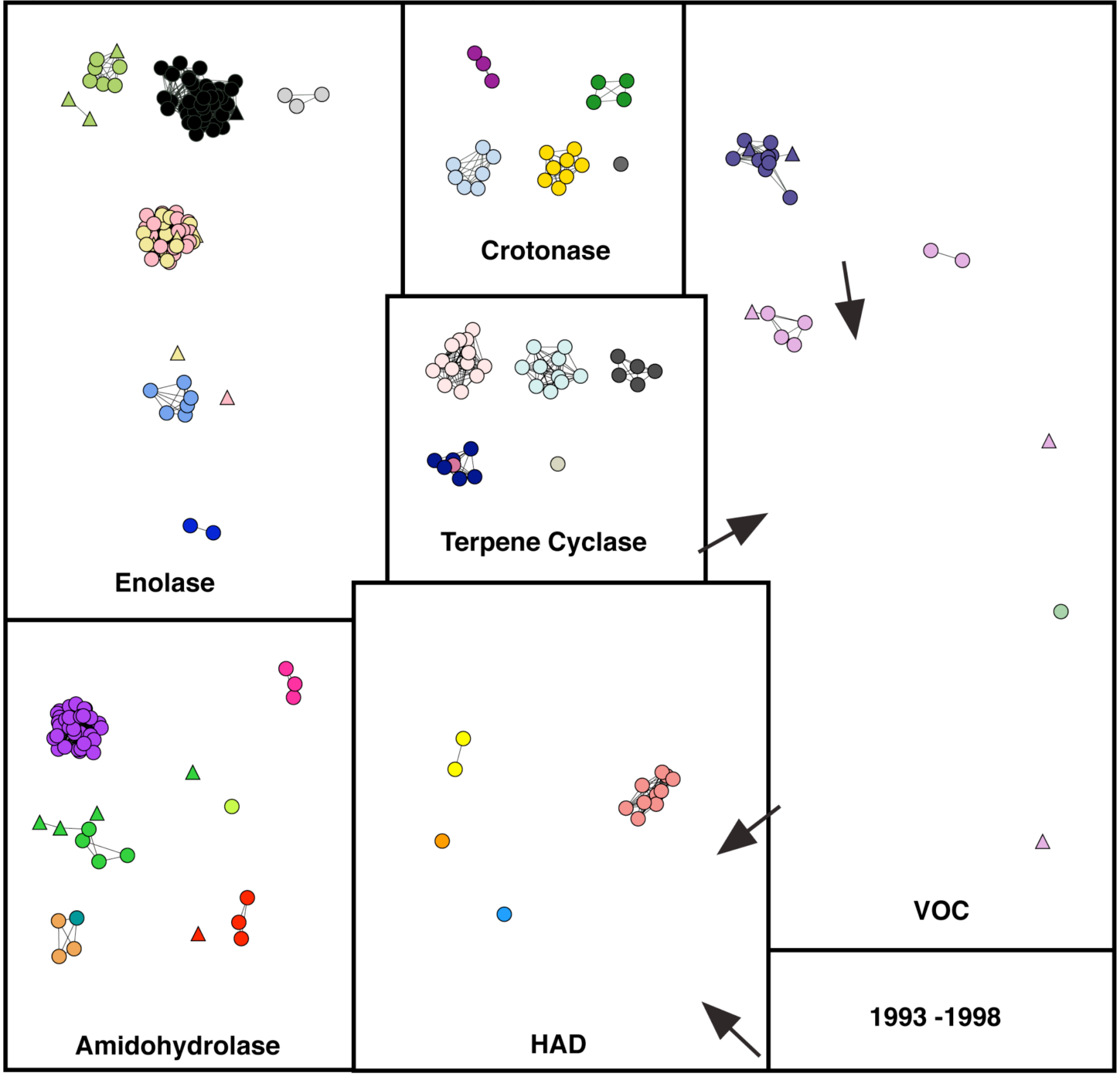


Figure B - 7. Sequence similarity network: years 1993-1999.

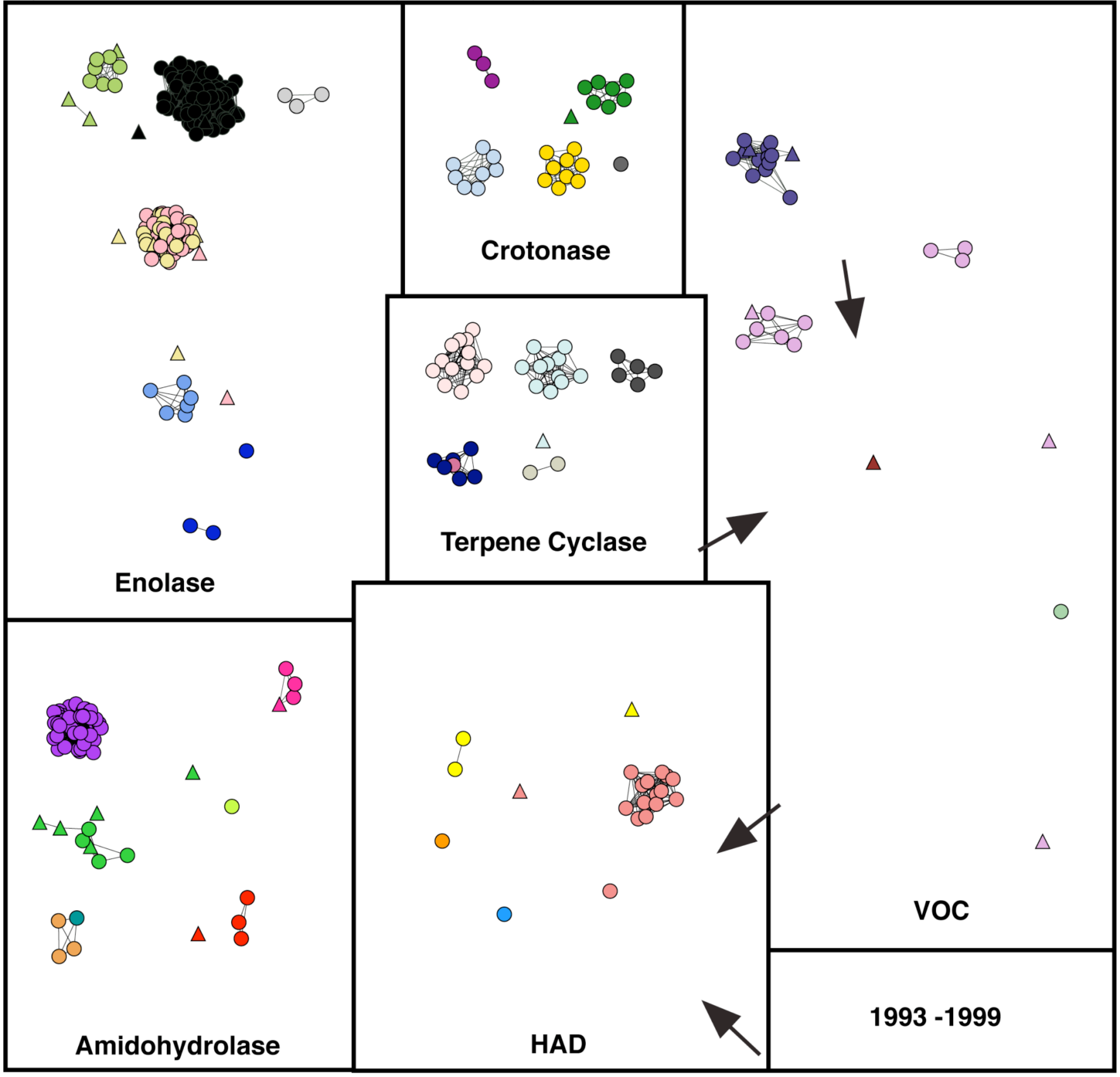


Figure B - 8. Sequence similarity network: years 1993-2000.

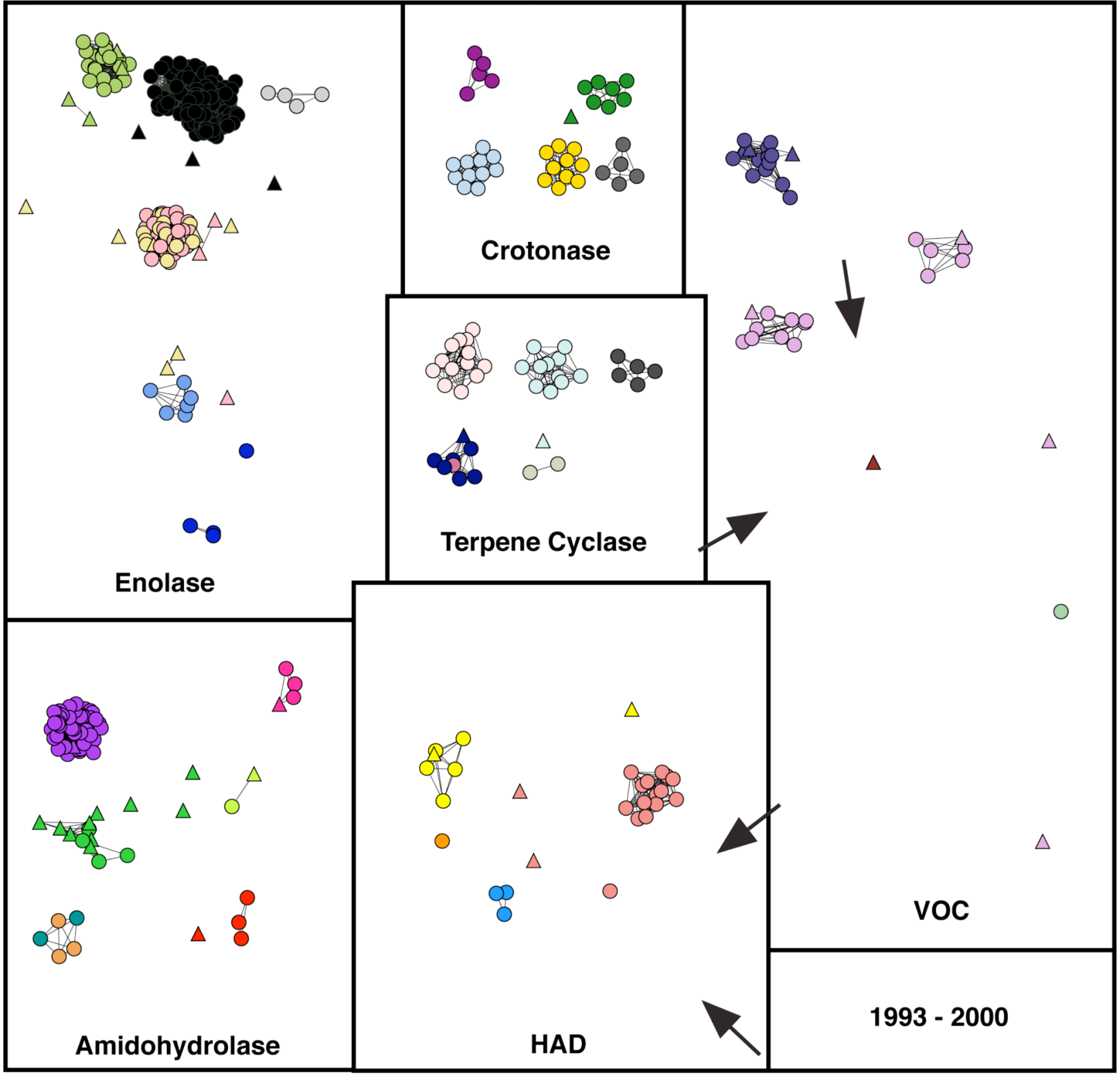


Figure B - 9. Sequence similarity network: years 1993-2001.

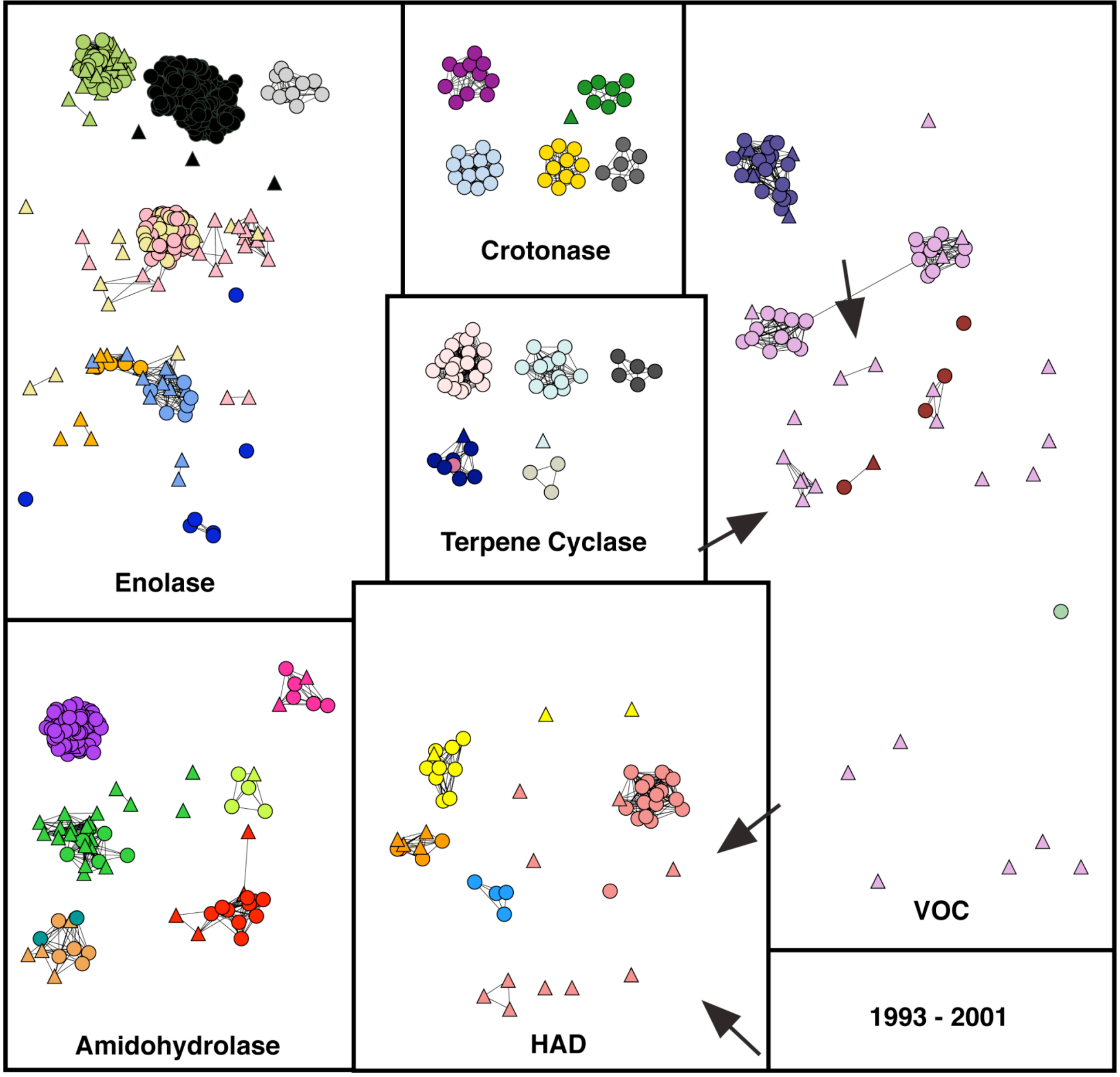


Figure B - 10. Sequence similarity network: years 1993-2002.

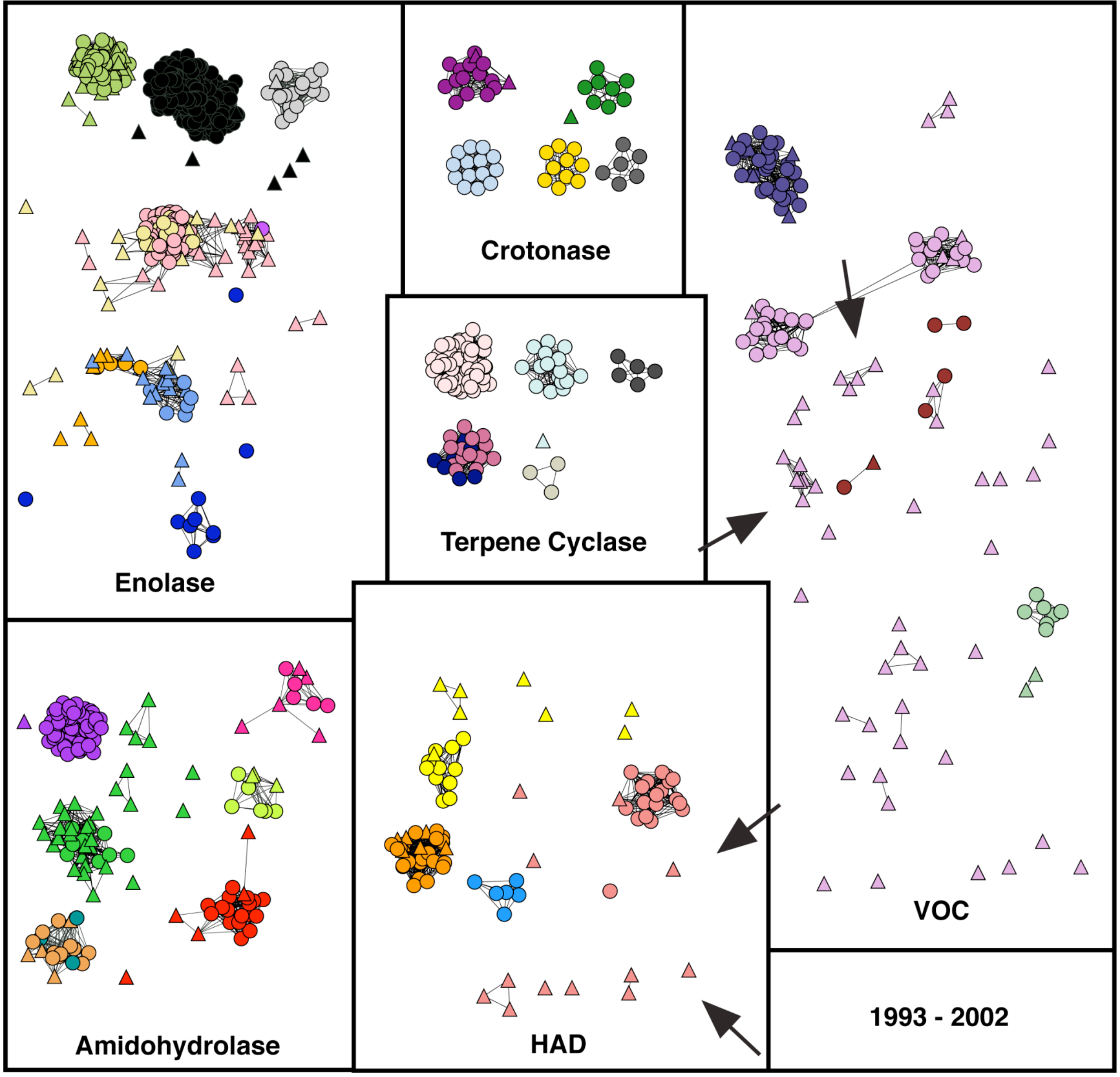


Figure B - 11. Sequence similarity network: years 1993-2003.

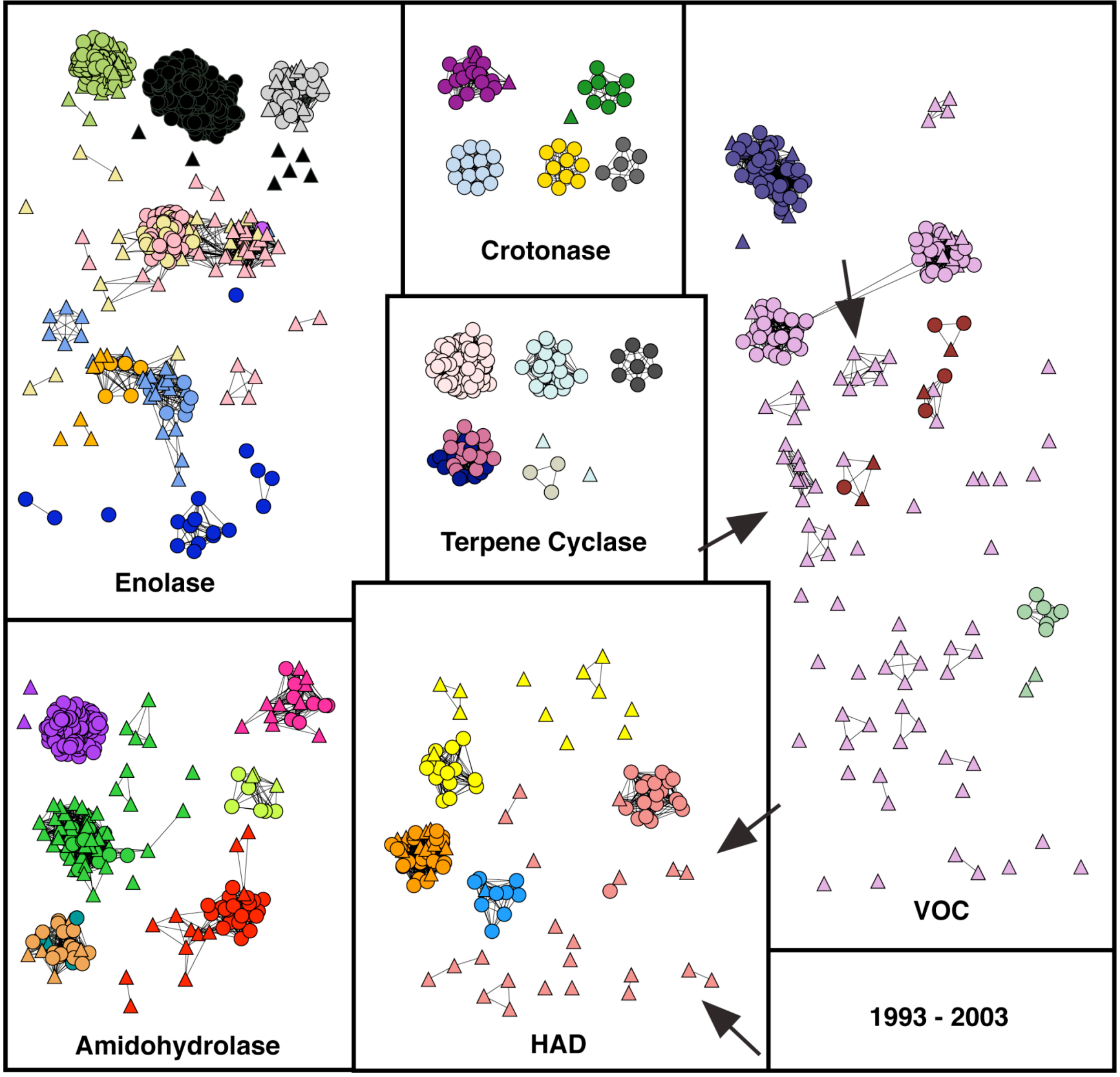


Figure B - 12. Sequence similarity network: years 1993-2004.

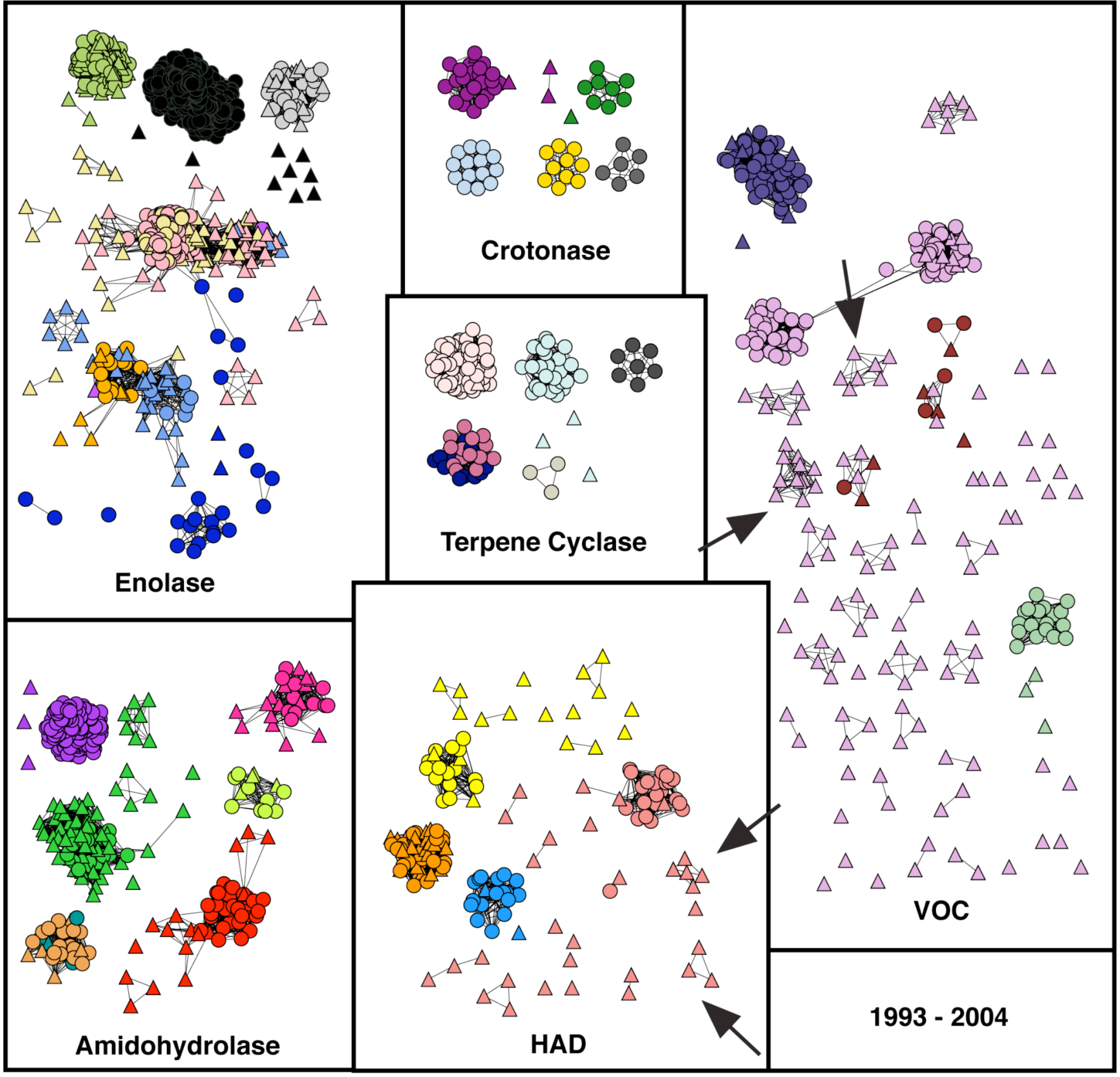
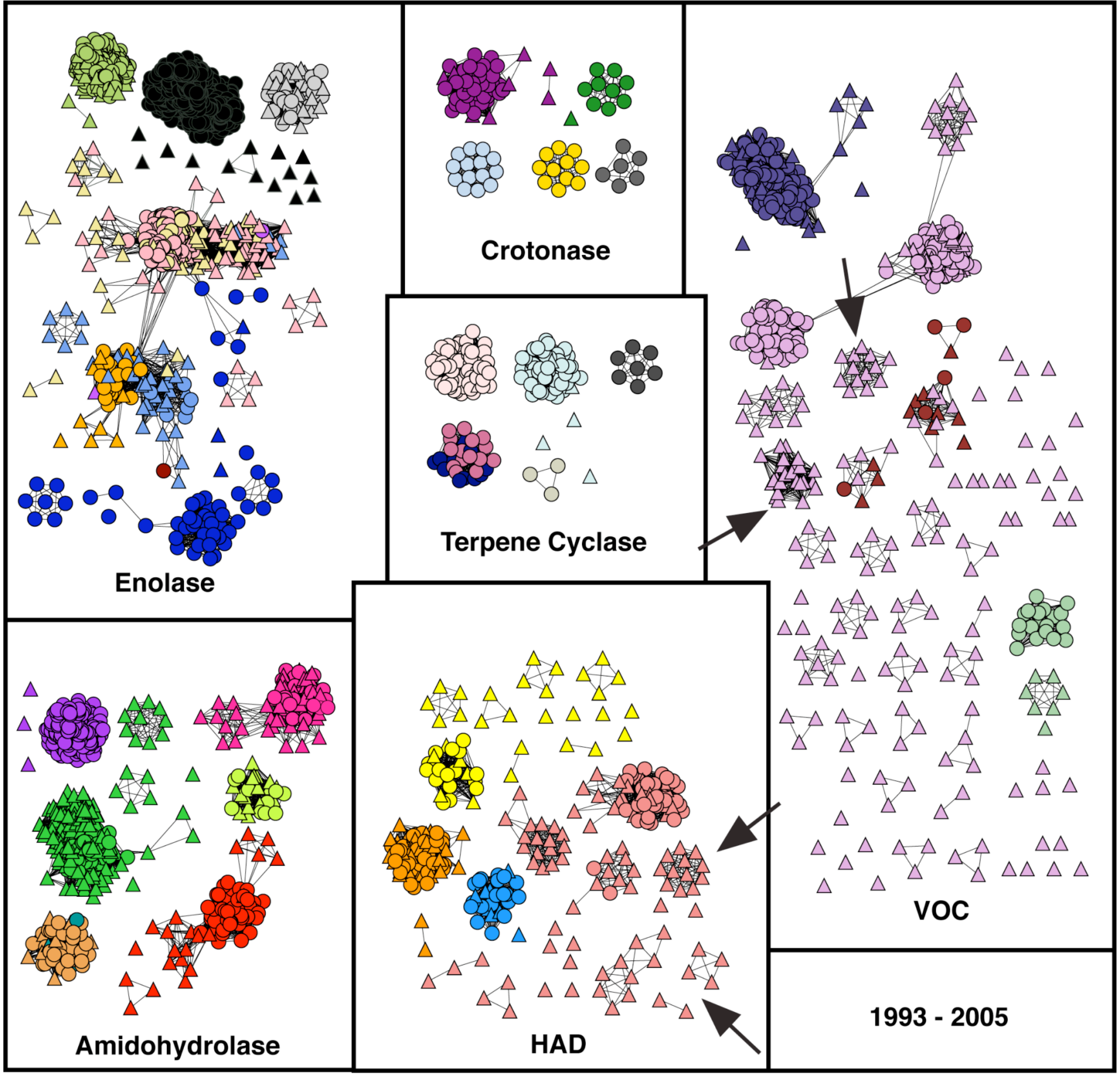


Figure B - 13. Sequence similarity network: years 1993-2005.



Appendix C. Program—checkKeywordMisannotation.py

```
#!/usr/bin/python2.4

"""checkKeywordMisannotation.py
  Usage: checkKeywordMisannotation.py --keyDictionary=<dictionaryFileName>
   --dbName=<databaseFileName> --runningPath=<path of working dir>
   --hmmPath=<path to the hmm files> --SFLDInfoFile=<file of all sfld info>
   --seqPath=<path to all fasta files in SFLD>
   --sequenceListFile=<file that lists all the fasta files>

  This program does the following:
     -inputs a keyword dictionary file
     -greps each of the keyword terms against the input databaseFileName
     -appends all of the grep results to one file keyDefLines.txt
     -parses keyDefLines.txt to get a file of non-redundant gi's keyGI.txt
     -take each gi, get its fasta file and run this file against all of the
        SFLD hmms (this produces a host of .hmmpfam files)
        => uses external program hmmpfam
        => uses external file filterHomolSeqs.py
        => uses external file parseHmmPfamKeyword.py



  INPUT:
   --keyDictionary=<dictionaryFileName>
   --dbName=<databaseFileName>
   --runningPath=<path of working dir>
   --hmmPath=<path to the hmm files>
   --SFLDInfoFile=<file of all sfld info>
   --seqPath=<path to all fasta files in SFLD>
   --sequenceListFile=<file that lists all the fasta files>
  OUTPUT:
     <keyDefLines.txt>: this is the file of all of the deflines that contain
     all of the keywords in the dictionaryFileName file.

     <keyGI.txt>: a non-redundant list of gi's that came up in the keyword
     search. These gi's are parsed from the keyDefLines.txt file

     <gi.hmmpfam>: each gi in keyGI.txt will be run against all of the SFLD
     hmm's using hmmpfam. the output of each run will be 'gi'.hmmpfam

     <dictionaryFileName.Results>: the parsed output of the found gi's
     format:
```

```
    Uses some modified code from updateSFLD.py by Shoshana Brown

    Alexandra M. Schnoes 04.12.05
    Last modified: 04.18.06 (AMS)

    """

import sys
import os
import os.path
import string
import getopt
import filterHomolSeqs
import parseHmmPfamKeyword


###############################################################################
# checkArg
###############################################################################
def checkArg(argv):
    """Exit with error and print usage if not enough arguments."""
    #am supposed to have 9 arguments assuming that the options are written
    #option=something
    #also assume that path is passed in with trailing '/'

    errorString = """Usage: checkKeywordMisannotation.py --keyDictionary=<dictio
    --dbName=<databaseFileName> --runningPath=<path of working dir>
    --hmmPath=<path to the hmm files> --SFLDInfoFile=<file of all sfld info>
    --seqPath=<path to all fasta files in SFLD>
    --sequenceListFile=<file that lists all the fasta files>"""

    if len(argv) == 10:
        pass
    else:
        print errorString
        sys.exit(1)


###############################################################################
# findKeywords
###############################################################################
def findKeywords(defFileName, keyList, dbFileName):
    """"Find the keywords in the database file and write them to a file"""

    print "findkeywords(defFileName, keyDictFileName, dbFileName)"
```

```
    sys.stdout.flush()

    os.system("rm -f " + defFileName)
    outFile = open(defFileName, 'w')
    for key in keyList:
        #os.system("grep -i \'%s\' %s >> %s" %(key, dbFileName, defFileName) )
        keyInfoObj = os.popen("grep -i \'%s\' %s" % (key, dbFileName))
        keyInfoStrs = keyInfoObj.read()
        outFile.write(keyInfoStrs)
        outFile.flush()
        keyInfoObj.close()

    outFile.close()

#######################################################################
# parseKeywordFile
#######################################################################
def parseKeywordFile(keyFileName):
    """Return the non-redundant list of gi's from the deflines in the file keyFileName
    print "parseKeywordFile(keyFileName)"
    sys.stdout.flush()

    inFile = open(keyFileName, "r")

    giList = []
    while 1: # DO NOT read in file all at once.... much too large!
        line = inFile.readline()
        #print line
        if not line: break

        gi_count = line.count('>gi|')
        #print "gi_count: " + str(gi_count)
        if gi_count > 1:
            while gi_count != 0:
                index_1 = line.find('>gi|')
                #print 'line: ' + line
                #print 'index_1: ' + str(index_1)
                if index_1 != -1:
                    start_next = index_1 + 1
                    index_2 = line[start_next :].find('>gi|')
                    #print "index_2 " + str(start_next + index_2)
                    if index_2 != -1:
                        #print "line 2: " + line[index_1 : (start_next + index_2)]
                        tmpList = line[index_1 : (start_next + index_2)].split('|')
                        if (str(tmpList[1])) not in giList:
                            giList.append(str(tmpList[1]))
```

```
                    else:
                        tmpList = line[index_1 :].split('|')
                        if (str(tmpList[1])) not in giList:
                            giList.append(str(tmpList[1]))

                    gi_count = gi_count - 1
                    line = line[(index_1 + 1) :]

                else: # don't think I should ever get here
                    #print "at break point I didn't think should happen"
                    break

        else:
            tmpList = line.split('|') #split on delimiter
            if len(tmpList) <  2: #it's not a gi line
                pass
            else:
                if (str(tmpList[1])) not in giList: #make non-redundant
                    giList.append(str(tmpList[1]))  #gi number in second position

    #print giList
    return giList

#######################################################################
# printGIList(giList, giFileName)
#######################################################################
def printGIList(giList, giFileName):
    """Print to giFileName the gi list"""
    print "printGIList(giList, giFileName)"
    sys.stdout.flush()

    outFile = open(giFileName, "w")

    for entry in giList:
        outFile.write(entry)
        outFile.write('\n')

    outFile.close()

#######################################################################
# getFastaDefLline
#######################################################################
def getFastaDefLine(fastaFileName, entry):
    """Return a list with fasta file name and the definition line from the fasta File"""
    #print "getFastaDefLine(fastaFileName, entry)"
```

```
    fastaDefList = []
    fastaFile = open(fastaFileName, "r")
    defLine = fastaFile.readline()
    defLine = defLine[:-1] #strip off the endl
    fastaDefList.extend([entry, defLine])
    fastaFile.close()

    return fastaDefList


##################################################################
# makeFastaFiles
##################################################################
def makeFastaFiles(giList, dbName, runningPath):
    """Return a list of fasta files made from the gi's in giList"""
    print "makeFastaFiles(giList, runningPath)"
    sys.stdout.flush()

    fastaList = []
    fastaDefDict = {}

    for entry in giList:
        fastaFileName = runningPath + entry + ".tmp.fa"
        os.system("fastacmd -d %s -tT -s%s > %s " % (dbName, entry, fastaFileNam
        fastaList.append(fastaFileName)
        fastaDefDict[fastaFileName] = getFastaDefLine(fastaFileName, entry)

    return fastaList, fastaDefDict

##################################################################
# runHmmPfam
##################################################################
def runHmmPfam(fastaList, hmmPath):
    """run hmmpfam for each file listed in fastaListFileName and return list of
    the hmmpfam files"""
    print "runHmmPfam(fastaList, hmmPath)"
    sys.stdout.flush()

    hmmpfamList = []

    #run hmmpfam
    for fastaFile in fastaList:
        cmd = "hmmpfam -E100 " + hmmPath + "all.hmm " + fastaFile + " > " + fasta
        os.system(cmd)
        hmmpfamList.append(fastaFile + ".hmmpfam")
```

```
    return hmmpfamList

############################################################################
# removeTmpFastaFiles
############################################################################
def removeTmpFastaFiles(fastaListFileName):
    """remove the fasta files listed in fastaListFileName"""
    print "removeTmpFastaFiles(fastaListFileName)"
    infile = open(fastaListFileName, 'r')

    for line in infile.readlines():
        line = line[:-1]
        os.system("rm -f " + line)

    infile.close()
############################################################################
# getSFLDInfo
############################################################################
def getSFLDInfo(infoFile):
    """Return a dict of SFLD hmm and related info.
    sfldHmmDict = [name, fam, sub, sf, align_file, cons_res_list]"""
    print "getSFLDInfo(infoFile)"
    sys.stdout.flush()

    sfldHmmDict = {}
    inFile = open(infoFile, 'r')
    firstTime = 1 #true
    consResList = []
    hmm = "null"
    holdHMM = "null"
    name = "null"
    fam = "null"
    sub = "null"
    sf = "null"
    align_file = "null"

    for line in inFile.readlines():
        line = line[:-1]
        tmpList = line.split(';')
        if len(tmpList) > 7:  # does the line have something in it
            hmm = tmpList[0]
            if firstTime == 1:
                firstTime = 0
                holdHMM = hmm
                name = tmpList[1]
                fam = tmpList[2]
```

```
                sub = tmpList[3]
                sf = tmpList[4]
                align_file = tmpList[5]
                consResList.append([tmpList[6], tmpList[7]])

            elif hmm == holdHMM:
                name = tmpList[1]
                fam = tmpList[2]
                sub = tmpList[3]
                sf = tmpList[4]
                align_file = tmpList[5]
                consResList.append([tmpList[6], tmpList[7]])
            else:
                #save old data
                sfldHmmDict[holdHMM] = [name, fam, sub, sf, align_file, consResList]
                #get the new stuff
                holdHMM = hmm
                consResList = []
                name = tmpList[1]
                fam = tmpList[2]
                sub = tmpList[3]
                sf = tmpList[4]
                align_file = tmpList[5]
                consResList.append([tmpList[6], tmpList[7]])
    # reached the end of the file
    # save the last hmm info
    #print "Reach last else...hmm sfld dict"
    #sys.stdout.flush()

    sfldHmmDict[holdHMM] = [name, fam, sub, sf, align_file, consResList]


    #for hmm in sfldHmmDict.keys():
    #   print "HMM"
    #   print hmm
    #   sys.stdout.flush()

        #print ":"
        #print sfldHmmDict[hmm]

    return sfldHmmDict

####################################################################
# getUngappedSeqsAndConsRes
####################################################################
def getUngappedSeqs(sfldDict, path):
```

```
    """Return a sfld dict with representative sequences for each SFLD alignment.
    sfldDict = [name, fam, sub, sf, align_file, Cons_Res_list, ungappedSeq]"""
    print "getUngappedSeqs(sfldDict, path)"
    sys.stdout.flush()

    for hmm in sfldDict.keys():
        info_list = sfldDict[hmm] #get the list that matches that hmm
        align_File = info_list[4] #get the alignment file name
        if align_File == 'None':
            align_File = None

        if align_File != None:
            gappedRepSeq = filterHomolSeqs.getRepSeq(path + align_File)
            #print gappedRepSeq
            ungappedSeq = filterHomolSeqs.removeGaps(gappedRepSeq)
            #print ungappedSeq
            res_list = info_list[5]
            #print res_list
            #get the sequence numbers in the ungapped sequence
            ungapped_res_list = filterHomolSeqs.getUngappedNumbers(res_list, gap
            #print ungapped_res_list
            #print hmm

            sfldDict[hmm][5] = ungapped_res_list
            #print "ungapped_res_list"
            #print ungapped_res_list
            #print "\n"
            sfldDict[hmm].append(ungappedSeq)

    return  sfldDict

######################################################################
# getSeq
######################################################################
def getSeq(fastaFileName):
    """Return the sequence from the fasta file as a string"""
    #print "getSeq(fastaFileName)"
    fastaFile = open(fastaFileName, "r")
    #get the defline
    defLine = fastaFile.readline()

    AAline = fastaFile.readline() #get the first AA line
    AAline = AAline[:-1]
    line = fastaFile.readline()
    while line:
        line = line[:-1]
```

```
        AAline = AAline + line
        line = fastaFile.readline()

    return AAline


###########################################################################
# addSeqAndDefLine
###########################################################################
def addSeqAndDefLine(hmm_data, fastaDefDict):
    """Return hmm_data with added gi num, sequence and definition line"""
    print "addSeqAndDefLine(hmm_data, fastaDefDict)"
    sys.stdout.flush()

    for entry in hmm_data:
        #actually I want the info even if there were no hits
        #if entry[1] == '[no': # there were no hits for this seq, move on
            #pass
        #else:
            fastaFileName = entry[0]
            #print "fastaFileName: "
            #print fastaFileName
            #print "entry: "
            #print entry
            fastaList = fastaDefDict[fastaFileName]
            #print fastaList
            gi = fastaList[0]
            #print gi
            defLine = fastaList[1]
            seq = getSeq(fastaFileName)
            #add the info to entry
            entry.insert(1, defLine)
            entry.insert(1, str(gi))
            entry.insert(len(entry), str(len(seq)))
            entry.insert(len(entry), seq)

    #print 'addSeqAndDefLine hmm_data '
    #print hmm_data
    #sys.stdout.flush()

    return hmm_data

###########################################################################
# parseEFDList
###########################################################################
def parseEFDList(efdFile):
```

```
    """Get the Info from the EFD file
    <gi> <name> <species> <fam ID> <fam ev code> <fam name> <sub id> <sub
    <sf id> <sf ev code> <sf name>"""

    print"parseEFDList"
    sys.stdout.flush()

    efdDict = {}

    inFile = open(efdFile, 'r')
    gi = "null"
    famID = "null"
    famEvCode = "null"
    famName = "null"
    subID = "null"
    subName = "null"
    sfID = "null"
    sfEvCode = "null"
    sfName = "null"

    for line in inFile.readlines():
        line = line[:-1]
        tmpList = line.split(';')
        if len(tmpList) > 7:  # does the line have something in it
            gi = tmpList[0]
            famID = tmpList[3]
            famEvCode = tmpList[4]
            famName = tmpList[5]
            subID = tmpList[6]
            subName = tmpList[7]
            sfID = tmpList[8]
            sfEvCode = tmpList[9]
            sfName = tmpList[10]

            efdDict[gi] = [famID, famEvCode, famName, subID, subName, sfID, sfEvC

    return efdDict




########################################################################
# getEvidenceCodes
########################################################################
def getEvidenceCodes(hmm_data_list, EFDFile):
    """get the evidence codes for any sequences that are in the sfld
```

```
hmm_data_list
<fastaFile> <accession> <defline> <HMM name> <score> <evalue> <hmm db
<seq len> <consRes> <seqFile> <inSFLD> <Sequence>
efddict
<fam ID> <fam ev code> <fam name> <sub id> <sub name>
<sf id> <sf ev code> <sf name>
"""
print 'getEvidenceCodes'
efdDict = parseEFDList(EFDFile)

for entry in hmm_data_list:
    sfld_seq_file = entry[9]
    period_index = sfld_seq_file.find('.')
    if period_index != -1: #there is a file
        gi = sfld_seq_file[: period_index]

        if gi in efdDict.keys():
            efd_entry = efdDict[gi]
            entry.insert(len(entry) -1, efd_entry[0])
            entry.insert(len(entry) -1, efd_entry[1])
            entry.insert(len(entry) -1, efd_entry[2])
            entry.insert(len(entry) -1, efd_entry[3])
            entry.insert(len(entry) -1, efd_entry[4])
            entry.insert(len(entry) -1, efd_entry[5])
            entry.insert(len(entry) -1, efd_entry[6])
            entry.insert(len(entry) -1, efd_entry[7])
        else: #it's not in the SFLD
            entry.insert(len(entry) -1, '[]')
            entry.insert(len(entry) -1, '[]')
            entry.insert(len(entry) -1, '[]')
            entry.insert(len(entry) -1, '[]')
            entry.insert(len(entry) -1, '[]')
            entry.insert(len(entry) -1, '[]')
            entry.insert(len(entry) -1, '[]')
            entry.insert(len(entry) -1, '[]')
    else: #there isn't a file
        entry.insert(len(entry) -1, '[]')
        entry.insert(len(entry) -1, '[]')
        entry.insert(len(entry) -1, '[]')
        entry.insert(len(entry) -1, '[]')
        entry.insert(len(entry) -1, '[]')
        entry.insert(len(entry) -1, '[]')
        entry.insert(len(entry) -1, '[]')
        entry.insert(len(entry) -1, '[]')

return hmm_data_list
```

```
####################################################################
# reformatConsRes
####################################################################
def reformatConsRes(sfldDict):
    """Return the sfld dict with reformated cons residues
    modified version of shoshona brown's code."""
    #print "reformatConsRes(sfldDict)"
    aaDict = {}
    aaDict['ALA'] = 'A'
    aaDict['ARG'] = 'R'
    aaDict['ASN'] = 'N'
    aaDict['ASP'] = 'D'
    aaDict['CYS'] = 'C'
    aaDict['GLN'] = 'Q'
    aaDict['GLU'] = 'E'
    aaDict['GLY'] = 'G'
    aaDict['HIS'] = 'H'
    aaDict['ILE'] = 'I'
    aaDict['LEU'] = 'L'
    aaDict['LYS'] = 'K'
    aaDict['MET'] = 'M'
    aaDict['PHE'] = 'F'
    aaDict['PRO'] = 'P'
    aaDict['SER'] = 'S'
    aaDict['THR'] = 'T'
    aaDict['TRP'] = 'W'
    aaDict['TYR'] = 'Y'
    aaDict['VAL'] = 'V'

    for hmm in sfldDict.keys():
        #consResList = sfldDict[hmm][5]
        for consResPair in sfldDict[hmm][5]:
            aaTypeString = consResPair[1]
            #print aaTypeString
            origAAList = string.split(aaTypeString, ",")
            reformattedAAList = []
            for aa in origAAList:
                aa = string.strip(aa)
                if len(aa) > 1:
                    try:
                        reformattedAAList.append(aaDict[aa])
                    except KeyError:
                        reformattedAAList.append('X')
                else:
```

```
                    reformattedAAList.append(aa)

            AA_num = consResPair[0]
            consResPair.pop()
            consResPair.pop()
            consResPair.insert(0,AA_num)
            consResPair.insert(1, reformattedAAList[:])
            #print "consResPair: "
            #print consResPair
            #print "\n"

        #sfldDict[hmm][5] = consResList
        #print sfldDict[hmm][5]
    return sfldDict
######################################################################
# checkIfConsRes
######################################################################
def checkIfConsRes(hmm_data_list, sfldDict, hmmPath):
    """Return data list that has marked whether the hits have conserved residues""
    print "checkIfConsRes(hmm_data_list, sfldDict, hmmPath)"
    sys.stdout.flush()

    for entry in hmm_data_list:
        if entry[1] == '[no': # there were no hits for this seq, add flag
            entry.insert((len(entry)-1), "nohits")
        elif entry[3] == '[no':
            entry.insert((len(entry)-1), "nohits")

        else:
            #print "ConsRes "
            #print entry
            fastaFileName = entry[0]
            hmm = entry[3]
            hmm_full = hmm + ".hmm"
            if (hmm_full.startswith("sub") and (hmm_full != 'subgroup112.listedited.fam
                entry.insert((len(entry)-1), "SUB, not check ConsRes")
            elif hmm_full == 'galD.hmm':
                entry.insert((len(entry)-1), "don't use, bad hmm")
            elif hmm_full == 'hydroxyphenylpyruvateDSub.60.hmm':
                entry.insert((len(entry)-1), "SUB, not check ConsRes")
            elif hmm_full == 'fosfoResSub.90.hmm':
                entry.insert((len(entry)-1), "SUB, not check ConsRes")
            elif hmm_full == 'kaurene.hmm':
                entry.insert((len(entry)-1), "FAM, no conserved res")
            elif hmm_full == 'mmceSub.90.hmm':
                entry.insert((len(entry)-1), "SUB, not check ConsRes")
```

```
elif hmm_full == 'AtzA.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'extraDioxSub.40.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'glyoxalaseISub.60.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'ureaseSmaller.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'dichlorohydroquinoneDSub.90.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == '4nitrophenylPhosphataseLike.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'atpase.exfgh.30.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'phosphataselike2.ref.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'phosphataselike3.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'hadsub.90.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'phosphataselike1.ref.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'enolasePhosphataseLike.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'epoxideHNLike.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'phosphonataseLike.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'polynucleotide5HKLike.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'nucleotidaseLike.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'IadSub.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'AdeC.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'NagAAgaASubShortFiltered.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'Daa.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'imidazolonepropionase.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'AtzB.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'AtzATriATrzA.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
```

```
elif hmm_full == 'Gda.90.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'Cyda.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'd-hydantoinaseSub.90.ref.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'dihydroorotase1.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'allantoinase.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'dihydroorotase2.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'phosphotriesterase.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'AMPda.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'Ada.90.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'dihydroorotase3.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'YecMSub.90.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'monoterpenes.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'sesquiterpenes.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'diterpenes.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'triterpenes.hmm':
    entry.insert((len(entry)-1), "SUB, not check ConsRes")
elif hmm_full == 'aminophenolD.90.hmm':
    entry.insert((len(entry)-1), "NOT SURE WHAT THIS IS")
else:
    sfld_list = sfldDict[hmm_full]
    repSeq = sfld_list[6]
    tmp_file = fastaFileName + ".temp"
    short_def_file = fastaFileName + ".short"
    os.system("cp %s %s" % (fastaFileName, tmp_file))
    filterHomolSeqs.addRepSeq(tmp_file, repSeq)
    alignFileName = fastaFileName + ".align"
    os.system("inspectDefline.py %s -o%s" % (tmp_file, short_def_file))
    os.system("mv %s %s" %(short_def_file, tmp_file))
    os.system("hmmalign -o %s  %s %s > screenOut" % (alignFileName, h
    consResList = sfld_list[5]
    validList, removedList = filterHomolSeqs.checkAlignmentForConsRes(
    if validList:
```

```
                    entry.insert((len(entry)-1), "VALID")
                else:
                    #print validList
                    #print removedList
                    #print consResList

                    entry.insert((len(entry)-1), "NOT_valid")

    os.system("rm -f *.temp")
    #print hmm_data_list
    return hmm_data_list

####################################################################
# checkIfInSFLD
####################################################################
def checkIfInSFLD(hmm_data_list, seqPath, sequenceListFile, runningPath):
    """Return data list in which it is marked if the hit is already in the sfld"""
    print "checkIfInSFLD(hmm_data_list, seqPath, sequenceListFile, runningPath)"
    sys.stdout.flush()
    seqFileList = filterHomolSeqs.getFileNameList(sequenceListFile)
    for entry in hmm_data_list:
        #actually I want to know if it was in the sfld or not even if there are no
        #hits
        #if entry[1] == '[no': # there were no hits for this seq, move on
         #   pass
        #else:
            #print "inSFLD "
            #print entry
            fastaFileName = entry[0]
            notOne = 1
            for seq_entry in seqFileList:
                seqFastFileName = seqPath + seq_entry
                commonList = filterHomolSeqs.getCommonSeqs(fastaFileName, seqFa
                if commonList: #the list exists, hit is in the SFLD
                    entry.insert((len(entry)-1), seq_entry)
                    entry.insert((len(entry)-1), 'IN_SFLD')
                    notOne = 0
                    break

            if notOne == 1: #this is not in the sfld
                entry.insert((len(entry)-1), '[]')
                entry.insert((len(entry)-1), '[]')

    #print hmm_data_list
    return hmm_data_list
```

```
############################################
# determineDomains
############################################
def determineDomains(hmm_data_list):
    """Return hmm data with domain info added"""
    print "determineDomains(hmm_data_list)"
    new_hmm_data_list = []
    for entry in hmm_data_list:
        if entry[1] == '[no': # there were no hits for this seq, move on
            pass
        else:
            #print entry
            fastaFileName = entry[0]
            outputFileName = runningPath + "rps.out"
            gi = entry[1]
            total_seq_len = len(entry[-1])

            os.system("rpsblast -i %s -d Cdd -m 8 -o %s" % (fastaFileName, outputFil
            hitList = filterHomolSeqs.parseRPSBlast(outputFileName)
            #print hitList

            hit_1 = hitList[0]
            entry_copy = entry[:]
            for item in hit_1:
                entry_copy.insert((len(entry_copy)-1), str(item))
            entry_copy.insert((len(entry_copy)-1), str(total_seq_len))
            new_hmm_data_list.append(entry_copy)
            hitList.pop(0)

            for hit in hitList:
                entry_copy = entry[:]
                for item in hit:
                    entry_copy.insert((len(entry_copy)-1), str(item))
                entry_copy.insert((len(entry_copy)-1), str(total_seq_len))
                entry_copy[1] = '[dup]'
                entry_copy[2] = '[dup]'
                entry_copy[3] = '[dup]'
                entry_copy[4] = '[dup]'
                entry_copy[5] = '[dup]'
                entry_copy[6] = '[dup]'
                entry_copy[7] = '[dup]'
                entry_copy[8] = '[dup]'
                entry_copy[9] = '[dup]'
                new_hmm_data_list.append(entry_copy)

    return new_hmm_data_list
```

```
#######################################################################
# printTheResults
#######################################################################
def printTheResults(hmm_data_list, resultsFile):
    """Print the results in the hmm_data_list to a file."""
    print "printTheResults(hmm_data_list, resultsFile)"
    sys.stdout.flush()

    fileOut = open(resultsFile, "w")
    for entry in hmm_data_list:
        #print entry
        #sys.stdout.flush()

        listString = '\t'.join(entry)
        fileOut.write(listString)
        fileOut.write("\n")

    fileOut.close()

#######################################################################
# getTheHmmPfamData
#######################################################################
def getTheHmmPfamData(hmmPfamFileList):
    """Return the data from all of the HmmPfam Files as a list"""
    print "getTheHmmPfamData(hmmPfamFileList)"
    all_file_data_list = []
    for file in hmmPfamFileList:
        #print "File:   "
        #print file
        #sys.stdout.flush()

        data_list = parseHmmPfamKeyword.getHmmPfamData(file)
        #print "data_list "
        #print data_list
        #sys.stdout.flush()

        all_file_data_list.extend(data_list)

    #print "all_file_data_list...get the hmmpfam data "
    #print all_file_data_list
    return all_file_data_list


#######################################################################
# getKeyList
```

```
##############################################################
def getKeyList(keyDictFileName):
    """return list of keywords."""
    inFile = open(keyDictFileName, "r")
    keyList = []
    for line in inFile.readlines():
        line = string.strip(line)
        keyList.append(line)

    inFile.close()

    return keyList

##############################################################
# MAIN
##############################################################
def checkKeywordMisannotation(argv):
    """Main program"""
    checkArg(argv)
    shortOpts = ''
    longOpts = ['keyDictionary=', 'dbName=', 'runningPath=', 'hmmPath=', 'SFLDInf
    'alignPath=', 'seqPath=', 'sequenceListFile=', 'efdFile=']
    opts, args = getopt.getopt(sys.argv[1:], shortOpts, longOpts)

    for option, value in opts:
        if option in ('--keyDictionary'):
            keyDictFileName = value
        elif option in ('--dbName'):
            dbFileName = value
        elif option in ('--runningPath'):
            runningPath = value
        elif option in ('--hmmPath'):
            hmmPath = value
        elif option in ('--SFLDInfoFile'):
            infoFile = value
        elif option in ('--alignPath'):
            alignPath = value
        elif option in ('--seqPath'):
            seqPath = value
        elif option in ('--sequenceListFile'):
            sequenceListFile = value
        elif option in ('--efdFile'):
            EFD_file = value

    #search the db for keywords
    keyList = getKeyList(keyDictFileName)
```

```
print 'findKeywords'
sys.stdout.flush()
defLineFileName = runningPath + 'keyDefLines.txt'
findKeywords(defLineFileName, keyList, dbFileName)

#get the gi's of the keywords
print 'parseKeywordFile'
sys.stdout.flush()
giFileName = runningPath + "keyGI.txt"
giList = parseKeywordFile(defLineFileName)
printGIList(giList, giFileName)

#run hmmpfam on the gi's (get the fasta files first)
print 'makeFastaFiles'
sys.stdout.flush()
fastaList, fastaDefDict = makeFastaFiles(giList, dbFileName, runningPath)
print 'runHmmpfam'
sys.stdout.flush()
hmmPfamList = runHmmPfam(fastaList, hmmPath)
#print hmmPfamList
#sys.stdout.flush()


#parse the hmmpfam files
#first get the info from the SFLD info file
sfldDict = getSFLDInfo(infoFile)

#update the cons res and get the ungapped represent. sequence
#sfldDict = [name, fam, sub, sf, align_file, Cons_Res_list, ungappedSeq]
print 'getUngappedSeqandConsRes'
sys.stdout.flush()
sfldDict = getUngappedSeqs(sfldDict, alignPath)

#reformat the cons res
sfldDict = reformatConsRes(sfldDict)

#parse the actual hmmpfam files
#returns data in list
#[sequence file, hmm, score, evalue, hmm_db filename]
print 'getTheHmmPfamData'
sys.stdout.flush()
hmm_data_list = getTheHmmPfamData(hmmPfamList)


#add gi, sequence and def line info
```

```
    print 'addSeqAndDefline'
    sys.stdout.flush()
    hmm_data_list = addSeqAndDefLine(hmm_data_list, fastaDefDict)

    #print "SFLD dict"
    #print sfldDict
    #sys.stdout.flush()

    #check if hits have conserved residues
    print 'checkIfConsRes'
    sys.stdout.flush()
    hmm_data_list = checkIfConsRes(hmm_data_list, sfldDict, hmmPath)

    #check if hits are already in the sfld
    print 'checkIfINSFLD'
    sys.stdout.flush()
    hmm_data_list = checkIfInSFLD(hmm_data_list, seqPath, sequenceListFile, ru

    #get the evidence codes for any of the sequences that are in the sfld
    print 'getEvidenceCodes'
    sys.stdout.flush()
    hmm_data_list = getEvidenceCodes(hmm_data_list, EFD_file)

    #don't use this now
    #check what the domains are that the sequence hits
    #hmm_data_list = determineDomains(hmm_data_list, runningPath)

    #print out the results
    resultsFile = keyDictFileName + ".results"
    #print "results file"
    #print resultsFile
    #sys.stdout.flush()

    #print hmm_data_list
    printTheResults(hmm_data_list, resultsFile)

    #removeTmpFastaFiles(fastaListFileName)

checkKeywordMisannotation(sys.argv)
```

Appendix D. Program—filterHomolSeqs.py

```
#!/usr/bin/python2.3

"""filterHomolSeqs.py
  MOdified from updateSFLD.py

  Uses SFLD HMMs to search the NCBI nr database for new superfamily
  sequences & structures.  Validates putative superfamily members by
  aligning them to existing family/subgroup/superfamily HMMs, and
  determining whether they have the conserved catalytic residues.

  Input (Optional):
    superfamilyList: A file listing the names of the superfamilies to be
                     updated, one per line.  Names should be the same as
                     those stored in the SFLD.  Default = all
                     superfamilies are updated.
    <SFName>FalsePos.gi: A file listing gi numbers for false positive
                         sequences in a given superfamily.  If these
                         sequences are obtained by hmmsearch, they will be
                         discarded without further analysis.
                         Note: <SFName> should correspond to a superfamily
                         name, as listed in the SFLD.  This file name is not
                         specified on the command line, but the script will
                         automatically use it if it is in the directory
                         where the script is run.


  Output: (All .gi and .pdb files list items in comma delimited format)

    SF<SFID>Fam<FamID>ValidatedHits.gi: Lists the gi numbers for all sequence
    found via hmmsearch against the nr database (with HMMs corresponding to
    the superfamily specified by SFID, or families & subgroups within that
    superfamily).  Sequences listed in this file must not be found in the
    corresponding false positive file.  They must also have the highest
    similarity to the family HMM specified by FamID, out of all the family
    HMMs in the superfamily specified by SFID, and they must conserve the
    family specific catalytic residues listed in the SFLD.

    SF<SFID>Sub<SubID>ValidatedHits.gi: Lists the gi numbers for all sequences
    found via hmmsearch against the nr database (with HMMs corresponding to
    the superfamily specified by SFID, or families & subgroups within that
    superfamily).  Sequences listed in this file must not be found in the
    corresponding false positive file or any of the validatedHits files for
    families within the superfamily.  They must also have the highest
    similarity to the subgroup HMM specified by SubID, out of all the subgroup
    HMMs in the superfamily specified by SFID, and they must conserve the
    subgroup specific catalytic residues listed in the SFLD.
```

SF<SFID>ValidatedHits.gi: Lists the gi numbers for all sequences found via hmmsearch against the nr database (with HMMs corresponding to the superfamily specified by SFID, or families & subgroups within that superfamily). Sequences listed in this file must not be found in the corresponding false positive file or any of the validatedHits file for subgroups or families within the superfamily. They must also conserve the superfamily specific catalytic residues listed in the SFLD.

SF<SFID>NonvalidatedHits.gi: Lists the gi numbers for all sequences found vi hmmsearch against the nr database (with HMMs corresponding to the superfamily specified by SFID, or families & subgroups within that superfamily) that are not in the corresponding false positive file, and that could not be validated as superfamily members based on conservation of catalytic residues.

SF<SFID>ValidatedStructs.pdb: Lists the pdb identifiers for all pdb structures that have an amino acid sequence identical to a sequence from file SF<SFID>ValidatedHits.gi, and that are not already in the SFLD.

SF<SFID>Fam<FamID>ValidatedStructs.pdb: Lists the pdb identifiers for all structures that have an amino acid sequence identical to a sequence from file SF<SFID>Fam<FamID>ValidatedHits.gi, and that are not already in the SFLD.

SF<SFID>Sub<SubID>ValidatedStructs.pdb: Lists the pdb identifiers for all structures that have an amino acid sequence identical to a sequence from file SF<SFID>Sub<SubID>ValidatedHits.gi, and that are not already in the SFLD.

SF<SFID>NonvalidatedStructs.pdb: Lists the pdb identifiers for all structures that have an amino acid sequence identical to a sequence from file SF<SFID>NonvalidatedHits.gi, and that are not already in the SFLD.

SF<SFID>ExistingSeqStructs.txt: Lists the gi number and corresponding PDB identifier(s) for any sequences already in the SFLD that have an identical amino acid sequence to a structure that is not in the SFLD. The gi number is seperated from the corresponding PDB identifier(s) by a single tab. If there is more than one corresponding PDB identifier, the PDB identifiers are seperated by a single space.

Other important info
Need python modules written in lab
  alignment.py
blastparser.py
common.py

```
    inspectDefline.py
    proteinGroup.py
    protein.py
    reducePwpidSander.py
    simPsiBlParse.pl

    Need to have programs set up
        NCBI (blast etc)
        (remember to have .ncbirc file in directory and set up correctly)
    HMMER package
         (make sure to have the fasta databases that this needs)

    Need to have variable $BLASTDB set appropriate e.g.
        setenv BLASTDB /usr/local/Blast/blastDBDir/

    Need to change following variables to propper locations
        hmmPath
    alignPath


Author: Shoshana Brown (some functions based on SFLDsql.py code by Scott Pe
Last Modified: 6/8/04

Modified: Alexandra M. Schnoes 8/26/04
    Added comments and changed paths
    Alexandra M. Schnoes 01/31/05
    Translating code to NOT use mysql so it can run on the clusters

"""

import sys
import os
import os.path
import string
import re
import common
from protein import *
from proteinGroup import *
from alignment import *
from blastparser import *

########################################################################
# Retrieves the name of the input files from the command line.  If an incorrect
# number of files are specified, prints an error message and exits the program.
########################################################################
def getInFileNames(argv):
```

```
  print 'getInFileNames'
  errorString = "Usage: updateSFLD.py [-l<superfamilyList>]"

  superfamilyListFileName = "all"
  print len(argv)
  if len(argv) > 2:
    print errorString
    sys.exit(0)
  elif len(argv) > 1:
    if argv[1][:2] == "-l" or argv[1][:2] == "-L":
      superfamilyListFileName = argv[1][2:]
    else:
      print errorString
      sys.exit(0)
  elif len(argv) == 1:
     print errorString
     sys.exit(0)

  return superfamilyListFileName

#######################################################################
# getFileNameList
#######################################################################
def getFileNameList(ListFileName):
  inFile = open(ListFileName, "r")
  FileNameList = []

  while 1:
    line = inFile.readline()
    if not line:
      break
    line = string.strip(line)
    if len(line) > 0:
      FileNameList.append(line)
  inFile.close()

  return FileNameList

#######################################################################
# MapSFNameToID
#######################################################################
def MapSFNameToID(SFName_and_ID_file):
   inFile = open(SFName_and_ID_file, 'r')
   Name_ID_dict = {}

   while 1:
```

```
        line = inFile.readline()
        line = line[:-1]
        tmpList = line.split(';')
        if len(tmpList) > 1:
            Name_ID_dict[tmpList[1]] = tmpList[0]
        else:
            break

    return Name_ID_dict

#############################################################
# MapSFIDToName
#############################################################
def MapSFIDToName(SFName_and_ID_file):
    inFile = open(SFName_and_ID_file, 'r')
    Name_ID_dict = {}

    while 1:
        line = inFile.readline()
        line = line[:-1]
        tmpList = line.split(';')
        if len(tmpList) > 1:
            Name_ID_dict[tmpList[0]] = tmpList[1]
        else:
            break

    return Name_ID_dict


#############################################################
# Input:
#  superfamilyListFileName: A string specifying either: (1) The name of a file
#                           which lists superfamily names, one per line, or (2)
#                           the value "all"
# Returns:
#  SFIDList: A list of identifiers from the SFLD that correspond to either: (1)
#            the superfamily names listed in the file referenced by
#            superfamilyListFileName, or (2) all superfamilies in the SFLD
#############################################################
def getSFIDList(superfamilyListFileName):
   if superfamilyListFileName != "all":
      SFNameList = getFileNameList(superfamilyListFileName)

      SFIDList = []

      SFName_and_ID_file = 'SF.colon'
```

```
    SFName_id_dict = MapSFNameToID(SFName_and_ID_file)
    size = len(SFNameList)
    i = 0
    while i < size:
      SFIDList.append(SFName_id_dict[SFNameList[i]])
      i = i + 1

  return SFIDList

########################################################################
# returnList
########################################################################
def returnList(fileName, num_elements):
  fileList = []

  inFile = open(fileName, 'r')

  while 1:
    line = inFile.readline()
    line = line[:-1]
    tmpList = line.split(';')
    if tmpList == ['']:
      break
    elif len(tmpList) == num_elements:
      for index in range(0, len(tmpList)):
         if tmpList[index] == 'None':
           tmpList[index] = None
      fileList.append(tmpList)
    else:
      break


  return fileList

########################################################################
# Retrieves the names of all superfamily, family & subgroup HMMs from the SFLD
# that correspond to the superfamilies specified in SFIDList.
#
# Input:
#  SFIDList: A list of superfamily identifiers from the SFLD
# Returns:
#  hmmDict: A dictionary with key = SFID, value = list with structure:
#         [superfamilyHMMName, famIDHMMDict, subIDHMMDict]
#         famIDHMMDict and subIDHMMDict are dictionaries with key =
#         family/subgroup ID, value = HMM file name.
########################################################################
```

```
def getHMMDict(SFIDList):

   hmmDict = {}

   SFHMMListName = 'SFHMM.colon'
   num_elements = 2
   SFHMMList = returnList(SFHMMListName, num_elements)
   #print SFHMMList

   SubHMMListName = 'SubHMM.colon'
   num_elements = 3
   SubHMMList = returnList(SubHMMListName, num_elements)
   #print SubHMMList

   FamHMMListName = 'FamHMM.colon'
   num_elements = 3
   FamHMMList = returnList(FamHMMListName, num_elements)
   #print FamHMMList

   for SFID in SFIDList:
      #print SFID

      for index in range(0, len(SFHMMList)):
         if SFID == SFHMMList[index][0]:
             SFHMM = SFHMMList[index][1]
         #print SFHMM

      famIDHMMDict = {}
      for index in range(0, len(FamHMMList)):
         if SFID == FamHMMList[index][0]:
             id = FamHMMList[index][1]
             hmmName = FamHMMList[index][2]
             if hmmName != None:
                 famIDHMMDict[id] = hmmName

      #print famIDHMMDict

      subIDHMMDict = {}
      for index in range(0, len(SubHMMList)):
         if SFID == SubHMMList[index][0]:
            id = SubHMMList[index][1]
            hmmName = SubHMMList[index][2]
            if hmmName != None:
                subIDHMMDict[id] = hmmName

      #print subIDHMMDict
```

```
    hmmDict[SFID] = [SFHMM, famIDHMMDict, subIDHMMDict]
    #print hmmDict
  return hmmDict


##########################################################################
# Input:
#  line: A string containing a gi identifier, from a hmmpfam search output
# Returns:
#  A long, specifying a gi identifier
##########################################################################
def getGI(line):

  index = string.find(line, "|")
  gi = line[index + 1:]
  index = string.find(gi, "|")
  if index == (-1):
    print "Error: Could not extract GI from line " + line
    sys.exit(0)
  else:
    gi = gi[:index]

  return long(gi)


##########################################################################
# Parses and hmmsearch output file to get gi numbers for all domain hits.
#
# Input:
#  fileName: A string specifying an output file from the program hmmsearch.
# Returns:
#  giList: A list of gi numbers for all domain hits in the hmmsearch output
#          file.
##########################################################################
def parseHmmsearchFile(fileName):
  print 'def parseHmmsearchFile(fileName):'

  inFile = open(fileName, "r")
  giList = []

  #discard lines up to domain e-value information
  while 1:
    line = inFile.readline()
    if not line or line[:19] == "Parsed for domains:":
      break
```

```
  #Collect gi numbers
  while 1:
    line = inFile.readline()
    if not line or line[:33] == "Alignments of top-scoring domains":
      break
    if line[:2] == "gi":
      gi = getGI(line)
      if gi not in giList:
        giList.append(gi)

  inFile.close()

  return giList


#######################################################################
# Input:
#  redundantList: A list that may have more than one identical entry.
# Returns:
#  nonredundantList: A list with no identical entries.
#######################################################################
def removeRedundantGIs(redundantList):

  nonredundantList = []

  for item in redundantList:
    if item not in nonredundantList:
      nonredundantList.append(item)

  return nonredundantList


#######################################################################
#
# Input:
#  hmmDict: A dictionary with key = SFID, value = list with structure:
#          [superfamilyHMMName, famIDHMMDict, subIDHMMDict]
#          famIDHMMDict and subIDHMMDict are dictionaries with key =
#          family/subgroup ID, value = HMM file name.
#  path: A string specifying the path for the directory that contains the SFLD
#        HMM files.
# Returns:
#  fastaDict: A dictionary with key = SFID, value = list of all fasta files
#            for the hits of each SF/Fam/Sub. Fasta will contain *all*
#            sequences for each hit file (the hit file name determined from
#            hmmdict).
```

```
#  giScoreEvalueDict: A dictonary with key SFID, value = list of all filenames
#           that contain the gi, score and evalue of each hit set.
#           file format:
#           <gi>    <score>    <evalue>
########################################################################
def runParseHMMSearch(hmmDict, path):
  print 'def runParseHMMSearch(hmmDict, path):'

  fastaDict = {}
  giScoreEvalueDict = {}

  for SFID in hmmDict.keys():

    tempHitGIList = []

    #Parse the HMMSearch output HMM in a given superfamily

    #First find the HMMSearch file with superfamily HMM, if present,
    if hmmDict[SFID][0] != None:
      hmmsearchOutFileName = "SF" + str(SFID) + ".hmmsearch"
      cmd = "giScoreParseList.pl %s" % (hmmsearchOutFileName)
      os.system(cmd)

      giScoreEvalueFileName = hmmsearchOutFileName + ".giScoreEval"
      cmd = "getGIfromList.pl %s" % (giScoreEvalueFileName)
      os.system(cmd)

      giFileName = giScoreEvalueFileName + ".giList"
      fastaFileName = giFileName + ".fasta"
      cmd = "fastacmd -d nr -i %s -t T -o %s" % (giFileName, fastaFileName)
      os.system(cmd)

      SFFastaFile = fastaFileName
      SFgiScoreEvalueFile =  giScoreEvalueFileName
    else:
      SFFastaFile = None
      SFgiScoreEvalueFile =  None

    #Then parse hmmsearch with each family HMM,
    famIDFastaDict = {}
    famIDgiScoreEvalueDict ={}
    famIDHMMDict = hmmDict[SFID][1]
    for famID in famIDHMMDict.keys():
      hmmsearchOutFileName = "SF" + str(SFID) + "Fam" + str(famID) + ".hmms
      cmd = "giScoreParseList.pl %s" % (hmmsearchOutFileName)
      os.system(cmd)
```

```
        giScoreEvalueFileName = hmmsearchOutFileName + ".giScoreEval"
        cmd = "getGIfromList.pl %s" % (giScoreEvalueFileName)
        os.system(cmd)

        giFileName = giScoreEvalueFileName + ".giList"
        fastaFileName = giFileName + ".fasta"
        cmd = "fastacmd -d nr -i %s -t T -o %s" % (giFileName, fastaFileName)
        os.system(cmd)

        famIDFastaDict[famID] = fastaFileName
        famIDgiScoreEvalueDict[famID] = giScoreEvalueFileName

      #Then run hmmsearch with each subgroup HMM
      SubIDFastaDict = {}
      SubIDgiScoreEvalueDict = {}
      subIDHMMDict = hmmDict[SFID][2]
      for subID in subIDHMMDict.keys():
        hmmsearchOutFileName = "SF" + str(SFID) + "Sub" + str(subID) + ".hmmse
        cmd = "giScoreParseList.pl %s" % (hmmsearchOutFileName)
        os.system(cmd)

        giScoreEvalueFileName = hmmsearchOutFileName + ".giScoreEval"
        cmd = "getGIfromList.pl %s" % (giScoreEvalueFileName)
        os.system(cmd)

        giFileName = giScoreEvalueFileName + ".giList"
        fastaFileName = giFileName + ".fasta"
        cmd = "fastacmd -d nr -i %s -t T -o %s" % (giFileName, fastaFileName)
        os.system(cmd)

        SubIDFastaDict[subID] = fastaFileName
        SubIDgiScoreEvalueDict[subID] = giScoreEvalueFileName


      #Make a fasta file dict and a gi/score/evalue dict for all the files
      fastaDict[SFID] = [SFFastaFile, famIDFastaDict, SubIDFastaDict]
      giScoreEvalueDict[SFID] = [SFgiScoreEvalueFile, famIDgiScoreEvalueDict, S

    return fastaDict, giScoreEvalueDict


##################################################################################
# Parses the output file from the NCBI nrdb program (specified by
# nrdbFileName) to determine the sequence overlap between two sets of
```

```
# files.
# Returns:
#  commonList: A list of GIs common to the two fasta files compared using
#  nrdb.  (If the GIs of the common sequence are identical, one copy is
#  added to the list.  Otherwise, both GIs are added to the list as
#  seperate entries
#########################################################################################
def parseNrdbOutput(nrdbFileName):

  commonList = []

  inFile = open(nrdbFileName, 'r')

  while 1:
    line = inFile.readline()
    if not line:
      break
    if line[:1] == '>':
      #Search for seperator '\x01' added by nrdb to determine if the
      #current sequence was present in both nrdb input files
      index = string.find(line, '\x01')
      if index != (-1):
        commonList.append('Seq in Common')
        break
      #else: pass

  inFile.close()

  return commonList


#########################################################################################
# Runs the NCBI program nrdb.  Uses the function parseNRDBOutput to parse
# the resulting output file
# Returns:
#  commonList: A list of GIs common to the two fasta files compared using
#  nrdb.  (If the GIs of the common sequence are identical, one copy is
#  added to the list.  Otherwise, both GIs are added to the list as
#  seperate entries
#########################################################################################
def getCommonSeqs(fastaFileName1, fastaFileName2, runningPath):

  nrdb_out = runningPath + 'temp.nrdb'
  cmd = 'nrdb -o%s %s %s  2> %sscreenOut' % (nrdb_out, fastaFileName1, fasta
  os.system(cmd)
```

```
    commonList = parseNrdbOutput(nrdb_out)

    #Remove temporary file
    os.system('rm %stemp.nrdb %sscreenOut' % (runningPath, runningPath))

    return commonList

###################################################################
# markingSeqs
###################################################################
def markingSeqs(gseList, seqPath, seqFileList, inSFLDList, notInList):
    """Mark seq's in gseList that are in the SFLD and write out to file
    and return lists of gi's that are in or not in the sfld
    The new format for the entryDict lists is--
    <gi>    <score>    <evalue>    <VALID/NOT_valid>    <IN_SFLD>    <fasta file na

    """
    #for entry in gseList:
    #    entry.append('[]')
    #    entry.append('[]')

    print "markingSeqs(gseFileName, gseList, seqPath, seqFileList, inSFLDList, no
    GIinSFLDList =[]
    for entry in inSFLDList:
        GIinSFLDList.append(entry[0])


    for entry in gseList:
            notOne = 1
            gi_GSE = entry[0]
            if gi_GSE in GIinSFLDList:
                entry.append('IN_SFLD')
                index = GIinSFLDList.index(gi_GSE)
                entry.append(inSFLDList[index][1])
            elif gi_GSE in notInList:
                 entry.append('[]')
                 entry.append('[]')

            else:
                tmpFastaFileName = gi_GSE + '.tmp'
                os.system("fastacmd -d nr -s%s -tT > %s" % (gi_GSE, tmpFastaFileName
                for seq_entry in seqFileList:
                    seqFastaFileName = seqPath + seq_entry
                    commonList = getCommonSeqs(tmpFastaFileName, seqFastaFileNam
                    if commonList:  #the list exists, hit is in SFLD
                        print commonList
```

```
            entry.append('IN_SFLD')
            entry.append(seq_entry)
            inSFLDList.append([gi_GSE, seq_entry])
            print "BREAK " + gi_GSE
            notOne = 0
            break
        if notOne == 1: #this is not in SFLD
          print "NO BREAK " + gi_GSE
          entry.append('[]')
          entry.append('[]')
          notInList.append(gi_GSE)

  os.system("rm -f *.tmp")


  return inSFLDList, notInList, gseList



########################################################################
# markIfInSFLD
########################################################################
def markIfInSFLD(seqPath, entryDict, seqFileName):
  """Mark any sequences that are in the SFLD sequence set and write out to a fil

  seqFileList = getFileNameList(seqPath + seqFileName)
  inSFLDList = []
  notInList = []
  newEntryDict = {}

  for SFID in entryDict.keys():
    #check the superfamily sequences
    SFgseList = entryDict[SFID][0]
    inSFLDList, notInList, SFgseList = markingSeqs(SFgseList, seqPath, seqFile

    #check the family sequences
    famEntryDict = {}
    FamGSEFileDict = entryDict[SFID][1]
    for famID in FamGSEFileDict.keys():
      FamGSEList = FamGSEFileDict[famID]
      inSFLDList, notInList, FamGSEList = markingSeqs(FamGSEList, seqPath,
      famEntryDict[famID] = FamGSEList

    #check the subgroup sequences
    subEntryDict = {}
    SubGSEFileDict = entryDict[SFID][2]
```

```
    for subID in SubGSEFileDict.keys():
      SubGSEList = SubGSEFileDict[subID]
      inSFLDList, notInList, SubGSEList = markingSeqs(SubGSEList, seqPath, s
      subEntryDict[subID] = SubGSEList

    newEntryDict[SFID]= [SFgseList, famEntryDict, subEntryDict]

  return newEntryDict

######################################################################
# Parses the fasta format sequence file referenced by fastaFileName and obtains
# a list of gi numbers for the sequences in the file (giList).  Returns giList.
######################################################################
def fastaToGI(fastaFileName):

  giList = []
  inFile = open(fastaFileName, "r")

  while 1:
    line = inFile.readline()
    if not line:
      break
    if line[:1] == ">":
      gi = getGI(line)
      giList.append(gi)

  inFile.close()
  return giList



######################################################################
# Queries the SFLD to determine the superfamily name that corresponds to a
# superfamily identifier.
#
# Input:
#  SFID: A superfamily identifier (type long).
# Returns:
#  SFName: A string specifying the name of the superfamily that corresponds to
#         SFID.
######################################################################
def getSFName(SFID):
  #SF.colon is the filename of the ID/Names for the SFLD
  SF_ID_filename = 'SF.colon'
  SFName_id_dict = MapSFIDToName(SF_ID_filename)
  SFName = SFName_id_dict[SFID]
```

```
  return SFName


######################################################################
# Input:
#  alignmentFileName: The name of an hmmeralign format sequence alignment.
# Returns:
#  repSeq: A string specifying the (gapped) amino acid sequence for the first
#          sequence in the alignment specified by alignmentFileName.
######################################################################
def getRepSeq(alignmentFileName):

  inFile = open(alignmentFileName, "r")

  #Get the identifier for the first sequence in the alignment
  while 1:
    line = inFile.readline()
    if not line:
      break
    line = string.strip(line)
    if line[:5] == "Name:":
      line = string.strip(line[5:])
      index = string.find(line, " ")
      repSeqID = line[:index]
      break

  #Get the amino acid sequence corresponding to repSeqID
  repSeq = ""
  while 1:
    line = inFile.readline()
    if not line:
      break
    line = string.strip(line)
    if line[:len(repSeqID)] == repSeqID:
      line = string.strip(line[len(repSeqID):])
      repSeq += string.replace(line, " ", "")

  inFile.close()

  return repSeq
```

```
###########################################################################
# Translates the sequence number num (obtained from a gapped sequence
# alignment) to the corresponding number with respect to the ungapped
# sequence equivalent of gappedRepSeq.
#
# Input:
#  gappedConsResTuple: A nested tuple of tuples.  Each inner tuple is of the
#                      form (AA#, AAType), where AA# references a specific
#                      amino acid in the string gappedRepSeq.
#  gappedRepSeq: A string specifying an amino acid sequence from a gapped
#                sequence alignment.
# Returns:
#  ungappedConsResList: The ungapped equivalent of gappedConsResTuple, bu
#                       list form.
#
# NOTE: If the alignment position specified by an entry in gappedConsResTuple
# corresponds to a gap character in gappedRepSeq, a zero will be placed in the
# corresponding entry in ungappedConsResList.
###########################################################################
def getUngappedNumbers(gappedConsResList, gappedRepSeq):

  ungappedConsResList = []
  seqList = list(gappedRepSeq)

  for consResPair in gappedConsResList:
    gappedNum = consResPair[0]
    #print gappedNum
    aaType = consResPair[1]
    ungappedCount = 0
    gappedCount = 0
    correctedNum = 0
    for letter in seqList:
      #clustalw specifies gaps with "-", while hmmeralign uses "." and "~"
      if letter == "-" or letter == "." or letter == "~":
        gappedCount += 1
        #print gappedCount
      else:

        gappedCount += 1
        ungappedCount += 1
        #stringie =  str(gappedCount) + " " + str(ungappedCount) + " " + gappedNu
        #print stringie
        if gappedCount == int(gappedNum):
          #print "hello?"
          correctedNum = ungappedCount
          ungappedConsResList.append([correctedNum, aaType])
```

```
  return ungappedConsResList


##############################################################
# Removes gap characters from the string gappedSequence.  Returns the ungap
# string.
##############################################################
def removeGaps(gappedSequence):

  ungappedSequence = string.replace(gappedSequence, ".", "")
  ungappedSequence = string.replace(ungappedSequence, "-", "")
  ungappedSequence = string.replace(ungappedSequence, "~", "")

  return ungappedSequence


##############################################################
# Input:
#  hmmDict: A dictionary with key = SFID, value = list with structure:
#          [superfamilyHMMName, famIDHMMDict, subIDHMMDict]
#          famIDHMMDict and subIDHMMDict are dictionaries with key =
#          family/subgroup ID, value = HMM file name.
#  path: A string specifying the path for the directory that contains the SFLD
#       HMM files.
# Returns:
#  consResDict: A dictionary with key = SFID, value = a list with the following
#              format: [consResList, familyConsResDict, subgroupConsResDict]
#              where family and subgroupConsResDict are dictionaries with
#              key = family/subgroup ID and value = consResList, and
#              consResList is a nested list where each inner list has the
#              format: [AA#, allowedAAType(s)]
#  repSeqDict: Dictionary with key = SFID, value = list with the following
#             format: [SFRepSeq, familyRepSeqDict, subgroupRepSeqDict]
#             where family and subgroupRepSeqDict are dictionaries with key =
#             family/subgroup ID and value = a string containing the amino
#             acid sequence for a representative sequence in the
#             family/subgroup, which corresponds to the conserved residue
#             numbering in consResDict.
##############################################################
def getConsResDict(hmmDict, path):
  consResDict = {}
  repSeqDict = {}

  align_file_name = 'SFalign.colon'
  num_elements = 2
```

```
SFalignList = returnList(align_file_name, num_elements)

cons_residue_file_name = 'SFConsRes.colon'
num_elements = 3
SFAllConsResList = returnList(cons_residue_file_name, num_elements)
#print SFAllConsResList


for SFID in hmmDict.keys():
  #get superfamily alignment file name
  for index in range(0, len(SFalignList)):
    if SFID == SFalignList[index][0]:
       alignmentFileName = SFalignList[index][1]

  if alignmentFileName != None:
    #Collect the representative sequence for the SF alignment
    gappedSFRepSeq = getRepSeq(path + alignmentFileName)
    SFRepSeq = removeGaps(gappedSFRepSeq)

    #Collect the conserved residues for the SF alignment
    SFCRList = []
    for index in range(0, len(SFAllConsResList)):
      if SFID == SFAllConsResList[index][0]:
         SFCRList.append([SFAllConsResList[index][1], SFAllConsResList[inde
         #print SFCRList
         #print gappedSFRepSeq

    SFConsResList = getUngappedNumbers(SFCRList, gappedSFRepSeq)
  else:
    SFConsResList = []
    SFRepSeq = None


  famConsResDict = {}
  famRepSeqDict = {}

  #get family alignment file names
  fam_align_file_name = 'FamAlign.colon'
  num_elements = 2
  FamAlignList = returnList(fam_align_file_name, num_elements)

  #get conserved residues for family alignments
  fam_cons_res_file_name = 'FamConsResList.colon'
  num_elements = 3
  FamConsResList = returnList(fam_cons_res_file_name, num_elements)
  #print FamConsResList
```

```
for famID in hmmDict[SFID][1].keys():
   #Collect the representative sequence for a family alignment
   for index in range(0, len(FamAlignList)):
      if famID == FamAlignList[index][0]:
         alignmentFileName = FamAlignList[index][1]
         gappedFamRepSeq = getRepSeq(path + alignmentFileName)
         famRepSeqDict[famID] = removeGaps(gappedFamRepSeq)

   #Collect the conserved residues for a family alignment
   FamCRList =[]
   for index in range(0, len(FamConsResList)):
      if famID == FamConsResList[index][0]:
         FamCRList.append([FamConsResList[index][1], FamConsResList[inde
         famConsResDict[famID] = getUngappedNumbers(FamCRList, gapped


subConsResDict = {}
subRepSeqDict = {}

#get subgroup alignment file names
sub_align_file_name = 'SubAlign.colon'
num_elements = 2
SubAlignList = returnList(sub_align_file_name, num_elements)

#get conserved residues for the subgroup alignments
sub_cons_res_file_name = 'SubConsResList.colon'
num_elements = 3
SubConsResList = returnList(sub_cons_res_file_name, num_elements)

for subID in hmmDict[SFID][2].keys():
   #Collect the representative sequence for a subgroup alignment
   for index in range(0, len(SubAlignList)):
      if subID == SubAlignList[index][0]:
         alignmentFileName = SubAlignList[index][1]
         gappedSubRepSeq = getRepSeq(path + alignmentFileName)
         subRepSeqDict[subID] = removeGaps(gappedSubRepSeq)

   #Collect the conserved residues for a subgroup alignment
   SubCRList = []
   for index in range(0, len(SubConsResList)):
      if subID == SubConsResList[index][0]:
         SubCRList.append([SubConsResList[index][1], SubConsResList[index
         subConsResDict[subID] = getUngappedNumbers(SubCRList, gappedS

#For each SFID make a dict holding the conserved residues and the rep
```

```
    #Sequences for each family/SF/Sub etc.
    consResDict[SFID] = [SFConsResList, famConsResDict, subConsResDict]
    repSeqDict[SFID] = [SFRepSeq, famRepSeqDict, subRepSeqDict]


  #print consResDict
  #print repSeqDict
  return consResDict, repSeqDict




######################################################################
# Input:
#  consResDict: A dictionary with key = SFID, value = a list with the following
#              format: [consResList, familyConsResDict, subgroupConsResDict]
#              where family and subgroupConsResDict are dictionaries with
#              key = family/subgroup ID and value = consResList, and
#              consResList is a nested list where each inner list has the
#              format: [AA#, allowedAAType(s)]
# Returns:
#  reformattedConsResDict: A dictionary with key = SFID, value = a list with the
#                          following format: [consResList, familyConsResDict,
#                          subgroupConsResDict], where family and
#                          subgroupConsResDict are dictionaries with key =
#                          family/subgroup ID and value = consResList, and
#                          consResList is a nested list where each inner list
#                          has the format: [AA#, [allowedAAType(s)]]
######################################################################
def reformatConsResDict(consResDict):

  #print consResDict
  reformattedConsResDict = {}

  aaDict = {}
  aaDict['ALA'] = 'A'
  aaDict['ARG'] = 'R'
  aaDict['ASN'] = 'N'
  aaDict['ASP'] = 'D'
  aaDict['CYS'] = 'C'
  aaDict['GLN'] = 'Q'
  aaDict['GLU'] = 'E'
  aaDict['GLY'] = 'G'
  aaDict['HIS'] = 'H'
  aaDict['ILE'] = 'I'
```

```
aaDict['LEU'] = 'L'
aaDict['LYS'] = 'K'
aaDict['MET'] = 'M'
aaDict['PHE'] = 'F'
aaDict['PRO'] = 'P'
aaDict['SER'] = 'S'
aaDict['THR'] = 'T'
aaDict['TRP'] = 'W'
aaDict['TYR'] = 'Y'
aaDict['VAL'] = 'V'

for SFID in consResDict.keys():
  SFConsResList = []
  for consResPair in consResDict[SFID][0]:
    aaTypeString = consResPair[1]
    origAAList = string.split(aaTypeString, ",")
    reformattedAAList = []
    for aa in origAAList:
      aa = string.strip(aa)
      if len(aa) > 1:
        try:
          reformattedAAList.append(aaDict[aa])
        except KeyError:
          reformattedAAList.append('X')
      else:
        reformattedAAList.append(aa)
    SFConsResList.append([consResPair[0], reformattedAAList[:]])
  famConsResDict = {}
  for famID in consResDict[SFID][1].keys():
    famConsResDict[famID] = []
    for consResPair in consResDict[SFID][1][famID]:
      aaTypeString = consResPair[1]
      origAAList = string.split(aaTypeString, ",")
      reformattedAAList = []
      for aa in origAAList:
        aa = string.strip(aa)
        if len(aa) > 1:
          try:
            reformattedAAList.append(aaDict[aa])
          except KeyError:
            reformattedAAList.append('X')
        else:
          reformattedAAList.append(aa)
      famConsResDict[famID].append([consResPair[0], reformattedAAList[:]])
  subConsResDict = {}
  for subID in consResDict[SFID][2].keys():
```

```
      subConsResDict[subID] = []
      for consResPair in consResDict[SFID][2][subID]:
        aaTypeString = consResPair[1]
        origAAList = string.split(aaTypeString, ",")
        reformattedAAList = []
        for aa in origAAList:
          aa = string.strip(aa)
          if len(aa) > 1:
            try:
              reformattedAAList.append(aaDict[aa])
            except KeyError:
              reformattedAAList.append('X')
          else:
            reformattedAAList.append(aa)
        subConsResDict[subID].append([consResPair[0], reformattedAAList[:]])
    reformattedConsResDict[SFID] = [SFConsResList, famConsResDict, subCon

  #print reformattedConsResDict
  return reformattedConsResDict



##########################################################################
# Adds the amino acid sequence specified by the string repSeq in fasta format
# to the fasta sequence file specified by the string fastaFileName.
##########################################################################
def addRepSeq(fastaFileName, repSeq):

  #print repSeq
  outFile = open(fastaFileName, "a")
  outFile.write(">gi|repSeq|\n")
  outFile.write(common.format(repSeq))
  outFile.close()


##########################################################################
# Aligns the hit sequences categorized in a given superfamily/family/subgroup,
# from categorizedHitsDict, along with the appropriate representative sequence,
# from repSeqDict, with the appropriate HMM, from hmmDict, using hmmalign.
#
# Input:
#  categorizedHitsDict: A dictionary with key = SFID, value = A list with
#                structure: [SFHitList, familyHitDict, subgroupHitDict],
#                where SFHitList is a list of gi numbers for all hits
#                from the superfamily, familyHitDict is a
#                dictionary with key = family ID, value = a list of gi
```

```
#                    numbers for hits classified with a given family, and
#                    subgroupHitDict is the equivalent to familyHitDict, but
#                    for a subgroup rather than a family.
#  repSeqDict: Dictionary with key = SFID, value = list with the following
#            format: [SFRepSeq, familyRepSeqDict, subgroupRepSeqDict]
#            where family and subgroupRepSeqDict are dictionaries with key =
#            family/subgroup ID and value = a string containing the amino
#            acid sequence for a representative sequence in the
#            family/subgroup, which corresponds to the conserved residue
#            numbering in consResDict.
#  hmmDict: A dictionary with key = SFID, value = list with structure:
#          [superfamilyHMMName, famIDHMMDict, subIDHMMDict]
#          famIDHMMDict and subIDHMMDict are dictionaries with key =
#          family/subgroup ID, value = HMM file name.
#  path: A string specifying the path for the directory that contains the SFLD
#        HMM files.
#######################################################################

def alignHits(fastaDict, repSeqDict, hmmDict, path):
  print 'def alignHits(fastaDict, repSeqDict, hmmDict, path):'

  alignHitDict = {}
  for SFID in hmmDict.keys():

    #First find the HMMSearch file with superfamily HMM, if present,
    if hmmDict[SFID][0] != None:
      hmmName = path + hmmDict[SFID][0]
      alignFileName = "SF" + str(SFID) + ".hmmalign"
      fastaFile = fastaDict[SFID][0]
      addRepSeq(fastaFile, repSeqDict[SFID][0])
      os.system("inspectDefline.py %s" % (fastaFile))
      os.system("mv shortDefline.fasta " + fastaFile)
      os.system("hmmalign -o %s  %s %s > screenOut" % (alignFileName, hmmN
      SFalignFileName = alignFileName
    else:
      SFalignFileName = None

    famAlignDict = {}
    famIDHMMDict = hmmDict[SFID][1]
    famFastaDict = fastaDict[SFID][1]
    for famID in famIDHMMDict.keys():
      hmmName = path + hmmDict[SFID][1][famID]
      alignFileName = "SF" + str(SFID) + "Fam" + str(famID) + ".hmmalign"
      fastaFile = famFastaDict[famID]
      addRepSeq(fastaFile, repSeqDict[SFID][1][famID])
      os.system("inspectDefline.py %s" % (fastaFile))
```

```
      os.system("mv shortDefline.fasta " + fastaFile)
      os.system("hmmalign -o %s  %s %s > screenOut" % (alignFileName, hmmN
      famAlignDict[famID] = alignFileName

    subAlignDict = {}
    subIDHMMDict = hmmDict[SFID][2]
    subFastaDict = fastaDict[SFID][2]
    for subID in subIDHMMDict.keys():
      hmmName = path + hmmDict[SFID][2][subID]
      alignFileName = "SF" + str(SFID) + "Sub" + str(subID) + ".hmmalign"
      fastaFile = subFastaDict[subID]
      addRepSeq(fastaFile, repSeqDict[SFID][2][subID])
      os.system("inspectDefline.py %s" % (fastaFile))
      os.system("mv shortDefline.fasta " + fastaFile)
      os.system("hmmalign -o %s  %s %s > screenOut" % (alignFileName, hmmN
      subAlignDict[subID] = alignFileName

    alignHitDict[SFID] = [SFalignFileName, famAlignDict, subAlignDict]
    #print alignHitDict

  return alignHitDict



####################################################################
# Input:
#  alignFileName: A string specifying the name of a hmmeralign format alignment
#  repSeq: A string specifying an (ungapped) amino acid sequence present in
#          the alignment specified by alignFileName
#  consResList: A nested list with format [AA#, [allowedAAType(s)]]
# Returns:
#  validatedHitList: A list containing the gi numbers for all sequences in
#                    alignFileName that conserve the residues specified in
#                    consResList, according to the alignment
####################################################################
def checkAlignmentForConsRes(alignFileName, repSeq, consResList):

  allowedMismatches = 0
  validatedHitList = []
  removedHitsList = []

  algnmnt = alignment(alignFileName)
  mismatchDict = {}
  for alignKey in algnmnt.alignDict.keys():
    #print "alignKey" + alignKey
    mismatchCounter = 0
```

```
        for resPair in consResList:
            resNum = resPair[0]
            #print "resNum" + str(resNum)
            correctedResNum = algnmnt.translateSeqNum(resNum, "repSeq")
            #subtract 1 from correctedResNum to convert to index
            #print resPair[1]
            if "X" in resPair[1]:
                #print "what?\n"
                pass
            elif algnmnt.alignDict[alignKey][correctedResNum - 1] not in resPair[1]:
                #print algnmnt.alignDict[alignKey][correctedResNum - 1]
                #print str(correctedResNum - 1)
                #print resPair[1]
                mismatchCounter += 1
        mismatchDict[alignKey] = mismatchCounter
        #print "mismatchCounter"
        #print mismatchCounter
    for key in mismatchDict.keys():
        #print "key"
        #print key
        #print "mismatchDict[key]"
        #print mismatchDict[key]
        if mismatchDict[key] <= allowedMismatches and key != "repSeq":
            validatedHitList.append(str(key))
            #print "VALID"
        elif key == "repSeq":
            pass
        else:
            removedHitsList.append(str(key))
#   os.system("rm " + alignFileName) #Delete temporary alignment file

    return validatedHitList, removedHitsList


######################################################################
# Validates hit sequences by verifying that they conserve the catalytic
# residues specified in consResDict.
#
# Input:
#  consResDict: A dictionary with key = SFID, value = a list with the following
#            format: [consResList, familyConsResDict, subgroupConsResDict]
#            where family and subgroupConsResDict are dictionaries with
#            key = family/subgroup ID and value = consResList, and
#            consResList is a nested list where each inner list has the
#            format: [AA#, allowedAAType(s)]
#  repSeqDict: Dictionary with key = SFID, value = list with the following
```

```
#            format: [SFRepSeq, familyRepSeqDict, subgroupRepSeqDict]
#            where family and subgroupRepSeqDict are dictionaries with key =
#            family/subgroup ID and value = a string containing the amino
#            acid sequence for a representative sequence in the
#            family/subgroup, which corresponds to the conserved residue
#            numbering in consResDict.
# Returns:
#  validatedHitsDict: Dictionary with key = SFID, value = list with structure:
#                 [validatedSFHitList, validatedFamHitDict,
#                 validatedSubHitDict], where validatedSFHitList is a list
#                 of gi numbers for validated hits categorized with the SF
#                 HMM, validatedFamHitDict is a dictionary with key =
#                 family ID, value = list of gi numbers for validated hits
#                 classified with a given family ID, and
#                 validatedSubHitDict is the equivalent to familyHitDict,
#                 but for a subgroup rather than a family.
######################################################################
def checkHitsForConsRes(hmmDict, consResDict, repSeqDict):
  print 'def checkHitsForConsRes(hmmDict, consResDict, repSeqDict):'
  validatedHitsDict = {}
  removedHitsDict = {}

  for SFID in hmmDict.keys():
    if SFID in consResDict.keys():
      SFAlignFileName = "SF" + str(SFID) + ".hmmalign"
      if os.path.isfile(SFAlignFileName):
        validatedSFHitList, removedSFHitsList = checkAlignmentForConsRes(SF
      else:
        validatedSFHitList = []
        removedSFHitsList = []
    else:
      SFAlignFileName = "SF" + str(SFID) + ".hmmalign" + ".noConsRes"
      openfile = open(subAlignFileName, "w")
      openfile.close()
      print "made an openfile for subgroup"

    validatedFamHitDict = {}
    removedFamHitsDict = {}
    famIDHMMDict = hmmDict[SFID][1]
    for famID in famIDHMMDict.keys():
      if famID in consResDict[SFID][1].keys():
        famAlignFileName = "SF" + str(SFID) + "Fam" + str(famID) + ".hmmalign"
        if os.path.isfile(famAlignFileName):
          #print "famID" + famID
          validatedFamHitDict[famID], removedFamHitsDict[famID] = checkAlign
        else:
```

```
                    print "No alignment file for family"
            else:
                famAlignFileName = "SF" + str(SFID) + "Fam" + str(famID) + ".hmmalign"
                openfile = open(famAlignFileName, "w")
                openfile.close()
                print "made an openfile for family"

        validatedSubHitDict = {}
        removedSubHitsDict = {}
        for subID in hmmDict[SFID][2].keys():
            if subID in consResDict[SFID][2].keys():
                subAlignFileName = "SF" + str(SFID) + "Sub" + str(subID) + ".hmmalign"
                if os.path.isfile(subAlignFileName):
                    validatedSubHitDict[subID], removedSubHitsDict[subID] = checkAlignme
                    print "No alignment file for subgroup"
            else:
                subAlignFileName = "SF" + str(SFID) + "Sub" + str(subID) + ".hmmalign" -
                openfile = open(subAlignFileName, "w")
                openfile.close()
                print "made an openfile for subgroup"


        validatedHitsDict[SFID] = [validatedSFHitList, validatedFamHitDict, validatedS
        print validatedSFHitList
        print validatedFamHitDict
        print validatedSubHitDict

        removedHitsDict[SFID] = [removedSFHitsList, removedFamHitsDict, removed
        print removedSFHitsList
        print removedFamHitsDict
        print removedSubHitsDict

    return validatedHitsDict, removedHitsDict



##################################################################
# gseLoadFile
##################################################################
def gseLoadFile(fileName):
    """Open the giScoreEvalue file and return contents in a list"""

    gseFileList = []
    gseINFile = open(fileName, 'r')

    for line in gseINFile.readlines():
```

```
        tmpList = line.split()
        gseFileList.append(tmpList)

    gseINFile.close()
    return gseFileList

###################################################################
# printGSEFile
###################################################################
def printGSEFile(fileList, filename):
    """Print out the fileList to the file named filename"""
    fileOut = open(filename, "w")
    for entry in fileList:
        listString = '    '.join(entry)
        fileOut.write(listString)
        fileOut.write("\n")

    fileOut.close()


###################################################################
# markIfValidHit
###################################################################
def markIfValidHit(validatedHitsDict, removedHitsDict, giScoreEvalueDict):
    """Mark the hits in giScoreEvalue files as valid or invalid hits.

    Input:
         validatedHitsDict: the Dict with the validated gi's for the SF's, Fams&
              Sub's
         removedHitsDict:  the dict with the invalidated gi's for the SF's Fams &
              Subs
         giScoreEvalueDict: the dict that holds all the files names for the
              parsed hmmsearch files (their file extension is .giScoreEvalue)
    This program will read in each .giScoreEvalue and mark each hit (line) as
    either valid or invalid and then

    Return: the dictionary holding all the updated entry information in entryDict
              The new entry format is:
              <gi>    <score>    <evalue>    <VALID/NOT_valid>
    """
    entryDict = {} #this holds all of the entry data from the flatfiles

    for SFID in giScoreEvalueDict.keys():
        # deal with the SF
        if giScoreEvalueDict[SFID][0] != None: #else pass
```

```
  validGISFList = validatedHitsDict[SFID][0]

  invalidGISFList = removedHitsDict[SFID][0]

  gseINFileList = gseLoadFile(giScoreEvalueDict[SFID][0])
  for entry in gseINFileList:
    if entry[0] in validGISFList:
      entry.insert(len(entry),"VALID")
    elif entry[0] in invalidGISFList:
      entry.insert(len(entry), "NOT_valid")
    else:
      print "This Didn't work!!!"

  SFentry = gseINFileList
  #printGSEFile(gseINFileList, giScoreEvalueDict[SFID][0])

else:
   SFentry = None

#deal with the families
famEntryDict ={}
famGSEDict = giScoreEvalueDict[SFID][1]
validFamDict = validatedHitsDict[SFID][1]
invalidFamDict = removedHitsDict[SFID][1]
for famID in famGSEDict.keys():
  famGSEFile = famGSEDict[famID] #get the family gse filename
  famINFileList = gseLoadFile(famGSEFile)

  validGIFamList = validFamDict[famID] #get the fam list of valid hits

  invalidGIFamList = invalidFamDict[famID] #get the fam list of invalid hits

  for entry in famINFileList:
    if entry[0] in validGIFamList:
      entry.insert(len(entry), "VALID")
    elif entry[0] in invalidGIFamList:
      entry.insert(len(entry), "NOT_valid")
    else:
      print "2 THis didn't work"

  famEntryDict[famID] = famINFileList
  #printGSEFile(famINFileList, famGSEFile)


#deal with the subgroups
subEntryDict = {}
```

```
        subGSEDict = giScoreEvalueDict[SFID][2]
        validSubDict = validatedHitsDict[SFID][2]
        invalidSubDict = removedHitsDict[SFID][2]
        for subID in subGSEDict.keys():
            subGSEFile = subGSEDict[subID] #get the family gse filename
            subINFileList = gseLoadFile(subGSEFile)

            validGISubList = validSubDict[subID] #get the fam list of valid hits

            invalidGISubList = invalidSubDict[subID] #get the fam list of invalid hits

            for entry in subINFileList:
                if entry[0] in validGISubList:
                    entry.insert(len(entry), "VALID")
                elif entry[0] in invalidGISubList:
                    entry.insert(len(entry),"NOT_valid")
                else:
                    print "3 THis didn't work"

            subEntryDict[subID] = subINFileList
            #printGSEFile(subINFileList, subGSEFile)

        entryDict[SFID] = [SFentry, famEntryDict, subEntryDict]

    return entryDict

########################################################################
#fastacmdDefSeq
########################################################################
def fastacmdDefSeq(entryList, fastaDict):
    """Return entry list with added def line and AA sequence.
    Input: entryList a list of the format
    <gi>    <def line>    <score>   <Evalue>    <VALID/NOT_valid>     <IN_SFLD>
    Return: entryList: a new list that has added the definition line and the AA seque
            of the format
    <gi>    <def line>    <score>   <Evalue>    <VALID/NOT_valid>     <IN_SFLD>

            fastaDict: key = gi number, value = fasta file name for that gi

    """
    gi = entryList[0]
    fastaFileName = gi + '.fasta'

    if gi not in fastaDict.keys():
        fastaDict[gi] = fastaFileName
        cmd = 'fastacmd -d nr -s%s -tT > %s' % (gi, fastaFileName)
```

```
        os.system(cmd)
    else:
        pass

    fastaFile = open(fastaFileName, "r")
    defLine = fastaFile.readline()
    defLine = defLine[:-1] #strip off the endl

    AAline = fastaFile.readline() #get the first AA line
    AAline = AAline[:-1]
    line = fastaFile.readline()
    while line:
        line = line[:-1]
        AAline = AAline + line
        line = fastaFile.readline()

    #insert def line in second position of list, after gi
    entryList.insert(1, defLine)

    #insert AA line at the end of the list
    entryList.insert(len(entryList), AAline)

    fastaFile.close()
    return entryList, fastaDict


##################################################
# getDefandSeq
##################################################
def getDefandSeq(entryDict):
    """Return new dict of the entries that includes the def line and AA sequence.
    Input:   entryDict--the dictionary key = SFID, value = lists of entry data
        for each SF/Fam/Sub.
    Return:    newEntryDict--dictionary key = SFID, value = updated lists of
        entry data for each SF/Fam/Sub in the format
        <gi>    <def line>    <score>   <Evalue>    <VALID/NOT_valid>     <IN_SFLD
               fastaDict--dictionary key = gi number, value = fasta file for that gi
    """
    newEntryDict = {}  #key SFID, value entry lists
    fastaDict = {}  # key gi number, value fasta file name
    for SFID in entryDict.keys():

        if entryDict[SFID][0] != None:
            SFentryList = entryDict[SFID][0]
            for entry in SFentryList:
                entry, fastaDict = fastacmdDefSeq(entry, fastaDict)
```

```
            newSFentryList = SFentryList
        else:
            newSFentryList = None

        famEntryDict = entryDict[SFID][1]
        newFamEntryDict = {}
        for famID in famEntryDict.keys():
            famEntryList = famEntryDict[famID]
            for entry in famEntryList:
                entry, fastaDict = fastacmdDefSeq(entry, fastaDict)
            newFamEntryDict[famID] = famEntryList

        subEntryDict = entryDict[SFID][2]
        newSubEntryDict = {}
        for subID in subEntryDict.keys():
            subEntryList = subEntryDict[famID]
            for entry in subEntryList:
                entry, fastaDict = fastacmdDefSeq(entry, fastaDict)
            newSubEntryDict[subID] = subEntryList

        newEntryDict[SFID] = [newSFentryList, newFamEntryDict, newSubEntryDict

    return newEntryDict, fastaDict

################################################################
#printOutput
################################################################
def printOutput(giScoreEvalueDict, entryDict, fileExt):
    """Print out the updated entries fo files listed in giScoreEvalueDict.
    format of file:
    <gi>    <def line>    <score>    <Evalue>    <VALID/NOT_valid>    <IN_SFLD>
    fileExt: if not empty, add this file extension to the filenames to write to

    """
    for SFID in giScoreEvalueDict.keys():
        if giScoreEvalueDict[SFID][0] != None:
            SFfileName = giScoreEvalueDict[SFID][0]
            SFfileName = SFfileName + fileExt
            SFfileList = entryDict[SFID][0]
            printGSEFile(SFfileList, SFfileName)
        else:
            pass

        famFileNameDict = giScoreEvalueDict[SFID][1]
        famEntryDict = entryDict[SFID][1]
        for famID in famFileNameDict.keys():
```

```
            famFileName = famFileNameDict[famID]
            famFileName = famFileName + fileExt
            famEntryList = famEntryDict[famID]
            printGSEFile(famEntryList, famFileName)

        subFileNameDict = giScoreEvalueDict[SFID][1]
        subEntryDict = entryDict[SFID][1]
        for subID in subFileNameDict.keys():
            subFileName = subFileNameDict[subID]
            subFileName = subFileName + fileExt
            subEntryList = subEntryDict[subID]
            printGSEFile(subEntryList, subFileName)

#################################################################
# seenThisDomain
#################################################################
def seenThisDomain(entry, hitList, hitDomainDict, entryList):
    """Return a Dict with cdd domain hits added to the info in 'entry'.
    INPUT:
        entry: a list of data for one gi
        hitList: a list of keys for hitDomainDict
        hitDomainDict: a dict with key = hit name ('gi_hit1' etc), value =
            domain hit information in the format
            <total length> <align. length> <query start> <query end> <percent ID>
                    <evalue> <bit score> <db>
        entryList: A list of lists (a list of entries) the
            entries are in the format
            <gi>    <def line>    <score>    <Evalue>    <VALID/NOT_valid>
                    <IN_SFLD>    <SFLD fasta filename>     <AA sequence>
    PROCESS:
        This gi has been seen before (and therefore the rpsblast has been done
        and the domain hits gotten) but we still need to add this info to the
        current entry being processed. This function will add the info in a
        series of new line additions to entryDict so that the fist updated
        entry is
            <gi>    <def line>    <score>    <Evalue>    <VALID/NOT_valid>
                    <IN_SFLD>    <SFLD fasta filename> <total length>
                    <align. length> <query start> <query end> <percent ID>
                    <evalue> <bit score> <db>  <AA sequence>
       the following entries are
            <gi>    <[dup]>    <[dup]>   <Evalue>    <[dup]>
                    <[dup]>    <[dup]> <total length>
                    <align. length> <query start> <query end> <percent ID>
                    <evalue> <bit score> <db>  <[dup]>
    RETURN:
        updatedEntryDict: a dict key = SFID, value = updated entries (see PROCES
```

```
    """
    updatedEntryList = entryList[:]
    entry_index = entryList.index(entry)
    entry_copy = entry[:]

    #deal with the first CDD hit
    if hitList:
        hit_1 = hitList.pop(0)
        domainHitList = hitDomainDict[hit_1]
        for datum in domainHitList:
            index = len(entry_copy) - 1 #insert before the last item
            entry_copy.insert(index, datum)

        updatedEntryList.pop(entry_index) #remove old entry
        updatedEntryList.insert(entry_index, entry_copy) #put in new entry into orig.

        #now deal with the rest of the CDD hits
        for hit in hitList:
            entry_copy = entry[:]
            domainHitList = hitDomainDict[hit]
            # get the domain data
            for datum in domainHitList:
                index = len(entry_copy) - 1 #insert before the last item
                entry_copy.insert(index, datum)

            # replace appropriate values with [dup] (duplicate)
            entry_copy[1] = '[dup]'   #def line
            entry_copy[2] = '[dup]'   #score
            entry_copy[4] = '[dup]'   #VALID/NOT_valid
            entry_copy[5] = '[dup]'   #IN_SFLD
            entry_copy[6] = '[dup]'   #SFLD fasta filename
            entry_copy[-1] = '[dup]'  # AA sequence

            entry_index = entry_index + 1
            updatedEntryList.insert(entry_index, entry_copy)
    else:
        for i in range(0, 8):
            index = len(entry_copy) - 1 #insert before the last item
            entry_copy.insert(index, '[]')
        updatedEntryList.pop(entry_index) #remove old entry
        updatedEntryList.insert(entry_index, entry_copy) #put in new entry into orig.

    return updatedEntryList

#################################################################################
```

```
# parseRPSBlast
###################################################################
def parseRPSBlast(rpsFileName):
    """Return a list holding the top five hits from the rpsFile.
    INPUT:
        rpsFileName: the filename of the output from an rpsblast run.
        file is in tabular format
            "Query id, Subject id, % identity, alignment length, mismatches,
                    gap openings, q. start, q. end, s. start, s. end,
                    e-value, bit score"
    PROCESS:
        Open the rps file and parse out the top five hits and put them into a
        list.
    RETURN:
         hitList: A list of lists of the top 5 rpsblast hits.

    """
    rpsFile = open(rpsFileName, 'r')
    #file is in tabular format with each line having the format
    #Query id, Subject id, % identity, alignment length, mismatches, gap openings,
    hitList = []
    i = 0
    for line in rpsFile.readlines():
        if i in range(0, 5):
            tmpList = line.split()

            db_info = str(tmpList[1])
            perc_id = str(tmpList[2])
            align_len = str(tmpList[3])
            q_start = str(tmpList[6])
            q_end = str(tmpList[7])
            evalue = str(tmpList[10])
            bit_score = str(tmpList[11])
            hitList.append([align_len, q_start, q_end, perc_id, evalue, bit_score, db_ir
            i += 1
        else:
            break

    return hitList


###################################################################
# runRPSBlast
###################################################################
def runRPSBlast(entry, haveDomainDict, hitDomainDict, fastaFileName):
    """Return two dictionaries that contian CDD domian data gathered from rpsblas
```

```
    INPUT:
        entry: the entry to run rpsblast on
        haveDomainDict: a dictionary Key = gi, value = list of keys for hitDomainDict
        hitDomainDict: a dictionary key = hit name ('gi_hit1' etc), value = cdd
            hit information in the format
            <total length> <length alignment> <query align start> <query align end>
            <percentID> <evalue of rpsblast> <bit score of rpsblast>  <rpsblast DB>
        fastaFileName: the filename of the fasta file to be run in rpsblast
        NOT PASSED:
            NOTE: this function calls the ncbi program rpsblast and therefore
            requires having an rpsblast formatted DB somewhere accessible and a
            .ncbirc file in the running directory
    PROCESS:
        This function will run rpsblast on the input fasta file and then open
        up the output and parse out the top 5 domain hits. This function has
        been hard-coded to use the CDD database. This function then updates
        haveDomainDict and hitDomainDict with the new gi/domain data.
    RETURN:
        updated haveDomainDict
        updated hitDomainDict

    """
    outputFile = fastaFileName + '.rpsblast'

    #get tabular output from rpsblast
    os.system('rpsblast -i %s -d Cdd -m 8 -o %s' % (fastaFileName, outputFile))
    hitList = parseRPSBlast(outputFile)
    total_seq_len = len(entry[-1])
    hitNum = 1
    gi = entry[0]
    keyList = []
    for hit in hitList:
        hit.insert(0, str(total_seq_len))
        hitKey = gi + '_hit_' + str(hitNum)
        hitDomainDict[hitKey] = hit
        keyList.append(hitKey)
        hitNum += 1

    haveDomainDict[gi] = keyList

    return haveDomainDict, hitDomainDict

########################################################################
# getDomainListing
########################################################################
def getDomainListing(entryDict, fastaDict):
```

```
"""Return updated entries with the top five domain hits (using CDD) for each se
Input: entryDict: key = SFID, value = lists of entries of the format...
    <gi>    <def line>    <score>    <Evalue>    <VALID/NOT_valid>    <IN_SFLD
       fastaDict: key = gi, value = fasta file name for that gi

Process: use rpsblast and the CDD database to determine the top five domains
         for each sequence. After this, remove all the fasta files in fastaDict.

Return:    newEntryDict: key = SFID, value = lists of entries of the format...
<gi> <def line>  <score>   <Evalue>    <VALID/NOT_valid>    <IN_SFLD>
        <SFLD fasta filename> <total length> <length alignment>
        <query align start> <query align end> <percentID> <evalue of rpsblast>
        <bit score of rpsblast>  <rpsblast DB> <AA sequence>

"""
# key = gi, value = list of keys for hitDomainDict
haveDomainDict = {}
# key = hit name ('gi_hit1' etc.), value = list of hit information
hitDomainDict = {}
newEntryDict = {}

for SFID in entryDict.keys():
    # do the SF hits
    if entryDict[SFID][0] != None:
        SFentryList = entryDict[SFID][0] #get the list
        newSFentryList = SFentryList[:] #this is the new list
        for entry in SFentryList:
            gi = entry[0]
            if gi in haveDomainDict.keys():
                hitList = haveDomainDict[gi]
                newSFentryList = seenThisDomain(entry, hitList, hitDomainDict, new

            else:
                fastaFileName = fastaDict[gi]
                haveDomainDict, hitDomainDict = runRPSBlast(entry, haveDomainD
                hitList = haveDomainDict[gi]
                newSFentryList = seenThisDomain(entry, hitList, hitDomainDict, new
    else:
        newSFentryList = None

    famEntryDict = entryDict[SFID][1]
    newFamEntryDict = {}
    for famID in famEntryDict.keys():
        famEntryList = famEntryDict[famID]
        newFamEntryList = famEntryList[:]
        for entry in famEntryList:
```

```
                gi = entry[0]
                if gi in haveDomainDict.keys():
                    hitList = haveDomainDict[gi]
                    newFamEntryList = seenThisDomain(entry, hitList, hitDomainDict, ne

                else:
                    fastaFileName = fastaDict[gi]
                    haveDomainDict, hitDomainDict = runRPSBlast(entry, haveDomainD
                    hitList = haveDomainDict[gi]
                    newFamEntryList = seenThisDomain(entry, hitList, hitDomainDict, ne
            newFamEntryDict[famID] = newFamEntryList

        subEntryDict = entryDict[SFID][2]
        newSubEntryDict = {}
        for subID in subEntryDict.keys():
            subEntryList = subEntryDict[famID]
            newSubEntryList = subEntryList[:]
            for entry in subEntryList:
                gi = entry[0]
                if gi in haveDomainDict.keys():
                    hitList = haveDomainDict[gi]
                    newSubEntryList = seenThisDomain(entry, hitList, hitDomainDict, ne
                else:
                    fastaFileName = fastaDict[gi]
                    haveDomainDict, hitDomainDict = runRPSBlast(entry, haveDomainD
                    hitList = haveDomainDict[gi]
                    newSubEntryList = seenThisDomain(entry, hitList, hitDomainDict, ne
            newSubEntryDict[subID] = newSubEntryList

        for gi in fastaDict.keys():
            os.system('rm -f %s' % (fastaDict[gi]))
        newEntryDict[SFID] = [newSFentryList, newFamEntryDict, newSubEntryDict
        print newSFentryList
        print newFamEntryDict
        print newSubEntryDict
    #print newEntryDict
    return newEntryDict
```

Appendix E. Program—parseHmmPfamKeyword.py

```
#!/usr/bin/python2.3

"""parseHmmPfamKeyword.py


Author: Alexandra M. Schnoes 12-02-04
last modified: 12-02-04
last modified: 03-31-05
"""

import sys
import os
import string

def getCommandLineArg(argv):
    """Return the a list of the command line input

    HmmPfamList    EFDfilename  SFfilename  SGfilename  Famfilename
    """
    commandList = []

    errorString = "Usage: parseHmmPfam_sfld.py <HmmPfamList> <EFDfilename

    if ((len(argv) < 6) | (len(argv) > 6)):
        print errorString
        sys.exit(0)
    else:
        i = 1
        while i < 6:
            commandList.append(argv[i])
            i = i + 1

    return commandList


def getFileList(input_filename):
    """Return a list of files to parse.

    INPUT: filename from main program call
        This file contains a list of filenames.
    The filenames are \n delimated

    RETURN: list_of_files
        The input file has been parsed and all of the filenames (in the input file)
    have been placed into a list->list_of_files
```

```
    """
    listFile = open(input_filename, "r")

    list_of_files = []

    for line in listFile.readlines():
        list_of_files.append(line[:-1])
        ##print line, #comma supresses extra endline

    listFile.close()

    return list_of_files

def getEFDdata(efd_filename):
    """Return the data in efd_filename as a list.

    'gi' 'family' 'family evidence' 'family reference' 'subgroup' 'superfamily' 'superfam
    """

    efd_data_list = []

    efd_file = open(efd_filename,"r")

    while 1:
        line = efd_file.readline()
        line = line[:-1]
        tmpList = line.split(';')
        if len(tmpList) > 7:
            efd_data_list.append(tmpList)
        else:
            break

    return efd_data_list

def getHeirarchyData(data_filename):
    """Return the data in efd_filename as a list.

    'id' 'name' 'align file name' 'hmm file name'
    """

    data_list = []

    data_file = open(data_filename,"r")

    while 1:
        line = data_file.readline()
```

```
        line = line[:-1]
        tmpList = line.split(';')
        if len(tmpList) > 3:
            data_list.append(tmpList)
        else:
            break

    data_file.close()

    return data_list


def getHmmPfamData(hmmPfamFileName, hmmPath):
    """Return all the needed data from the input HmmPfam file."""
    file_data = []
    hmmPfam_file = open(hmmPfamFileName, "r")
    i = 1 #keep while loop going
    hmm_db = ''
    sequence_file = ''

    while i:
        line = hmmPfam_file.readline()
        lineList = line.split()

        if len(lineList) > 2:
            if ((lineList[0] == "HMM") & (lineList[1] == "file:")):
                hmm_db = lineList[2]
                hmm_db = hmm_db[len(hmmPath):]
            elif ((lineList[0] == "Sequence") & (lineList[1] == "file:")):
                sequence_file = lineList[2]
                #sequence_file = sequence_file[49:]
            elif lineList[1] == "Description": #where to start
                looseLine = hmmPfam_file.readline() #get rid of useless line

                #get the gi, score and evalue
                while 1:
                    scoreLine = hmmPfam_file.readline()
                    tmpList = scoreLine.split()
                    if len(tmpList) > 3:  #make sure line has something in it
                        if tmpList[0] != "Parsed":
                            hmm = tmpList[0] #model is first in position
                            score = scoreLine[55:62] #score is positions 55 to 61
                            evalue = scoreLine[64:73] #evalue is positions 64 to 72
                            file_data.append([sequence_file, hmm, score, evalue, hmm_db]
                    else: #got what we need, break out of while loop
                        i = 0
```

```
                        break
    return file_data

def doesItBelong(hmmPfamDataList, efdList, sfList, subList, famList):
    """Return a list that indicates if query sequence has hit an hmm (read sf/sub/fa

    [sequence_file, hmm, yes/no, score, evalue, sf id, sf name, sub id, sub name, f
    """
    listOlists = []
    yesNoUnk_list = []
    trouble_list = []
    efd_gi_list = []
    sf_hmm_list = []
    sub_hmm_list = []
    fam_hmm_list = []
    no_hit_list = []

    for i in efdList:
        efd_gi_list.append(i[0])

    for j in sfList:
        sf_hmm_list.append(j[3])

    for k in subList:
        sub_hmm_list.append(k[3])

    for m in famList:
        fam_hmm_list.append(m[3])

    for entry in hmmPfamDataList:
        tmp_gi = entry[0][:-3] #get the gi of the entry, loose the '.fa' file extension
        #tmp_gi = tmp_gi[27:]
        if tmp_gi in efd_gi_list: # make sure that this gi is in the list (some aren't)
            tmp_hmm = entry[1]
            if tmp_hmm == "Enolase":
                tmp_hmm = "enolase.60"
            elif tmp_hmm == "g-humulene-tmp":
                tmp_hmm = "g-humulene"
            elif tmp_hmm == "galD":
                tmp_hmm = "gald.90"
            tmp_hmm = tmp_hmm + ".hmm"  # get the hmm filename from the entry,

            if tmp_hmm in sf_hmm_list: # is this filename a SF hmm file?
                index_sflist = sf_hmm_list.index(tmp_hmm) # what index of the SF list
                SFid_hit = sfList[index_sflist][0] # get the id of this SF, the SFid of the 'h
```

```
        index_efdlist = efd_gi_list.index(tmp_gi) # find the index of the gi entry i
        SFid_real = efdList[index_efdlist][5] # get the real SFid of the gi number

        if SFid_hit != SFid_real: # the two id's don't match, this gi has hit an hm
                                     # doesn't belong to!
            sfName = sfList[index_sflist][1]
            # add to the yes/no list with the following format
            #              seq file, hmm file hit, yes/no,  score,   evalue,  sf id hit, sf
            yesNoUnk_list.append([entry[0], entry[1],    "NO",   (entry[2]), (entry[3
        else: # this gi has hit it's own SF
            sfName = sfList[index_sflist][1]
            # add to the yes/no list with the following format
            #              seq file, hmm file hit, yes/no,  score,   evalue,  sf id hit, sf
            yesNoUnk_list.append([entry[0], entry[1],    "YES",   (entry[2]), (entry[

    elif tmp_hmm in sub_hmm_list: # is this filename a Subgroup hmm file?
        index_sub = sub_hmm_list.index(tmp_hmm) # what index of the subgrc
        subid_hit = subList[index_sub][0] # get the id of this subgroup, the subic

        index_efdlist = efd_gi_list.index(tmp_gi) # find the index of the gi entry i
        subid_real = efdList[index_efdlist][4] # get the real sub id of the gi numb
        subName = subList[index_sub][1]

        if subid_hit != subid_real: # the two id's don't match, this gi has hit an hr
                                       # doesn't belong to!
            # add to the yes/no list with the following format
            #              seq file, hmm file hit, yes/no,  score,   evalue,  sf id hit, sf
            yesNoUnk_list.append([entry[0], entry[1],    "NO",   (entry[2]), (entry[3
        else: # this gi has hit it's own subgroup
            # add to the yes/no list with the following format
            #              seq file, hmm file hit, yes/no,  score,   evalue,  sf id hit, sf
            yesNoUnk_list.append([entry[0], entry[1],    "YES",   (entry[2]), (entry[
    elif tmp_hmm in fam_hmm_list:
        index_fam = fam_hmm_list.index(tmp_hmm) # what index of the family
        famid_hit = famList[index_fam][0] # get the id of this family, the subid of

        index_efdlist = efd_gi_list.index(tmp_gi) # find the index of the gi entry i
        famid_real = efdList[index_efdlist][1] # get the real fam id of the gi numb
        famName = famList[index_fam][1]

        if famid_hit != famid_real: # the two id's don't match, this gi has hit an hi
                                      # doesn't belong to!
            # add to the yes/no list with the following format
            #              seq file, hmm file hit, yes/no,  score,   evalue,  sf id hit, sf
            yesNoUnk_list.append([entry[0], entry[1],    "NO",   (entry[2]), (entry[3
        else: # this gi has hit it's own family
```

```
                    # add to the yes/no list with the following format
                    #              seq file, hmm file hit, yes/no,  score,   evalue,  sf id hit, sf
                    yesNoUnk_list.append([entry[0], entry[1],    "YES",   (entry[2]), (entry[
            else: # no hit was found
                no_hit_list.append(entry)


        else: #gi is not in the the gi (efd) list, classify as unknown
            yesNoUnk_list.append([entry[0], entry[1], "UNK", (entry[2]), (entry[3]), "X",

    #check that identifier exists in the set I"m looking at

    listOlists.append(yesNoUnk_list)
    listOlists.append(no_hit_list)
    #print yesNoUnk_list
    return listOlists

def printOutList(inputList, fileOutName):
    """Print out the input list  sorted by a element of the internal list

    INPUT: (1) inputList
        This is a list of data in the format
    [sequence_file, hmm, yes/no, score, evalue, sf id, sf name, sub id, sub name, f

    (2) fileOutName
    This is the name of the output file to be opened and written to in this
    function
     OUTPUT: file named 'fileOutName'
        The output in the file is sorted and grouped by the 2nd element in the file
        There is a blank line in between each file
    grouping in the file
     Nothing returned.

    """
    fileOut = open(fileOutName, "w")

    inputList.sort(lambda x, y: cmp(x[1], y[1])) # sort by 'hmm file', 2nd element
                                                 # in internal list

    hold = inputList[0][1]
    for entry in inputList:
        compare_to = entry[1]
        if hold == compare_to: # print out the entry
            outString = ';'.join(entry)
            fileOut.write(outString)
            fileOut.write("\n")
```

```
    else:
        fileOut.write("\n") # blank line between file entries
        hold = entry[1] #update hold
        outString = ';'.join(entry) #print out the entry
        fileOut.write(outString)
        fileOut.write("\n")

fileOut.close()
return
```

Appendix F. Keyword Dictionaries for Misannotation Analysis

F.1. Enolase

enolase
phosphopyruvate
2\-phospho\-D\-glycerate
phosphoglycerate
4\.2\.1\.11
phosphoenolpyruvate

F.2. Galactonate dehydratase

galactonate
4\.2\.1\.6
galactonate dehydratase
galactonate dehydrase
galactonate hydro-lyase

F.3. Mandelate racemase

5\.1\.2\.2
mandelate
mandelate racemase

F.4. Glucarate dehydratase

4\.2\.1\.40
glucarate
glucarate hydro-lyase
glucarate dehydratase

F.5. Methylaspartate ammonia-lyase

methylaspartate

ammonia-lyase
methylaspartase
4\.3\.1\.2
methylaspartate ammonia-lyase
b-methylaspartase
3-methylaspartase

F.6. Ortho-succinyl benzoate synthase

succinylbenzoate
succinylbenzoyl
succinylbenzoic
OSBS
OXYBUTYRIC
menC
chorismate
OSB

F.7. Dipeptide epimerase

L\-Ala\-DL\-Glu Epimerase
L\-alanine\-DL\-glutamate epimerase
dipeptide epimerase
dipeptide
epimerase

F.8. Chloromuconate cycloisomerase

5\.5\.1\.7
2\-chloro\-2\,5\-dihydro\-5\-oxofuran\-2\-acetate lyase \(decyclizing\)
Chloromuconate cycloisomerase
chloromuconate lactonizing enzyme
muconate lactonizing enzyme II
muconate lactonizing enzyme 2
MLE2
MLE 2
muconate cycloisomerase II
Chloromuconate
MLE II
MLEII

F.9. Muconate cycloisomerase

5\.5\.1\.1
4\-carboxymethyl\-4\-hydroxyisocrotonolactone lyase \(decyclizing\)

MLE
muconate
MLE I
MLEI
MLE1
MLE 1
muconate lactonizing enzyme

F.10. L-Fuconate dehydratase

fuconate
fuconate dehydratase
2\-keto\-3\-deoxy\-L\-fuconate
L\-fucose
fucose
4\.2\.1\.68

F.11. Dodecenoyl-CoA delta-isomerase (mitochondrial)

dodecenoyl\-CoA delta\-isomerase \(mitochondrial\)
dodecenoyl\-CoA isomerase
dodecenoyl\-CoA \(3Z\)\-\(2E\)\-isomerase
dodecenoyl\-CoA D\-isomerase
D3\-cis\-D2\-trans\-enoyl\-CoA isomerase
acetylene\-allene isomerase
dodecenoyl\-CoA D\-isomerase
dodecenoyl\-CoA D3\-cis\-D2\-trans\-isomerase
3\-2trans\-enoyl\-CoA isomerase
Mitochondrial 3\,2\-Enoyl\-Coa
3\,2\-Enoyl\-Coa
dodecenoyl\-CoA
3\-2trans\-enoyl\-CoA
3\-2trans\-enoyl
3\,2\-Enoyl\
5\.3\.3\.8

F.12. Delta(3,5)-delta(2,4)-dienoyl-CoA isomerase

delta\(3\,5\)\-delta\(2\,4\)\-dienoyl\-CoA isomerase
delta\(3\,5\)\-delta\(2\,4\)\-dienoyl\-CoA
delta\(3\,5\)\-delta\(2\,4\)\-dienoyl
3\,5\-dienoyl\-CoA
2\,4\-dienoyl\-CoA
dienoyl\-CoA isomerase
dienoyl\-CoA

F.13. Methylmalonyl-CoA decarboxylase

methylmalonyl\-CoA decarboxylase
methylmalonyl\-CoA
methylmalonyl
propionyl\-CoA carboxylase
methylmalonyl coenzyme A
propionyl coenzyme A carboxylase
methylmalonyl\-coenzyme A decarboxylase
\(S\)\-methylmalonyl\-CoA carboxy\-lyase
propionyl\-CoA
propionyl coenzyme A
4\.1\.1\.41

F.14. 3-Hydroxyisobutyryl-CoA hydrolase

3\-hydroxyisobutyryl\-CoA hydrolase
hydroxyisobutyryl
3\-hydroxyisobutyryl\-CoA
3\-hydroxyisobutyrate
hydroxyisobutyrate
3\-hydroxy\-isobutyryl CoA hydrolase
HIB CoA deacylase
3\-hydroxy\-2\-methylpropanoyl\-CoA hydrolase
isobutyryl
methylpropanoyl
3\.1\.2\.4

F.15. 4-Chlorobenzoate dehalogenase

3\.8\.1\.7
4\-chlorobenzoate dehalogenase
chlorobenzoate dehalogenase
chlorobenzoate
4\-chlorobenzoyl\-CoA
4\-hydroxybenzoyl\-CoA
chlorobenzoyl
chlorohydrolase
4\-CBA\-CoA dehalogenase
4\-CBA\-CoA
4\-chlorobenzoyl CoA chlorohydrolase

F.16. 1,4-Dihydroxy-2-napthoyl-CoA synthase

1\,4\-dihydroxy\-2\-napthoyl\-CoA synthase
1\,4\-dihydroxy\-2\-napthoyl\-CoA

napthoyl
napthoate
dihydroxynaphthoic

F.17. Methylmalonyl-CoA epimerase

5\.1\.99\.1
methylmalonyl\-CoA epimerase
mmce
\(2R\)\-methylmalonyl\-CoA
\(2S\)\-methylmalonyl\-CoA
methylmalonyl\-CoA racemase
methylmalonyl coenzyme A racemase
DL\-methylmalonyl\-CoA racemase
methylmalonyl\-CoA 2\-epimerase
methylmalonyl\-CoA

F.18. 4-Hydroxyphenylpyruvate dioxygenase

4\-hydroxyphenylpyruvate dioxygenase
hydroxyphenylpyruvate dioxygenase
4\-hydroxyphenylpyruvate
homogentisate
hydroxyphenylpyruvate
p\-hydroxyphenylpyruvic hydroxylase
p\-hydroxyphenylpyruvate hydroxylase
p\-hydroxyphenylpyruvate oxidase
p\-hydroxyphenylpyruvic oxidase
p\-hydroxyphenylpyruvate dioxygenase
p\-hydroxyphenylpyruvic acid hydroxylase
4\-hydroxyphenylpyruvic acid dioxygenase
4\-hydroxyphenylpyruvate\:oxygen oxidoreductase \(hydroxylating\, decarboxylating\)
hydroxyphenylpyruvic
1\.13\.11\.27
4HPPD
HPD
HPPDase

F.19. FosA

2\.5\.1\.18
fosfomycin resistance protein FosA
FosA
fosfomycin

F.20. Glyoxalase I

4\.4\.1\.5
glyoxalase I
glyoxalase
S\-D\-lactoylglutathione
lactoylglutathione lyase
lactoylglutathione
methylglyoxal
methylglyoxalase
aldoketomutase
ketone\-aldehyde mutase
\(R\)\-S\-lactoylglutathione methylglyoxal\-lyase \(isomerizing\)

F.21. 5-Epi-aristolochene synthase

epi\-aristolochene synthase
epi\-aristolochene cyclase
farnesyl diphosphate \(FPP\)
5\-epi\-aristolochene
epi\-aristolochene
aristolochene
farnesyl diphosphate

F.22. Bornyl diphosphate synthase

5\.5\.1\.8
bornyl diphosphate synthase
bornyl diphosphate cyclase
bornyl synthase
bornyl cyclase
bornyl pyrophosphate synthase
bornyl pyrophosphate synthetase
\(\+\)\-bornylpyrophosphate cyclase
\(\+\)\-bornyl\-diphosphate lyase \(decyclizing\)
bornyl
geranyl\-diphosphate cyclase
geranyl

F.23. Pentalenene synthase

4\.2\.3\.7
pentalenene synthase
pentalenene cyclase
pentalenene
pentalenene synthetase

2\-trans\,6\-trans\-farnesyldiphosphate diphosphate\-lyase \(cyclizing\, pentalenene\-forming\)
farnesyldiphosphate
farnesyl diphosphate

F.24. Squalene-hopene synthase

5\.4\.99\.17
squalene\-hopene synthase
squalene\-hopene cyclase
squalene
hopene
squalene mutase \(cyclizing\)

F.25. Trichodiene synthase

4\.2\.3\.6
trichodiene synthase
trichodiene cyclase
trichodiene synthetase
trans\,trans\-farnesyl\-diphosphate sesquiterpenoid\-lyase
trans\,trans\-farnesyl\-diphosphate diphosphate\-lyase \(cyclizing\, trichodiene\-forming\)
trichodiene
farnesyl\-diphosphate

F.26. Aristolochene synthase

4\.2\.3\.9
aristolochene synthase
aristolochene cyclase
trans\,trans\-farnesyl diphosphate aristolochene\-lyase
trans\,trans\-farnesyl\-diphosphate diphosphate\-lyase \(cyclizing\, aristolochene\-forming\)
aristolochene
farnesyl diphosphate
farnesyl\-diphosphate

F.27. Deoxy-d-mannose-octulosonate 8-phosphate phosphatase

3\.1\.3\.45
deoxy\-d\-mannose\-octulosonate 8\-phosphate phosphatase
octulosonate
3\-deoxy\-D\-manno\-octulosonate 8\-phosphate

3\-deoxy\-d\-manno\-octulosonate
3\-deoxy\-manno\-octulosonate\-8\-phosphatase
3\-deoxy\-D\-manno\-octulosonate\-8\-phosphate 8\-phosphohydrolase
8\-phosphate phosphatase
8\-phosphohydrolase
8\-phosphate
deoxy\-d\-mannose
3\-deoxy\-D\-manno
deoxy\-D\-manno

F.28. Phosphonoacetaldehyde hydrolase

3\.11\.1\.1
phosphonoacetaldehyde hydrolase
phosphonoacetaldehyde
phosphonatase
2\-phosphonoacetylaldehyde phosphonohydrolase
2\-oxoethylphosphonate phosphonohydrolase
phosphonohydrolase

F.29. 2-Haloacid dehalogenase

3\.8\.1\.2
2\-haloacid dehalogenase
haloacid
HAD
\(S\)\-2\-haloacid dehalogenase
2\-haloacid halidohydrolase
2\-haloalkanoic acid dehalogenase
haloalkanoic
2\-haloalkanoid acid halidohydrolase
haloalkanoid
2\-halocarboxylic acid dehalogenase II
halocarboxylic
DL\-2\-haloacid dehalogenase
L\-2\-haloacid dehalogenase
L\-DEX\,\(S\)\-2\-haloacid halidohydrolase
halocarboxylic acid halidohydrolase
L\-2\-halo acid dehalogenase
halo acid
halo\-acid

F.30. Beta-phosphoglucomutase

5\.4\.2\.6
beta\-phosphoglucomutase

d\-glucose 1\-phosphate
d\-glucose 6\-phosphate
phosphoglucomutase
b\-phosphoglucomutase
b\-D\-glucose 1\,6\-phosphomutase
b\-glucose 1\-phosphate
phosphomutase

F.31. Cytosine deaminase

3\.5\.4\.1
cytosine deaminase
cytosine
uracil
isocytosine deaminase
cytosine aminohydrolase
CDA
isocytosine

F.32. Adenosine deaminase

3\.5\.4\.4
adenosine deaminase
deoxyadenosine deaminase
adenosine aminohydrolase

F.33. N-acyl-d-amino-acid deacyclase

3\.5\.1\.81
n\-acyl\-d\-amino\-acid deacylase
Daa
N\-acyl\-D\-amino acid
N\-acyl\-D\-amino acid amidohydrolase
D\-aminoacylase
N\-acyl\-D\-aspartate deacylase
N\-acyl\-D\-glutamate deacylase
aminoacylase
n\-acyl\-d\-amino\-acid
N\-acyl\-D\-aspartate
N\-acyl\-D\-glutamate

F.34. L-hydantoinase

L\-hydantoinase
L\-hyd

L\-selective hydantoinase
dihydropyrimidinase
hydantoinase
hydropyrimidine hydrase
hydantoin peptidase
hydantoin
pyrimidine hydrase
5\,6\-dihydropyrimidine amidohydrolase
3\.5\.2\.2

F.35. D-hydantoinase

D\-hydantoinase
hydantoinase
5\,6\-dihydrouracil
3\.5\.2\.2
dihydropyrimidinase
hydantoinase
hydropyrimidine hydrase
hydantoin peptidase
pyrimidine hydrase
5\,6\-dihydropyrimidine amidohydrolase

F.36. Urease

3\.5\.1\.5
urease
UreC
urea
urea amidohydrolase
UreB

F.37. Isoaspartyl dipeptidase

isoaspartyl dipeptidase
Iad
beta\-aspartyl dipeptidase
isoaspartyl
beta\-aspartyl

Appendix G. R Scripts for Analysis and Figures (Chapter 2)

```
#AHFamilyMisKey.r, Example r script for making the family/DB misannotation
plots

Sys.setenv(R_GSCMD="/sw/bin/gs")
dbNames=c("NR",  "TrEMBL", "KEGG", "Swiss-Prot")

#basic background
ahSFDB=read.table("ahSFMisKeyallDB.dat", header = T)
ahSFDBmatrix=as.matrix(ahSFDB)
ahBarLocations = c(0.7, 1.9, 3.1, 4.3)
#bitmap(file="/Users/schnoes/Alex/Misannotation/AnnotationWork/
MisannotationPaper/FiguresTables/PercentMisannotationFigs/TEST/
ahFamilyMis.tiff", type="tiff24nc", height=5.2, width=8.9, res=600, pointsize=14)
postscript(file="/Users/schnoes/Alex/Misannotation/AnnotationWork/
MisannotationPaper/FiguresTables/PercentMisannotationFigs/TEST/
ahFamilyMis.eps",  height=4, width=5.5,  pointsize=10, onefile=FALSE,
horizontal=FALSE)
par(cex.axis=1.25)
par(mar=c(5.1, 6,4.1, 2.1), font.lab=2, font.main=2, font.axis=1, cex.main=2,
cex.lab=1.5)
barplot( height=c(0,0,0,0), main="AH Superfamily", names.arg=dbNames,
ylim=c(-15,119), xlab="Database", ylab="Percent Misannotation",col=c("black",
"black", "black", "black"))
barplot( height=c(100, 100, 100, 100),  add=TRUE, axes=FALSE, col=c("white",
"white", "white", "white"))
symbols(ahBarLocations[1], ahSFDBmatrix[1], rectangles=matrix(c(1,1.5),
nrow=1, ncol=2), inches=FALSE, add=TRUE, fg="black", bg="black")
symbols(ahBarLocations[2], ahSFDBmatrix[2], rectangles=matrix(c(1,1.5),
nrow=1, ncol=2), inches=FALSE, add=TRUE, fg="black", bg="black")
symbols(ahBarLocations[3], ahSFDBmatrix[3], rectangles=matrix(c(1,1.5),
nrow=1, ncol=2), inches=FALSE, add=TRUE, fg="black", bg="black")
symbols(ahBarLocations[4], ahSFDBmatrix[4], rectangles=matrix(c(1,1.5),
nrow=1, ncol=2), inches=FALSE, add=TRUE, fg="black", bg="black")




#NR
ahNRFam=read.table("ahFamNR.dat", header = T, as.is=T)
ahNRFamData=data.frame(ahNRFam)
points(ahNRFamData[,1], ahNRFamData[,2], col=ahNRFamData[,3],
pch=ahNRFamData[,4], cex=ahNRFamData[,5])


#TR
ahTRFam=read.table("ahFamTR.dat", header = T, as.is=T)
```

```
ahTRFamData=data.frame(ahTRFam)
points(ahTRFamData[,1], ahTRFamData[,2], col=ahTRFamData[,3],
pch=ahTRFamData[,4], cex=ahTRFamData[,5])

#KG
ahKGFam=read.table("ahFamKG.dat", header = T, as.is=T)
ahKGFamData=data.frame(ahKGFam)
points(ahKGFamData[,1], ahKGFamData[,2], col=ahKGFamData[,3],
pch=ahKGFamData[,4], cex=ahKGFamData[,5])


#SP
ahSPFam=read.table("ahFamSP.dat", header = T, as.is=T)
ahSPFamData=data.frame(ahSPFam)
points(ahSPFamData[,1], ahSPFamData[,2], col=ahSPFamData[,3],
pch=ahSPFamData[,4], cex=ahSPFamData[,5])

dev.off()

------------------------------------------------------------------#legend.r, code to
make the legend for the family/DB misannotation plots
Sys.setenv(R_GSCMD="/sw/bin/gs")
dbNames=c("NR",  "TrEMBL", "KEGG", "Swiss-Prot")

#basic background
#bitmap(file="/Users/schnoes/Alex/Misannotation/AnnotationWork/
MisannotationPaper/FiguresTables/PercentMisannotationFigs/TEST/legend.tiff",
type="tiff24nc", height=5.2, width=8.9, res=600, pointsize=14)
postscript(file="/Users/schnoes/Alex/Misannotation/AnnotationWork/
MisannotationPaper/FiguresTables/PercentMisannotationFigs/TEST/legend.eps
",  height=4, width=5.5,  pointsize=10, onefile=FALSE, horizontal=FALSE)
par(cex.axis=1.25)
par(mar=c(5.1, 6,4.1, 2.1), font.lab=2, font.main=2, font.axis=1, cex.main=2,
cex.lab=1.5)
barplot( height=c(0,0,0,0), main=" Superfamily", names.arg=dbNames,
ylim=c(-15,119), xlab="Database", ylab="Percent Misannotation",col=c("black",
"black", "black", "black"))
barplot( height=c(100, 100, 100, 100),  add=TRUE, axes=FALSE, col=c("white",
"white", "white", "white"))

points(.5, 50, col="black", pch=19, cex=4.4)
points(1.7, 50, col="black", pch=19, cex=3)
points(2.8, 50, col="black", pch=19, cex=2)
points(4, 20, col="black", pch=21, cex=2)
points(4, 20, col="black", pch=4, cex=3)
```

```
dev.off()

--------------------------------------------------------------------------------# FracIncorFigure.r,
part of the misannotation over time figure

Sys.setenv(R_GSCMD="/sw/bin/gs")
incYears=read.table("incorrect.year.list")
allYears=read.table("all.year.list")

bin=seq(1992.5, 2006.5, by=1)
histAll=hist(allYears$V1, breaks=bin)
histInc = hist(incYears$V1, breaks = bin)

fractionIncorrect=histInc$counts/histAll$counts
postscript(file="/Users/schnoes/Alex/Writing/Thesis/Chapter3/MisOverTime/
fractIncorrect.eps", height=5, width=7,  pointsize=12, onefile=FALSE,
horizontal=FALSE)
par(cex.axis=1)
par(mar=c(5.1, 6,4.1, 4), font.lab=2, font.main=2, font.axis=1, cex.lab=1.15)

plot(histAll$mids[1:13], fractionIncorrect[1:13], type='b', xlab="Year",
ylab="Fraction of Total Sequences", main='Fraction of Misannotated Sequences
Deposited per Year\n (NR DB)', axes=FALSE, frame.plot=T, ylim=c(0, 0.5))

axis(2, at=seq(0.1:0.6, by=0.1), labels=seq(0.1:0.6, by=0.1))
axis(1, at=c(1993:2005),  labels=c(1993:2005))
dev.off()

--------------------------------------------------------------------------------#timeVmis-noadd.r,
second part of the misannotation over time figure

Sys.setenv(R_GSCMD="/sw/bin/gs")
incYears=read.table("incorrect.year.list")
corYears=read.table("correct.year.list")

bin=seq(1992.5, 2006.5, by=1)
histInc = hist(incYears$V1, breaks = bin)
histCor = hist(corYears$V1, breaks = bin)
temp1 = histCor$counts

temp2 = histInc$counts


matrixCounts= matrix(data= c(temp1, temp2), ncol=2)
matrixCountsTrans= t(matrixCounts)
#bitmap(file="/Users/schnoes/Alex/Misannotation/AnnotationWork/
```

```
MisannotationPaper/FiguresTables/Time:Misannotation/timeVMis.tiff",
height=5.2, width=8.9, res=600, pointsize=14)
postscript(file="/Users/schnoes/Alex/Misannotation/AnnotationWork/
MisannotationPaper/FiguresTables/Time:Misannotation/timeVMis.eps",
height=5, width=7,  pointsize=12, onefile=FALSE, horizontal=FALSE)
par(cex.axis=1)
par(mar=c(5.1, 6,4.1, 4), font.lab=2, font.main=2, font.axis=1, cex.lab=1.15)

barplot(matrixCountsTrans[,1:13], beside=FALSE,
names.arg=histInc$mids[1:13], ylim=c(0, 1200), col=c("forestgreen", "firebrick"),
, main="All Superfamily Sequences Deposited by Year\n (NR DB)", xlab="Year",
ylab="Number of Sequences")

legend(x=1, y=800, legend=c("Correct Annotations", "Incorrect Annotations"),
col=c("black", "black"), pch=22, pt.bg=c("forestgreen", "firebrick"),
pt.cex=c(1.75,1.75))
dev.off()

-------------------------------------------------------------------------------
#evCodesPie.r, misannotation code pie chart

Sys.setenv(R_GSCMD="/sw/bin/gs")
evCodes=read.table("evidenceCodesPer.dat", header=T, as.is=T)
evCodesData=data.frame(evCodes)
evCodeNames=c("NSA", "MFR", "SFA", "BTC")
#bitmap(file="/Users/schnoes/Alex/Misannotation/AnnotationWork/
MisannotationPaper/FiguresTables/EvidenceCodesFigure/evCodesPie.tiff",
type="tiff24nc", height=5.2, width=8.9, res=600, pointsize=14)
postscript(file="/Users/schnoes/Alex/Misannotation/AnnotationWork/
MisannotationPaper/FiguresTables/EvidenceCodesFigure/evCodesPie.eps",
height=5, width=7,  pointsize=12, onefile=FALSE, horizontal=FALSE)
par(cex.axis=1.25)
par(mar=c(10, 20, 20, 20), font.lab=2, font.main=2, font.axis=1, cex.main=2,
cex.lab=1.5)
bisectors = pie3D(evCodesData[,1],  col=c("slategray1", "slategray1",
"royalblue4", "royalblue4" ), explode=0, labelcex=2.5, font=2, theta=.4,
labelcol="black", radius=.9, main="Types of Misannotation")
pie3D.labels(bisectors, radius=.7, labels=evCodeNames)
legend(1,1, legend = c("Misannotations due to overprediction", "Missanotations
not due to overprediction"),col=c("black", "black"), pch=22, pt.bg=c("slategray1",
"royalblue4"), pt.cex=c(1.75,1.75))
dev.off()


#legend
postscript(file="/Users/schnoes/Alex/Misannotation/AnnotationWork/
```

```
MisannotationPaper/FiguresTables/EvidenceCodesFigure/legend.eps",
height=5, width=7,  pointsize=12, onefile=FALSE, horizontal=FALSE)
barplot( height=c(0,0,0,0),  ylim=c(-15,119), col=c("black", "black", "black",
"black"))
legend(1, 100, legend = c("Misannotations due to overprediction",
"Missanotations not due to overprediction"),col=c("black", "black"), pch=22,
pt.bg=c( "royalblue4", "slategray1"), pt.cex=c(1.75,1.75))
dev.off()
```

Appendix H. Program—runHMMSearchSFLD.py

```
#!/usr/bin/python2.3

"""runHMMSearchSFLD.py
    This program takes in superfamily info and database info and runns hmmsearc
    on the databases using the specified superfamily HMMs.

    INPUT:
        --dbName=<name of the database>
        --supFamListFile=<list of Superfamilies>
        --SFFile=<super Fam data file>
        --SFHMMFile=<superfam HMM file>
        --FamHMMFile=<Fam HMM file>
        --SubHMMFile=<Subgroup HMM File>
        --hmmPath=<path to hmms>
        --runningPath=<path to working directory>

   OUTPUT:
        A '.hmmsearch' file for every HMM specified against the input DB.


     Other important info
     Need python modules written in lab
    common.py

    Need to have programs set up
        NCBI (blast etc)
        (remember to have .ncbirc file in directory and set up correctly)
    HMMER package
         (make sure to have the fasta databases that this needs)

    Need to have variable $BLASTDB set appropriate e.g.
        setenv BLASTDB /usr/local/Blast/blastDBDir/

Author: Alexandra M. Schnoes from code by
Shoshana Brown (some functions based on SFLDsql.py code by Scott Pegg)
Last Modified: 6/8/04

Modified: Alexandra M. Schnoes 8/26/04
    Added comments and changed paths
    Alexandra M. Schnoes 01/31/05
    Translating code to NOT use mysql so it can run on the clusters
    Alexandra M. Schnoes 01/10/06:
        Updating comments.

"""
```

```
import sys
import os
import os.path
import string
import getopt
import re
import common


######################################################################
# checkArg
######################################################################
def checkArg(argv):
    """Exit with error and print usage if not enough arguments."""
    #am supposed to have 9 arguments assuming that the options are written
    #option=something
    #also assume that path is passed in with trailing '/'

    errorString = """Usage:runHMMSearchSFLD.py --dbName=<name of the datab
        --supFamListFile=<list of Superfamilies> --SFFile=<super Fam data file>
        --SFHMMFile=<superfam HMM file> --FamHMMFile=<Fam HMM file>
        --SubHMMFile=<Subgroup HMM File> --hmmPath=<path to hmms>
        --runningPath=<path to working directory>"""

    if len(argv) == 9:
        pass
    else:
        print errorString
        sys.exit(1)


######################################################################
# getSFNameList
######################################################################
def getSFNameList(superfamilyListFileName):
   inFile = open(superfamilyListFileName, "r")
   SFNameList = []

   while 1:
      line = inFile.readline()
      if not line:
         break
      line = string.strip(line)
      if len(line) > 0:
         SFNameList.append(line)
   inFile.close()
```

```
   return SFNameList

######################################################
# MapSFNameToID
######################################################
def MapSFNameToID(SFName_and_ID_file):
    inFile = open(SFName_and_ID_file, 'r')
    Name_ID_dict = {}

    while 1:
        line = inFile.readline()
    line = line[:-1]
    tmpList = line.split(';')
    if len(tmpList) > 1:
        Name_ID_dict[tmpList[1]] = tmpList[0]
    else:
        break

    return Name_ID_dict

######################################################
# getSFIDList
######################################################
def getSFIDList(superfamilyListFileName, SFName_and_ID_file):
    SFNameList = getSFNameList(superfamilyListFileName)
    SFIDList = []
    SFName_id_dict = MapSFNameToID(SFName_and_ID_file)
    size = len(SFNameList)
    i = 0
    while i < size:
       SFIDList.append(SFName_id_dict[SFNameList[i]])
       i = i + 1

    return SFIDList

######################################################
# returnList
######################################################
def returnList(fileName, num_elements):
   fileList = []

   inFile = open(fileName, 'r')

   while 1:
      line = inFile.readline()
```

```
    line = line[:-1]
    tmpList = line.split(';')
    if tmpList == ['']:
      break
    elif len(tmpList) == num_elements:
      for index in range(0, len(tmpList)):
     if tmpList[index] == 'None':
        tmpList[index] = None
      fileList.append(tmpList)
    else:
      break


  return fileList


######################################################################
# STAY
# Retrieves the names of all superfamily, family & subgroup HMMs from the SFLD
# that correspond to the superfamilies specified in SFIDList.
#
# Input:
#  SFIDList: A list of superfamily identifiers from the SFLD
# Returns:
#  hmmDict: A dictionary with key = SFID, value = list with structure:
#          [superfamilyHMMName, famIDHMMDict, subIDHMMDict]
#          famIDHMMDict and subIDHMMDict are dictionaries with key =
#          family/subgroup ID, value = HMM file name.
######################################################################
def getHMMDict(SFIDList, SFHMMListName, FamHMMListName, SubHMMListN

  hmmDict = {}

  num_elements = 2
  SFHMMList = returnList(SFHMMListName, num_elements)
  #print SFHMMList

  num_elements = 3
  SubHMMList = returnList(SubHMMListName, num_elements)
  #print SubHMMList

  num_elements = 3
  FamHMMList = returnList(FamHMMListName, num_elements)
  #print FamHMMList

  for SFID in SFIDList:
```

```
    #print SFID

    for index in range(0, len(SFHMMList)):
      if SFID == SFHMMList[index][0]:
      SFHMM = SFHMMList[index][1]
      #print SFHMM


    famIDHMMDict = {}
    for index in range(0, len(FamHMMList)):
      if SFID == FamHMMList[index][0]:
      id = FamHMMList[index][1]
      hmmName = FamHMMList[index][2]
      if hmmName != None:
        famIDHMMDict[id] = hmmName

    #print famIDHMMDict

    subIDHMMDict = {}
    for index in range(0, len(SubHMMList)):
      if SFID == SubHMMList[index][0]:
     id = SubHMMList[index][1]
     hmmName = SubHMMList[index][2]
     if hmmName != None:
       subIDHMMDict[id] = hmmName

    #print subIDHMMDict
    hmmDict[SFID] = [SFHMM, famIDHMMDict, subIDHMMDict]

  return hmmDict


#####################################################################
#
# Runs hmmsearch against the NCBI nr database at an e-value cutoff of
# eValueCutoff, using each HMM in hmmDict.  Parses each hmmsearch output fil
# to get the domain hits, and stores each unique hit in SFHitsDict according
# to the superfamily of the HMM that found it.
#
# Input:
#  hmmDict: A dictionary with key = SFID, value = list with structure:
#          [superfamilyHMMName, famIDHMMDict, subIDHMMDict]
#          famIDHMMDict and subIDHMMDict are dictionaries with key =
#          family/subgroup ID, value = HMM file name.
#  path: A string specifying the path for the directory that contains the SFLD
#        HMM files.
```

```
# Returns:
#  SFHitsDict: A dictionary with key = SFID, value = list of all unique gi
#            numbers found by hmmsearch at an e-value cutoff of eValueCutoff,
#            using the HMMs corresponding to SFID in hmmDict.
######################################################################
def runHMMSearch(dbName, hmmDict, hmmPath, runningPath):
  print 'def runHMMSearch(dbName, hmmDict, hmmPath, runningPath):'
  sys.stdout.flush()

  eValueCutoff = "10"
  bitscore = "10"
  SFHitsDict = {}

  for SFID in hmmDict.keys():

    tempHitGIList = []

    #Run hmmsearch for each HMM in a given superfamily, & parse the results

    #First run hmmsearch with superfamily HMM, if present, & parse results
    if hmmDict[SFID][0] != None:
      superfamilyHMMFileName = hmmPath + hmmDict[SFID][0]
      hmmsearchOutFileName = runningPath + "SF" + str(SFID) + ".hmmsearch"
      cmd = "hmmsearch -T %s %s %s > %s" % (bitscore, superfamilyHMMFileN
      os.system(cmd)

    #Then run hmmsearch with each family HMM, & parse the results
    famIDHMMDict = hmmDict[SFID][1]
    for famID in famIDHMMDict.keys():
      famHMMFileName = hmmPath + famIDHMMDict[famID]
      hmmsearchOutFileName = runningPath + "SF" + str(SFID) + "Fam" + str(fa
      cmd = "hmmsearch -T %s %s %s > %s" % (bitscore, famHMMFileName, db
      os.system(cmd)

    #Then run hmmsearch with each subgroup HMM
    subIDHMMDict = hmmDict[SFID][2]
    for subID in subIDHMMDict.keys():
      subHMMFileName = hmmPath + subIDHMMDict[subID]
      hmmsearchOutFileName = runningPath + "SF" + str(SFID) + "Sub" + str(su
      cmd = "hmmsearch -T %s %s %s > %s" % (bitscore, subHMMFileName, db
      os.system(cmd)


######################################################################
# Main program
######################################################################
```

```
def runHMMSearchSFLD(argv):
    """Main program."""
    print "checkArg(argv)"
    sys.stdout.flush()
    checkArg(argv)
    shortOpts = ''
    longOpts = ['dbName=', 'supFamListFile=', 'SFFile=', 'SFHMMFile=', 'FamHMMF
        'SubHMMFile=', 'hmmPath=', 'runningPath=']
    opts, args = getopt.getopt(sys.argv[1:], shortOpts, longOpts)

    for option, value in opts:
        if option in ('--dbName'):
            dbName = value
        elif option in ('--supFamListFile'):
            superfamilyListFileName = value
        elif option in ('--SFFile'):
            SFName_and_ID_file = value
        elif option in ('--SFHMMFile'):
            SFHMMListName = value
        elif option in ('--FamHMMFile'):
            FamHMMListName = value
        elif option in ('--SubHMMFile'):
            SubHMMListName = value
        elif option in ('--hmmPath'):
            hmmPath = value
        elif option in ('--runningPath'):
            runningPath = value

    print 'SFIDList = getSFIDList(superfamilyListFileName, SFName_and_ID_file)'
    sys.stdout.flush()
    SFIDList = getSFIDList(superfamilyListFileName, SFName_and_ID_file)

    print 'hmmDict = getHMMDict( SFIDList, SFHMMListName, FamHMMListName
    sys.stdout.flush()
    hmmDict = getHMMDict( SFIDList, SFHMMListName, FamHMMListName, Sub

    print 'runHMMSearch(dbName, hmmDict, hmmPath, runningPath)'
    sys.stdout.flush()
    runHMMSearch(dbName, hmmDict, hmmPath, runningPath)


runHMMSearchSFLD(sys.argv)
```

Appendix I. Program—filterHomolSearchSFLD.py

```
#!/usr/bin/python2.3

"""filterHomolSearchSFLD.py
   This program parses hmmsearch files relative to the SFLD.

   Usage:filterHomolSearchSFLD.py  --supFamListFile=<list of superfamilies>
     --hmmPath=<path to hmmfiles> --alignPath=<path to align files> --seqPath=<
     --seqFileName=<file of all sfld seq file names> --SFFile=<SF info file>
     --SFHMMFile=<SF HMM file> --SubHMMFile=<subgroup HMM file>
     --FamHMMFile=<fam HMM file>   --runningDir=<running directory>
     --dbName=<database name> --sfAlignFile=<sf alignment file>
     --sfConsRes=<sf conserv. residue file> --famAlignFile=<fam alignment file>
     --famConsRes=<fam conserved residue file> --subAlignFile=<subgroup align
     --subConsRes=<subgroup conserved resiude file>

   INPUT:
      --supFamListFile= List of the names of the superfamilies
      --hmmPath= path to the hmmfiles
      --alignPath= path to the hmm alignment files
      --seqPath= path to the SFLD seqeunce files
      --seqFileName= file containing the names of all sfld seq file names
      --SFFile= SF SFLD info file
      --SFHMMFile= SF SFLD HMM file
      --SubHMMFile= subgroup SFLD HMM file
      --FamHMMFile= fam SFLD HMM file
      --runningDir= paht of running directory
      --dbName= database name
      --sfAlignFile= sf SFLD alignment file
      --sfConsRes= sf SFLD conserv. residue file
      --famAlignFile= fam SFLD alignment file
      --famConsRes= fam SFLD conserved residue file
      --subAlignFile= subgroup SFLD alignm. file
      --subConsRes= subgroup SFLD conserved resiude file

   OUTPUT:
      - *.giScoreEval = space delimited file with <gi> <score> <evalue> from the
            hmmsearch files
      - *.giScoreEval.giList = gi list from the giScoreEval file
      - *.giScoreEval.giList.fasta = the fasta file generated from the gi list
      - *.giScoreEval.mark = semicolon delimited file of the format
      <


    Other important info
    Need python modules written in lab
   alignment.py
```

```
    common.py
    inspectDefline.py

    Need to have programs set up
    giScoreParseList.pl
    getGIfromList.pl
    fastacmd
    nrdb
    rpsblast
    inspectDefline.py
    hmmer package

      remember to have .ncbirc file in directory and set up correctly

    Need to have variable $BLASTDB set appropriate e.g.
        setenv BLASTDB /usr/local/Blast/blastDBDir/


Author: Alexandra M. Schnoes from code written by
Shoshana Brown(updateSFLD.py) (some functions based on SFLDsql.py code by
Last Modified: 6/8/04

Modified: Alexandra M. Schnoes 8/26/04
    Added comments and changed paths
    Alexandra M. Schnoes 01/31/05
    Translating code to NOT use mysql so it can run on the clusters
    Alexandra M. Schnoes 01/10/06:
    Commenting
    AMS: add seq len 06/24/06

"""

import sys
import os
import os.path
import string
import getopt
import re
import common
from alignment import *
############
# need related programs
# giScoreParseList.pl
# getGIfromList.pl
# fastacmd
# nrdb
```

```
# rpsblast
# inspectDefline.py
# hmmer package
###############

######################################################################
# checkArg
######################################################################

def checkArg(argv):
   """Exit with error and print usage if not enough arguments."""
   #am supposed to have 18 arguments assuming that the options are written
   #option=something
   #also assume that path is passed in with trailing '/'

   errorString = """length is """ + str(len(argv)) + """. Usage:filterHomolSearchSFL
     --hmmPath=<path to hmmfiles> --alignPath=<path to align files> --seqPath=
     --seqFileName=<file of all sfld seq file names> --SFFile=<SF info file>
     --SFHMMFile=<SF HMM file> --SubHMMFile=<subgroup HMM file>
     --FamHMMFile=<fam HMM file>   --runningDir=<running directory>
     --dbName=<database name> --sfAlignFile=<sf alignment file>
     --sfConsRes=<sf conserv. residue file> --famAlignFile=<fam alignment file>
     --famConsRes=<fam conserved residue file> --subAlignFile=<subgroup align
     --subConsRes=<subgroup conserved resiude file> --efdFile=<enzymefunctio
     file>"""


   if len(argv) == 19:
      pass
   else:
      print errorString
      sys.exit(1)



######################################################################
# getFileNameList
######################################################################
def getFileNameList(ListFileName):
  inFile = open(ListFileName, "r")
  FileNameList = []

  while 1:
    line = inFile.readline()
    if not line:
      break
```

```
      line = string.strip(line)
      if len(line) > 0:
         FileNameList.append(line)
   inFile.close()

   return FileNameList

##############################################################################
# MapSFNameToID
##############################################################################
def MapSFNameToID(SFName_and_ID_file):
    inFile = open(SFName_and_ID_file, 'r')
    Name_ID_dict = {}

    while 1:
        line = inFile.readline()
        line = line[:-1]
        tmpList = line.split(';')
        if len(tmpList) > 1:
            Name_ID_dict[tmpList[1]] = tmpList[0]
        else:
            break

    return Name_ID_dict


##############################################################################
# Input:
#  superfamilyListFileName: A string specifying either: (1) The name of a file
#                           which lists superfamily names, one per line, or (2)
#                           the value "all"
#  SFName_and_ID_file
# Returns:
#  SFIDList: A list of identifiers from the SFLD that correspond to either: (1)
#            the superfamily names listed in the file referenced by
#            superfamilyListFileName, or (2) all superfamilies in the SFLD
##############################################################################
def getSFIDList(superfamilyListFileName, SFName_and_ID_file):
   if superfamilyListFileName != "all":
      SFIDList = []
      SFNameList = getFileNameList(superfamilyListFileName)
      SFName_id_dict = MapSFNameToID(SFName_and_ID_file)

      size = len(SFNameList)
      i = 0
      while i < size:
```

```
      SFIDList.append(SFName_id_dict[SFNameList[i]])
      i = i + 1

  return SFIDList

####################################################################
# returnList
####################################################################
def returnList(fileName, num_elements):
  fileList = []

  inFile = open(fileName, 'r')

  while 1:
    line = inFile.readline()
    line = line[:-1]
    tmpList = line.split(';')
    if tmpList == ['']:
      break
    elif len(tmpList) == num_elements:
      for index in range(0, len(tmpList)):
        if tmpList[index] == 'None':
          tmpList[index] = None
      fileList.append(tmpList)
    else:
      break


  return fileList

####################################################################
# Retrieves the names of all superfamily, family & subgroup HMMs from the SFL
# that correspond to the superfamilies specified in SFIDList.
#
# Input:
#  SFIDList: A list of superfamily identifiers from the SFLD
#  SFHMMListName, SubHMMListName, FamHMMListName
# Returns:
#  hmmDict: A dictionary with key = SFID, value = list with structure:
#          [superfamilyHMMName, famIDHMMDict, subIDHMMDict]
#          famIDHMMDict and subIDHMMDict are dictionaries with key =
#          family/subgroup ID, value = HMM file name.
####################################################################
def getHMMDict(SFIDList, SFHMMListName, SubHMMListName, FamHMMListN

  hmmDict = {}
```

```
num_elements = 2
SFHMMList = returnList(SFHMMListName, num_elements)
#print SFHMMList

num_elements = 3
SubHMMList = returnList(SubHMMListName, num_elements)
#print SubHMMList

num_elements = 3
FamHMMList = returnList(FamHMMListName, num_elements)
#print FamHMMList

for SFID in SFIDList:
  #print SFID

  for index in range(0, len(SFHMMList)):
    if SFID == SFHMMList[index][0]:
       SFHMM = SFHMMList[index][1]
    #print SFHMM

  famIDHMMDict = {}
  for index in range(0, len(FamHMMList)):
    if SFID == FamHMMList[index][0]:
       id = FamHMMList[index][1]
       hmmName = FamHMMList[index][2]
       if hmmName != None:
         famIDHMMDict[id] = hmmName

  #print famIDHMMDict

  subIDHMMDict = {}
  for index in range(0, len(SubHMMList)):
    if SFID == SubHMMList[index][0]:
      id = SubHMMList[index][1]
      hmmName = SubHMMList[index][2]
      if hmmName != None:
        subIDHMMDict[id] = hmmName

  #print "subIDHMMDict"
  #print subIDHMMDict
  hmmDict[SFID] = [SFHMM, famIDHMMDict, subIDHMMDict]
  #print hmmDict
return hmmDict
```

```
###########################################################################
#
# Input:
#  hmmDict: A dictionary with key = SFID, value = list with structure:
#         [superfamilyHMMName, famIDHMMDict, subIDHMMDict]
#         famIDHMMDict and subIDHMMDict are dictionaries with key =
#         family/subgroup ID, value = HMM file name.
#  path: A string specifying the path for the directory that contains the SFLD
#       HMM files.
# Returns:
#  fastaDict: A dictionary with key = SFID, value = list of all fasta files
#           for the hits of each SF/Fam/Sub. Fasta will contain *all*
#           sequences for each hit file (the hit file name determined from
#           hmmdict).
#  giScoreEvalueDict: A dictonary with key SFID, value = list of all filenames
#           that contain the gi, score and evalue of each hit set.
#           file format:
#           <gi>    <score>    <evalue>
###########################################################################
def runParseHMMSearch(hmmDict, runningDir, dbName):
  print 'def runParseHMMSearch(hmmDict, runningDir, dbName):'

  fastaDict = {}
  giScoreEvalueDict = {}

  for SFID in hmmDict.keys():

    tempHitGIList = []

    #Parse the HMMSearch output HMM in a given superfamily

    #First find the HMMSearch file with superfamily HMM, if present,
    if hmmDict[SFID][0] != None:
      hmmsearchOutFileName = runningDir + "SF" + str(SFID) + ".hmmsearch"
      cmd = "giScoreParseList.pl %s" % (hmmsearchOutFileName)
      os.system(cmd)

      giScoreEvalueFileName = hmmsearchOutFileName + ".giScoreEval"
      cmd = "getGIfromList.pl %s" % (giScoreEvalueFileName)
      os.system(cmd)

      giFileName = giScoreEvalueFileName + ".giList"
      fastaFileName = giFileName + ".fasta"
      cmd = "fastacmd -d %s -i %s -t T -o %s" % (dbName, giFileName, fastaFileI
      os.system(cmd)
```

```
    SFFastaFile = fastaFileName
    SFgiScoreEvalueFile =  giScoreEvalueFileName
else:
    SFFastaFile = None
    SFgiScoreEvalueFile =  None

#Then parse hmmsearch with each family HMM,
famIDFastaDict = {}
famIDgiScoreEvalueDict ={}
famIDHMMDict = hmmDict[SFID][1]
for famID in famIDHMMDict.keys():
    hmmsearchOutFileName = runningDir + "SF" + str(SFID) + "Fam" + str(famI
    cmd = "giScoreParseList.pl %s" % (hmmsearchOutFileName)
    os.system(cmd)

    giScoreEvalueFileName = hmmsearchOutFileName + ".giScoreEval"
    cmd = "getGIfromList.pl %s" % (giScoreEvalueFileName)
    os.system(cmd)

    giFileName = giScoreEvalueFileName + ".giList"
    fastaFileName = giFileName + ".fasta"
    cmd = "fastacmd -d %s -i %s -t T -o %s" % (dbName, giFileName, fastaFile
    os.system(cmd)

    famIDFastaDict[famID] = fastaFileName
    famIDgiScoreEvalueDict[famID] = giScoreEvalueFileName

#Then run hmmsearch with each subgroup HMM
SubIDFastaDict = {}
SubIDgiScoreEvalueDict = {}
subIDHMMDict = hmmDict[SFID][2]
for subID in subIDHMMDict.keys():
    hmmsearchOutFileName = runningDir + "SF" + str(SFID) + "Sub" + str(subI
    cmd = "giScoreParseList.pl %s" % (hmmsearchOutFileName)
    os.system(cmd)

    giScoreEvalueFileName = hmmsearchOutFileName + ".giScoreEval"
    cmd = "getGIfromList.pl %s" % (giScoreEvalueFileName)
    os.system(cmd)

    giFileName = giScoreEvalueFileName + ".giList"
    fastaFileName = giFileName + ".fasta"
    cmd = "fastacmd -d %s -i %s -t T -o %s" % (dbName, giFileName, fastaFile
    os.system(cmd)
```

```
      SubIDFastaDict[subID] = fastaFileName
      SubIDgiScoreEvalueDict[subID] = giScoreEvalueFileName


    #Make a fasta file dict and a gi/score/evalue dict for all the files
    fastaDict[SFID] = [SFFastaFile, famIDFastaDict, SubIDFastaDict]
    giScoreEvalueDict[SFID] = [SFgiScoreEvalueFile, famIDgiScoreEvalueDict, S

  return fastaDict, giScoreEvalueDict



######################################################################
# Parses the output file from the NCBI nrdb program (specified by
# nrdbFileName) to determine the sequence overlap between two sets of
# files.
# Returns:
#  commonList: A list of GIs common to the two fasta files compared using
#  nrdb.  (If the GIs of the common sequence are identical, one copy is
#  added to the list.  Otherwise, both GIs are added to the list as
#  seperate entries
######################################################################
def parseNrdbOutput(nrdbFileName):

  commonList = []

  inFile = open(nrdbFileName, 'r')

  while 1:
    line = inFile.readline()
    if not line:
      break
    if line[:1] == '>':
      #Search for seperator '\x01' added by nrdb to determine if the
      #current sequence was present in both nrdb input files
      index = string.find(line, '\x01')
      if index != (-1):
        commonList.append('Seq in Common')
        break
      #else: pass

  inFile.close()

  return commonList
```

```
#####################################################################
# Runs the NCBI program nrdb.  Uses the function parseNRDBOutput to parse
# the resulting output file
# Returns:
#  commonList: A list of GIs common to the two fasta files compared using
#  nrdb.  (If the GIs of the common sequence are identical, one copy is
#  added to the list.  Otherwise, both GIs are added to the list as
#  seperate entries
#####################################################################
def getCommonSeqs(fastaFileName1, fastaFileName2, runningDir):

  tmp_out = runningDir + 'temp.nrdb'
  cmd = 'nrdb -o%s %s %s  2> screenOut' % (tmp_out, fastaFileName1, fastaFile
  os.system(cmd)

  commonList = parseNrdbOutput(tmp_out)

  #Remove temporary file
  os.system('rm %s screenOut' % (tmp_out))

  return commonList

#####################################################################
# markingSeqs
#####################################################################
def markingSeqs(gseList, seqPath, seqFileList, inSFLDList, notInList, runningDir,
  """Mark seq's in gseList that are in the SFLD and write out to file
  and return lists of gi's that are in or not in the sfld
  The new format for the entryDict lists is--
  <gi>    <score>    <evalue>    <VALID/NOT_valid>    <IN_SFLD>    <fasta file na

  """
  #for entry in gseList:
  #    entry.append('[]')
  #    entry.append('[]')

  print "markingSeqs(gseFileName, gseList, seqPath, seqFileList, inSFLDList, no
  GIinSFLDList =[]
  for entry in inSFLDList:
    GIinSFLDList.append(entry[0])


  for entry in gseList:
      notOne = 1
      gi_GSE = entry[0]
      if gi_GSE in GIinSFLDList:
```

```
            entry.append('IN_SFLD')
            index = GIinSFLDList.index(gi_GSE)
            entry.append(inSFLDList[index][1])
         elif gi_GSE in notInList:
             entry.append('[]')
             entry.append('[]')

         else:
            tmpFastaFileName = runningDir + gi_GSE + '.tmp'
            os.system("fastacmd -d %s -s%s -tT > %s" % (dbName, gi_GSE, tmpFast
            for seq_entry in seqFileList:
                seqFastaFileName = seqPath + seq_entry
                commonList = getCommonSeqs(tmpFastaFileName, seqFastaFileNam
                if commonList:  #the list exists, hit is in SFLD
                   #print commonList
                   entry.append('IN_SFLD')
                   entry.append(seq_entry)
                   inSFLDList.append([gi_GSE, seq_entry])
                   #print "BREAK " + gi_GSE
                   notOne = 0
                   break
            if notOne == 1: #this is not in SFLD
               #print "NO BREAK " + gi_GSE
               entry.append('[]')
               entry.append('[]')
               notInList.append(gi_GSE)



   return inSFLDList, notInList, gseList



######################################################################
# markIfInSFLD
######################################################################
def markIfInSFLD(seqPath, entryDict, seqFileName, runningDir, dbName):
   """Mark any sequences that are in the SFLD sequence set and write out to a fil

   seqFileList = getFileNameList(seqPath + seqFileName)
   inSFLDList = []
   notInList = []
   newEntryDict = {}

   for SFID in entryDict.keys():
      #check the superfamily sequences
```

```
    SFgseList = entryDict[SFID][0]
    print "SFgseList"
    print SFgseList
    if SFgseList == None:
      print "Pass SFgseList"
      pass
    else:
      inSFLDList, notInList, SFgseList = markingSeqs(SFgseList, seqPath, seqFi

    #check the family sequences
    famEntryDict = {}
    FamGSEFileDict = entryDict[SFID][1]
    for famID in FamGSEFileDict.keys():
      FamGSEList = FamGSEFileDict[famID]
      inSFLDList, notInList, FamGSEList = markingSeqs(FamGSEList, seqPath, s
      famEntryDict[famID] = FamGSEList

    #check the subgroup sequences
    subEntryDict = {}
    SubGSEFileDict = entryDict[SFID][2]
    for subID in SubGSEFileDict.keys():
      SubGSEList = SubGSEFileDict[subID]
      inSFLDList, notInList, SubGSEList = markingSeqs(SubGSEList, seqPath, se
      subEntryDict[subID] = SubGSEList

    newEntryDict[SFID]= [SFgseList, famEntryDict, subEntryDict]

  return newEntryDict


##################################################################################
# Input:
#  alignmentFileName: The name of an hmmeralign format sequence alignment.
# Returns:
#  repSeq: A string specifying the (gapped) amino acid sequence for the first
#          sequence in the alignment specified by alignmentFileName.
##################################################################################
def getRepSeq(alignmentFileName):

  inFile = open(alignmentFileName, "r")

  #Get the identifier for the first sequence in the alignment
  while 1:
    line = inFile.readline()
    if not line:
      break
```

```
    line = string.strip(line)
    if line[:5] == "Name:":
      line = string.strip(line[5:])
      index = string.find(line, " ")
      repSeqID = line[:index]
      break

  #Get the amino acid sequence corresponding to repSeqID
  repSeq = ""
  while 1:
    line = inFile.readline()
    if not line:
      break
    line = string.strip(line)
    if line[:len(repSeqID)] == repSeqID:
      line = string.strip(line[len(repSeqID):])
      repSeq += string.replace(line, " ", "")

  inFile.close()

  return repSeq


##########################################################
# Translates the sequence number num (obtained from a gapped sequence
# alignment) to the corresponding number with respect to the ungapped
# sequence equivalent of gappedRepSeq.
#
# Input:
#  gappedConsResTuple: A nested tuple of tuples.  Each inner tuple is of the
#                      form (AA#, AAType), where AA# references a specific
#                      amino acid in the string gappedRepSeq.
#  gappedRepSeq: A string specifying an amino acid sequence from a gapped
#                sequence alignment.
# Returns:
#  ungappedConsResList: The ungapped equivalent of gappedConsResTuple, bu
#                       list form.
#
# NOTE: If the alignment position specified by an entry in gappedConsResTuple
# corresponds to a gap character in gappedRepSeq, a zero will be placed in the
# corresponding entry in ungappedConsResList.
##########################################################
def getUngappedNumbers(gappedConsResList, gappedRepSeq):

  ungappedConsResList = []
  seqList = list(gappedRepSeq)
```

```
  for consResPair in gappedConsResList:
    gappedNum = consResPair[0]
    #print gappedNum
    aaType = consResPair[1]
    ungappedCount = 0
    gappedCount = 0
    correctedNum = 0
    for letter in seqList:
      #clustalw specifies gaps with "-", while hmmeralign uses "." and "~"
      if letter == "-" or letter == "." or letter == "~":
        gappedCount += 1
        #print gappedCount
      else:

        gappedCount += 1
        ungappedCount += 1
        #stringie =  str(gappedCount) + " " + str(ungappedCount) + " " + gappedN
        #print stringie
        if gappedCount == int(gappedNum):
          #print "hello?"
          correctedNum = ungappedCount
          ungappedConsResList.append([correctedNum, aaType])

  return ungappedConsResList


######################################################################
# Removes gap characters from the string gappedSequence.  Returns the ungap
# string.
######################################################################
def removeGaps(gappedSequence):

  ungappedSequence = string.replace(gappedSequence, ".", "")
  ungappedSequence = string.replace(ungappedSequence, "-", "")
  ungappedSequence = string.replace(ungappedSequence, "~", "")

  return ungappedSequence


######################################################################
# Input:
#  hmmDict: A dictionary with key = SFID, value = list with structure:
#          [superfamilyHMMName, famIDHMMDict, subIDHMMDict]
#          famIDHMMDict and subIDHMMDict are dictionaries with key =
#          family/subgroup ID, value = HMM file name.
```

```
#  path: A string specifying the path for the directory that contains the SFLD
#       HMM files.
# Returns:
#  consResDict: A dictionary with key = SFID, value = a list with the following
#             format: [consResList, familyConsResDict, subgroupConsResDict]
#             where family and subgroupConsResDict are dictionaries with
#             key = family/subgroup ID and value = consResList, and
#             consResList is a nested list where each inner list has the
#             format: [AA#, allowedAAType(s)]
#  repSeqDict: Dictionary with key = SFID, value = list with the following
#            format: [SFRepSeq, familyRepSeqDict, subgroupRepSeqDict]
#            where family and subgroupRepSeqDict are dictionaries with key =
#            family/subgroup ID and value = a string containing the amino
#            acid sequence for a representative sequence in the
#            family/subgroup, which corresponds to the conserved residue
#            numbering in consResDict.
######################################################################
def getConsResDict(hmmDict, alignPath, sf_align_file_name,
    sf_cons_residue_file_name, fam_align_file_name, fam_cons_res_file_name,
    sub_align_file_name, sub_cons_res_file_name):

    consResDict = {}
    repSeqDict = {}

    num_elements = 2
    SFalignList = returnList(sf_align_file_name, num_elements)

    num_elements = 3
    SFAllConsResList = returnList(sf_cons_residue_file_name, num_elements)
    #print SFAllConsResList


    for SFID in hmmDict.keys():
        #get superfamily alignment file name
        for index in range(0, len(SFalignList)):
            if SFID == SFalignList[index][0]:
                alignmentFileName = SFalignList[index][1]

        if alignmentFileName != None:
            #Collect the representative sequence for the SF alignment
            gappedSFRepSeq = getRepSeq(alignPath + alignmentFileName)
            SFRepSeq = removeGaps(gappedSFRepSeq)

            #Collect the conserved residues for the SF alignment
            SFCRList = []
            for index in range(0, len(SFAllConsResList)):
```

```
      if SFID == SFAllConsResList[index][0]:
         SFCRList.append([SFAllConsResList[index][1], SFAllConsResList[inde
         #print SFCRList
         #print gappedSFRepSeq

  SFConsResList = getUngappedNumbers(SFCRList, gappedSFRepSeq)
else:
  SFConsResList = []
  SFRepSeq = None


famConsResDict = {}
famRepSeqDict = {}

#get family alignment file names
num_elements = 2
FamAlignList = returnList(fam_align_file_name, num_elements)

#get conserved residues for family alignments
num_elements = 3
FamConsResList = returnList(fam_cons_res_file_name, num_elements)
#print FamConsResList

for famID in hmmDict[SFID][1].keys():
  #Collect the representative sequence for a family alignment
  for index in range(0, len(FamAlignList)):
     if famID == FamAlignList[index][0]:
        alignmentFileName = FamAlignList[index][1]
        gappedFamRepSeq = getRepSeq(alignPath + alignmentFileName)
        famRepSeqDict[famID] = removeGaps(gappedFamRepSeq)

  #Collect the conserved residues for a family alignment
  FamCRList =[]
  for index in range(0, len(FamConsResList)):
     if famID == FamConsResList[index][0]:
        FamCRList.append([FamConsResList[index][1], FamConsResList[inde
        famConsResDict[famID] = getUngappedNumbers(FamCRList, gapped


subConsResDict = {}
subRepSeqDict = {}

#get subgroup alignment file names
num_elements = 2
SubAlignList = returnList(sub_align_file_name, num_elements)
#print "SubAlignList"
```

```
    #print SubAlignList

    #get conserved residues for the subgroup alignments
    num_elements = 3
    SubConsResList = returnList(sub_cons_res_file_name, num_elements)
    #print "SubConsList"
    #print SubConsResList
    for subID in hmmDict[SFID][2].keys():
      #Collect the representative sequence for a subgroup alignment
      for index in range(0, len(SubAlignList)):
        if subID == SubAlignList[index][0]:
          #print "subID Align " + subID + "\n"
          alignmentFileName = SubAlignList[index][1]
          gappedSubRepSeq = getRepSeq(alignPath + alignmentFileName)
          subRepSeqDict[subID] = removeGaps(gappedSubRepSeq)

      #Collect the conserved residues for a subgroup alignment
      SubCRList = []
      for index in range(0, len(SubConsResList)):
        if subID == SubConsResList[index][0]:
          #print "subID Cons " + subID + "\n"
          SubCRList.append([SubConsResList[index][1], SubConsResList[index
          subConsResDict[subID] = getUngappedNumbers(SubCRList, gapped

    #For each SFID make a dict holding the conserved residues and the rep
    #Sequences for each family/SF/Sub etc.
    consResDict[SFID] = [SFConsResList, famConsResDict, subConsResDict]
    repSeqDict[SFID] = [SFRepSeq, famRepSeqDict, subRepSeqDict]


  #print consResDict
  #print repSeqDict
  return consResDict, repSeqDict


################################################################
# Input:
#  consResDict: A dictionary with key = SFID, value = a list with the following
#              format: [consResList, familyConsResDict, subgroupConsResDict]
#              where family and subgroupConsResDict are dictionaries with
#              key = family/subgroup ID and value = consResList, and
#              consResList is a nested list where each inner list has the
#              format: [AA#, allowedAAType(s)]
# Returns:
#  reformattedConsResDict: A dictionary with key = SFID, value = a list with the
#                        following format: [consResList, familyConsResDict,
```

```
#                       subgroupConsResDict], where family and
#                       subgroupConsResDict are dictionaries with key =
#                       family/subgroup ID and value = consResList, and
#                       consResList is a nested list where each inner list
#                       has the format: [AA#, [allowedAAType(s)]]
####################################################################################
def reformatConsResDict(consResDict):

  #print consResDict
  reformattedConsResDict = {}

  aaDict = {}
  aaDict['ALA'] = 'A'
  aaDict['ARG'] = 'R'
  aaDict['ASN'] = 'N'
  aaDict['ASP'] = 'D'
  aaDict['CYS'] = 'C'
  aaDict['GLN'] = 'Q'
  aaDict['GLU'] = 'E'
  aaDict['GLY'] = 'G'
  aaDict['HIS'] = 'H'
  aaDict['ILE'] = 'I'
  aaDict['LEU'] = 'L'
  aaDict['LYS'] = 'K'
  aaDict['MET'] = 'M'
  aaDict['PHE'] = 'F'
  aaDict['PRO'] = 'P'
  aaDict['SER'] = 'S'
  aaDict['THR'] = 'T'
  aaDict['TRP'] = 'W'
  aaDict['TYR'] = 'Y'
  aaDict['VAL'] = 'V'

  for SFID in consResDict.keys():
    SFConsResList = []
    for consResPair in consResDict[SFID][0]:
      aaTypeString = consResPair[1]
      origAAList = string.split(aaTypeString, ",")
      reformattedAAList = []
      for aa in origAAList:
        aa = string.strip(aa)
        if len(aa) > 1:
          try:
            reformattedAAList.append(aaDict[aa])
          except KeyError:
            reformattedAAList.append('X')
```

```
                else:
                    reformattedAAList.append(aa)
            SFConsResList.append([consResPair[0], reformattedAAList[:]])
        famConsResDict = {}
        for famID in consResDict[SFID][1].keys():
            famConsResDict[famID] = []
            for consResPair in consResDict[SFID][1][famID]:
                aaTypeString = consResPair[1]
                origAAList = string.split(aaTypeString, ",")
                reformattedAAList = []
                for aa in origAAList:
                    aa = string.strip(aa)
                    if len(aa) > 1:
                        try:
                            reformattedAAList.append(aaDict[aa])
                        except KeyError:
                            reformattedAAList.append('X')
                    else:
                        reformattedAAList.append(aa)
                famConsResDict[famID].append([consResPair[0], reformattedAAList[:]])
        subConsResDict = {}
        for subID in consResDict[SFID][2].keys():
            subConsResDict[subID] = []
            for consResPair in consResDict[SFID][2][subID]:
                aaTypeString = consResPair[1]
                origAAList = string.split(aaTypeString, ",")
                reformattedAAList = []
                for aa in origAAList:
                    aa = string.strip(aa)
                    if len(aa) > 1:
                        try:
                            reformattedAAList.append(aaDict[aa])
                        except KeyError:
                            reformattedAAList.append('X')
                    else:
                        reformattedAAList.append(aa)
                subConsResDict[subID].append([consResPair[0], reformattedAAList[:]])
        reformattedConsResDict[SFID] = [SFConsResList, famConsResDict, subCon

    #print reformattedConsResDict
    return reformattedConsResDict


################################################################
# Adds the amino acid sequence specified by the string repSeq in fasta format
```

```
# to the fasta sequence file specified by the string fastaFileName.
######################################################################
def addRepSeq(fastaFileName, repSeq):

  #print repSeq
  outFile = open(fastaFileName, "a")
  outFile.write(">gi|repSeq|\n")
  outFile.write(common.format(repSeq))
  outFile.close()


######################################################################
# Aligns the hit sequences categorized in a given superfamily/family/subgroup,
# from categorizedHitsDict, along with the appropriate representative sequence,
# from repSeqDict, with the appropriate HMM, from hmmDict, using hmmalign.
#
# Input:
#  categorizedHitsDict: A dictionary with key = SFID, value = A list with
#                       structure: [SFHitList, familyHitDict, subgroupHitDict],
#                       where SFHitList is a list of gi numbers for all hits
#                       from the superfamily, familyHitDict is a
#                       dictionary with key = family ID, value = a list of gi
#                       numbers for hits classified with a given family, and
#                       subgroupHitDict is the equivalent to familyHitDict, but
#                       for a subgroup rather than a family.
#  repSeqDict: Dictionary with key = SFID, value = list with the following
#              format: [SFRepSeq, familyRepSeqDict, subgroupRepSeqDict]
#              where family and subgroupRepSeqDict are dictionaries with key =
#              family/subgroup ID and value = a string containing the amino
#              acid sequence for a representative sequence in the
#              family/subgroup, which corresponds to the conserved residue
#              numbering in consResDict.
#  hmmDict: A dictionary with key = SFID, value = list with structure:
#           [superfamilyHMMName, famIDHMMDict, subIDHMMDict]
#           famIDHMMDict and subIDHMMDict are dictionaries with key =
#           family/subgroup ID, value = HMM file name.
#  path: A string specifying the path for the directory that contains the SFLD
#        HMM files.
######################################################################

def alignHits(fastaDict, repSeqDict, hmmDict, hmmPath, runningDir):
  print 'def alignHits(fastaDict, repSeqDict, hmmDict, hmmPath, runningDir):'

  alignHitDict = {}
  for SFID in hmmDict.keys():
```

```
  #First find the HMMSearch file with superfamily HMM, if present,
  if hmmDict[SFID][0] != None:
    hmmName = hmmPath + hmmDict[SFID][0]
    alignFileName = runningDir + "SF" + str(SFID) + ".hmmalign"
    fastaFile = fastaDict[SFID][0]
    addRepSeq(fastaFile, repSeqDict[SFID][0])
    os.system("inspectDefline.py %s" % (fastaFile))
    os.system("mv shortDefline.fasta " + fastaFile)
    os.system("hmmalign -o %s  %s %s" % (alignFileName, hmmName, fastaFi
    SFalignFileName = alignFileName
  else:
    SFalignFileName = None

  famAlignDict = {}
  famIDHMMDict = hmmDict[SFID][1]
  famFastaDict = fastaDict[SFID][1]
  for famID in famIDHMMDict.keys():
    hmmName = hmmPath + hmmDict[SFID][1][famID]
    alignFileName = runningDir + "SF" + str(SFID) + "Fam" + str(famID) + ".hmr
    fastaFile = famFastaDict[famID]
    addRepSeq(fastaFile, repSeqDict[SFID][1][famID])
    os.system("inspectDefline.py %s" % (fastaFile))
    os.system("mv shortDefline.fasta " + fastaFile)
    os.system("hmmalign -o %s  %s %s" % (alignFileName, hmmName, fastaFi
    famAlignDict[famID] = alignFileName

  subAlignDict = {}
  subIDHMMDict = hmmDict[SFID][2]
  subFastaDict = fastaDict[SFID][2]
  for subID in subIDHMMDict.keys():
    hmmName = hmmPath + hmmDict[SFID][2][subID]
    alignFileName = runningDir + "SF" + str(SFID) + "Sub" + str(subID) + ".hmm
    fastaFile = subFastaDict[subID]
    addRepSeq(fastaFile, repSeqDict[SFID][2][subID])
    os.system("inspectDefline.py %s" % (fastaFile))
    os.system("mv shortDefline.fasta " + fastaFile)
    os.system("hmmalign -o %s  %s %s" % (alignFileName, hmmName, fastaFi
    subAlignDict[subID] = alignFileName

  alignHitDict[SFID] = [SFalignFileName, famAlignDict, subAlignDict]
  #print alignHitDict

return alignHitDict
```

```
##################################################################
# Input:
#  alignFileName: A string specifying the name of a hmmeralign format alignment
#  repSeq: A string specifying an (ungapped) amino acid sequence present in
#          the alignment specified by alignFileName
#  consResList: A nested list with format [AA#, [allowedAAType(s)]]
# Returns:
#  validatedHitList: A list containing the gi numbers for all sequences in
#                    alignFileName that conserve the residues specified in
#                    consResList, according to the alignment
##################################################################
def checkAlignmentForConsRes(alignFileName, repSeq, consResList):

  allowedMismatches = 0
  validatedHitList = []
  removedHitsList = []

  algnmnt = alignment(alignFileName)
  mismatchDict = {}
  for alignKey in algnmnt.alignDict.keys():
    #print "alignKey" + alignKey
    mismatchCounter = 0
    for resPair in consResList:
      resNum = resPair[0]
      #print "resNum" + str(resNum)
      correctedResNum = algnmnt.translateSeqNum(resNum, "repSeq")
      #subtract 1 from correctedResNum to convert to index
      if "X" in resPair[1]:
        #print "I REACH HERE!!"
        #Any residue can be at this position do not increment
        #mismatchCounter
        pass
      elif algnmnt.alignDict[alignKey][correctedResNum - 1] not in resPair[1]:
        #print algnmnt.alignDict[alignKey][correctedResNum - 1]
        #print str(correctedResNum - 1)
        #print resPair[1]
        mismatchCounter += 1
    mismatchDict[alignKey] = mismatchCounter
    #print mismatchCounter
  for key in mismatchDict.keys():
    if mismatchDict[key] <= allowedMismatches and key != "repSeq":
      validatedHitList.append(str(key))
    elif key == "repSeq":
      pass
    else:
      removedHitsList.append(str(key))
```

```
#   os.system("rm " + alignFileName) #Delete temporary alignment file

  return validatedHitList, removedHitsList


###################################################################
# Validates hit sequences by verifying that they conserve the catalytic
# residues specified in consResDict.
#
# Input:
#  consResDict: A dictionary with key = SFID, value = a list with the following
#              format: [consResList, familyConsResDict, subgroupConsResDict]
#              where family and subgroupConsResDict are dictionaries with
#              key = family/subgroup ID and value = consResList, and
#              consResList is a nested list where each inner list has the
#              format: [AA#, allowedAAType(s)]
#  repSeqDict: Dictionary with key = SFID, value = list with the following
#             format: [SFRepSeq, familyRepSeqDict, subgroupRepSeqDict]
#             where family and subgroupRepSeqDict are dictionaries with key =
#             family/subgroup ID and value = a string containing the amino
#             acid sequence for a representative sequence in the
#             family/subgroup, which corresponds to the conserved residue
#             numbering in consResDict.
# Returns:
#  validatedHitsDict: Dictionary with key = SFID, value = list with structure:
#                    [validatedSFHitList, validatedFamHitDict,
#                    validatedSubHitDict], where validatedSFHitList is a list
#                    of gi numbers for validated hits categorized with the SF
#                    HMM, validatedFamHitDict is a dictionary with key =
#                    family ID, value = list of gi numbers for validated hits
#                    classified with a given family ID, and
#                    validatedSubHitDict is the equivalent to familyHitDict,
#                    but for a subgroup rather than a family.
###################################################################
def checkHitsForConsRes(hmmDict, consResDict, repSeqDict, runningDir):
  print 'def checkHitsForConsRes(hmmDict, consResDict, repSeqDict):'
  validatedHitsDict = {}
  removedHitsDict = {}

  for SFID in hmmDict.keys():
    if SFID in consResDict.keys():
      SFAlignFileName = runningDir + "SF" + str(SFID) + ".hmmalign"
      if os.path.isfile(SFAlignFileName):
        validatedSFHitList, removedSFHitsList = checkAlignmentForConsRes(SF
        print "Checking file %s" % (SFAlignFileName)
      else:
```

```
        validatedSFHitList = []
        removedSFHitsList = []
        print "NO alignment file for SF %s" % (SFID)
else:
    SFAlignFileName = runningDir + "SF" + str(SFID) + ".hmmalign" + ".noCons
    openfile = open(subAlignFileName, "w")
    openfile.close()
    validatedSFHitList = []
    removedSFHitsList = []

    print "no ConsRes for SF ID %s. File %s made" % (SFID, SFAlignFileName

validatedFamHitDict = {}
removedFamHitsDict = {}
famIDHMMDict = hmmDict[SFID][1]
for famID in famIDHMMDict.keys():
    if famID in consResDict[SFID][1].keys():
        famAlignFileName = runningDir + "SF" + str(SFID) + "Fam" + str(famID) +
        if os.path.isfile(famAlignFileName):
            #print "famID" + famID
            validatedFamHitDict[famID], removedFamHitsDict[famID] = checkAlignm
            print "checking file for fam file %s" % (famAlignFileName)
        else:
            print "No alignment file for family ID %s" % (famID)
            validatedFamHitDict[famID] = []
            removedFamHitsDict[famID] = []
    else:
        famAlignFileName = runningDir + "SF" + str(SFID) + "Fam" + str(famID) +
        openfile = open(famAlignFileName, "w")
        openfile.close()
        validatedFamHitDict[famID] = []
        removedFamHitsDict[famID] = []
        print "no ConsRes for FamilyID %s. famAlignFileName %s made" % (famI

validatedSubHitDict = {}
removedSubHitsDict = {}
for subID in hmmDict[SFID][2].keys():
    if subID in consResDict[SFID][2].keys():
        subAlignFileName = runningDir + "SF" + str(SFID) + "Sub" + str(subID) +
        if os.path.isfile(subAlignFileName):
            validatedSubHitDict[subID], removedSubHitsDict[subID] = checkAlignme
            print "checking file for sub family %s" % (subAlignFileName)
        else:
            print "No alignment file for subgroup ID %s" % (subID)
            validatedSubHitDict[subID] = []
            removedSubHitsDict[subID] = []
```

```
      else:
        subAlignFileName = runningDir + "SF" + str(SFID) + "Sub" + str(subID) + '
        openfile = open(subAlignFileName, "w")
        openfile.close()
        validatedSubHitDict[subID] = []
        removedSubHitsDict[subID] = []
        print "No ConsRes for subgroup ID %s. File %s made" % (subID, subAligr


    validatedHitsDict[SFID] = [validatedSFHitList, validatedFamHitDict, validatedS
    print "validatedSFHitList"
    print validatedSFHitList
    print "validatedFamHitDict"
    print validatedFamHitDict
    print "validatedSubHitDict"
    print validatedSubHitDict

    removedHitsDict[SFID] = [removedSFHitsList, removedFamHitsDict, removed
    print "removedSFHitsList"
    print removedSFHitsList
    print "removedFamHitsDict"
    print removedFamHitsDict
    print "removedSubHitsDict"
    print removedSubHitsDict

  return validatedHitsDict, removedHitsDict



##################################################################
# gseLoadFile
##################################################################
def gseLoadFile(fileName):
  """Open the giScoreEvalue file and return contents in a list"""

  gseFileList = []
  gseINFile = open(fileName, 'r')

  for line in gseINFile.readlines():
    tmpList = line.split()
    gseFileList.append(tmpList)

  gseINFile.close()
  return gseFileList

##################################################################
```

```
# printGSEFile
##################################################################################
def printGSEFile(fileList, filename):
  """Print out the fileList to the file named filename"""
  fileOut = open(filename, "w")
  for entry in fileList:
    listString = '\t'.join((entry))
    fileOut.write(listString)
    fileOut.write("\n")

  fileOut.close()


##################################################################################
# markIfValidHit
##################################################################################
def markIfValidHit(validatedHitsDict, removedHitsDict, giScoreEvalueDict):
  """Mark the hits in giScoreEvalue files as valid or invalid hits.

  Input:
     validatedHitsDict: the Dict with the validated gi's for the SF's, Fams&
        Sub's
     removedHitsDict:  the dict with the invalidated gi's for the SF's Fams &
        Subs
     giScoreEvalueDict: the dict that holds all the files names for the
        parsed hmmsearch files (their file extension is .giScoreEvalue)
  This program will read in each .giScoreEvalue and mark each hit (line) as
  either valid or invalid and then

  Return: the dictionary holding all the updated entry information in entryDict
        The new entry format is:
        <gi>    <score>    <evalue>    <VALID/NOT_valid>
  """
  entryDict = {} #this holds all of the entry data from the flatfiles

  for SFID in giScoreEvalueDict.keys():
    # deal with the SF
    if giScoreEvalueDict[SFID][0] != None: #else pass

      validGISFList = validatedHitsDict[SFID][0]

      invalidGISFList = removedHitsDict[SFID][0]

      gseINFileList = gseLoadFile(giScoreEvalueDict[SFID][0])
      for entry in gseINFileList:
        if entry[0] in validGISFList:
```

```
      entry.insert(len(entry),"VALID")
    elif entry[0] in invalidGISFList:
      entry.insert(len(entry), "NOT_valid")
    else:
      print "This Didn't work!!! NO hits? SFID = %s. entry = %s" % (SFID, entr

  SFentry = gseINFileList
  #printGSEFile(gseINFileList, giScoreEvalueDict[SFID][0])

else:
   SFentry = None

#deal with the families
famEntryDict ={}
famGSEDict = giScoreEvalueDict[SFID][1]
validFamDict = validatedHitsDict[SFID][1]
invalidFamDict = removedHitsDict[SFID][1]
for famID in famGSEDict.keys():
  famGSEFile = famGSEDict[famID] #get the family gse filename
  famINFileList = gseLoadFile(famGSEFile)

  validGIFamList = validFamDict[famID] #get the fam list of valid hits

  invalidGIFamList = invalidFamDict[famID] #get the fam list of invalid hits

  for entry in famINFileList:
    if entry[0] in validGIFamList:
      entry.insert(len(entry), "VALID")
    elif entry[0] in invalidGIFamList:
      entry.insert(len(entry), "NOT_valid")
    else:
      print "2 THis didn't work. NO hits? famID = %s. entry = %s" % (famID, e

  famEntryDict[famID] = famINFileList
  #printGSEFile(famINFileList, famGSEFile)


#deal with the subgroups
subEntryDict = {}
subGSEDict = giScoreEvalueDict[SFID][2]
validSubDict = validatedHitsDict[SFID][2]
invalidSubDict = removedHitsDict[SFID][2]
for subID in subGSEDict.keys():
  subGSEFile = subGSEDict[subID] #get the sub gse filename
  subINFileList = gseLoadFile(subGSEFile)
```

```
            validGISubList = validSubDict[subID] #get the sub list of valid hits

            invalidGISubList = invalidSubDict[subID] #get the sub list of invalid hits

            for entry in subINFileList:
                if entry[0] in validGISubList:
                    entry.insert(len(entry), "VALID")
                elif entry[0] in invalidGISubList:
                    entry.insert(len(entry),"NOT_valid")
                else:
                    print "3 THis didn't work. NO hits? subID = %s. entry = %s" % (subID, er

            subEntryDict[subID] = subINFileList
            #printGSEFile(subINFileList, subGSEFile)

        entryDict[SFID] = [SFentry, famEntryDict, subEntryDict]

    return entryDict

#####################################################################################
#fastacmdDefSeq
#####################################################################################
def fastacmdDefSeq(entryList, fastaDict, runningDir, dbName):
    """Return entry list with added def line and AA sequence.
    Input: entryList a list of the format
    <gi>    <def line>    <score>   <Evalue>    <VALID/NOT_valid>     <IN_SFLD>
    Return: entryList: a new list that has added the definition line and the AA seque
            of the format
    <gi>    <def line>    <score>   <Evalue>    <VALID/NOT_valid>     <IN_SFLD>

            fastaDict: key = gi number, value = fasta file name for that gi

    """
    gi = entryList[0]
    fastaFileName = runningDir + gi + '.fasta'

    if gi not in fastaDict.keys():
        fastaDict[gi] = fastaFileName
        cmd = 'fastacmd -d %s -s%s -tT > %s' % (dbName, gi, fastaFileName)
        os.system(cmd)
    else:
        pass

    fastaFile = open(fastaFileName, "r")
    defLine = fastaFile.readline()
    defLine = defLine[:-1] #strip off the endl
```

```
    AAline = fastaFile.readline() #get the first AA line
    AAline = AAline[:-1]
    line = fastaFile.readline()
    while line:
        line = line[:-1]
        AAline = AAline + line
        line = fastaFile.readline()

    #insert def line in second position of list, after gi
    entryList.insert(1, defLine)

    #insert lenght AA line at the end of the list
    entryList.insert(len(entryList), str(len(AAline)))

    #insert AA line at the end of the list
    entryList.insert(len(entryList), AAline)

    fastaFile.close()
    return entryList, fastaDict


######################################################
# getDefandSeq
######################################################
def getDefandSeq(entryDict, runningDir, dbName):
    """Return new dict of the entries that includes the def line and AA sequence.
    Input:   entryDict--the dictionary key = SFID, value = lists of entry data
        for each SF/Fam/Sub.
    Return:    newEntryDict--dictionary key = SFID, value = updated lists of
        entry data for each SF/Fam/Sub in the format
        <gi>    <def line>    <score>   <Evalue>    <VALID/NOT_valid>     <IN_SFLD
               fastaDict--dictionary key = gi number, value = fasta file for that gi
    """
    newEntryDict = {}  #key SFID, value entry lists
    fastaDict = {}  # key gi number, value fasta file name
    for SFID in entryDict.keys():

        if entryDict[SFID][0] != None:
            SFentryList = entryDict[SFID][0]
            for entry in SFentryList:
                entry, fastaDict = fastacmdDefSeq(entry, fastaDict, runningDir, dbName
            newSFentryList = SFentryList
        else:
            newSFentryList = None
```

```
        famEntryDict = entryDict[SFID][1]
        newFamEntryDict = {}
        for famID in famEntryDict.keys():
            famEntryList = famEntryDict[famID]
            for entry in famEntryList:
                entry, fastaDict = fastacmdDefSeq(entry, fastaDict, runningDir, dbName
            newFamEntryDict[famID] = famEntryList

        subEntryDict = entryDict[SFID][2]
        newSubEntryDict = {}
        for subID in subEntryDict.keys():
            subEntryList = subEntryDict[subID]
            for entry in subEntryList:
                entry, fastaDict = fastacmdDefSeq(entry, fastaDict, runningDir, dbName
            newSubEntryDict[subID] = subEntryList

        newEntryDict[SFID] = [newSFentryList, newFamEntryDict, newSubEntryDict

    return newEntryDict, fastaDict

######################################################################
#printOutput
######################################################################
def printOutput(giScoreEvalueDict, entryDict, fileExt):
    """Print out the updated entries fo files listed in giScoreEvalueDict.
    format of file:
    <gi>    <def line>    <score>    <Evalue>    <VALID/NOT_valid>    <IN_SFLD>
    fileExt: if not empty, add this file extension to the filenames to write to

    """
    for SFID in giScoreEvalueDict.keys():
        if giScoreEvalueDict[SFID][0] != None:
            SFfileName = giScoreEvalueDict[SFID][0]
            SFfileName = SFfileName + fileExt
            SFfileList = entryDict[SFID][0]
            printGSEFile(SFfileList, SFfileName)
        else:
            pass

        famFileNameDict = giScoreEvalueDict[SFID][1]
        famEntryDict = entryDict[SFID][1]
        for famID in famFileNameDict.keys():
            famFileName = famFileNameDict[famID]
            famFileName = famFileName + fileExt
            famEntryList = famEntryDict[famID]
            printGSEFile(famEntryList, famFileName)
```

```
        subFileNameDict = giScoreEvalueDict[SFID][2]
        subEntryDict = entryDict[SFID][2]
        for subID in subFileNameDict.keys():
            subFileName = subFileNameDict[subID]
            subFileName = subFileName + fileExt
            subEntryList = subEntryDict[subID]
            printGSEFile(subEntryList, subFileName)

######################################################################
# seenThisDomain
######################################################################
def seenThisDomain(entry, hitList, hitDomainDict, entryList):
    """Return a Dict with cdd domain hits added to the info in 'entry'.
    INPUT:
        entry: a list of data for one gi
        hitList: a list of keys for hitDomainDict
        hitDomainDict: a dict with key = hit name ('gi_hit1' etc), value =
            domain hit information in the format
            <total length> <align. length> <query start> <query end> <percent ID>
                    <evalue> <bit score> <db>
        entryList: A list of lists (a list of entries) the
            entries are in the format
            <gi>    <def line>    <score>    <Evalue>    <VALID/NOT_valid>
                    <IN_SFLD>    <SFLD fasta filename>     <AA sequence>
    PROCESS:
        This gi has been seen before (and therefore the rpsblast has been done
        and the domain hits gotten) but we still need to add this info to the
        current entry being processed. This function will add the info in a
        series of new line additions to entryDict so that the fist updated
        entry is
            <gi>    <def line>    <score>    <Evalue>    <VALID/NOT_valid>
                    <IN_SFLD>    <SFLD fasta filename> <total length>
                    <align. length> <query start> <query end> <percent ID>
                    <evalue> <bit score> <db>  <AA sequence>
       the following entries are
            <gi>    <[dup]>    <[dup]>   <Evalue>    <[dup]>
                    <[dup]>    <[dup]> <total length>
                    <align. length> <query start> <query end> <percent ID>
                    <evalue> <bit score> <db>  <[dup]>
    RETURN:
        updatedEntryDict: a dict key = SFID, value = updated entries (see PROCES

    """
    updatedEntryList = entryList[:]
    entry_index = entryList.index(entry)
```

```
    entry_copy = entry[:]

    #deal with the first CDD hit
    if hitList:
        hit_1 = hitList.pop(0)
        domainHitList = hitDomainDict[hit_1]
        for datum in domainHitList:
            index = len(entry_copy) - 1 #insert before the last item
            entry_copy.insert(index, datum)

        updatedEntryList.pop(entry_index) #remove old entry
        updatedEntryList.insert(entry_index, entry_copy) #put in new entry into orig.

        #now deal with the rest of the CDD hits
        for hit in hitList:
            entry_copy = entry[:]
            domainHitList = hitDomainDict[hit]
            # get the domain data
            for datum in domainHitList:
                index = len(entry_copy) - 1 #insert before the last item
                entry_copy.insert(index, datum)

            # replace appropriate values with [dup] (duplicate)
            entry_copy[1] = '[dup]'   #def line
            entry_copy[2] = '[dup]'   #score
            entry_copy[4] = '[dup]'   #VALID/NOT_valid
            entry_copy[5] = '[dup]'   #IN_SFLD
            entry_copy[6] = '[dup]'   #SFLD fasta filename
            entry_copy[-1] = '[dup]'  # AA sequence

            entry_index = entry_index + 1
            updatedEntryList.insert(entry_index, entry_copy)
    else:
        for i in range(0, 8):
            index = len(entry_copy) - 1 #insert before the last item
            entry_copy.insert(index, '[]')
        updatedEntryList.pop(entry_index) #remove old entry
        updatedEntryList.insert(entry_index, entry_copy) #put in new entry into orig.

    return updatedEntryList

########################################################################
# parseRPSBlast
########################################################################
def parseRPSBlast(rpsFileName):
    """Return a list holding the top five hits from the rpsFile.
```

```
    INPUT:
        rpsFileName: the filename of the output from an rpsblast run.
        file is in tabular format
            "Query id, Subject id, % identity, alignment length, mismatches,
                    gap openings, q. start, q. end, s. start, s. end,
                    e-value, bit score"
    PROCESS:
        Open the rps file and parse out the top five hits and put them into a
        list.
    RETURN:
         hitList: A list of lists of the top 5 rpsblast hits.

    """
    rpsFile = open(rpsFileName, 'r')
    #file is in tabular format with each line having the format
    #Query id, Subject id, % identity, alignment length, mismatches, gap openings,
    hitList = []
    i = 0
    for line in rpsFile.readlines():
        if i in range(0, 5):
            tmpList = line.split()

            db_info = str(tmpList[1])
            perc_id = str(tmpList[2])
            align_len = str(tmpList[3])
            q_start = str(tmpList[6])
            q_end = str(tmpList[7])
            evalue = str(tmpList[10])
            bit_score = str(tmpList[11])
            hitList.append([align_len, q_start, q_end, perc_id, evalue, bit_score, db_ir
            i += 1
        else:
            break

    return hitList


###############################################################
# runRPSBlast
###############################################################
def runRPSBlast(entry, haveDomainDict, hitDomainDict, fastaFileName):
    """Return two dictionaries that contian CDD domian data gathered from rpsblas
    INPUT:
        entry: the entry to run rpsblast on
        haveDomainDict: a dictionary Key = gi, value = list of keys for hitDomainDict
        hitDomainDict: a dictionary key = hit name ('gi_hit1' etc), value = cdd
```

```
            hit information in the format
            <total length> <length alignment> <query align start> <query align end>
            <percentID> <evalue of rpsblast> <bit score of rpsblast>  <rpsblast DB>
        fastaFileName: the filename of the fasta file to be run in rpsblast
        NOT PASSED:
            NOTE: this function calls the ncbi program rpsblast and therefore
            requires having an rpsblast formatted DB somewhere accessible and a
            .ncbirc file in the running directory
    PROCESS:
        This function will run rpsblast on the input fasta file and then open
        up the output and parse out the top 5 domain hits. This function has
        been hard-coded to use the CDD database. This function then updates
        haveDomainDict and hitDomainDict with the new gi/domain data.
    RETURN:
        updated haveDomainDict
        updated hitDomainDict

    """
    outputFile = fastaFileName + '.rpsblast'

    #get tabular output from rpsblast
    os.system('rpsblast -i %s -d Cdd -m 8 -o %s' % (fastaFileName, outputFile))
    hitList = parseRPSBlast(outputFile)
    total_seq_len = len(entry[-1])
    hitNum = 1
    gi = entry[0]
    keyList = []
    for hit in hitList:
        hit.insert(0, str(total_seq_len))
        hitKey = gi + '_hit_' + str(hitNum)
        hitDomainDict[hitKey] = hit
        keyList.append(hitKey)
        hitNum += 1

    haveDomainDict[gi] = keyList

    return haveDomainDict, hitDomainDict

##################################################################
# getDomainListing
##################################################################
def getDomainListing(entryDict, fastaDict, runningDir):
    """Return updated entries with the top five domain hits (using CDD) for each se
    Input: entryDict: key = SFID, value = lists of entries of the format...
        <gi>    <def line>    <score>    <Evalue>    <VALID/NOT_valid>    <IN_SFLD:
           fastaDict: key = gi, value = fasta file name for that gi
```

```
Process: use rpsblast and the CDD database to determine the top five domains
        for each sequence. After this, remove all the fasta files in fastaDict.

Return:    newEntryDict: key = SFID, value = lists of entries of the format...
<gi> <def line>  <score>   <Evalue>    <VALID/NOT_valid>     <IN_SFLD>
       <SFLD fasta filename> <total length> <length alignment>
       <query align start> <query align end> <percentID> <evalue of rpsblast>
       <bit score of rpsblast>  <rpsblast DB> <AA sequence>

"""
# key = gi, value = list of keys for hitDomainDict
haveDomainDict = {}
# key = hit name ('gi_hit1' etc.), value = list of hit information
hitDomainDict = {}
newEntryDict = {}

for SFID in entryDict.keys():
    # do the SF hits
    if entryDict[SFID][0] != None:
        SFentryList = entryDict[SFID][0] #get the list
        newSFentryList = SFentryList[:] #this is the new list
        for entry in SFentryList:
            gi = entry[0]
            if gi in haveDomainDict.keys():
                hitList = haveDomainDict[gi]
                newSFentryList = seenThisDomain(entry, hitList, hitDomainDict, new

            else:
                fastaFileName = fastaDict[gi]
                haveDomainDict, hitDomainDict = runRPSBlast(entry, haveDomainD
                hitList = haveDomainDict[gi]
                newSFentryList = seenThisDomain(entry, hitList, hitDomainDict, new
    else:
        newSFentryList = None

    famEntryDict = entryDict[SFID][1]
    newFamEntryDict = {}
    for famID in famEntryDict.keys():
        famEntryList = famEntryDict[famID]
        newFamEntryList = famEntryList[:]
        for entry in famEntryList:
            gi = entry[0]
            if gi in haveDomainDict.keys():
                hitList = haveDomainDict[gi]
                newFamEntryList = seenThisDomain(entry, hitList, hitDomainDict, ne
```

```
                else:
                    fastaFileName = fastaDict[gi]
                    haveDomainDict, hitDomainDict = runRPSBlast(entry, haveDomainD
                    hitList = haveDomainDict[gi]
                    newFamEntryList = seenThisDomain(entry, hitList, hitDomainDict, ne
            newFamEntryDict[famID] = newFamEntryList

        subEntryDict = entryDict[SFID][2]
        newSubEntryDict = {}
        for subID in subEntryDict.keys():
            subEntryList = subEntryDict[subID]
            newSubEntryList = subEntryList[:]
            for entry in subEntryList:
                gi = entry[0]
                if gi in haveDomainDict.keys():
                    hitList = haveDomainDict[gi]
                    newSubEntryList = seenThisDomain(entry, hitList, hitDomainDict, ne
                else:
                    fastaFileName = fastaDict[gi]
                    haveDomainDict, hitDomainDict = runRPSBlast(entry, haveDomainD
                    hitList = haveDomainDict[gi]
                    newSubEntryList = seenThisDomain(entry, hitList, hitDomainDict, ne
            newSubEntryDict[subID] = newSubEntryList

        for gi in fastaDict.keys():
            os.system('rm -f %s' % (fastaDict[gi]))
        newEntryDict[SFID] = [newSFentryList, newFamEntryDict, newSubEntryDict
        #print newSFentryList
        #print newFamEntryDict
        #print newSubEntryDict
    #print newEntryDict
    return newEntryDict

################################################################
# parseEFDList
################################################################
def parseEFDList(efdFile):
    """Get the Info from the EFD file
    <gi> <name> <species> <fam ID> <fam ev code> <fam name> <sub id> <sub
    <sf id> <sf ev code> <sf name>"""

    print"parseEFDList"
    sys.stdout.flush()

    efdDict = {}
```

```
    inFile = open(efdFile, 'r')
    gi = "null"
    famID = "null"
    famEvCode = "null"
    famName = "null"
    subID = "null"
    subName = "null"
    sfID = "null"
    sfEvCode = "null"
    sfName = "null"

    for line in inFile.readlines():
        line = line[:-1]
        tmpList = line.split(';')
        if len(tmpList) > 7:  # does the line have something in it
            gi = tmpList[0]
            famID = tmpList[3]
            famEvCode = tmpList[4]
            famName = tmpList[5]
            subID = tmpList[6]
            subName = tmpList[7]
            sfID = tmpList[8]
            sfEvCode = tmpList[9]
            sfName = tmpList[10]

            efdDict[gi] = [famID, famEvCode, famName, subID, subName, sfID, sfEvC

    return efdDict


################################################################################
# getEvidenceCodes
################################################################################
def getEvidenceCodes(entryDict, EFDFile):
    """get the evidence codes for any sequences that are in the sfld
    entryDict list
        <gi>    <def line>    <score>   <Evalue>    <VALID/NOT_valid>
        <IN_SFLD>    <SFLD fasta filename>   <len AA seq>  <AA sequence>
    efddict
    <fam ID> <fam ev code> <fam name> <sub id> <sub name>
    <sf id> <sf ev code> <sf name>
    output entry dict
        <gi>    <def line>    <score>   <Evalue>    <VALID/NOT_valid>
        <IN_SFLD>    <SFLD fasta filename>   <len AA seq>  <AA sequence>
        <fam ID> <fam ev code> <fam name> <sub id> <sub name>
```

```
    <sf id> <sf ev code> <sf name>

"""
print 'getEvidenceCodes'
efdDict = parseEFDList(EFDFile)
newEntryDict = {}  #key SFID, value entry lists

for SFID in entryDict.keys():
   if entryDict[SFID][0] != None:
       SFentryList = entryDict[SFID][0]
       for entry in SFentryList:
          sfld_seq_file = entry[6]
          period_index = sfld_seq_file.find('.')
          if period_index != -1: #there is a file
              gi = sfld_seq_file[: period_index]

              if gi in efdDict.keys():
                  efd_entry = efdDict[gi]
                  entry.insert(len(entry) -1, str(efd_entry[0]))
                  entry.insert(len(entry) -1, str(efd_entry[1]))
                  entry.insert(len(entry) -1, str(efd_entry[2]))
                  entry.insert(len(entry) -1, str(efd_entry[3]))
                  entry.insert(len(entry) -1, str(efd_entry[4]))
                  entry.insert(len(entry) -1, str(efd_entry[5]))
                  entry.insert(len(entry) -1, str(efd_entry[6]))
                  entry.insert(len(entry) -1, str(efd_entry[7]))
              else: #isn't in the sfld
                  entry.insert(len(entry) -1, '[]')
                  entry.insert(len(entry) -1, '[]')
                  entry.insert(len(entry) -1, '[]')
                  entry.insert(len(entry) -1, '[]')
                  entry.insert(len(entry) -1, '[]')
                  entry.insert(len(entry) -1, '[]')
                  entry.insert(len(entry) -1, '[]')
                  entry.insert(len(entry) -1, '[]')
          else: #there isn't a file
              entry.insert(len(entry) -1, '[]')
              entry.insert(len(entry) -1, '[]')
              entry.insert(len(entry) -1, '[]')
              entry.insert(len(entry) -1, '[]')
              entry.insert(len(entry) -1, '[]')
              entry.insert(len(entry) -1, '[]')
              entry.insert(len(entry) -1, '[]')
              entry.insert(len(entry) -1, '[]')

       newSFentryList = SFentryList
```

```
else:
    newSFentryList = None

famEntryDict = entryDict[SFID][1]
newFamEntryDict = {}
for famID in famEntryDict.keys():
    famEntryList = famEntryDict[famID]
    for entry in famEntryList:
        sfld_seq_file = entry[6]
        period_index = sfld_seq_file.find('.')
        if period_index != -1: #there is a file
            gi = sfld_seq_file[: period_index]

            if gi in efdDict.keys():
              efd_entry = efdDict[gi]
              entry.insert(len(entry) -1, str(efd_entry[0]))
              entry.insert(len(entry) -1, str(efd_entry[1]))
              entry.insert(len(entry) -1, str(efd_entry[2]))
              entry.insert(len(entry) -1, str(efd_entry[3]))
              entry.insert(len(entry) -1, str(efd_entry[4]))
              entry.insert(len(entry) -1, str(efd_entry[5]))
              entry.insert(len(entry) -1, str(efd_entry[6]))
              entry.insert(len(entry) -1, str(efd_entry[7]))
            else: #isn't in the sfld
              entry.insert(len(entry) -1, '[]')
              entry.insert(len(entry) -1, '[]')
              entry.insert(len(entry) -1, '[]')
              entry.insert(len(entry) -1, '[]')
              entry.insert(len(entry) -1, '[]')
              entry.insert(len(entry) -1, '[]')
              entry.insert(len(entry) -1, '[]')
              entry.insert(len(entry) -1, '[]')
        else: #there isn't a file
          entry.insert(len(entry) -1, '[]')
          entry.insert(len(entry) -1, '[]')
          entry.insert(len(entry) -1, '[]')
          entry.insert(len(entry) -1, '[]')
          entry.insert(len(entry) -1, '[]')
          entry.insert(len(entry) -1, '[]')
          entry.insert(len(entry) -1, '[]')
          entry.insert(len(entry) -1, '[]')

    newFamEntryDict[famID] = famEntryList

subEntryDict = entryDict[SFID][2]
newSubEntryDict = {}
```

```
        for subID in subEntryDict.keys():
            subEntryList = subEntryDict[subID]
            for entry in subEntryList:
                sfld_seq_file = entry[6]
                period_index = sfld_seq_file.find('.')
                if period_index != -1: #there is a file
                    gi = sfld_seq_file[: period_index]
                    if gi in efdDict.keys():
                        efd_entry = efdDict[gi]
                        entry.insert(len(entry) -1, str(efd_entry[0]))
                        entry.insert(len(entry) -1, str(efd_entry[1]))
                        entry.insert(len(entry) -1, str(efd_entry[2]))
                        entry.insert(len(entry) -1, str(efd_entry[3]))
                        entry.insert(len(entry) -1, str(efd_entry[4]))
                        entry.insert(len(entry) -1, str(efd_entry[5]))
                        entry.insert(len(entry) -1, str(efd_entry[6]))
                        entry.insert(len(entry) -1, str(efd_entry[7]))
                    else: #isn't in the sfld
                        entry.insert(len(entry) -1, '[]')
                        entry.insert(len(entry) -1, '[]')
                        entry.insert(len(entry) -1, '[]')
                        entry.insert(len(entry) -1, '[]')
                        entry.insert(len(entry) -1, '[]')
                        entry.insert(len(entry) -1, '[]')
                        entry.insert(len(entry) -1, '[]')
                        entry.insert(len(entry) -1, '[]')
                else: #there isn't a file
                    entry.insert(len(entry) -1, '[]')
                    entry.insert(len(entry) -1, '[]')
                    entry.insert(len(entry) -1, '[]')
                    entry.insert(len(entry) -1, '[]')
                    entry.insert(len(entry) -1, '[]')
                    entry.insert(len(entry) -1, '[]')
                    entry.insert(len(entry) -1, '[]')
                    entry.insert(len(entry) -1, '[]')


            newSubEntryDict[subID] = subEntryList

        newEntryDict[SFID] = [newSFentryList, newFamEntryDict, newSubEntryDict]


    return newEntryDict

################################################################
```

```
# getMultGI
######################################################################
def getMultGI(entryDict, dbName, runningDir):
   """expand entry dict to include duplicate sequences (with dif gi numbers)
         <gi>    <def line>    <score>   <Evalue>    <VALID/NOT_valid>
      <IN_SFLD>    <SFLD fasta filename>   <len AA seq>  <AA sequence>
      <fam ID> <fam ev code> <fam name> <sub id> <sub name>
      <sf id> <sf ev code> <sf name>

   """
   print "getMultGI(entryDict, dbName, runningDir)"
   newEntryDict = {}  #key SFID, value entry lists
   newSFList = []

   for SFID in entryDict.keys():
      if entryDict[SFID][0] != None:
         SFentryList = entryDict[SFID][0]
         for entry in SFentryList:
            fastaFileName = runningDir + 'temp.fa'
            gi = entry[0]
            cmd = 'fastacmd -d %s -s%s  > %s' % (dbName, gi, fastaFileName)
            os.system(cmd)

            fastaFile = open(fastaFileName, "r")
            defLine = fastaFile.readline()
            defLine = defLine[:-1] #strip off the endl
            fastaFile.close()
            gi_count = defLine.count('>gi|')
            #print "gi_count: " + str(gi_count)
            if gi_count > 1:
               while gi_count != 0:
                  index_1 = defLine.find('>gi|') # find the gi start
                  #print 'line: ' + defLine
                  #print 'index_1: ' + str(index_1)
                  if index_1 != -1: #there's a gi
                     start_next = index_1 + 1
                     index_2 = defLine[start_next :].find('>gi|')
                     #print "index_2 " + str(start_next + index_2)
                     if index_2 != -1: #it's not the end of the line
                        #print "defLine 2: " + defLine[index_1 : (start_next + index_2)]
                        tmpList = defLine[index_1 : (start_next + index_2)].split('|')
                        newGI = str(tmpList[1])
                        cmd = 'fastacmd -d %s -s%s -tT > %s' % (dbName, newGI, fas
                        fastaFile = open(fastaFileName, "r")
                        line = fastaFile.readline()
                        line = line[:-1] #strip off the endl
```

```
                       fastaFile.close()
                       entry_copy = entry[:]
                       entry_copy[0] = str(newGI)
                       entry_copy[1] = line
                       newSFList.append(entry_copy)

                   else: # at the end of the line
                       tmpList = defLine[index_1 :].split('|')
                       if len(tmpList) < 2:
                           print "tmpList SF: "
                           print tmpList
                           print 'defLine SF: '
                           print defLine
                       else:
                          newGI = str(tmpList[1])
                          cmd = 'fastacmd -d %s -s%s -tT > %s' % (dbName, newGI, f
                          fastaFile = open(fastaFileName, "r")
                          line = fastaFile.readline()
                          line = line[:-1] #strip off the endl
                          fastaFile.close()
                          entry_copy = entry[:]
                          entry_copy[0] = str(newGI)
                          entry_copy[1] = line
                          newSFList.append(entry_copy)




               else: # don't think I should ever get here
                   print "at break point I didn't think should happen"
                   break

               gi_count = gi_count - 1
               defLine = defLine[(index_1 + 1) :]

        else: #not a multiple gi
           newSFList.append(entry) #just put in the orig entry

else:
     newSFList = None



famEntryDict = entryDict[SFID][1]
newFamEntryDict = {}
for famID in famEntryDict.keys():
```

```
famEntryList = famEntryDict[famID]
newFamList = []
for entry in famEntryList:
    fastaFileName = runningDir + 'temp.fa'
    gi = entry[0]
    cmd = 'fastacmd -d %s -s%s  > %s' % (dbName, gi, fastaFileName)
    os.system(cmd)

    fastaFile = open(fastaFileName, "r")
    defLine = fastaFile.readline()
    defLine = defLine[:-1] #strip off the endl
    fastaFile.close()
    gi_count = defLine.count('>gi|')
    print "gi_count: " + str(gi_count)

    if gi_count > 1:
        while gi_count != 0:
            index_1 = defLine.find('>gi|') # find the gi start
            print 'line: ' + defLine
            print 'index_1: ' + str(index_1)
            if index_1 != -1: #there's a gi
                start_next = index_1 + 1
                index_2 = defLine[start_next :].find('>gi|')
                print "index_2 " + str(start_next + index_2)
                if index_2 != -1: #it's not the end of the line
                    print "defLine 2: " + defLine[index_1 : (start_next + index_2)]
                    tmpList = defLine[index_1 : (start_next + index_2)].split('|')
                    newGI = str(tmpList[1])
                    print "newGI " + newGI
                    #cmd = 'fastacmd -d %s -s%s -tT > %s' % (dbName, newGI, fa
                    #fastaFile = open(fastaFileName, "r")
                    #line = fastaFile.readline()
                    #line = line[:-1] #strip off the endl
                    #fastaFile.close()
                    entry_copy = entry[:]
                    entry_copy[0] = str(newGI)
                    #entry_copy[1] = line
                    entry_copy[1] = defLine[index_1 : (start_next + index_2)]
                    newFamList.append(entry_copy)
                    #defLine = defLine[(start_next + index_2) :]

                else: # at the end of the line
                    tmpList = defLine[index_1 :].split('|')
                    if len(tmpList) < 2:
                        print "tmpList FAM: "
                        print tmpList
```

```
                           print 'defLine FAM: '
                           print defLine

                       else:
                          newGI = str(tmpList[1])
                          print "newGI 2:" + newGI
                          #cmd = 'fastacmd -d %s -s%s -tT > %s' % (dbName, newGI,
                          #fastaFile = open(fastaFileName, "r")
                          #line = fastaFile.readline()
                          #line = line[:-1] #strip off the endl
                          #fastaFile.close()
                          entry_copy = entry[:]
                          entry_copy[0] = str(newGI)
                          #entry_copy[1] = line
                          entry_copy[1] = defLine[index_1 :]
                          newFamList.append(entry_copy)



               else: # don't think I should ever get here
                   print "at break point I didn't think should happen"
                   break

               gi_count = gi_count - 1
               #defLine = defLine[(index_1 + 1) :]
               defLine = defLine[(start_next + index_2) :]

        else: #no multiple gi's
           newFamList.append(entry) #just put in the orig entry

    newFamEntryDict[famID] = newFamList


subEntryDict = entryDict[SFID][2]
newSubEntryDict = {}
for subID in subEntryDict.keys():
     subEntryList = subEntryDict[subID]
     newSubList = []
     for entry in subEntryList:
        fastaFileName = runningDir + 'temp.fa'
        gi = entry[0]
        cmd = 'fastacmd -d %s -s%s  > %s' % (dbName, gi, fastaFileName)
        os.system(cmd)

        fastaFile = open(fastaFileName, "r")
```

```
defLine = fastaFile.readline()
defLine = defLine[:-1] #strip off the endl
fastaFile.close()
gi_count = defLine.count('>gi|')
#print "gi_count: " + str(gi_count)

if gi_count > 1:
    while gi_count != 0:
       index_1 = defLine.find('>gi|') # find the gi start
       #print 'line: ' + defLine
       #print 'index_1: ' + str(index_1)
       if index_1 != -1: #there's a gi
           start_next = index_1 + 1
           index_2 = defLine[start_next :].find('>gi|')
           #print "index_2 " + str(start_next + index_2)
           if index_2 != -1: #it's not the end of the line
               #print "defLine 2: " + defLine[index_1 : (start_next + index_2)]
               tmpList = defLine[index_1 : (start_next + index_2)].split('|')
               newGI = str(tmpList[1])
               cmd = 'fastacmd -d %s -s%s -tT > %s' % (dbName, newGI, fas
               fastaFile = open(fastaFileName, "r")
               line = fastaFile.readline()
               line = line[:-1] #strip off the endl
               fastaFile.close()
               entry_copy = entry[:]
               entry_copy[0] = str(newGI)
               entry_copy[1] = line
               newSubList.append(entry_copy)

           else: # at the end of the line
               tmpList = defLine[index_1 :].split('|')
               if len(tmpList) < 2:
                   print "tmpList SUB: "
                   print tmpList
                   print 'defLine: '
                   print defLine
               else:
                  newGI = str(tmpList[1])
                  cmd = 'fastacmd -d %s -s%s -tT > %s' % (dbName, newGI, f
                  fastaFile = open(fastaFileName, "r")
                  line = fastaFile.readline()
                  line = line[:-1] #strip off the endl
                  fastaFile.close()
                  entry_copy = entry[:]
                  entry_copy[0] = str(newGI)
                  entry_copy[1] = line
```

```
                                  newSubList.append(entry_copy)




                      else: # don't think I should ever get here
                          print "at break point I didn't think should happen"
                          break

                      gi_count = gi_count - 1
                      defLine = defLine[(index_1 + 1) :]

               else: #not a new gi
                  newSubList.append(entry) #just put in the orig entry

            newSubEntryDict[subID] = subEntryList

       newEntryDict[SFID] = [newSFList, newFamEntryDict, newSubEntryDict]


    return newEntryDict



####################################################################
# Main program
####################################################################
def filterHomolSearchSFLD(argv):
   """Main program."""
   checkArg(argv)
   shortOpts = ''
   longOpts = ['supFamListFile=', 'hmmPath=', 'alignPath=', 'seqPath=', 'seqFileNa
      'SFFile=',  'SFHMMFile=', 'SubHMMFile=', 'FamHMMFile=', 'runningPath=',
      'dbName=', 'sfAlignFile=', 'sfConsRes=', 'famAlignFile=', 'famConsRes=',
      'subAlignFile=', 'subConsRes=', 'efdFile=']
   opts,args = getopt.getopt(sys.argv[1:], shortOpts, longOpts)

   for option, value in opts:
      if option in ('--supFamListFile'):
         superfamilyListFileName = value
      elif option in ('--hmmPath'):
         hmmPath = value
      elif option in ('--alignPath'):
         alignPath = value
      elif option in ('--seqPath'):
         seqPath = value
```

```
  elif option in ('--seqFileName'):
    seqFileName = value
  elif option in ('--SFFile'):
    SFName_and_ID_file = value
  elif option in ('--SFHMMFile'):
    SFHMMListName = value
  elif option in ('--SubHMMFile'):
    SubHMMListName = value
  elif option in ('--FamHMMFile'):
    FamHMMListName = value
  elif option in ('--runningPath'):
    runningDir = value
  elif option in ('--dbName'):
    dbName = value
  elif option in ('--sfAlignFile'):
    sf_align_file_name = value
  elif option in ('--sfConsRes'):
    sf_cons_residue_file_name = value
  elif option in ('--famAlignFile'):
    fam_align_file_name = value
  elif option in ('--famConsRes'):
    fam_cons_res_file_name = value
  elif option in ('--subAlignFile'):
    sub_align_file_name = value
  elif option in ('--subConsRes'):
    sub_cons_res_file_name = value
  elif option in ('--efdFile'):
    EFD_file = value

print 'SFIDList = getSFIDList(superfamilyListFileName, SFName_and_ID_file)'
SFIDList = getSFIDList(superfamilyListFileName, SFName_and_ID_file)

print 'hmmDict = getHMMDict(SFIDList, SFHMMListName, SubHMMListName,
hmmDict = getHMMDict(SFIDList, SFHMMListName, SubHMMListName, FamH

print 'fastaDict, giScoreEvalueDict = runParseHMMSearch(hmmDict, runningDi
fastaDict, giScoreEvalueDict = runParseHMMSearch(hmmDict, runningDir, dbN

print """consResDict, repSeqDict = getConsResDict(hmmDict, alignPath,
  sf_align_file_name, sf_cons_residue_file_name, fam_align_file_name,
  fam_cons_res_file_name, sub_align_file_name, sub_cons_res_file_name)"""
consResDict, repSeqDict = getConsResDict(hmmDict, alignPath,
  sf_align_file_name, sf_cons_residue_file_name, fam_align_file_name,
  fam_cons_res_file_name, sub_align_file_name, sub_cons_res_file_name)

print 'consResDict = reformatConsResDict(consResDict)'
```

```
    consResDict = reformatConsResDict(consResDict)

    print 'alignHits(fastaDict, repSeqDict, hmmDict, hmmPath)'
    alignHitDict = alignHits(fastaDict, repSeqDict, hmmDict, hmmPath, runningDir)

    print 'validatedHitsDict, removedHitsDict = checkHitsForConsRes(hmmDict, cor
    validatedHitsDict, removedHitsDict = checkHitsForConsRes(hmmDict, consRes
    #print validatedHitsDict
    #print removedHitsDict

    print 'markIfValidHit(validatedHitsDict, removedHitsDict, giScoreEvalueDict)'
    entryDict = markIfValidHit(validatedHitsDict, removedHitsDict, giScoreEvalueDi

    print 'markIfInSFLD(seqPath, giScoreEvalueDict, seqFileName, runningDir, db
    entryDict = markIfInSFLD(seqPath, entryDict, seqFileName, runningDir, dbNam

    print 'getDefandSeq(entryDict, runningDir)'
    entryDict, allSeqFastaDict = getDefandSeq(entryDict, runningDir, dbName)

    #get the evidence codes for any of the sequences that are in the sfld
    print 'getEvidenceCodes'
    sys.stdout.flush()
    entryDict = getEvidenceCodes(entryDict, EFD_file)

    # get multiple gi's if there are any
    print 'getMultGI(entryDict, dbName, runningDir)'
    sys.stdout.flush()
    entryDict = getMultGI(entryDict, dbName, runningDir)

    fileExt = '.mark'
    print 'printOuput(giScoreEvalueDict, entryDict, fileExt)'
    printOutput(giScoreEvalueDict, entryDict, fileExt)


    #not doing rpsblast, never found the results to be useful
    #print 'getDomainListing(entryDict, allSeqFastaDict, runningDir)'
    #entryDict = getDomainListing(entryDict, allSeqFastaDict, runningDir)

    #fileExt = '.mark.cdd'
    #print 'printOutput(giScoreEvalueDict, entryDict, fileExt)'
    #printOutput(giScoreEvalueDict, entryDict, fileExt)

    #remove tmp files
    os.system('rm -f *.tmp')

filterHomolSearchSFLD(sys.argv)
```

Appendix J. R Scripts for Analysis and Figures (Chapter 3)

```
# AH.Sim.r, example of family/DB r code to make figure
Sys.setenv(R_GSCMD="/sw/bin/gs")
dbNames=c("NR",  "TrEMBL", "KEGG", "Swiss-Prot")
#NR

postscript(file="/Users/schnoes/Alex/Writing/Thesis/Chapter3/
PercentMisannotationFigure/AH.NR.sim.eps",  height=4, width=3.5,  pointsize=10
onefile=FALSE, horizontal=FALSE)
par(cex.axis=1.25)
par(mar=c(5.1, 6,4.1, 2.1), font.lab=2, font.main=2, font.axis=1, cex.main=2,
cex.lab=1.5)

#NR
ahNRFam=read.table("ahFamNRSim.dat", header = T, as.is=T)
ahNRFamData=data.frame(ahNRFam)
ahNRmatrix=matrix(c(ahNRFamData[,3], ahNRFamData[,4], ahNRFamData[,5],
ahNRFamData[,6]), nrow=7, ncol=4)
tmatrix = t(ahNRmatrix)
tmatrix
pnts = barplot(tmatrix, width=0.1, beside=FALSE,  col=c('grey27', 'black',
'white', 'khaki'), border=c("black","black", "black", "black"), xlab='NR',
ylab='Percent')
points(pnts, ahNRFamData[,7], col=ahNRFamData[,8], pch=ahNRFamData[,9],
cex=ahNRFamData[,10])
dev.off()

#TR
postscript(file="/Users/schnoes/Alex/Writing/Thesis/Chapter3/
PercentMisannotationFigure/AH.TR.sim.eps",  height=4, width=3.5,  pointsize=10
onefile=FALSE, horizontal=FALSE)
par(cex.axis=1.25)
par(mar=c(5.1, 6,4.1, 2.1), font.lab=2, font.main=2, font.axis=1, cex.main=2,
cex.lab=1.5)

#TR
ahNRFam=read.table("ahFamTRSim.dat", header = T, as.is=T)
ahNRFamData=data.frame(ahNRFam)
ahNRmatrix=matrix(c(ahNRFamData[,3], ahNRFamData[,4], ahNRFamData[,5],
ahNRFamData[,6]), nrow=7, ncol=4)
tmatrix = t(ahNRmatrix)
tmatrix
pnts = barplot(tmatrix, width=0.1, beside=FALSE,  col=c('grey27', 'black',
'white', 'khaki'), border=c("black","black", "black", "black"), xlab='NR',
ylab='Percent')
points(pnts, ahNRFamData[,7], col=ahNRFamData[,8], pch=ahNRFamData[,9],
cex=ahNRFamData[,10])
```

```
dev.off()

#KG
postscript(file="/Users/schnoes/Alex/Writing/Thesis/Chapter3/
PercentMisannotationFigure/AH.KG.sim.eps",  height=4, width=3.5,  pointsize=10
onefile=FALSE, horizontal=FALSE)
par(cex.axis=1.25)
par(mar=c(5.1, 6,4.1, 2.1), font.lab=2, font.main=2, font.axis=1, cex.main=2,
cex.lab=1.5)

#KG
ahNRFam=read.table("ahFamKGSim.dat", header = T, as.is=T)
ahNRFamData=data.frame(ahNRFam)
ahNRmatrix=matrix(c(ahNRFamData[,3], ahNRFamData[,4], ahNRFamData[,5],
ahNRFamData[,6]), nrow=7, ncol=4)
tmatrix = t(ahNRmatrix)
tmatrix
pnts = barplot(tmatrix, width=0.1, beside=FALSE,  col=c('grey27', 'black',
'white', 'khaki'), border=c("black","black", "black", "black"), xlab='NR',
ylab='Percent')
points(pnts, ahNRFamData[,7], col=ahNRFamData[,8], pch=ahNRFamData[,9],
cex=ahNRFamData[,10])

dev.off()

#SP
postscript(file="/Users/schnoes/Alex/Writing/Thesis/Chapter3/
PercentMisannotationFigure/AH.SP.sim.eps",  height=4, width=3.5,  pointsize=10
onefile=FALSE, horizontal=FALSE)
par(cex.axis=1.25)
par(mar=c(5.1, 6,4.1, 2.1), font.lab=2, font.main=2, font.axis=1, cex.main=2,
cex.lab=1.5)

#SP
ahNRFam=read.table("ahFamSPSim.dat", header = T, as.is=T)
ahNRFamData=data.frame(ahNRFam)
ahNRmatrix=matrix(c(ahNRFamData[,3], ahNRFamData[,4], ahNRFamData[,5],
ahNRFamData[,6]), nrow=7, ncol=4)
tmatrix = t(ahNRmatrix)
tmatrix
pnts = barplot(tmatrix, width=0.1, beside=FALSE,  col=c('grey27', 'black',
'white', 'khaki'), border=c("black","black", "black", "black"), xlab='NR',
ylab='Percent')
points(pnts, ahNRFamData[,7], col=ahNRFamData[,8], pch=ahNRFamData[,9],
cex=ahNRFamData[,10])
```

```
dev.off()


-------------------------------------------
#timeVmis-noadd-4.r, to make the misannotation/time figure

Sys.setenv(R_GSCMD="/sw/bin/gs")
incYears=read.table("incorrect.year.list")
corYears=read.table("correct.year.list")
equivYears=read.table("equiv.year.list")
genYears=read.table("general.year.list")

bin=seq(1992.5, 2006.5, by=1)
histInc = hist(incYears$V1, breaks = bin)
histCor = hist(corYears$V1, breaks = bin)
histEqv = hist(equivYears$V1, breaks = bin)
histGen = hist(genYears$V1, breaks = bin)
temp1 = histCor$counts

temp2 = histInc$counts
temp3 = histEqv$counts

temp4 = histGen$counts


matrixCounts= matrix(data= c(temp3, temp2, temp1, temp4), ncol=4)
matrixCountsTrans= t(matrixCounts)
#bitmap(file="/Users/schnoes/Alex/Misannotation/AnnotationWork/
MisannotationPaper/FiguresTables/Time:Misannotation/timeVMis.tiff", height=5.2
width=8.9, res=600, pointsize=14)
postscript(file="/Users/schnoes/Alex/Writing/Thesis/Chapter3/MisOverTime/
timeVMis-4.eps", height=5, width=7,  pointsize=12, onefile=FALSE,
horizontal=FALSE)
par(cex.axis=1)
par(mar=c(5.1, 6,4.1, 4), font.lab=2, font.main=2, font.axis=1, cex.lab=1.15)

barplot(matrixCountsTrans[,1:13], beside=FALSE, names.arg=histInc$mids[1:13]
ylim=c(0, 2500), col=c("grey27", "black", "white", "khaki"), , main="All
Superfamily Sequences Deposited by Year\n (NR DB)", xlab="Year", ylab="Numb
Sequences")

legend(x=1, y=2000, legend=c( "Equiv. Annotations","Incorrect Annotations",
"Correct Annotations", "General Annotations"), col=c("black", "black", "black",
"black"), pch=22, pt.bg=c("grey27", "black", "white", "khaki"),
pt.cex=c(1.75,1.75, 1.75,1.75))
```

```
dev.off()
-----------------------------------------
#FracIncorFigure.r, to make the misannotation/time figure

Sys.setenv(R_GSCMD="/sw/bin/gs")
incYears=read.table("incorrect.year.list")
allYears=read.table("all.year.list")

bin=seq(1992.5, 2006.5, by=1)
histAll=hist(allYears$V1, breaks=bin)
histInc = hist(incYears$V1, breaks = bin)

fractionIncorrect=histInc$counts/histAll$counts
postscript(file="/Users/schnoes/Alex/Writing/Thesis/Chapter3/MisOverTime/
fractIncorrect.eps", height=5, width=7,  pointsize=12, onefile=FALSE,
horizontal=FALSE)
par(cex.axis=1)
par(mar=c(5.1, 6,4.1, 4), font.lab=2, font.main=2, font.axis=1, cex.lab=1.15)

plot(histAll$mids[1:13], fractionIncorrect[1:13], type='b', xlab="Year",
ylab="Fraction of Total Sequences", main='Fraction of Misannotated Sequences
Deposited per Year\n (NR DB)', axes=FALSE, frame.plot=T, ylim=c(0, 0.5))

axis(2, at=seq(0.1:0.6, by=0.1), labels=seq(0.1:0.6, by=0.1))
axis(1, at=c(1993:2005),  labels=c(1993:2005))
dev.off()
```

Appendix K. Data, Keyword-Based Misannotation Analysis (Chapter 2)

K.1. Table K-1. GenBank NR Data (Chapter 2)

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
1311141	>gi|1311141|pdb|1PDZ| Mol_id: 1; Molecule: Enolase; Chain: Null; Synonym: 2-Phospho-D-Glycerate Dehydratase; Ec: 4.2.1.11; Heterogen: Phosphoglycolate; Heterogen: Mn 2+			x
231253	>gi|231253|pdb|7ENL| Enolase (E.C.4.2.1.11) (2-Phospho-D-Glycerate Hydrolase) Complex With 2-Phospho-D-Glyceric Acid And Magnesium			x
2914550	>gi|2914550|pdb|2ONE|B Chain B, Asymmetric Yeast Enolase Dimer Complexed With Resolved 2'-Phosphoglycerate And Phosphoenolpyruvate			x
16975440	>gi|16975440|pdb|1E9I|D Chain D, Enolase From E.Coli			x
39654416	>gi|39654416|pdb|1P43|B Chain B, Reverse Protonation Is The Key To General Acid-Base Catalysis In Enolase			x
55669907	>gi|55669907|pdb|1TE6|B Chain B, Crystal Structure Of Human Neuron Specific Enolase At 1.8 Angstrom			x
30749888	>gi|30749888|pdb|1OEP|A Chain A, Structure Of Trypanosoma Brucei Enolase Reveals The Inhibitory Divalent Metal Site			x
74313351	>gi|74313351|ref|YP_311770.1| phosphopyruvate hydratase [Shigella sonnei Ss046]			x
75765318	>gi|75765318|pdb|1W6T|B Chain B, Crystal Structure Of Octameric Enolase From Streptococcus Pneumoniae			x
12517248	>gi|12517248|gb|AAG57892.1| enolase [Escherichia coli O157:H7 EDL933]			x
119336	>gi|119336|sp|P00924|ENO1_YEAST Enolase 1 (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x
1169529	>gi|1169529|sp|P42897|ENO_ALLMI Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
13124708	>gi|13124708|sp|O29133|ENO_ARCFU Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
6015094	>gi|6015094|sp|P42040|ENO_CLAHE Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Allergen Cla h 6) (Cla h VI)			x
13124709	>gi|13124709|sp|O32513|ENO_DESVM Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
57015278	>gi|57015278|sp|Q5XD01|ENO_STRP6 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
6226608	>gi|6226608|sp|P42848|ENO_THEMA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
59802545	>gi|59802545|sp|P33675|ENO_ZYMMO Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
780372	>gi|780372|gb|AAC49173.1| enolase			x
3089611	>gi|3089611|gb|AAC70360.1| enolase [Zymomonas mobilis]			x
3023703	>gi|3023703|sp|P56252|ENO_HOMGA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
13124712	>gi|13124712|sp|Q60173|ENO_METJA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
59797564	>gi|59797564|sp|Q6M075|ENO_METMP Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
21263608	>gi|21263608|sp|Q9CD42|ENO_MYCLE Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
50400247	>gi|50400247|sp|Q9UAL5|ENO_PLAFG Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
50400235	>gi|50400235|sp|Q7RA60|ENO_PLAYO Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
13124159	>gi|13124159|sp|Q9UXZ0|ENO_PYRAB Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
3023710	>gi|3023710|sp|Q27877|ENO_SCHMA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
30315823	>gi|30315823|sp|Q8EBR0|ENO_SHEON Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
13124161	>gi|13124161|sp|Q9XDS7|ENO_STRIT Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
59797608	>gi|59797608|sp|Q7MHQ1|ENO_VIBVY Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
13124145	>gi|13124145|sp|Q9PDT8|ENO_XYLFA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
29835068	>gi|29835068|gb|AAP05702.1| enolase [Chlamydophila caviae GPIC]			x
2921237	>gi|2921237|gb|AAC64907.1| enolase [Streptococcus thermophilus]			x
82737565	>gi|82737565|ref|ZP_00900413.1| Enolase [Pseudomonas putida F1]			x
59712682	>gi|59712682|ref|YP_205458.1| phosphopyruvate hydratase [Vibrio fischeri ES114]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
82746640	>gi|82746640|ref|ZP_00909145.1| Enolase [Clostridium beijerincki NCIMB 8052]			x
83371294	>gi|83371294|ref|ZP_00916109.1| Enolase [Rhodobacter sphaeroides ATCC 17025]			x
58003118	>gi|58003118|gb|AAW62012.1| Enolase [Gluconobacter oxydans 621H]			x
78707886	>gi|78707886|gb|ABB46861.1| enolase [Oryza sativa (japonica cultivar-group)]			x
78707887	>gi|78707887|gb|ABB46862.1| enolase [Oryza sativa (japonica cultivar-group)]			x
1590967	>gi|1590967|gb|AAB98220.1| enolase (eno) [Methanocaldococcus jannaschii DSM 2661]			x
42410100	>gi|42410100|gb|AAS14211.1| enolase [Wolbachia endosymbiont of Drosophila melanogaster]			x
499267	>gi|499267|gb|AAA57450.1| enolase [Fasciola hepatica]			x
2983135	>gi|2983135|gb|AAC06738.1| enolase [Aquifex aeolicus VF5]			x
83748260	>gi|83748260|ref|ZP_00945286.1| Enolase [Ralstonia solanacearum UW551]			x
83751193	>gi|83751193|ref|ZP_00947607.1| COG0148: Enolase [Bartonella bacilliformis KC583]			x
3323125	>gi|3323125|gb|AAC65781.1| enolase (eno) [Treponema pallidum subsp. pallidum str. Nichols]			x
4981411	>gi|4981411|gb|AAD35958.1| enolase [Thermotoga maritima MSB8]			x
33237212	>gi|33237212|gb|AAP99281.1| Enolase [Prochlorococcus marinus subsp. marinus str. CCMP1375]			x
6460466	>gi|6460466|gb|AAF12173.1| enolase [Deinococcus radiodurans R1]			x
32262179	>gi|32262179|gb|AAP77228.1| enolase [Helicobacter hepaticus ATCC 51449]			x
33147912	>gi|33147912|gb|AAP95433.1| enolase [Haemophilus ducreyi 35000HP]			x
83856594	>gi|83856594|ref|ZP_00950123.1| enolase [Croceibacter atlanticus HTCC2559]			x
83942542	>gi|83942542|ref|ZP_00955003.1| enolase [Sulfitobacter sp. EE-36]			x
83952177	>gi|83952177|ref|ZP_00960909.1| enolase [Roseovarius nubinhibens ISM]			x
83953763	>gi|83953763|ref|ZP_00962484.1| enolase [Sulfitobacter sp. NAS-14.1]			x
29898732	>gi|29898732|gb|AAP12004.1| Enolase [Bacillus cereus ATCC 14579]			x
27904258	>gi|27904258|gb|AAO27091.1| enolase [Buchnera aphidicola str. Bp (Baizongia pistaciae)]			x
84319615	>gi|84319615|ref|ZP_00968009.1| COG0148: Enolase [Pseudomonas aeruginosa C3719]			x
27361094	>gi|27361094|gb|AAO10003.1| Enolase [Vibrio vulnificus CMCP6]			x
2621078	>gi|2621078|gb|AAB84550.1| enolase [Methanothermobacter thermautotrophicus str. Delta H]			x
84501065	>gi|84501065|ref|ZP_00999300.1| Enolase [Oceanicola batsensis HTCC2597]			x
84515610	>gi|84515610|ref|ZP_01002972.1| enolase [Loktanella vestfoldensis SKA53]			x
84518726	>gi|84518726|ref|ZP_01006075.1| Enolase [Prochlorococcus marinus str. MIT 9211]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
82752500	>gi|82752500|ref|XP_727327.1| enolase [Plasmodium yoelii yoelii str. 17XNL]			x
84489662	>gi|84489662|ref|YP_447894.1| enolase [Methanosphaera stadtmanae DSM 3091]			x
54020356	>gi|54020356|ref|YP_115643.1| phosphopyruvate hydratase [Mycoplasma hyopneumoniae 232]			x
28202574	>gi|28202574|gb|AAO35019.1| enolase [Clostridium tetani E88]			x
15835490	>gi|15835490|ref|NP_297249.1| phosphopyruvate hydratase [Chlamydia muridarum Nigg]			x
58254511	>gi|58254511|gb|AAV42748.1| 2-phosphoglycerate dehydratase [Lactobacillus acidophilus NCFM]			x
5305421	>gi|5305421|gb|AAD41643.1| alpha enolase [Alligator mississippiensis]			x
5305423	>gi|5305423|gb|AAD41644.1| alpha enolase [Sceloporus undulatus]			x
5305427	>gi|5305427|gb|AAD41646.1| alpha enolase [Python regius]			x
84684859	>gi|84684859|ref|ZP_01012759.1| enolase [Rhodobacterales bacterium HTCC2654]			x
84714102	>gi|84714102|ref|ZP_01021631.1| Enolase [Polaromonas naphthalenivorans CJ2]			x
10580680	>gi|10580680|gb|AAG19526.1| phosphopyruvate hydratase; Eno [Halobacterium sp. NRC-1]			x
46578738	>gi|46578738|ref|YP_009546.1| enolase [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]			x
15644783	>gi|15644783|ref|NP_206953.1| phosphopyruvate hydratase [Helicobacter pylori 26695]			x
26988344	>gi|26988344|ref|NP_743769.1| phosphopyruvate hydratase [Pseudomonas putida KT2440]			x
28198453	>gi|28198453|ref|NP_778767.1| phosphopyruvate hydratase [Xylella fastidiosa Temecula1]			x
23465590	>gi|23465590|ref|NP_696193.1| enolase [Bifidobacterium longum NCC2705]			x
24374950	>gi|24374950|ref|NP_718993.1| enolase [Shewanella oneidensis MR-1]			x
42784284	>gi|42784284|ref|NP_981531.1| enolase [Bacillus cereus ATCC 10987]			x
28868760	>gi|28868760|ref|NP_791379.1| phosphopyruvate hydratase [Pseudomonas syringae pv. tomato str. DC3000]			x
28871748	>gi|28871748|ref|NP_794367.1| enolase [Pseudomonas syringae pv. tomato str. DC3000]			x
11498732	>gi|11498732|ref|NP_069961.1| phosphopyruvate hydratase [Archaeoglobus fulgidus DSM 4304]			x
29349980	>gi|29349980|ref|NP_813483.1| phosphopyruvate hydratase [Bacteroides thetaiotaomicron VPI-5482]			x
59801045	>gi|59801045|ref|YP_207757.1| phosphopyruvate hydratase [Neisseria gonorrhoeae FA 1090]			x
34541443	>gi|34541443|ref|NP_905922.1| phosphopyruvate hydratase [Porphyromonas gingivalis W83]			x
12045269	>gi|12045269|ref|NP_073080.1| phosphopyruvate hydratase [Mycoplasma genitalium G37]			x

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>42526461</td><td>>gi|42526461|ref|NP_971559.1| enolase [Treponema denticola ATCC 35405]</td><td></td><td></td><td>x</td></tr>
<tr><td>41407088</td><td>>gi|41407088|ref|NP_959924.1| phosphopyruvate hydratase [Mycobacterium avium subsp. paratuberculosis K-10]</td><td></td><td></td><td>x</td></tr>
<tr><td>83721440</td><td>>gi|83721440|ref|YP_442424.1| enolase [Burkholderia thailandensis E264]</td><td></td><td></td><td>x</td></tr>
<tr><td>55377005</td><td>>gi|55377005|ref|YP_134855.1| phosphopyruvate hydratase [Haloarcula marismortui ATCC 43049]</td><td></td><td></td><td>x</td></tr>
<tr><td>13508345</td><td>>gi|13508345|ref|NP_110295.1| phosphopyruvate hydratase [Mycoplasma pneumoniae M129]</td><td></td><td></td><td>x</td></tr>
<tr><td>563868</td><td>>gi|563868|emb|CAA57795.1| enolase; phosphopyruvate hydratase [Escherichia coli]</td><td></td><td></td><td>x</td></tr>
<tr><td>58582586</td><td>>gi|58582586|ref|YP_201602.1| phosphopyruvate hydratase [Xanthomonas oryzae pv. oryzae KACC10331]</td><td></td><td></td><td>x</td></tr>
<tr><td>37359341</td><td>>gi|37359341|gb|AAP24058.1| enolase 1 [Toxoplasma gondii]</td><td></td><td></td><td>x</td></tr>
<tr><td>82702357</td><td>>gi|82702357|ref|YP_411923.1| enolase [Nitrosospira multiformis ATCC 25196]</td><td></td><td></td><td>x</td></tr>
<tr><td>83319528</td><td>>gi|83319528|ref|YP_424200.1| enolase [Mycoplasma capricolum subsp. capricolum ATCC 27343]</td><td></td><td></td><td>x</td></tr>
<tr><td>28476792</td><td>>gi|28476792|gb|AAO44880.1| enolase [Tropheryma whipplei str. Twist]</td><td></td><td></td><td>x</td></tr>
<tr><td>83644694</td><td>>gi|83644694|ref|YP_433129.1| enolase [Hahella chejuensis KCTC 2396]</td><td></td><td></td><td>x</td></tr>
<tr><td>85057717</td><td>>gi|85057717|ref|YP_456633.1| enolase [Aster yellows witches'-broom phytoplasma AYWB]</td><td></td><td></td><td>x</td></tr>
<tr><td>4154655</td><td>>gi|4154655|gb|AAD05723.1| ENOLASE [Helicobacter pylori J99]</td><td></td><td></td><td>x</td></tr>
<tr><td>15023593</td><td>>gi|15023593|gb|AAK78690.1| Enolase [Clostridium acetobutylicum ATCC 824]</td><td></td><td></td><td>x</td></tr>
<tr><td>22852211</td><td>>gi|22852211|dbj|BAC16223.1| enolase [Enterococcus hirae]</td><td></td><td></td><td>x</td></tr>
<tr><td>71796051</td><td>>gi|71796051|gb|AAZ40802.1| enolase [Candidatus Blochmannia pennsylvanicus str. BPEN]</td><td></td><td></td><td>x</td></tr>
<tr><td>85089455</td><td>>gi|85089455|ref|XP_957959.1| ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) [Neurospora crassa N150]</td><td></td><td></td><td>x</td></tr>
<tr><td>34392443</td><td>>gi|34392443|dbj|BAC82549.1| enolase [Penicillium chrysogenum]</td><td></td><td></td><td>x</td></tr>
<tr><td>62424027</td><td>>gi|62424027|ref|ZP_00379179.1| COG0148: Enolase [Brevibacterium linens BL2]</td><td></td><td></td><td>x</td></tr>
<tr><td>47567341</td><td>>gi|47567341|ref|ZP_00238054.1| enolase [Bacillus cereus G9241]</td><td></td><td></td><td>x</td></tr>
<tr><td>62463961</td><td>>gi|62463961|ref|ZP_00383267.1| COG0148: Enolase [Lactococcus lactis subsp. cremoris SK11]</td><td></td><td></td><td>x</td></tr>
<tr><td>62513221</td><td>>gi|62513221|ref|ZP_00384782.1| COG0148: Enolase [Lactobacillus casei ATCC 334]</td><td></td><td></td><td>x</td></tr>
<tr><td>62515717</td><td>>gi|62515717|ref|ZP_00387107.1| COG0148: Enolase [Lactobacillus delbrueckii subsp. bulgaricus ATCC BAA-365]</td><td></td><td></td><td>x</td></tr>
<tr><td>39721879</td><td>>gi|39721879|dbj|BAD04369.1| enolase [Onion yellows phytoplasma OY-M]</td><td></td><td></td><td>x</td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
62528387	>gi|62528387|ref|ZP_00389641.1| COG0148: Enolase [Streptococcus thermophilus LMD-9]			x
48869740	>gi|48869740|ref|ZP_00322483.1| COG0148: Enolase [Pediococcus pentosaceus ATCC 25745]			x
23003759	>gi|23003759|ref|ZP_00047409.1| COG0148: Enolase [Lactobacillus gasseri]			x
23002885	>gi|23002885|ref|ZP_00046557.1| COG0148: Enolase [Lactobacillus gasseri]			x
23015298	>gi|23015298|ref|ZP_00055078.1| COG0148: Enolase [Magnetospirillum magnetotacticum MS-1]			x
54018341	>gi|54018341|dbj|BAD59711.1| putative enolase [Nocardia farcinica IFM 10152]			x
23128142	>gi|23128142|ref|ZP_00109996.1| COG0148: Enolase [Nostoc punctiforme PCC 73102]			x
46191081	>gi|46191081|ref|ZP_00120494.2| COG0148: Enolase [Bifidobacterium longum DJO10A]			x
46164345	>gi|46164345|ref|ZP_00137024.2| COG0148: Enolase [Pseudomonas aeruginosa UCBPP-PA14]			x
32029561	>gi|32029561|ref|ZP_00132564.1| COG0148: Enolase [Haemophilus somnus 2336]			x
32035526	>gi|32035526|ref|ZP_00135469.1| COG0148: Enolase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]			x
46129115	>gi|46129115|ref|ZP_00202000.1| COG0148: Enolase [Haemophilus influenzae R2846]			x
46133204	>gi|46133204|ref|ZP_00156796.2| COG0148: Enolase [Haemophilus influenzae R2866]			x
47574355	>gi|47574355|ref|ZP_00244391.1| COG0148: Enolase [Rubrivivax gelatinosus PM1]			x
21228938	>gi|21228938|ref|NP_634860.1| Enolase [Methanosarcina mazei Go1]			x
27806645	>gi|27806645|ref|NP_776474.1| enolase 1 [Bos taurus]			x
17982798	>gi|17982798|gb|AAL52032.1| ENOLASE [Brucella melitensis 16M]			x
14021357	>gi|14021357|dbj|BAB47970.1| enolase [Mesorhizobium loti MAFF303099]			x
17132671	>gi|17132671|dbj|BAB75237.1| enolase [Nostoc sp. PCC 7120]			x
26453833	>gi|26453833|dbj|BAC44164.1| enolase [Mycoplasma penetrans HF-2]			x
23492880	>gi|23492880|dbj|BAC17852.1| putative enolase [Corynebacterium efficiens YS-314]			x
22294379	>gi|22294379|dbj|BAC08209.1| enolase [Thermosynechococcus elongatus BP-1]			x
27353058	>gi|27353058|dbj|BAC50059.1| enolase [Bradyrhizobium japonicum USDA 110]			x
35212688	>gi|35212688|dbj|BAC90062.1| enolase [Gloeobacter violaceus PCC 7421]			x
18144961	>gi|18144961|dbj|BAB81005.1| enolase [Clostridium perfringens str. 13]			x
55771384	>gi|55771384|dbj|BAD69825.1| enolase (2-phosphoglycerate dehydratase) [Thermus thermophilus HB8]			x
53757045	>gi|53757045|gb|AAU91336.1| enolase [Methylococcus capsulatus str. Bath]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
53757787	>gi|53757787|gb|AAU92078.1| enolase [Methylococcus capsulatus str. Bath]			x
8979174	>gi|8979174|dbj|BAA99008.1| enolase [Chlamydophila pneumoniae J138]			x
56381431	>gi|56381431|dbj|BAD77339.1| enolase (2-phosphoglycerate dehydratase) [Geobacillus kaustophilus HTA426]			x
10176180	>gi|10176180|dbj|BAB07275.1| enolase (2-phosphoglycerate dehydratase) [Bacillus halodurans C-125]			x
22778120	>gi|22778120|dbj|BAC14390.1| enolase (2-phosphoglycerate dehydratase) [Oceanobacillus iheyensis HTE831]			x
10039081	>gi|10039081|dbj|BAB13115.1| enolase [Buchnera aphidicola str. APS (Acyrthosiphon pisum)]			x
14325249	>gi|14325249|dbj|BAB60153.1| enolase [Thermoplasma volcanium GSS1]			x
5106162	>gi|5106162|dbj|BAA81473.1| 432aa long hypothetical enolase [Aeropyrum pernix K1]			x
3258386	>gi|3258386|dbj|BAA31069.1| 428aa long hypothetical phosphoglycerate dehydratase [Pyrococcus horikoshii OT3]			x
1653839	>gi|1653839|dbj|BAA18749.1| enolase [Synechocystis sp. PCC 6803]			x
24377625	>gi|24377625|gb|AAN58930.1| putative enolase [Streptococcus mutans UA159]			x
46908628	>gi|46908628|ref|YP_015017.1| enolase [Listeria monocytogenes str. 4b F2365]			x
13242907	>gi|13242907|gb|AAG42022.2| enolase [Alternaria alternata]			x
21646048	>gi|21646048|gb|AAM71393.1| enolase [Chlorobium tepidum TLS]			x
21647988	>gi|21647988|gb|AAM73181.1| enolase [Chlorobium tepidum TLS]			x
71062748	>gi|71062748|gb|AAZ21751.1| Enolase [Candidatus Pelagibacter ubique HTCC1062]			x
4377111	>gi|4377111|gb|AAD18938.1| Enolase [Chlamydophila pneumoniae CWL029]			x
13569595	>gi|13569595|gb|AAK31161.1| enolase [Mastigamoeba balamuthi]			x
13774515	>gi|13774515|gb|AAK38886.1| enolase [Eimeria tenella]			x
13925873	>gi|13925873|gb|AAK49451.1| enolase [Aspergillus fumigatus]			x
13991101	>gi|13991101|gb|AAK51201.1| enolase [Penicillium citrinum]			x
16878083	>gi|16878083|gb|AAH17249.1| Enolase 3 [Homo sapiens]			x
57240685	>gi|57240685|ref|ZP_00368633.1| enolase [Campylobacter lari RM2100]			x
57504666	>gi|57504666|ref|ZP_00370744.1| enolase [Campylobacter coli RM2228]			x
57505300	>gi|57505300|ref|ZP_00371229.1| enolase [Campylobacter upsaliensis RM3195]			x
58698888	>gi|58698888|ref|ZP_00373755.1| enolase [Wolbachia endosymbiont of Drosophila ananassae]			x
2688240	>gi|2688240|gb|AAC66719.1| enolase (eno) [Borrelia burgdorferi B31]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
69928271	>gi|69928271|ref|ZP_00625432.1| Enolase [Nitrobacter hamburgensis X14]			x
21623311	>gi|21623311|gb|AAM67951.1| enolase [Buchnera aphidicola str. Sg (Schizaphis graminum)]			x
69933446	>gi|69933446|ref|ZP_00628648.1| Enolase [Paracoccus denitrificans PD1222]			x
69953339	>gi|69953339|ref|ZP_00640506.1| Enolase [Shewanella frigidimarina NCIMB 400]			x
30314940	>gi|30314940|gb|AAP30720.1| enolase [Rhodotorula mucilaginosa]			x
85858513	>gi|85858513|ref|YP_460715.1| enolase [Syntrophus aciditrophicus SB]			x
14585753	>gi|14585753|gb|AAK67491.1| enolase [Curvularia lunata]			x
19713005	>gi|19713005|gb|AAL93877.1| Enolase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]			x
1087071	>gi|1087071|gb|AAB34986.1| 2-phospho-D-glycerate hydrolase; enolase [Mesembryanthemum crystallinum]			x
12619316	>gi|12619316|gb|AAG60329.1| enolase [Toxoplasma gondii]			x
56178891	>gi|56178891|gb|AAV81613.1| Enolase [Idiomarina loihiensis L2TR]			x
18159635	>gi|18159635|gb|AAL63046.1| enolase [Pyrobaculum aerophilum str. IM2]			x
56911024	>gi|56911024|dbj|BAD65551.1| enolase [Bacillus clausii KSM-K16]			x
29607186	>gi|29607186|dbj|BAC71245.1| putative enolase [Streptomyces avermitilis MA-4680]			x
28807571	>gi|28807571|dbj|BAC60824.1| enolase [Vibrio parahaemolyticus RIMD 2210633]			x
18892150	>gi|18892150|gb|AAL80339.1| enolase (2-phosphoglycerate dehydratase) [Pyrococcus furiosus DSM 3638]			x
57160365	>gi|57160365|dbj|BAD86295.1| enolase [Thermococcus kodakarensis KOD1]			x
71000211	>gi|71000211|dbj|BAE07163.1| enolase 2 [Karenia brevis]			x
71000213	>gi|71000213|dbj|BAE07164.1| enolase 2 [Karenia brevis]			x
71000219	>gi|71000219|dbj|BAE07165.1| enolase 3 [Karenia brevis]			x
71000227	>gi|71000227|dbj|BAE07167.1| enolase 3 [Karenia brevis]			x
71000239	>gi|71000239|dbj|BAE07170.1| enolase 2 [Karenia mikimotoi]			x
71000241	>gi|71000241|dbj|BAE07171.1| enolase 3 [Karenia mikimotoi]			x
71000247	>gi|71000247|dbj|BAE07173.1| enolase 3 [Karenia mikimotoi]			x
24195632	>gi|24195632|gb|AAN49150.1| Enolase [Leptospira interrogans serovar Lai str. 56601]			x
19915551	>gi|19915551|gb|AAM05080.1| phosphopyruvate hydratase [Methanosarcina acetivorans C2A]			x
21107915	>gi|21107915|gb|AAM36586.1| enolase [Xanthomonas axonopodis pv. citri str. 306]			x
85703404	>gi|85703404|ref|ZP_01034508.1| enolase [Roseovarius sp. 217]			x

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>85708563</td><td>>gi|85708563|ref|ZP_01039629.1| enolase [Erythrobacter sp. NAP1]</td><td></td><td></td><td>x</td></tr>
<tr><td>85712138</td><td>>gi|85712138|ref|ZP_01043191.1| Enolase [Idiomarina baltica OS145]</td><td></td><td></td><td>x</td></tr>
<tr><td>85716527</td><td>>gi|85716527|ref|ZP_01047498.1| enolase [Nitrobacter sp. Nb-311A]</td><td></td><td></td><td>x</td></tr>
<tr><td>14141143</td><td>>gi|14141143|gb|AAF71925.2| beta beta enolase [Oryctolagus cuniculus]</td><td></td><td></td><td>x</td></tr>
<tr><td>13423140</td><td>>gi|13423140|gb|AAK23700.1| enolase [Caulobacter crescentus CB15]</td><td></td><td></td><td>x</td></tr>
<tr><td>86132574</td><td>>gi|86132574|ref|ZP_01051167.1| enolase [Cellulophaga sp. MED134]</td><td></td><td></td><td>x</td></tr>
<tr><td>86135551</td><td>>gi|86135551|ref|ZP_01054132.1| enolase [Tenacibaculum sp. MED152]</td><td></td><td></td><td>x</td></tr>
<tr><td>86138676</td><td>>gi|86138676|ref|ZP_01057249.1| enolase [Roseobacter sp. MED193]</td><td></td><td></td><td>x</td></tr>
<tr><td>86141170</td><td>>gi|86141170|ref|ZP_01059716.1| enolase [Flavobacterium sp. MED217]</td><td></td><td></td><td>x</td></tr>
<tr><td>86152289</td><td>>gi|86152289|ref|ZP_01070500.1| enolase [Campylobacter jejuni subsp. jejuni 260.94]</td><td></td><td></td><td>x</td></tr>
<tr><td>86169224</td><td>>gi|86169224|gb|EAQ70480.1| Enolase [Synechococcus sp. RS9917]</td><td></td><td></td><td>x</td></tr>
<tr><td>42518800</td><td>>gi|42518800|ref|NP_964730.1| enolase [Lactobacillus johnsonii NCC 533]</td><td></td><td></td><td>x</td></tr>
<tr><td>42519171</td><td>>gi|42519171|ref|NP_965101.1| phosphopyruvate hydratase [Lactobacillus johnsonii NCC 533]</td><td></td><td></td><td>x</td></tr>
<tr><td>42519286</td><td>>gi|42519286|ref|NP_965216.1| phosphopyruvate hydratase [Lactobacillus johnsonii NCC 533]</td><td></td><td></td><td>x</td></tr>
<tr><td>86357552</td><td>>gi|86357552|ref|YP_469444.1| 2-phosphoglycerate dehydratase (enolase) protein [Rhizobium etli CFN 42]</td><td></td><td></td><td>x</td></tr>
<tr><td>68567781</td><td>>gi|68567781|gb|AAY80710.1| enolase [Sulfolobus acidocaldarius DSM 639]</td><td></td><td></td><td>x</td></tr>
<tr><td>45382393</td><td>>gi|45382393|ref|NP_990207.1| enolase 2 (gamma, neuronal) [Gallus gallus]</td><td></td><td></td><td>x</td></tr>
<tr><td>74316639</td><td>>gi|74316639|ref|YP_314379.1| phosphopyruvate hydratase [Thiobacillus denitrificans ATCC 25259]</td><td></td><td></td><td>x</td></tr>
<tr><td>30583767</td><td>>gi|30583767|gb|AAP36132.1| Homo sapiens enolase 1, (alpha) [synthetic construct]</td><td></td><td></td><td>x</td></tr>
<tr><td>68342877</td><td>>gi|68342877|gb|AAY90483.1| enolase [Pseudomonas fluorescens Pf-5]</td><td></td><td></td><td>x</td></tr>
<tr><td>70885013</td><td>>gi|70885013|gb|EAN97849.1| enolase, putative [Trypanosoma cruzi]</td><td></td><td></td><td>x</td></tr>
<tr><td>71364941</td><td>>gi|71364941|ref|ZP_00655507.1| Enolase [Psychrobacter cryohalolentis K5]</td><td></td><td></td><td>x</td></tr>
<tr><td>71368692</td><td>>gi|71368692|ref|ZP_00659180.1| Enolase [Nocardioides sp. JS614]</td><td></td><td></td><td>x</td></tr>
<tr><td>71481429</td><td>>gi|71481429|ref|ZP_00661136.1| Enolase [Prosthecochloris vibrioformis DSM 265]</td><td></td><td></td><td>x</td></tr>
<tr><td>71546423</td><td>>gi|71546423|ref|ZP_00667224.1| Enolase [Syntrophobacter fumaroxidans MPOB]</td><td></td><td></td><td>x</td></tr>
<tr><td>71548704</td><td>>gi|71548704|ref|ZP_00668928.1| Enolase [Nitrosomonas eutropha C71]</td><td></td><td></td><td>x</td></tr>
<tr><td>71064151</td><td>>gi|71064151|gb|AAZ22544.1| alpha-enolase [Bifidobacterium animalis subsp. lactis]</td><td></td><td></td><td>x</td></tr>
<tr><td>71839487</td><td>>gi|71839487|ref|ZP_00679235.1| Enolase [Pelobacter propionicus DSM 2379]</td><td></td><td></td><td>x</td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
29542233	>gi|29542233|gb|AAO91170.1| enolase [Coxiella burnetii RSA 493]			x
71145813	>gi|71145813|gb|AAZ26286.1| enolase [Colwellia psychrerythraea 34H]			x
72003261	>gi|72003261|gb|AAZ59063.1| enolase [Prochlorococcus marinus str. NATL2A]			x
72495736	>gi|72495736|dbj|BAE19057.1| enolase [Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305]			x
25989631	>gi|25989631|gb|AAN28926.1| enolase [Aeromonas hydrophila]			x
33236671	>gi|33236671|gb|AAP98758.1| enolase [Chlamydophila pneumoniae TW-183]			x
32880095	>gi|32880095|gb|AAP88878.1| enolase 2, (gamma, neuronal) [synthetic construct]			x
71850822	>gi|71850822|gb|AAZ43431.1| enolase [Mycoplasma synoviae 53]			x
51973903	>gi|51973903|gb|AAU15453.1| enolase [Bacillus cereus E33L]			x
37199752	>gi|37199752|dbj|BAC95582.1| enolase [Vibrio vulnificus YJ016]			x
15622261	>gi|15622261|dbj|BAB66253.1| 416aa long hypothetical enolase [Sulfolobus tokodaii str. 7]			x
68447834	>gi|68447834|dbj|BAE05418.1| enolase [Staphylococcus haemolyticus JCSC1435]			x
51855076	>gi|51855076|dbj|BAD39234.1| enolase [Symbiobacterium thermophilum IAM 14863]			x
82945763	>gi|82945763|dbj|BAE50627.1| Enolase [Magnetospirillum magneticum AMB-1]			x
84368411	>gi|84368411|dbj|BAE69569.1| enolase [Xanthomonas oryzae pv. oryzae MAFF 311018]			x
84779011	>gi|84779011|dbj|BAE73788.1| enolase [Sodalis glossinidius str. 'morsitans']			x
37147852	>gi|37147852|gb|AAQ88397.1| enolase [Tuber borchii]			x
40806812	>gi|40806812|gb|AAR92205.1| enolase [Cryphonectria parasitica]			x
9581744	>gi|9581744|emb|CAC00532.1| enolase, isoform 1 [Hevea brasiliensis]			x
9581746	>gi|9581746|emb|CAC00533.1| enolase, isoform 2 [Hevea brasiliensis]			x
5459136	>gi|5459136|emb|CAB50622.1| eno enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (EC 4.2.1.11) [Pyrococcus abyssi GE5]			x
8670811	>gi|8670811|emb|CAB94910.1| enolase [Enterococcus faecalis]			x
74420888	>gi|74420888|gb|ABA05087.1| enolase [Nitrobacter winogradskyi Nb-255]			x
71557144	>gi|71557144|gb|AAZ36355.1| enolase [Pseudomonas syringae pv. phaseolicola 1448A]			x
56604320	>gi|56604320|emb|CAG45342.1| Enolase (2-phosphoglycerate dehydratase) [Francisella tularensis subsp. tularensis SCHU S4]			x
6969088	>gi|6969088|emb|CAB73659.1| enolase [Campylobacter jejuni subsp. jejuni NCTC 11168]			x
71851725	>gi|71851725|gb|AAZ44333.1| enolase [Mycoplasma hyopneumoniae J]			x
71913713	>gi|71913713|gb|AAZ53624.1| enolase [Mycoplasma hyopneumoniae 7448]			x
7380143	>gi|7380143|emb|CAB84728.1| enolase [Neisseria meningitidis Z2491]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
13092594	>gi|13092594|emb|CAC29763.1| putative enolase [Mycobacterium leprae]			x
17428142	>gi|17428142|emb|CAD14831.1| PROBABLE ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) PROTEIN [Ralstonia solanacearum]			x
28271404	>gi|28271404|emb|CAD64309.1| phosphopyruvate hydratase [Lactobacillus plantarum WCFS1]			x
10241779	>gi|10241779|emb|CAC09537.1| enolase [Streptomyces coelicolor A3(2)]			x
11323224	>gi|11323224|emb|CAC16971.1| enolase [Streptomyces coelicolor A3(2)]			x
31617802	>gi|31617802|emb|CAD93911.1| PROBABLE ENOLASE ENO [Mycobacterium bovis AF2122/97]			x
38199773	>gi|38199773|emb|CAE49433.1| Enolase [Corynebacterium diphtheriae]			x
33517294	>gi|33517294|emb|CAD83678.1| enolase [Candidatus Blochmannia floridanus]			x
28411067	>gi|28411067|emb|CAD67452.1| enolase [Tropheryma whipplei TW08/27]			x
32448033	>gi|32448033|emb|CAD77550.1| enolase (2-phosphoglycerate dehydratase) [Rhodopirellula baltica SH 1]			x
34483549	>gi|34483549|emb|CAE10546.1| PUTATIVE ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) [Wolinella succinogenes]			x
49244091	>gi|49244091|emb|CAG42517.1| putative enolase [Staphylococcus aureus subsp. aureus MSSA476]			x
36784331	>gi|36784331|emb|CAE13208.1| Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) [Photorhabdus luminescens subsp. laumondii TTO1]			x
33577120	>gi|33577120|emb|CAE35677.1| enolase [Bordetella bronchiseptica RB50]			x
49238171	>gi|49238171|emb|CAF27380.1| Enolase [Bartonella henselae str. Houston-1]			x
49239628	>gi|49239628|emb|CAF25987.1| Enolase [Bartonella quintana str. Toulouse]			x
46399418	>gi|46399418|emb|CAF22867.1| probable phosphopyruvate hydratase (enolase) [Parachlamydia sp. UWE25]			x
41325200	>gi|41325200|emb|CAF19681.1| ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE [Corynebacterium glutamicum ATCC 13032]			x
42492297	>gi|42492297|emb|CAE76894.1| phosphopyruvate hydratase [Mycoplasma mycoides subsp. mycoides SC]			x
49613013	>gi|49613013|emb|CAG76464.1| enolase [Erwinia carotovora subsp. atroseptica SCRI1043]			x
44920716	>gi|44920716|emb|CAF29952.1| Enolase [Methanococcus maripaludis S2]			x
46914618	>gi|46914618|emb|CAG21395.1| putative enolase [Photobacterium profundum SS9]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
39574904	>gi|39574904|emb|CAE78745.1| phosphopyruvate hydratase [Bdellovibrio bacteriovorus HD100]			x
50876688	>gi|50876688|emb|CAG36528.1| probable enolase [Desulfotalea psychrophila LSv54]			x
49531112	>gi|49531112|emb|CAG68824.1| enolase [Acinetobacter sp. ADP1]			x
56315000	>gi|56315000|emb|CAI09645.1| Enolase [Azoarcus sp. EbN1]			x
53751750	>gi|53751750|emb|CAH13172.1| enolase [Legionella pneumophila str. Paris]			x
53754768	>gi|53754768|emb|CAH16255.1| enolase [Legionella pneumophila str. Lens]			x
467660	>gi|467660|emb|CAA55070.1| enolase; phosphopyruvate hydratase [Davidiella tassiana]			x
693933	>gi|693933|emb|CAA59331.1| 2-phosphopyruvate-hydratase alpha-enolase; carbonate dehydratase [Homo sapiens]			x
1041245	>gi|1041245|emb|CAA63121.1| enolase [Alnus glutinosa]			x
3367647	>gi|3367647|emb|CAA76735.1| enolase [Cunninghamella elegans]			x
2635903	>gi|2635903|emb|CAB15395.1| enolase [Bacillus subtilis subsp. subtilis str. 168]			x
76167854	>gi|76167854|gb|AAX50862.1| enolase [Chlamydia trachomatis A/HAR-13]			x
76365089	>gi|76365089|gb|AAR00929.2| enolase [Davidiella tassiana]			x
57866440	>gi|57866440|ref|YP_188039.1| enolase [Staphylococcus epidermidis RP62A]			x
17739845	>gi|17739845|gb|AAL42432.1| enolase [Agrobacterium tumefaciens str. C58]			x
12723138	>gi|12723138|gb|AAK04374.1| 2-phosphoglycerate dehydratase (EC 4.2.1.11) [Lactococcus lactis subsp. lactis Il1403]			x
12723548	>gi|12723548|gb|AAK04742.1| enolase (EC 4.2.1.11) [Lactococcus lactis subsp. lactis Il1403]			x
13621912	>gi|13621912|gb|AAK33680.1| putative enolase [Streptococcus pyogenes M1 GAS]			x
13814095	>gi|13814095|gb|AAK41195.1| Enolase [Sulfolobus solfataricus P2]			x
20516770	>gi|20516770|gb|AAM24953.1| Enolase [Thermoanaerobacter tengcongensis MB4]			x
6899148	>gi|6899148|gb|AAF30591.1| enolase [Ureaplasma parvum serovar 3 str. ATCC 700970]			x
9106280	>gi|9106280|gb|AAF84100.1| enolase [Xylella fastidiosa 9a5c]			x
19281	>gi|19281|emb|CAA41115.1| enolase [Lycopersicon esculentum]			x
39984275	>gi|39984275|gb|AAR35662.1| enolase [Geobacter sulfurreducens PCA]			x
50363841	>gi|50363841|gb|AAT75826.1| enolase [Mesoplasma florum L1]			x
74017775	>gi|74017775|ref|ZP_00688398.1| Enolase [Burkholderia ambifaria AMMD]			x
74022142	>gi|74022142|ref|ZP_00692726.1| Enolase [Rhodoferax ferrireducens DSM 15236]			x
50839631	>gi|50839631|gb|AAT82298.1| enolase [Propionibacterium acnes KPA171202]			x
50951779	>gi|50951779|gb|AAT89480.1| enolase [Leifsonia xyli subsp. xyli str. CTCB07]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
75763414	>gi|75763414|ref|ZP_00743143.1| Enolase [Bacillus thuringiensis serovar israelensis ATCC 35646]			x
75828720	>gi|75828720|ref|ZP_00758069.1| COG0148: Enolase [Vibrio cholerae MO10]			x
15074376	>gi|15074376|emb|CAC46022.1| PROBABLE ENOLASE PROTEIN [Sinorhizobium meliloti]			x
71853151	>gi|71853151|gb|AAZ51174.1| enolase [Streptococcus pyogenes MGAS5005]			x
74830117	>gi|74830117|emb|CAI39008.1| enolase, putative [Paramecium tetraurelia]			x
74830161	>gi|74830161|emb|CAI39017.1| enolase, putative [Paramecium tetraurelia]			x
76556213	>gi|76556213|emb|CAD48739.1| enolase 2 [Propionibacterium freudenreichii subsp. shermanii]			x
76556211	>gi|76556211|emb|CAD48738.1| enolase 1 [Propionibacterium freudenreichii subsp. shermanii]			x
47458343	>gi|47458343|gb|AAT27666.1| enolase [Mycoplasma mobile 163K]			x
15458655	>gi|15458655|gb|AAK99840.1| Enolase [Streptococcus pneumoniae R6]			x
76557930	>gi|76557930|emb|CAI49514.1| phosphopyruvate hydratase (EC 4.2.1.11) (enolase) [Natronomonas pharaonis DSM 2160]			x
76874604	>gi|76874604|emb|CAI85825.1| enolase [Pseudoalteromonas haloplanktis TAC125]			x
78035738	>gi|78035738|emb|CAJ23429.1| Enolase [Xanthomonas campestris pv. vesicatoria str. 85-10]			x
73660149	>gi|73660149|emb|CAI82756.1| enolase [Dehalococcoides sp. CBDB1]			x
77176833	>gi|77176833|gb|ABA64522.1| enolase [Leishmania mexicana]			x
52629365	>gi|52629365|gb|AAU28106.1| enolase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]			x
77544917	>gi|77544917|gb|ABA88479.1| enolase [Pelobacter carbinolicus DSM 2380]			x
23495020	>gi|23495020|gb|AAN35353.1| enolase [Plasmodium falciparum 3D7]			x
76785279	>gi|76785279|ref|ZP_00772451.1| COG0148: Enolase [Mycobacterium tuberculosis F11]			x
76792445	>gi|76792445|ref|ZP_00774944.1| Enolase [Pseudoalteromonas atlantica T6c]			x
76797225	>gi|76797225|ref|ZP_00779559.1| Enolase [Thermoanaerobacter ethanolicus ATCC 33223]			x
77406132	>gi|77406132|ref|ZP_00783205.1| enolase [Streptococcus agalactiae H36B]			x
77407751	>gi|77407751|ref|ZP_00784505.1| enolase [Streptococcus agalactiae COH1]			x
77411108	>gi|77411108|ref|ZP_00787461.1| enolase [Streptococcus agalactiae CJB111]			x
77414276	>gi|77414276|ref|ZP_00790435.1| enolase [Streptococcus agalactiae 515]			x
77631732	>gi|77631732|ref|ZP_00794318.1| COG0148: Enolase [Yersinia pseudotuberculosis IP 31758]			x
77635114	>gi|77635114|ref|ZP_00797203.1| COG0148: Enolase [Yersinia pestis Angola]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
77689478	>gi|77689478|ref|ZP_00804659.1| Enolase [Rhodopseudomonas palustris BisB5]			x
77994855	>gi|77994855|gb|ABB13754.1| enolase [Carboxydothermus hydrogenoformans Z-2901]			x
46048768	>gi|46048768|ref|NP_990451.1| enolase 1 [Gallus gallus]			x
77742416	>gi|77742416|ref|ZP_00810894.1| Enolase [Rhodopseudomonas palustris BisA53]			x
69159144	>gi|69159144|gb|EAN71282.1| Enolase [Shewanella denitrificans OS217]			x
78167716	>gi|78167716|gb|ABB24814.1| Enolase [Pelodictyon luteolum DSM 273]			x
78170022	>gi|78170022|gb|ABB27119.1| Enolase [Synechococcus sp. CC9902]			x
78170524	>gi|78170524|gb|ABB27620.1| Enolase [Chlorobium chlorochromatii CaD3]			x
77815272	>gi|77815272|ref|ZP_00814510.1| Enolase [Shewanella putrefaciens CN-32]			x
78198443	>gi|78198443|gb|ABB36208.1| enolase [Synechococcus sp. CC9605]			x
77952809	>gi|77952809|ref|ZP_00817222.1| Enolase [Marinobacter aquaeolei VT8]			x
77962820	>gi|77962820|ref|ZP_00826636.1| COG0148: Enolase [Yersinia mollaretii ATCC 43969]			x
77976028	>gi|77976028|ref|ZP_00831561.1| COG0148: Enolase [Yersinia frederiksenii ATCC 33641]			x
77979609	>gi|77979609|ref|ZP_00835026.1| COG0148: Enolase [Yersinia intermedia ATCC 29909]			x
55590655	>gi|55590655|ref|XP_514354.1| PREDICTED: enolase 1 [Pan troglodytes]			x
78363890	>gi|78363890|gb|ABB41855.1| enolase [Thiomicrospira crunogena XCL-2]			x
78712095	>gi|78712095|gb|ABB49272.1| enolase [Prochlorococcus marinus str. MIT 9312]			x
19888365	>gi|19888365|gb|AAM02860.1| Enolase [Methanopyrus kandleri AV19]			x
51573166	>gi|51573166|gb|AAU07191.1| enolase [Borrelia garinii PBi]			x
3152725	>gi|3152725|gb|AAC17130.1| enolase [Staphylococcus aureus]			x
55738590	>gi|55738590|gb|AAV62231.1| 2-phosphoglycerate dehydratase, enolase [Streptococcus thermophilus CNRZ1066]			x
56679062	>gi|56679062|gb|AAV95728.1| enolase [Silicibacter pomeroyi DSS-3]			x
24053192	>gi|24053192|gb|AAN44282.1| enolase [Shigella flexneri 2a str. 301]			x
57225057	>gi|57225057|gb|AAW40114.1| enolase [Dehalococcoides ethenogenes 195]			x
57167487	>gi|57167487|gb|AAW36266.1| enolase [Campylobacter jejuni RM1221]			x
78365755	>gi|78365755|ref|ZP_00836040.1| Enolase [Shewanella sp. PV-4]			x
78492903	>gi|78492903|ref|ZP_00845138.1| Enolase [Rhodopseudomonas palustris BisB18]			x
78685818	>gi|78685818|ref|ZP_00850593.1| Enolase [Shewanella sp. ANA-3]			x
78691419	>gi|78691419|ref|ZP_00856036.1| Enolase [Shewanella sp. MR-7]			x
78702809	>gi|78702809|ref|ZP_00867233.1| Enolase [Alkalilimnicola ehrlichei MLHE-1]			x
78704928	>gi|78704928|ref|ZP_00869322.1| Enolase [Methanospirillum hungatei JF-1]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
78705604	>gi|78705604|ref|ZP_00869981.1| Enolase [Methanospirillum hungatei JF-1]			x
78695164	>gi|78695164|ref|ZP_00859676.1| Enolase [Bradyrhizobium sp. BTAi1]			x
78706225	>gi|78706225|ref|ZP_00870566.1| Enolase [Methanospirillum hungatei JF-1]			x
42545184	>gi|42545184|gb|EAA68027.1| ENO_ALTAL Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Major allergen Alt a 11) (Alt a XI) [Gibberella zeae PH-1]			x
66848203	>gi|66848203|gb|EAL88532.1| enolase [Aspergillus fumigatus Af293]			x
66797943	>gi|66797943|ref|ZP_00396700.1| Enolase [Deinococcus geothermalis DSM 11300]			x
66879038	>gi|66879038|ref|ZP_00404072.1| COG0148: Enolase [Streptococcus pneumoniae TIGR4]			x
67676250	>gi|67676250|ref|ZP_00473001.1| Enolase [Chromohalobacter salexigens DSM 3043]			x
67657013	>gi|67657013|ref|ZP_00454393.1| Enolase [Burkholderia cenocepacia AU 1054]			x
67917474	>gi|67917474|ref|ZP_00511080.1| Enolase [Chlorobium limicola DSM 245]			x
67934468	>gi|67934468|ref|ZP_00527517.1| Enolase [Solibacter usitatus Ellin6076]			x
67935050	>gi|67935050|ref|ZP_00528074.1| Enolase [Chlorobium phaeobacteroides DSM 266]			x
67940099	>gi|67940099|ref|ZP_00532567.1| Enolase [Chlorobium phaeobacteroides BS1]			x
67941827	>gi|67941827|ref|ZP_00533828.1| Enolase [Chlorobium phaeobacteroides BS1]			x
67988318	>gi|67988318|gb|EAM76098.1| Enolase [Kineococcus radiotolerans SRS30216]			x
68056418	>gi|68056418|ref|ZP_00540539.1| Enolase [Exiguobacterium sp. 255-15]			x
68171488	>gi|68171488|ref|ZP_00544872.1| Enolase [Ehrlichia chaffeensis str. Sapulpa]			x
68179394	>gi|68179394|ref|ZP_00552459.1| Enolase [Desulfuromonas acetoxidans DSM 684]			x
68182317	>gi|68182317|ref|ZP_00555297.1| Enolase [Jannaschia sp. CCS1]			x
68234022	>gi|68234022|ref|ZP_00573122.1| Enolase [Frankia sp. EAN1pec]			x
68351290	>gi|68351290|gb|EAN32053.1| enolase, putative [Theileria parva]			x
68539232	>gi|68539232|ref|ZP_00579005.1| Enolase [Sphingopyxis alaskensis RB2256]			x
68551301	>gi|68551301|ref|ZP_00590717.1| Enolase [Pelodictyon phaeoclathratiforme BU-1]			x
68551717	>gi|68551717|ref|ZP_00591111.1| Enolase [Prosthecochloris aestuarii DSM 271]			x
68546866	>gi|68546866|ref|ZP_00586410.1| Enolase [Shewanella amazonensis SB2B]			x
68543414	>gi|68543414|ref|ZP_00583120.1| Enolase [Shewanella baltica OS155]			x
56685854	>gi|56685854|dbj|BAD79076.1| enolase [Synechococcus elongatus PCC 6301]			x
66044611	>gi|66044611|ref|YP_234452.1| phosphopyruvate hydratase [Pseudomonas syringae pv. syringae B728a]			x
66044729	>gi|66044729|ref|YP_234570.1| Enolase [Pseudomonas syringae pv. syringae B728a]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
3023709	>gi|3023709|sp|Q27727|ENO_PLAFA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
460259	>gi|460259|gb|AAA21681.1| enolase			x
37805239	>gi|37805239|gb|AAH60310.1| Enolase 2, gamma [Rattus norvegicus]			x
155581	>gi|155581|gb|AAA27686.1| enolase			x
56416785	>gi|56416785|ref|YP_153859.1| Enolase 1 (2-phosphoglycerate dehydratase 1) [Anaplasma marginale str. St. Maries]			x
182118	>gi|182118|gb|AAA52388.1| gamma enolase			x
6624229	>gi|6624229|dbj|BAA88479.1| enolase [Eptatretus burgeri]			x
6624235	>gi|6624235|dbj|BAA88482.1| enolase-1 [Lethenteron reissneri]			x
46048765	>gi|46048765|ref|NP_990450.1| enolase [Gallus gallus]			x
6624237	>gi|6624237|dbj|BAA88483.1| enolase-2 [Lethenteron reissneri]			x
34762728	>gi|34762728|ref|ZP_00143718.1| Enolase [Fusobacterium nucleatum subsp. vincentii ATCC 49256]			x
535442	>gi|535442|gb|AAA70080.1| enolase			x
38636433	>gi|38636433|emb|CAE81969.1| probable enolase [Neurospora crassa]			x
18481669	>gi|18481669|gb|AAL73509.1| enolase [Giardia intestinalis]			x
67466006	>gi|67466006|ref|XP_649161.1| enolase [Entamoeba histolytica HM-1:IMSS]			x
458897	>gi|458897|gb|AAB68019.1| Eno2p: Enolase 2; 2-phosphoglycerate dehydratase [Saccharomyces cerevisiae]			x
31165	>gi|31165|emb|CAA36215.1| human gamma enolase [Homo sapiens]			x
16504025	>gi|16504025|emb|CAD06058.1| enolase [Salmonella enterica subsp. enterica serovar Typhi]			x
34789	>gi|34789|emb|CAA36216.1| muscle-specific enolase [Homo sapiens]			x
21112791	>gi|21112791|gb|AAM40994.1| enolase [Xanthomonas campestris pv. campestris str. ATCC 33913]			x
65317107	>gi|65317107|ref|ZP_00390066.1| COG0148: Enolase [Bacillus anthracis str. A2012]			x
23347962	>gi|23347962|gb|AAN30052.1| enolase [Brucella suis 1330]			x
62148599	>gi|62148599|emb|CAH64371.1| enolase [Chlamydophila abortus S26/3]			x
58417796	>gi|58417796|emb|CAI27000.1| Enolase (2-phosphoglycerate dehydratase) [Ehrlichia ruminantium str. Welgevonden]			x
48430954	>gi|48430954|gb|AAT43819.1| enolase [Picrophilus torridus DSM 9790]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
60492114	>gi|60492114|emb|CAH06877.1| putative heme-binding enolase [Bacteroides fragilis NCTC 9343]			x
67642981	>gi|67642981|ref|ZP_00441731.1| COG0148: Enolase [Burkholderia mallei GB8 horse 4]			x
52005169	>gi|52005169|gb|AAU25111.1| enolase [Bacillus licheniformis ATCC 14580]			x
58418695	>gi|58418695|gb|AAW70710.1| Enolase [Wolbachia endosymbiont strain TRS of Brugia malayi]			x
58416835	>gi|58416835|emb|CAI27948.1| Enolase (2-phosphoglycerate dehydratase) [Ehrlichia ruminantium str. Gardel]			x
13937125	>gi|13937125|gb|AAK50056.1| enolase [Trichinella spiralis]			x
22273	>gi|22273|emb|CAA39454.1| enolase [Zea mays]			x
37222051	>gi|37222051|gb|AAQ17040.2| pollen 2-phosphoglycerate dehydrogenase 2 precursor [Cynodon dactylon]			x
54673814	>gi|54673814|gb|AAH85098.1| Enolase 1, alpha non-neuron [Mus musculus]			x
31167	>gi|31167|emb|CAA40163.1| muscle specific enolase [Homo sapiens]			x
6679651	>gi|6679651|ref|NP_031959.1| enolase 3, beta muscle [Mus musculus]			x
21618816	>gi|21618816|gb|AAH31739.1| Enolase 2, gamma neuronal [Mus musculus]			x
15227987	>gi|15227987|ref|NP_181192.1| LOS2; phosphopyruvate hydratase [Arabidopsis thaliana]			x
16272869	>gi|16272869|ref|NP_439092.1| phosphopyruvate hydratase [Haemophilus influenzae Rd KW20]			x
14089932	>gi|14089932|emb|CAC13691.1| ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) [Mycoplasma pulmonis]			x
7226525	>gi|7226525|gb|AAF41661.1| enolase [Neisseria meningitidis MC58]			x
433609	>gi|433609|emb|CAA82232.1| enolase [Ricinus communis]			x
31179	>gi|31179|emb|CAA47179.1| enolase [Homo sapiens]			x
30138660	>gi|30138660|emb|CAD84955.1| Enolase [Nitrosomonas europaea ATCC 19718]			x
56496865	>gi|56496865|emb|CAH99714.1| enolase, putative [Plasmodium berghei]			x
28270478	>gi|28270478|emb|CAD63380.1| phosphopyruvate hydratase [Lactobacillus plantarum WCFS1]			x
1911573	>gi|1911573|gb|AAB50731.1| enolase [Loligo pealei]			x
515827	>gi|515827|emb|CAA56645.1| enolase [Neocallimastix frontalis]			x
33641127	>gi|33641127|emb|CAE22257.1| Enolase [Prochlorococcus marinus str. MIT 9313]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
33633710	>gi|33633710|emb|CAE18667.1| Enolase [Prochlorococcus marinus subsp. pastoris str. CCMP1986]			x
39649793	>gi|39649793|emb|CAE28315.1| enolase [Rhodopseudomonas palustris CGA009]			x
33639479	>gi|33639479|emb|CAE08863.1| Enolase [Synechococcus sp. WH 8102]			x
83589135	>gi|83589135|ref|YP_429144.1| enolase [Moorella thermoacetica ATCC 39073]			x
58429954	>gi|58429954|gb|AAW78351.1| enolase [Trichomonas vaginalis]			x
81096520	>gi|81096520|ref|ZP_00874861.1| Enolase [Streptococcus suis 89/1591]			x
67762048	>gi|67762048|ref|ZP_00500752.1| COG0148: Enolase [Burkholderia pseudomallei S13]			x
4416379	>gi|4416379|gb|AAD20342.1| alpha enolase [Caiman crocodilus]			x
4416381	>gi|4416381|gb|AAD20343.1| alpha enolase [Sphenodon punctatus]			x
4416383	>gi|4416383|gb|AAD20344.1| alpha enolase [Eumeces inexpectatus]			x
4416385	>gi|4416385|gb|AAD20345.1| alpha enolase [Trachemys scripta]			x
4416387	>gi|4416387|gb|AAD20346.1| alpha enolase [Pelusios subniger]			x
77387470	>gi|77387470|gb|ABA78655.1| Enolase [Rhodobacter sphaeroides 2.4.1]			x
19074779	>gi|19074779|ref|NP_586285.1| ENOLASE [Encephalitozoon cuniculi GB-M1]			x
59808815	>gi|59808815|gb|AAH90069.1| Enolase 1, alpha [Rattus norvegicus]			x
48762657	>gi|48762657|ref|NP_997887.1| enolase 1, (alpha) [Danio rerio]			x
69298335	>gi|69298335|ref|ZP_00620615.1| Enolase [Silicibacter sp. TM1040]			x
60099812	>gi|60099812|gb|AAX13040.1| enolase [Drosophila pseudoobscura]			x
60099838	>gi|60099838|gb|AAX13053.1| enolase [Drosophila miranda]			x
60099832	>gi|60099832|gb|AAX13050.1| enolase [Drosophila miranda]			x
68194237	>gi|68194237|gb|EAN08760.1| Enolase [Enterococcus faecium DO]			x
68245979	>gi|68245979|gb|EAN28087.1| Enolase [Magnetococcus sp. MC-1]			x
68193510	>gi|68193510|gb|EAN08162.1| Enolase [Mesorhizobium sp. BNC1]			x
71847604	>gi|71847604|gb|AAZ47100.1| Enolase [Dechloromonas aromatica RCB]			x
78217747	>gi|78217747|gb|ABB37096.1| enolase [Desulfovibrio desulfuricans G20]			x
75703448	>gi|75703448|gb|ABA23124.1| Enolase [Anabaena variabilis ATCC 29413]			x
5566201	>gi|5566201|gb|AAD45332.1| enolase 2 [Monocercomonas ATCC50210]			x
5566203	>gi|5566203|gb|AAD45334.1| enolase 1 [Trichomonas vaginalis]			x
5566204	>gi|5566204|gb|AAD45335.1| enolase 2 [Trichomonas vaginalis]			x
5566205	>gi|5566205|gb|AAD45336.1| enolase 3 [Trichomonas vaginalis]			x
5566206	>gi|5566206|gb|AAD45337.1| enolase 4 [Trichomonas vaginalis]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
5566207	>gi|5566207|gb|AAD45338.1| enolase 5 [Trichomonas vaginalis]			x
5566208	>gi|5566208|gb|AAD45339.1| enolase [Trypanosoma brucei]			x
65304337	>gi|65304337|emb|CAI76716.1| enolase, putative [Theileria annulata]			x
71039176	>gi|71039176|gb|AAZ19484.1| enolase [Psychrobacter arcticus 273-4]			x
72118206	>gi|72118206|gb|AAZ60469.1| Enolase [Ralstonia eutropha JMP134]			x
72394249	>gi|72394249|gb|AAZ68526.1| Enolase [Ehrlichia canis str. Jake]			x
78194830	>gi|78194830|gb|ABB32597.1| Enolase [Geobacter metallireducens GS-15]			x
71914564	>gi|71914564|gb|AAZ54466.1| enolase [Thermobifida fusca YX]			x
70832210	>gi|70832210|gb|EAN77714.1| enolase [Trypanosoma brucei]			x
27262298	>gi|27262298|gb|AAN87430.1| Enolase [Heliobacillus mobilis]			x
68057718	>gi|68057718|gb|AAX87971.1| enolase [Haemophilus influenzae 86-028NP]			x
40949670	>gi|40949670|gb|AAR97546.1| enolase 1 [Apodachlya brachynema]			x
40949672	>gi|40949672|gb|AAR97547.1| enolase 2 [Apodachlya brachynema]			x
40949674	>gi|40949674|gb|AAR97548.1| enolase [Heterosigma akashiwo]			x
40949676	>gi|40949676|gb|AAR97549.1| enolase [Isochrysis galbana]			x
40949680	>gi|40949680|gb|AAR97551.1| enolase [Phaeodactylum tricornutum]			x
40949682	>gi|40949682|gb|AAR97552.1| enolase [Phytophthora palmivora]			x
40949684	>gi|40949684|gb|AAR97553.1| enolase [Prymnesium parvum]			x
40949686	>gi|40949686|gb|AAR97554.1| enolase [Thraustotheca clavata]			x
40949688	>gi|40949688|gb|AAR97555.1| enolase [Heterocapsa triquetra]			x
57227282	>gi|57227282|gb|AAW43741.1| enolase 1, putative [Cryptococcus neoformans var. neoformans JEC21]			x
37572552	>gi|37572552|dbj|BAC98826.1| enolase [Trichonympha agilis]			x
84787058	>gi|84787058|gb|ABC63240.1| enolase [Erythrobacter litoralis HTCC2594]			x
66357920	>gi|66357920|ref|XP_626138.1| enolase (2-phosphoglycerate dehydratase) [Cryptosporidium parvum]			x
48787796	>gi|48787796|ref|ZP_00283775.1| COG0148: Enolase [Burkholderia fungorum LB400]			x
48855292	>gi|48855292|ref|ZP_00309451.1| COG0148: Enolase [Cytophaga hutchinsonii]			x
48861278	>gi|48861278|ref|ZP_00315181.1| COG0148: Enolase [Microbulbifer degradans 2-40]			x
48865594	>gi|48865594|ref|ZP_00319453.1| COG0148: Enolase [Oenococcus oeni PSU-1]			x
67539152	>gi|67539152|ref|XP_663350.1| enolase [Aspergillus nidulans FGSC A4]			x
55297212	>gi|55297212|dbj|BAD68886.1| putative enolase [Oryza sativa (japonica cultivar-group)]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
23024413	>gi|23024413|ref|ZP_00063626.1| COG0148: Enolase [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]			x
38511762	>gi|38511762|gb|AAH61287.1| Enolase (2-phosphoglycerate dehydratase) [Xenopus tropicalis]			x
49257392	>gi|49257392|gb|AAH72713.1| Enolase 2 [Danio rerio]			x
34597330	>gi|34597330|gb|AAQ77240.1| enolase [Brassica rapa]			x
60280039	>gi|60280039|gb|AAX16379.1| enolase [uncultured murine large bowel bacterium BAC 31B]			x
11999247	>gi|11999247|gb|AAG16301.1| alpha enolase-1 [Amia calva]			x
11999249	>gi|11999249|gb|AAG16302.1| beta enolase-1 [Amia calva]			x
11999251	>gi|11999251|gb|AAG16303.1| alpha enolase-1 [Latimeria chalumnae]			x
11999257	>gi|11999257|gb|AAG16306.1| beta enolase-1 [Lepidosiren paradoxa]			x
11999259	>gi|11999259|gb|AAG16307.1| beta enolase-1 [Neoceratodus forsteri]			x
11999261	>gi|11999261|gb|AAG16308.1| alpha enolase-1 [Chiloscyllium punctatum]			x
11999263	>gi|11999263|gb|AAG16309.1| beta enolase-1 [Chiloscyllium punctatum]			x
11999265	>gi|11999265|gb|AAG16310.1| alpha-1 enolase-1 [Salmo trutta]			x
11999267	>gi|11999267|gb|AAG16311.1| alpha-2 enolase-1 [Salmo trutta]			x
15221107	>gi|15221107|ref|NP_177543.1| phosphopyruvate hydratase [Arabidopsis thaliana]			x
2655161	>gi|2655161|gb|AAB87890.1| enolase [Drosophila pseudoobscura]			x
2655163	>gi|2655163|gb|AAB87891.1| enolase [Drosophila subobscura]			x
8101740	>gi|8101740|gb|AAF72639.1| enolase [Polyxenus fasciculatus]			x
8101742	>gi|8101742|gb|AAF72640.1| enolase [Scolopendra polymorpha]			x
8101744	>gi|8101744|gb|AAF72641.1| enolase [Tomocerus sp. 'Tom']			x
29650775	>gi|29650775|gb|AAO86694.1| enolase [Dunaliella salina]			x
86158067	>gi|86158067|ref|YP_464852.1| enolase [Anaeromyxobacter dehalogenans 2CP-C]			x
15667704	>gi|15667704|gb|AAL05459.1| enolase 1 [Mastocarpus papillatus]			x
15667706	>gi|15667706|gb|AAL05460.1| enolase 2 [Mastocarpus papillatus]			x
15667709	>gi|15667709|gb|AAL05461.1| enolase 1 [Prionitis lanceolata]			x
15667711	>gi|15667711|gb|AAL05462.1| enolase 2 [Prionitis lanceolata]			x
15667717	>gi|15667717|gb|AAL05465.1| enolase [Paramecium tetraurelia]			x
15667719	>gi|15667719|gb|AAL05466.1| enolase [Colpidium aqueous]			x
15667721	>gi|15667721|gb|AAL05467.1| enolase [Tetrahymena thermophila]			x
15667723	>gi|15667723|gb|AAL05468.1| enolase [Tetrahymena bergeri]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
41033679	>gi|41033679|emb|CAF18506.1| enolase [Thermoproteus tenax]			x
19171969	>gi|19171969|gb|AAL85688.1| enolase [Streptococcus agalactiae]			x
14161523	>gi|14161523|gb|AAK54778.1| enolase [Hypocryphalus mangiferae]			x
4106354	>gi|4106354|gb|AAD02812.1| enolase [Pneumocystis carinii f. sp. ratti]			x
62896593	>gi|62896593|dbj|BAD96237.1| enolase 1 variant [Homo sapiens]			x
62897945	>gi|62897945|dbj|BAD96912.1| enolase 1 variant [Homo sapiens]			x
15227561	>gi|15227561|ref|NP_180516.1| phosphopyruvate hydratase [Arabidopsis thaliana]	fixd		x
20260174	>gi|20260174|gb|AAM12985.1| enolase (2-phospho-D-glycerate hydroylase) [Arabidopsis thaliana]			x
21325986	>gi|21325986|gb|AAM47554.1| alpha-enolase [Crocodylus palustris]			x
68086449	>gi|68086449|gb|AAH92869.2| Enolase 3, (beta, muscle) [Danio rerio]			x
86572923	>gi|86572923|gb|ABD07480.1| enolase [Rhodopseudomonas palustris HaA2]			x
71274918	>gi|71274918|ref|ZP_00651206.1| Enolase [Xylella fastidiosa Dixon]			x
71674738	>gi|71674738|ref|ZP_00672484.1| Enolase [Trichodesmium erythraeum IMS101]			x
71898806	>gi|71898806|ref|ZP_00680974.1| Enolase [Xylella fastidiosa Ann-1]			x
37531422	>gi|37531422|ref|NP_920013.1| putative enolase (2-phospho-D-glycerate hydroylase) [Oryza sativa (japonica cultivar-group)]			x
18175728	>gi|18175728|gb|AAL59917.1| putative enolase (2-phospho-D-glycerate hydroylase) [Arabidopsis thaliana]			x
32440997	>gi|32440997|gb|AAP81756.1| enolase [Onchocerca volvulus]			x
33113259	>gi|33113259|gb|AAP94211.1| enolase [Oryza sativa (japonica cultivar-group)]			x
23394379	>gi|23394379|gb|AAN31479.1| enolase [Phytophthora infestans]			x
33415263	>gi|33415263|gb|AAQ18140.1| enolase [Gossypium barbadense]			x
22652630	>gi|22652630|gb|AAN03783.1| enolase [Clonorchis sinensis]			x
34597332	>gi|34597332|gb|AAQ77241.1| enolase [Brassica napus]			x
27902665	>gi|27902665|gb|AAO24625.1| enolase [Methylobacterium extorquens]			x
40063045	>gi|40063045|gb|AAR37901.1| enolase [uncultured bacterium 560]			x
33465417	>gi|33465417|gb|AAQ19194.1| enolase [Tritrichomonas foetus]			x
33465419	>gi|33465419|gb|AAQ19195.1| enolase [Tetratrichomonas gallinarum]			x
40063711	>gi|40063711|gb|AAR38492.1| enolase [uncultured bacterium 583]			x
37681795	>gi|37681795|gb|AAQ97775.1| enolase 1, (alpha) [Danio rerio]			x
42521309	>gi|42521309|gb|AAS18240.1| enolase [Glycine max]			x

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>8919731</td><td>>gi|8919731|emb|CAB96173.1| enolase [Spinacia oleracea]</td><td></td><td></td><td>x</td></tr>
<tr><td>6996529</td><td>>gi|6996529|emb|CAB75428.1| enolase [Lupinus luteus]</td><td></td><td></td><td>x</td></tr>
<tr><td>8919600</td><td>>gi|8919600|emb|CAB96125.1| enolase [Euglena gracilis]</td><td></td><td></td><td>x</td></tr>
<tr><td>8919602</td><td>>gi|8919602|emb|CAB96126.1| chloroplast enolase [Euglena gracilis]</td><td></td><td></td><td>x</td></tr>
<tr><td>16151617</td><td>>gi|16151617|emb|CAC83091.1| alpha-enolase [Streptococcus pneumoniae]</td><td></td><td></td><td>x</td></tr>
<tr><td>22035897</td><td>>gi|22035897|emb|CAD43170.1| enolase [Anisakis simplex]</td><td></td><td></td><td>x</td></tr>
<tr><td>28866546</td><td>>gi|28866546|emb|CAD60544.1| enolase [Streptococcus sobrinus]</td><td></td><td></td><td>x</td></tr>
<tr><td>56711110</td><td>>gi|56711110|emb|CAD98929.1| enolase [Lactobacillus sakei]</td><td></td><td></td><td>x</td></tr>
<tr><td>57336904</td><td>>gi|57336904|emb|CAH60998.1| alpha-enolase [Lactobacillus crispatus]</td><td></td><td></td><td>x</td></tr>
<tr><td>6978809</td><td>>gi|6978809|ref|NP_036686.1| enolase 1, alpha [Rattus norvegicus]</td><td></td><td></td><td>x</td></tr>
<tr><td>930101</td><td>>gi|930101|emb|CAA32505.1| gamma enolase [Homo sapiens]</td><td></td><td></td><td>x</td></tr>
<tr><td>39598758</td><td>>gi|39598758|gb|AAR28936.1| enolase [Zootermopsis parabasalian symbiont 11]</td><td></td><td></td><td>x</td></tr>
<tr><td>39598760</td><td>>gi|39598760|gb|AAR28937.1| enolase [Zootermopsis parabasalian symbiont 13]</td><td></td><td></td><td>x</td></tr>
<tr><td>39598762</td><td>>gi|39598762|gb|AAR28938.1| enolase [Zootermopsis parabasalian symbiont 17]</td><td></td><td></td><td>x</td></tr>
<tr><td>39598764</td><td>>gi|39598764|gb|AAR28939.1| enolase [Zootermopsis parabasalian symbiont 19]</td><td></td><td></td><td>x</td></tr>
<tr><td>39598766</td><td>>gi|39598766|gb|AAR28940.1| enolase [Zootermopsis parabasalian symbiont 22]</td><td></td><td></td><td>x</td></tr>
<tr><td>39598768</td><td>>gi|39598768|gb|AAR28941.1| enolase [Zootermopsis parabasalian symbiont 29]</td><td></td><td></td><td>x</td></tr>
<tr><td>39598770</td><td>>gi|39598770|gb|AAR28942.1| enolase [Zootermopsis parabasalian symbiont 30]</td><td></td><td></td><td>x</td></tr>
<tr><td>39598772</td><td>>gi|39598772|gb|AAR28943.1| enolase [Zootermopsis parabasalian symbiont 31]</td><td></td><td></td><td>x</td></tr>
<tr><td>39598774</td><td>>gi|39598774|gb|AAR28944.1| enolase [Zootermopsis parabasalian symbiont 33]</td><td></td><td></td><td>x</td></tr>
<tr><td>37590349</td><td>>gi|37590349|gb|AAH59511.1| Enolase 1, (alpha) [Danio rerio]</td><td></td><td></td><td>x</td></tr>
<tr><td>76257976</td><td>>gi|76257976|ref|ZP_00765633.1| Enolase [Chloroflexus aurantiacus J-10-fl]</td><td></td><td></td><td>x</td></tr>
<tr><td>68125330</td><td>>gi|68125330|emb|CAJ03181.1| enolase [Leishmania major]</td><td></td><td></td><td>x</td></tr>
<tr><td>52550388</td><td>>gi|52550388|gb|AAU84237.1| phosphopyruvate hydratase enolase [uncultured archaeon GZfos3D4]</td><td></td><td></td><td>x</td></tr>
<tr><td>53830714</td><td>>gi|53830714|gb|AAU95200.1| enolase [Oncometopia nigricans]</td><td></td><td></td><td>x</td></tr>
<tr><td>54035288</td><td>>gi|54035288|gb|AAH83566.1| Enolase 3, beta [Rattus norvegicus]</td><td></td><td></td><td>x</td></tr>
<tr><td>51980244</td><td>>gi|51980244|gb|AAU20794.1| enolase 2 [Heterocapsa triquetra]</td><td></td><td></td><td>x</td></tr>
<tr><td>55846716</td><td>>gi|55846716|gb|AAV67362.1| enolase 2 [Macaca fascicularis]</td><td></td><td></td><td>x</td></tr>
<tr><td>79042712</td><td>>gi|79042712|ref|ZP_00873466.1| Enolase [Novosphingobium aromaticivorans DSM 12444]</td><td></td><td></td><td>x</td></tr>
<tr><td>66964439</td><td>>gi|66964439|ref|ZP_00412009.1| Enolase [Arthrobacter sp. FB24]</td><td></td><td></td><td>x</td></tr>
<tr><td>67157908</td><td>>gi|67157908|ref|ZP_00419053.1| Enolase [Azotobacter vinelandii AvOP]</td><td></td><td></td><td>x</td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>67157754</td><td>>gi|67157754|ref|ZP_00418949.1| Enolase [Azotobacter vinelandii AvOP]</td><td></td><td></td><td>x</td></tr>
<tr><td>67156392</td><td>>gi|67156392|ref|ZP_00417985.1| Enolase [Azotobacter vinelandii AvOP]</td><td></td><td></td><td>x</td></tr>
<tr><td>67154735</td><td>>gi|67154735|ref|ZP_00416480.1| Enolase [Azotobacter vinelandii AvOP]</td><td></td><td></td><td>x</td></tr>
<tr><td>67549711</td><td>>gi|67549711|ref|ZP_00427562.1| Enolase [Burkholderia vietnamiensis G4]</td><td></td><td></td><td>x</td></tr>
<tr><td>67910846</td><td>>gi|67910846|ref|ZP_00509232.1| Enolase [Polaromonas sp. JS666]</td><td></td><td></td><td>x</td></tr>
<tr><td>67924949</td><td>>gi|67924949|ref|ZP_00518338.1| Enolase [Crocosphaera watsonii WH 8501]</td><td></td><td></td><td>x</td></tr>
<tr><td>68207426</td><td>>gi|68207426|ref|ZP_00559588.1| Enolase [Desulfitobacterium hafniense DCB-2]</td><td></td><td></td><td>x</td></tr>
<tr><td>68210333</td><td>>gi|68210333|ref|ZP_00562199.1| Enolase [Methanococcoides burtonii DSM 6242]</td><td></td><td></td><td>x</td></tr>
<tr><td>68188665</td><td>>gi|68188665|gb|EAN03344.1| Enolase [Methylobacillus flagellatus KT]</td><td></td><td></td><td>x</td></tr>
<tr><td>68561157</td><td>>gi|68561157|ref|ZP_00600460.1| Enolase [Rubrobacter xylanophilus DSM 9941]</td><td></td><td></td><td>x</td></tr>
<tr><td>68555733</td><td>>gi|68555733|ref|ZP_00595077.1| Enolase [Ralstonia metallidurans CH34]</td><td></td><td></td><td>x</td></tr>
<tr><td>68555849</td><td>>gi|68555849|ref|ZP_00595193.1| Enolase [Ralstonia metallidurans CH34]</td><td></td><td></td><td>x</td></tr>
<tr><td>1363309</td><td>>gi|1363309|pir||JC1039 phosphopyruvate hydratase (EC 4.2.1.11) - rat</td><td></td><td></td><td>x</td></tr>
<tr><td>84390114</td><td>>gi|84390114|ref|ZP_00991376.1| phosphopyruvate hydratase [Vibrio splendidus 12B01]</td><td></td><td></td><td>x</td></tr>
<tr><td>84497843</td><td>>gi|84497843|ref|ZP_00996640.1| phosphopyruvate hydratase [Janibacter sp. HTCC2649]</td><td></td><td></td><td>x</td></tr>
<tr><td>81428222</td><td>>gi|81428222|ref|YP_395222.1| Phosphopyruvate hydratase [Lactobacillus sakei subsp. sakei 23K]</td><td></td><td></td><td>x</td></tr>
<tr><td>83816221</td><td>>gi|83816221|ref|YP_444923.1| phosphopyruvate hydratase [Salinibacter ruber DSM 13855]</td><td></td><td></td><td>x</td></tr>
<tr><td>86146349</td><td>>gi|86146349|ref|ZP_01064673.1| phosphopyruvate hydratase [Vibrio sp. MED222]</td><td></td><td></td><td>x</td></tr>
<tr><td>86153067</td><td>>gi|86153067|ref|ZP_01071272.1| phosphopyruvate hydratase [Campylobacter jejuni subsp. jejuni HB93-13]</td><td></td><td></td><td>x</td></tr>
<tr><td>86154615</td><td>>gi|86154615|ref|ZP_01072782.1| phosphopyruvate hydratase [Campylobacter fetus subsp. fetus 82-40]</td><td></td><td></td><td>x</td></tr>
<tr><td>86166241</td><td>>gi|86166241|gb|EAQ67507.1| phosphopyruvate hydratase [Marinomonas sp. MED121]</td><td></td><td></td><td>x</td></tr>
<tr><td>86607174</td><td>>gi|86607174|ref|YP_475937.1| phosphopyruvate hydratase [Cyanobacteria bacterium Yellowstone A-Prime]</td><td></td><td></td><td>x</td></tr>
<tr><td>86609966</td><td>>gi|86609966|ref|YP_478728.1| phosphopyruvate hydratase [Cyanobacteria bacterium Yellowstone B-Prime]</td><td></td><td></td><td>x</td></tr>
<tr><td>76882684</td><td>>gi|76882684|gb|ABA57365.1| Phosphopyruvate hydratase [Nitrosococcus oceani ATCC 19707]</td><td></td><td></td><td>x</td></tr>
<tr><td>66811048</td><td>>gi|66811048|ref|XP_639231.1| 2-phospho-D-glycerate hydrolase [Dictyostelium discoideum]</td><td></td><td></td><td>x</td></tr>
<tr><td>66828593</td><td>>gi|66828593|ref|XP_647650.1| 2-phospho-D-glycerate hydrolase [Dictyostelium discoideum]</td><td></td><td></td><td>x</td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
627094	>gi|627094|pir||A53665 phosphopyruvate hydratase (EC 4.2.1.11) - liver fluke			x
83593220	>gi|83593220|ref|YP_426972.1| Phosphopyruvate hydratase [Rhodospirillum rubrum ATCC 11170]			x
77967627	>gi|77967627|gb|ABB09007.1| Phosphopyruvate hydratase [Burkholderia sp. 383]			x
3885968	>gi|3885968|gb|AAC78141.1| phosphopyruvate hydratase [Penaeus monodon]			x
68140076	>gi|68140076|gb|EAM93386.1| Phosphopyruvate hydratase [Ferroplasma acidarmanus Fer1]			x
57225611	>gi|57225611|gb|AAW42072.1| phosphopyruvate hydratase, putative [Cryptococcus neoformans var. neoformans JEC21]			x
77381351	>gi|77381351|gb|ABA72864.1| Phosphopyruvate hydratase [Pseudomonas fluorescens PfO-1]			x
72397477	>gi|72397477|gb|AAZ71750.1| phosphopyruvate hydratase [Methanosarcina barkeri str. fusaro]			x
86742602	>gi|86742602|ref|YP_483002.1| Phosphopyruvate hydratase [Frankia sp. CcI3]			x
78778195	>gi|78778195|ref|YP_394510.1| Phosphopyruvate hydratase [Thiomicrospira denitrificans ATCC 33889]			x
533474	>gi|533474|gb|AAA21277.1| 2-phospho-D-glycerate hydrolase			x
41394387	>gi|41394387|gb|AAS02297.1| 2-phospho-D-glycerate hydrolase [Lithobius sp. SBH266126]			x
41394389	>gi|41394389|gb|AAS02298.1| 2-phospho-D-glycerate hydrolase [Diplopoda sp. SBH266145]			x
41394391	>gi|41394391|gb|AAS02299.1| 2-phospho-D-glycerate hydrolase [Phormictopus sp. SBH266263]			x
41394393	>gi|41394393|gb|AAS02300.1| 2-phospho-D-glycerate hydrolase [Limulus polyphemus]			x
41394395	>gi|41394395|gb|AAS02301.1| 2-phospho-D-glycerate hydrolase [Artemia sp. SBH266677]			x
41394397	>gi|41394397|gb|AAS02302.1| 2-phospho-D-glycerate hydrolase [Daphnia magna]			x
41394399	>gi|41394399|gb|AAS02303.1| 2-phospho-D-glycerate hydrolase [Callinectes sapidus]			x
41394401	>gi|41394401|gb|AAS02304.1| 2-phospho-D-glycerate hydrolase [Nereis macrydi]			x
41394403	>gi|41394403|gb|AAS02305.1| 2-phospho-D-glycerate hydrolase [Ostracoda sp. SBH266127]			x
41394405	>gi|41394405|gb|AAS02306.1| 2-phospho-D-glycerate hydrolase [Centruroides sp. SBH266264]			x
148781	>gi|148781|gb|AAA73101.1| 2-phosphoglycerate dehydratase			x
17066742	>gi|17066742|gb|AAL35382.1| 2-phosphoglycerate dehydratase [Streptococcus thermophilus]			x
83375076	>gi|83375076|ref|ZP_00919840.1| probable galactonate dehydratase protein [Rhodobacter sphaeroides ATCC 17029]			x
83363605	>gi|83363605|gb|EAP67101.1| probable galactonate dehydratase protein [Rhodobacter sphaeroides ATCC 17029]			x

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>86359287</td><td>>gi|86359287|ref|YP_471179.1| galactonate dehydratase protein [Rhizobium etli CFN 42]</td><td></td><td></td><td>x</td></tr>
<tr><td>86283389</td><td>>gi|86283389|gb|ABC92452.1| galactonate dehydratase protein [Rhizobium etli CFN 42]</td><td></td><td></td><td>x</td></tr>
<tr><td>71554501</td><td>>gi|71554501|gb|AAZ33712.1| galactonate dehydratase [Pseudomonas syringae pv. phaseolicola 1448A]</td><td></td><td></td><td>x</td></tr>
<tr><td>71733948</td><td>>gi|71733948|ref|YP_274182.1| galactonate dehydratase [Pseudomonas syringae pv. phaseolicola 1448A]</td><td></td><td></td><td>x</td></tr>
<tr><td>15140365</td><td>>gi|15140365|emb|CAC48892.1| probable galactonate dehydratase protein [Sinorhizobium meliloti 1021]</td><td></td><td></td><td>x</td></tr>
<tr><td>16264240</td><td>>gi|16264240|ref|NP_437032.1| probable galactonate dehydratase protein [Sinorhizobium meliloti 1021]</td><td></td><td></td><td>x</td></tr>
<tr><td>48994953</td><td>>gi|48994953|gb|AAT48197.1| galactonate dehydratase [Escherichia coli K12]</td><td></td><td></td><td>x</td></tr>
<tr><td>85676352</td><td>>gi|85676352|dbj|BAE77602.1| galactonate dehydratase [Escherichia coli W3110]</td><td></td><td></td><td>x</td></tr>
<tr><td>49176390</td><td>>gi|49176390|ref|YP_026237.1| galactonate dehydratase [Escherichia coli K12]</td><td></td><td></td><td>x</td></tr>
<tr><td>55977863</td><td>>gi|55977863|sp|Q6BF17|DGOD_ECOLI Galactonate dehydratase</td><td></td><td></td><td>x</td></tr>
<tr><td>78035782</td><td>>gi|78035782|emb|CAJ23473.1| Galactonate dehydratase [Xanthomonas campestris pv. vesicatoria str. 85-10]</td><td></td><td></td><td>x</td></tr>
<tr><td>78047352</td><td>>gi|78047352|ref|YP_363527.1| Galactonate dehydratase [Xanthomonas campestris pv. vesicatoria str. 85-10]</td><td></td><td></td><td>x</td></tr>
<tr><td>56908537</td><td>>gi|56908537|dbj|BAD63064.1| galactonate dehydratase [Bacillus clausii KSM-K16]</td><td></td><td></td><td>x</td></tr>
<tr><td>56962300</td><td>>gi|56962300|ref|YP_174025.1| galactonate dehydratase [Bacillus clausii KSM-K16]</td><td></td><td></td><td>x</td></tr>
<tr><td>37201785</td><td>>gi|37201785|dbj|BAC97606.1| probable galactonate dehydratase protein [Vibrio vulnificus YJ016]</td><td></td><td></td><td>x</td></tr>
<tr><td>37677240</td><td>>gi|37677240|ref|NP_937636.1| probable galactonate dehydratase protein [Vibrio vulnificus YJ016]</td><td></td><td></td><td>x</td></tr>
<tr><td>52208756</td><td>>gi|52208756|emb|CAH34692.1| putative galactonate dehydratase protein [Burkholderia pseudomallei K96243]</td><td></td><td></td><td>x</td></tr>
<tr><td>53718342</td><td>>gi|53718342|ref|YP_107328.1| putative galactonate dehydratase protein [Burkholderia pseudomallei K96243]</td><td></td><td></td><td>x</td></tr>
<tr><td>62182315</td><td>>gi|62182315|ref|YP_218732.1| galactonate dehydratase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]</td><td></td><td></td><td>x</td></tr>
<tr><td>62129948</td><td>>gi|62129948|gb|AAX67651.1| galactonate dehydratase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]</td><td></td><td></td><td>x</td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>56380332</td><td>>gi|56380332|dbj|BAD76240.1| galactonate dehydratase [Geobacillus kaustophilus HTA426]</td><td></td><td></td><td>x</td></tr>
<tr><td>56420490</td><td>>gi|56420490|ref|YP_147808.1| galactonate dehydratase [Geobacillus kaustophilus HTA426]</td><td></td><td></td><td>x</td></tr>
<tr><td>17429773</td><td>>gi|17429773|emb|CAD16458.1| PUTATIVE GALACTONATE DEHYDRATASE PROTEIN [Ralstonia solanacearum]</td><td></td><td></td><td>x</td></tr>
<tr><td>17547470</td><td>>gi|17547470|ref|NP_520872.1| PUTATIVE GALACTONATE DEHYDRATASE PROTEIN [Ralstonia solanacearum GMI1000]</td><td></td><td></td><td>x</td></tr>
<tr><td>494811</td><td>>gi|494811|pdb|2MNR| Mandelate Racemase (E.C.5.1.2.2)</td><td></td><td></td><td>x</td></tr>
<tr><td>443131</td><td>>gi|443131|pdb|1MNS| Mandelate Racemase (E.C.5.1.2.2)</td><td></td><td></td><td>x</td></tr>
<tr><td>151356</td><td>>gi|151356|gb|AAC15504.1| mandelate racemase [Pseudomonas putida]</td><td></td><td></td><td>x</td></tr>
<tr><td>126731</td><td>>gi|126731|sp|P11444|MANR_PSEPU Mandelate racemase (MR)</td><td></td><td></td><td>x</td></tr>
<tr><td>151352</td><td>>gi|151352|gb|AAA25887.1| mandelate racemase (EC 5.1.2.2)</td><td></td><td></td><td>x</td></tr>
<tr><td>640264</td><td>>gi|640264|pdb|1MDR| Mandelate Racemase (E.C.5.1.2.2)</td><td></td><td></td><td>x</td></tr>
<tr><td>16504040</td><td>>gi|16504040|emb|CAD06074.1| probable glucarate dehydratase 1 [Salmonella enterica subsp. enterica serovar Typhi]</td><td></td><td></td><td>x</td></tr>
<tr><td>29138856</td><td>>gi|29138856|gb|AAO70425.1| probable glucarate dehydratase 1 [Salmonella enterica subsp. enterica serovar Typhi Ty2]</td><td></td><td></td><td>x</td></tr>
<tr><td>16761739</td><td>>gi|16761739|ref|NP_457356.1| probable glucarate dehydratase 1 [Salmonella enterica subsp. enterica serovar Typhi str. CT18]</td><td></td><td></td><td>x</td></tr>
<tr><td>29143223</td><td>>gi|29143223|ref|NP_806565.1| probable glucarate dehydratase 1 [Salmonella enterica subsp. enterica serovar Typhi Ty2]</td><td></td><td></td><td>x</td></tr>
<tr><td>25291986</td><td>>gi|25291986|pir||AC0861 glucarate dehydratase (EC 4.2.1.40) - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)</td><td></td><td></td><td>x</td></tr>
<tr><td>74313359</td><td>>gi|74313359|ref|YP_311778.1| putative glucarate dehydratase [Shigella sonnei Ss046]</td><td></td><td></td><td>x</td></tr>
<tr><td>73856836</td><td>>gi|73856836|gb|AAZ89543.1| putative glucarate dehydratase [Shigella sonnei Ss046]</td><td></td><td></td><td>x</td></tr>
<tr><td>12517262</td><td>>gi|12517262|gb|AAG57900.1| putative glucarate dehydratase [Escherichia coli O157:H7 EDL933]</td><td></td><td></td><td>x</td></tr>
<tr><td>15803308</td><td>>gi|15803308|ref|NP_289341.1| putative glucarate dehydratase [Escherichia coli O157:H7 EDL933]</td><td></td><td></td><td>x</td></tr>
<tr><td>25291985</td><td>>gi|25291985|pir||H85929 probable glucarate dehydratase ygcX [imported] - Escherichia coli (strain O157:H7, substrain EDL933)</td><td></td><td></td><td>x</td></tr>
<tr><td>1170131</td><td>>gi|1170131|sp|P42206|GUDH_PSEPU Glucarate dehydratase (GDH) (GlucD)</td><td></td><td></td><td>x</td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>5107516</td><td>>gi|5107516|pdb|1BQG| The Structure Of The D-Glucarate Dehydratase Protein From Pseudomonas Putida</td><td></td><td></td><td>x</td></tr>
<tr><td>151315</td><td>>gi|151315|gb|AAA25868.1| glucarate dehydratase</td><td></td><td></td><td>x</td></tr>
<tr><td>82740091</td><td>>gi|82740091|ref|ZP_00902855.1| glucarate dehydratase [Pseudomonas putida F1]</td><td></td><td></td><td>x</td></tr>
<tr><td>82712829</td><td>>gi|82712829|gb|EAP47979.1| glucarate dehydratase [Pseudomonas putida F1]</td><td></td><td></td><td>x</td></tr>
<tr><td>83748918</td><td>>gi|83748918|ref|ZP_00945928.1| Glucarate dehydratase [Ralstonia solanacearum UW551]</td><td></td><td></td><td>x</td></tr>
<tr><td>83724417</td><td>>gi|83724417|gb|EAP71585.1| Glucarate dehydratase [Ralstonia solanacearum UW551]</td><td></td><td></td><td>x</td></tr>
<tr><td>83749284</td><td>>gi|83749284|ref|ZP_00946283.1| Glucarate dehydratase [Ralstonia solanacearum UW551]</td><td></td><td></td><td>x</td></tr>
<tr><td>83724065</td><td>>gi|83724065|gb|EAP71244.1| Glucarate dehydratase [Ralstonia solanacearum UW551]</td><td></td><td></td><td>x</td></tr>
<tr><td>84715424</td><td>>gi|84715424|ref|ZP_01022525.1| glucarate dehydratase [Polaromonas naphthalenivorans CJ2]</td><td></td><td></td><td>x</td></tr>
<tr><td>84693248</td><td>>gi|84693248|gb|EAQ19050.1| glucarate dehydratase [Polaromonas naphthalenivorans CJ2]</td><td></td><td></td><td>x</td></tr>
<tr><td>83719461</td><td>>gi|83719461|ref|YP_440747.1| glucarate dehydratase [Burkholderia thailandensis E264]</td><td></td><td></td><td>x</td></tr>
<tr><td>83653286</td><td>>gi|83653286|gb|ABC37349.1| glucarate dehydratase [Burkholderia thailandensis E264]</td><td></td><td></td><td>x</td></tr>
<tr><td>82545086</td><td>>gi|82545086|ref|YP_409033.1| putative glucarate dehydratase [Shigella boydii Sb227]</td><td></td><td></td><td>x</td></tr>
<tr><td>81246497</td><td>>gi|81246497|gb|ABB67205.1| putative glucarate dehydratase [Shigella boydii Sb227]</td><td></td><td></td><td>x</td></tr>
<tr><td>1789150</td><td>>gi|1789150|gb|AAC75829.1| (D)-glucarate dehydratase 1 [Escherichia coli K12]</td><td></td><td></td><td>x</td></tr>
<tr><td>85675606</td><td>>gi|85675606|dbj|BAA16572.2| (D)-glucarate dehydratase 1 [Escherichia coli W3110]</td><td></td><td></td><td>x</td></tr>
<tr><td>13363118</td><td>>gi|13363118|dbj|BAB37070.1| putative glucarate dehydratase [Escherichia coli O157:H7]</td><td></td><td></td><td>x</td></tr>
<tr><td>16130694</td><td>>gi|16130694|ref|NP_417267.1| (D)-glucarate dehydratase 1 [Escherichia coli K12]</td><td></td><td></td><td>x</td></tr>
<tr><td>15832901</td><td>>gi|15832901|ref|NP_311674.1| putative glucarate dehydratase [Escherichia coli O157:H7]</td><td></td><td></td><td>x</td></tr>
<tr><td>84028816</td><td>>gi|84028816|sp|P0AES2|GUDH_ECOLI Glucarate dehydratase (GDH) (GlucD)</td><td></td><td></td><td>x</td></tr>
<tr><td>84028815</td><td>>gi|84028815|sp|P0AES3|GUDH_ECO57 Glucarate dehydratase (GDH) (GlucD)</td><td></td><td></td><td>x</td></tr>
<tr><td>8569464</td><td>>gi|8569464|pdb|1EC7|D Chain D, E. Coli Glucarate Dehydratase Native Enzyme</td><td></td><td></td><td>x</td></tr>
<tr><td>8569463</td><td>>gi|8569463|pdb|1EC7|C Chain C, E. Coli Glucarate Dehydratase Native Enzyme</td><td></td><td></td><td>x</td></tr>
<tr><td>8569462</td><td>>gi|8569462|pdb|1EC7|B Chain B, E. Coli Glucarate Dehydratase Native Enzyme</td><td></td><td></td><td>x</td></tr>
<tr><td>8569461</td><td>>gi|8569461|pdb|1EC7|A Chain A, E. Coli Glucarate Dehydratase Native Enzyme</td><td></td><td></td><td>x</td></tr>
<tr><td>8569476</td><td>>gi|8569476|pdb|1ECQ|D Chain D, E. Coli Glucarate Dehydratase Bound To 4-Deoxyglucarate</td><td></td><td></td><td>x</td></tr>
<tr><td>8569475</td><td>>gi|8569475|pdb|1ECQ|C Chain C, E. Coli Glucarate Dehydratase Bound To 4-Deoxyglucarate</td><td></td><td></td><td>x</td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
8569474	>gi|8569474|pdb|1ECQ|B Chain B, E. Coli Glucarate Dehydratase Bound To 4-Deoxyglucarate			x
8569473	>gi|8569473|pdb|1ECQ|A Chain A, E. Coli Glucarate Dehydratase Bound To 4-Deoxyglucarate			x
8569472	>gi|8569472|pdb|1EC9|D Chain D, E. Coli Glucarate Dehydratase Bound To Xylarohydroxamate			x
8569471	>gi|8569471|pdb|1EC9|C Chain C, E. Coli Glucarate Dehydratase Bound To Xylarohydroxamate			x
8569470	>gi|8569470|pdb|1EC9|B Chain B, E. Coli Glucarate Dehydratase Bound To Xylarohydroxamate			x
8569469	>gi|8569469|pdb|1EC9|A Chain A, E. Coli Glucarate Dehydratase Bound To Xylarohydroxamate			x
8569468	>gi|8569468|pdb|1EC8|D Chain D, E. Coli Glucarate Dehydratase Bound To Product 2,3- Dihydroxy-5-Oxo-Hexanedioate			x
8569467	>gi|8569467|pdb|1EC8|C Chain C, E. Coli Glucarate Dehydratase Bound To Product 2,3- Dihydroxy-5-Oxo-Hexanedioate			x
8569466	>gi|8569466|pdb|1EC8|B Chain B, E. Coli Glucarate Dehydratase Bound To Product 2,3- Dihydroxy-5-Oxo-Hexanedioate			x
8569465	>gi|8569465|pdb|1EC8|A Chain A, E. Coli Glucarate Dehydratase Bound To Product 2,3- Dihydroxy-5-Oxo-Hexanedioate			x
74019874	>gi|74019874|ref|ZP_00690485.1| Glucarate dehydratase [Burkholderia ambifaria AMMD]			x
72607384	>gi|72607384|gb|EAO43345.1| Glucarate dehydratase [Burkholderia ambifaria AMMD]			x
75428530	>gi|75428530|ref|ZP_00731732.1| Glucarate dehydratase [Actinobacillus succinogenes 130Z]			x
74277622	>gi|74277622|gb|EAO51194.1| Glucarate dehydratase [Actinobacillus succinogenes 130Z]			x
77965618	>gi|77965618|gb|ABB06998.1| Glucarate dehydratase [Burkholderia sp. 383]			x
78064873	>gi|78064873|ref|YP_367642.1| Glucarate dehydratase [Burkholderia sp. 383]			x
78694788	>gi|78694788|ref|ZP_00859301.1| Glucarate dehydratase [Bradyrhizobium sp. BTAi1]			x
78517904	>gi|78517904|gb|EAP31202.1| Glucarate dehydratase [Bradyrhizobium sp. BTAi1]			x
67666682	>gi|67666682|ref|ZP_00463925.1| Glucarate dehydratase [Burkholderia cenocepacia HI2424]			x
67661211	>gi|67661211|ref|ZP_00458533.1| Glucarate dehydratase [Burkholderia cenocepacia AU 1054]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
67099777	>gi|67099777|gb|EAM16944.1| Glucarate dehydratase [Burkholderia cenocepacia HI2424]			x
67091199	>gi|67091199|gb|EAM08786.1| Glucarate dehydratase [Burkholderia cenocepacia AU 1054]			x
28870449	>gi|28870449|ref|NP_793068.1| glucarate dehydratase [Pseudomonas syringae pv. tomato str. DC3000]			x
28853696	>gi|28853696|gb|AAO56763.1| glucarate dehydratase [Pseudomonas syringae pv. tomato str. DC3000]			x
66046349	>gi|66046349|ref|YP_236190.1| Glucarate dehydratase [Pseudomonas syringae pv. syringae B728a]			x
63257056	>gi|63257056|gb|AAY38152.1| Glucarate dehydratase [Pseudomonas syringae pv. syringae B728a]			x
21114479	>gi|21114479|gb|AAM42512.1| glucarate hydratase [Xanthomonas campestris pv. campestris str. ATCC 33913]			x
66572615	>gi|66572615|gb|AAY48025.1| glucarate hydratase [Xanthomonas campestris pv. campestris str. 8004]			x
66767283	>gi|66767283|ref|YP_242045.1| glucarate hydratase [Xanthomonas campestris pv. campestris str. 8004]			x
21232671	>gi|21232671|ref|NP_638588.1| glucarate hydratase [Xanthomonas campestris pv. campestris str. ATCC 33913]			x
49613022	>gi|49613022|emb|CAG76473.1| glucarate dehydratase [Erwinia carotovora subsp. atroseptica SCRI1043]			x
50122496	>gi|50122496|ref|YP_051663.1| glucarate dehydratase [Erwinia carotovora subsp. atroseptica SCRI1043]			x
22778523	>gi|22778523|dbj|BAC14792.1| glucarate dehydratase [Oceanobacillus iheyensis HTE831]			x
23100291	>gi|23100291|ref|NP_693758.1| glucarate dehydratase [Oceanobacillus iheyensis HTE831]			x
1170130	>gi|1170130|sp|P42238|GUDH_BACSU Probable glucarate dehydratase (GDH) (GlucD)			x
710000	>gi|710000|dbj|BAA06470.1| glucarate dehydratase [Bacillus subtilis]			x
27354149	>gi|27354149|dbj|BAC51137.1| glucarate dehydratase [Bradyrhizobium japonicum USDA 110]			x
27380983	>gi|27380983|ref|NP_772512.1| glucarate dehydratase [Bradyrhizobium japonicum USDA 110]			x
56129169	>gi|56129169|gb|AAV78675.1| probable glucarate dehydratase 1 [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]			x

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>56414912</td><td>>gi|56414912|ref|YP_151987.1| probable glucarate dehydratase 1 [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]</td><td></td><td></td><td>x</td></tr>
<tr><td>16421511</td><td>>gi|16421511|gb|AAL21840.1| d-glucarate dehydratase [Salmonella typhimurium LT2]</td><td></td><td></td><td>x</td></tr>
<tr><td>62181470</td><td>>gi|62181470|ref|YP_217887.1| d-glucarate dehydratase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]</td><td></td><td></td><td>x</td></tr>
<tr><td>62129103</td><td>>gi|62129103|gb|AAX66806.1| d-glucarate dehydratase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]</td><td></td><td></td><td>x</td></tr>
<tr><td>16766266</td><td>>gi|16766266|ref|NP_461881.1| d-glucarate dehydratase [Salmonella typhimurium LT2]</td><td></td><td></td><td>x</td></tr>
<tr><td>26991438</td><td>>gi|26991438|ref|NP_746863.1| glucarate dehydratase [Pseudomonas putida KT2440]</td><td></td><td></td><td>x</td></tr>
<tr><td>24986512</td><td>>gi|24986512|gb|AAN70327.1| glucarate dehydratase [Pseudomonas putida KT2440]</td><td></td><td></td><td>x</td></tr>
<tr><td>49529393</td><td>>gi|49529393|emb|CAG67105.1| D-glucarate dehydratase [Acinetobacter sp. ADP1]</td><td></td><td></td><td>x</td></tr>
<tr><td>50083417</td><td>>gi|50083417|ref|YP_044927.1| D-glucarate dehydratase [Acinetobacter sp. ADP1]</td><td></td><td></td><td>x</td></tr>
<tr><td>24053199</td><td>>gi|24053199|gb|AAN44288.1| putative glucarate dehydratase [Shigella flexneri 2a str. 301]</td><td></td><td></td><td>x</td></tr>
<tr><td>30042388</td><td>>gi|30042388|gb|AAP18113.1| putative glucarate dehydratase [Shigella flexneri 2a str. 2457T]</td><td></td><td></td><td>x</td></tr>
<tr><td>30064132</td><td>>gi|30064132|ref|NP_838303.1| putative glucarate dehydratase [Shigella flexneri 2a str. 2457T]</td><td></td><td></td><td>x</td></tr>
<tr><td>24114071</td><td>>gi|24114071|ref|NP_708581.1| putative glucarate dehydratase [Shigella flexneri 2a str. 301]</td><td></td><td></td><td>x</td></tr>
<tr><td>72120887</td><td>>gi|72120887|gb|AAZ63073.1| Glucarate dehydratase [Ralstonia eutropha JMP134]</td><td></td><td></td><td>x</td></tr>
<tr><td>73537550</td><td>>gi|73537550|ref|YP_297917.1| Glucarate dehydratase [Ralstonia eutropha JMP134]</td><td></td><td></td><td>x</td></tr>
<tr><td>17428092</td><td>>gi|17428092|emb|CAD14781.1| PROBABLE GLUCARATE DEHYDRATASE PROTEIN [Ralstonia solanacearum]</td><td></td><td></td><td>x</td></tr>
<tr><td>17545798</td><td>>gi|17545798|ref|NP_519200.1| PROBABLE GLUCARATE DEHYDRATASE PROTEIN [Ralstonia solanacearum GMI1000]</td><td></td><td></td><td>x</td></tr>
<tr><td>17431301</td><td>>gi|17431301|emb|CAD17980.1| PROBABLE GLUCARATE DEHYDRATASE PROTEIN [Ralstonia solanacearum]</td><td></td><td></td><td>x</td></tr>
<tr><td>17549050</td><td>>gi|17549050|ref|NP_522390.1| PROBABLE GLUCARATE DEHYDRATASE PROTEIN [Ralstonia solanacearum GMI1000]</td><td></td><td></td><td>x</td></tr>
<tr><td>67549363</td><td>>gi|67549363|ref|ZP_00427228.1| Glucarate dehydratase [Burkholderia vietnamiensis G4]</td><td></td><td></td><td>x</td></tr>
<tr><td>67529304</td><td>>gi|67529304|gb|EAM26174.1| Glucarate dehydratase [Burkholderia vietnamiensis G4]</td><td></td><td></td><td>x</td></tr>
<tr><td>67778298</td><td>>gi|67778298|gb|EAM37921.1| Glucarate dehydratase [Polaromonas sp. JS666]</td><td></td><td></td><td>x</td></tr>
<tr><td>67909708</td><td>>gi|67909708|ref|ZP_00508103.1| Glucarate dehydratase [Polaromonas sp. JS666]</td><td></td><td></td><td>x</td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
68555520	>gi|68555520|ref|ZP_00594864.1| Glucarate dehydratase [Ralstonia metallidurans CH34]			x
68529990	>gi|68529990|gb|EAN52952.1| Glucarate dehydratase [Ralstonia metallidurans CH34]			x
18655552	>gi|18655552|pdb|1KKR|B Chain B, Crystal Structure Of Citrobacter Amalonaticus Methylaspartate Ammonia Lyase Containing (2s,3s)-3- Methylaspartic Acid			x
18655551	>gi|18655551|pdb|1KKR|A Chain A, Crystal Structure Of Citrobacter Amalonaticus Methylaspartate Ammonia Lyase Containing (2s,3s)-3- Methylaspartic Acid			x
18655550	>gi|18655550|pdb|1KKO|B Chain B, Crystal Structure Of Citrobacter Amalonaticus Methylaspartate Ammonia Lyase			x
18655549	>gi|18655549|pdb|1KKO|A Chain A, Crystal Structure Of Citrobacter Amalonaticus Methylaspartate Ammonia Lyase			x
82776003	>gi|82776003|ref|YP_402350.1| putative methylaspartate ammonia-lyase [Shigella dysenteriae Sd197]			x
81240151	>gi|81240151|gb|ABB60861.1| putative methylaspartate ammonia-lyase [Shigella dysenteriae Sd197]			x
68206184	>gi|68206184|ref|ZP_00558376.1| Methylaspartate ammonia-lyase [Desulfitobacterium hafniense DCB-2]			x
68169895	>gi|68169895|gb|EAM97789.1| Methylaspartate ammonia-lyase [Desulfitobacterium hafniense DCB-2]			x
3184397	>gi|3184397|dbj|BAA28709.1| 3-methylaspartate ammonia-lyase [Citrobacter amalonaticus]			x
10581701	>gi|10581701|gb|AAG20402.1| methylaspartate ammonia-lyase; Mal [Halobacterium sp. NRC-1]			x
15791098	>gi|15791098|ref|NP_280922.1| Mal [Halobacterium sp. NRC-1]			x
13360220	>gi|13360220|dbj|BAB34184.1| 3-methylaspartate ammonia-lyase [Escherichia coli O157:H7]			x
15830015	>gi|15830015|ref|NP_308788.1| 3-methylaspartate ammonia-lyase [Escherichia coli O157:H7]			x
12513655	>gi|12513655|gb|AAG55061.1| putative methylaspartate ammonia-lyase [Escherichia coli O157:H7 EDL933]			x
15800441	>gi|15800441|ref|NP_286453.1| putative methylaspartate ammonia-lyase [Escherichia coli O157:H7 EDL933]			x
14025840	>gi|14025840|dbj|BAB52439.1| 3-methylaspartate ammonia-lyase [Mesorhizobium loti MAFF303099]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
13475089	>gi|13475089|ref|NP_106653.1| 3-methylaspartate ammonia-lyase [Mesorhizobium loti MAFF303099]			x
259429	>gi|259429|gb|AAB24070.1| beta-methylaspartase; 3-methylaspartate ammonia-lyase [Clostridium tetanomorphum]			x
729971	>gi|729971|sp|Q05514|MAAL_CLOTT Methylaspartate ammonia-lyase (Beta-methylaspartase)			x
28204585	>gi|28204585|gb|AAO37022.1| methylaspartate ammonia-lyase [Clostridium tetani E88]			x
28212141	>gi|28212141|ref|NP_783085.1| methylaspartate ammonia-lyase [Clostridium tetani E88]			x
18159000	>gi|18159000|pdb|1KCZ|B Chain B, Crystal Structure Of Beta-Methylaspartase From Clostridium Tetanomorphum. Mg-Complex			x
18158999	>gi|18158999|pdb|1KCZ|A Chain A, Crystal Structure Of Beta-Methylaspartase From Clostridium Tetanomorphum. Mg-Complex			x
18159002	>gi|18159002|pdb|1KD0|B Chain B, Crystal Structure Of Beta-Methylaspartase From Clostridium Tetanomorphum. Apo-Structure			x
18159001	>gi|18159001|pdb|1KD0|A Chain A, Crystal Structure Of Beta-Methylaspartase From Clostridium Tetanomorphum. Apo-Structure			x
10120813	>gi|10120813|pdb|1FHV|A Chain A, Crystal Structure Analysis Of O-Succinylbenzoate Synthase From E. Coli Complexed With Mg And Osb			x
74312783	>gi|74312783|ref|YP_311202.1| O-succinylbenzoate synthase [Shigella sonnei Ss046]			x
17380438	>gi|17380438|sp|P44961|MENC_HAEIN O-succinylbenzoate synthase (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x
30995414	>gi|30995414|ref|NP_439130.2| O-succinylbenzoate synthase [Haemophilus influenzae Rd KW20]			x
84387750	>gi|84387750|ref|ZP_00990766.1| O-succinylbenzoate synthase [Vibrio splendidus 12B01]			x
23467878	>gi|23467878|ref|ZP_00123455.1| COG1441: O-succinylbenzoate synthase [Haemophilus somnus 129PT]			x
32029563	>gi|32029563|ref|ZP_00132566.1| COG1441: O-succinylbenzoate synthase [Haemophilus somnus 2336]			x
46143800	>gi|46143800|ref|ZP_00133907.2| COG1441: O-succinylbenzoate synthase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]			x
46129092	>gi|46129092|ref|ZP_00155737.2| COG1441: O-succinylbenzoate synthase [Haemophilus influenzae R2846]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
42631291	>gi|42631291|ref|ZP_00156829.1| COG1441: O-succinylbenzoate synthase [Haemophilus influenzae R2866]			x
85860671	>gi|85860671|ref|YP_462873.1| o-succinylbenzoate synthase [Syntrophus aciditrophicus SB]			x
86148507	>gi|86148507|ref|ZP_01066795.1| O-succinylbenzoate synthase [Vibrio sp. MED222]			x
86169287	>gi|86169287|gb|EAQ70543.1| putative O-succinylbenzoate synthase [Synechococcus sp. RS9917]			x
86605931	>gi|86605931|ref|YP_474694.1| O-succinylbenzoate synthetase [Cyanobacteria bacterium Yellowstone A-Prime]			x
86608214	>gi|86608214|ref|YP_476976.1| O-succinylbenzoate synthetase [Cyanobacteria bacterium Yellowstone B-Prime]			x
71481154	>gi|71481154|ref|ZP_00660862.1| O-succinylbenzoate-CoA synthase [Prosthecochloris vibrioformis DSM 265]			x
75177946	>gi|75177946|ref|ZP_00698008.1| COG1441: O-succinylbenzoate synthase [Shigella boydii BS512]			x
75196304	>gi|75196304|ref|ZP_00706374.1| COG1441: O-succinylbenzoate synthase [Escherichia coli HS]			x
75230352	>gi|75230352|ref|ZP_00716842.1| COG1441: O-succinylbenzoate synthase [Escherichia coli B7A]			x
75238050	>gi|75238050|ref|ZP_00722055.1| COG1441: O-succinylbenzoate synthase [Escherichia coli E110019]			x
75243077	>gi|75243077|ref|ZP_00726783.1| COG1441: O-succinylbenzoate synthase [Escherichia coli F11]			x
75259725	>gi|75259725|ref|ZP_00731027.1| COG1441: O-succinylbenzoate synthase [Escherichia coli E22]			x
75512739	>gi|75512739|ref|ZP_00735241.1| COG1441: O-succinylbenzoate synthase [Escherichia coli 53638]			x
75818947	>gi|75818947|ref|ZP_00749056.1| COG1441: O-succinylbenzoate synthase [Vibrio cholerae V51]			x
75823556	>gi|75823556|ref|ZP_00753049.1| COG1441: O-succinylbenzoate synthase [Vibrio cholerae RC385]			x
75827285	>gi|75827285|ref|ZP_00756720.1| COG1441: O-succinylbenzoate synthase [Vibrio cholerae O395]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
75830779	>gi|75830779|ref|ZP_00760051.1| COG1441: O-succinylbenzoate synthase [Vibrio cholerae MO10]			x
75854299	>gi|75854299|ref|ZP_00762001.1| COG1441: O-succinylbenzoate synthase [Vibrio sp. Ex25]			x
77629610	>gi|77629610|ref|ZP_00792196.1| COG1441: O-succinylbenzoate synthase [Yersinia pseudotuberculosis IP 31758]			x
77636599	>gi|77636599|ref|ZP_00798672.1| COG1441: O-succinylbenzoate synthase [Yersinia pestis Angola]			x
78169979	>gi|78169979|gb|ABB27076.1| putative O-succinylbenzoate synthase [Synechococcus sp. CC9902]			x
78171873	>gi|78171873|gb|ABB28969.1| O-succinylbenzoate-CoA synthase [Chlorobium chlorochromatii CaD3]			x
78198404	>gi|78198404|gb|ABB36169.1| putative O-succinylbenzoate synthase [Synechococcus sp. CC9605]			x
77957630	>gi|77957630|ref|ZP_00821681.1| COG1441: O-succinylbenzoate synthase [Yersinia bercovieri ATCC 43970]			x
77961210	>gi|77961210|ref|ZP_00825054.1| COG1441: O-succinylbenzoate synthase [Yersinia mollaretii ATCC 43969]			x
77975452	>gi|77975452|ref|ZP_00830987.1| COG1441: O-succinylbenzoate synthase [Yersinia frederiksenii ATCC 33641]			x
77976638	>gi|77976638|ref|ZP_00832116.1| COG1441: O-succinylbenzoate synthase [Yersinia intermedia ATCC 29909]			x
78712062	>gi|78712062|gb|ABB49239.1| putative O-succinylbenzoate synthase [Prochlorococcus marinus str. MIT 9312]			x
49259032	>gi|49259032|pdb|1SJD|D Chain D, X-Ray Structure Of O-Succinylbenzoate Synthase Complexed With N-Succinyl Phenylglycine			x
37198046	>gi|37198046|dbj|BAC93883.1| O-succinylbenzoate synthase [Vibrio vulnificus YJ016]			x
27362631	>gi|27362631|gb|AAO11485.1| O-succinylbenzoate synthase [Vibrio vulnificus CMCP6]			x
51974118	>gi|51974118|gb|AAU15668.1| possible N-acylamino acid racemase; possible O-succinylbenzoate synthase [Bacillus cereus E33L]			x
59712274	>gi|59712274|ref|YP_205050.1| O-succinylbenzoate synthase [Vibrio fischeri ES114]			x
41410148	>gi|41410148|ref|NP_962984.1| O-succinylbenzoate synthase [Mycobacterium avium subsp. paratuberculosis K-10]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
17135012	>gi|17135012|dbj|BAB77558.1| O-succinylbenzoic acid synthase [Nostoc sp. PCC 7120]			x
24376048	>gi|24376048|ref|NP_720091.1| O-succinylbenzoate synthase [Shewanella oneidensis MR-1]			x
33633677	>gi|33633677|emb|CAE18634.1| putative O-succinylbenzoate synthase [Prochlorococcus marinus subsp. pastoris str. CCMP1986]			x
33641103	>gi|33641103|emb|CAE22232.1| putative O-succinylbenzoate synthase [Prochlorococcus marinus str. MIT 9313]			x
33639437	>gi|33639437|emb|CAE08821.1| putative O-succinylbenzoate synthase [Synechococcus sp. WH 8102]			x
75702573	>gi|75702573|gb|ABA22249.1| O-succinylbenzoic acid synthase [Anabaena variabilis ATCC 29413]			x
68057755	>gi|68057755|gb|AAX88008.1| O-succinylbenzoate synthase [Haemophilus influenzae 86-028NP]			x
82751377	>gi|82751377|ref|YP_417118.1| o-succinylbenzoic acid synthetase [Staphylococcus aureus RF122]			x
47568030	>gi|47568030|ref|ZP_00238736.1| O-succinylbenzoic acid (OSB) synthetase [Bacillus cereus G9241]			x
83814286	>gi|83814286|ref|YP_445478.1| o-succinylbenzoic acid (OSB) synthetase [Salinibacter ruber DSM 13855]			x
72494795	>gi|72494795|dbj|BAE18116.1| O-succinylbenzoic acid synthetase [Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305]			x
68446858	>gi|68446858|dbj|BAE04442.1| O-succinylbenzoic acid (OSB) synthetase [Staphylococcus haemolyticus JCSC1435]			x
57284767	>gi|57284767|gb|AAW36861.1| o-succinylbenzoic acid (OSB) synthetase, putative [Staphylococcus aureus subsp. aureus COL]			x
27315928	>gi|27315928|gb|AAO05062.1| o-succinylbenzoic acid (OSB) synthetase [Staphylococcus epidermidis ATCC 12228]			x
57867276	>gi|57867276|ref|YP_188928.1| O-succinylbenzoic acid synthetase, putative [Staphylococcus epidermidis RP62A]			x
14247568	>gi|14247568|dbj|BAB57958.1| o-succinylbenzoic acid synthetase [Staphylococcus aureus subsp. aureus Mu50]			x
146811	>gi|146811|gb|AAA71917.1| 4-(2'-carboxyphenyl)-4-oxybutyric acid synthase			x

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>6466408</td><td>>gi|6466408|gb|AAF12990.1| unknown; 4-(2'-carboxyphenyl)-4-oxybutyric acid synthase [Cyanidium caldarium]</td><td></td><td></td><td>x</td></tr>
<tr><td>30409241</td><td>>gi|30409241|dbj|BAC76190.1| 4-(2'-carboxyphenyl)-4-oxybutyric acid synthase [Cyanidioschyzon merolae]</td><td>GSA</td><td></td><td>x</td></tr>
<tr><td>18158849</td><td>>gi|18158849|pdb|1JPD|X Chain X, L-Ala-DL-Glu Epimerase</td><td></td><td></td><td>x</td></tr>
<tr><td>49176883</td><td>>gi|49176883|ref|YP_025386.1| chloromuconate cycloisomerase [Ralstonia eutropha JMP134]</td><td></td><td></td><td>x</td></tr>
<tr><td>39777463</td><td>>gi|39777463|gb|AAR31038.1| chloromuconate cycloisomerase [Ralstonia eutropha JMP134]</td><td></td><td></td><td>x</td></tr>
<tr><td>150768</td><td>>gi|150768|gb|AAA98263.1| chloromuconate cycloisomerase [Ralstonia eutropha]</td><td></td><td></td><td>x</td></tr>
<tr><td>135651</td><td>>gi|135651|sp|P05404|TFDD1_RALEJ Chloromuconate cycloisomerase (Muconate cycloisomerase II)</td><td></td><td></td><td>x</td></tr>
<tr><td>1127206</td><td>>gi|1127206|pdb|2CHR| Chloromuconate Cycloisomerase (Cmci) (E.C.5.5.1.7)</td><td></td><td></td><td>x</td></tr>
<tr><td>442737</td><td>>gi|442737|pdb|1CHR|B Chain B, Chloromuconate Cycloisomerase (E.C.5.5.1.7)</td><td></td><td></td><td>x</td></tr>
<tr><td>442736</td><td>>gi|442736|pdb|1CHR|A Chain A, Chloromuconate Cycloisomerase (E.C.5.5.1.7)</td><td></td><td></td><td>x</td></tr>
<tr><td>116506</td><td>>gi|116506|sp|P11452|CLCB_PSEPU Chloromuconate cycloisomerase (Muconate cycloisomerase II)</td><td></td><td></td><td>x</td></tr>
<tr><td>15026865</td><td>>gi|15026865|gb|AAK81674.1| chloromuconate cycloisomerase [Burkholderia cepacia]</td><td></td><td></td><td>x</td></tr>
<tr><td>6521701</td><td>>gi|6521701|dbj|BAA88065.1| chloromuconate cycloisomerase [Variovorax paradoxus]</td><td></td><td></td><td>x</td></tr>
<tr><td>14209510</td><td>>gi|14209510|dbj|BAB56010.1| chloromuconate cycloisomerase [Burkholderia sp. NK8]</td><td></td><td></td><td>x</td></tr>
<tr><td>26185980</td><td>>gi|26185980|emb|CAD56207.1| chloromuconate cycloisomerase [Achromobacter xylosoxidans]</td><td></td><td></td><td>x</td></tr>
<tr><td>19386505</td><td>>gi|19386505|gb|AAK57008.2| chloromuconate cycloisomerase [Delftia acidovorans]</td><td></td><td></td><td>x</td></tr>
<tr><td>44888544</td><td>>gi|44888544|sp|Q9RNZ9|TFDD_COMAC Chloromuconate cycloisomerase</td><td></td><td></td><td>x</td></tr>
<tr><td>58616645</td><td>>gi|58616645|ref|YP_195854.1| chloromuconate cycloisomerase [Achromobacter xylosoxidans]</td><td></td><td></td><td>x</td></tr>
<tr><td>54035685</td><td>>gi|54035685|sp|P83763|CBNB_RALEU Chloromuconate cycloisomerase cbnB (Muconate cycloisomerase II cbnB)</td><td></td><td></td><td>x</td></tr>
<tr><td>4210466</td><td>>gi|4210466|dbj|BAA74531.1| chloromuconate cycloisomerase [Ralstonia eutropha]</td><td></td><td></td><td>x</td></tr>
<tr><td>135517</td><td>>gi|135517|sp|P27099|TCBD_PSESQ Chloromuconate cycloisomerase (Muconate cycloisomerase II)</td><td></td><td></td><td>x</td></tr>
<tr><td>151578</td><td>>gi|151578|gb|AAD13626.1| cycloisomerase II [Pseudomonas sp.]</td><td></td><td></td><td>x</td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>40889146</td><td>>gi|40889146|pdb|1NU5|A Chain A, Crystal Structure Of Pseudomonas Sp. P51 Chloromuconate Lactonizing Enzyme</td><td></td><td></td><td>x</td></tr>
<tr><td>2935031</td><td>>gi|2935031|gb|AAC38249.1| chloromuconate cycloisomerase [Rhodococcus opacus]</td><td></td><td></td><td>x</td></tr>
<tr><td>6002915</td><td>>gi|6002915|gb|AAF00196.1| chloromuconate cycloisomerase [Pseudomonas aeruginosa]</td><td></td><td></td><td>x</td></tr>
<tr><td>3643989</td><td>>gi|3643989|gb|AAC69475.1| chloromuconate cycloisomerase [Pseudomonas aeruginosa]</td><td></td><td></td><td>x</td></tr>
<tr><td>40019136</td><td>>gi|40019136|emb|CAE92860.1| chloromuconate cycloisomerase [Pseudomonas putida]</td><td></td><td></td><td>x</td></tr>
<tr><td>6002924</td><td>>gi|6002924|gb|AAF00202.1| chloromuconate cycloisomerase [Pseudomonas aeruginosa]</td><td></td><td></td><td>x</td></tr>
<tr><td>23094408</td><td>>gi|23094408|emb|CAD28144.1| chloromuconate cycloisomerase [Rhodococcus opacus]</td><td></td><td></td><td>x</td></tr>
<tr><td>141917</td><td>>gi|141917|gb|AAA98282.1| muconate cycloisomerase II</td><td></td><td></td><td>x</td></tr>
<tr><td>151123</td><td>>gi|151123|gb|AAA25765.1| cis,cis-muconate lactonizing enzyme I (E.C. 5.5.1.1)</td><td></td><td></td><td>x</td></tr>
<tr><td>151125</td><td>>gi|151125|gb|AAA25766.1| cis,cis-muconate lactonizing enzyme I (EC 5.5.1.1)</td><td></td><td></td><td>x</td></tr>
<tr><td>13399453</td><td>>gi|13399453|pdb|1F9C|B Chain B, Crystal Structure Of Mle D178n Variant</td><td></td><td></td><td>x</td></tr>
<tr><td>13399452</td><td>>gi|13399452|pdb|1F9C|A Chain A, Crystal Structure Of Mle D178n Variant</td><td></td><td></td><td>x</td></tr>
<tr><td>3419684</td><td>>gi|3419684|gb|AAC31766.1| cic,cis-muconate lactonizing enzyme I [Acinetobacter lwoffii K24]</td><td></td><td></td><td>x</td></tr>
<tr><td>115713</td><td>>gi|115713|sp|P08310|CATB_PSEPU Muconate cycloisomerase I (Cis,cis-muconate lactonizing enzyme I) (MLE)</td><td></td><td></td><td>x</td></tr>
<tr><td>225599</td><td>>gi|225599|prf||1307186A muconate lactonizing enzyme I</td><td></td><td></td><td>x</td></tr>
<tr><td>2589174</td><td>>gi|2589174|gb|AAC46226.1| cic,cis-muconate lactonizing enzyme I [Acinetobacter lwoffii K24]</td><td></td><td></td><td>x</td></tr>
<tr><td>6014740</td><td>>gi|6014740|sp|O33946|CATB1_ACILW Muconate cycloisomerase I 1 (Cis,cis-muconate lactonizing enzyme I 1) (MLE 1)</td><td></td><td></td><td>x</td></tr>
<tr><td>49530597</td><td>>gi|49530597|emb|CAG68309.1| muconate cycloisomerase I (Cis,cis-muconate lactonizing enzyme I) (MLE) [Acinetobacter sp. ADP1]</td><td></td><td></td><td>x</td></tr>
<tr><td>50084621</td><td>>gi|50084621|ref|YP_046131.1| muconate cycloisomerase I (Cis,cis-muconate lactonizing enzyme I) (MLE) [Acinetobacter sp. ADP1]</td><td></td><td></td><td>x</td></tr>
<tr><td>51704317</td><td>>gi|51704317|sp|Q43931|CATB_ACIAD Muconate cycloisomerase I (Cis,cis-muconate lactonizing enzyme I) (MLE)</td><td></td><td></td><td>x</td></tr>
<tr><td>1771524</td><td>>gi|1771524|emb|CAA67934.1| muconate cycloisomerase [Rhodococcus opacus]</td><td></td><td></td><td>x</td></tr>
<tr><td>5915882</td><td>>gi|5915882|sp|P95608|CATB_RHOOP Muconate cycloisomerase I (Cis,cis-muconate lactonizing enzyme I) (MLE)</td><td></td><td></td><td>x</td></tr>
<tr><td>3891690</td><td>>gi|3891690|pdb|1BKH|A Chain A, Muconate Lactonizing Enzyme From Pseudomonas Putida</td><td></td><td></td><td>x</td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>3891691</td><td>>gi|3891691|pdb|1BKH|B Chain B, Muconate Lactonizing Enzyme From Pseudomonas Putida</td><td></td><td></td><td>x</td></tr>
<tr><td>3891692</td><td>>gi|3891692|pdb|1BKH|C Chain C, Muconate Lactonizing Enzyme From Pseudomonas Putida</td><td></td><td></td><td>x</td></tr>
<tr><td>6730024</td><td>>gi|6730024|pdb|2MUC|B Chain B, Muconate Cycloisomerase Variant F329i</td><td></td><td></td><td>x</td></tr>
<tr><td>6730023</td><td>>gi|6730023|pdb|2MUC|A Chain A, Muconate Cycloisomerase Variant F329i</td><td></td><td></td><td>x</td></tr>
<tr><td>6730036</td><td>>gi|6730036|pdb|3MUC|B Chain B, Muconate Cycloisomerase Variant I54v</td><td></td><td></td><td>x</td></tr>
<tr><td>6730035</td><td>>gi|6730035|pdb|3MUC|A Chain A, Muconate Cycloisomerase Variant I54v</td><td></td><td></td><td>x</td></tr>
<tr><td>82735481</td><td>>gi|82735481|ref|ZP_00898343.1| muconate cycloisomerase [Pseudomonas putida F1]</td><td></td><td></td><td>x</td></tr>
<tr><td>82717114</td><td>>gi|82717114|gb|EAP52166.1| muconate cycloisomerase [Pseudomonas putida F1]</td><td></td><td></td><td>x</td></tr>
<tr><td>83749259</td><td>>gi|83749259|ref|ZP_00946259.1| Muconate cycloisomerase [Ralstonia solanacearum UW551]</td><td></td><td></td><td>x</td></tr>
<tr><td>83724099</td><td>>gi|83724099|gb|EAP71277.1| Muconate cycloisomerase [Ralstonia solanacearum UW551]</td><td></td><td></td><td>x</td></tr>
<tr><td>83716982</td><td>>gi|83716982|ref|YP_438685.1| muconate cycloisomerase [Burkholderia thailandensis E264]</td><td></td><td></td><td>x</td></tr>
<tr><td>83650807</td><td>>gi|83650807|gb|ABC34871.1| muconate cycloisomerase [Burkholderia thailandensis E264]</td><td></td><td></td><td>x</td></tr>
<tr><td>69936817</td><td>>gi|69936817|ref|ZP_00631572.1| Muconate cycloisomerase [Paracoccus denitrificans PD1222]</td><td></td><td></td><td>x</td></tr>
<tr><td>69151840</td><td>>gi|69151840|gb|EAN65022.1| Muconate cycloisomerase [Paracoccus denitrificans PD1222]</td><td></td><td></td><td>x</td></tr>
<tr><td>2996615</td><td>>gi|2996615|gb|AAC46430.1| muconate cycloisomerase [Acinetobacter sp. ADP1]</td><td></td><td></td><td>x</td></tr>
<tr><td>740997</td><td>>gi|740997|prf||2006268E muconate cycloisomerase</td><td></td><td></td><td>x</td></tr>
<tr><td>1633162</td><td>>gi|1633162|pdb|1MUC|B Chain B, Structure Of Muconate Lactonizing Enzyme At 1.85 Angstroms Resolution</td><td></td><td></td><td>x</td></tr>
<tr><td>1633161</td><td>>gi|1633161|pdb|1MUC|A Chain A, Structure Of Muconate Lactonizing Enzyme At 1.85 Angstroms Resolution</td><td></td><td></td><td>x</td></tr>
<tr><td>68345520</td><td>>gi|68345520|gb|AAY93126.1| muconate cycloisomerase [Pseudomonas fluorescens Pf-5]</td><td></td><td></td><td>x</td></tr>
<tr><td>70731221</td><td>>gi|70731221|ref|YP_260962.1| muconate cycloisomerase [Pseudomonas fluorescens Pf-5]</td><td></td><td></td><td>x</td></tr>
<tr><td>77362681</td><td>>gi|77362681|dbj|BAE46388.1| cis,cis-muconate cycloisomerase [Rhodococcus sp. AN-22]</td><td>ESA</td><td></td><td>x</td></tr>
<tr><td>67665468</td><td>>gi|67665468|ref|ZP_00462731.1| Muconate cycloisomerase [Burkholderia cenocepacia HI2424]</td><td></td><td></td><td>x</td></tr>
<tr><td>67656859</td><td>>gi|67656859|ref|ZP_00454240.1| Muconate cycloisomerase [Burkholderia cenocepacia AU 1054]</td><td></td><td></td><td>x</td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
67101001	>gi|67101001|gb|EAM18148.1| Muconate cycloisomerase [Burkholderia cenocepacia HI2424]			x
67095576	>gi|67095576|gb|EAM13104.1| Muconate cycloisomerase [Burkholderia cenocepacia AU 1054]			x
34392416	>gi|34392416|dbj|BAC82532.1| muconate cycloisomerase [Frateuria sp. ANA-18]			x
4579699	>gi|4579699|dbj|BAA75205.1| muconate cycloisomerase [Frateuria sp. ANA-18]			x
4579705	>gi|4579705|dbj|BAA75210.1| muconate cycloisomerase [Frateuria sp. ANA-18]			x
12539415	>gi|12539415|dbj|BAB21460.1| muconate cycloisomerase [Burkholderia sp. NK8]			x
607908	>gi|607908|gb|AAA66202.1| muconate lactonizing enzyme			x
23494145	>gi|23494145|dbj|BAC19113.1| putative muconate cycloisomerase [Corynebacterium efficiens YS-314]			x
25028859	>gi|25028859|ref|NP_738913.1| putative muconate cycloisomerase [Corynebacterium efficiens YS-314]			x
76583804	>gi|76583804|gb|ABA53278.1| muconate cycloisomerase [Burkholderia pseudomallei 1710b]			x
76819331	>gi|76819331|ref|YP_336144.1| muconate cycloisomerase [Burkholderia pseudomallei 1710b]			x
52422485	>gi|52422485|gb|AAU46055.1| muconate cycloisomerase [Burkholderia mallei ATCC 23344]			x
53716515	>gi|53716515|ref|YP_105027.1| muconate cycloisomerase [Burkholderia mallei ATCC 23344]			x
9948563	>gi|9948563|gb|AAG05897.1| muconate cycloisomerase I [Pseudomonas aeruginosa PAO1]			x
15597705	>gi|15597705|ref|NP_251199.1| muconate cycloisomerase I [Pseudomonas aeruginosa PAO1]			x
23491535	>gi|23491535|dbj|BAC16768.1| cis,cis-muconate lactonizing enzyme [Burkholderia sp. TH2]			x
23491545	>gi|23491545|dbj|BAC16777.1| cis,cis-muconate lactonizing enzyme [Burkholderia sp. TH2]			x
26990423	>gi|26990423|ref|NP_745848.1| muconate cycloisomerase [Pseudomonas putida KT2440]			x
24985391	>gi|24985391|gb|AAN69312.1| muconate cycloisomerase [Pseudomonas putida KT2440]			x
77971060	>gi|77971060|gb|ABB12439.1| Muconate cycloisomerase [Burkholderia sp. 383]			x
78063175	>gi|78063175|ref|YP_373083.1| Muconate cycloisomerase [Burkholderia sp. 383]			x
52213326	>gi|52213326|emb|CAH39369.1| muconate cycloisomerase I [Burkholderia pseudomallei K96243]			x
53722912	>gi|53722912|ref|YP_111897.1| muconate cycloisomerase I [Burkholderia pseudomallei K96243]			x
42627730	>gi|42627730|dbj|BAD11152.1| cis,cis-muconate cycloisomerase [Arthrobacter sp. BA-5-17]	ESA		x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
12862418	>gi|12862418|dbj|BAB32456.1| cis,cis-muconate cycloisomerase CatB [Pseudomonas sp. CA10]			x
14132758	>gi|14132758|gb|AAK52296.1| putative muconate cycloisomerase I CatB [Pseudomonas putida]			x
11967279	>gi|11967279|gb|AAG42035.1| putative muconate cycloisomerase [Ralstonia eutropha]			x
13660733	>gi|13660733|gb|AAK33064.1| cis,cis-muconate lactonizing enzyme [Pseudomonas putida]			x
56710236	>gi|56710236|dbj|BAD80960.1| muconate lactonizing enzyme I [uncultured bacterium]			x
38638055	>gi|38638055|ref|NP_943029.1| putative muconate cycloisomerase [Cupriavidus necator]			x
32527393	>gi|32527393|gb|AAP86143.1| putative muconate cycloisomerase [Ralstonia eutropha]			x
38638066	>gi|38638066|ref|NP_943040.1| putative muconate cycloisomerase [Cupriavidus necator]			x
32527404	>gi|32527404|gb|AAP86154.1| putative muconate cycloisomerase [Ralstonia eutropha]			x
60594324	>gi|60594324|pdb|1YEY|D Chain D, Crystal Structure Of L-Fuconate Dehydratase From Xanthomonas Campestris Pv. Campestris Str. Atcc 33913			x
1169205	>gi|1169205|sp|P42125|D3D2_MOUSE 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor (Dodecenoyl-CoA isomerase) (Delta(3),delta(2)-enoyl-CoA isomerase) (D3,D2-enoyl-CoA isomerase)			x
817974	>gi|817974|emb|CAA78418.1| dodecenoyl-CoA delta isomerase [Mus musculus]			x
414902	>gi|414902|emb|CAA78417.1| dodecenoyl-CoA delta-isomerase [Mus musculus]			x
62530384	>gi|62530384|ref|NP_001910.2| dodecenoyl-Coenzyme A delta isomerase precursor [Homo sapiens]			x
1169204	>gi|1169204|sp|P42126|D3D2_HUMAN 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor (Dodecenoyl-CoA isomerase) (Delta(3),delta(2)-enoyl-CoA isomerase) (D3,D2-enoyl-CoA isomerase)			x
825689	>gi|825689|emb|CAA81066.1| dodecenoyl-CoA delta-isomerase [Homo sapiens]			x
8393243	>gi|8393243|ref|NP_059002.1| dodecenoyl-coenzyme A delta isomerase [Rattus norvegicus]			x
57333	>gi|57333|emb|CAA43488.1| 3-2trans-enoyl-CoA isomerase [Rattus norvegicus]			x
118210	>gi|118210|sp|P23965|D3D2_RAT 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor (Dodecenoyl-CoA isomerase) (Delta(3),delta(2)-enoyl-CoA isomerase) (D3,D2-enoyl-CoA isomerase)			x
56967286	>gi|56967286|pdb|1XX4|A Chain A, Crystal Structure Of Rat Mitochondrial 3,2-Enoyl-Coa			x
472987	>gi|472987|emb|CAA81065.1| dodecenoyl-CoA delta-isomerase [Homo sapiens]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
6015047	>gi|6015047|sp|Q62651|ECH1_RAT Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor			x
75055278	>gi|75055278|sp|Q5RFG0|ECH1_PONPY Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor			x
82654933	>gi|82654933|sp|Q13011|ECH1_HUMAN Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor			x
3122065	>gi|3122065|sp|O35459|ECH1_MOUSE Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor			x
4699609	>gi|4699609|pdb|1DCI|C Chain C, Dienoyl-Coa Isomerase			x
4699608	>gi|4699608|pdb|1DCI|B Chain B, Dienoyl-Coa Isomerase			x
4699607	>gi|4699607|pdb|1DCI|A Chain A, Dienoyl-Coa Isomerase			x
18307432	>gi|18307432|emb|CAD21495.1| probable DELTA3, 5-DELTA2, 4-DIENOYL-COA ISOMERASE PRECURSOR (ECH1) [Neurospora crassa]			x
2623168	>gi|2623168|gb|AAB86485.1| putative dienoyl-CoA isomerase [Homo sapiens]			x
85675730	>gi|85675730|dbj|BAE76983.1| methylmalonyl-CoA decarboxylase, biotin-independent [Escherichia coli W3110]			x
1723839	>gi|1723839|sp|P52045|MMCD_ECOLI Methylmalonyl-CoA decarboxylase (Transcarboxylase) (MMCD)			x
8569417	>gi|8569417|pdb|1EF9|A Chain A, The Crystal Structure Of Methylmalonyl Coa Decarboxylase Complexed With 2s-Carboxypropyl Coa			x
8569416	>gi|8569416|pdb|1EF8|C Chain C, Crystal Structure Of Methylmalonyl Coa Decarboxylase			x
8569415	>gi|8569415|pdb|1EF8|B Chain B, Crystal Structure Of Methylmalonyl Coa Decarboxylase			x
8569414	>gi|8569414|pdb|1EF8|A Chain A, Crystal Structure Of Methylmalonyl Coa Decarboxylase			x
49176283	>gi|49176283|ref|NP_417394.3| methylmalonyl-CoA decarboxylase, biotin-independent [Escherichia coli K12]			x
83747299	>gi|83747299|ref|ZP_00944340.1| 3-hydroxyisobutyryl-CoA hydrolase [Ralstonia solanacearum UW551]			x
83725999	>gi|83725999|gb|EAP73136.1| 3-hydroxyisobutyryl-CoA hydrolase [Ralstonia solanacearum UW551]			x
83749668	>gi|83749668|ref|ZP_00946649.1| 3-hydroxyisobutyryl-CoA hydrolase [Ralstonia solanacearum UW551]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
83723670	>gi|83723670|gb|EAP70867.1| 3-hydroxyisobutyryl-CoA hydrolase [Ralstonia solanacearum UW551]			x
79332547	>gi|79332547|ref|NP_001032155.1| CHY1 (BETA-HYDROXYISOBUTYRYL-COA HYDROLASE 1); 3-hydroxyisobutyryl-CoA hydrolase [Arabidopsis thaliana]			x
15239206	>gi|15239206|ref|NP_201395.1| CHY1 (BETA-HYDROXYISOBUTYRYL-COA HYDROLASE 1); 3-hydroxyisobutyryl-CoA hydrolase [Arabidopsis thaliana]			x
24030391	>gi|24030391|gb|AAN41356.1| putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]			x
9759578	>gi|9759578|dbj|BAB11141.1| 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]			x
42565158	>gi|42565158|ref|NP_189079.2| 3-hydroxyisobutyryl-CoA hydrolase/ catalytic [Arabidopsis thaliana]			x
30679729	>gi|30679729|ref|NP_172142.2| 3-hydroxyisobutyryl-CoA hydrolase/ catalytic [Arabidopsis thaliana]			x
62320504	>gi|62320504|dbj|BAD95058.1| 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]			x
66851010	>gi|66851010|gb|EAL91336.1| mitochondrial 3-hydroxyisobutyryl-CoA hydrolase, putative [Aspergillus fumigatus Af293]			x
70997244	>gi|70997244|ref|XP_753374.1| mitochondrial 3-hydroxyisobutyryl-CoA hydrolase [Aspergillus fumigatus Af293]			x
22329062	>gi|22329062|ref|NP_194909.2| 3-hydroxyisobutyryl-CoA hydrolase/ catalytic [Arabidopsis thaliana]			x
77554202	>gi|77554202|gb|ABA96998.1| 3-hydroxyisobutyryl-coenzyme A hydrolase, putative [Oryza sativa (japonica cultivar-group)]			x
77554203	>gi|77554203|gb|ABA96999.1| 3-hydroxyisobutyryl-coenzyme A hydrolase, putative [Oryza sativa (japonica cultivar-group)]			x
84717486	>gi|84717486|ref|ZP_01023545.1| probable enoyl(3-hydroxyisobutyryl)-coenzyme A hydratase protein [Polaromonas naphthalenivorans CJ2]			x
84692147	>gi|84692147|gb|EAQ17970.1| probable enoyl(3-hydroxyisobutyryl)-coenzyme A hydratase protein [Polaromonas naphthalenivorans CJ2]			x
37594469	>gi|37594469|ref|NP_932164.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase isoform 2 [Homo sapiens]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
29895975	>gi|29895975|gb|AAP09256.1| 3-hydroxyisobutyryl-coenzyme A hydrolase [Bacillus cereus ATCC 14579]			x
14027690	>gi|14027690|dbj|BAB54283.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase [Mesorhizobium loti MAFF303099]			x
49238423	>gi|49238423|emb|CAF27650.1| 3-hydroxyisobutyryl-coenzyme A hydrolase [Bartonella henselae str. Houston-1]			x
51976589	>gi|51976589|gb|AAU18139.1| 3-hydroxyisobutyryl-coenzyme A hydrolase [Bacillus cereus E33L]			x
52628217	>gi|52628217|gb|AAU26958.1| 3-hydroxyisobutyryl Coenzyme A hydrolase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]			x
52841106	>gi|52841106|ref|YP_094905.1| 3-hydroxyisobutyryl Coenzyme A hydrolase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]			x
3320120	>gi|3320120|gb|AAC52114.1| 3-hydroxyisobutyryl-coenzyme A hydrolase [Homo sapiens]			x
53733532	>gi|53733532|gb|AAH83737.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase (predicted) [Rattus norvegicus]			x
61556993	>gi|61556993|ref|NP_001013130.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase (predicted) [Rattus norvegicus]			x
17428312	>gi|17428312|emb|CAD15000.1| PROBABLE ENOYL(3-HYDROXYISOBUTYRYL)-COENZYME A HYDRATASE PROTEIN [Ralstonia solanacearum]			x
49329189	>gi|49329189|gb|AAT59835.1| 3-hydroxyisobutyryl-coenzyme A hydrolase [Bacillus thuringiensis serovar konkukian str. 97-27]			x
50725651	>gi|50725651|dbj|BAD33117.1| putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Oryza sativa (japonica cultivar-group)]			x
50725401	>gi|50725401|dbj|BAD32875.1| putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Oryza sativa (japonica cultivar-group)]			x
62897519	>gi|62897519|dbj|BAD96699.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase isoform 1 variant [Homo sapiens]			x
62897607	>gi|62897607|dbj|BAD96743.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase isoform 1 variant [Homo sapiens]			x
2880043	>gi|2880043|gb|AAC02737.1| 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
2880042	>gi|2880042|gb|AAC02736.1| 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]			x
22122625	>gi|22122625|ref|NP_666220.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase [Mus musculus]			x
20071741	>gi|20071741|gb|AAH26437.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase [Mus musculus]			x
45767881	>gi|45767881|gb|AAH67822.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase, isoform 1 [Homo sapiens]			x
61403546	>gi|61403546|gb|AAH91995.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase [Danio rerio]			x
62122813	>gi|62122813|ref|NP_001014338.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase [Danio rerio]			x
71895123	>gi|71895123|ref|NP_001026414.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase [Gallus gallus]			x
37594471	>gi|37594471|ref|NP_055177.2| 3-hydroxyisobutyryl-Coenzyme A hydrolase isoform 1 [Homo sapiens]			x
419529	>gi|419529|pir||A42560 4-chlorobenzoate dehalogenase (EC 3.8.1.6), 30K chain - Pseudomonas sp. (strain CBS-3)			x
4584855	>gi|4584855|gb|AAD25164.1| 4-chlorobenzoyl CoA dehalogenase [Arthrobacter sp. SU]			x
8517279	>gi|8517279|gb|AAF76241.1| 4-chlorobenzoyl CoA dehalogenase [Arthrobacter sp. TM1]			x
11991170	>gi|11991170|gb|AAG42236.1| 4-chlorobenzoate Co-A dehalogenase [Arthrobacter globiformis]			x
142207	>gi|142207|gb|AAC80223.1| 4-chlorobenzoyl CoA dehalogenase [Arthrobacter sp. SU]			x
477389	>gi|477389|pir||A48956 4-chlorobenzoate-CoA dehalogenase - Arthrobacter sp			x
2392483	>gi|2392483|pdb|1NZY|B Chain B, 4-Chlorobenzoyl Coenzyme A Dehalogenase From Pseudomonas Sp. Strain Cbs-3			x
2392484	>gi|2392484|pdb|1NZY|C Chain C, 4-Chlorobenzoyl Coenzyme A Dehalogenase From Pseudomonas Sp. Strain Cbs-3			x
2392482	>gi|2392482|pdb|1NZY|A Chain A, 4-Chlorobenzoyl Coenzyme A Dehalogenase From Pseudomonas Sp. Strain Cbs-3			x
2952540	>gi|2952540|gb|AAC05576.1| 4-chlorobenzoyl CoA dehalogenase [Pseudomonas sp. DJ-12]			x
8712875	>gi|8712875|gb|AAF78820.1| 4-chlorobenzoyl CoA dehalogenase [Arthrobacter sp. TM1]			x
22901870	>gi|22901870|gb|AAN10108.1| 4-chlorobenzoyl CoA dehalogenase [Alcaligenes sp. AL3007]			x
13516855	>gi|13516855|dbj|BAB40580.1| 4-CBA-CoA dehalogenase [Arthrobacter sp. FHP1]			x
13516852	>gi|13516852|dbj|BAB40577.1| 4-CBA-CoA dehalogenase [Arthrobacter sp. FHP1]			x
15826387	>gi|15826387|pdb|1JC4|D Chain D, Crystal Structure Of Se-Met Methylmalonyl-Coa Epimerase			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
21314762	>gi|21314762|ref|NP_115990.2| methylmalonyl-CoA epimerase [Homo sapiens]			x
22022367	>gi|22022367|gb|AAL02261.1| methylmalonyl-CoA epimerase [Propionibacterium freudenreichii subsp. shermanii]			x
14010614	>gi|14010614|gb|AAK52052.1| methylmalonyl-CoA epimerase [Homo sapiens]			x
14010616	>gi|14010616|gb|AAK52053.1| methylmalonyl-CoA epimerase [Pyrococcus horikoshii]			x
52695751	>gi|52695751|pdb|1TG5|A Chain A, Crystal Structures Of Plant 4-Hydroxyphenylpyruvate Dioxygenases Complexed With Das645			x
55669756	>gi|55669756|pdb|1SP8|D Chain D, 4-Hydroxyphenylpyruvate Dioxygenase			x
74846152	>gi|74846152|sp|Q60Y65|HPPD_CAEBR 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase)			x
82735751	>gi|82735751|ref|ZP_00898613.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida F1]			x
82740811	>gi|82740811|ref|ZP_00903545.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. W3-18-1]			x
83746408	>gi|83746408|ref|ZP_00943460.1| 4-hydroxyphenylpyruvate dioxygenase [Ralstonia solanacearum UW551]			x
83855941	>gi|83855941|ref|ZP_00949470.1| 4-hydroxyphenylpyruvate dioxygenase [Croceibacter atlanticus HTCC2559]			x
83858849	>gi|83858849|ref|ZP_00952371.1| 4-hydroxyphenylpyruvate dioxygenase [Oceanicaulis alexandrii HTCC2633]			x
83942846	>gi|83942846|ref|ZP_00955307.1| 4-hydroxyphenylpyruvate dioxygenase [Sulfitobacter sp. EE-36]			x
83955679	>gi|83955679|ref|ZP_00964259.1| 4-hydroxyphenylpyruvate dioxygenase [Sulfitobacter sp. NAS-14.1]			x
84386189	>gi|84386189|ref|ZP_00989218.1| 4-hydroxyphenylpyruvate dioxygenase [Vibrio splendidus 12B01]			x
84494414	>gi|84494414|ref|ZP_00993533.1| putative 4-hydroxyphenylpyruvate dioxygenase [Janibacter sp. HTCC2649]			x
84500900	>gi|84500900|ref|ZP_00999135.1| 4-hydroxyphenylpyruvate dioxygenase [Oceanicola batsensis HTCC2597]			x
84715414	>gi|84715414|ref|ZP_01022515.1| 4-hydroxyphenylpyruvate dioxygenase [Polaromonas naphthalenivorans CJ2]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
13810184	>gi|13810184|emb|CAC37394.1| 4-hydroxyphenylpyruvate dioxygenase [Solenostemon scutellarioides]			x
83716682	>gi|83716682|ref|YP_439418.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia thailandensis E264]			x
83718326	>gi|83718326|ref|YP_440247.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Burkholderia thailandensis E264]			x
83720009	>gi|83720009|ref|YP_443601.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia thailandensis E264]			x
83643833	>gi|83643833|ref|YP_432268.1| 4-hydroxyphenylpyruvate dioxygenase [Hahella chejuensis KCTC 2396]			x
47567476	>gi|47567476|ref|ZP_00238188.1| 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus G9241]			x
47523532	>gi|47523532|ref|NP_999389.1| 4-hydroxyphenylpyruvic acid dioxygenase [Sus scrofa]			x
83816571	>gi|83816571|ref|YP_445494.1| 4-hydroxyphenylpyruvate dioxygenase [Salinibacter ruber DSM 13855]			x
69934333	>gi|69934333|ref|ZP_00629411.1| 4-hydroxyphenylpyruvate dioxygenase [Paracoccus denitrificans PD1222]			x
69951167	>gi|69951167|ref|ZP_00638934.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella frigidimarina NCIMB 400]			x
83744141	>gi|83744141|gb|ABC42332.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas chlororaphis]			x
29608808	>gi|29608808|dbj|BAC72861.1| 4-hydroxyphenylpyruvate dioxygenase [Streptomyces avermitilis MA-4680]			x
86360259	>gi|86360259|ref|YP_472148.1| putative 4-hydroxyphenylpyruvate dioxygenase protein [Rhizobium etli CFN 42]			x
85710284	>gi|85710284|ref|ZP_01041349.1| 4-hydroxyphenylpyruvate dioxygenase [Erythrobacter sp. NAP1]			x
85712096	>gi|85712096|ref|ZP_01043149.1| 4-hydroxyphenylpyruvate dioxygenase [Idiomarina baltica OS145]			x
86130810	>gi|86130810|ref|ZP_01049409.1| 4-hydroxyphenylpyruvate dioxygenase [Cellulophaga sp. MED134]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
86134911	>gi|86134911|ref|ZP_01053493.1| 4-hydroxyphenylpyruvate dioxygenase [Tenacibaculum sp. MED152]			x
86137851	>gi|86137851|ref|ZP_01056427.1| 4-hydroxyphenylpyruvate dioxygenase [Roseobacter sp. MED193]			x
86143740	>gi|86143740|ref|ZP_01062116.1| 4-hydroxyphenylpyruvate dioxygenase [Flavobacterium sp. MED217]			x
86144791	>gi|86144791|ref|ZP_01063123.1| 4-hydroxyphenylpyruvate dioxygenase [Vibrio sp. MED222]			x
86277802	>gi|86277802|gb|ABC88387.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas fluorescens]			x
86166180	>gi|86166180|gb|EAQ67446.1| 4-hydroxyphenylpyruvate dioxygenase [Marinomonas sp. MED121]			x
86357375	>gi|86357375|ref|YP_469267.1| probable 4-hydroxyphenylpyruvate dioxygenase protein [Rhizobium etli CFN 42]			x
68345050	>gi|68345050|gb|AAY92656.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas fluorescens Pf-5]			x
68346989	>gi|68346989|gb|AAY94595.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas fluorescens Pf-5]			x
71364775	>gi|71364775|ref|ZP_00655353.1| 4-hydroxyphenylpyruvate dioxygenase [Psychrobacter cryohalolentis K5]			x
71366476	>gi|71366476|ref|ZP_00657018.1| 4-hydroxyphenylpyruvate dioxygenase [Nocardioides sp. JS614]			x
71147316	>gi|71147316|gb|AAZ27789.1| 4-hydroxyphenylpyruvate dioxygenase [Colwellia psychrerythraea 34H]			x
72122197	>gi|72122197|gb|AAZ64383.1| 4-hydroxyphenylpyruvate dioxygenase [Ralstonia eutropha JMP134]			x
60552039	>gi|60552039|gb|AAH91035.1| Hpd-prov protein [Xenopus tropicalis]			x
84369443	>gi|84369443|dbj|BAE70601.1| 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas oryzae pv. oryzae MAFF 311018]			x
71557567	>gi|71557567|gb|AAZ36778.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. phaseolicola 1448A]			x
71557637	>gi|71557637|gb|AAZ36848.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas syringae pv. phaseolicola 1448A]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
5531376	>gi|5531376|emb|CAB51008.1| putative 4-hydroxyphenylpyruvate dioxygenase [Streptomyces coelicolor A3(2)]			x
28881241	>gi|28881241|emb|CAD70479.1| probable 4-hydroxyphenylpyruvate dioxygenase [Neurospora crassa]			x
62751490	>gi|62751490|ref|NP_001015611.1| 4-hydroxyphenylpyruvate dioxygenase [Bos taurus]			x
74016264	>gi|74016264|ref|ZP_00686890.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria AMMD]			x
74018538	>gi|74018538|ref|ZP_00689158.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria AMMD]			x
74020299	>gi|74020299|ref|ZP_00690899.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria AMMD]			x
75760149	>gi|75760149|ref|ZP_00740208.1| 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar israelensis ATCC 35646]			x
76883245	>gi|76883245|gb|ABA57926.1| 4-hydroxyphenylpyruvate dioxygenase [Nitrosococcus oceani ATCC 19707]			x
51980500	>gi|51980500|gb|AAH81819.1| 4-hydroxyphenylpyruvic acid dioxygenase [Rattus norvegicus]			x
76876002	>gi|76876002|emb|CAI87224.1| 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) [Pseudoalteromonas haloplanktis TAC125]			x
78034468	>gi|78034468|emb|CAJ22113.1| 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas campestris pv. vesicatoria str. 85-10]			x
52629602	>gi|52629602|gb|AAU28343.1| 4-hydroxyphenylpyruvate dioxygenase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]			x
76791393	>gi|76791393|ref|ZP_00773900.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudoalteromonas atlantica T6c]			x
76791947	>gi|76791947|ref|ZP_00774450.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudoalteromonas atlantica T6c]			x
77970360	>gi|77970360|gb|ABB11739.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. 383]			x
2231615	>gi|2231615|gb|AAC49815.1| 4-hydroxyphenylpyruvate dioxygenase [Daucus carota]			x
22136134	>gi|22136134|gb|AAM91145.1| 4-hydroxyphenylpyruvate dioxygenase (HPD) [Arabidopsis thaliana]			x
3334221	>gi|3334221|sp|O42764|HPPD_MYCGR 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase)			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
849053	>gi|849053|dbj|BAA06267.1| 4-hydroxyphenylpyruvate dioxygenase [Mus musculus]			x
69157650	>gi|69157650|gb|EAN69869.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella denitrificans OS217]			x
77816006	>gi|77816006|ref|ZP_00815218.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella putrefaciens CN-32]			x
55666795	>gi|55666795|ref|XP_528667.1| PREDICTED: 4-hydroxyphenylpyruvate dioxygenase [Pan troglodytes]			x
37681833	>gi|37681833|gb|AAQ97794.1| 4-hydroxyphenylpyruvate dioxygenase [Danio rerio]			x
78368776	>gi|78368776|ref|ZP_00838982.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. PV-4]			x
78691757	>gi|78691757|ref|ZP_00856354.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. MR-7]			x
78694655	>gi|78694655|ref|ZP_00859168.1| 4-hydroxyphenylpyruvate dioxygenase [Bradyrhizobium sp. BTAi1]			x
78696078	>gi|78696078|ref|ZP_00860588.1| 4-hydroxyphenylpyruvate dioxygenase [Bradyrhizobium sp. BTAi1]			x
66849398	>gi|66849398|gb|EAL89726.1| 4-hydroxyphenylpyruvate dioxygenase [Aspergillus fumigatus Af293]			x
66847183	>gi|66847183|gb|EAL87514.1| 4-hydroxyphenylpyruvate dioxygenase [Aspergillus fumigatus Af293]			x
67542525	>gi|67542525|ref|ZP_00420461.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia vietnamiensis G4]			x
67549551	>gi|67549551|ref|ZP_00427409.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia vietnamiensis G4]			x
67667845	>gi|67667845|ref|ZP_00465053.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia HI2424]			x
67664502	>gi|67664502|ref|ZP_00461775.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia HI2424]			x
67667262	>gi|67667262|ref|ZP_00464490.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia HI2424]			x
67928870	>gi|67928870|ref|ZP_00522055.1| 4-hydroxyphenylpyruvate dioxygenase [Solibacter usitatus Ellin6076]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
68182021	>gi|68182021|ref|ZP_00555002.1| 4-hydroxyphenylpyruvate dioxygenase [Jannaschia sp. CCS1]			x
68232050	>gi|68232050|ref|ZP_00571206.1| 4-hydroxyphenylpyruvate dioxygenase [Frankia sp. EAN1pec]			x
68189545	>gi|68189545|gb|EAN04210.1| 4-hydroxyphenylpyruvate dioxygenase [Mesorhizobium sp. BNC1]			x
68540317	>gi|68540317|ref|ZP_00580078.1| 4-hydroxyphenylpyruvate dioxygenase [Sphingopyxis alaskensis RB2256]			x
68542976	>gi|68542976|ref|ZP_00582695.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella baltica OS155]			x
68547720	>gi|68547720|ref|ZP_00587251.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella amazonensis SB2B]			x
28869544	>gi|28869544|ref|NP_792163.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas syringae pv. tomato str. DC3000]			x
28870714	>gi|28870714|ref|NP_793333.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. tomato str. DC3000]			x
66045370	>gi|66045370|ref|YP_235211.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. syringae B728a]			x
66046559	>gi|66046559|ref|YP_236400.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. syringae B728a]			x
4504477	>gi|4504477|ref|NP_002141.1| 4-hydroxyphenylpyruvate dioxygenase [Homo sapiens]			x
3334224	>gi|3334224|sp|Q00415|HPPD_COCIM 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) (T-cell reactive protein)			x
3334226	>gi|3334226|sp|Q27203|HPPD_TETTH 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) (F-antigen homolog) (TF-AG)			x
50057356	>gi|50057356|emb|CAH03340.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Paramecium tetraurelia]			x
21111421	>gi|21111421|gb|AAM39754.1| 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas campestris pv. campestris str. ATCC 33913]			x
28806337	>gi|28806337|dbj|BAC59612.1| 4-hydroxyphenylpyruvate dioxygenase [Vibrio parahaemolyticus RIMD 2210633]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
27348587	>gi|27348587|dbj|BAC45604.1| 4-hydroxyphenylpyruvate dioxygenase [Bradyrhizobium japonicum USDA 110]			x
29894029	>gi|29894029|gb|AAP07321.1| 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus ATCC 14579]			x
54018563	>gi|54018563|dbj|BAD59933.1| putative 4-hydroxyphenylpyruvate dioxygenase [Nocardia farcinica IFM 10152]			x
39577105	>gi|39577105|emb|CAE78334.1| 4-hydroxyphenylpyruvate dioxygenase [Bdellovibrio bacteriovorus HD100]			x
15075967	>gi|15075967|emb|CAC47521.1| PUTATIVE 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE PROTEIN [Sinorhizobium meliloti]			x
14027622	>gi|14027622|dbj|BAB53891.1| 4-hydroxyphenylpyruvate dioxygenase [Mesorhizobium loti MAFF303099]			x
56178841	>gi|56178841|gb|AAV81563.1| 4-hydroxyphenylpyruvate dioxygenase [Idiomarina loihiensis L2TR]			x
53754956	>gi|53754956|emb|CAH16444.1| 4-hydroxyphenylpyruvate dioxygenase (legiolysin) [Legionella pneumophila str. Lens]			x
53751960	>gi|53751960|emb|CAH13384.1| 4-hydroxyphenylpyruvate dioxygenase (legiolysin) [Legionella pneumophila str. Paris]			x
15426479	>gi|15426479|gb|AAH13343.1| 4-hydroxyphenylpyruvic acid dioxygenase [Mus musculus]			x
58583694	>gi|58583694|ref|YP_202710.1| 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas oryzae pv. oryzae KACC10331]			x
248959	>gi|248959|gb|AAB22111.1| 4-hydroxyphenylpyruvate dioxygenase {EC 1.13.11.27} [Pseudomonas, P.J. 874, Peptide, 357 aa]			x
26989274	>gi|26989274|ref|NP_744699.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas putida KT2440]			x
34496424	>gi|34496424|ref|NP_900639.1| 4-hydroxyphenylpyruvate dioxygenase [Chromobacterium violaceum ATCC 12472]			x
9946763	>gi|9946763|gb|AAG04254.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas aeruginosa PAO1]			x
26990146	>gi|26990146|ref|NP_745571.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida KT2440]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
69298020	>gi|69298020|ref|ZP_00620300.1| 4-hydroxyphenylpyruvate dioxygenase [Silicibacter sp. TM1040]			x
62003087	>gi|62003087|gb|AAX59006.1| 4-hydroxyphenylpyruvate dioxygenase [Medicago truncatula]			x
68192496	>gi|68192496|gb|EAN07150.1| 4-hydroxyphenylpyruvate dioxygenase [Mesorhizobium sp. BNC1]			x
24373526	>gi|24373526|ref|NP_717569.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella oneidensis MR-1]			x
21106538	>gi|21106538|gb|AAM35343.1| 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas axonopodis pv. citri str. 306]			x
56678047	>gi|56678047|gb|AAV94713.1| 4-hydroxyphenylpyruvate dioxygenase [Silicibacter pomeroyi DSS-3]			x
39652710	>gi|39652710|emb|CAE25449.1| 4-hydroxyphenylpyruvate dioxygenase [Rhodopseudomonas palustris CGA009]			x
72121665	>gi|72121665|gb|AAZ63851.1| 4-hydroxyphenylpyruvate dioxygenase [Ralstonia eutropha JMP134]			x
72122190	>gi|72122190|gb|AAZ64376.1| 4-hydroxyphenylpyruvate dioxygenase [Ralstonia eutropha JMP134]			x
17430127	>gi|17430127|emb|CAD16812.1| PROBABLE 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE OXIDOREDUCTASE PROTEIN [Ralstonia solanacearum]			x
17431820	>gi|17431820|emb|CAD18498.1| PROBABLE 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE OXIDOREDUCTASE PROTEIN [Ralstonia solanacearum]			x
77965642	>gi|77965642|gb|ABB07022.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. 383]			x
77969080	>gi|77969080|gb|ABB10459.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. 383]			x
46916283	>gi|46916283|emb|CAG23052.1| putative 4-hydroxyphenylpyruvate dioxygenase [Photobacterium profundum SS9]			x
84787193	>gi|84787193|gb|ABC63375.1| 4-hydroxyphenylpyruvate dioxygenase [Erythrobacter litoralis HTCC2594]			x
13424094	>gi|13424094|gb|AAK24504.1| 4-hydroxyphenylpyruvate dioxygenase [Caulobacter crescentus CB15]			x
77383145	>gi|77383145|gb|ABA74658.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas fluorescens PfO-1]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
77385129	>gi|77385129|gb|ABA76642.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas fluorescens PfO-1]			x
50905533	>gi|50905533|ref|XP_464255.1| putative 4-hydroxyphenylpyruvate dioxygenase [Oryza sativa (japonica cultivar-group)]			x
18104608	>gi|18104608|gb|AAL59614.1| 4-hydroxyphenylpyruvate dioxygenase [Listonella anguillarum]			x
22530912	>gi|22530912|gb|AAM96960.1| 4-hydroxyphenylpyruvate dioxygenase HPD [Arabidopsis thaliana]			x
31324014	>gi|31324014|gb|AAP47152.1| 4-hydroxyphenylpyruvate dioxygenase [uncultured soil bacterium]			x
76261015	>gi|76261015|ref|ZP_00768638.1| 4-hydroxyphenylpyruvate dioxygenase [Chloroflexus aurantiacus J-10-fl]			x
79040915	>gi|79040915|ref|ZP_00872288.1| 4-hydroxyphenylpyruvate dioxygenase [Novosphingobium aromaticivorans DSM 12444]			x
79039649	>gi|79039649|ref|ZP_00871355.1| 4-hydroxyphenylpyruvate dioxygenase [Novosphingobium aromaticivorans DSM 12444]			x
67157862	>gi|67157862|ref|ZP_00419007.1| 4-hydroxyphenylpyruvate dioxygenase [Azotobacter vinelandii AvOP]			x
67156324	>gi|67156324|ref|ZP_00417917.1| 4-hydroxyphenylpyruvate dioxygenase [Azotobacter vinelandii AvOP]			x
67155173	>gi|67155173|ref|ZP_00416801.1| 4-hydroxyphenylpyruvate dioxygenase [Azotobacter vinelandii AvOP]			x
67542103	>gi|67542103|ref|ZP_00420040.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia vietnamiensis G4]			x
67780042	>gi|67780042|gb|EAM39659.1| 4-hydroxyphenylpyruvate dioxygenase [Polaromonas sp. JS666]			x
68556085	>gi|68556085|ref|ZP_00595428.1| 4-hydroxyphenylpyruvate dioxygenase [Ralstonia metallidurans CH34]			x
3694811	>gi|3694811|gb|AAC62457.1| p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana]			x
37727200	>gi|37727200|gb|AAO12525.1| p-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida]			x
3860238	>gi|3860238|gb|AAC73008.1| 4-hydroxyphenylpyruvate-dioxygenase [Homo sapiens]			x
555806	>gi|555806|gb|AAA50231.1| 4-hydroxyphenylpyruvate acid dioxygenase			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
46395699	>gi|46395699|sp|Q56415|FOSA_SERMA Glutathione transferase fosA (Fosfomycin resistance protein)			x
46014944	>gi|46014944|pdb|1NPB|F Chain F, Crystal Structure Of The Fosfomycin Resistance Protein From Transposon Tn2921			x
46014943	>gi|46014943|pdb|1NPB|E Chain E, Crystal Structure Of The Fosfomycin Resistance Protein From Transposon Tn2921			x
46014942	>gi|46014942|pdb|1NPB|D Chain D, Crystal Structure Of The Fosfomycin Resistance Protein From Transposon Tn2921			x
46014941	>gi|46014941|pdb|1NPB|C Chain C, Crystal Structure Of The Fosfomycin Resistance Protein From Transposon Tn2921			x
46014940	>gi|46014940|pdb|1NPB|B Chain B, Crystal Structure Of The Fosfomycin Resistance Protein From Transposon Tn2921			x
46014939	>gi|46014939|pdb|1NPB|A Chain A, Crystal Structure Of The Fosfomycin Resistance Protein From Transposon Tn2921			x
320413	>gi|320413|pir||A60635 glutathione transferase (EC 2.5.1.18), fosfomycin-modifying - Escherichia coli plasmid pSU961 transposon Tn2921			x
46395995	>gi|46395995|sp|Q9I4K6|FOSA_PSEAE Glutathione transferase fosA (Fosfomycin resistance protein)			x
42543104	>gi|42543104|pdb|1NNR|B Chain B, Crystal Structure Of A Probable Fosfomycin Resistance Protein (Pa1129) From Pseudomonas Aeruginosa With Sulfate Present In The Active Site			x
42543103	>gi|42543103|pdb|1NNR|A Chain A, Crystal Structure Of A Probable Fosfomycin Resistance Protein (Pa1129) From Pseudomonas Aeruginosa With Sulfate Present In The Active Site			x
42543067	>gi|42543067|pdb|1NKI|B Chain B, Crystal Strucure Of The Fosfomycin Resistance Protein A (Fosa) Containing Bound Phosphonoformate			x
42543066	>gi|42543066|pdb|1NKI|A Chain A, Crystal Strucure Of The Fosfomycin Resistance Protein A (Fosa) Containing Bound Phosphonoformate			x
24158887	>gi|24158887|pdb|1LQO|B Chain B, Crystal Strutcure Of The Fosfomycin Resistance Protein A (Fosa) Containing Bound Thallium Cations			x
24158886	>gi|24158886|pdb|1LQO|A Chain A, Crystal Strutcure Of The Fosfomycin Resistance Protein A (Fosa) Containing Bound Thallium Cations			x
24158889	>gi|24158889|pdb|1LQP|B Chain B, Crystal Structure Of The Fosfomycin Resistance Protein (Fosa) Containing Bound Substrate			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
24158888	>gi|24158888|pdb|1LQP|A Chain A, Crystal Structure Of The Fosfomycin Resistance Protein (Fosa) Containing Bound Substrate			x
24158885	>gi|24158885|pdb|1LQK|B Chain B, High Resolution Structure Of Fosfomycin Resistance Protein A (Fosa)			x
24158884	>gi|24158884|pdb|1LQK|A Chain A, High Resolution Structure Of Fosfomycin Resistance Protein A (Fosa)			x
16502774	>gi|16502774|emb|CAD01932.1| lactoylglutathione lyase [Salmonella enterica subsp. enterica serovar Typhi]			x
16580747	>gi|16580747|dbj|BAB71741.1| glyoxalase I [Oryza sativa (japonica cultivar-group)]			x
6573422	>gi|6573422|pdb|1QIP|D Chain D, Human Glyoxalase I Complexed With S-P-Nitrobenzyloxycarbonylglutathione			x
82735426	>gi|82735426|ref|ZP_00898288.1| Glyoxalase I [Pseudomonas putida F1]			x
15030212	>gi|15030212|gb|AAH11365.1| Glyoxalase I [Homo sapiens]			x
84715589	>gi|84715589|ref|ZP_01022618.1| Glyoxalase I [Polaromonas naphthalenivorans CJ2]			x
82703738	>gi|82703738|ref|YP_413304.1| Glyoxalase I [Nitrosospira multiformis ATCC 25196]			x
28807102	>gi|28807102|dbj|BAC60372.1| lactoylglutathione lyase [Vibrio parahaemolyticus RIMD 2210633]			x
71550295	>gi|71550295|ref|ZP_00670425.1| Glyoxalase I [Nitrosomonas eutropha C71]			x
9655474	>gi|9655474|gb|AAF94171.1| lactoylglutathione lyase [Vibrio cholerae O1 biovar eltor str. N16961]			x
2909424	>gi|2909424|emb|CAA12028.1| Glyoxalase I [Cicer arietinum]			x
11182130	>gi|11182130|emb|CAC16163.1| glyoxalase I [Saccharomyces cerevisiae]			x
2113825	>gi|2113825|emb|CAA73691.1| Glyoxalase I [Brassica juncea]			x
38181954	>gi|38181954|gb|AAH61570.1| Glyoxylase 1 [Rattus norvegicus]			x
74014235	>gi|74014235|ref|ZP_00684864.1| Glyoxalase I [Burkholderia ambifaria AMMD]			x
76884453	>gi|76884453|gb|ABA59134.1| Glyoxalase I [Nitrosococcus oceani ATCC 19707]			x
76875453	>gi|76875453|emb|CAI86674.1| Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase) [Pseudoalteromonas haloplanktis TAC125]			x
76791872	>gi|76791872|ref|ZP_00774376.1| Glyoxalase I [Pseudoalteromonas atlantica T6c]			x
77968247	>gi|77968247|gb|ABB09627.1| Glyoxalase I [Burkholderia sp. 383]			x
54696834	>gi|54696834|gb|AAV38789.1| glyoxalase I [synthetic construct]			x

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>77953933</td><td>>gi|77953933|ref|ZP_00818336.1| Glyoxalase I [Marinobacter aquaeolei VT8]</td><td></td><td></td><td>x</td></tr>
<tr><td>50941905</td><td>>gi|50941905|ref|XP_480480.1| glyoxalase I [Oryza sativa (japonica cultivar-group)]</td><td></td><td></td><td>x</td></tr>
<tr><td>30680509</td><td>>gi|30680509|ref|NP_849609.1| calmodulin binding / lactoylglutathione lyase [Arabidopsis thaliana]</td><td></td><td></td><td>x</td></tr>
<tr><td>24052010</td><td>>gi|24052010|gb|AAN43259.1| lactoylglutathione lyase [Shigella flexneri 2a str. 301]</td><td></td><td></td><td>x</td></tr>
<tr><td>67674810</td><td>>gi|67674810|ref|ZP_00471570.1| Glyoxalase I [Chromohalobacter salexigens DSM 3043]</td><td></td><td></td><td>x</td></tr>
<tr><td>67663996</td><td>>gi|67663996|ref|ZP_00461274.1| Glyoxalase I [Burkholderia cenocepacia HI2424]</td><td></td><td></td><td>x</td></tr>
<tr><td>67777486</td><td>>gi|67777486|gb|EAM37113.1| Glyoxalase I [Polaromonas sp. JS666]</td><td></td><td></td><td>x</td></tr>
<tr><td>68188408</td><td>>gi|68188408|gb|EAN03088.1| Glyoxalase I [Methylobacillus flagellatus KT]</td><td></td><td></td><td>x</td></tr>
<tr><td>56685855</td><td>>gi|56685855|dbj|BAD79077.1| lactoylglutathione lyase [Synechococcus elongatus PCC 6301]</td><td></td><td></td><td>x</td></tr>
<tr><td>66046204</td><td>>gi|66046204|ref|YP_236045.1| Glyoxalase I [Pseudomonas syringae pv. syringae B728a]</td><td></td><td></td><td>x</td></tr>
<tr><td>16198506</td><td>>gi|16198506|gb|AAH15934.1| Glyoxalase I [Homo sapiens]</td><td></td><td></td><td>x</td></tr>
<tr><td>2506469</td><td>>gi|2506469|sp|P16635|LGUL_PSEPU Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>68057128</td><td>>gi|68057128|gb|AAX87381.1| lactoylglutathione lyase [Haemophilus influenzae 86-028NP]</td><td></td><td></td><td>x</td></tr>
<tr><td>2281946</td><td>>gi|2281946|emb|CAA74673.1| lactoylglutathione lyase [Neisseria meningitidis]</td><td></td><td></td><td>x</td></tr>
<tr><td>79317664</td><td>>gi|79317664|ref|NP_001031025.1| ATGLX1 (GLYOXALASE I HOMOLOG); lactoylglutathione lyase [Arabidopsis thaliana]</td><td></td><td></td><td>x</td></tr>
<tr><td>56495052</td><td>>gi|56495052|emb|CAH99110.1| glyoxalase I, putative [Plasmodium berghei]</td><td></td><td></td><td>x</td></tr>
<tr><td>70950284</td><td>>gi|70950284|ref|XP_744478.1| glyoxalase I [Plasmodium chabaudi chabaudi]</td><td></td><td></td><td>x</td></tr>
<tr><td>1177314</td><td>>gi|1177314|emb|CAA88233.1| glyoxalase-I [Lycopersicon esculentum]</td><td></td><td></td><td>x</td></tr>
<tr><td>54696838</td><td>>gi|54696838|gb|AAV38791.1| glyoxalase I [Homo sapiens]</td><td></td><td></td><td>x</td></tr>
<tr><td>71848772</td><td>>gi|71848772|gb|AAZ48268.1| Glyoxalase I [Dechloromonas aromatica RCB]</td><td></td><td></td><td>x</td></tr>
<tr><td>75700089</td><td>>gi|75700089|gb|ABA19765.1| Glyoxalase I [Anabaena variabilis ATCC 29413]</td><td></td><td></td><td>x</td></tr>
<tr><td>72117622</td><td>>gi|72117622|gb|AAZ59885.1| Glyoxalase I [Ralstonia eutropha JMP134]</td><td></td><td></td><td>x</td></tr>
<tr><td>77383151</td><td>>gi|77383151|gb|ABA74664.1| Glyoxalase I [Pseudomonas fluorescens PfO-1]</td><td></td><td></td><td>x</td></tr>
<tr><td>50252391</td><td>>gi|50252391|dbj|BAD28547.1| putative glyoxalase I [Oryza sativa (japonica cultivar-group)]</td><td></td><td></td><td>x</td></tr>
<tr><td>68473834</td><td>>gi|68473834|ref|XP_719020.1| glyoxalase I [Candida albicans SC5314]</td><td></td><td></td><td>x</td></tr>
<tr><td>12744892</td><td>>gi|12744892|gb|AAK06838.1| glyoxalase I [Avicennia marina]</td><td></td><td></td><td>x</td></tr>
<tr><td>30016920</td><td>>gi|30016920|gb|AAP03992.1| glyoxalase I [Paracoccidioides brasiliensis]</td><td></td><td></td><td>x</td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
21537360	>gi|21537360|gb|AAM61701.1| glyoxalase I, putative [Arabidopsis thaliana]			x
62089188	>gi|62089188|dbj|BAD93038.1| glyoxalase I variant [Homo sapiens]			x
71900928	>gi|71900928|ref|ZP_00683042.1| Glyoxalase I [Xylella fastidiosa Ann-1]			x
71677562	>gi|71677562|ref|ZP_00675298.1| Glyoxalase I [Trichodesmium erythraeum IMS101]			x
71897576	>gi|71897576|ref|ZP_00679821.1| Glyoxalase I [Xylella fastidiosa Ann-1]			x
23508336	>gi|23508336|ref|NP_701005.1| glyoxalase I, putative [Plasmodium falciparum 3D7]			x
4127862	>gi|4127862|emb|CAA09177.1| glyoxalase I [Glycine max]			x
7619802	>gi|7619802|emb|CAB50787.2| putative glyoxalase I [Triticum aestivum]			x
37932483	>gi|37932483|gb|AAP76396.1| glyoxalase I [Zea mays]			x
52839948	>gi|52839948|gb|AAU87880.1| glyoxalase I [Leishmania donovani]	ESA		x
67157387	>gi|67157387|ref|ZP_00418689.1| Glyoxalase I [Azotobacter vinelandii AvOP]			x
67547158	>gi|67547158|ref|ZP_00425064.1| Glyoxalase I [Burkholderia vietnamiensis G4]			x
67920488	>gi|67920488|ref|ZP_00514008.1| Glyoxalase I [Crocosphaera watsonii WH 8501]			x
36785924	>gi|36785924|emb|CAE14976.1| lactoylglutathione lyase (methylglyoxalase) (S-D-lactolyglutathione methylglyoxal lyase) [Photorhabdus luminescens subsp. laumondii TTO1]			x
19354350	>gi|19354350|gb|AAH24663.1| Glyoxalase 1 [Mus musculus]			x
47085917	>gi|47085917|ref|NP_998316.1| glyoxalase 1 [Danio rerio]			x
83720549	>gi|83720549|ref|YP_441137.1| lactoylglutathione lyase [Burkholderia thailandensis E264]			x
85712601	>gi|85712601|ref|ZP_01043648.1| Lactoylglutathione lyase [Idiomarina baltica OS145]			x
86147966	>gi|86147966|ref|ZP_01066270.1| lactoylglutathione lyase [Vibrio sp. MED222]			x
86605927	>gi|86605927|ref|YP_474690.1| lactoylglutathione lyase [Cyanobacteria bacterium Yellowstone A-Prime]			x
68345056	>gi|68345056|gb|AAY92662.1| lactoylglutathione lyase [Pseudomonas fluorescens Pf-5]			x
84366281	>gi|84366281|dbj|BAE67439.1| lactoylglutathione lyase [Xanthomonas oryzae pv. oryzae MAFF 311018]			x
71554395	>gi|71554395|gb|AAZ33606.1| lactoylglutathione lyase [Pseudomonas syringae pv. phaseolicola 1448A]			x
76578699	>gi|76578699|gb|ABA48174.1| lactoylglutathione lyase [Burkholderia pseudomallei 1710b]			x
75431428	>gi|75431428|ref|ZP_00733000.1| Lactoylglutathione lyase [Actinobacillus succinogenes 130Z]			x
78037735	>gi|78037735|emb|CAJ25480.1| Lactoylglutathione lyase [Xanthomonas campestris pv. vesicatoria str. 85-10]			x

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>79317307</td><td>>gi|79317307|ref|NP_001030996.1| calmodulin binding / lactoylglutathione lyase [Arabidopsis thaliana]</td><td></td><td></td><td>x</td></tr>
<tr><td>28870279</td><td>>gi|28870279|ref|NP_792898.1| lactoylglutathione lyase [Pseudomonas syringae pv. tomato str. DC3000]</td><td></td><td></td><td>x</td></tr>
<tr><td>82597002</td><td>>gi|82597002|ref|XP_726497.1| lactoylglutathione lyase [Plasmodium yoelii yoelii str. 17XNL]</td><td></td><td></td><td>x</td></tr>
<tr><td>9106409</td><td>>gi|9106409|gb|AAF84208.1| lactoylglutathione lyase [Xylella fastidiosa 9a5c]</td><td></td><td></td><td>x</td></tr>
<tr><td>21111572</td><td>>gi|21111572|gb|AAM39891.1| lactoylglutathione lyase [Xanthomonas campestris pv. campestris str. ATCC 33913]</td><td></td><td></td><td>x</td></tr>
<tr><td>37198112</td><td>>gi|37198112|dbj|BAC93949.1| lactoylglutathione lyase [Vibrio vulnificus YJ016]</td><td></td><td></td><td>x</td></tr>
<tr><td>49611385</td><td>>gi|49611385|emb|CAG74832.1| lactoylglutathione lyase [Erwinia carotovora subsp. atroseptica SCRI1043]</td><td></td><td></td><td>x</td></tr>
<tr><td>39576464</td><td>>gi|39576464|emb|CAE80629.1| lactoylglutathione lyase [Bdellovibrio bacteriovorus HD100]</td><td></td><td></td><td>x</td></tr>
<tr><td>56180743</td><td>>gi|56180743|gb|AAV83465.1| Lactoylglutathione lyase [Idiomarina loihiensis L2TR]</td><td></td><td></td><td>x</td></tr>
<tr><td>58580377</td><td>>gi|58580377|ref|YP_199393.1| lactoylglutathione lyase [Xanthomonas oryzae pv. oryzae KACC10331]</td><td></td><td></td><td>x</td></tr>
<tr><td>28198538</td><td>>gi|28198538|ref|NP_778852.1| lactoylglutathione lyase [Xylella fastidiosa Temecula1]</td><td></td><td></td><td>x</td></tr>
<tr><td>59711535</td><td>>gi|59711535|ref|YP_204311.1| lactoylglutathione lyase [Vibrio fischeri ES114]</td><td></td><td></td><td>x</td></tr>
<tr><td>34497115</td><td>>gi|34497115|ref|NP_901330.1| lactoylglutathione lyase [Chromobacterium violaceum ATCC 12472]</td><td></td><td></td><td>x</td></tr>
<tr><td>9951408</td><td>>gi|9951408|gb|AAG08496.1| lactoylglutathione lyase [Pseudomonas aeruginosa PAO1]</td><td></td><td></td><td>x</td></tr>
<tr><td>17131413</td><td>>gi|17131413|dbj|BAB74020.1| lactoylglutathione lyase [Nostoc sp. PCC 7120]</td><td></td><td></td><td>x</td></tr>
<tr><td>9949673</td><td>>gi|9949673|gb|AAG06912.1| lactoylglutathione lyase [Pseudomonas aeruginosa PAO1]</td><td></td><td></td><td>x</td></tr>
<tr><td>26990471</td><td>>gi|26990471|ref|NP_745896.1| lactoylglutathione lyase [Pseudomonas putida KT2440]</td><td></td><td></td><td>x</td></tr>
<tr><td>49531298</td><td>>gi|49531298|emb|CAG69010.1| lactoylglutathione lyase [Acinetobacter sp. ADP1]</td><td></td><td></td><td>x</td></tr>
<tr><td>56313950</td><td>>gi|56313950|emb|CAI08595.1| Lactoylglutathione lyase [Azoarcus sp. EbN1]</td><td></td><td></td><td>x</td></tr>
<tr><td>33639478</td><td>>gi|33639478|emb|CAE08862.1| lactoylglutathione lyase [Synechococcus sp. WH 8102]</td><td></td><td></td><td>x</td></tr>
<tr><td>21110013</td><td>>gi|21110013|gb|AAM38475.1| lactoylglutathione lyase [Xanthomonas axonopodis pv. citri str. 306]</td><td></td><td></td><td>x</td></tr>
<tr><td>28809009</td><td>>gi|28809009|dbj|BAC62117.1| lactoylglutathione lyase [Vibrio parahaemolyticus RIMD 2210633]</td><td></td><td></td><td>x</td></tr>
<tr><td>30138761</td><td>>gi|30138761|emb|CAD85338.1| possible gloA; lactoylglutathione lyase [Nitrosomonas europaea ATCC 19718]</td><td></td><td></td><td>x</td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
45436822	>gi|45436822|gb|AAS62375.1| lactoylglutathione lyase [Yersinia pestis biovar Medievalis str. 91001]			x
33568699	>gi|33568699|emb|CAE34457.1| lactoylglutathione lyase [Bordetella bronchiseptica RB50]			x
15220397	>gi|15220397|ref|NP_176896.1| lactoylglutathione lyase [Arabidopsis thaliana]			x
66848318	>gi|66848318|gb|EAL88647.1| lactoylglutathione lyase [Aspergillus fumigatus Af293]			x
15810219	>gi|15810219|gb|AAL07227.1| putative lactoylglutathione lyase [Arabidopsis thaliana]			x
1354847	>gi|1354847|gb|AAC44877.1| S-D-lactolyglutathione methylglyoxal lyase			x
2624696	>gi|2624696|pdb|5EAS| 5-Epi-Aristolochene Synthase From Nicotiana Tabacum			x
2624425	>gi|2624425|pdb|5EAT| 5-Epi-Aristolochene Synthase From Nicotiana Tabacum With Substrate Analog Farnesyl Hydroxyphosphonate			x
3121724	>gi|3121724|sp|Q40577|5EAS_TOBAC Aristolchene synthase (5-epi-aristolochene synthase) (EAS)			x
3114378	>gi|3114378|pdb|5EAU| 5-Epi-Aristolochene Synthase From Nicotiana Tabacum			x
505588	>gi|505588|gb|AAA19216.1| 5-epi-aristolochene synthase			x
29468500	>gi|29468500|gb|AAO85555.1| 5-epi-aristolochene synthase [Nicotiana attenuata]			x
29837351	>gi|29837351|gb|AAP05760.1| 5-epi-aristolochene synthase 12 [Nicotiana attenuata]			x
29837353	>gi|29837353|gb|AAP05761.1| 5-epi-aristolochene synthase 34 [Nicotiana attenuata]			x
29837355	>gi|29837355|gb|AAP05762.1| 5-epi-aristolochene synthase 37 [Nicotiana attenuata]			x
3687297	>gi|3687297|emb|CAA06614.1| 5-epi-aristolochene synthase [Capsicum annuum var. annuum]			x
27065865	>gi|27065865|pdb|1N24|B Chain B, (+)-Bornyl Diphosphate Synthase: Complex With Mg And Product			x
27065864	>gi|27065864|pdb|1N24|A Chain A, (+)-Bornyl Diphosphate Synthase: Complex With Mg And Product			x
27065862	>gi|27065862|pdb|1N23|B Chain B, (+)-Bornyl Diphosphate Synthase: Complex With Mg, Pyrophosphate, And (1r,4s)-2-Azabornane			x
27065861	>gi|27065861|pdb|1N23|A Chain A, (+)-Bornyl Diphosphate Synthase: Complex With Mg, Pyrophosphate, And (1r,4s)-2-Azabornane			x
27065855	>gi|27065855|pdb|1N22|B Chain B, (+)-Bornyl Diphosphate Synthase: Complex With Mg, Pyrophosphate, And (4r)-7-Aza-7,8-Dihydrolimonene			x
27065854	>gi|27065854|pdb|1N22|A Chain A, (+)-Bornyl Diphosphate Synthase: Complex With Mg, Pyrophosphate, And (4r)-7-Aza-7,8-Dihydrolimonene			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
27065853	>gi|27065853|pdb|1N21|A Chain A, (+)-Bornyl Diphosphate Synthase: Cocrystal With Mg And 3-Aza-2,3-Dihydrogeranyl Diphosphate			x
27065851	>gi|27065851|pdb|1N20|B Chain B, (+)-Bornyl Diphosphate Synthase: Complex With Mg And 3-Aza-2,3-Dihydrogeranyl Diphosphate			x
27065850	>gi|27065850|pdb|1N20|A Chain A, (+)-Bornyl Diphosphate Synthase: Complex With Mg And 3-Aza-2,3-Dihydrogeranyl Diphosphate			x
27065849	>gi|27065849|pdb|1N1Z|B Chain B, (+)-Bornyl Diphosphate Synthase: Complex With Mg And Pyrophosphate			x
27065848	>gi|27065848|pdb|1N1Z|A Chain A, (+)-Bornyl Diphosphate Synthase: Complex With Mg And Pyrophosphate			x
27065842	>gi|27065842|pdb|1N1B|B Chain B, Crystal Structure Of (+)-Bornyl Diphosphate Synthase From Sage			x
27065841	>gi|27065841|pdb|1N1B|A Chain A, Crystal Structure Of (+)-Bornyl Diphosphate Synthase From Sage			x
62899675	>gi|62899675|sp|O81192|BPPS_SALOF (+)-bornyl diphosphate synthase, chloroplast precursor (SBS) (BPPS)			x
3309119	>gi|3309119|gb|AAC26017.1| (+)-bornyl diphosphate synthase [Salvia officinalis]			x
2833457	>gi|2833457|sp|Q55012|PTLS_STRS3 Pentalenene synthase			x
2127584	>gi|2127584|pir||A54214 C 4.2.3.7 pentalenene synthase () - Streptomyces sp. (strain UC5319)			x
3114507	>gi|3114507|pdb|1PS1|B Chain B, Pentalenene Synthase			x
3114506	>gi|3114506|pdb|1PS1|A Chain A, Pentalenene Synthase			x
451846	>gi|451846|gb|AAA19131.1| pentalenene synthase			x
29606648	>gi|29606648|dbj|BAC70709.1| pentalenene synthase [Streptomyces avermitilis MA-4680]			x
29829540	>gi|29829540|ref|NP_824174.1| pentalenene synthase [Streptomyces avermitilis MA-4680]			x
2851526	>gi|2851526|sp|P33247|SQHC_ALIAC Squalene--hopene cyclase			x
83716953	>gi|83716953|ref|YP_440546.1| squalene-hopene cyclase [Burkholderia thailandensis E264]			x
27351262	>gi|27351262|dbj|BAC48269.1| squalene-hopene cyclase [Bradyrhizobium japonicum USDA 110]			x
2113823	>gi|2113823|emb|CAA60250.1| squalene-hopene cyclase [Bradyrhizobium japonicum]			x
76583469	>gi|76583469|gb|ABA52943.1| squalene-hopene cyclase [Burkholderia pseudomallei 1710b]			x
77544139	>gi|77544139|gb|ABA87701.1| squalene-hopene cyclase [Pelobacter carbinolicus DSM 2380]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
65320833	>gi|65320833|ref|ZP_00393792.1| COG1657: Squalene cyclase [Bacillus anthracis str. A2012]			x
32468770	>gi|32468770|emb|CAB13824.2| squalene-hopene cyclase [Bacillus subtilis subsp. subtilis str. 168]			x
35214631	>gi|35214631|dbj|BAC91998.1| squalene-hopene cyclase [Gloeobacter violaceus PCC 7421]			x
51975448	>gi|51975448|gb|AAU16998.1| squalene-hopene cyclase [Bacillus cereus E33L]			x
58003100	>gi|58003100|gb|AAW61994.1| Squalene-hopene cyclase [Gluconobacter oxydans 621H]			x
42782622	>gi|42782622|ref|NP_979869.1| squalene-hopene cyclase [Bacillus cereus ATCC 10987]			x
677871	>gi|677871|emb|CAA56749.1| squalene-hopene cyclase [Zymomonas mobilis]			x
29605294	>gi|29605294|dbj|BAC69361.1| squalene-hopene cyclase [Streptomyces avermitilis MA-4680]			x
52421851	>gi|52421851|gb|AAU45421.1| squalene-hopene cyclase [Burkholderia mallei ATCC 23344]			x
39982558	>gi|39982558|gb|AAR34018.1| squalene-hopene cyclase [Geobacter sulfurreducens PCA]			x
39985098	>gi|39985098|gb|AAR36453.1| squalene-hopene cyclase [Geobacter sulfurreducens PCA]			x
53758581	>gi|53758581|gb|AAU92872.1| squalene-hopene cyclase [Methylococcus capsulatus str. Bath]			x
49329830	>gi|49329830|gb|AAT60476.1| squalene-hopene cyclase [Bacillus thuringiensis serovar konkukian str. 97-27]			x
4539168	>gi|4539168|emb|CAB39697.1| putative squalene-hopene cyclase [Streptomyces coelicolor A3(2)]			x
927384	>gi|927384|emb|CAA61950.1| squalene-hopene cyclase [Alicyclobacillus acidoterrestris]			x
3164082	>gi|3164082|emb|CAA71098.1| squalene-hopene cyclase [Methylococcus capsulatus str. Bath]			x
3164106	>gi|3164106|emb|CAA71101.1| squalene-hopene cyclase [Rhodopseudomonas palustris]			x
987617	>gi|987617|gb|AAA75452.1| squalene-hopene-cyclase			x
59803022	>gi|59803022|sp|P33990|SQHC_ZYMMO Squalene--hopene cyclase			x
84352143	>gi|84352143|ref|ZP_00977114.1| COG1657: Squalene cyclase [Burkholderia cenocepacia PC184]			x
84353268	>gi|84353268|ref|ZP_00978203.1| COG1657: Squalene cyclase [Burkholderia cenocepacia PC184]			x
84358827	>gi|84358827|ref|ZP_00983594.1| COG1657: Squalene cyclase [Burkholderia dolosa AUO158]			x
82703671	>gi|82703671|ref|YP_413237.1| Squalene cyclase [Nitrosospira multiformis ATCC 25196]			x

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>47568915</td><td>>gi|47568915|ref|ZP_00239607.1| squalene--hopene cyclase [Bacillus cereus G9241]</td><td></td><td></td><td>x</td></tr>
<tr><td>46203107</td><td>>gi|46203107|ref|ZP_00052068.2| COG1657: Squalene cyclase [Magnetospirillum magnetotacticum MS-1]</td><td></td><td></td><td>x</td></tr>
<tr><td>23126680</td><td>>gi|23126680|ref|ZP_00108569.1| COG1657: Squalene cyclase [Nostoc punctiforme PCC 73102]</td><td></td><td></td><td>x</td></tr>
<tr><td>85716675</td><td>>gi|85716675|ref|ZP_01047644.1| terpene synthase/Squalene cyclase [Nitrobacter sp. Nb-311A]</td><td></td><td></td><td>x</td></tr>
<tr><td>74421324</td><td>>gi|74421324|gb|ABA05523.1| terpene synthase/Squalene cyclase [Nitrobacter winogradskyi Nb-255]</td><td></td><td></td><td>x</td></tr>
<tr><td>76883137</td><td>>gi|76883137|gb|ABA57818.1| Terpene synthase/Squalene cyclase [Nitrosococcus oceani ATCC 19707]</td><td></td><td></td><td>x</td></tr>
<tr><td>77544053</td><td>>gi|77544053|gb|ABA87615.1| squalene--hopene cyclase [Pelobacter carbinolicus DSM 2380]</td><td></td><td></td><td>x</td></tr>
<tr><td>77690249</td><td>>gi|77690249|ref|ZP_00805427.1| Terpene synthase:Squalene cyclase [Rhodopseudomonas palustris BisB5]</td><td></td><td></td><td>x</td></tr>
<tr><td>77965182</td><td>>gi|77965182|gb|ABB06563.1| Terpene synthase/Squalene cyclase [Burkholderia sp. 383]</td><td></td><td></td><td>x</td></tr>
<tr><td>78492501</td><td>>gi|78492501|ref|ZP_00844737.1| Terpene synthase:Squalene cyclase [Rhodopseudomonas palustris BisB18]</td><td></td><td></td><td>x</td></tr>
<tr><td>67759490</td><td>>gi|67759490|ref|ZP_00498226.1| COG1657: Squalene cyclase [Burkholderia pseudomallei S13]</td><td></td><td></td><td>x</td></tr>
<tr><td>56552444</td><td>>gi|56552444|ref|YP_163283.1| squalene--hopene cyclase [Zymomonas mobilis subsp. mobilis ZM4]</td><td></td><td></td><td>x</td></tr>
<tr><td>22296036</td><td>>gi|22296036|dbj|BAC09861.1| squalene-hopene-cyclase [Thermosynechococcus elongatus BP-1]</td><td></td><td></td><td>x</td></tr>
<tr><td>29897214</td><td>>gi|29897214|gb|AAP10491.1| Squalene--hopene cyclase [Bacillus cereus ATCC 14579]</td><td></td><td></td><td>x</td></tr>
<tr><td>83591402</td><td>>gi|83591402|ref|YP_425154.1| terpene synthase, squalene cyclase [Rhodospirillum rubrum ATCC 11170]</td><td></td><td></td><td>x</td></tr>
<tr><td>67680231</td><td>>gi|67680231|ref|ZP_00474818.1| COG1657: Squalene cyclase [Burkholderia pseudomallei 1710a]</td><td></td><td></td><td>x</td></tr>
<tr><td>67645915</td><td>>gi|67645915|ref|ZP_00444187.1| COG1657: Squalene cyclase [Burkholderia mallei NCTC 10247]</td><td></td><td></td><td>x</td></tr>
<tr><td>17130120</td><td>>gi|17130120|dbj|BAB72732.1| squalene-hopene-cyclase [Nostoc sp. PCC 7120]</td><td></td><td></td><td>x</td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
1653061	>gi|1653061|dbj|BAA17978.1| squalene-hopene-cyclase [Synechocystis sp. PCC 6803]			x
39650658	>gi|39650658|emb|CAE29181.1| squalene-hopene-cyclase [Rhodopseudomonas palustris CGA009]			x
72122116	>gi|72122116|gb|AAZ64302.1| Terpene synthase:Squalene cyclase [Ralstonia eutropha JMP134]			x
77968757	>gi|77968757|gb|ABB10136.1| Terpene synthase/Squalene cyclase [Burkholderia sp. 383]			x
78192895	>gi|78192895|gb|ABB30662.1| Terpene synthase:Squalene cyclase [Geobacter metallireducens GS-15]			x
78195271	>gi|78195271|gb|ABB33038.1| Terpene synthase:Squalene cyclase [Geobacter metallireducens GS-15]			x
48782682	>gi|48782682|ref|ZP_00279188.1| COG1657: Squalene cyclase [Burkholderia fungorum LB400]			x
86571877	>gi|86571877|gb|ABD06434.1| Squalene cyclase [Rhodopseudomonas palustris HaA2]			x
86739536	>gi|86739536|ref|YP_479936.1| Squalene cyclase [Frankia sp. CcI3]			x
13621069	>gi|13621069|gb|AAK33074.1| trichodiene synthase [Fusarium sporotrichioides]			x
168160	>gi|168160|gb|AAD13657.1| trichodiene synthase TRI5 [Fusarium sporotrichioides]			x
15054400	>gi|15054400|gb|AAK77935.1| trichodiene synthase [Fusarium sporotrichioides]			x
68280	>gi|68280|pir||SYFUTP trichodiene synthase (EC 4.2.3.6) - fungus (Fusarium sporotrichioides)			x
136010	>gi|136010|sp|P13513|TRI5_FUSSP Trichodiene synthase (Sesquiterpene cyclase) (TS)			x
17942972	>gi|17942972|pdb|1JFA|B Chain B, Trichodiene Synthase From Fusarium Sporotrichioides			x
17942971	>gi|17942971|pdb|1JFA|A Chain A, Trichodiene Synthase From Fusarium Sporotrichioides			x
17942970	>gi|17942970|pdb|1JFG|B Chain B, Trichodiene Synthase From Fusarium Sporotrichioides Complexed With Diphosphate			x
17942969	>gi|17942969|pdb|1JFG|A Chain A, Trichodiene Synthase From Fusarium Sporotrichioides Complexed With Diphosphate			x
2267599	>gi|2267599|gb|AAC49957.1| trichodiene synthase [Myrothecium roridum]			x
4033476	>gi|4033476|sp|O13489|TRI5_MYRRO Trichodiene synthase (Sesquiterpene cyclase) (TS)			x
21429542	>gi|21429542|gb|AAM49006.1| trichodiene synthase [Gibberella zeae]			x
558954	>gi|558954|gb|AAA50765.1| trichodiene synthase [Fusarium poae]			x
4033478	>gi|4033478|sp|Q00835|TRI5_FUSPO Trichodiene synthase (Sesquiterpene cyclase) (TS)			x
33413587	>gi|33413587|gb|AAN05032.1| trichodiene synthase [Gibberella zeae]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
42549660	>gi|42549660|gb|EAA72503.1| TRI5_GIBZE Trichodiene synthase (Sesquiterpene cyclase) (TS) [Gibberella zeae PH-1]			x
46115390	>gi|46115390|ref|XP_383713.1| TRI5_GIBZE Trichodiene synthase (Sesquiterpene cyclase) (TS) [Gibberella zeae PH-1]			x
13621080	>gi|13621080|gb|AAK33084.1| trichodiene synthase [Gibberella zeae]			x
14091070	>gi|14091070|gb|AAK53586.1| trichodiene synthase [Gibberella zeae]			x
4033479	>gi|4033479|sp|Q00909|TRI5_GIBZE Trichodiene synthase (Sesquiterpene cyclase) (TS)			x
21429596	>gi|21429596|gb|AAM49054.1| trichodiene synthase [Gibberella zeae]			x
21429578	>gi|21429578|gb|AAM49038.1| trichodiene synthase [Gibberella zeae]			x
21429380	>gi|21429380|gb|AAM48862.1| trichodiene synthase [Gibberella zeae]			x
2218058	>gi|2218058|gb|AAB72033.1| trichodiene synthase [Gibberella zeae]			x
12584945	>gi|12584945|gb|AAG59895.1| trichodiene synthase [Stachybotrys chartarum]			x
3023077	>gi|3023077|gb|AAC12640.1| trichodiene synthase [Stachybotrys chartarum]			x
4033477	>gi|4033477|sp|O59947|TRI5_STACH Trichodiene synthase (Sesquiterpene cyclase) (TS)			x
168190	>gi|168190|gb|AAB02038.1| trichodiene synthase			x
136011	>gi|136011|sp|P27679|TRI5_GIBPU Trichodiene synthase (Sesquiterpene cyclase) (TS)			x
21429434	>gi|21429434|gb|AAM48910.1| trichodiene synthase [Gibberella zeae]			x
21429353	>gi|21429353|gb|AAM48838.1| trichodiene synthase [Fusarium acaciae-mearnsii]			x
21429344	>gi|21429344|gb|AAM48830.1| trichodiene synthase [Fusarium acaciae-mearnsii]			x
21429335	>gi|21429335|gb|AAM48822.1| trichodiene synthase [Fusarium acaciae-mearnsii]			x
21429308	>gi|21429308|gb|AAM48798.1| trichodiene synthase [Fusarium mesoamericanum]			x
21429254	>gi|21429254|gb|AAM48750.1| trichodiene synthase [Gibberella zeae]			x
21429263	>gi|21429263|gb|AAM48758.1| trichodiene synthase [Fusarium lunulosporum]			x
21429317	>gi|21429317|gb|AAM48806.1| trichodiene synthase [Fusarium cerealis]			x
21429299	>gi|21429299|gb|AAM48790.1| trichodiene synthase [Fusarium cerealis]			x
21429281	>gi|21429281|gb|AAM48774.1| trichodiene synthase [Fusarium asiaticum]			x
21429272	>gi|21429272|gb|AAM48766.1| trichodiene synthase [Fusarium cerealis]			x
21429569	>gi|21429569|gb|AAM49030.1| trichodiene synthase [Fusarium culmorum]			x
21429407	>gi|21429407|gb|AAM48886.1| trichodiene synthase [Gibberella zeae]			x
21429290	>gi|21429290|gb|AAM48782.1| trichodiene synthase [Fusarium culmorum]			x
24371019	>gi|24371019|dbj|BAC22117.1| trichodiene synthase [Gibberella zeae]			x
21429326	>gi|21429326|gb|AAM48814.1| trichodiene synthase [Fusarium asiaticum]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
21429524	>gi|21429524|gb|AAM48990.1| trichodiene synthase [Fusarium boothii]			x
21429506	>gi|21429506|gb|AAM48974.1| trichodiene synthase [Fusarium boothii]			x
21429497	>gi|21429497|gb|AAM48966.1| trichodiene synthase [Fusarium boothii]			x
21429362	>gi|21429362|gb|AAM48846.1| trichodiene synthase [Fusarium boothii]			x
21429416	>gi|21429416|gb|AAM48894.1| trichodiene synthase [Fusarium pseudograminearum]			x
21429398	>gi|21429398|gb|AAM48878.1| trichodiene synthase [Fusarium pseudograminearum]			x
21429371	>gi|21429371|gb|AAM48854.1| trichodiene synthase [Fusarium pseudograminearum]			x
21429389	>gi|21429389|gb|AAM48870.1| trichodiene synthase [Fusarium pseudograminearum]			x
21429560	>gi|21429560|gb|AAM49022.1| trichodiene synthase [Fusarium cortaderiae]			x
21429551	>gi|21429551|gb|AAM49014.1| trichodiene synthase [Fusarium cortaderiae]			x
21429488	>gi|21429488|gb|AAM48958.1| trichodiene synthase [Fusarium meridionale]			x
21429479	>gi|21429479|gb|AAM48950.1| trichodiene synthase [Fusarium meridionale]			x
21429470	>gi|21429470|gb|AAM48942.1| trichodiene synthase [Gibberella zeae]			x
21429443	>gi|21429443|gb|AAM48918.1| trichodiene synthase [Fusarium austroamericanum]			x
21429425	>gi|21429425|gb|AAM48902.1| trichodiene synthase [Fusarium meridionale]			x
21429515	>gi|21429515|gb|AAM48982.1| trichodiene synthase [Fusarium austroamericanum]			x
21429452	>gi|21429452|gb|AAM48926.1| trichodiene synthase [Fusarium austroamericanum]			x
21429587	>gi|21429587|gb|AAM49046.1| trichodiene synthase [Fusarium asiaticum]			x
21429461	>gi|21429461|gb|AAM48934.1| trichodiene synthase [Fusarium asiaticum]			x
21429533	>gi|21429533|gb|AAM48998.1| trichodiene synthase [Fusarium mesoamericanum]			x
14091062	>gi|14091062|gb|AAK53579.1| trichodiene synthase [Gibberella zeae]			x
33413589	>gi|33413589|gb|AAN05033.1| trichodiene synthase [Fusarium culmorum]			x
33413593	>gi|33413593|gb|AAN05035.1| trichodiene synthase [Fusarium sporotrichioides]			x
33413595	>gi|33413595|gb|AAN05036.1| trichodiene synthase [Fusarium poae]			x
22087477	>gi|22087477|gb|AAM90953.1| trichodiene synthetase [Gibberella zeae]			x
22087480	>gi|22087480|gb|AAM90954.1| trichodiene synthetase [Gibberella zeae]			x
13096103	>gi|13096103|pdb|1DGP|B Chain B, Aristolochene Synthase Farnesol Complex			x
416643	>gi|416643|sp|Q03471|ARIS_PENRO Aristolochene synthase (Sesquiterpene cyclase) (AS)			x
6467980	>gi|6467980|gb|AAF13264.1| aristolochene synthase [Aspergillus terreus]			x
20150364	>gi|20150364|pdb|1J8D|D Chain D, Structure Of The Metal-Free Form Of The Deoxy-D-Mannose-Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
20150363	>gi|20150363|pdb|1J8D|C Chain C, Structure Of The Metal-Free Form Of The Deoxy-D-Mannose-Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x
20150362	>gi|20150362|pdb|1J8D|B Chain B, Structure Of The Metal-Free Form Of The Deoxy-D-Mannose-Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x
20150361	>gi|20150361|pdb|1J8D|A Chain A, Structure Of The Metal-Free Form Of The Deoxy-D-Mannose-Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x
68342600	>gi|68342600|gb|AAY90206.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Pseudomonas fluorescens Pf-5]			x
70728301	>gi|70728301|ref|YP_258050.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Pseudomonas fluorescens Pf-5]			x
85675992	>gi|85675992|dbj|BAE77242.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Escherichia coli W3110]	ESA, swissprot		x
16131088	>gi|16131088|ref|NP_417665.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Escherichia coli K12]	ESA, swissprot		x
81170926	>gi|81170926|sp|P0ABZ4|KDSC_ECOLI 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (KDO 8-P phosphatase)	ESA, swissprot		x
81170925	>gi|81170925|sp|P0ABZ5|KDSC_ECO57 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (KDO 8-P phosphatase)	ESA, swissprot		x
15833331	>gi|15833331|ref|NP_312104.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Escherichia coli O157:H7]	ESA, swissprot		x
74313735	>gi|74313735|ref|YP_312154.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Shigella sonnei Ss046]	ESA, swissprot		x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
15803738	>gi|15803738|ref|NP_289772.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Escherichia coli O157:H7 EDL933]	ESA, swissprot		x
75431114	>gi|75431114|ref|ZP_00732941.1| 3-deoxy-manno-octulosonate-8-phosphatase [Actinobacillus succinogenes 130Z]			x
74276377	>gi|74276377|gb|EAO49988.1| 3-deoxy-manno-octulosonate-8-phosphatase [Actinobacillus succinogenes 130Z]			x
30064536	>gi|30064536|ref|NP_838707.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Shigella flexneri 2a str. 2457T]	ESA, swissprot		x
24114487	>gi|24114487|ref|NP_708997.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Shigella flexneri 2a str. 301]	ESA, swissprot		x
54037513	>gi|54037513|sp|P67654|KDSC_SHIFL 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (KDO 8-P phosphatase)	ESA, swissprot		x
26249784	>gi|26249784|ref|NP_755824.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Escherichia coli CFT073]	ESA, swissprot		x
54041561	>gi|54041561|sp|P67653|KDSC_ECOL6 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (KDO 8-P phosphatase)	ESA, swissprot		x
1176845	>gi|1176845|sp|P45314|KDOP_HAEIN 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (KDO 8-P phosphatase)			x
20150637	>gi|20150637|pdb|1K1E|L Chain L, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose-Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x
20150636	>gi|20150636|pdb|1K1E|K Chain K, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
20150635	>gi|20150635|pdb|1K1E|J Chain J, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose-Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x
20150634	>gi|20150634|pdb|1K1E|I Chain I, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose-Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x
20150633	>gi|20150633|pdb|1K1E|H Chain H, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x
20150632	>gi|20150632|pdb|1K1E|G Chain G, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x
20150631	>gi|20150631|pdb|1K1E|F Chain F, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose-Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x
20150630	>gi|20150630|pdb|1K1E|E Chain E, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x
20150629	>gi|20150629|pdb|1K1E|D Chain D, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x
20150628	>gi|20150628|pdb|1K1E|C Chain C, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x
20150627	>gi|20150627|pdb|1K1E|B Chain B, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x
20150626	>gi|20150626|pdb|1K1E|A Chain A, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x
68058479	>gi|68058479|gb|AAX88732.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Haemophilus influenzae 86-028NP]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
68250280	>gi|68250280|ref|YP_249392.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Haemophilus influenzae 86-028NP]			x
10835408	>gi|10835408|pdb|1FEZ|D Chain D, The Crystal Structure Of Bacillus Cereus Phosphonoacetaldehyde Hydrolase Complexed With Tungstate, A Product Analog			x
48425373	>gi|48425373|pdb|1RQN|B Chain B, Phosphonoacetaldehyde Hydrolase Complexed With Magnesium			x
52695385	>gi|52695385|pdb|1RDF|F Chain F, G50p Mutant Of Phosphonoacetaldehyde Hydrolase In Complex With Substrate Analogue Vinyl Sulfonate			x
55669792	>gi|55669792|pdb|1SWW|B Chain B, Crystal Structure Of The Phosphonoacetaldehyde Hydrolase D12a Mutant Complexed With Magnesium And Substrate Phosphonoacetaldehyde			x
68345624	>gi|68345624|gb|AAY93230.1| 2-phosphonoacetaldehyde hydrolase [Pseudomonas fluorescens Pf-5]			x
49331329	>gi|49331329|gb|AAT61975.1| possible phosphonoacetaldehyde hydrolase [Bacillus thuringiensis serovar konkukian str. 97-27]			x
51977481	>gi|51977481|gb|AAU19031.1| possible phosphonoacetaldehyde hydrolase [Bacillus cereus E33L]			x
26988932	>gi|26988932|ref|NP_744357.1| 2-phosphonoacetaldehyde hydrolase [Pseudomonas putida KT2440]			x
28270410	>gi|28270410|emb|CAD63313.1| phosphonoacetaldehyde hydrolase [Lactobacillus plantarum WCFS1]			x
9947248	>gi|9947248|gb|AAG04700.1| 2-phosphonoacetaldehyde hydrolase [Pseudomonas aeruginosa PAO1]			x
77383909	>gi|77383909|gb|ABA75422.1| Phosphonoacetaldehyde hydrolase [Pseudomonas fluorescens PfO-1]			x
18254515	>gi|18254515|gb|AAB86434.2| phosphonoacetaldehyde hydrolase [Bacillus cereus]			x
18996325	>gi|18996325|emb|CAD24489.1| 2-phosphonoacetaldehyde hydrolase [Pseudomonas putida]			x
47566213	>gi|47566213|ref|ZP_00237241.1| phosphonoacetaldehyde phosphonohydrolase VCA0606 [Bacillus cereus G9241]			x
16501700	>gi|16501700|emb|CAD08888.1| phosphonoacetaldehyde phosphonohydrolase [Salmonella enterica subsp. enterica serovar Typhi]			x
37200675	>gi|37200675|dbj|BAC96500.1| phosphonoacetaldehyde phosphonohydrolase [Vibrio vulnificus YJ016]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
56128670	>gi|56128670|gb|AAV78176.1| phosphonoacetaldehyde phosphonohydrolase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]			x
42780513	>gi|42780513|ref|NP_977760.1| phosphonoacetaldehyde phosphonohydrolase [Bacillus cereus ATCC 10987]			x
28808371	>gi|28808371|dbj|BAC61576.1| phosphonoacetaldehyde phosphonohydrolase [Vibrio parahaemolyticus RIMD 2210633]			x
4699780	>gi|4699780|pdb|1ZRN| Intermediate Structure Of L-2-Haloacid Dehalogenase With Monochloroacetate			x
6435583	>gi|6435583|pdb|1QQ5|B Chain B, Structure Of L-2-Haloacid Dehalogenase From Xanthobacter Autotrophicus			x
6435569	>gi|6435569|pdb|1QQ7|B Chain B, Structure Of L-2-Haloacid Dehalogenase From Xanthobacter Autotrophicus With Chloropropionic Acid Covalently Bound			X
3122193	>gi|3122193|sp|Q59728|HAD9_PSEPU (S)-2-haloacid dehalogenase H-109 (2-haloalkanoic acid dehalogenase H-109) (L-2-haloacid dehalogenase H-109) (Halocarboxylic acid halidohydrolase H-109)			x
3122178	>gi|3122178|sp|Q60099|HAD_XANAU (S)-2-haloacid dehalogenase (2-haloalkanoic acid dehalogenase) (L-2-haloacid dehalogenase) (Halocarboxylic acid halidohydrolase)			x
44887977	>gi|44887977|sp|P60527|HAD_AGRTR 2-haloalkanoic acid dehalogenase (L-2-haloacid dehalogenase) (Halocarboxylic acid halidohydrolase) (L-DEX) (Cryptic L-isomer-specific dehalogenase) (DhlS5I)			x
6580616	>gi|6580616|emb|CAA63861.2| 2-haloacid dehalogenase; L-2-halidohydrolase [Pseudomonas fluorescens]			x
396771	>gi|396771|emb|CAA46976.1| 2-haloacid halidohydrolase IVa [Burkholderia cepacia]			x
3122191	>gi|3122191|sp|Q52087|HADL_PSEPU (S)-2-haloacid dehalogenase (2-haloalkanoic acid dehalogenase) (L-2-haloacid dehalogenase) (Halocarboxylic acid halidohydrolase)			x
122212	>gi|122212|sp|P24070|HAD2_PSEUC (S)-2-haloacid dehalogenase II (2-haloalkanoic acid dehalogenase II) (L-2-haloacid dehalogenase II) (Halocarboxylic acid halidohydrolase II) (DEHCII)			x
691747	>gi|691747|gb|AAB32245.1| L-2-halo acid dehalogenase; L-DEX [Pseudomonas sp.]			x
417106	>gi|417106|sp|P24069|HAD1_PSEUC (S)-2-haloacid dehalogenase I (2-haloalkanoic acid dehalogenase I) (L-2-haloacid dehalogenase I) (Halocarboxylic acid halidohydrolase I) (DEHCI)			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
62086241	>gi|62086241|dbj|BAD91552.1| L-2-haloacid dehalogenase [Burkholderia sp. WS]			x
83719028	>gi|83719028|ref|YP_442519.1| haloacid dehalogenase, type II [Burkholderia thailandensis E264]			x
76578370	>gi|76578370|gb|ABA47845.1| haloacid dehalogenase, type II [Burkholderia pseudomallei 1710b]			x
77967574	>gi|77967574|gb|ABB08954.1| Haloacid dehalogenase, type II [Burkholderia sp. 383]			x
23347357	>gi|23347357|gb|AAN29496.1| haloacid dehalogenase, type II [Brucella suis 1330]			x
78693202	>gi|78693202|ref|ZP_00857716.1| Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2:HAD-superfamily hydrolase, subfamily IA, variant 1 [Bradyrhizobium sp. BTAi1]			x
321693	>gi|321693|pir||S29096 2-haloacid halidohydrolase IVa - Pseudomonas cepacia			x
14027103	>gi|14027103|dbj|BAB54057.1| 2-haloacid halidohydrolase Iva [Mesorhizobium loti MAFF303099]			x
52427537	>gi|52427537|gb|AAU48130.1| haloacid dehalogenase, type II [Burkholderia mallei ATCC 23344]			x
39651117	>gi|39651117|emb|CAE29640.1| putative 2-haloacid halidohydrolase Iva [Rhodopseudomonas palustris CGA009]			x
72119053	>gi|72119053|gb|AAZ61316.1| Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2 [Ralstonia eutropha JMP134]			x
4127501	>gi|4127501|emb|CAA06738.1| cryptic haloacid dehalogenase 1 [Burkholderia cepacia]			x
86160229	>gi|86160229|ref|YP_467014.1| haloacid dehalogenase, type II [Anaeromyxobacter dehalogenans 2CP-C]			x
76259263	>gi|76259263|ref|ZP_00766913.1| Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2 [Chloroflexus aurantiacus J-10-fl]			x
74017830	>gi|74017830|ref|ZP_00688453.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Burkholderia ambifaria AMMD]			X
67666092	>gi|67666092|ref|ZP_00463346.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Burkholderia cenocepacia HI2424]			X
68189622	>gi|68189622|gb|EAN04287.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Mesorhizobium sp. BNC1]			X
67907457	>gi|67907457|ref|ZP_00505859.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Polaromonas sp. JS666]			X

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
67777344	>gi|67777344|gb|EAM36972.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Polaromonas sp. JS666]			X
68559621	>gi|68559621|ref|ZP_00598953.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Ralstonia metallidurans CH34]			X
27355843	>gi|27355843|dbj|BAC52825.1| 2-haloalkanoic acid dehalogenase [Bradyrhizobium japonicum USDA 110]			X
56311903	>gi|56311903|emb|CAI06548.1| putative 2-haloalkanoic acid dehalogenase [Azoarcus sp. EbN1]			X
17428377	>gi|17428377|emb|CAD15064.1| PUTATIVE 2-HALOALKANOIC ACID DEHALOGENASE PROTEIN [Ralstonia solanacearum]			X
4468652	>gi|4468652|emb|CAB38090.1| haloalkanoic acid dehalogenase [Pseudomonas putida]			x
155350	>gi|155350|gb|AAA27590.1| halocarboxylic acid halidohydrolase			x
15073899	>gi|15073899|emb|CAC45540.1| PUTATIVE ALPHA-HALOCARBOXYLIC ACID DEHALOGENASE PROTEIN [Sinorhizobium meliloti]			x
12723306	>gi|12723306|gb|AAK04527.1| beta-phosphoglucomutase (EC 5.4.2.6) [Lactococcus lactis subsp. lactis Il1403]			x
23200375	>gi|23200375|pdb|1LVH|B Chain B, The Structure Of Phosphorylated Beta-Phosphoglucomutase From Lactoccocus Lactis To 2.3 Angstrom Resolution			x
74312316	>gi|74312316|ref|YP_310735.1| putative beta-phosphoglucomutase [Shigella sonnei Ss046]			x
1495997	>gi|1495997|emb|CAA94734.1| beta-phosphoglucomutase [Lactococcus lactis]			x
47093202	>gi|47093202|ref|ZP_00230975.1| beta-phosphoglucomutase [Listeria monocytogenes str. 4b H7858]			x
47097361	>gi|47097361|ref|ZP_00234914.1| beta-phosphoglucomutase [Listeria monocytogenes str. 1/2a F6854]			x
13361361	>gi|13361361|dbj|BAB35319.1| putative beta-phosphoglucomutase [Escherichia coli O157:H7]			x
29342999	>gi|29342999|gb|AAO80763.1| beta-phosphoglucomutase [Enterococcus faecalis V583]			x
46909020	>gi|46909020|ref|YP_015409.1| beta-phosphoglucomutase [Listeria monocytogenes str. 4b F2365]			x
28269830	>gi|28269830|emb|CAD62727.1| beta-phosphoglucomutase [Lactobacillus plantarum WCFS1]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
28269859	>gi|28269859|emb|CAD62756.1| beta-phosphoglucomutase [Lactobacillus plantarum WCFS1]			x
7225613	>gi|7225613|gb|AAF40831.1| beta-phosphoglucomutase [Neisseria meningitidis MC58]			x
7380718	>gi|7380718|emb|CAB85309.1| beta-phosphoglucomutase [Neisseria meningitidis Z2491]			x
7380722	>gi|7380722|emb|CAB85313.1| beta-phosphoglucomutase [Neisseria meningitidis Z2491]			x
24051633	>gi|24051633|gb|AAN42930.1| putative beta-phosphoglucomutase [Shigella flexneri 2a str. 301]			x
15025638	>gi|15025638|gb|AAK80561.1| Beta-phosphoglucomutase [Clostridium acetobutylicum ATCC 824]			x
14090050	>gi|14090050|emb|CAC13808.1| BETA-PHOSPHOGLUCOMUTASE (BETA-PGM) [Mycoplasma pulmonis]			x
3724126	>gi|3724126|emb|CAA11906.1| beta-phosphoglucomutase [Lactobacillus sanfranciscensis]			x
18655482	>gi|18655482|pdb|1K70|A Chain A, The Structure Of Escherichia Coli Cytosine Deaminase Bound To 4-Hydroxy-3,4-Dihydro-1h-Pyrimidin-2-One			x
55669648	>gi|55669648|pdb|1RA0|A Chain A, Bacterial Cytosine Deaminase D314g Mutant Bound To 5-Fluoro- 4-(S)-Hydroxy-3,4-Dihydropyrimidine			x
55669649	>gi|55669649|pdb|1RA5|A Chain A, Bacterial Cytosine Deaminase D314a Mutant Bound To 5-Fluoro- 4-(S)-Hydroxyl-3,4-Dihydropyrimidine			x
55669650	>gi|55669650|pdb|1RAK|A Chain A, Bacterial Cytosine Deaminase D314s Mutant Bound To 5-Fluoro- 4-(S)-Hydroxyl-3,4-Dihydropyrimidine			x
1246363	>gi|1246363|gb|AAA93512.1| cytosine deaminase:uracil phosphoribosyltransferase fusion protein			x
82736446	>gi|82736446|ref|ZP_00899304.1| cytosine deaminase [Pseudomonas putida F1]			x
1657533	>gi|1657533|gb|AAB18061.1| cytosine deaminase [Escherichia coli]			x
83745851	>gi|83745851|ref|ZP_00942908.1| Cytosine deaminase [Ralstonia solanacearum UW551]			x
83952722	>gi|83952722|ref|ZP_00961452.1| cytosine deaminase [Roseovarius nubinhibens ISM]			x
84387544	>gi|84387544|ref|ZP_00990562.1| cytosine deaminase [Vibrio splendidus 12B01]			x
84714350	>gi|84714350|ref|ZP_01021815.1| codA, RSc1594; probable cytosine deaminase (cytosine aminohydrolase) protein [Polaromonas naphthalenivorans CJ2]			x
83717088	>gi|83717088|ref|YP_439833.1| cytosine deaminase [Burkholderia thailandensis E264]			x
86359986	>gi|86359986|ref|YP_471876.1| cytosine deaminase protein [Rhizobium etli CFN 42]			x
85705815	>gi|85705815|ref|ZP_01036912.1| cytosine deaminase [Roseovarius sp. 217]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
86135886	>gi|86135886|ref|ZP_01054465.1| Cytosine deaminase [Roseobacter sp. MED193]			x
86144452	>gi|86144452|ref|ZP_01062784.1| cytosine deaminase [Vibrio sp. MED222]			x
86163518	>gi|86163518|gb|EAQ64793.1| cytosine deaminase [Marinomonas sp. MED121]			x
68567500	>gi|68567500|gb|AAY80429.1| cytosine deaminase [Sulfolobus acidocaldarius DSM 639]			x
86606249	>gi|86606249|ref|YP_475012.1| cytosine deaminase [Cyanobacteria bacterium Yellowstone A-Prime]			x
86607889	>gi|86607889|ref|YP_476651.1| cytosine deaminase [Cyanobacteria bacterium Yellowstone B-Prime]			x
68345688	>gi|68345688|gb|AAY93294.1| cytosine deaminase [Pseudomonas fluorescens Pf-5]			x
57339189	>gi|57339189|gb|AAW49583.1| cytosine deaminase [Bifidobacterium breve]			x
67664077	>gi|67664077|ref|ZP_00461354.1| Cytosine deaminase [Burkholderia cenocepacia HI2424]			x
23464639	>gi|23464639|ref|NP_695242.1| cytosine deaminase [Bifidobacterium longum NCC2705]			x
56912036	>gi|56912036|dbj|BAD66563.1| cytosine deaminase [Bacillus clausii KSM-K16]			x
13359847	>gi|13359847|dbj|BAB33813.1| cytosine deaminase [Escherichia coli O157:H7]			x
16504399	>gi|16504399|emb|CAD07851.1| cytosine deaminase [Salmonella enterica subsp. enterica serovar Typhi]			x
23494693	>gi|23494693|dbj|BAC19659.1| putative cytosine deaminase [Corynebacterium efficiens YS-314]			x
37201459	>gi|37201459|dbj|BAC97281.1| cytosine deaminase [Vibrio vulnificus YJ016]			x
26106750	>gi|26106750|gb|AAN78935.1| Cytosine deaminase [Escherichia coli CFT073]			x
27358767	>gi|27358767|gb|AAO07716.1| Cytosine deaminase [Vibrio vulnificus CMCP6]			x
35213096	>gi|35213096|dbj|BAC90469.1| cytosine deaminase [Gloeobacter violaceus PCC 7421]			x
14524455	>gi|14524455|gb|AAK65940.1| putative CodA1 cytosine deaminase [Sinorhizobium meliloti 1021]			x
14025224	>gi|14025224|dbj|BAB51825.1| creatinine deaminase [Mesorhizobium loti MAFF303099]			x
13816107	>gi|13816107|gb|AAK42880.1| Cytosine deaminase (codA) [Sulfolobus solfataricus P2]			x
15623524	>gi|15623524|dbj|BAB67512.1| 412aa long hypothetical cytosine deaminase [Sulfolobus tokodaii str. 7]			x
56129520	>gi|56129520|gb|AAV79026.1| cytosine deaminase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]			x
581052	>gi|581052|emb|CAA45196.1| cytosine deaminase [Escherichia coli]			x
16421892	>gi|16421892|gb|AAL22203.1| putative cytosine deaminase [Salmonella typhimurium LT2]			x

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>59711138</td><td>>gi|59711138|ref|YP_203914.1| cytosine deaminase [Vibrio fischeri ES114]</td><td></td><td></td><td>x</td></tr>
<tr><td>28203958</td><td>>gi|28203958|gb|AAO36398.1| cytosine deaminase [Clostridium tetani E88]</td><td></td><td></td><td>x</td></tr>
<tr><td>26989908</td><td>>gi|26989908|ref|NP_745333.1| cytosine deaminase [Pseudomonas putida KT2440]</td><td></td><td></td><td>x</td></tr>
<tr><td>62181842</td><td>>gi|62181842|ref|YP_218259.1| cytosine deaminase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]</td><td></td><td></td><td>x</td></tr>
<tr><td>18144416</td><td>>gi|18144416|dbj|BAB80462.1| cytosine deaminase [Clostridium perfringens str. 13]</td><td></td><td></td><td>x</td></tr>
<tr><td>28809611</td><td>>gi|28809611|dbj|BAC62586.1| putative cytosine deaminase [Vibrio parahaemolyticus RIMD 2210633]</td><td></td><td></td><td>x</td></tr>
<tr><td>56679381</td><td>>gi|56679381|gb|AAV96047.1| cytosine deaminase, putative [Silicibacter pomeroyi DSS-3]</td><td></td><td></td><td>x</td></tr>
<tr><td>17428610</td><td>>gi|17428610|emb|CAD15296.1| PROBABLE CYTOSINE DEAMINASE (CYTOSINE AMINOHYDROLASE) PROTEIN [Ralstonia solanacearum]</td><td></td><td></td><td>x</td></tr>
<tr><td>77388331</td><td>>gi|77388331|gb|ABA79516.1| Cytosine deaminase [Rhodobacter sphaeroides 2.4.1]</td><td></td><td></td><td>x</td></tr>
<tr><td>51591311</td><td>>gi|51591311|emb|CAH22977.1| cytosine deaminase [Yersinia pseudotuberculosis IP 32953]</td><td></td><td></td><td>x</td></tr>
<tr><td>46916477</td><td>>gi|46916477|emb|CAG23242.1| putative cytosine deaminase [Photobacterium profundum SS9]</td><td></td><td></td><td>x</td></tr>
<tr><td>36958684</td><td>>gi|36958684|gb|AAQ87152.1| Cytosine deaminase [Rhizobium sp. NGR234]</td><td></td><td></td><td>x</td></tr>
<tr><td>45356869</td><td>>gi|45356869|gb|AAS58473.1| cytosine deaminase [Escherichia coli]</td><td></td><td></td><td>x</td></tr>
<tr><td>51493749</td><td>>gi|51493749|gb|AAU04862.1| cytosine deaminase [Tamarix chinensis]</td><td></td><td></td><td>x</td></tr>
<tr><td>67153359</td><td>>gi|67153359|ref|ZP_00415104.1| Cytosine deaminase [Azotobacter vinelandii AvOP]</td><td></td><td></td><td>x</td></tr>
<tr><td>67779564</td><td>>gi|67779564|gb|EAM39182.1| Cytosine deaminase [Polaromonas sp. JS666]</td><td></td><td></td><td>x</td></tr>
<tr><td>68560577</td><td>>gi|68560577|ref|ZP_00599889.1| Cytosine deaminase [Rubrobacter xylanophilus DSM 9941]</td><td></td><td></td><td>x</td></tr>
<tr><td>3892031</td><td>>gi|3892031|pdb|1A4M|D Chain D, Ada Structure Complexed With Purine Riboside At Ph 7.0</td><td></td><td></td><td>x</td></tr>
<tr><td>55669583</td><td>>gi|55669583|pdb|1QXL|A Chain A, Crystal Structure Of Adenosine Deaminase Complexed With Fr235380</td><td></td><td></td><td>x</td></tr>
<tr><td>55670514</td><td>>gi|55670514|pdb|1W1I|H Chain H, Crystal Structure Of Dipeptidyl Peptidase Iv (Dppiv Or Cd26) In Complex With Adenosine Deaminase</td><td></td><td></td><td>x</td></tr>
<tr><td>1518868</td><td>>gi|1518868|gb|AAB07142.1| adenosine deaminase (ADA) [Mus musculus]</td><td></td><td></td><td>x</td></tr>
<tr><td>74312050</td><td>>gi|74312050|ref|YP_310469.1| adenosine deaminase [Shigella sonnei Ss046]</td><td></td><td></td><td>x</td></tr>
<tr><td>75765416</td><td>>gi|75765416|pdb|1WXZ|A Chain A, Crystal Structure Of Adenosine Deaminase Ligated With A Potent Inhibitor</td><td></td><td></td><td>x</td></tr>
<tr><td>82497819</td><td>>gi|82497819|ref|ZP_00883345.1| Adenosine deaminase [Shewanella sp. MR-4]</td><td></td><td></td><td>x</td></tr>
<tr><td>82743060</td><td>>gi|82743060|ref|ZP_00905728.1| Adenosine deaminase [Shewanella sp. W3-18-1]</td><td></td><td></td><td>x</td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
83571009	>gi|83571009|ref|ZP_00922451.1| COG1816: Adenosine deaminase [Shigella dysenteriae 1012]			x
24376203	>gi|24376203|ref|NP_720247.1| adenosine deaminase [Shewanella oneidensis MR-1]			x
82777097	>gi|82777097|ref|YP_403446.1| adenosine deaminase [Shigella dysenteriae Sd197]			x
13361798	>gi|13361798|dbj|BAB35754.1| adenosine deaminase [Escherichia coli O157:H7]			x
69951986	>gi|69951986|ref|ZP_00639598.1| Adenosine deaminase [Shewanella frigidimarina NCIMB 400]			x
28805098	>gi|28805098|dbj|BAC58379.1| adenosine deaminase [Vibrio parahaemolyticus RIMD 2210633]			x
62898355	>gi|62898355|dbj|BAD97117.1| adenosine deaminase variant [Homo sapiens]			x
16419984	>gi|16419984|gb|AAL20385.1| adenosine deaminase [Salmonella typhimurium LT2]			x
52354740	>gi|52354740|gb|AAH82820.1| Adenosine deaminase [Xenopus tropicalis]			x
16502746	>gi|16502746|emb|CAD01904.1| adenosine deaminase [Salmonella enterica subsp. enterica serovar Typhi]			x
1197210	>gi|1197210|emb|CAA26130.1| adenosine deaminase [Homo sapiens]			x
75178481	>gi|75178481|ref|ZP_00698527.1| COG1816: Adenosine deaminase [Shigella boydii BS512]			x
75238816	>gi|75238816|ref|ZP_00722800.1| COG1816: Adenosine deaminase [Escherichia coli F11]			x
75257042	>gi|75257042|ref|ZP_00728602.1| COG1816: Adenosine deaminase [Escherichia coli E22]			x
75512944	>gi|75512944|ref|ZP_00735425.1| COG1816: Adenosine deaminase [Escherichia coli 53638]			x
75820650	>gi|75820650|ref|ZP_00750693.1| COG1816: Adenosine deaminase [Vibrio cholerae V51]			x
75822633	>gi|75822633|ref|ZP_00752223.1| COG1816: Adenosine deaminase [Vibrio cholerae RC385]			x
75830675	>gi|75830675|ref|ZP_00759949.1| COG1816: Adenosine deaminase [Vibrio cholerae MO10]			x
75855670	>gi|75855670|ref|ZP_00763315.1| COG1816: Adenosine deaminase [Vibrio sp. Ex25]			x
27806933	>gi|27806933|ref|NP_776312.1| adenosine deaminase [Bos taurus]			x
77629257	>gi|77629257|ref|ZP_00791843.1| COG1816: Adenosine deaminase [Yersinia pseudotuberculosis IP 31758]			x
69159081	>gi|69159081|gb|EAN71219.1| Adenosine deaminase [Shewanella denitrificans OS217]			x
77816434	>gi|77816434|ref|ZP_00815623.1| Adenosine deaminase [Shewanella putrefaciens CN-32]			x
77956975	>gi|77956975|ref|ZP_00821045.1| COG1816: Adenosine deaminase [Yersinia bercovieri ATCC 43970]			x
77963273	>gi|77963273|ref|ZP_00827084.1| COG1816: Adenosine deaminase [Yersinia mollaretii ATCC 43969]			x

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>77973198</td><td>>gi|77973198|ref|ZP_00828749.1| COG1816: Adenosine deaminase [Yersinia frederiksenii ATCC 33641]</td><td></td><td></td><td>x</td></tr>
<tr><td>77976844</td><td>>gi|77976844|ref|ZP_00832313.1| COG1816: Adenosine deaminase [Yersinia intermedia ATCC 29909]</td><td></td><td></td><td>x</td></tr>
<tr><td>56789878</td><td>>gi|56789878|gb|AAH88116.1| Adenosine deaminase [Rattus norvegicus]</td><td></td><td></td><td>x</td></tr>
<tr><td>24051977</td><td>>gi|24051977|gb|AAN43230.1| adenosine deaminase [Shigella flexneri 2a str. 301]</td><td></td><td></td><td>x</td></tr>
<tr><td>78368950</td><td>>gi|78368950|ref|ZP_00839137.1| Adenosine deaminase [Shewanella sp. PV-4]</td><td></td><td></td><td>x</td></tr>
<tr><td>78688097</td><td>>gi|78688097|ref|ZP_00852819.1| Adenosine deaminase [Shewanella sp. ANA-3]</td><td></td><td></td><td>x</td></tr>
<tr><td>78691154</td><td>>gi|78691154|ref|ZP_00855782.1| Adenosine deaminase [Shewanella sp. MR-7]</td><td></td><td></td><td>x</td></tr>
<tr><td>68544028</td><td>>gi|68544028|ref|ZP_00583706.1| Adenosine deaminase [Shewanella baltica OS155]</td><td></td><td></td><td>x</td></tr>
<tr><td>68547729</td><td>>gi|68547729|ref|ZP_00587259.1| Adenosine deaminase [Shewanella amazonensis SB2B]</td><td></td><td></td><td>x</td></tr>
<tr><td>145201</td><td>>gi|145201|gb|AAA23419.1| adenosine deaminase</td><td></td><td></td><td>x</td></tr>
<tr><td>25955532</td><td>>gi|25955532|gb|AAH40226.1| Adenosine deaminase [Homo sapiens]</td><td></td><td></td><td>x</td></tr>
<tr><td>62180050</td><td>>gi|62180050|ref|YP_216467.1| adenosine deaminase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]</td><td></td><td></td><td>x</td></tr>
<tr><td>51589788</td><td>>gi|51589788|emb|CAH21418.1| adenosine deaminase [Yersinia pseudotuberculosis IP 32953]</td><td></td><td></td><td>x</td></tr>
<tr><td>46914992</td><td>>gi|46914992|emb|CAG21767.1| putative adenosine deaminase [Photobacterium profundum SS9]</td><td></td><td></td><td>x</td></tr>
<tr><td>76259953</td><td>>gi|76259953|ref|ZP_00767596.1| Adenosine deaminase [Chloroflexus aurantiacus J-10-fl]</td><td></td><td></td><td>x</td></tr>
<tr><td>83719564</td><td>>gi|83719564|ref|YP_441103.1| N-acyl-D-amino-acid deacylase family protein [Burkholderia thailandensis E264]</td><td></td><td></td><td>x</td></tr>
<tr><td>74014202</td><td>>gi|74014202|ref|ZP_00684831.1| N-acyl-D-amino-acid deacylase [Burkholderia ambifaria AMMD]</td><td></td><td></td><td>x</td></tr>
<tr><td>67667435</td><td>>gi|67667435|ref|ZP_00464658.1| N-acyl-D-amino-acid deacylase [Burkholderia cenocepacia HI2424]</td><td></td><td></td><td>x</td></tr>
<tr><td>66043682</td><td>>gi|66043682|ref|YP_233523.1| N-acyl-D-amino-acid deacylase [Pseudomonas syringae pv. syringae B728a]</td><td></td><td></td><td>x</td></tr>
<tr><td>1488357</td><td>>gi|1488357|gb|AAB35881.1| D-aminoacylase; N-acyl-D-amino acid amidohydrolase [Achromobacter xylosoxidans]</td><td></td><td></td><td>x</td></tr>
<tr><td>67647671</td><td>>gi|67647671|ref|ZP_00445910.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia mallei NCTC 10247]</td><td></td><td></td><td>x</td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
72121190	>gi|72121190|gb|AAZ63376.1| N-acyl-D-amino-acid deacylase [Ralstonia eutropha JMP134]			x
77968282	>gi|77968282|gb|ABB09662.1| N-acyl-D-amino-acid deacylase [Burkholderia sp. 383]			x
67547194	>gi|67547194|ref|ZP_00425100.1| N-acyl-D-amino-acid deacylase [Burkholderia vietnamiensis G4]			x
68559991	>gi|68559991|ref|ZP_00599319.1| N-acyl-D-amino-acid deacylase [Ralstonia metallidurans CH34]			x
68556229	>gi|68556229|ref|ZP_00595572.1| N-acyl-D-amino-acid deacylase [Ralstonia metallidurans CH34]			x
3287879	>gi|3287879|sp|P94212|NDDD_ALCXX N-acyl-D-aspartate deacylase (N-acyl-D-aspartate amidohydrolase)			x
1707291	>gi|1707291|dbj|BAA08778.1| N-acyl-D-amino acids amidohydrolase [Achromobacter xylosoxidans]			x
48425876	>gi|48425876|pdb|1V51|A Chain A, The Functional Role Of The Binuclear Metal Center In D-Aminoacylase. One-Metal Activation And Second-Metal Attenuation			x
83745626	>gi|83745626|ref|ZP_00942684.1| D-aminoacylase [Ralstonia solanacearum UW551]			x
13194736	>gi|13194736|gb|AAK15530.1| D-aminoacylase [Alcaligenes faecalis]			x
52208687	>gi|52208687|emb|CAH34623.1| D-aminoacylase [Burkholderia pseudomallei K96243]			x
67757137	>gi|67757137|ref|ZP_00496015.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia pseudomallei Pasteur]			x
33576700	>gi|33576700|emb|CAE33777.1| N-acyl-D-glutamate deacylase [Bordetella bronchiseptica RB50]	ESA		x
33566217	>gi|33566217|emb|CAE37123.1| N-acyl-D-glutamate deacylase [Bordetella parapertussis]	ESA		x
33571981	>gi|33571981|emb|CAE41503.1| N-acyl-D-glutamate deacylase [Bordetella pertussis Tohama I]	ESA		x
17431661	>gi|17431661|emb|CAD18338.1| PROBABLE N-ACYL-D-GLUTAMATE DEACYLASE PROTEIN [Ralstonia solanacearum]			x
84355751	>gi|84355751|ref|ZP_00980625.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia cenocepacia PC184]			x
84362911	>gi|84362911|ref|ZP_00987522.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia dolosa AUO158]			x
67670108	>gi|67670108|ref|ZP_00466921.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia pseudomallei 1655]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
67762107	>gi|67762107|ref|ZP_00500810.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia pseudomallei S13]			x
48786563	>gi|48786563|ref|ZP_00282697.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia fungorum LB400]			x
22218652	>gi|22218652|pdb|1GKR|D Chain D, L-Hydantoinase (Dihydropyrimidinase) From Arthrobacter Aurescens			x
9931313	>gi|9931313|gb|AAG02130.1| L-hydantoinase HyuH [Arthrobacter aurescens]			x
3122243	>gi|3122243|sp|P81006|HYDL_ARTAU Non-ATP-dependent L-selective hydantoinase			x
21730180	>gi|21730180|pdb|1GKQ|D Chain D, D-Hydantoinase (Dihydropyrimidinase) From Thermus Sp. In Space Group P212121			x
23200227	>gi|23200227|pdb|1K1D|H Chain H, Crystal Structure Of D-Hydantoinase			x
34811416	>gi|34811416|pdb|1NFG|D Chain D, Structure Of D-Hydantoinase			x
82739934	>gi|82739934|ref|ZP_00902711.1| D-hydantoinase [Pseudomonas putida F1]			x
82747261	>gi|82747261|ref|ZP_00909760.1| D-hydantoinase [Clostridium beijerincki NCIMB 8052]			x
83369112	>gi|83369112|ref|ZP_00913970.1| D-hydantoinase [Rhodobacter sphaeroides ATCC 17025]			x
83368213	>gi|83368213|ref|ZP_00913078.1| D-hydantoinase [Rhodobacter sphaeroides ATCC 17025]			x
83374693	>gi|83374693|ref|ZP_00919463.1| D-hydantoinase [Rhodobacter sphaeroides ATCC 17029]			x
83374826	>gi|83374826|ref|ZP_00919594.1| D-hydantoinase [Rhodobacter sphaeroides ATCC 17029]			x
84686022	>gi|84686022|ref|ZP_01013918.1| D-hydantoinase [Rhodobacterales bacterium HTCC2654]			x
84711150	>gi|84711150|ref|ZP_01019452.1| D-hydantoinase [Polaromonas naphthalenivorans CJ2]			x
71146703	>gi|71146703|gb|AAZ27176.1| D-hydantoinase [Colwellia psychrerythraea 34H]			x
72117164	>gi|72117164|gb|AAZ59427.1| D-hydantoinase [Ralstonia eutropha JMP134]			x
3127836	>gi|3127836|emb|CAA18902.1| putative D-hydantoinase [Streptomyces coelicolor A3(2)]			x
1296441	>gi|1296441|emb|CAA62549.1| D-hydantoinase [Agrobacterium tumefaciens]			x
77388169	>gi|77388169|gb|ABA79354.1| putative D-hydantoinase (dihydropyrimidinase) [Rhodobacter sphaeroides 2.4.1]			x
3334230	>gi|3334230|sp|Q59699|HYDA_PSEPU D-hydantoinase (Dihydropyrimidinase) (DHPase)			x
78693606	>gi|78693606|ref|ZP_00858120.1| D-hydantoinase [Bradyrhizobium sp. BTAi1]			x
78694838	>gi|78694838|ref|ZP_00859351.1| D-hydantoinase [Bradyrhizobium sp. BTAi1]			x
78696155	>gi|78696155|ref|ZP_00860665.1| D-hydantoinase [Bradyrhizobium sp. BTAi1]			x
56911787	>gi|56911787|dbj|BAD66314.1| D-hydantoinase [Bacillus clausii KSM-K16]			x
23347063	>gi|23347063|gb|AAN29227.1| D-hydantoinase [Brucella suis 1330]			x

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>55794125</td><td>>gi|55794125|gb|AAV65953.1| D-hydantoinase [Bacillus sp. AR9]</td><td></td><td></td><td>x</td></tr>
<tr><td>27351554</td><td>>gi|27351554|dbj|BAC48560.1| D-hydantoinase [Bradyrhizobium japonicum USDA 110]</td><td></td><td></td><td>x</td></tr>
<tr><td>27351592</td><td>>gi|27351592|dbj|BAC48598.1| D-hydantoinase [Bradyrhizobium japonicum USDA 110]</td><td></td><td></td><td>x</td></tr>
<tr><td>17983665</td><td>>gi|17983665|gb|AAL52825.1| D-HYDANTOINASE [Brucella melitensis 16M]</td><td></td><td></td><td>x</td></tr>
<tr><td>15075477</td><td>>gi|15075477|emb|CAC47033.1| PUTATIVE D-HYDANTOINASE (DIHYDROPYRIMIDINASE) PROTEIN [Sinorhizobium meliloti]</td><td></td><td></td><td>x</td></tr>
<tr><td>28203869</td><td>>gi|28203869|gb|AAO36309.1| D-hydantoinase [Clostridium tetani E88]</td><td></td><td></td><td>x</td></tr>
<tr><td>56379800</td><td>>gi|56379800|dbj|BAD75708.1| dihydropyrimidinase (D-hydantoinase) [Geobacillus kaustophilus HTA426]</td><td></td><td></td><td>x</td></tr>
<tr><td>56678396</td><td>>gi|56678396|gb|AAV95062.1| D-hydantoinase [Silicibacter pomeroyi DSS-3]</td><td></td><td></td><td>x</td></tr>
<tr><td>77964327</td><td>>gi|77964327|gb|ABB05708.1| D-hydantoinase [Burkholderia sp. 383]</td><td></td><td></td><td>x</td></tr>
<tr><td>77389882</td><td>>gi|77389882|gb|ABA81066.1| putative D-hydantoinase dihydropyrimidinase [Rhodobacter sphaeroides 2.4.1]</td><td></td><td></td><td>x</td></tr>
<tr><td>77383666</td><td>>gi|77383666|gb|ABA75179.1| D-hydantoinase [Pseudomonas fluorescens PfO-1]</td><td></td><td></td><td>x</td></tr>
<tr><td>27903506</td><td>>gi|27903506|gb|AAO24771.1| D-hydantoinase [Arthrobacter crystallopoietes]</td><td></td><td></td><td>x</td></tr>
<tr><td>18478562</td><td>>gi|18478562|gb|AAL73199.1| D-hydantoinase [Agrobacterium sp. IP I-671]</td><td></td><td></td><td>x</td></tr>
<tr><td>37222601</td><td>>gi|37222601|gb|AAQ90019.1| D-hydantoinase [Pseudomonas putida]</td><td></td><td></td><td>x</td></tr>
<tr><td>85675686</td><td>>gi|85675686|dbj|BAE76939.1| D-stereospecific phenylhydantoinase [Escherichia coli W3110]</td><td></td><td></td><td>x</td></tr>
<tr><td>1311330</td><td>>gi|1311330|pdb|1KRB|C Chain C, Active Site Mutant, Nickel Metalloenzyme Mol_id: 1; Molecule: Urease; Chain: A, B, C; Ec: 3.5.1.5; Mutation: H(C 219)a; Heterogen: Carbon Dioxide; Heterogen: Nickel</td><td></td><td></td><td>x</td></tr>
<tr><td>1311327</td><td>>gi|1311327|pdb|1KRC|C Chain C, Active Site Mutant, Nickel Metalloenzyme Mol_id: 1; Molecule: Urease; Chain: A, B, C; Ec: 3.5.1.5; Mutation: H(C 320)a; Heterogen: Carbon Dioxide; Heterogen: Nickel</td><td></td><td></td><td>x</td></tr>
<tr><td>76557515</td><td>>gi|76557515|emb|CAI49096.1| urease (EC 3.5.1.5), alpha subunit [Natronomonas pharaonis DSM 2160]</td><td></td><td></td><td>x</td></tr>
<tr><td>137070</td><td>>gi|137070|sp|P18314|URE1_KLEAE Urease alpha subunit (Urea amidohydrolase)</td><td></td><td></td><td>x</td></tr>
<tr><td>224797</td><td>>gi|224797|prf||1201293A urease</td><td></td><td></td><td>x</td></tr>
<tr><td>227457</td><td>>gi|227457|prf||1704174C urease alpha</td><td></td><td></td><td>x</td></tr>
<tr><td>7245287</td><td>>gi|7245287|pdb|1EF2|A Chain A, Crystal Structure Of Manganese-Substituted Klebsiella Aerogenes Urease</td><td></td><td></td><td>x</td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
16974909	>gi|16974909|pdb|1E9Y|B Chain B, Crystal Structure Of Helicobacter Pylori Urease In Complex With Acetohydroxamic Acid			x
16974911	>gi|16974911|pdb|1E9Z|B Chain B, Crystal Structure Of Helicobacter Pylori Urease			x
14278353	>gi|14278353|pdb|1IE7|C Chain C, Phosphate Inhibited Bacillus Pasteurii Urease Crystal Structure			x
39654041	>gi|39654041|pdb|1EJW|C Chain C, Crystal Structure Of Wild-Type Klebsiella Aerogenes Urease At 298k			x
7245484	>gi|7245484|pdb|4UBP|C Chain C, Structure Of Bacillus Pasteurii Urease Inhibited With Acetohydroxamic Acid At 1.55 A Resolution			x
85541984	>gi|85541984|sp|Q6A3P9|UREA_ASPFU Urease (Urea amidohydrolase)			x
2130642	>gi|2130642|gb|AAC46128.1| urease structural subunit C [Bordetella bronchiseptica]			x
82500240	>gi|82500240|ref|ZP_00885663.1| Urease, alpha subunit [Caldicellulosiruptor saccharolyticus DSM 8903]			x
82735364	>gi|82735364|ref|ZP_00898227.1| Urease, alpha subunit [Pseudomonas putida F1]			x
83368250	>gi|83368250|ref|ZP_00913114.1| Urease, alpha subunit [Rhodobacter sphaeroides ATCC 17025]			x
83373265	>gi|83373265|ref|ZP_00918044.1| Urease, alpha subunit [Rhodobacter sphaeroides ATCC 17029]			x
83680720	>gi|83680720|ref|ZP_00942424.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia pseudomallei 406e]			x
3915207	>gi|3915207|sp|O54420|URE1_ACTPL Urease alpha subunit (Urea amidohydrolase)			x
137071	>gi|137071|sp|P26929|URE1_LACFE Acid urease alpha subunit (Urea amidohydrolase)			x
83748047	>gi|83748047|ref|ZP_00945076.1| Urease alpha subunit [Ralstonia solanacearum UW551]			x
83944265	>gi|83944265|ref|ZP_00956720.1| urease, alpha subunit [Sulfitobacter sp. EE-36]			x
83953306	>gi|83953306|ref|ZP_00962028.1| urease, alpha subunit [Sulfitobacter sp. NAS-14.1]			x
84317527	>gi|84317527|ref|ZP_00965968.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Pseudomonas aeruginosa C3719]			x
84357037	>gi|84357037|ref|ZP_00981867.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia cenocepacia PC184]			x
84361059	>gi|84361059|ref|ZP_00985743.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia dolosa AUO158]			x
84387642	>gi|84387642|ref|ZP_00990659.1| urease, alpha subunit [Vibrio splendidus 12B01]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
84499667	>gi|84499667|ref|ZP_00997955.1| urease, alpha subunit [Oceanicola batsensis HTCC2597]			x
84503105	>gi|84503105|ref|ZP_01001201.1| Urease [Oceanicola batsensis HTCC2597]			x
84515944	>gi|84515944|ref|ZP_01003305.1| urease, alpha subunit [Loktanella vestfoldensis SKA53]			x
84685183	>gi|84685183|ref|ZP_01013082.1| urease, alpha subunit [Rhodobacterales bacterium HTCC2654]			x
84714992	>gi|84714992|ref|ZP_01022214.1| Urease, alpha subunit [Polaromonas naphthalenivorans CJ2]			x
83720169	>gi|83720169|ref|YP_442042.1| urease, alpha subunit [Burkholderia thailandensis E264]			x
580821	>gi|580821|emb|CAA55175.1| urease [Sporosarcina pasteurii]			x
82751878	>gi|82751878|ref|YP_417619.1| urease alpha subunit [Staphylococcus aureus RF122]			x
82702370	>gi|82702370|ref|YP_411936.1| urease, alpha subunit [Nitrosospira multiformis ATCC 25196]			x
83647213	>gi|83647213|ref|YP_435648.1| urease, alpha subunit [Hahella chejuensis KCTC 2396]			x
71796401	>gi|71796401|gb|AAZ41152.1| putative urease structural subunit C (alpha) [Candidatus Blochmannia pennsylvanicus str. BPEN]			x
62527922	>gi|62527922|ref|ZP_00389185.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Streptococcus thermophilus LMD-9]			x
48782084	>gi|48782084|ref|ZP_00278657.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia fungorum LB400]			x
48855146	>gi|48855146|ref|ZP_00309306.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Cytophaga hutchinsonii]			x
23005331	>gi|23005331|ref|ZP_00048203.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Magnetospirillum magnetotacticum MS-1]			x
53687606	>gi|53687606|ref|ZP_00107943.2| COG0804: Urea amidohydrolase (urease) alpha subunit [Nostoc punctiforme PCC 73102]			x
32044238	>gi|32044238|ref|ZP_00141339.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Pseudomonas aeruginosa UCBPP-PA14]			x
53729261	>gi|53729261|ref|ZP_00133792.2| COG0804: Urea amidohydrolase (urease) alpha subunit [Actinobacillus pleuropneumoniae serovar 1 str. 4074]			x
53733072	>gi|53733072|ref|ZP_00155532.2| COG0804: Urea amidohydrolase (urease) alpha subunit [Haemophilus influenzae R2846]			x
47574669	>gi|47574669|ref|ZP_00244705.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Rubrivivax gelatinosus PM1]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
1185472	>gi|1185472|gb|AAA87854.1| urease alpha subunit [Yersinia pseudotuberculosis]			x
3688063	>gi|3688063|gb|AAC62257.1| urease [Cryptococcus neoformans var. grubii]			x
1652159	>gi|1652159|dbj|BAA17083.1| urease alpha subunit [Synechocystis sp. PCC 6803]			x
69936847	>gi|69936847|ref|ZP_00631602.1| Urease [Paracoccus denitrificans PD1222]			x
85700461	>gi|85700461|gb|ABC74584.1| urease structural subunit [Yersinia enterocolitica]			x
85704480	>gi|85704480|ref|ZP_01035582.1| urease, alpha subunit [Roseovarius sp. 217]			x
85705527	>gi|85705527|ref|ZP_01036625.1| Urease [Roseovarius sp. 217]			x
86137786	>gi|86137786|ref|ZP_01056362.1| urease, alpha subunit [Roseobacter sp. MED193]			x
86163898	>gi|86163898|gb|EAQ65170.1| urease, alpha subunit [Marinomonas sp. MED121]			x
86169120	>gi|86169120|gb|EAQ70376.1| urease, alpha subunit [Synechococcus sp. RS9917]			x
86358904	>gi|86358904|ref|YP_470796.1| urease (urea amidohydrolase) alpha subunit protein [Rhizobium etli CFN 42]			x
21958000	>gi|21958000|gb|AAM84814.1| urease (urea amidohydrolase) alpha subunit [Yersinia pestis KIM]			x
86605319	>gi|86605319|ref|YP_474082.1| urease, alpha subunit [Cyanobacteria bacterium Yellowstone A-Prime]			x
86607525	>gi|86607525|ref|YP_476287.1| urease, alpha subunit [Cyanobacteria bacterium Yellowstone B-Prime]			x
86571954	>gi|86571954|gb|ABD06511.1| urease, alpha subunit [Rhodopseudomonas palustris HaA2]			x
68348432	>gi|68348432|gb|AAY96038.1| urease, alpha subunit [Pseudomonas fluorescens Pf-5]			x
71361909	>gi|71361909|ref|ZP_00653069.1| Urease [Psychrobacter cryohalolentis K5]			x
71362355	>gi|71362355|ref|ZP_00653514.1| Urease [Psychrobacter cryohalolentis K5]			x
72002743	>gi|72002743|gb|AAZ58545.1| urease, alpha subunit [Prochlorococcus marinus str. NATL2A]			x
72494087	>gi|72494087|dbj|BAE17408.1| urease alpha subunit [Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305]			x
50788080	>gi|50788080|emb|CAE17672.1| putative urease [Aspergillus fumigatus]			x
1167544	>gi|1167544|gb|AAC43564.1| urease alpha subunit [Streptococcus salivarius]			x
74099907	>gi|74099907|gb|AAZ99164.1| urease alpha subunit [Streptococcus vestibularis]			x
71556913	>gi|71556913|gb|AAZ36124.1| urease, alpha subunit [Pseudomonas syringae pv. phaseolicola 1448A]			x
75703548	>gi|75703548|gb|ABA23224.1| Urease, alpha subunit [Anabaena variabilis ATCC 29413]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
17429050	>gi|17429050|emb|CAD15734.1| PROBABLE UREASE (ALPHA SUBUNIT) PROTEIN [Ralstonia solanacearum]			x
49242634	>gi|49242634|emb|CAG41355.1| urease alpha subunit [Staphylococcus aureus subsp. aureus MRSA252]			x
49245514	>gi|49245514|emb|CAG43991.1| urease alpha subunit [Staphylococcus aureus subsp. aureus MSSA476]			x
33574493	>gi|33574493|emb|CAE39138.1| urease alpha subunit [Bordetella parapertussis]			x
33577421	>gi|33577421|emb|CAE34686.1| urease alpha subunit [Bordetella bronchiseptica RB50]			x
914897	>gi|914897|emb|CAA35697.1| urease alpha subunit [Ureaplasma urealyticum]			x
1780784	>gi|1780784|emb|CAA71385.1| urease catalytic subunit [Clostridium perfringens]			x
2636189	>gi|2636189|emb|CAB15681.1| urease (alpha subunit) [Bacillus subtilis subsp. subtilis str. 168]			x
57867797	>gi|57867797|ref|YP_189432.1| urease, alpha subunit [Staphylococcus epidermidis RP62A]			x
1174891	>gi|1174891|sp|P42823|URE2_HELHE Urease beta subunit (Urea amidohydrolase)			x
76579628	>gi|76579628|gb|ABA49103.1| urease, alpha subunit [Burkholderia pseudomallei 1710b]			x
74016945	>gi|74016945|ref|ZP_00687570.1| Urease [Burkholderia ambifaria AMMD]			x
74020417	>gi|74020417|ref|ZP_00691006.1| Urease [Rhodoferax ferrireducens DSM 15236]			x
75234470	>gi|75234470|ref|ZP_00718825.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Escherichia coli E110019]			x
15075493	>gi|15075493|emb|CAC47049.1| UREASE ALPHA SUBUNIT PROTEIN [Sinorhizobium meliloti]			x
76884645	>gi|76884645|gb|ABA59326.1| Urease, alpha subunit [Nitrosococcus oceani ATCC 19707]			x
77388295	>gi|77388295|gb|ABA79480.1| Urea amidohydrolase (urease) alpha subunit [Rhodobacter sphaeroides 2.4.1]			x
76875610	>gi|76875610|emb|CAI86831.1| urease, alpha subunit [Pseudoalteromonas haloplanktis TAC125]			x
9967061	>gi|9967061|gb|AAD28133.2| urease complex component UreC [Ureaplasma urealyticum serovar 13]			x
9967077	>gi|9967077|gb|AAD28139.2| urease complex component UreC [Ureaplasma parvum serovar 1]			x
9967085	>gi|9967085|gb|AAD28145.2| urease complex component UreC [Ureaplasma parvum serovar 14]			x
77543439	>gi|77543439|gb|ABA87133.1| urease B [Helicobacter pylori]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
77635026	>gi|77635026|ref|ZP_00797116.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Yersinia pestis Angola]			x
77966223	>gi|77966223|gb|ABB07603.1| Urease, alpha subunit [Burkholderia sp. 383]			x
77688020	>gi|77688020|ref|ZP_00803205.1| Urease, alpha subunit [Rhodopseudomonas palustris BisB5]			x
77740711	>gi|77740711|ref|ZP_00809197.1| Urease, alpha subunit [Rhodopseudomonas palustris BisA53]			x
78170118	>gi|78170118|gb|ABB27215.1| Urease, alpha subunit [Synechococcus sp. CC9902]			x
78198587	>gi|78198587|gb|ABB36352.1| urease, alpha subunit [Synechococcus sp. CC9605]			x
77955793	>gi|77955793|ref|ZP_00820133.1| Urease, alpha subunit [Marinobacter aquaeolei VT8]			x
77957751	>gi|77957751|ref|ZP_00821799.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Yersinia bercovieri ATCC 43970]			x
77973096	>gi|77973096|ref|ZP_00828648.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Yersinia frederiksenii ATCC 33641]			x
77978460	>gi|77978460|ref|ZP_00833889.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Yersinia intermedia ATCC 29909]			x
78712719	>gi|78712719|gb|ABB49896.1| urease, alpha subunit [Prochlorococcus marinus str. MIT 9312]			x
78494014	>gi|78494014|ref|ZP_00846244.1| Urease, alpha subunit [Rhodopseudomonas palustris BisB18]			x
78692690	>gi|78692690|ref|ZP_00857204.1| Urease, alpha subunit [Bradyrhizobium sp. BTAi1]			x
78693475	>gi|78693475|ref|ZP_00857989.1| Urease, alpha subunit [Bradyrhizobium sp. BTAi1]			x
78701765	>gi|78701765|ref|ZP_00866213.1| Urease, alpha subunit [Alkalilimnicola ehrlichei MLHE-1]			x
78695136	>gi|78695136|ref|ZP_00859648.1| Urease, alpha subunit [Bradyrhizobium sp. BTAi1]			x
66847836	>gi|66847836|gb|EAL88166.1| urease [Aspergillus fumigatus Af293]			x
67545844	>gi|67545844|ref|ZP_00423763.1| Urease [Burkholderia vietnamiensis G4]			x
67648604	>gi|67648604|ref|ZP_00446833.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia mallei NCTC 10247]			x
67665979	>gi|67665979|ref|ZP_00463234.1| Urease [Burkholderia cenocepacia HI2424]			x
67677174	>gi|67677174|ref|ZP_00473914.1| Urease [Chromohalobacter salexigens DSM 3043]			x
67739644	>gi|67739644|ref|ZP_00490204.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia pseudomallei 668]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
67757584	>gi|67757584|ref|ZP_00496460.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia pseudomallei Pasteur]			x
67761072	>gi|67761072|ref|ZP_00499785.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia pseudomallei S13]			x
67985209	>gi|67985209|gb|EAM73168.1| Urease [Kineococcus radiotolerans SRS30216]			x
68182273	>gi|68182273|ref|ZP_00555253.1| Urease [Jannaschia sp. CCS1]			x
68234677	>gi|68234677|ref|ZP_00573744.1| Urease [Frankia sp. EAN1pec]			x
68246713	>gi|68246713|gb|EAN28807.1| Urease [Magnetococcus sp. MC-1]			x
225714	>gi|225714|prf||1311327A urease			x
28872010	>gi|28872010|ref|NP_794629.1| urease, alpha subunit [Pseudomonas syringae pv. tomato str. DC3000]			x
66045437	>gi|66045437|ref|YP_235278.1| Urease [Pseudomonas syringae pv. syringae B728a]			x
66047663	>gi|66047663|ref|YP_237504.1| Urease [Pseudomonas syringae pv. syringae B728a]			x
17402589	>gi|17402589|dbj|BAB78715.1| urease [Oryza sativa (indica cultivar-group)]			x
4154576	>gi|4154576|gb|AAD05651.1| UREASE BETA SUBUNIT [Helicobacter pylori J99]			x
137073	>gi|137073|sp|P17086|URE1_PROMI Urease alpha subunit (Urea amidohydrolase)			x
12313641	>gi|12313641|dbj|BAB21067.1| alpha subunit of urease [Rhodobacter capsulatus]			x
5913962	>gi|5913962|dbj|BAA84533.1| urease B [Helicobacter pylori]			x
586164	>gi|586164|sp|Q07397|URE1_BACSB Urease alpha subunit (Urea amidohydrolase)			x
1174889	>gi|1174889|sp|P31494|URE1_YEREN Urease alpha subunit (Urea amidohydrolase)			x
55738254	>gi|55738254|gb|AAV61895.1| urea amidohydrolase (urease) alpha subunit [Streptococcus thermophilus CNRZ1066]			x
38567277	>gi|38567277|emb|CAE76567.1| probable urease [Neurospora crassa]			x
167228	>gi|167228|gb|AAA83831.1| urease			x
13360784	>gi|13360784|dbj|BAB34747.1| urease alpha subunit [Escherichia coli O157:H7]			x
17740887	>gi|17740887|gb|AAL43389.1| urease alpha subunit [Agrobacterium tumefaciens str. C58]			x
23492833	>gi|23492833|dbj|BAC17805.1| urease alpha subunit [Corynebacterium efficiens YS-314]			x
22293726	>gi|22293726|dbj|BAC07558.1| urease alpha subunit [Thermosynechococcus elongatus BP-1]			x
33504317	>gi|33504317|emb|CAD83209.1| putative urease structural subunit C (alpha) [Candidatus Blochmannia floridanus]			x
23347054	>gi|23347054|gb|AAN29219.1| urease, alpha subunit [Brucella suis 1330]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
23348201	>gi|23348201|gb|AAN30272.1| urease, alpha subunit [Brucella suis 1330]			x
27349709	>gi|27349709|dbj|BAC46722.1| urease alpha subunit [Bradyrhizobium japonicum USDA 110]			x
17982574	>gi|17982574|gb|AAL51828.1| UREASE ALPHA SUBUNIT [Brucella melitensis 16M]			x
17983673	>gi|17983673|gb|AAL52833.1| UREASE ALPHA SUBUNIT [Brucella melitensis 16M]			x
14579320	>gi|14579320|gb|AAK69199.1| urease beta subunit UreB [Helicobacter hepaticus]			x
6460756	>gi|6460756|gb|AAF12461.1| urease, alpha subunit [Deinococcus radiodurans R1]			x
36785519	>gi|36785519|emb|CAE14466.1| urease alpha subunit [Photorhabdus luminescens subsp. laumondii TTO1]			x
54016003	>gi|54016003|dbj|BAD57373.1| putative urease alpha subunit [Nocardia farcinica IFM 10152]			x
14024880	>gi|14024880|dbj|BAB51482.1| urease alpha subunit [Mesorhizobium loti MAFF303099]			x
10172866	>gi|10172866|dbj|BAB03973.1| urease alpha subunit [Bacillus halodurans C-125]			x
52210683	>gi|52210683|emb|CAH36667.1| urease alpha subunit [Burkholderia pseudomallei K96243]			x
55229415	>gi|55229415|gb|AAV44835.1| urease alpha subunit [Haloarcula marismortui ATCC 43049]			x
15622060	>gi|15622060|dbj|BAB66053.1| 493aa long hypothetical urease alpha subunit [Sulfolobus tokodaii str. 7]			x
396162	>gi|396162|emb|CAA48826.1| urease beta-6 subunit [Helicobacter felis]			x
2708800	>gi|2708800|gb|AAC26155.1| urease alpha subunit [Synechococcus sp. PCC 7002]			x
76784366	>gi|76784366|ref|ZP_00771551.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Mycobacterium tuberculosis F11]			x
13959023	>gi|13959023|gb|AAK51069.1| urease alpha subunit UreC [Brucella melitensis biovar Abortus]			x
62290254	>gi|62290254|ref|YP_222047.1| UreC-2, urease, alpha subunit [Brucella abortus biovar 1 str. 9-941]			x
21637179	>gi|21637179|gb|AAM70367.1| urease UreB [Helicobacter pylori 26695]			x
21637192	>gi|21637192|gb|AAM70375.1| urease UreB [Candidatus Helicobacter heilmannii]			x
21637202	>gi|21637202|gb|AAM70382.1| urease UreB [Helicobacter bizzozeronii]			x
21637205	>gi|21637205|gb|AAM70384.1| urease UreB [Helicobacter bizzozeronii]			x
21637208	>gi|21637208|gb|AAM70386.1| urease UreB [Helicobacter felis]			x
21637244	>gi|21637244|gb|AAM70410.1| urease UreB [Helicobacter pylori SS1]			x
59711280	>gi|59711280|ref|YP_204056.1| urease alpha subunit [Vibrio fischeri ES114]			x
4249613	>gi|4249613|gb|AAD13732.1| urease alpha subunit UreC [Actinomyces naeslundii]			x
3659633	>gi|3659633|gb|AAC61502.1| urease alpha subunit [Synechococcus sp. WH 7805]			x
4545295	>gi|4545295|gb|AAD22480.1| urease alpha subunit [Lactobacillus fermentum]			x

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>67644011</td><td>>gi|67644011|ref|ZP_00442754.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia mallei GB8 horse 4]</td><td></td><td></td><td>x</td></tr>
<tr><td>42782712</td><td>>gi|42782712|ref|NP_979959.1| urease alpha subunit [Bacillus cereus ATCC 10987]</td><td></td><td></td><td>x</td></tr>
<tr><td>16272483</td><td>>gi|16272483|ref|NP_438697.1| urease alpha subunit [Haemophilus influenzae Rd KW20]</td><td></td><td></td><td>x</td></tr>
<tr><td>410516</td><td>>gi|410516|emb|CAA52680.1| urease alpha subunit [Staphylococcus xylosus]</td><td></td><td></td><td>x</td></tr>
<tr><td>465008</td><td>>gi|465008|sp|P07374|UREA_CANEN Urease (Urea amidohydrolase)</td><td></td><td></td><td>x</td></tr>
<tr><td>57228623</td><td>>gi|57228623|gb|AAW45058.1| urease [Cryptococcus neoformans var. neoformans JEC21]</td><td></td><td></td><td>x</td></tr>
<tr><td>60280325</td><td>>gi|60280325|gb|AAC49868.3| urease [Coccidioides posadasii]</td><td></td><td></td><td>x</td></tr>
<tr><td>9951141</td><td>>gi|9951141|gb|AAG08253.1| urease alpha subunit [Pseudomonas aeruginosa PAO1]</td><td></td><td></td><td>x</td></tr>
<tr><td>41324314</td><td>>gi|41324314|emb|CAF18654.1| UREASE ALPHA SUBUNIT [Corynebacterium glutamicum ATCC 13032]</td><td></td><td></td><td>x</td></tr>
<tr><td>17132803</td><td>>gi|17132803|dbj|BAB75369.1| urease alpha subunit [Nostoc sp. PCC 7120]</td><td></td><td></td><td>x</td></tr>
<tr><td>26989564</td><td>>gi|26989564|ref|NP_744989.1| urease, alpha subunit [Pseudomonas putida KT2440]</td><td></td><td></td><td>x</td></tr>
<tr><td>69298861</td><td>>gi|69298861|ref|ZP_00620990.1| Urease [Silicibacter sp. TM1040]</td><td></td><td></td><td>x</td></tr>
<tr><td>68192333</td><td>>gi|68192333|gb|EAN06987.1| Urease [Mesorhizobium sp. BNC1]</td><td></td><td></td><td>x</td></tr>
<tr><td>33634096</td><td>>gi|33634096|emb|CAE19422.1| Urease alpha subunit [Prochlorococcus marinus subsp. pastoris str. CCMP1986]</td><td></td><td></td><td>x</td></tr>
<tr><td>49530264</td><td>>gi|49530264|emb|CAG67976.1| urease alpha subunit [Acinetobacter sp. ADP1]</td><td></td><td></td><td>x</td></tr>
<tr><td>33641280</td><td>>gi|33641280|emb|CAE22410.1| Urease alpha subunit [Prochlorococcus marinus str. MIT 9313]</td><td></td><td></td><td>x</td></tr>
<tr><td>33639580</td><td>>gi|33639580|emb|CAE08964.1| urease alpha subunit [Synechococcus sp. WH 8102]</td><td></td><td></td><td>x</td></tr>
<tr><td>71846680</td><td>>gi|71846680|gb|AAZ46176.1| Urease, alpha subunit [Dechloromonas aromatica RCB]</td><td></td><td></td><td>x</td></tr>
<tr><td>29606364</td><td>>gi|29606364|dbj|BAC70426.1| putative urease alpha subunit [Streptomyces avermitilis MA-4680]</td><td></td><td></td><td>x</td></tr>
<tr><td>29610772</td><td>>gi|29610772|dbj|BAC74817.1| putative urease alpha subunit [Streptomyces avermitilis MA-4680]</td><td></td><td></td><td>x</td></tr>
<tr><td>56380307</td><td>>gi|56380307|dbj|BAD76215.1| urease alpha subunit (urea amidohydrolase) [Geobacillus kaustophilus HTA426]</td><td></td><td></td><td>x</td></tr>
<tr><td>56678330</td><td>>gi|56678330|gb|AAV94996.1| urease, alpha subunit [Silicibacter pomeroyi DSS-3]</td><td></td><td></td><td>x</td></tr>
<tr><td>33564160</td><td>>gi|33564160|emb|CAE43436.1| urease alpha subunit [Bordetella pertussis Tohama I]</td><td></td><td></td><td>x</td></tr>
<tr><td>39650578</td><td>>gi|39650578|emb|CAE29101.1| urease alpha subunit [Rhodopseudomonas palustris CGA009]</td><td></td><td></td><td>x</td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
72118111	>gi|72118111|gb|AAZ60374.1| Urease, alpha subunit [Ralstonia eutropha JMP134]			x
68057335	>gi|68057335|gb|AAX87588.1| Urease alpha subunit [Haemophilus influenzae 86-028NP]			x
77380811	>gi|77380811|gb|ABA72324.1| Urease, alpha subunit [Pseudomonas fluorescens PfO-1]			x
48958361	>gi|48958361|dbj|BAD23924.1| urease beta subunit [Campylobacter lari]			x
48958364	>gi|48958364|dbj|BAD23926.1| urease beta subunit [Campylobacter lari]			x
48958367	>gi|48958367|dbj|BAD23928.1| urease beta subunit [Campylobacter lari]			x
48958373	>gi|48958373|dbj|BAD23932.1| urease beta subunit [Campylobacter lari]			x
48958376	>gi|48958376|dbj|BAD23934.1| urease beta subunit [Campylobacter lari]			x
48958379	>gi|48958379|dbj|BAD23936.1| urease beta subunit [Campylobacter lari]			x
48958382	>gi|48958382|dbj|BAD23938.1| urease beta subunit [Campylobacter lari]			x
48958385	>gi|48958385|dbj|BAD23940.1| urease beta subunit [Campylobacter lari]			x
48958388	>gi|48958388|dbj|BAD23942.1| urease beta subunit [Campylobacter lari]			x
48958391	>gi|48958391|dbj|BAD23944.1| urease beta subunit [Campylobacter lari]			x
48864341	>gi|48864341|ref|ZP_00318234.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Microbulbifer degradans 2-40]			x
28372407	>gi|28372407|gb|AAO34403.1| urease beta; urease subunit B; urease large subunit [Helicobacter pylori]			x
22831365	>gi|22831365|gb|AAN08919.1| urease JBURE-II [Canavalia ensiformis]			x
41350153	>gi|41350153|gb|AAS00415.1| urease alpha subunit [Saccharopolyspora spinosa]			x
15220459	>gi|15220459|ref|NP_176922.1| hydrolase/ nickel ion binding / urease [Arabidopsis thaliana]			x
9716120	>gi|9716120|emb|CAC01458.1| urease alpha subunit [Streptomyces coelicolor A3(2)]			x
3355674	>gi|3355674|emb|CAA19974.1| urease alpha subunit [Streptomyces coelicolor A3(2)]			x
13605430	>gi|13605430|gb|AAK32714.1| urease B [Helicobacter pylori]			x
58801243	>gi|58801243|dbj|BAD89502.1| urease B subunit [Campylobacter lari]			x
27462198	>gi|27462198|gb|AAO15374.1| urease B [Helicobacter bizzozeronii]			x
86739545	>gi|86739545|ref|YP_479945.1| urease, alpha subunit [Frankia sp. CcI3]			x
71676622	>gi|71676622|ref|ZP_00674363.1| Urease [Trichodesmium erythraeum IMS101]			x
31580721	>gi|31580721|gb|AAP51176.1| urease B [Helicobacter pylori]			x
32170829	>gi|32170829|gb|AAO85884.1| embryo-specific urease [Glycine max]			x
14599161	>gi|14599161|emb|CAC43845.1| urease [Glycine max]			x
37731823	>gi|37731823|gb|AAO63582.1| urease C [Nitrosomonas cryotolerans]			x

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
77961632	>gi|77961632|ref|ZP_00825465.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Yersinia mollaretii ATCC 43969]			x
14599435	>gi|14599435|emb|CAC43859.1| urease [Solanum tuberosum]			x
14599413	>gi|14599413|emb|CAC43857.1| urease [Solanum tuberosum]			x
37726861	>gi|37726861|gb|AAO38226.1| urease subunit C [Nitrosospira multiformis]			x
32966209	>gi|32966209|gb|AAP92141.1| urease C subunit [Nitrosospira multiformis]			x
2340847	>gi|2340847|emb|CAA74065.1| urease, structural subunit [Cupriavidus necator]			x
19338960	>gi|19338960|gb|AAL86896.1| urease B subunit [Helicobacter pylori]			x
14599415	>gi|14599415|emb|CAC43858.1| urease [Solanum tuberosum]			x
52429706	>gi|52429706|gb|AAU50299.1| urease, alpha subunit [Burkholderia mallei ATCC 23344]			x
66963659	>gi|66963659|ref|ZP_00411230.1| Urease [Arthrobacter sp. FB24]			x
67156658	>gi|67156658|ref|ZP_00418155.1| Urease [Azotobacter vinelandii AvOP]			x
67686103	>gi|67686103|ref|ZP_00479859.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia pseudomallei 1710a]			x
67850889	>gi|67850889|gb|EAM46460.1| Urease [Clostridium thermocellum ATCC 27405]			x
68187175	>gi|68187175|gb|EAN01866.1| Urease [Methylobacillus flagellatus KT]			x
68555641	>gi|68555641|ref|ZP_00594985.1| Urease [Ralstonia metallidurans CH34]			x
7272374	>gi|7272374|gb|AAA89189.2| UreC [Ureaplasma urealyticum]			x
10336584	>gi|10336584|dbj|BAB13788.1| UreC [Vibrio parahaemolyticus]			x
6633958	>gi|6633958|dbj|BAA88554.1| UreC [Corynebacterium glutamicum]			x
38489172	>gi|38489172|gb|AAR21273.1| UreC protein [Streptococcus thermophilus]			x
886331	>gi|886331|gb|AAC37007.1| ureC gene product			x
28208583	>gi|28208583|gb|AAO37372.1| UreC [Streptococcus thermophilus]			x
545801	>gi|545801|gb|AAB30138.1| UreC [Sinorhizobium meliloti]			x
19070377	>gi|19070377|gb|AAL83830.1| UreC [Rhizobium leguminosarum bv. viciae]			x
45774390	>gi|45774390|gb|AAN76657.2| UreC [Nitrosospira sp. NpAV]			x
38232576	>gi|38232576|gb|AAR15086.1| UreC [Yersinia aldovae]			x
38232585	>gi|38232585|gb|AAR15094.1| UreC [Yersinia bercovieri]			x
38232594	>gi|38232594|gb|AAR15102.1| UreC [Yersinia frederiksenii]			x
38232603	>gi|38232603|gb|AAR15110.1| UreC [Yersinia intermedia]			x
38232613	>gi|38232613|gb|AAR15119.1| UreC [Yersinia kristensenii]			x
38232633	>gi|38232633|gb|AAR15137.1| UreC [Yersinia rohdei]			x

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>28411228</td><td>>gi|28411228|emb|CAD67483.1| ureC protein [Streptococcus thermophilus]</td><td></td><td></td><td>x</td></tr>
<tr><td>40888979</td><td>>gi|40888979|gb|AAR97335.1| UreC [Nitrosospira tenuis]</td><td></td><td></td><td>x</td></tr>
<tr><td>37724518</td><td>>gi|37724518|gb|AAO17783.1| urea amidohydrolase alpha subunit [Nitrosospira briensis]</td><td></td><td></td><td>x</td></tr>
<tr><td>19310948</td><td>>gi|19310948|gb|AAL86691.1| urea amidohydrolase alpha subunit [Nitrosococcus oceani]</td><td></td><td></td><td>x</td></tr>
<tr><td>40737715</td><td>>gi|40737715|gb|AAR89361.1| UreB [Helicobacter felis]</td><td></td><td></td><td>x</td></tr>
<tr><td>40737730</td><td>>gi|40737730|gb|AAR89371.1| UreB [Helicobacter pylori]</td><td></td><td></td><td>x</td></tr>
<tr><td>40737733</td><td>>gi|40737733|gb|AAR89373.1| UreB [Helicobacter pylori]</td><td></td><td></td><td>x</td></tr>
<tr><td>51989332</td><td>>gi|51989332|gb|AAU21200.1| UreB [Helicobacter pylori]</td><td></td><td></td><td>x</td></tr>
<tr><td>50513301</td><td>>gi|50513301|pdb|1POK|A Chain A, Crystal Structure Of Isoaspartyl Dipeptidase</td><td></td><td></td><td>x</td></tr>
<tr><td>16505629</td><td>>gi|16505629|emb|CAD03357.1| probable isoaspartyl dipeptidase [Salmonella enterica subsp. enterica serovar Typhi]</td><td></td><td></td><td>x</td></tr>
<tr><td>13364764</td><td>>gi|13364764|dbj|BAB38709.1| isoaspartyl dipeptidase [Escherichia coli O157:H7]</td><td></td><td></td><td>x</td></tr>
<tr><td>26111649</td><td>>gi|26111649|gb|AAN83830.1| Isoaspartyl dipeptidase [Escherichia coli CFT073]</td><td></td><td></td><td>x</td></tr>
<tr><td>56130553</td><td>>gi|56130553|gb|AAV80059.1| probable isoaspartyl dipeptidase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]</td><td></td><td></td><td>x</td></tr>
<tr><td>1790784</td><td>>gi|1790784|gb|AAC77284.1| isoaspartyl dipeptidase [Escherichia coli K12]</td><td></td><td></td><td>x</td></tr>
<tr><td>16423078</td><td>>gi|16423078|gb|AAL23330.1| isoaspartyl dipeptidase [Salmonella typhimurium LT2]</td><td></td><td></td><td>x</td></tr>
<tr><td>62182937</td><td>>gi|62182937|ref|YP_219354.1| isoaspartyl dipeptidase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]</td><td></td><td></td><td>x</td></tr>
<tr><td>24054703</td><td>>gi|24054703|gb|AAN45611.1| isoaspartyl dipeptidase [Shigella flexneri 2a str. 301]</td><td></td><td></td><td>x</td></tr>
<tr><td>52420926</td><td>>gi|52420926|emb|CAH55805.1| isoaspartyl dipeptidase yadA [Escherichia coli]</td><td></td><td></td><td>x</td></tr>
<tr><td>226366</td><td>>gi|226366|prf||1508181A enolase</td><td>NSA</td><td>x</td><td></td></tr>
<tr><td>5305425</td><td>>gi|5305425|gb|AAD41645.1| alpha enolase [Trachemys scripta elegans]</td><td>MFR</td><td>x</td><td></td></tr>
<tr><td>48864450</td><td>>gi|48864450|ref|ZP_00318343.1| COG0148: Enolase [Microbulbifer degradans 2-40]</td><td>NSA</td><td>x</td><td></td></tr>
<tr><td>23014637</td><td>>gi|23014637|ref|ZP_00054443.1| COG0148: Enolase [Magnetospirillum magnetotacticum MS-1]</td><td>NSA</td><td>x</td><td></td></tr>
<tr><td>30584989</td><td>>gi|30584989|gb|AAP36767.1| Homo sapiens enolase 1, (alpha) [synthetic construct]</td><td>NSA</td><td>x</td><td></td></tr>
<tr><td>70865791</td><td>>gi|70865791|gb|EAN81679.1| enolase, putative [Trypanosoma cruzi]</td><td>NSA</td><td>x</td><td></td></tr>
<tr><td>70880803</td><td>>gi|70880803|gb|EAN93876.1| enolase, putative [Trypanosoma cruzi]</td><td>NSA</td><td>x</td><td></td></tr>
<tr><td>70835084</td><td>>gi|70835084|gb|EAN80586.1| enolase, putative [Trypanosoma brucei]</td><td>NSA</td><td>x</td><td></td></tr>
<tr><td>18893794</td><td>>gi|18893794|gb|AAL81765.1| enolase (2-phosphoglycerate dehydratase) [Pyrococcus furiosus DSM 3638]</td><td>NSA</td><td>x</td><td></td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
58428815	>gi|58428815|gb|AAW77852.1| Enolase [Xanthomonas oryzae pv. oryzae KACC10331]	NSA	x	
5566199	>gi|5566199|gb|AAD45330.1| enolase 2 [Trichomitus batrachorum]	BTC	x	
5566200	>gi|5566200|gb|AAD45331.1| enolase 1 [Trichomitus batrachorum]	BTC	x	
5566202	>gi|5566202|gb|AAD45333.1| enolase 1 [Monocercomonas ATCC50210]	BTC	x	
45047757	>gi|45047757|emb|CAF30884.1| Enolase [Methanococcus maripaludis S2]	NSA	x	
28630228	>gi|28630228|gb|AAM88900.1| enolase 3 [Branchiostoma lanceolatum]	MFR	x	
33465413	>gi|33465413|gb|AAQ19192.1| enolase 1 [Hypotrichomonas acosta]	BTC	x	
33465415	>gi|33465415|gb|AAQ19193.1| enolase 2 [Hypotrichomonas acosta]	BTC	x	
5881830	>gi|5881830|emb|CAB55631.1| putative enolase [Gluconobacter oxydans]	NSA	x	
11292212	>gi|11292212|pir||T45116 phosphopyruvate hydratase (EC 4.2.1.11) [imported] - fission yeast (Schizosaccharomyces pombe)	NSA	x	
7473329	>gi|7473329|pir||C75251 phosphopyruvate hydratase - Deinococcus radiodurans (strain R1)	NSA	x	
83952176	>gi|83952176|ref|ZP_00960908.1| probable phosphopyruvate hydratase [Roseovarius nubinhibens ISM]	NSA	x	
84501066	>gi|84501066|ref|ZP_00999301.1| probable phosphopyruvate hydratase [Oceanicola batsensis HTCC2597]	NSA	x	
84787057	>gi|84787057|gb|ABC63239.1| probable phosphopyruvate hydratase [Erythrobacter litoralis HTCC2594]	NSA	x	
34498913	>gi|34498913|ref|NP_903128.1| probable phosphopyruvate hydratase [Chromobacterium violaceum ATCC 12472]	NSA	x	
16082480	>gi|16082480|ref|NP_393564.1| Galactonate dehydratase [Thermoplasma acidophilum DSM 1728]	BTC, MOF	x	
86360374	>gi|86360374|ref|YP_472262.1| putative galactonate dehydratase protein [Rhizobium etli CFN 42]	BTC	x	
86284476	>gi|86284476|gb|ABC93535.1| putative galactonate dehydratase protein [Rhizobium etli CFN 42]	BTC	x	
56680714	>gi|56680714|gb|AAV97379.1| galactonate dehydratase, putative [Silicibacter pomeroyi DSS-3]	SFA	x	
56709029	>gi|56709029|ref|YP_165074.1| galactonate dehydratase, putative [Silicibacter pomeroyi DSS-3]	SFA	x	
13540999	>gi|13540999|ref|NP_110687.1| Galactonate dehydratase [Thermoplasma volcanium GSS1]	BTC, MOF	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
13542025	>gi|13542025|ref|NP_111713.1| Galactonate dehydratase [Thermoplasma volcanium GSS1]	BTC, MOF	x	
16420830	>gi|16420830|gb|AAL21192.1| putative galactonate dehydratase [Salmonella typhimurium LT2]	SFA	x	
16765618	>gi|16765618|ref|NP_461233.1| putative galactonate dehydratase [Salmonella typhimurium LT2]	SFA	x	
62180864	>gi|62180864|ref|YP_217281.1| paral putative galactonate dehydratase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]	SFA	x	
62128497	>gi|62128497|gb|AAX66200.1| paral putative galactonate dehydratase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]	SFA	x	
17984511	>gi|17984511|gb|AAL53598.1| GALACTONATE DEHYDRATASE [Brucella melitensis 16M]	NSA	x	
82499349	>gi|82499349|ref|ZP_00884796.1| conserved hypothetical mandelate racemase [Caldicellulosiruptor saccharolyticus DSM 8903]	BTC, MOF	x	
82402672	>gi|82402672|gb|EAP43446.1| conserved hypothetical mandelate racemase [Caldicellulosiruptor saccharolyticus DSM 8903]	BTC, MOF	x	
82746834	>gi|82746834|ref|ZP_00909337.1| putative mandelate racemase [Clostridium beijerincki NCIMB 8052]	SFA	x	
82725330	>gi|82725330|gb|EAP60076.1| putative mandelate racemase [Clostridium beijerincki NCIMB 8052]	SFA	x	
86360704	>gi|86360704|ref|YP_472592.1| probable mandelate racemase protein [Rhizobium etli CFN 42]	SFA	x	
86284806	>gi|86284806|gb|ABC93865.1| probable mandelate racemase protein [Rhizobium etli CFN 42]	SFA	x	
86361111	>gi|86361111|ref|YP_472998.1| putative mandelate racemase protein [Rhizobium etli CFN 42]	BTC, MOF	x	
86285213	>gi|86285213|gb|ABC94271.1| putative mandelate racemase protein [Rhizobium etli CFN 42]	BTC, MOF	x	
86165177	>gi|86165177|gb|EAQ66445.1| probable mandelate racemase [Marinomonas sp. MED121]	BTC	x	
68568553	>gi|68568553|gb|AAY81482.1| mandelate racemase [Sulfolobus acidocaldarius DSM 639]	SFA	x	
70607905	>gi|70607905|ref|YP_256775.1| mandelate racemase [Sulfolobus acidocaldarius DSM 639]	SFA	x	
33577784	>gi|33577784|emb|CAE35049.1| putative mandelate racemase [Bordetella bronchiseptica RB50]	BTC, MOF	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
33603659	>gi|33603659|ref|NP_891219.1| putative mandelate racemase [Bordetella bronchiseptica RB50]	BTC, MOF	x	
77359254	>gi|77359254|ref|YP_338829.1| mandelate racemase [Pseudoalteromonas haloplanktis TAC125]	SFA	x	
78695260	>gi|78695260|ref|ZP_00859772.1| probable mandelate racemase [Bradyrhizobium sp. BTAi1]	BTC	x	
78516934	>gi|78516934|gb|EAP30233.1| probable mandelate racemase [Bradyrhizobium sp. BTAi1]	BTC	x	
29137654	>gi|29137654|gb|AAO69216.1| putative mandelate racemase [Salmonella enterica subsp. enterica serovar Typhi Ty2]	SFA	x	
56552124	>gi|56552124|ref|YP_162963.1| mandelate racemase [Zymomonas mobilis subsp. mobilis ZM4]	SFA	x	
56543698	>gi|56543698|gb|AAV89852.1| mandelate racemase [Zymomonas mobilis subsp. mobilis ZM4]	SFA	x	
56552160	>gi|56552160|ref|YP_162999.1| putative mandelate racemase [Zymomonas mobilis subsp. mobilis ZM4]	SFA	x	
56543734	>gi|56543734|gb|AAV89888.1| putative mandelate racemase [Zymomonas mobilis subsp. mobilis ZM4]	SFA	x	
17983732	>gi|17983732|gb|AAL52888.1| MANDELATE RACEMASE [Brucella melitensis 16M]	SFA	x	
17987990	>gi|17987990|ref|NP_540624.1| MANDELATE RACEMASE [Brucella melitensis 16M]	SFA	x	
49610464	>gi|49610464|emb|CAG73909.1| putative mandelate racemase [Erwinia carotovora subsp. atroseptica SCRI1043]	BTC	x	
50119938	>gi|50119938|ref|YP_049105.1| putative mandelate racemase [Erwinia carotovora subsp. atroseptica SCRI1043]	BTC	x	
27381460	>gi|27381460|ref|NP_772989.1| putative mandelate racemase [Bradyrhizobium japonicum USDA 110]	SFA	x	
27382736	>gi|27382736|ref|NP_774265.1| probable mandelate racemase [Bradyrhizobium japonicum USDA 110]	BTC	x	
17983738	>gi|17983738|gb|AAL52893.1| MANDELATE RACEMASE [Brucella melitensis 16M]	BTC	x	
17987995	>gi|17987995|ref|NP_540629.1| MANDELATE RACEMASE [Brucella melitensis 16M]	BTC	x	
14026713	>gi|14026713|dbj|BAB53309.1| mandelate racemase [Mesorhizobium loti MAFF303099]	BTC	x	
13475953	>gi|13475953|ref|NP_107523.1| mandelate racemase [Mesorhizobium loti MAFF303099]	BTC	x	
52208779	>gi|52208779|emb|CAH34717.1| putative mandelate racemase [Burkholderia pseudomallei K96243]	BTC	x	

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>53718365</td><td>>gi|53718365|ref|YP_107351.1| putative mandelate racemase [Burkholderia pseudomallei K96243]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>15622149</td><td>>gi|15622149|dbj|BAB66141.1| 373aa long hypothetical mandelate racemase [Sulfolobus tokodaii str. 7]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>15921363</td><td>>gi|15921363|ref|NP_377032.1| hypothetical mandelate racemase [Sulfolobus tokodaii str. 7]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>56127654</td><td>>gi|56127654|gb|AAV77160.1| putative mandelate racemase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>56413397</td><td>>gi|56413397|ref|YP_150472.1| putative mandelate racemase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>16422264</td><td>>gi|16422264|gb|AAL22556.1| putative mandelate racemase [Salmonella typhimurium LT2]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>16766982</td><td>>gi|16766982|ref|NP_462597.1| putative mandelate racemase [Salmonella typhimurium LT2]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>16422406</td><td>>gi|16422406|gb|AAL22692.1| putative mandelate racemase [Salmonella typhimurium LT2]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>16767118</td><td>>gi|16767118|ref|NP_462733.1| putative mandelate racemase [Salmonella typhimurium LT2]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>76579348</td><td>>gi|76579348|gb|ABA48823.1| mandelate racemase [Burkholderia pseudomallei 1710b]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>76809895</td><td>>gi|76809895|ref|YP_332360.1| mandelate racemase [Burkholderia pseudomallei 1710b]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>29610948</td><td>>gi|29610948|dbj|BAC74993.1| putative mandelate racemase [Streptomyces avermitilis MA-4680]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>29833824</td><td>>gi|29833824|ref|NP_828458.1| putative mandelate racemase [Streptomyces avermitilis MA-4680]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>33576228</td><td>>gi|33576228|emb|CAE33307.1| putative mandelate racemase [Bordetella bronchiseptica RB50]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>33573688</td><td>>gi|33573688|emb|CAE37980.1| putative mandelate racemase [Bordetella parapertussis]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>33572111</td><td>>gi|33572111|emb|CAE41651.1| putative mandelate racemase [Bordetella pertussis Tohama I]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>33592465</td><td>>gi|33592465|ref|NP_880109.1| putative mandelate racemase [Bordetella pertussis Tohama I]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>33597261</td><td>>gi|33597261|ref|NP_884904.1| putative mandelate racemase [Bordetella parapertussis 12822]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>33601791</td><td>>gi|33601791|ref|NP_889351.1| putative mandelate racemase [Bordetella bronchiseptica RB50]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>16504041</td><td>>gi|16504041|emb|CAD06075.1| probable glucarate dehydratase 2 [Salmonella enterica subsp. enterica serovar Typhi]</td><td>BTC</td><td>x</td><td></td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
29138857	>gi|29138857|gb|AAO70426.1| probable glucarate dehydratase 2 [Salmonella enterica subsp. enterica serovar Typhi Ty2]	BTC	x	
16761740	>gi|16761740|ref|NP_457357.1| probable glucarate dehydratase 2 [Salmonella enterica subsp. enterica serovar Typhi str. CT18]	BTC	x	
29143224	>gi|29143224|ref|NP_806566.1| probable glucarate dehydratase 2 [Salmonella enterica subsp. enterica serovar Typhi Ty2]	BTC	x	
25291987	>gi|25291987|pir||AD0861 glucarate dehydratase (EC 4.2.1.40) - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)	BTC	x	
74313360	>gi|74313360|ref|YP_311779.1| putative glucarate dehydratase [Shigella sonnei Ss046]	BTC	x	
73856837	>gi|73856837|gb|AAZ89544.1| putative glucarate dehydratase [Shigella sonnei Ss046]	BTC	x	
151314	>gi|151314|gb|AAA25867.1| glucarate dehydratase	NSF	x	
82545087	>gi|82545087|ref|YP_409034.1| putative glucarate dehydratase [Shigella boydii Sb227]	BTC	x	
81246498	>gi|81246498|gb|ABB67206.1| putative glucarate dehydratase [Shigella boydii Sb227]	BTC	x	
1789151	>gi|1789151|gb|AAC75830.1| putative (D)-glucarate dehydratase 2 [Escherichia coli K12]	BTC	x	
85675607	>gi|85675607|dbj|BAE76860.1| predicted glucarate dehydratase [Escherichia coli W3110]	BTC	x	
16130695	>gi|16130695|ref|NP_417268.1| putative (D)-glucarate dehydratase 2 [Escherichia coli K12]	BTC	x	
6714756	>gi|6714756|emb|CAB66220.1| putative glucarate dehydratase. [Streptomyces coelicolor A3(2)]	BTC	x	
21221001	>gi|21221001|ref|NP_626780.1| glucarate dehydratase [Streptomyces coelicolor A3(2)]	BTC	x	
9910726	>gi|9910726|sp|Q9RDE9|GUDH_STRCO Probable glucarate dehydratase (GDH) (GlucD)	BTC	x	
75428535	>gi|75428535|ref|ZP_00731737.1| putative d-glucarate dehydratase [Actinobacillus succinogenes 130Z]	BTC	x	
74277627	>gi|74277627|gb|EAO51199.1| putative d-glucarate dehydratase [Actinobacillus succinogenes 130Z]	BTC	x	
67675577	>gi|67675577|ref|ZP_00472333.1| Glucarate dehydratase [Chromohalobacter salexigens DSM 3043]	BTC	x	
67520396	>gi|67520396|gb|EAM24340.1| Glucarate dehydratase [Chromohalobacter salexigens DSM 3043]	BTC	x	
12517263	>gi|12517263|gb|AAG57901.1| putative glucarate dehydratase [Escherichia coli O157:H7 EDL933]	BTC	x	
15803309	>gi|15803309|ref|NP_289342.1| putative glucarate dehydratase [Escherichia coli O157:H7 EDL933]	BTC	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
17741388	>gi|17741388|gb|AAL43845.1| glucarate dehydratase [Agrobacterium tumefaciens str. C58]	BTC	x	
17936740	>gi|17936740|ref|NP_533529.1| glucarate dehydratase [Agrobacterium tumefaciens str. C58]	BTC	x	
26109595	>gi|26109595|gb|AAN81798.1| Glucarate dehydratase [Escherichia coli CFT073]	BTC	x	
26249188	>gi|26249188|ref|NP_755228.1| Glucarate dehydratase [Escherichia coli CFT073]	BTC	x	
49610404	>gi|49610404|emb|CAG73848.1| putative glucarate dehydratase [Erwinia carotovora subsp. atroseptica SCRI1043]	BTC	x	
50119878	>gi|50119878|ref|YP_049045.1| putative glucarate dehydratase [Erwinia carotovora subsp. atroseptica SCRI1043]	BTC	x	
49613023	>gi|49613023|emb|CAG76474.1| probable glucarate dehydratase [Erwinia carotovora subsp. atroseptica SCRI1043]	BTC	x	
50122497	>gi|50122497|ref|YP_051664.1| probable glucarate dehydratase [Erwinia carotovora subsp. atroseptica SCRI1043]	BTC	x	
709999	>gi|709999|dbj|BAA06469.1| glucarate dehydratase [Bacillus subtilis]	NSF	x	
54016985	>gi|54016985|dbj|BAD58355.1| putative glucarate dehydratase [Nocardia farcinica IFM 10152]	BTC	x	
54025477	>gi|54025477|ref|YP_119719.1| putative glucarate dehydratase [Nocardia farcinica IFM 10152]	BTC	x	
13363119	>gi|13363119|dbj|BAB37071.1| putative glucarate dehydratase [Escherichia coli O157:H7]	BTC	x	
15832902	>gi|15832902|ref|NP_311675.1| putative glucarate dehydratase [Escherichia coli O157:H7]	BTC	x	
16421512	>gi|16421512|gb|AAL21841.1| putative d-glucarate dehydratase [Salmonella typhimurium LT2]	BTC	x	
16766267	>gi|16766267|ref|NP_461882.1| putative D-glucarate dehydratase [Salmonella typhimurium LT2]	BTC	x	
56383734	>gi|56383734|gb|AAN44289.2| putative glucarate dehydratase [Shigella flexneri 2a str. 301]	BTC	x	
30042389	>gi|30042389|gb|AAP18114.1| putative glucarate dehydratase [Shigella flexneri 2a str. 2457T]	BTC	x	
30064133	>gi|30064133|ref|NP_838304.1| putative glucarate dehydratase [Shigella flexneri 2a str. 2457T]	BTC	x	
56480183	>gi|56480183|ref|NP_708582.2| putative glucarate dehydratase [Shigella flexneri 2a str. 301]	BTC	x	
29609242	>gi|29609242|dbj|BAC73293.1| putative glucarate dehydratase [Streptomyces avermitilis MA-4680]	BTC	x	

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>29832124</td><td>>gi|29832124|ref|NP_826758.1| putative glucarate dehydratase [Streptomyces avermitilis MA-4680]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>77684111</td><td>>gi|77684111|ref|ZP_00799549.1| Methylaspartate ammonia-lyase [Alkaliphilus metalliredigenes QYMF]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>77640128</td><td>>gi|77640128|gb|EAO82478.1| Methylaspartate ammonia-lyase [Alkaliphilus metalliredigenes QYMF]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>77997310</td><td>>gi|77997310|gb|ABB16209.1| methylaspartate ammonia-lyase [Carboxydothermus hydrogenoformans Z-2901]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>78045195</td><td>>gi|78045195|ref|YP_359438.1| methylaspartate ammonia-lyase [Carboxydothermus hydrogenoformans Z-2901]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>77997332</td><td>>gi|77997332|gb|ABB16231.1| methylaspartate ammonia-lyase [Carboxydothermus hydrogenoformans Z-2901]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>78045217</td><td>>gi|78045217|ref|YP_359342.1| methylaspartate ammonia-lyase [Carboxydothermus hydrogenoformans Z-2901]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>77975622</td><td>>gi|77975622|ref|ZP_00831157.1| COG3799: Methylaspartate ammonia-lyase [Yersinia frederiksenii ATCC 33641]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>77976541</td><td>>gi|77976541|ref|ZP_00832024.1| COG3799: Methylaspartate ammonia-lyase [Yersinia intermedia ATCC 29909]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>42527737</td><td>>gi|42527737|ref|NP_972835.1| methylaspartate ammonia-lyase [Treponema denticola ATCC 35405]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>41818565</td><td>>gi|41818565|gb|AAS12754.1| methylaspartate ammonia-lyase [Treponema denticola ATCC 35405]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>55377543</td><td>>gi|55377543|ref|YP_135393.1| methylaspartate ammonia-lyase [Haloarcula marismortui ATCC 43049]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>55230268</td><td>>gi|55230268|gb|AAV45687.1| methylaspartate ammonia-lyase [Haloarcula marismortui ATCC 43049]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>33577289</td><td>>gi|33577289|emb|CAE35846.1| methylaspartate ammonia-lyase [Bordetella bronchiseptica RB50]</td><td>BTC</td><td>X</td><td></td></tr>
<tr><td>33571620</td><td>>gi|33571620|emb|CAE41110.1| methylaspartate ammonia-lyase [Bordetella pertussis Tohama I]</td><td>BTC</td><td>X</td><td></td></tr>
<tr><td>33591976</td><td>>gi|33591976|ref|NP_879620.1| methylaspartate ammonia-lyase [Bordetella pertussis Tohama I]</td><td>BTC</td><td>X</td><td></td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
33602847	>gi|33602847|ref|NP_890407.1| methylaspartate ammonia-lyase [Bordetella bronchiseptica RB50]	BTC	X	
33577435	>gi|33577435|emb|CAE34700.1| putative methylaspartate ammonia-lyase [Bordetella bronchiseptica RB50]	BTC	X	
33564168	>gi|33564168|emb|CAE43445.1| putative methylaspartate ammonia-lyase [Bordetella pertussis Tohama I]	BTC	X	
33594094	>gi|33594094|ref|NP_881738.1| putative methylaspartate ammonia-lyase [Bordetella pertussis Tohama I]	BTC	X	
33603311	>gi|33603311|ref|NP_890871.1| putative methylaspartate ammonia-lyase [Bordetella bronchiseptica RB50]	BTC	X	
33574369	>gi|33574369|emb|CAE38707.1| methylaspartate ammonia-lyase [Bordetella parapertussis]	BTC	X	
33597940	>gi|33597940|ref|NP_885583.1| methylaspartate ammonia-lyase [Bordetella parapertussis 12822]	BTC	X	
33574502	>gi|33574502|emb|CAE39147.1| putative methylaspartate ammonia-lyase [Bordetella parapertussis]	BTC	X	
33598373	>gi|33598373|ref|NP_886016.1| putative methylaspartate ammonia-lyase [Bordetella parapertussis 12822]	BTC	X	
66846029	>gi|66846029|gb|EAL86362.1| methylaspartate ammonia-lyase [Aspergillus fumigatus Af293]	BTC	x	
70985789	>gi|70985789|ref|XP_748400.1| methylaspartate ammonia-lyase [Aspergillus fumigatus Af293]	BTC	x	
20804010	>gi|20804010|emb|CAD31587.1| PUTATIVE METHYLASPARTATE AMMONIA-LYASE PROTEIN [Mesorhizobium loti]	BTC	x	
71915096	>gi|71915096|gb|AAZ54998.1| n-acylamino acid racemase : O-succinylbenzoate-CoA synthase [Thermobifida fusca YX]	MFR	x	
46400938	>gi|46400938|emb|CAF24387.1| putative o-succinylbenzoate synthase II, menC [Parachlamydia sp. UWE25]	SFA	x	
52004778	>gi|52004778|gb|AAU24720.1| o-succinylbenzoate synthase [Bacillus licheniformis ATCC 14580]	NSF	x	
48428779	>gi|48428779|gb|AAT42427.1| L-alanine-DL-glutamate epimerase [Collimonas fungivorans]	SFA	x	
83857375	>gi|83857375|ref|ZP_00950903.1| chloromuconate cycloisomerase [Croceibacter atlanticus HTCC2559]	SFA	x	
83848742	>gi|83848742|gb|EAP86611.1| chloromuconate cycloisomerase [Croceibacter atlanticus HTCC2559]	SFA	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
86131888	>gi|86131888|ref|ZP_01050485.1| chloromuconate cycloisomerase [Cellulophaga sp. MED134]	SFA	x	
85817710	>gi|85817710|gb|EAQ38884.1| chloromuconate cycloisomerase [Cellulophaga sp. MED134]	SFA	x	
86133686	>gi|86133686|ref|ZP_01052268.1| chloromuconate cycloisomerase [Tenacibaculum sp. MED152]	SFA	x	
85820549	>gi|85820549|gb|EAQ41696.1| chloromuconate cycloisomerase [Tenacibaculum sp. MED152]	SFA	x	
78037966	>gi|78037966|emb|CAJ25711.1| putative chloromuconate cycloisomerase [Xanthomonas campestris pv. vesicatoria str. 85-10]	BTC, MOF	x	
78049536	>gi|78049536|ref|YP_365711.1| putative chloromuconate cycloisomerase [Xanthomonas campestris pv. vesicatoria str. 85-10]	BTC, MOF	x	
49176892	>gi|49176892|ref|YP_025395.1| chloromuconate cycloisomerase [Ralstonia eutropha JMP134]	BTC	x	
39777472	>gi|39777472|gb|AAR31047.1| chloromuconate cycloisomerase [Ralstonia eutropha JMP134]	BTC	x	
60415960	>gi|60415960|sp|P42428|TFDD2_RALEJ Chloromuconate cycloisomerase (Muconate cycloisomerase II)	BTC	x	
10580624	>gi|10580624|gb|AAG19476.1| chloromuconate cycloisomerase; YkfB2 [Halobacterium sp. NRC-1]	SFA	x	
10581283	>gi|10581283|gb|AAG20045.1| chloromuconate cycloisomerase; YkfB1 [Halobacterium sp. NRC-1]	BTC, MOF	x	
17743934	>gi|17743934|gb|AAL46164.1| chloromuconate cycloisomerase [Agrobacterium tumefaciens str. C58]	SFA	x	
17939060	>gi|17939060|ref|NP_535848.1| chloromuconate cycloisomerase [Agrobacterium tumefaciens str. C58]	SFA	x	
21115078	>gi|21115078|gb|AAM43053.1| chloromuconate cycloisomerase [Xanthomonas campestris pv. campestris str. ATCC 33913]	BTC, MOF	x	
21233235	>gi|21233235|ref|NP_639152.1| chloromuconate cycloisomerase [Xanthomonas campestris pv. campestris str. ATCC 33913]	BTC, MOF	x	
6459649	>gi|6459649|gb|AAF11422.1| chloromuconate cycloisomerase, putative [Deinococcus radiodurans R1]	BTC	x	
15806871	>gi|15806871|ref|NP_295594.1| chloromuconate cycloisomerase, putative [Deinococcus radiodurans R1]	BTC	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
14026881	>gi|14026881|dbj|BAB53477.1| chloromuconate cycloisomerase [Mesorhizobium loti MAFF303099]	MFR	x	
13476121	>gi|13476121|ref|NP_107691.1| chloromuconate cycloisomerase [Mesorhizobium loti MAFF303099]	MFR	x	
52215476	>gi|52215476|dbj|BAD48069.1| chloromuconate cycloisomerase [Bacteroides fragilis YCH46]	SFA	x	
53712611	>gi|53712611|ref|YP_098603.1| chloromuconate cycloisomerase [Bacteroides fragilis YCH46]	SFA	x	
55773206	>gi|55773206|dbj|BAD71647.1| chloromuconate cycloisomerase [Thermus thermophilus HB8]	SFA	x	
55981793	>gi|55981793|ref|YP_145090.1| chloromuconate cycloisomerase [Thermus thermophilus HB8]	SFA	x	
2599298	>gi|2599298|gb|AAB86807.1| putative chloromuconate cycloisomerase [Burkholderia cepacia]	MFR	x	
1747426	>gi|1747426|gb|AAC44729.1| chloromuconate cycloisomerase [Ralstonia eutropha]	BTC	x	
84369475	>gi|84369475|dbj|BAE70633.1| chloromuconate cycloisomerase [Xanthomonas oryzae pv. oryzae MAFF 311018]	BTC, MOF	x	
84625535	>gi|84625535|ref|YP_452907.1| chloromuconate cycloisomerase [Xanthomonas oryzae pv. oryzae MAFF 311018]	BTC, MOF	x	
58583725	>gi|58583725|ref|YP_202741.1| chloromuconate cycloisomerase [Xanthomonas oryzae pv. oryzae KACC10331]	BTC, MOF	x	
58428319	>gi|58428319|gb|AAW77356.1| chloromuconate cycloisomerase [Xanthomonas oryzae pv. oryzae KACC10331]	BTC, MOF	x	
16765024	>gi|16765024|ref|NP_460639.1| putative chloromuconate cycloisomerase [Salmonella typhimurium LT2]	SFA	x	
29350111	>gi|29350111|ref|NP_813614.1| chloromuconate cycloisomerase [Bacteroides thetaiotaomicron VPI-5482]	SFA	x	
29342023	>gi|29342023|gb|AAO79808.1| chloromuconate cycloisomerase [Bacteroides thetaiotaomicron VPI-5482]	SFA	x	
55377148	>gi|55377148|ref|YP_134998.1| chloromuconate cycloisomerase [Haloarcula marismortui ATCC 43049]	BTC, MOF	x	
55229873	>gi|55229873|gb|AAV45292.1| chloromuconate cycloisomerase [Haloarcula marismortui ATCC 43049]	BTC, MOF	x	
55377682	>gi|55377682|ref|YP_135532.1| chloromuconate cycloisomerase [Haloarcula marismortui ATCC 43049]	SFA	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
55230407	>gi|55230407|gb|AAV45826.1| chloromuconate cycloisomerase [Haloarcula marismortui ATCC 43049]	SFA	x	
55379988	>gi|55379988|ref|YP_137838.1| chloromuconate cycloisomerase [Haloarcula marismortui ATCC 43049]	SFA	x	
55232713	>gi|55232713|gb|AAV48132.1| chloromuconate cycloisomerase [Haloarcula marismortui ATCC 43049]	SFA	x	
41326584	>gi|41326584|emb|CAF21066.1| CHLOROMUCONATE CYCLOISOMERASE [Corynebacterium glutamicum ATCC 13032]	BTC, MOF	x	
62391244	>gi|62391244|ref|YP_226646.1| CHLOROMUCONATE CYCLOISOMERASE [Corynebacterium glutamicum ATCC 13032]	BTC, MOF	x	
23308936	>gi|23308936|ref|NP_601602.2| putative chloromuconate cycloisomerase [Corynebacterium glutamicum ATCC 13032]	BTC, MOF	x	
62180244	>gi|62180244|ref|YP_216661.1| putative chloromuconate cycloisomerase (muconate cycloisomerase) [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]	SFA	x	
62127877	>gi|62127877|gb|AAX65580.1| putative chloromuconate cycloisomerase (muconate cycloisomerase) [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]	SFA	x	
21110264	>gi|21110264|gb|AAM38704.1| chloromuconate cycloisomerase [Xanthomonas axonopodis pv. citri str. 306]	BTC, MOF	x	
21244586	>gi|21244586|ref|NP_644168.1| chloromuconate cycloisomerase [Xanthomonas axonopodis pv. citri str. 306]	BTC, MOF	x	
32446038	>gi|32446038|emb|CAD75867.1| chloromuconate cycloisomerase YkfB1 [Rhodopirellula baltica SH 1]	SFA	x	
32475496	>gi|32475496|ref|NP_868490.1| chloromuconate cycloisomerase YkfB1 [Rhodopirellula baltica SH 1]	SFA	x	
32447344	>gi|32447344|emb|CAD77170.1| chloromuconate cycloisomerase YkfB1 [Rhodopirellula baltica SH 1]	SFA	x	
32476798	>gi|32476798|ref|NP_869792.1| chloromuconate cycloisomerase YkfB1 [Rhodopirellula baltica SH 1]	SFA	x	
53757661	>gi|53757661|gb|AAU91952.1| putative chloromuconate cycloisomerase [Methylococcus capsulatus str. Bath]	BTC, MOF	x	
53803900	>gi|53803900|ref|YP_114271.1| chloromuconate cycloisomerase, putative [Methylococcus capsulatus str. Bath]	BTC, MOF	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
52629284	>gi|52629284|gb|AAU28025.1| chloromuconate cycloisomerase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]	BTC, MOF	x	
52842173	>gi|52842173|ref|YP_095972.1| chloromuconate cycloisomerase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]	BTC, MOF	x	
66575509	>gi|66575509|gb|AAY50919.1| chloromuconate cycloisomerase [Xanthomonas campestris pv. campestris str. 8004]	BTC, MOF	x	
66770177	>gi|66770177|ref|YP_244939.1| chloromuconate cycloisomerase [Xanthomonas campestris pv. campestris str. 8004]	BTC, MOF	x	
11499682	>gi|11499682|ref|NP_070924.1| muconate cycloisomerase II (clcB) [Archaeoglobus fulgidus DSM 4304]	SFA	x	
2648434	>gi|2648434|gb|AAB89156.1| muconate cycloisomerase II (clcB) [Archaeoglobus fulgidus DSM 4304]	SFA	x	
13880091	>gi|13880091|gb|AAK44802.1| muconate cycloisomerase I, putative [Mycobacterium tuberculosis CDC1551]	SGA	x	
3261782	>gi|3261782|emb|CAB08964.1| PROBABLE MUCONATE CYCLOISOMERASE MENC (CIS,CIS-MUCONATE LACTONIZING ENZYME) (MLE) [Mycobacterium tuberculosis H37Rv]	SGA	x	
31617321	>gi|31617321|emb|CAD93430.1| PROBABLE MUCONATE CYCLOISOMERASE MENC (CIS,CIS-MUCONATE LACTONIZING ENZYME) (MLE) [Mycobacterium bovis AF2122/97]	SGA	x	
82548049	>gi|82548049|gb|ABB82573.1| cis-muconate cycloisomerase [Nocardia sp. C-14-1]	BTC	x	
74312308	>gi|74312308|ref|YP_310727.1| putative muconate cycloisomerase I [Shigella sonnei Ss046]	SGA	x	
73855785	>gi|73855785|gb|AAZ88492.1| putative muconate cycloisomerase I [Shigella sonnei Ss046]	SGA	x	
38703962	>gi|38703962|ref|NP_309931.2| putative muconate cycloisomerase I [Escherichia coli O157:H7]	SGA	x	
82500522	>gi|82500522|ref|ZP_00885932.1| muconate cycloisomerase [Caldicellulosiruptor saccharolyticus DSM 8903]	SGA	x	
82401463	>gi|82401463|gb|EAP42274.1| muconate cycloisomerase [Caldicellulosiruptor saccharolyticus DSM 8903]	SGA	x	
84389418	>gi|84389418|ref|ZP_00991224.1| putative muconate cycloisomerase I [Vibrio splendidus 12B01]	SGA	x	
84376933	>gi|84376933|gb|EAP93806.1| putative muconate cycloisomerase I [Vibrio splendidus 12B01]	SGA	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
84713193	>gi|84713193|ref|ZP_01020979.1| muconate cycloisomerase I [Polaromonas naphthalenivorans CJ2]	BTC	x	
84694767	>gi|84694767|gb|EAQ20559.1| muconate cycloisomerase I [Polaromonas naphthalenivorans CJ2]	BTC	x	
84713395	>gi|84713395|ref|ZP_01021160.1| putative cis-muconate cycloisomerase [Polaromonas naphthalenivorans CJ2]	NSF	x	
84694572	>gi|84694572|gb|EAQ20365.1| putative cis-muconate cycloisomerase [Polaromonas naphthalenivorans CJ2]	NSF	x	
82776689	>gi|82776689|ref|YP_403038.1| putative muconate cycloisomerase I [Shigella dysenteriae Sd197]	SGA	x	
81240837	>gi|81240837|gb|ABB61547.1| putative muconate cycloisomerase I [Shigella dysenteriae Sd197]	SGA	x	
82544227	>gi|82544227|ref|YP_408174.1| putative muconate cycloisomerase I [Shigella boydii Sb227]	SGA	x	
81245638	>gi|81245638|gb|ABB66346.1| putative muconate cycloisomerase I [Shigella boydii Sb227]	SGA	x	
14026882	>gi|14026882|dbj|BAB53478.1| muconate lactonizing enzyme [Mesorhizobium loti MAFF303099]	SGA	x	
13476122	>gi|13476122|ref|NP_107692.1| muconate lactonizing enzyme [Mesorhizobium loti MAFF303099]	SGA	x	
86140323	>gi|86140323|ref|ZP_01058882.1| putative muconate cycloisomerase [Flavobacterium sp. MED217]	SGA	x	
85832265	>gi|85832265|gb|EAQ50714.1| putative muconate cycloisomerase [Flavobacterium sp. MED217]	SGA	x	
86145024	>gi|86145024|ref|ZP_01063356.1| putative muconate cycloisomerase I [Vibrio sp. MED222]	SGA	x	
85837923	>gi|85837923|gb|EAQ56035.1| putative muconate cycloisomerase I [Vibrio sp. MED222]	SGA	x	
86357965	>gi|86357965|ref|YP_469857.1| probable muconate cycloisomerase I protein [Rhizobium etli CFN 42]	sGA	x	
86282067	>gi|86282067|gb|ABC91130.1| probable muconate cycloisomerase I protein [Rhizobium etli CFN 42]	SGA	x	
68183493	>gi|68183493|ref|ZP_00556468.1| Muconate cycloisomerase [Jannaschia sp. CCS1]	BTC, MOF	x	
67976423	>gi|67976423|gb|EAM66050.1| Muconate cycloisomerase [Jannaschia sp. CCS1]	BTC, MOF	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
56911020	>gi|56911020|dbj|BAD65547.1| muconate cycloisomerase [Bacillus clausii KSM-K16]	SFA	x	
56964777	>gi|56964777|ref|YP_176508.1| muconate cycloisomerase [Bacillus clausii KSM-K16]	SFA	x	
15801845	>gi|15801845|ref|NP_287863.1| putative muconate cycloisomerase I [Escherichia coli O157:H7 EDL933]	SGA	x	
23492313	>gi|23492313|dbj|BAC17287.1| putative muconate cycloisomerase [Corynebacterium efficiens YS-314]	SGA	x	
22778530	>gi|22778530|dbj|BAC14799.1| muconate cycloisomerase [Oceanobacillus iheyensis HTE831]	SFA	x	
23100298	>gi|23100298|ref|NP_693765.1| muconate cycloisomerase [Oceanobacillus iheyensis HTE831]	SFA	x	
22778653	>gi|22778653|dbj|BAC14921.1| muconate cycloisomerase [Oceanobacillus iheyensis HTE831]	BTC, MOF	x	
23100420	>gi|23100420|ref|NP_693887.1| muconate cycloisomerase [Oceanobacillus iheyensis HTE831]	BTC, MOF	x	
17982924	>gi|17982924|gb|AAL52147.1| MUCONATE CYCLOISOMERASE I [Brucella melitensis 16M]	SGA	x	
17987249	>gi|17987249|ref|NP_539883.1| MUCONATE CYCLOISOMERASE I [Brucella melitensis 16M]	SGA	x	
4980489	>gi|4980489|gb|AAD35100.1| muconate cycloisomerase [Thermotoga maritima MSB8]	SGA	x	
15642781	>gi|15642781|ref|NP_227822.1| muconate cycloisomerase [Thermotoga maritima MSB8]	SGA	x	
54016999	>gi|54016999|dbj|BAD58369.1| putative muconate cycloisomerase [Nocardia farcinica IFM 10152]	BTC, MOF	x	
54025491	>gi|54025491|ref|YP_119733.1| putative muconate cycloisomerase [Nocardia farcinica IFM 10152]	BTC, MOF	x	
72123629	>gi|72123629|gb|AAZ65772.1| Muconate cycloisomerase [Ralstonia eutropha JMP134]	BTC, MOF	x	
72384276	>gi|72384276|ref|YP_293629.1| Muconate cycloisomerase [Ralstonia eutropha JMP134]	BTC, MOF	x	
14523923	>gi|14523923|gb|AAK65455.1| Putative muconate cycloisomerase [Sinorhizobium meliloti 1021]	SGA	x	
16263250	>gi|16263250|ref|NP_436043.1| Putative muconate cycloisomerase [Sinorhizobium meliloti 1021]	SGA	x	
14021703	>gi|14021703|dbj|BAB48315.1| probable muconate cycloisomerase [Mesorhizobium loti MAFF303099]	SGA	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
13470960	>gi|13470960|ref|NP_102529.1| probable muconate cycloisomerase [Mesorhizobium loti MAFF303099]	SGA	x	
10175628	>gi|10175628|dbj|BAB06725.1| muconate cycloisomerase [Bacillus halodurans C-125]	SGA	x	
15615568	>gi|15615568|ref|NP_243872.1| muconate cycloisomerase [Bacillus halodurans C-125]	SGA	x	
60492256	>gi|60492256|emb|CAH07021.1| putative muconate cycloisomerase [Bacteroides fragilis NCTC 9343]	SGA	x	
60680822	>gi|60680822|ref|YP_210966.1| putative muconate cycloisomerase [Bacteroides fragilis NCTC 9343]	SGA	x	
60493669	>gi|60493669|emb|CAH08458.1| putative muconate cycloisomerase [Bacteroides fragilis NCTC 9343]	SGA	x	
60682235	>gi|60682235|ref|YP_212379.1| putative muconate cycloisomerase [Bacteroides fragilis NCTC 9343]	SGA	x	
52003007	>gi|52003007|gb|AAU22949.1| putative muconate cycloisomerase [Bacillus subtilis phage PBSX]	BTC, MOF	x	
52079796	>gi|52079796|ref|YP_078587.1| putative muconate cycloisomerase [Bacillus licheniformis ATCC 14580]	BTC, MOF	x	
52216903	>gi|52216903|dbj|BAD49496.1| muconate cycloisomerase [Bacteroides fragilis YCH46]	SGA	x	
53714038	>gi|53714038|ref|YP_100030.1| muconate cycloisomerase [Bacteroides fragilis YCH46]	SGA	x	
46199775	>gi|46199775|ref|YP_005442.1| muconate cycloisomerase [Thermus thermophilus HB27]	SGA	x	
46197402	>gi|46197402|gb|AAS81815.1| muconate cycloisomerase [Thermus thermophilus HB27]	SGA	x	
29346723	>gi|29346723|ref|NP_810226.1| muconate cycloisomerase [Bacteroides thetaiotaomicron VPI-5482]	SGA	x	
29338620	>gi|29338620|gb|AAO76420.1| muconate cycloisomerase [Bacteroides thetaiotaomicron VPI-5482]	SGA	x	
17132665	>gi|17132665|dbj|BAB75231.1| muconate cycloisomerase [Nostoc sp. PCC 7120]	SGA	x	
30698534	>gi|30698534|dbj|BAC76455.1| cis,cis-muconate cycloisomerase [Rhodococcus erythropolis]	BTC	x	
56383430	>gi|56383430|gb|AAN42937.2| putative muconate cycloisomerase I [Shigella flexneri 2a str. 301]	SGA	x	
30041091	>gi|30041091|gb|AAP16821.1| putative muconate cycloisomerase I [Shigella flexneri 2a str. 2457T]	SGA	x	
30062843	>gi|30062843|ref|NP_837014.1| putative muconate cycloisomerase I [Shigella flexneri 2a str. 2457T]	SGA	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
56479879	>gi|56479879|ref|NP_707230.2| putative muconate cycloisomerase I [Shigella flexneri 2a str. 301]	SGA	x	
21958818	>gi|21958818|gb|AAM85557.1| putative muconate cycloisomerase I [Yersinia pestis KIM]	SGA	x	
22125883	>gi|22125883|ref|NP_669306.1| muconate cycloisomerase I [Yersinia pestis KIM]	SGA	x	
28808495	>gi|28808495|dbj|BAC61672.1| putative muconate cycloisomerase I [Vibrio parahaemolyticus RIMD 2210633]	SGA	x	
28900184	>gi|28900184|ref|NP_799839.1| putative muconate cycloisomerase I [Vibrio parahaemolyticus RIMD 2210633]	SGA	x	
32447201	>gi|32447201|emb|CAD77027.1| muconate cycloisomerase I [Rhodopirellula baltica SH 1]	SGA	x	
32476655	>gi|32476655|ref|NP_869649.1| muconate cycloisomerase I [Rhodopirellula baltica SH 1]	SGA	x	
56680224	>gi|56680224|gb|AAV96890.1| muconate cycloisomerase I [Silicibacter pomeroyi DSS-3]	BTC, MOF	x	
56698487	>gi|56698487|ref|YP_168862.1| muconate cycloisomerase I [Silicibacter pomeroyi DSS-3]	BTC, MOF	x	
39650882	>gi|39650882|emb|CAE29405.1| putative muconate cycloisomerase [Rhodopseudomonas palustris CGA009]	SGA	x	
39937025	>gi|39937025|ref|NP_949301.1| putative muconate cycloisomerase [Rhodopseudomonas palustris CGA009]	SGA	x	
46913516	>gi|46913516|emb|CAG20302.1| Hypothetical muconate cycloisomerase I [Photobacterium profundum SS9]	SGA	x	
54309084	>gi|54309084|ref|YP_130104.1| Hypothetical muconate cycloisomerase I [Photobacterium profundum SS9]	SGA	x	
38198158	>gi|38198158|emb|CAE53842.1| muconate cycloisomerase [Rhodococcus erythropolis]	BTC	x	
13361369	>gi|13361369|dbj|BAB35327.1| putative muconate cycloisomerase I [Escherichia coli O157:H7]	SGA	x	
25990736	>gi|25990736|gb|AAN76672.1| muconate cycloisomerase [Streptomyces setonii]	SGA	x	
61611869	>gi|61611869|gb|AAX47261.1| muconate cycloisomerase [Delftia tsuruhatensis]	BTC	x	
68560306	>gi|68560306|ref|ZP_00599621.1| Muconate cycloisomerase [Rubrobacter xylanophilus DSM 9941]	MFR	x	
68513655	>gi|68513655|gb|EAN37447.1| Muconate cycloisomerase [Rubrobacter xylanophilus DSM 9941]	MFR	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
6324754	>gi|6324754|ref|NP_014823.1| Peroxisomal delta(3,5)-delta(2,4)-dienoyl-CoA isomerase, involved in fatty acid metabolism, contains peroxisome targeting signals at amino and carboxy termini; Dci1p [Saccharomyces cerevisiae]	SFA	x	
75764210	>gi|75764210|ref|ZP_00743772.1| 3-hydroxyisobutyryl-CoA hydrolase [Bacillus thuringiensis serovar israelensis ATCC 35646]	BTC	x	
74488304	>gi|74488304|gb|EAO51958.1| 3-hydroxyisobutyryl-CoA hydrolase [Bacillus thuringiensis serovar israelensis ATCC 35646]	BTC	x	
57222845	>gi|57222845|gb|AAW40889.1| 3-hydroxyisobutyryl-CoA hydrolase, putative [Cryptococcus neoformans var. neoformans JEC21]	BTC	x	
58258591	>gi|58258591|ref|XP_566708.1| 3-hydroxyisobutyryl-CoA hydrolase [Cryptococcus neoformans var. neoformans JEC21]	BTC	x	
77554204	>gi|77554204|gb|ABA97000.1| 3-hydroxyisobutyryl-coenzyme A hydrolase, putative [Oryza sativa (japonica cultivar-group)]	BTC	x	
83286275	>gi|83286275|ref|XP_730090.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase [Plasmodium yoelii yoelii str. 17XNL]	NSF	x	
52628216	>gi|52628216|gb|AAU26957.1| 3-hydroxyisobutyryl Coenzyme A hydrolase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]	SFA	x	
52841105	>gi|52841105|ref|YP_094904.1| 3-hydroxyisobutyryl Coenzyme A hydrolase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]	SFA	x	
23509082	>gi|23509082|ref|NP_701750.1| 3-hydroxyisobutyryl-coenzyme A hydrolase, putative [Plasmodium falciparum 3D7]	BTC	x	
23496922	>gi|23496922|gb|AAN36474.1| 3-hydroxyisobutyryl-coenzyme A hydrolase, putative [Plasmodium falciparum 3D7]	BTC	x	
83369758	>gi|83369758|ref|ZP_00914609.1| methylmalonyl-CoA epimerase [Rhodobacter sphaeroides ATCC 17025]	BTC	x	
83373654	>gi|83373654|ref|ZP_00918432.1| methylmalonyl-CoA epimerase [Rhodobacter sphaeroides ATCC 17029]	BTC	x	
83952781	>gi|83952781|ref|ZP_00961511.1| methylmalonyl-CoA epimerase [Roseovarius nubinhibens ISM]	BTC	x	
84499556	>gi|84499556|ref|ZP_00997844.1| methylmalonyl-CoA epimerase [Oceanicola batsensis HTCC2597]	BTC	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
84514460	>gi|84514460|ref|ZP_01001824.1| methylmalonyl-CoA epimerase [Loktanella vestfoldensis SKA53]	BTC	x	
84685301	>gi|84685301|ref|ZP_01013199.1| methylmalonyl-CoA epimerase [Rhodobacterales bacterium HTCC2654]	BTC	x	
85704719	>gi|85704719|ref|ZP_01035820.1| methylmalonyl-CoA epimerase [Roseovarius sp. 217]	BTC	x	
86131463	>gi|86131463|ref|ZP_01050061.1| methylmalonyl-CoA epimerase [Cellulophaga sp. MED134]	BTC	x	
86136527	>gi|86136527|ref|ZP_01055106.1| methylmalonyl-CoA epimerase [Roseobacter sp. MED193]	BTC	x	
66820506	>gi|66820506|ref|XP_643859.1| methylmalonyl coenzyme A racemase [Dictyostelium discoideum]	BTC	x	
38199911	>gi|38199911|emb|CAE49577.1| Putative methylmalonyl-CoA epimerase [Corynebacterium diphtheriae]	BTC	x	
55771774	>gi|55771774|dbj|BAD70215.1| probable methylmalonyl-CoA epimerase [Thermus thermophilus HB8]	BTC	x	
5457681	>gi|5457681|emb|CAB49172.1| Methylmalonyl-coA epimerase [Pyrococcus abyssi GE5]	BTC	x	
57158589	>gi|57158589|dbj|BAD84519.1| methylmalonyl-CoA epimerase [Thermococcus kodakarensis KOD1]	BTC	x	
39985338	>gi|39985338|gb|AAR36693.1| methylmalonyl-CoA epimerase [Geobacter sulfurreducens PCA]	BTC	x	
56677571	>gi|56677571|gb|AAV94237.1| methylmalonyl-CoA epimerase [Silicibacter pomeroyi DSS-3]	BTC	x	
28207558	>gi|28207558|gb|AAO32148.1| methylmalonyl-CoA epimerase [Methylobacterium extorquens]	BTC	x	
83318921	>gi|83318921|emb|CAJ38798.1| 4-hydroxyphenylpyruvate dioxygenase protein [Platynereis dumerilii]	BTC	x	
84712295	>gi|84712295|ref|ZP_01020207.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Polaromonas naphthalenivorans CJ2]	BTC	x	
84715779	>gi|84715779|ref|ZP_01022729.1| 4-hydroxyphenylpyruvate dioxygenase [Polaromonas naphthalenivorans CJ2]	NSF	x	
86605196	>gi|86605196|ref|YP_473959.1| putative 4-hydroxyphenylpyruvate dioxygenase [Cyanobacteria bacterium Yellowstone A-Prime]	BTC	x	
86607745	>gi|86607745|ref|YP_476507.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Cyanobacteria bacterium Yellowstone B-Prime]	BTC	x	
72256523	>gi|72256523|gb|AAZ67144.1| 4-hydroxyphenylpyruvate dioxygenase [Triticum aestivum]	BTC	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
2695710	>gi|2695710|emb|CAA04245.1| 4-hydroxyphenylpyruvate dioxygenase [Hordeum vulgare subsp. vulgare]	BTC	x	
78696458	>gi|78696458|ref|ZP_00860968.1| 4-hydroxyphenylpyruvate dioxygenase [Bradyrhizobium sp. BTAi1]	NSF	x	
67677616	>gi|67677616|ref|ZP_00474345.1| 4-hydroxyphenylpyruvate dioxygenase [Chromohalobacter salexigens DSM 3043]	BTC	x	
67779648	>gi|67779648|gb|EAM39266.1| 4-hydroxyphenylpyruvate dioxygenase [Polaromonas sp. JS666]	NSF	x	
35213661	>gi|35213661|dbj|BAC91032.1| 4-hydroxyphenylpyruvate dioxygenase [Gloeobacter violaceus PCC 7421]	BTC	x	
48431089	>gi|48431089|gb|AAT43954.1| 4-hydroxyphenylpyruvate dioxygenase [Picrophilus torridus DSM 9790]	BTC	x	
58001357	>gi|58001357|gb|AAW60251.1| Putative 4-hydroxyphenylpyruvate dioxygenase [Gluconobacter oxydans 621H]	NSF	x	
17130116	>gi|17130116|dbj|BAB72728.1| 4-hydroxyphenylpyruvate dioxygenase [Nostoc sp. PCC 7120]	BTC	x	
68139770	>gi|68139770|gb|EAM93093.1| 4-hydroxyphenylpyruvate dioxygenase [Ferroplasma acidarmanus Fer1]	BTC	x	
75704587	>gi|75704587|gb|ABA24263.1| 4-hydroxyphenylpyruvate dioxygenase [Anabaena variabilis ATCC 29413]	BTC	x	
15141381	>gi|15141381|emb|CAC49893.1| putative 4-hydroxyphenylpyruvate dioxygenase protein [Sinorhizobium meliloti 1021]	BTC	x	
68489346	>gi|68489346|ref|XP_711514.1| 4-hydroxyphenylpyruvate dioxygenase [Candida albicans SC5314]	BTC	x	
86159841	>gi|86159841|ref|YP_466626.1| 4-hydroxyphenylpyruvate dioxygenase [Anaeromyxobacter dehalogenans 2CP-C]	BTC	x	
66843900	>gi|66843900|gb|EAL84241.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Aspergillus fumigatus Af293]	NSF	x	
66846300	>gi|66846300|gb|EAL86633.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Aspergillus fumigatus Af293]	NSF	x	
66848396	>gi|66848396|gb|EAL88725.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Aspergillus fumigatus Af293]	NSF	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
66850157	>gi|66850157|gb|EAL90484.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Aspergillus fumigatus Af293]	NSF	x	
66851780	>gi|66851780|gb|EAL92105.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Aspergillus fumigatus Af293]	NSF	x	
86741150	>gi|86741150|ref|YP_481550.1| 4-hydroxyphenylpyruvate dioxygenase [Frankia sp. CcI3]	BTC	x	
71673567	>gi|71673567|ref|ZP_00671315.1| 4-hydroxyphenylpyruvate dioxygenase [Trichodesmium erythraeum IMS101]	BTC	x	
32394683	>gi|32394683|gb|AAN39008.1| putative 4-hydroxyphenylpyruvate dioxygenase oxidoreductase protein [Griffithsia japonica]	NSF	x	
23505684	>gi|23505684|gb|AAN28922.1| 4-hydroxyphenylpyruvate dioxygenase [Abutilon theophrasti]	BTC	x	
67909206	>gi|67909206|ref|ZP_00507603.1| 4-hydroxyphenylpyruvate dioxygenase [Polaromonas sp. JS666]	BTC	x	
67922247	>gi|67922247|ref|ZP_00515761.1| 4-hydroxyphenylpyruvate dioxygenase [Crocosphaera watsonii WH 8501]	BTC	x	
42600537	>gi|42600537|emb|CAD24031.1| p-hydroxyphenylpyruvate dioxigenase [Chlamydomonas reinhardtii]	BTC	x	
4481935	>gi|4481935|emb|CAB38519.1| putative 4-hydroxyphenylpyruvic acid dioxygenase [Streptomyces coelicolor A3(2)]	BTC	x	
1001726	>gi|1001726|dbj|BAA10563.1| 4-hydroxyphenylpyruvic acid dioxgenase [Synechocystis sp. PCC 6803]	BTC	x	
78167527	>gi|78167527|gb|ABB24625.1| glutathione S-transferase, fosfomycin resistance protein, putative [Pelodictyon luteolum DSM 273]	SFA	x	
78187625	>gi|78187625|ref|YP_375668.1| glutathione S-transferase, fosfomycin resistance protein, putative [Pelodictyon luteolum DSM 273]	SFA	x	
78171614	>gi|78171614|gb|ABB28710.1| glutathione S-transferase, fosfomycin resistance protein, putative [Chlorobium chlorochromatii CaD3]	SFA	x	
78189415	>gi|78189415|ref|YP_379753.1| glutathione S-transferase, fosfomycin resistance protein, putative [Chlorobium chlorochromatii CaD3]	SFA	x	
21646159	>gi|21646159|gb|AAM71495.1| glutathione S-transferase, fosfomycin resistance protein, putative [Chlorobium tepidum TLS]	SFA	x	
21673088	>gi|21673088|ref|NP_661153.1| glutathione S-transferase, fosfomycin resistance protein, putative [Chlorobium tepidum TLS]	SFA	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
42737746	>gi|42737746|gb|AAS41677.1| fosfomycin resistance protein (glutathione transferase) BH1778 [Bacillus cereus ATCC 10987]	SFA	x	
216886	>gi|216886|dbj|BAA00248.1| glyoxalase I [Pseudomonas putida]	BTC	x	
82495720	>gi|82495720|ref|ZP_00881294.1| Glyoxalase I [Shewanella sp. MR-4]	BTC	x	
82746264	>gi|82746264|ref|ZP_00908771.1| glyoxalase I [Clostridium beijerincki NCIMB 8052]	SFA	x	
82749136	>gi|82749136|ref|ZP_00911603.1| glyoxalase I (glyoxalase family) [Clostridium beijerincki NCIMB 8052]	SFA	x	
83701621	>gi|83701621|gb|ABC41262.1| glyoxalase I [Leishmania infantum]	BTC	x	
83953359	>gi|83953359|ref|ZP_00962081.1| Glyoxalase I (lactoylglutathione lyase) [Sulfitobacter sp. NAS-14.1]	SFA	x	
69952143	>gi|69952143|ref|ZP_00639697.1| Glyoxalase I [Shewanella frigidimarina NCIMB 400]	BTC	x	
69953426	>gi|69953426|ref|ZP_00640556.1| Glyoxalase I [Shewanella frigidimarina NCIMB 400]	BTC	x	
71362651	>gi|71362651|ref|ZP_00653802.1| Glyoxalase I [Psychrobacter cryohalolentis K5]	BTC	x	
505585	>gi|505585|emb|CAA48717.1| lactoylglutathione lyase [Glycine max]	NSF	x	
74023999	>gi|74023999|ref|ZP_00694563.1| Glyoxalase I [Rhodoferax ferrireducens DSM 15236]	BTC	x	
76874945	>gi|76874945|emb|CAI86166.1| glyoxalase I, nickel isomerase (Lactoylglutathione lyase) [Pseudoalteromonas haloplanktis TAC125]	BTC	x	
78034245	>gi|78034245|emb|CAJ21890.1| putative glyoxalase I [Xanthomonas campestris pv. vesicatoria str. 85-10]	NSF	x	
76792566	>gi|76792566|ref|ZP_00775064.1| Glyoxalase I [Pseudoalteromonas atlantica T6c]	BTC	x	
69156636	>gi|69156636|gb|EAN68934.1| Glyoxalase I [Shewanella denitrificans OS217]	BTC	x	
78170021	>gi|78170021|gb|ABB27118.1| Glyoxalase I [Synechococcus sp. CC9902]	BTC	x	
77815744	>gi|77815744|ref|ZP_00814966.1| Glyoxalase I [Shewanella putrefaciens CN-32]	BTC	x	
78198442	>gi|78198442|gb|ABB36207.1| Glyoxalase I [Synechococcus sp. CC9605]	BTC	x	
78364163	>gi|78364163|gb|ABB42128.1| Glyoxalase I [Thiomicrospira crunogena XCL-2]	BTC	x	
78712536	>gi|78712536|gb|ABB49713.1| Glyoxalase I [Prochlorococcus marinus str. MIT 9312]	BTC	x	
79317690	>gi|79317690|ref|NP_001031026.1| ATGLX1 (GLYOXALASE I HOMOLOG); lactoylglutathione lyase [Arabidopsis thaliana]	BTC	x	
78366563	>gi|78366563|ref|ZP_00836842.1| Glyoxalase I [Shewanella sp. PV-4]	BTC	x	
78686502	>gi|78686502|ref|ZP_00851269.1| Glyoxalase I [Shewanella sp. ANA-3]	BTC	x	
78690516	>gi|78690516|ref|ZP_00855161.1| Glyoxalase I [Shewanella sp. MR-7]	BTC	x	
68542244	>gi|68542244|ref|ZP_00581978.1| Glyoxalase I [Shewanella baltica OS155]	BTC	x	

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>68547433</td><td>>gi|68547433|ref|ZP_00586969.1| Glyoxalase I [Shewanella amazonensis SB2B]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>55739422</td><td>>gi|55739422|gb|AAV63063.1| glyoxalase I/lactoylglutathione lyase [Streptococcus thermophilus CNRZ1066]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>23348107</td><td>>gi|23348107|gb|AAN30186.1| lactoylglutathione lyase [Brucella suis 1330]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>13815730</td><td>>gi|13815730|gb|AAK42570.1| Lactoylglutathione lyase (glyoxalase I), putative [Sulfolobus solfataricus P2]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>52002505</td><td>>gi|52002505|gb|AAU22447.1| Glyoxalase I YfiE [Bacillus licheniformis ATCC 14580]</td><td>NSF</td><td>x</td><td></td></tr>
<tr><td>51973817</td><td>>gi|51973817|gb|AAU15367.1| lactoylglutathione lyase (glyoxalase I) [Bacillus cereus E33L]</td><td>NSF</td><td>x</td><td></td></tr>
<tr><td>82698979</td><td>>gi|82698979|ref|YP_413553.1| Glyoxalase/Bleomycin resistance protein/dioxygenase domain:Glyoxalase I [Brucella melitensis biovar Abortus 2308]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>56491581</td><td>>gi|56491581|emb|CAI02444.1| glyoxalase I, putative [Plasmodium berghei]</td><td>NSF</td><td>x</td><td></td></tr>
<tr><td>70946959</td><td>>gi|70946959|ref|XP_743141.1| glyoxalase I [Plasmodium chabaudi chabaudi]</td><td>NSF</td><td>x</td><td></td></tr>
<tr><td>28204236</td><td>>gi|28204236|gb|AAO36675.1| putative lactoylglutathione lyase [Clostridium tetani E88]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>70905885</td><td>>gi|70905885|gb|AAZ14524.1| trypanothione-dependent glyoxalase I [Leishmania major strain Friedlin]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>77388805</td><td>>gi|77388805|gb|ABA79990.1| Glyoxalase I (lactoylglutathione lyase) [Rhodobacter sphaeroides 2.4.1]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>52005756</td><td>>gi|52005756|gb|AAU25698.1| Glyoxalase I [Bacillus licheniformis ATCC 14580]</td><td>NSF</td><td>x</td><td></td></tr>
<tr><td>49332759</td><td>>gi|49332759|gb|AAT63405.1| lactoylglutathione lyase (glyoxalase I) [Bacillus thuringiensis serovar konkukian str. 97-27]</td><td>NSF</td><td>x</td><td></td></tr>
<tr><td>46362279</td><td>>gi|46362279|emb|CAG25217.1| glyoxalase I, putative [Plasmodium falciparum 3D7]</td><td>NSF</td><td>x</td><td></td></tr>
<tr><td>68555141</td><td>>gi|68555141|ref|ZP_00594486.1| Glyoxalase I [Ralstonia metallidurans CH34]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>86357507</td><td>>gi|86357507|ref|YP_469399.1| lactoylglutathione lyase methylglyoxalase protein [Rhizobium etli CFN 42]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>15074653</td><td>>gi|15074653|emb|CAC46298.1| PROBABLE LACTOYLGLUTATHIONE LYASE METHYLGLYOXALASE PROTEIN [Sinorhizobium meliloti]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>33639942</td><td>>gi|33639942|emb|CAE19112.1| LACTOYLGLUTATHIONE LYASE [Prochlorococcus marinus subsp. pastoris str. CCMP1986]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>33641128</td><td>>gi|33641128|emb|CAE22258.1| lactoylglutathione lyase; Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily [Prochlorococcus marinus str. MIT 9313]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>17427530</td><td>>gi|17427530|emb|CAD14048.1| PROBABLE LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE) PROTEIN [Ralstonia solanacearum]</td><td>BTC</td><td>x</td><td></td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
49330669	>gi|49330669|gb|AAT61315.1| lactoylglutathione lyase, glyoxalase family protein [Bacillus thuringiensis serovar konkukian str. 97-27]	SFA	x	
2621847	>gi|2621847|gb|AAB85261.1| S-D-lactoylglutathione methylglyoxal lyase [Methanothermobacter thermautotrophicus str. Delta H]	SFA	x	
82748396	>gi|82748396|ref|ZP_00910881.1| lactoylglutathione lyase [Clostridium beijerincki NCIMB 8052]	BTC	x	
83368940	>gi|83368940|ref|ZP_00913800.1| lactoylglutathione lyase [Rhodobacter sphaeroides ATCC 17025]	BTC	x	
83369976	>gi|83369976|ref|ZP_00914824.1| lactoylglutathione lyase, putative [Rhodobacter sphaeroides ATCC 17025]	BTC	x	
83372766	>gi|83372766|ref|ZP_00917545.1| lactoylglutathione lyase [Rhodobacter sphaeroides ATCC 17029]	BTC	x	
83373191	>gi|83373191|ref|ZP_00917970.1| lactoylglutathione lyase, putative [Rhodobacter sphaeroides ATCC 17029]	BTC	x	
83747838	>gi|83747838|ref|ZP_00944871.1| Lactoylglutathione lyase [Ralstonia solanacearum UW551]	SFA	x	
83749342	>gi|83749342|ref|ZP_00946339.1| Lactoylglutathione lyase [Ralstonia solanacearum UW551]	BTC	x	
83858397	>gi|83858397|ref|ZP_00951919.1| lactoylglutathione lyase, putative [Oceanicaulis alexandrii HTCC2633]	SFA	x	
83943291	>gi|83943291|ref|ZP_00955751.1| lactoylglutathione lyase [Sulfitobacter sp. EE-36]	NSF	x	
83945063	>gi|83945063|ref|ZP_00957429.1| lactoylglutathione lyase [Oceanicaulis alexandrii HTCC2633]	BTC	x	
83950701	>gi|83950701|ref|ZP_00959434.1| Lactoylglutathione lyase [Roseovarius nubinhibens ISM]	BTC	x	
83951513	>gi|83951513|ref|ZP_00960245.1| lactoylglutathione lyase, putative [Roseovarius nubinhibens ISM]	BTC	x	
83954069	>gi|83954069|ref|ZP_00962789.1| lactoylglutathione lyase, putative [Sulfitobacter sp. NAS-14.1]	BTC	x	
84360451	>gi|84360451|ref|ZP_00985153.1| COG3607: Predicted lactoylglutathione lyase [Burkholderia dolosa AUO158]	SFA	x	
84385192	>gi|84385192|ref|ZP_00988224.1| putative lactoylglutathione lyase [Vibrio splendidus 12B01]	SFA	x	
84386626	>gi|84386626|ref|ZP_00989652.1| lactoylglutathione lyase [Vibrio splendidus 12B01]	BTC	x	
84386685	>gi|84386685|ref|ZP_00989711.1| Lactoylglutathione lyase [Vibrio splendidus 12B01]	SFA	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
84501614	>gi|84501614|ref|ZP_00999786.1| lactoylglutathione lyase, putative [Oceanicola batsensis HTCC2597]	BTC	x	
84515363	>gi|84515363|ref|ZP_01002725.1| probable lactoylglutathione lyase [Loktanella vestfoldensis SKA53]	BTC	x	
84685556	>gi|84685556|ref|ZP_01013454.1| GloA, lactoylglutathione lyase [Rhodobacterales bacterium HTCC2654]	BTC	x	
84686020	>gi|84686020|ref|ZP_01013916.1| lactoylglutathione lyase [Rhodobacterales bacterium HTCC2654]	SFA	x	
84711566	>gi|84711566|ref|ZP_01019712.1| lactoylglutathione lyase [Polaromonas naphthalenivorans CJ2]	NSF	x	
83644418	>gi|83644418|ref|YP_432853.1| Lactoylglutathione lyase [Hahella chejuensis KCTC 2396]	SFA	x	
83644521	>gi|83644521|ref|YP_432956.1| Lactoylglutathione lyase [Hahella chejuensis KCTC 2396]	SFA	x	
83644845	>gi|83644845|ref|YP_433280.1| Lactoylglutathione lyase [Hahella chejuensis KCTC 2396]	NSF	x	
83646548	>gi|83646548|ref|YP_434983.1| Lactoylglutathione lyase [Hahella chejuensis KCTC 2396]	NSF	x	
83646952	>gi|83646952|ref|YP_435387.1| Lactoylglutathione lyase [Hahella chejuensis KCTC 2396]	SFA	x	
83647341	>gi|83647341|ref|YP_435776.1| Lactoylglutathione lyase [Hahella chejuensis KCTC 2396]	NSF	x	
83647554	>gi|83647554|ref|YP_435989.1| Lactoylglutathione lyase [Hahella chejuensis KCTC 2396]	NSF	x	
83648464	>gi|83648464|ref|YP_436899.1| Lactoylglutathione lyase [Hahella chejuensis KCTC 2396]	SFA	x	
83649126	>gi|83649126|ref|YP_437561.1| Lactoylglutathione lyase [Hahella chejuensis KCTC 2396]	NSF	x	
83649348	>gi|83649348|ref|YP_437783.1| Lactoylglutathione lyase [Hahella chejuensis KCTC 2396]	NSF	x	
47095742	>gi|47095742|ref|ZP_00233348.1| lactoylglutathione lyase, putative [Listeria monocytogenes str. 1/2a F6854]	BTC	x	
47564331	>gi|47564331|ref|ZP_00235376.1| lactoylglutathione lyase [Bacillus cereus G9241]	SFA	x	
47564348	>gi|47564348|ref|ZP_00235393.1| lactoylglutathione lyase [Bacillus cereus G9241]	BTC	x	
47564484	>gi|47564484|ref|ZP_00235529.1| lactoylglutathione lyase [Bacillus cereus G9241]	SFA	x	
47564743	>gi|47564743|ref|ZP_00235787.1| lactoylglutathione lyase [Bacillus cereus G9241]	SFA	x	
62464063	>gi|62464063|ref|ZP_00383365.1| COG3607: Predicted lactoylglutathione lyase [Lactococcus lactis subsp. cremoris SK11]	NSF	x	
47570268	>gi|47570268|ref|ZP_00240918.1| lactoylglutathione lyase, putative [Bacillus cereus G9241]	NSF	X	
53688539	>gi|53688539|ref|ZP_00110851.2| COG3607: Predicted lactoylglutathione lyase [Nostoc punctiforme PCC 73102]	NSF	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
47572332	>gi|47572332|ref|ZP_00242377.1| COG3607: Predicted lactoylglutathione lyase [Rubrivivax gelatinosus PM1]	NSF	x	
71062469	>gi|71062469|gb|AAZ21472.1| lactoylglutathione lyase [Candidatus Pelagibacter ubique HTCC1062]	BTC	x	
85859982	>gi|85859982|ref|YP_462184.1| lactoylglutathione lyase [Syntrophus aciditrophicus SB]	SFA	x	
85703449	>gi|85703449|ref|ZP_01034553.1| Lactoylglutathione lyase [Roseovarius sp. 217]	BTC	x	
85704765	>gi|85704765|ref|ZP_01035866.1| Lactoylglutathione lyase [Roseovarius sp. 217]	SFA	x	
85707130	>gi|85707130|ref|ZP_01038218.1| probable lactoylglutathione lyase [Roseovarius sp. 217]	BTC	x	
85707649	>gi|85707649|ref|ZP_01038715.1| lactoylglutathione lyase [Erythrobacter sp. NAP1]	BTC	x	
85708379	>gi|85708379|ref|ZP_01039445.1| lactoylglutathione lyase, putative [Erythrobacter sp. NAP1]	SFA	x	
86137415	>gi|86137415|ref|ZP_01055992.1| lactoylglutathione lyase, putative [Roseobacter sp. MED193]	BTC	x	
86145772	>gi|86145772|ref|ZP_01064101.1| putative lactoylglutathione lyase [Vibrio sp. MED222]	SFA	x	
86146970	>gi|86146970|ref|ZP_01065288.1| lactoylglutathione lyase [Vibrio sp. MED222]	BTC	x	
86162424	>gi|86162424|gb|EAQ63707.1| lactoylglutathione lyase [Marinomonas sp. MED121]	BTC	x	
86166361	>gi|86166361|gb|EAQ67627.1| putative lactoylglutathione lyase [Marinomonas sp. MED121]	SFA	x	
86356019	>gi|86356019|ref|YP_467911.1| probable lactoylglutathione lyase protein [Rhizobium etli CFN 42]	SFA	x	
86356437	>gi|86356437|ref|YP_468329.1| putative lactoylglutathione lyase protein [Rhizobium etli CFN 42]	NSF	x	
86356906	>gi|86356906|ref|YP_468798.1| probable lactoylglutathione lyase protein [Rhizobium etli CFN 42]	NSF	x	
86357255	>gi|86357255|ref|YP_469147.1| putative lactoylglutathione lyase protein [Rhizobium etli CFN 42]	SFA	x	
86358230	>gi|86358230|ref|YP_470122.1| probable lactoylglutathione lyase protein [Rhizobium etli CFN 42]	SFA	x	
74318361	>gi|74318361|ref|YP_316101.1| lactoylglutathione lyase [Thiobacillus denitrificans ATCC 25259]	BTC	x	
68164578	>gi|68164578|gb|AAY87307.1| predicted lactoylglutathione lyase [uncultured bacterium BAC17H8]	BTC	x	
71144858	>gi|71144858|gb|AAZ25331.1| lactoylglutathione lyase [Colwellia psychrerythraea 34H]	BTC	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
72495716	>gi|72495716|dbj|BAE19037.1| putative lactoylglutathione lyase [Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305]	NSF	x	
71802610	>gi|71802610|gb|AAX71963.1| lactoylglutathione lyase [Streptococcus pyogenes MGAS6180]	SFA	x	
74023435	>gi|74023435|ref|ZP_00694008.1| putative lactoylglutathione lyase [Rhodoferax ferrireducens DSM 15236]	NSF	x	
75759432	>gi|75759432|ref|ZP_00739526.1| Lactoylglutathione lyase [Bacillus thuringiensis serovar israelensis ATCC 35646]	NSF	x	
75760536	>gi|75760536|ref|ZP_00740571.1| Lactoylglutathione lyase [Bacillus thuringiensis serovar israelensis ATCC 35646]	SFA	x	
75763726	>gi|75763726|ref|ZP_00743400.1| Lactoylglutathione lyase [Bacillus thuringiensis serovar israelensis ATCC 35646]	BTC	x	
75763843	>gi|75763843|ref|ZP_00743493.1| Lactoylglutathione lyase [Bacillus thuringiensis serovar israelensis ATCC 35646]	SFA	x	
71853471	>gi|71853471|gb|AAZ51494.1| lactoylglutathione lyase [Streptococcus pyogenes MGAS5005]	SFA	x	
77389666	>gi|77389666|gb|ABA80850.1| Lactoylglutathione lyase [Rhodobacter sphaeroides 2.4.1]	BTC	x	
77544204	>gi|77544204|gb|ABA87766.1| lactoylglutathione lyase [Pelobacter carbinolicus DSM 2380]	BTC	x	
77545161	>gi|77545161|gb|ABA88723.1| lactoylglutathione lyase [Pelobacter carbinolicus DSM 2380]	BTC	x	
77546720	>gi|77546720|gb|ABA90282.1| lactoylglutathione lyase [Pelobacter carbinolicus DSM 2380]	SFA	x	
77408563	>gi|77408563|ref|ZP_00785299.1| lactoylglutathione lyase [Streptococcus agalactiae COH1]	BTC	x	
78167051	>gi|78167051|gb|ABB24149.1| lactoylglutathione lyase [Pelodictyon luteolum DSM 273]	SFA	x	
77952624	>gi|77952624|ref|ZP_00817038.1| lactoylglutathione lyase [Marinobacter aquaeolei VT8]	BTC	x	
78693250	>gi|78693250|ref|ZP_00857764.1| lactoylglutathione lyase [Bradyrhizobium sp. BTAi1]	BTC	x	
78700706	>gi|78700706|ref|ZP_00865161.1| lactoylglutathione lyase [Alkalilimnicola ehrlichei MLHE-1]	BTC	x	
78696758	>gi|78696758|ref|ZP_00861267.1| lactoylglutathione lyase [Bradyrhizobium sp. BTAi1]	BTC	x	
34763440	>gi|34763440|ref|ZP_00144387.1| Lactoylglutathione lyase [Fusobacterium nucleatum subsp. vincentii ATCC 49256]	BTC	x	
34763318	>gi|34763318|ref|ZP_00144274.1| Lactoylglutathione lyase [Fusobacterium nucleatum subsp. vincentii ATCC 49256]	NSF	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
34762987	>gi|34762987|ref|ZP_00143964.1| Lactoylglutathione lyase [Fusobacterium nucleatum subsp. vincentii ATCC 49256]	SFA	x	
66802462	>gi|66802462|ref|XP_635103.1| glyoxylase I [Dictyostelium discoideum]	BTC	x	
56550926	>gi|56550926|ref|YP_161765.1| lactoylglutathione lyase [Zymomonas mobilis subsp. mobilis ZM4]	NSF	x	
56551657	>gi|56551657|ref|YP_162496.1| lactoylglutathione lyase [Zymomonas mobilis subsp. mobilis ZM4]	NSF	x	
56552617	>gi|56552617|ref|YP_163456.1| lactoylglutathione lyase [Zymomonas mobilis subsp. mobilis ZM4]	NSF	x	
56908846	>gi|56908846|dbj|BAD63373.1| lactoylglutathione lyase [Bacillus clausii KSM-K16]	SFA	x	
56909760	>gi|56909760|dbj|BAD64287.1| lactoylglutathione lyase [Bacillus clausii KSM-K16]	SFA	x	
17740245	>gi|17740245|gb|AAL42800.1| lactoylglutathione lyase [Agrobacterium tumefaciens str. C58]	BTC	x	
17740947	>gi|17740947|gb|AAL43444.1| lactoylglutathione lyase [Agrobacterium tumefaciens str. C58]	BTC	x	
17740826	>gi|17740826|gb|AAL43333.1| lactoylglutathione lyase [Agrobacterium tumefaciens str. C58]	SFA	x	
17741988	>gi|17741988|gb|AAL44391.1| lactoylglutathione lyase [Agrobacterium tumefaciens str. C58]	SFA	x	
24195004	>gi|24195004|gb|AAN48616.1| Lactoylglutathione lyase, putative [Leptospira interrogans serovar Lai str. 56601]	SFA	x	
19713822	>gi|19713822|gb|AAL94559.1| Lactoylglutathione lyase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]	BTC	x	
19714549	>gi|19714549|gb|AAL95170.1| Lactoylglutathione lyase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]	SFA	x	
19714639	>gi|19714639|gb|AAL95246.1| Lactoylglutathione lyase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]	NSF	x	
21111152	>gi|21111152|gb|AAM39511.1| lactoylglutathione lyase [Xanthomonas campestris pv. campestris str. ATCC 33913]	SFA	x	
37197078	>gi|37197078|dbj|BAC92919.1| lactoylglutathione lyase [Vibrio vulnificus YJ016]	BTC	x	
37198867	>gi|37198867|dbj|BAC94701.1| lactoylglutathione lyase [Vibrio vulnificus YJ016]	SFA	x	
37198983	>gi|37198983|dbj|BAC94816.1| lactoylglutathione lyase [Vibrio vulnificus YJ016]	SFA	x	
37199332	>gi|37199332|dbj|BAC95164.1| lactoylglutathione lyase [Vibrio vulnificus YJ016]	BTC	x	
37200497	>gi|37200497|dbj|BAC96323.1| lactoylglutathione lyase [Vibrio vulnificus YJ016]	SFA	x	
37201361	>gi|37201361|dbj|BAC97183.1| lactoylglutathione lyase [Vibrio vulnificus YJ016]	SFA	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
49333330	>gi|49333330|gb|AAT63976.1| lactoylglutathione lyase [Bacillus thuringiensis serovar konkukian str. 97-27]	NSF	x	
24377970	>gi|24377970|gb|AAN59245.1| putative lactoylglutathione lyase [Streptococcus mutans UA159]	BTC	x	
27361504	>gi|27361504|gb|AAO10412.1| Lactoylglutathione lyase [Vibrio vulnificus CMCP6]	BTC	x	
27361763	>gi|27361763|gb|AAO10670.1| Lactoylglutathione lyase [Vibrio vulnificus CMCP6]	SFA	x	
27361919	>gi|27361919|gb|AAO10825.1| Lactoylglutathione lyase [Vibrio vulnificus CMCP6]	SFA	x	
27361948	>gi|27361948|gb|AAO10854.1| Lactoylglutathione lyase [Vibrio vulnificus CMCP6]	SFA	x	
27361997	>gi|27361997|gb|AAO10903.1| Lactoylglutathione lyase [Vibrio vulnificus CMCP6]	SFA	x	
27358602	>gi|27358602|gb|AAO07551.1| Lactoylglutathione lyase [Vibrio vulnificus CMCP6]	SFA	x	
27359219	>gi|27359219|gb|AAO08164.1| Lactoylglutathione lyase [Vibrio vulnificus CMCP6]	SFA	x	
27359402	>gi|27359402|gb|AAO08346.1| Lactoylglutathione lyase [Vibrio vulnificus CMCP6]	SFA	x	
22777545	>gi|22777545|dbj|BAC13817.1| lactoylglutathione lyase [Oceanobacillus iheyensis HTE831]	SFA	x	
28807159	>gi|28807159|dbj|BAC60429.1| putative lactoylglutathione lyase [Vibrio parahaemolyticus RIMD 2210633]	BTC	x	
27352662	>gi|27352662|dbj|BAC49664.1| lactoylglutathione lyase [Bradyrhizobium japonicum USDA 110]	BTC	x	
27355772	>gi|27355772|dbj|BAC52754.1| lactoylglutathione lyase [Bradyrhizobium japonicum USDA 110]	BTC	x	
17982044	>gi|17982044|gb|AAL51346.1| PROBABLE LACTOYLGLUTATHIONE LYASE [Brucella melitensis 16M]	SFA	x	
17982666	>gi|17982666|gb|AAL51911.1| LACTOYLGLUTATHIONE LYASE [Brucella melitensis 16M]	BTC	x	
17983931	>gi|17983931|gb|AAL53069.1| LACTOYLGLUTATHIONE LYASE [Brucella melitensis 16M]	BTC	x	
29894336	>gi|29894336|gb|AAP07627.1| Lactoylglutathione lyase [Bacillus cereus ATCC 14579]	SFA	x	
29894525	>gi|29894525|gb|AAP07815.1| Lactoylglutathione lyase [Bacillus cereus ATCC 14579]	SFA	x	
51976787	>gi|51976787|gb|AAU18337.1| lactoylglutathione lyase [Bacillus cereus E33L]	NSF	x	
29896623	>gi|29896623|gb|AAP09902.1| Lactoylglutathione lyase [Bacillus cereus ATCC 14579]	SFA	x	
29896661	>gi|29896661|gb|AAP09940.1| Lactoylglutathione lyase [Bacillus cereus ATCC 14579]	SFA	x	
29896818	>gi|29896818|gb|AAP10096.1| Lactoylglutathione lyase [Bacillus cereus ATCC 14579]	SFA	x	
29896842	>gi|29896842|gb|AAP10120.1| Lactoylglutathione lyase [Bacillus cereus ATCC 14579]	BTC	x	
29898812	>gi|29898812|gb|AAP12084.1| Lactoylglutathione lyase [Bacillus cereus ATCC 14579]	NSF	x	
29343177	>gi|29343177|gb|AAO80940.1| lactoylglutathione lyase [Enterococcus faecalis V583]	BTC	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
33148019	>gi|33148019|gb|AAP95540.1| lactoylglutathione lyase [Haemophilus ducreyi 35000HP]	BTC	x	
35214133	>gi|35214133|dbj|BAC91502.1| lactoylglutathione lyase [Gloeobacter violaceus PCC 7421]	BTC	x	
14021196	>gi|14021196|dbj|BAB47809.1| lactoylglutathione lyase [Mesorhizobium loti MAFF303099]	BTC	x	
14022819	>gi|14022819|dbj|BAB49427.1| probable lactoylglutathione lyase [Mesorhizobium loti MAFF303099]	NSF	x	
14024632	>gi|14024632|dbj|BAB51235.1| lactoylglutathione lyase [Mesorhizobium loti MAFF303099]	SFA	x	
60492330	>gi|60492330|emb|CAH07095.1| putative lactoylglutathione lyase [Bacteroides fragilis NCTC 9343]	BTC	x	
56179552	>gi|56179552|gb|AAV82274.1| Lactoylglutathione lyase [Idiomarina loihiensis L2TR]	BTC	x	
71853016	>gi|71853016|gb|AAZ51039.1| lactoylglutathione lyase [Streptococcus pyogenes MGAS5005]	BTC	x	
50903292	>gi|50903292|gb|AAT87007.1| Lactoylglutathione lyase [Streptococcus pyogenes MGAS10394]	SFA	x	
51977990	>gi|51977990|gb|AAU19540.1| lactoylglutathione lyase [Bacillus cereus E33L]	NSF	x	
51978173	>gi|51978173|gb|AAU19723.1| lactoylglutathione lyase (glyoxylase I) [Bacillus cereus E33L]	SFA	x	
58002669	>gi|58002669|gb|AAW61563.1| Lactoylglutathione lyase [Gluconobacter oxydans 621H]	BTC	x	
51856015	>gi|51856015|dbj|BAD40173.1| putative lactoylglutathione lyase [Symbiobacterium thermophilum IAM 14863]	SFA	x	
16418740	>gi|16418740|gb|AAL19199.1| putative lactoylglutathione lyase [Salmonella typhimurium LT2]	SFA	x	
52214981	>gi|52214981|dbj|BAD47574.1| putative lactoylglutathione lyase [Bacteroides fragilis YCH46]	SFA	x	
52629211	>gi|52629211|gb|AAU27952.1| lactoylglutathione lyase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]	BTC	x	
46908401	>gi|46908401|ref|YP_014790.1| lactoylglutathione lyase, putative [Listeria monocytogenes str. 4b F2365]	BTC	x	
41325166	>gi|41325166|emb|CAF19647.1| Predicted lactoylglutathione lyase [Corynebacterium glutamicum ATCC 13032]	SFA	x	
79317995	>gi|79317995|ref|NP_001031049.1| lactoylglutathione lyase [Arabidopsis thaliana]	SFA	x	
21229131	>gi|21229131|ref|NP_635053.1| Lactoylglutathione lyase [Methanosarcina mazei Go1]	SFA	x	
16421670	>gi|16421670|gb|AAL21991.1| putative lactoylglutathione lyase [Salmonella typhimurium LT2]	SFA	x	
59713823	>gi|59713823|ref|YP_206598.1| lactoylglutathione lyase [Vibrio fischeri ES114]	NSF	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
59713972	>gi|59713972|ref|YP_206747.1| lactoylglutathione lyase [Vibrio fischeri ES114]	SFA	x	
9946593	>gi|9946593|gb|AAG04099.1| lactoylglutathione lyase [Pseudomonas aeruginosa PAO1]	BTC	x	
45658176	>gi|45658176|ref|YP_002262.1| putative lactoylglutathione lyase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]	SFA	x	
29346990	>gi|29346990|ref|NP_810493.1| lactoylglutathione lyase [Bacteroides thetaiotaomicron VPI-5482]	BTC	x	
55378194	>gi|55378194|ref|YP_136044.1| lactoylglutathione lyase [Haloarcula marismortui ATCC 43049]	BTC	x	
55378690	>gi|55378690|ref|YP_136540.1| lactoylglutathione lyase [Haloarcula marismortui ATCC 43049]	BTC	x	
77414114	>gi|77414114|ref|ZP_00790281.1| lactoylglutathione lyase [Streptococcus agalactiae 515]	BTC	x	
34540535	>gi|34540535|ref|NP_905014.1| lactoylglutathione lyase, putative [Porphyromonas gingivalis W83]	BTC	x	
24373604	>gi|24373604|ref|NP_717647.1| lactoylglutathione lyase [Shewanella oneidensis MR-1]	BTC	x	
71845563	>gi|71845563|gb|AAZ45059.1| lactoylglutathione lyase [Dechloromonas aromatica RCB]	SFA	x	
15458468	>gi|15458468|gb|AAK99668.1| Lactoylglutathione lyase [Streptococcus pneumoniae R6]	BTC	x	
21106272	>gi|21106272|gb|AAM35103.1| lactoylglutathione lyase [Xanthomonas axonopodis pv. citri str. 306]	SFA	x	
18144105	>gi|18144105|dbj|BAB80153.1| lactoylglutathione lyase [Clostridium perfringens str. 13]	BTC	x	
28810087	>gi|28810087|dbj|BAC63028.1| putative lactoylglutathione lyase [Vibrio parahaemolyticus RIMD 2210633]	SFA	x	
29609062	>gi|29609062|dbj|BAC73114.1| putative lactoylglutathione lyase [Streptomyces avermitilis MA-4680]	SFA	x	
56380727	>gi|56380727|dbj|BAD76635.1| lactoylglutathione lyase [Geobacillus kaustophilus HTA426]	SFA	x	
42571377	>gi|42571377|ref|NP_973779.1| catalytic/ lactoylglutathione lyase [Arabidopsis thaliana]	NSF	x	
53758036	>gi|53758036|gb|AAU92327.1| lactoylglutathione lyase [Methylococcus capsulatus str. Bath]	BTC	x	
56677896	>gi|56677896|gb|AAV94562.1| lactoylglutathione lyase, putative [Silicibacter pomeroyi DSS-3]	BTC	x	
39649388	>gi|39649388|emb|CAE27910.1| putative lactoylglutathione lyase [Rhodopseudomonas palustris CGA009]	SFA	x	
39649442	>gi|39649442|emb|CAE27964.1| putative lactoylglutathione lyase [Rhodopseudomonas palustris CGA009]	BTC	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
71037783	>gi|71037783|gb|AAZ18091.1| probable lactoylglutathione lyase [Psychrobacter arcticus 273-4]	BTC	x	
15025187	>gi|15025187|gb|AAK80149.1| Lactoylglutathione lyase, YQJC B.subtilis ortholog [Clostridium acetobutylicum ATCC 824]	SFA	x	
77388381	>gi|77388381|gb|ABA79566.1| probable lactoylglutathione lyase [Rhodobacter sphaeroides 2.4.1]	BTC	x	
49328358	>gi|49328358|gb|AAT59004.1| lactoylglutathione lyase [Bacillus thuringiensis serovar konkukian str. 97-27]	SFA	x	
49329075	>gi|49329075|gb|AAT59721.1| lactoylglutathione lyase [Bacillus thuringiensis serovar konkukian str. 97-27]	NSF	x	
49331751	>gi|49331751|gb|AAT62397.1| lactoylglutathione lyase (glyoxylase I) [Bacillus thuringiensis serovar konkukian str. 97-27]	SFA	x	
46913068	>gi|46913068|emb|CAG19857.1| Putative lactoylglutathione lyase [Photobacterium profundum SS9]	NSF	x	
57229143	>gi|57229143|gb|AAW45577.1| lactoylglutathione lyase, putative [Cryptococcus neoformans var. neoformans JEC21]	BTC	x	
84786157	>gi|84786157|gb|ABC62339.1| lactoylglutathione lyase, putative [Erythrobacter litoralis HTCC2594]	BTC	x	
84786889	>gi|84786889|gb|ABC63071.1| lactoylglutathione lyase, putative [Erythrobacter litoralis HTCC2594]	SFA	x	
13422656	>gi|13422656|gb|AAK23296.1| lactoylglutathione lyase, putative [Caulobacter crescentus CB15]	BTC	x	
13423390	>gi|13423390|gb|AAK23908.1| lactoylglutathione lyase, putative [Caulobacter crescentus CB15]	SFA	x	
15242020	>gi|15242020|ref|NP_200514.1| catalytic/ lactoylglutathione lyase [Arabidopsis thaliana]	NSF	x	
48789047	>gi|48789047|ref|ZP_00285026.1| COG3607: Predicted lactoylglutathione lyase [Burkholderia fungorum LB400]	NSF	x	
48854992	>gi|48854992|ref|ZP_00309152.1| COG3607: Predicted lactoylglutathione lyase [Cytophaga hutchinsonii]	NSF	x	
48856747	>gi|48856747|ref|ZP_00310904.1| COG3607: Predicted lactoylglutathione lyase [Cytophaga hutchinsonii]	NSF	x	
18412683	>gi|18412683|ref|NP_565231.1| lactoylglutathione lyase [Arabidopsis thaliana]	NSF	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
18402873	>gi|18402873|ref|NP_565737.1| lactoylglutathione lyase [Arabidopsis thaliana]	SFA	x	
18401734	>gi|18401734|ref|NP_029429.1| lactoylglutathione lyase [Arabidopsis thaliana]	SFA	x	
66853326	>gi|66853326|gb|EAL93650.1| lactoylglutathione lyase [Aspergillus fumigatus Af293]	BTC	x	
67906790	>gi|67906790|gb|AAY82853.1| predicted lactoylglutathione lyase [uncultured bacterium MedeBAC46A06]	NSF	x	
31789451	>gi|31789451|gb|AAP58565.1| putative lactoylglutathione lyase [uncultured Acidobacteria bacterium]	SFA	x	
40063586	>gi|40063586|gb|AAR38375.1| lactoylglutathione lyase [uncultured bacterium 582]	BTC	x	
79041861	>gi|79041861|ref|ZP_00872997.1| lactoylglutathione lyase, putative [Novosphingobium aromaticivorans DSM 12444]	BTC	x	
79039852	>gi|79039852|ref|ZP_00871558.1| lactoylglutathione lyase, putative [Novosphingobium aromaticivorans DSM 12444]	SFA	x	
67907184	>gi|67907184|ref|ZP_00505589.1| lactoylglutathione lyase, putative [Polaromonas sp. JS666]	NSF	x	
10444007	>gi|10444007|gb|AAG17667.1| 5-epi-aristolochene synthase [Nicotiana tabacum]	BTC	x	
5458240	>gi|5458240|emb|CAB49729.1| Squalene-hopene cyclase, putative [Pyrococcus abyssi GE5]	NSF	x	
32444518	>gi|32444518|emb|CAD74517.1| probable squalene-hopene cyclase [Rhodopirellula baltica SH 1]	NSF	x	
66844527	>gi|66844527|gb|EAL84865.1| squalene-hopene cyclase [Aspergillus fumigatus Af293]	BTC	x	
77741245	>gi|77741245|ref|ZP_00809729.1| Terpene synthase:Squalene cyclase [Rhodopseudomonas palustris BisA53]	BTC	x	
78697648	>gi|78697648|ref|ZP_00862154.1| Terpene synthase:Squalene cyclase [Bradyrhizobium sp. BTAi1]	BTC	x	
48861106	>gi|48861106|ref|ZP_00315011.1| COG1657: Squalene cyclase [Microbulbifer degradans 2-40]	NSF	X	
50787825	>gi|50787825|emb|CAH05021.1| putative trichodiene synthase [Hypocrea lixii]	BTC	x	
83746572	>gi|83746572|ref|ZP_00943622.1| 3-deoxy-manno-octulosonate-8-phosphatase [Ralstonia solanacearum UW551]	BTC	x	
83726706	>gi|83726706|gb|EAP73834.1| 3-deoxy-manno-octulosonate-8-phosphatase [Ralstonia solanacearum UW551]	BTC	x	
24375444	>gi|24375444|ref|NP_719487.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Shewanella oneidensis MR-1]	BTC	x	

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>85859054</td><td>>gi|85859054|ref|YP_461256.1| 3-deoxy-manno-octulosonate-8-phosphatase [Syntrophus aciditrophicus SB]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>85722145</td><td>>gi|85722145|gb|ABC77088.1| 3-deoxy-manno-octulosonate-8-phosphatase [Syntrophus aciditrophicus SB]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>86147576</td><td>>gi|86147576|ref|ZP_01065886.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Vibrio sp. MED222]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>85834615</td><td>>gi|85834615|gb|EAQ52763.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Vibrio sp. MED222]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>86153227</td><td>>gi|86153227|ref|ZP_01071431.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Campylobacter jejuni subsp. jejuni HB93-13]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>85842953</td><td>>gi|85842953|gb|EAQ60164.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Campylobacter jejuni subsp. jejuni HB93-13]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>86154279</td><td>>gi|86154279|ref|ZP_01072447.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Campylobacter fetus subsp. fetus 82-40]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>85845514</td><td>>gi|85845514|gb|EAQ62715.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Campylobacter fetus subsp. fetus 82-40]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>86163942</td><td>>gi|86163942|gb|EAQ65214.1| 3-deoxy-manno-octulosonate-8-phosphatase [Marinomonas sp. MED121]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>71280996</td><td>>gi|71280996|ref|YP_271187.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Colwellia psychrerythraea 34H]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>16766611</td><td>>gi|16766611|ref|NP_462226.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Salmonella typhimurium LT2]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>37079527</td><td>>gi|37079527|sp|Q8ZLS0|KDSC_SALTY 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (KDO 8-P phosphatase)</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>76876373</td><td>>gi|76876373|emb|CAI87595.1| 3-Deoxy-D-manno-octulosonate 8-phosphate (KDO 8-P) phosphatase [Pseudoalteromonas haloplanktis TAC125]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>77361462</td><td>>gi|77361462|ref|YP_341037.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Pseudoalteromonas haloplanktis TAC125]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>78172127</td><td>>gi|78172127|gb|ABB29223.1| putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Chlorobium chlorochromatii CaD3]</td><td>MFR</td><td>x</td><td></td></tr>
<tr><td>78189928</td><td>>gi|78189928|ref|YP_380266.1| putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Chlorobium chlorochromatii CaD3]</td><td>MFR</td><td>x</td><td></td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
56415245	>gi|56415245|ref|YP_152320.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]	BTC	x	
16762078	>gi|16762078|ref|NP_457695.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Salmonella enterica subsp. enterica serovar Typhi str. CT18]	BTC	x	
29143567	>gi|29143567|ref|NP_806909.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Salmonella enterica subsp. enterica serovar Typhi Ty2]	BTC	x	
37079509	>gi|37079509|sp|Q8Z3G5|KDSC_SALTI 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (KDO 8-P phosphatase)	BTC	x	
22124070	>gi|22124070|ref|NP_667493.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Yersinia pestis KIM]	BTC	x	
51597814	>gi|51597814|ref|YP_072005.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Yersinia pseudotuberculosis IP 32953]	BTC	x	
45443564	>gi|45443564|ref|NP_995103.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Yersinia pestis biovar Medievalis str. 91001]	BTC	x	
16123722	>gi|16123722|ref|NP_407035.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Yersinia pestis CO92]	BTC	x	
37079519	>gi|37079519|sp|Q8ZB47|KDSC_YERPE 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (KDO 8-P phosphatase)	BTC	x	
37678636	>gi|37678636|ref|NP_933245.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Vibrio vulnificus YJ016]	BTC	x	
27364145	>gi|27364145|ref|NP_759673.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Vibrio vulnificus CMCP6]	BTC	x	
50119252	>gi|50119252|ref|YP_048419.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Erwinia carotovora subsp. atroseptica SCRI1043]	BTC	x	
37527889	>gi|37527889|ref|NP_931234.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Photorhabdus luminescens subsp. laumondii TTO1]	BTC	x	
76580258	>gi|76580258|gb|ABA49733.1| 3-deoxy-manno-octulosonate-8-phosphatase [Burkholderia pseudomallei 1710b]	BTC	x	
76810805	>gi|76810805|ref|YP_334634.1| 3-deoxy-manno-octulosonate-8-phosphatase [Burkholderia pseudomallei 1710b]	BTC	x	
56459511	>gi|56459511|ref|YP_154792.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Idiomarina loihiensis L2TR]	BTC	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
59710784	>gi|59710784|ref|YP_203560.1| 3-deoxy-manno-octulosonate-8-phosphatase [Vibrio fischeri ES114]	BTC	x	
59478885	>gi|59478885|gb|AAW84672.1| 3-deoxy-manno-octulosonate-8-phosphatase [Vibrio fischeri ES114]	BTC	x	
59710998	>gi|59710998|ref|YP_203774.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Vibrio fischeri ES114]	BTC	x	
59479099	>gi|59479099|gb|AAW84886.1| 3-deoxy-manno-octulosonate-8-phosphatase [Vibrio fischeri ES114]	BTC	x	
62181824	>gi|62181824|ref|YP_218241.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]	BTC	x	
49530630	>gi|49530630|emb|CAG68342.1| 3-Deoxy-D-manno-octulosonate 8-phosphate (KDO 8-P) phosphatase [Acinetobacter sp. ADP1]	BTC	x	
50084654	>gi|50084654|ref|YP_046164.1| 3-Deoxy-D-manno-octulosonate 8-phosphate (KDO 8-P) phosphatase [Acinetobacter sp. ADP1]	BTC	x	
56604608	>gi|56604608|emb|CAG45660.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Francisella tularensis subsp. tularensis SCHU S4]	BTC	x	
56708116	>gi|56708116|ref|YP_170012.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Francisella tularensis subsp. tularensis SCHU S4]	BTC	x	
15642520	>gi|15642520|ref|NP_232153.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Vibrio cholerae O1 biovar eltor str. N16961]	BTC	x	
54310339	>gi|54310339|ref|YP_131359.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Photobacterium profundum SS9]	BTC	x	
83749932	>gi|83749932|ref|ZP_00946890.1| Possible phosphonoacetaldehyde hydrolase [Ralstonia solanacearum UW551]	BTC	x	
29895021	>gi|29895021|gb|AAP08309.1| phosphonoacetaldehyde hydrolase [Bacillus cereus ATCC 14579]	BTC	x	
81429277	>gi|81429277|ref|YP_396278.1| Phosphonoacetaldehyde hydrolase [Lactobacillus sakei subsp. sakei 23K]	BTC	x	
83645840	>gi|83645840|ref|YP_434275.1| phosphonoacetaldehyde hydrolase [Hahella chejuensis KCTC 2396]	BTC	x	
71543658	>gi|71543658|ref|ZP_00664735.1| Phosphonoacetaldehyde hydrolase [Syntrophobacter fumaroxidans MPOB]	BTC	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
71546673	>gi|71546673|ref|ZP_00667446.1| Phosphonoacetaldehyde hydrolase [Syntrophobacter fumaroxidans MPOB]	BTC	x	
68195077	>gi|68195077|gb|EAN09538.1| Phosphonoacetaldehyde hydrolase [Enterococcus faecium DO]	BTC	x	
50950950	>gi|50950950|gb|AAT88651.1| phosphonoacetaldehyde hydrolase [Leifsonia xyli subsp. xyli str. CTCB07]	NSF	x	
86166076	>gi|86166076|gb|EAQ67342.1| phosphonoacetaldehyde phosphonohydrolase [Marinomonas sp. MED121]	BTC	x	
71061958	>gi|71061958|gb|AAZ20961.1| (S)-2-haloacid dehalogenase [Candidatus Pelagibacter ubique HTCC1062]	BTC	x	
28272147	>gi|28272147|emb|CAD65051.1| 2-haloacid dehalogenase (putative) [Lactobacillus plantarum WCFS1]	SFA	x	
83749723	>gi|83749723|ref|ZP_00946701.1| Probable 2-haloacid halidohydrolase IVa [Ralstonia solanacearum UW551]	SFA	x	
83854744	>gi|83854744|ref|ZP_00948274.1| haloacid dehalogenase, type II [Sulfitobacter sp. NAS-14.1]	BTC	x	
83941267	>gi|83941267|ref|ZP_00953729.1| haloacid dehalogenase, type II [Sulfitobacter sp. EE-36]	BTC	x	
83943521	>gi|83943521|ref|ZP_00955980.1| probable Haloacid dehalogenase, type II [Sulfitobacter sp. EE-36]	BTC	x	
83949587	>gi|83949587|ref|ZP_00958320.1| haloacid dehalogenase, type II [Roseovarius nubinhibens ISM]	BTC	x	
83954905	>gi|83954905|ref|ZP_00963583.1| probable Haloacid dehalogenase, type II [Sulfitobacter sp. NAS-14.1]	BTC	x	
84517059	>gi|84517059|ref|ZP_01004416.1| haloacid dehalogenase, type II [Loktanella vestfoldensis SKA53]	BTC	x	
84687508	>gi|84687508|ref|ZP_01015385.1| haloacid dehalogenase, type II [Rhodobacterales bacterium HTCC2654]	BTC	x	
84714733	>gi|84714733|ref|ZP_01022025.1| Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2 [Polaromonas naphthalenivorans CJ2]	BTC	x	
83717933	>gi|83717933|ref|YP_438707.1| haloacid dehalogenase, type II [Burkholderia thailandensis E264]	SFA	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
82750318	>gi|82750318|ref|YP_416059.1| probable haloacid dehalogenase hydrolase [Staphylococcus aureus RF122]	SFA	x	
83816227	>gi|83816227|ref|YP_445384.1| haloacid dehalogenase type II [Salinibacter ruber DSM 13855]	SFA	x	
85706310	>gi|85706310|ref|ZP_01037404.1| haloacid dehalogenase, type II [Roseovarius sp. 217]	BTC	x	
86130983	>gi|86130983|ref|ZP_01049582.1| Cryptic haloacid dehalogenase 1 [Cellulophaga sp. MED134]	BTC	x	
86136004	>gi|86136004|ref|ZP_01054583.1| haloacid dehalogenase, type II [Roseobacter sp. MED193]	BTC	x	
71145189	>gi|71145189|gb|AAZ25662.1| haloacid dehalogenase, type II [Colwellia psychrerythraea 34H]	BTC	x	
72122818	>gi|72122818|gb|AAZ65004.1| Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2 [Ralstonia eutropha JMP134]	SFA	x	
72122821	>gi|72122821|gb|AAZ65007.1| Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2 [Ralstonia eutropha JMP134]	SFA	x	
71556271	>gi|71556271|gb|AAZ35482.1| haloacid dehalogenase, type II [Pseudomonas syringae pv. phaseolicola 1448A]	SFA	x	
71558624	>gi|71558624|gb|AAZ37835.1| haloacid dehalogenase, type II [Pseudomonas syringae pv. phaseolicola 1448A]	SFA	x	
32397860	>gi|32397860|emb|CAD73861.1| cryptic haloacid dehalogenase 1 [Rhodopirellula baltica SH 1]	BTC	x	
76795038	>gi|76795038|ref|ZP_00777483.1| Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2:HAD-superfamily hydrolase, subfamily IA, variant 3 [Pseudoalteromonas atlantica T6c]	BTC	x	
77691950	>gi|77691950|ref|ZP_00807116.1| Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2 [Rhodopseudomonas palustris BisB5]	SFA	x	
77740310	>gi|77740310|ref|ZP_00808798.1| Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2 [Rhodopseudomonas palustris BisA53]	SFA	x	
78492307	>gi|78492307|ref|ZP_00844544.1| Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2 [Rhodopseudomonas palustris BisB18]	SFA	x	
78693432	>gi|78693432|ref|ZP_00857946.1| Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2 [Bradyrhizobium sp. BTAi1]	SFA	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
78696732	>gi|78696732|ref|ZP_00861241.1| Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2 [Bradyrhizobium sp. BTAi1]	SFA	x	
28867479	>gi|28867479|ref|NP_790098.1| haloacid dehalogenase, type II [Pseudomonas syringae pv. tomato str. DC3000]	SFA	x	
56680903	>gi|56680903|gb|AAV97568.1| haloacid dehalogenase, type II [Silicibacter pomeroyi DSS-3]	BTC	x	
9946703	>gi|9946703|gb|AAG04199.1| probable haloacid dehalogenase [Pseudomonas aeruginosa PAO1]	BTC	x	
56604165	>gi|56604165|emb|CAG45174.1| haloacid dehalogenase [Francisella tularensis subsp. tularensis SCHU S4]	SFA	x	
56679061	>gi|56679061|gb|AAV95727.1| haloacid dehalogenase, type II, putative [Silicibacter pomeroyi DSS-3]	BTC	x	
33567032	>gi|33567032|emb|CAE30945.1| probable haloacid dehalogenase [Bordetella bronchiseptica RB50]	SFA	x	
71038936	>gi|71038936|gb|AAZ19244.1| probable Haloacid dehalogenase, type II [Psychrobacter arcticus 273-4]	BTC	x	
77970761	>gi|77970761|gb|ABB12140.1| Haloacid dehalogenase, type II [Burkholderia sp. 383]	BTC	x	
76583431	>gi|76583431|gb|ABA52905.1| haloacid dehalogenase, type II [Burkholderia pseudomallei 1710b]	SFA	x	
57229109	>gi|57229109|gb|AAW45543.1| haloacid dehalogenase, putative [Cryptococcus neoformans var. neoformans JEC21]	NSF	x	
77384027	>gi|77384027|gb|ABA75540.1| Haloacid dehalogenase, type II [Pseudomonas fluorescens PfO-1]	SFA	x	
66850829	>gi|66850829|gb|EAL91155.1| haloacid dehalogenase, type II [Aspergillus fumigatus Af293]	BTC	x	
66852748	>gi|66852748|gb|EAL93072.1| haloacid dehalogenase, type II [Aspergillus fumigatus Af293]	SFA	x	
86573108	>gi|86573108|gb|ABD07665.1| haloacid dehalogenase, type II [Rhodopseudomonas palustris HaA2]	SFA	x	
36959128	>gi|36959128|gb|AAQ87553.1| 2-haloacid halidohydrolase IVa [Rhizobium sp. NGR234]	SFA	x	
36959159	>gi|36959159|gb|AAQ87584.1| 2-haloacid halidohydrolase IVa [Rhizobium sp. NGR234]	SFA	x	
36959162	>gi|36959162|gb|AAQ87587.1| 2-haloacid halidohydrolase IVa [Rhizobium sp. NGR234]	SFA	x	
68056242	>gi|68056242|ref|ZP_00540371.1| Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2:HAD-superfamily hydrolase, subfamily IA, variant 1 [Exiguobacterium sp. 255-15]	BTC	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
84499630	>gi|84499630|ref|ZP_00997918.1| L-2-haloalkanoic acid dehalogenase, HAD superfamily protein [Oceanicola batsensis HTCC2597]	BTC	X	
69937246	>gi|69937246|ref|ZP_00631938.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Paracoccus denitrificans PD1222]	SFA	X	
69937252	>gi|69937252|ref|ZP_00631944.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Paracoccus denitrificans PD1222]	SFA	X	
69952780	>gi|69952780|ref|ZP_00640147.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Shewanella frigidimarina NCIMB 400]	BTC	X	
69953831	>gi|69953831|ref|ZP_00640782.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Shewanella frigidimarina NCIMB 400]	BTC	X	
86166360	>gi|86166360|gb|EAQ67626.1| L-2-haloalkanoic acid dehalogenase, HAD superfamily protein [Marinomonas sp. MED121]	BTC	X	
71362373	>gi|71362373|ref|ZP_00653532.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Psychrobacter cryohalolentis K5]	BTC	X	
71366969	>gi|71366969|ref|ZP_00657503.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Nocardioides sp. JS614]	BTC	X	
74016581	>gi|74016581|ref|ZP_00687207.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Burkholderia ambifaria AMMD]	BTC	X	
74014423	>gi|74014423|ref|ZP_00685052.1| HAD-superfamily hydrolase, subfamily IA, variant 2:HAD-superfamily hydrolase, subfamily IA, variant 1 [Burkholderia ambifaria AMMD]	SFA	X	
74014492	>gi|74014492|ref|ZP_00685121.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Burkholderia ambifaria AMMD]	BTC	X	
74024447	>gi|74024447|ref|ZP_00694997.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Rhodoferax ferrireducens DSM 15236]	BTC	X	
78693435	>gi|78693435|ref|ZP_00857949.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Bradyrhizobium sp. BTAi1]	SFA	X	
67667932	>gi|67667932|ref|ZP_00465136.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Burkholderia cenocepacia HI2424]	BTC	X	
67675308	>gi|67675308|ref|ZP_00472066.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Chromohalobacter salexigens DSM 3043]	BTC	X	
67934346	>gi|67934346|ref|ZP_00527413.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Solibacter usitatus Ellin6076]	MFR	X	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
67938584	>gi|67938584|ref|ZP_00531107.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Chlorobium phaeobacteroides BS1]	BTC	X	
68183273	>gi|68183273|ref|ZP_00556249.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Jannaschia sp. CCS1]	BTC	X	
68551689	>gi|68551689|ref|ZP_00591084.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Prosthecochloris aestuarii DSM 271]	BTC	X	
68562756	>gi|68562756|ref|ZP_00601996.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Rubrobacter xylanophilus DSM 9941]	BTC	X	
66043429	>gi|66043429|ref|YP_233270.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Pseudomonas syringae pv. syringae B728a]	SFA	X	
66045035	>gi|66045035|ref|YP_234876.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Pseudomonas syringae pv. syringae B728a]	SFA	X	
56179691	>gi|56179691|gb|AAV82413.1| L-2-haloalkanoic acid dehalogenase, HAD superfamily [Idiomarina loihiensis L2TR]	BTC	x	
69299585	>gi|69299585|ref|ZP_00621572.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Silicibacter sp. TM1040]	BTC	X	
67909226	>gi|67909226|ref|ZP_00507623.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Polaromonas sp. JS666]	BTC	X	
67847238	>gi|67847238|ref|ZP_00502357.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Polaromonas sp. JS666]	SFA	X	
67847249	>gi|67847249|ref|ZP_00502368.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Polaromonas sp. JS666]	SFA	X	
68560337	>gi|68560337|ref|ZP_00599651.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Rubrobacter xylanophilus DSM 9941]	BTC	X	
22776613	>gi|22776613|dbj|BAC12888.1| L-2-haloalkanoic acid dehalogenase [Oceanobacillus iheyensis HTE831]	SFA	X	
27355108	>gi|27355108|dbj|BAC52092.1| 2-haloalkanoic acid dehalogenase [Bradyrhizobium japonicum USDA 110]	SFA	X	
17983363	>gi|17983363|gb|AAL52549.1| 2-HALOALKANOIC ACID DEHALOGENASE I [Brucella melitensis 16M]	MFR	X	
29896404	>gi|29896404|gb|AAP09684.1| 2-haloalkanoic acid dehalogenase [Bacillus cereus ATCC 14579]	NSF	X	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
29896996	>gi|29896996|gb|AAP10274.1| 2-haloalkanoic acid dehalogenase [Bacillus cereus ATCC 14579]	SFA	X	
29898999	>gi|29898999|gb|AAP12270.1| 2-haloalkanoic acid dehalogenase [Bacillus cereus ATCC 14579]	SFA	X	
14024598	>gi|14024598|dbj|BAB51201.1| 2-haloalkanoic acid dehalogenase [Mesorhizobium loti MAFF303099]	SFA	X	
13813894	>gi|13813894|gb|AAK41024.1| 2-haloalkanoic acid dehalogenase, putative [Sulfolobus solfataricus P2]	NSF	X	
13815156	>gi|13815156|gb|AAK42086.1| 2-haloalkanoic acid dehalogenase [Sulfolobus solfataricus P2]	NSF	X	
13815309	>gi|13815309|gb|AAK42215.1| 2-haloalkanoic acid dehalogenase [Sulfolobus solfataricus P2]	NSF	X	
13815455	>gi|13815455|gb|AAK42335.1| 2-haloalkanoic acid dehalogenase [Sulfolobus solfataricus P2]	NSF	X	
15623694	>gi|15623694|dbj|BAB67681.1| 201aa long hypothetical 2-haloalkanoic acid dehalogenase [Sulfolobus tokodaii str. 7]	BTC	X	
27314846	>gi|27314846|gb|AAO03982.1| L-2-haloalkanoic acid dehalogenase [Staphylococcus epidermidis ATCC 12228]	SFA	X	
28203997	>gi|28203997|gb|AAO36437.1| 2-haloalkanoic acid dehalogenase I [Clostridium tetani E88]	NSF	X	
42783986	>gi|42783986|ref|NP_981233.1| L-2-haloalkanoic acid dehalogenase [Bacillus cereus ATCC 10987]	NSF	X	
55377155	>gi|55377155|ref|YP_135005.1| 2-haloalkanoic acid dehalogenase [Haloarcula marismortui ATCC 43049]	BTC	X	
29604376	>gi|29604376|dbj|BAC68447.1| putative 2-haloalkanoic acid dehalogenase [Streptomyces avermitilis MA-4680]	BTC	X	
6138872	>gi|6138872|emb|CAB59701.1| putative 2-haloalkanoic acid dehalogenase [Streptomyces coelicolor A3(2)]	SFA	X	
66845015	>gi|66845015|gb|EAL85351.1| 2-haloalkanoic acid dehalogenase, putative [Aspergillus fumigatus Af293]	NSF	X	
66848953	>gi|66848953|gb|EAL89282.1| 2-haloalkanoic acid dehalogenase [Aspergillus fumigatus Af293]	SFA	X	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
17741799	>gi|17741799|gb|AAL44218.1| haloalkanoic acid dehalogenase [Agrobacterium tumefaciens str. C58]	SFA	X	
78709032	>gi|78709032|gb|ABB48007.1| beta-phosphoglucomutase, putative [Oryza sativa (japonica cultivar-group)]	SFA	x	
4981809	>gi|4981809|gb|AAD36329.1| beta-phosphoglucomutase, putative [Thermotoga maritima MSB8]	BTC	x	
86133112	>gi|86133112|ref|ZP_01051694.1| Beta-phosphoglucomutase [Tenacibaculum sp. MED152]	BTC	x	
68566592	>gi|68566592|gb|AAY79521.1| beta-phosphoglucomutase [Sulfolobus acidocaldarius DSM 639]	SFA	x	
71147190	>gi|71147190|gb|AAZ27663.1| putative beta-phosphoglucomutase [Colwellia psychrerythraea 34H]	BTC	x	
71850918	>gi|71850918|gb|AAZ43527.1| beta-phosphoglucomutase [Mycoplasma synoviae 53]	BTC	x	
71802268	>gi|71802268|gb|AAX71621.1| beta-phosphoglucomutase [Streptococcus pyogenes MGAS6180]	SFA	x	
78167074	>gi|78167074|gb|ABB24172.1| Beta-phosphoglucomutase hydrolase [Pelodictyon luteolum DSM 273]	BTC	x	
78167835	>gi|78167835|gb|ABB24933.1| Beta-phosphoglucomutase hydrolase [Pelodictyon luteolum DSM 273]	BTC	x	
78170254	>gi|78170254|gb|ABB27350.1| Beta-phosphoglucomutase hydrolase [Chlorobium chlorochromatii CaD3]	BTC	x	
78171094	>gi|78171094|gb|ABB28190.1| Beta-phosphoglucomutase hydrolase [Chlorobium chlorochromatii CaD3]	BTC	x	
68549482	>gi|68549482|ref|ZP_00588945.1| Beta-phosphoglucomutase hydrolase [Pelodictyon phaeoclathratiforme BU-1]	BTC	x	
55820471	>gi|55820471|ref|YP_138913.1| beta-phosphoglucomutase, putative [Streptococcus thermophilus LMG 18311]	SFA	x	
23492927	>gi|23492927|dbj|BAC17899.1| putative beta-phosphoglucomutase [Corynebacterium efficiens YS-314]	BTC	x	
27361675	>gi|27361675|gb|AAO10582.1| Beta-phosphoglucomutase [Vibrio vulnificus CMCP6]	SFA	x	
47458560	>gi|47458560|gb|AAT27882.1| beta-phosphoglucomutase [Mycoplasma mobile 163K]	BTC	x	
10176489	>gi|10176489|dbj|BAB07583.1| beta-phosphoglucomutase [Bacillus halodurans C-125]	BTC	x	
58255432	>gi|58255432|gb|AAV43669.1| beta-phosphoglucomutase [Lactobacillus acidophilus NCFM]	BTC	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
52217963	>gi|52217963|dbj|BAD50556.1| putative beta-phosphoglucomutase [Bacteroides fragilis YCH46]	SFA	x	
21226798	>gi|21226798|ref|NP_632720.1| Beta-phosphoglucomutase [Methanosarcina mazei Go1]	SFA	x	
21227737	>gi|21227737|ref|NP_633659.1| Beta-phosphoglucomutase [Methanosarcina mazei Go1]	SFA	x	
42518300	>gi|42518300|ref|NP_964230.1| beta-phosphoglucomutase [Lactobacillus johnsonii NCC 533]	BTC	x	
34496849	>gi|34496849|ref|NP_901064.1| probable beta-phosphoglucomutase [Chromobacterium violaceum ATCC 12472]	SFA	x	
34496852	>gi|34496852|ref|NP_901067.1| probable beta-phosphoglucomutase [Chromobacterium violaceum ATCC 12472]	SFA	x	
29347537	>gi|29347537|ref|NP_811040.1| putative beta-phosphoglucomutase [Bacteroides thetaiotaomicron VPI-5482]	SFA	x	
19914233	>gi|19914233|gb|AAM03897.1| beta-phosphoglucomutase [Methanosarcina acetivorans C2A]	SFA	x	
15022982	>gi|15022982|gb|AAK78137.1| Beta-phosphoglucomutase, putative [Clostridium acetobutylicum ATCC 824]	BTC	x	
52628437	>gi|52628437|gb|AAU27178.1| beta-phosphoglucomutase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]	SFA	x	
55738341	>gi|55738341|gb|AAV61982.1| beta-phosphoglucomutase, putative [Streptococcus thermophilus CNRZ1066]	SFA	x	
72394903	>gi|72394903|gb|AAZ69176.1| beta-phosphoglucomutase [Methanosarcina barkeri str. fusaro]	SFA	x	
72395447	>gi|72395447|gb|AAZ69720.1| beta-phosphoglucomutase [Methanosarcina barkeri str. fusaro]	SFA	x	
37536998	>gi|37536998|ref|NP_922801.1| putative beta-phosphoglucomutase [Oryza sativa (japonica cultivar-group)]	SFA	x	
74310904	>gi|74310904|ref|YP_309323.1| cytosine deaminase [Shigella sonnei Ss046]	SFA	x	
84517580	>gi|84517580|ref|ZP_01004929.1| possible cytosine deaminase [Prochlorococcus marinus str. MIT 9211]	SFA	x	
86360352	>gi|86360352|ref|YP_472240.1| probable cytosine deaminase protein [Rhizobium etli CFN 42]	SFA	x	
86166819	>gi|86166819|gb|EAQ68081.1| possible cytosine deaminase [Synechococcus sp. RS9917]	SFA	x	
86357662	>gi|86357662|ref|YP_469554.1| cytosine deaminase protein [Rhizobium etli CFN 42]	SFA	x	
72002559	>gi|72002559|gb|AAZ58361.1| possible cytosine deaminase [Prochlorococcus marinus str. NATL2A]	SFA	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
75760736	>gi|75760736|ref|ZP_00740758.1| Cytosine deaminase [Bacillus thuringiensis serovar israelensis ATCC 35646]	SFA	x	
78169399	>gi|78169399|gb|ABB26496.1| possible cytosine deaminase [Synechococcus sp. CC9902]	SFA	x	
78196857	>gi|78196857|gb|ABB34622.1| possible cytosine deaminase [Synechococcus sp. CC9605]	SFA	x	
81299379	>gi|81299379|ref|YP_399587.1| cytosine deaminase [Synechococcus elongatus PCC 7942]	SFA	x	
13359830	>gi|13359830|dbj|BAB33796.1| putative deaminase [Escherichia coli O157:H7]	SFA	x	
33238356	>gi|33238356|gb|AAQ00422.1| Cytosine deaminase [Prochlorococcus marinus subsp. marinus str. CCMP1375]	SFA	x	
37199997	>gi|37199997|dbj|BAC95826.1| cytosine deaminase [Vibrio vulnificus YJ016]	SFA	x	
27360848	>gi|27360848|gb|AAO09758.1| Cytosine deaminase [Vibrio vulnificus CMCP6]	SFA	x	
29898140	>gi|29898140|gb|AAP11414.1| Cytosine deaminase [Bacillus cereus ATCC 14579]	SFA	x	
14022090	>gi|14022090|dbj|BAB48700.1| cytosine deaminase [Mesorhizobium loti MAFF303099]	SFA	x	
14022678	>gi|14022678|dbj|BAB49287.1| cytosine deaminase [Mesorhizobium loti MAFF303099]	BAC	X	
55229512	>gi|55229512|gb|AAV44932.1| cytosine deaminase [Haloarcula marismortui ATCC 43049]	SFA	x	
42783674	>gi|42783674|ref|NP_980921.1| cytosine deaminase [Bacillus cereus ATCC 10987]	SFA	x	
1652606	>gi|1652606|dbj|BAA17527.1| cytosine deaminase [Synechocystis sp. PCC 6803]	BAC	x	
33640228	>gi|33640228|emb|CAE19763.1| possible cytosine deaminase [Prochlorococcus marinus subsp. pastoris str. CCMP1986]	SFA	x	
49529401	>gi|49529401|emb|CAG67113.1| conserved hypothetical protein; putative cytosine deaminase [Acinetobacter sp. ADP1]	NSF	X	
33634515	>gi|33634515|emb|CAE20501.1| possible cytosine deaminase [Prochlorococcus marinus str. MIT 9313]	SFA	x	
33639147	>gi|33639147|emb|CAE08153.1| possible cytosine deaminase [Synechococcus sp. WH 8102]	SFA	x	
56685922	>gi|56685922|dbj|BAD79144.1| cytosine deaminase [Synechococcus elongatus PCC 6301]	SFA	x	
32455877	>gi|32455877|ref|NP_862530.1| putative cytosine deaminase [Pseudomonas sp. ADP]	SFA	x	
12723150	>gi|12723150|gb|AAK04385.1| adenosine deaminase (EC 3.5.4.4) [Lactococcus lactis subsp. lactis Il1403]	MFR	x	
1703170	>gi|1703170|sp|P53984|ADD_STRVG Adenosine deaminase (Adenosine aminohydrolase)	BTC	x	
78101384	>gi|78101384|pdb|2AMX|B Chain B, Crystal Structure Of Plasmodium Yoelii Adenosine Deaminase (Py02076)	BTC	x	
81167689	>gi|81167689|sp|Q6DG22|ADA_BRARE Adenosine deaminase (Adenosine aminohydrolase)	BTC	x	
78609339	>gi|78609339|emb|CAI54385.1| Adenosine deaminase [Lactobacillus sakei subsp. sakei 23K]	BTC	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
15073060	>gi|15073060|emb|CAC41519.1| PUTATIVE ADENOSINE DEAMINASE PROTEIN [Sinorhizobium meliloti]	BTC	x	
74039773	>gi|74039773|gb|AAZ94911.1| putative adenosine deaminase [Moneuplotes crassus]	SFA	x	
82737003	>gi|82737003|ref|ZP_00899857.1| Adenosine deaminase [Pseudomonas putida F1]	BTC	x	
83369663	>gi|83369663|ref|ZP_00914515.1| Adenosine deaminase [Rhodobacter sphaeroides ATCC 17025]	BTC	x	
83372006	>gi|83372006|ref|ZP_00916786.1| Adenosine deaminase [Rhodobacter sphaeroides ATCC 17029]	BTC	x	
83748873	>gi|83748873|ref|ZP_00945884.1| Adenosine deaminase [Ralstonia solanacearum UW551]	BTC	x	
3322300	>gi|3322300|gb|AAC65039.1| adenosine deaminase, putative [Treponema pallidum subsp. pallidum str. Nichols]	NSF	x	
33147825	>gi|33147825|gb|AAP95347.1| probable adenosine deaminase [Haemophilus ducreyi 35000HP]	MFR	x	
29342279	>gi|29342279|gb|AAO80045.1| adenosine deaminase [Enterococcus faecalis V583]	MFR	x	
84318459	>gi|84318459|ref|ZP_00966883.1| COG1816: Adenosine deaminase [Pseudomonas aeruginosa C3719]	BTC	x	
84352861	>gi|84352861|ref|ZP_00977807.1| COG1816: Adenosine deaminase [Burkholderia cenocepacia PC184]	BTC	x	
84357185	>gi|84357185|ref|ZP_00982013.1| COG1816: Adenosine deaminase [Burkholderia cenocepacia PC184]	BTC	x	
84361177	>gi|84361177|ref|ZP_00985857.1| COG1816: Adenosine deaminase [Burkholderia dolosa AUO158]	BTC	x	
27358471	>gi|27358471|gb|AAO07421.1| Adenosine deaminase [Vibrio vulnificus CMCP6]	MFR	x	
84385821	>gi|84385821|ref|ZP_00988851.1| adenosine deaminase [Vibrio splendidus 12B01]	BTC	x	
84386552	>gi|84386552|ref|ZP_00989579.1| adenosine deaminase [Vibrio splendidus 12B01]	MFR	x	
84387206	>gi|84387206|ref|ZP_00990227.1| adenosine deaminase [Vibrio splendidus 12B01]	BTC	x	
84494818	>gi|84494818|ref|ZP_00993937.1| putative adenosine deaminase [Janibacter sp. HTCC2649]	BTC	x	
84496719	>gi|84496719|ref|ZP_00995573.1| adenosine deaminase [Janibacter sp. HTCC2649]	BTC	x	
84498036	>gi|84498036|ref|ZP_00996833.1| adenosine deaminase [Janibacter sp. HTCC2649]	MFR	x	
84499523	>gi|84499523|ref|ZP_00997811.1| adenosine deaminase [Oceanicola batsensis HTCC2597]	BTC	x	
84514417	>gi|84514417|ref|ZP_01001781.1| adenosine deaminase [Loktanella vestfoldensis SKA53]	BTC	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
84683858	>gi|84683858|ref|ZP_01011761.1| adenosine deaminase [Rhodobacterales bacterium HTCC2654]	BTC	x	
84704670	>gi|84704670|ref|ZP_01018170.1| adenosine deaminase [Parvularcula bermudensis HTCC2503]	SFA	x	
84715335	>gi|84715335|ref|ZP_01022436.1| Adenosine deaminase [Polaromonas naphthalenivorans CJ2]	BTC	x	
26987329	>gi|26987329|ref|NP_742754.1| adenosine deaminase [Pseudomonas putida KT2440]	BTC	x	
77748521	>gi|77748521|ref|NP_640664.2| adenosine deaminase [Xanthomonas axonopodis pv. citri str. 306]	SFA	x	
28867985	>gi|28867985|ref|NP_790604.1| adenosine deaminase [Pseudomonas syringae pv. tomato str. DC3000]	BTC	x	
17546817	>gi|17546817|ref|NP_520219.1| adenosine deaminase [Ralstonia solanacearum GMI1000]	BTC	x	
83721046	>gi|83721046|ref|YP_442150.1| adenosine deaminase [Burkholderia thailandensis E264]	BTC	x	
77761081	>gi|77761081|ref|YP_241410.2| adenosine deaminase [Xanthomonas campestris pv. campestris str. 8004]	SFA	x	
83644351	>gi|83644351|ref|YP_432786.1| adenosine deaminase [Hahella chejuensis KCTC 2396]	BTC	x	
15026062	>gi|15026062|gb|AAK80946.1| Adenosine deaminase [Clostridium acetobutylicum ATCC 824]	MFR	x	
62464326	>gi|62464326|ref|ZP_00383620.1| COG1816: Adenosine deaminase [Lactococcus lactis subsp. cremoris SK11]	MFR	x	
62516339	>gi|62516339|ref|ZP_00387694.1| COG1816: Adenosine deaminase [Lactobacillus delbrueckii subsp. bulgaricus ATCC BAA-365]	MFR	x	
62528085	>gi|62528085|ref|ZP_00389344.1| COG1816: Adenosine deaminase [Streptococcus thermophilus LMD-9]	MFR	x	
9945979	>gi|9945979|gb|AAG03538.1| probable adenosine deaminase [Pseudomonas aeruginosa PAO1]	BTC	x	
53686932	>gi|53686932|ref|ZP_00106539.2| COG1816: Adenosine deaminase [Nostoc punctiforme PCC 73102]	SFA	x	
23129077	>gi|23129077|ref|ZP_00110911.1| COG1816: Adenosine deaminase [Nostoc punctiforme PCC 73102]	SFA	x	
23024940	>gi|23024940|ref|ZP_00064127.1| COG1816: Adenosine deaminase [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]	BTC	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
32043305	>gi|32043305|ref|ZP_00140567.1| COG1816: Adenosine deaminase [Pseudomonas aeruginosa UCBPP-PA14]	BTC	x	
47573398	>gi|47573398|ref|ZP_00243437.1| COG1816: Adenosine deaminase [Rubrivivax gelatinosus PM1]	BTC	x	
83814751	>gi|83814751|ref|YP_444811.1| adenosine deaminase [Salinibacter ruber DSM 13855]	MFR	x	
14023508	>gi|14023508|dbj|BAB50114.1| Adenosine Deaminase [Mesorhizobium loti MAFF303099]	BTC	x	
49904346	>gi|49904346|gb|AAH76532.1| Adenosine deaminase [Danio rerio]	BTC	x	
18146172	>gi|18146172|dbj|BAB82212.1| probable adenosine deaminase [Clostridium perfringens str. 13]	MFR	x	
24377670	>gi|24377670|gb|AAN58972.1| putative adenosine deaminase [Streptococcus mutans UA159]	MFR	x	
69936059	>gi|69936059|ref|ZP_00630919.1| Adenosine deaminase [Paracoccus denitrificans PD1222]	BTC	x	
28809660	>gi|28809660|dbj|BAC62635.1| adenosine deaminase [Vibrio parahaemolyticus RIMD 2210633]	BTC	x	
85709314	>gi|85709314|ref|ZP_01040379.1| adenosine deaminase [Erythrobacter sp. NAP1]	BTC	x	
85712769	>gi|85712769|ref|ZP_01043813.1| Adenosine deaminase [Idiomarina baltica OS145]	MFR	x	
13424854	>gi|13424854|gb|AAK25142.1| adenosine deaminase [Caulobacter crescentus CB15]	BTC	x	
86144727	>gi|86144727|ref|ZP_01063059.1| adenosine deaminase [Vibrio sp. MED222]	MFR	x	
86163110	>gi|86163110|gb|EAQ64387.1| adenosine deaminase [Marinomonas sp. MED121]	BTC	x	
86163133	>gi|86163133|gb|EAQ64410.1| adenosine deaminase [Marinomonas sp. MED121]	MFR	x	
86164135	>gi|86164135|gb|EAQ65406.1| adenosine deaminase [Marinomonas sp. MED121]	BTC	x	
86355856	>gi|86355856|ref|YP_467748.1| adenosine deaminase protein [Rhizobium etli CFN 42]	BTC	x	
86606562	>gi|86606562|ref|YP_475325.1| putative adenosine deaminase [Cyanobacteria bacterium Yellowstone A-Prime]	SFA	x	
86609455	>gi|86609455|ref|YP_478217.1| adenosine deaminase, putative [Cyanobacteria bacterium Yellowstone B-Prime]	SFA	x	
68348520	>gi|68348520|gb|AAY96126.1| adenosine deaminase [Pseudomonas fluorescens Pf-5]	BTC	x	
71364008	>gi|71364008|ref|ZP_00654607.1| Adenosine deaminase [Psychrobacter cryohalolentis K5]	BTC	x	
71365621	>gi|71365621|ref|ZP_00656172.1| Adenosine deaminase [Nocardioides sp. JS614]	MFR	x	
71366810	>gi|71366810|ref|ZP_00657347.1| Adenosine deaminase [Nocardioides sp. JS614]	BTC	x	
71366934	>gi|71366934|ref|ZP_00657469.1| Adenosine deaminase [Nocardioides sp. JS614]	BTC	x	
71144852	>gi|71144852|gb|AAZ25325.1| adenosine deaminase [Colwellia psychrerythraea 34H]	BTC	x	
71148192	>gi|71148192|gb|AAZ28665.1| adenosine deaminase [Colwellia psychrerythraea 34H]	BTC	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
72496222	>gi|72496222|dbj|BAE19543.1| putative adenosine deaminase [Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305]	MFR	x	
37201223	>gi|37201223|dbj|BAC97046.1| adenosine deaminase [Vibrio vulnificus YJ016]	MFR	x	
71555915	>gi|71555915|gb|AAZ35126.1| adenosine deaminase [Pseudomonas syringae pv. phaseolicola 1448A]	BTC	x	
13092845	>gi|13092845|emb|CAC30209.1| putative adenosine deaminase [Mycobacterium leprae]	MFR	x	
6714760	>gi|6714760|emb|CAB66224.1| probable adenosine deaminase [Streptomyces coelicolor A3(2)]	BTC	x	
7248338	>gi|7248338|emb|CAB77418.1| adenosine deaminase [Streptomyces coelicolor A3(2)]	BTC	x	
13162090	>gi|13162090|emb|CAC33066.1| putative adenosine deaminase [Streptomyces coelicolor A3(2)]	MFR	x	
3319724	>gi|3319724|emb|CAA19890.1| putative adenosine deaminase [Streptomyces coelicolor A3(2)]	BTC	x	
4835327	>gi|4835327|emb|CAB42949.1| putative adenosine deaminase [Streptomyces coelicolor A3(2)]	MFR	x	
34482857	>gi|34482857|emb|CAE09856.1| PUTATIVE ADENOSINE DEAMINASE [Wolinella succinogenes]	BTC	x	
36785694	>gi|36785694|emb|CAE14655.1| adenosine deaminase (adenosine aminohydrolase) [Photorhabdus luminescens subsp. laumondii TTO1]	BTC	x	
33567838	>gi|33567838|emb|CAE31752.1| adenosine deaminase [Bordetella bronchiseptica RB50]	BTC	x	
76563285	>gi|76563285|gb|ABA45869.1| adenosine deaminase [Streptococcus agalactiae A909]	MFR	x	
76580731	>gi|76580731|gb|ABA50206.1| adenosine deaminase [Burkholderia pseudomallei 1710b]	BTC	x	
17738457	>gi|17738457|gb|AAL41160.1| adenosine deaminase [Agrobacterium tumefaciens str. C58]	BTC	x	
74015908	>gi|74015908|ref|ZP_00686535.1| Adenosine deaminase [Burkholderia ambifaria AMMD]	BTC	x	
74018265	>gi|74018265|ref|ZP_00688886.1| Adenosine deaminase [Burkholderia ambifaria AMMD]	BTC	x	
74020523	>gi|74020523|ref|ZP_00691112.1| Adenosine deaminase [Rhodoferax ferrireducens DSM 15236]	BTC	x	
76260060	>gi|76260060|ref|ZP_00767701.1| Adenosine deaminase [Chloroflexus aurantiacus J-10-fl]	BTC	x	
76873990	>gi|76873990|emb|CAI85211.1| adenosine deaminase [Pseudoalteromonas haloplanktis TAC125]	BTC	x	
70905801	>gi|70905801|gb|AAZ14440.1| adenosine deaminase, putative [Leishmania major strain Friedlin]	BTC	x	

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>78034303</td><td>>gi|78034303|emb|CAJ21948.1| putative adenosine deaminase [Xanthomonas campestris pv. vesicatoria str. 85-10]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>76782997</td><td>>gi|76782997|ref|ZP_00770191.1| COG1816: Adenosine deaminase [Mycobacterium tuberculosis F11]</td><td>MFR</td><td>x</td><td></td></tr>
<tr><td>76794044</td><td>>gi|76794044|ref|ZP_00776521.1| Adenosine deaminase [Pseudoalteromonas atlantica T6c]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>76794867</td><td>>gi|76794867|ref|ZP_00777322.1| Adenosine deaminase [Pseudoalteromonas atlantica T6c]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>77408515</td><td>>gi|77408515|ref|ZP_00785252.1| adenosine deaminase [Streptococcus agalactiae COH1]</td><td>MFR</td><td>x</td><td></td></tr>
<tr><td>77413694</td><td>>gi|77413694|ref|ZP_00789877.1| adenosine deaminase [Streptococcus agalactiae 515]</td><td>MFR</td><td>x</td><td></td></tr>
<tr><td>54697118</td><td>>gi|54697118|gb|AAV38931.1| adenosine deaminase [synthetic construct]</td><td>MFR</td><td>x</td><td></td></tr>
<tr><td>78167283</td><td>>gi|78167283|gb|ABB24381.1| Adenosine deaminase [Pelodictyon luteolum DSM 273]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>78493342</td><td>>gi|78493342|ref|ZP_00845576.1| Adenosine deaminase [Rhodopseudomonas palustris BisB18]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>67677253</td><td>>gi|67677253|ref|ZP_00473992.1| Adenosine deaminase [Chromohalobacter salexigens DSM 3043]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>67735855</td><td>>gi|67735855|ref|ZP_00486789.1| COG1816: Adenosine deaminase [Burkholderia pseudomallei 668]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>67665401</td><td>>gi|67665401|ref|ZP_00462665.1| Adenosine deaminase [Burkholderia cenocepacia HI2424]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>67777791</td><td>>gi|67777791|gb|EAM37416.1| Adenosine deaminase [Polaromonas sp. JS666]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>67935693</td><td>>gi|67935693|ref|ZP_00528712.1| Adenosine deaminase [Chlorobium phaeobacteroides DSM 266]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>67938139</td><td>>gi|67938139|ref|ZP_00530668.1| Adenosine deaminase [Chlorobium phaeobacteroides BS1]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>67928188</td><td>>gi|67928188|ref|ZP_00521377.1| Adenosine deaminase [Solibacter usitatus Ellin6076]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>67987878</td><td>>gi|67987878|gb|EAM75664.1| Adenosine deaminase [Kineococcus radiotolerans SRS30216]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>67988152</td><td>>gi|67988152|gb|EAM75934.1| Adenosine deaminase [Kineococcus radiotolerans SRS30216]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>67988687</td><td>>gi|67988687|gb|EAM76464.1| Adenosine deaminase [Kineococcus radiotolerans SRS30216]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>67987476</td><td>>gi|67987476|gb|EAM75271.1| Adenosine deaminase [Kineococcus radiotolerans SRS30216]</td><td>BTC</td><td>x</td><td></td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
67985535	>gi|67985535|gb|EAM73395.1| Adenosine deaminase [Kineococcus radiotolerans SRS30216]	MFR	x	
67668081	>gi|67668081|ref|ZP_00465276.1| Adenosine deaminase [Burkholderia cenocepacia HI2424]	BTC	x	
68183558	>gi|68183558|ref|ZP_00556532.1| Adenosine deaminase [Jannaschia sp. CCS1]	BTC	x	
68229598	>gi|68229598|ref|ZP_00568791.1| Adenosine deaminase [Frankia sp. EAN1pec]	MFR	x	
68230521	>gi|68230521|ref|ZP_00569703.1| Adenosine deaminase [Frankia sp. EAN1pec]	BTC	x	
68234903	>gi|68234903|ref|ZP_00573955.1| Adenosine deaminase [Frankia sp. EAN1pec]	BTC	x	
68538871	>gi|68538871|ref|ZP_00578646.1| Adenosine deaminase [Sphingopyxis alaskensis RB2256]	BTC	x	
66043928	>gi|66043928|ref|YP_233769.1| adenosine deaminase [Pseudomonas syringae pv. syringae B728a]	BTC	x	
55820814	>gi|55820814|ref|YP_139256.1| adenosine deaminase [Streptococcus thermophilus LMG 18311]	MFR	x	
83285917	>gi|83285917|ref|XP_729933.1| adenosine deaminase [Plasmodium yoelii yoelii str. 17XNL]	BTC	x	
66807095	>gi|66807095|ref|XP_637270.1| adenosine deaminase [Dictyostelium discoideum]	MFR	x	
56551551	>gi|56551551|ref|YP_162390.1| adenosine deaminase [Zymomonas mobilis subsp. mobilis ZM4]	SFA	x	
56551867	>gi|56551867|ref|YP_162706.1| adenosine deaminase [Zymomonas mobilis subsp. mobilis ZM4]	BTC	x	
24197788	>gi|24197788|gb|AAN50981.1| Adenosine deaminase [Leptospira interrogans serovar Lai str. 56601]	BTC	x	
49611720	>gi|49611720|emb|CAG75169.1| adenosine deaminase [Erwinia carotovora subsp. atroseptica SCRI1043]	BTC	x	
54014428	>gi|54014428|dbj|BAD55798.1| putative adenosine deaminase [Nocardia farcinica IFM 10152]	MFR	x	
50363587	>gi|50363587|gb|AAT75572.1| adenosine deaminase [Mesoplasma florum L1]	SFA	x	
67758351	>gi|67758351|ref|ZP_00497121.1| COG1816: Adenosine deaminase [Burkholderia pseudomallei S13]	BTC	x	
58255117	>gi|58255117|gb|AAV43354.1| adenosine deaminase [Lactobacillus acidophilus NCFM]	BTC	x	
56178481	>gi|56178481|gb|AAV81203.1| Adenosine deaminase [Idiomarina loihiensis L2TR]	MFR	x	
58002292	>gi|58002292|gb|AAW61186.1| Adenosine deaminase [Gluconobacter oxydans 621H]	SFA	x	
52217988	>gi|52217988|dbj|BAD50581.1| putative adenosine deaminase [Bacteroides fragilis YCH46]	SFA	x	
854497	>gi|854497|emb|CAA86885.1| adenosine deaminase (putative) [Saccharomyces cerevisiae]	BTC	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
68070263	>gi|68070263|ref|XP_677043.1| adenosine deaminase [Plasmodium berghei strain ANKA]	BTC	x	
83592105	>gi|83592105|ref|YP_425857.1| Adenosine deaminase [Rhodospirillum rubrum ATCC 11170]	BTC	x	
70945981	>gi|70945981|ref|XP_742752.1| adenosine deaminase [Plasmodium chabaudi chabaudi]	BTC	x	
42519515	>gi|42519515|ref|NP_965445.1| adenosine deaminase [Lactobacillus johnsonii NCC 533]	MFR	x	
81096978	>gi|81096978|ref|ZP_00875297.1| Adenosine deaminase [Streptococcus suis 89/1591]	MFR	x	
67646444	>gi|67646444|ref|ZP_00444703.1| COG1816: Adenosine deaminase [Burkholderia mallei NCTC 10247]	BTC	x	
41409536	>gi|41409536|ref|NP_962372.1| adenosine deaminase [Mycobacterium avium subsp. paratuberculosis K-10]	MFR	x	
68192770	>gi|68192770|gb|EAN07423.1| Adenosine deaminase [Mesorhizobium sp. BNC1]	BTC	x	
67986152	>gi|67986152|gb|EAM73984.1| Adenosine deaminase [Kineococcus radiotolerans SRS30216]	SFA	x	
49530407	>gi|49530407|emb|CAG68119.1| adenosine deaminase [Acinetobacter sp. ADP1]	BTC	x	
56604528	>gi|56604528|emb|CAG45572.1| adenosine deaminase [Francisella tularensis subsp. tularensis SCHU S4]	BTC	x	
29604806	>gi|29604806|dbj|BAC68875.1| putative adenosine deaminase [Streptomyces avermitilis MA-4680]	MFR	x	
29606243	>gi|29606243|dbj|BAC70306.1| putative adenosine deaminase [Streptomyces avermitilis MA-4680]	BTC	x	
29607009	>gi|29607009|dbj|BAC71069.1| putative adenosine deaminase [Streptomyces avermitilis MA-4680]	MFR	x	
29608564	>gi|29608564|dbj|BAC72618.1| putative adenosine deaminase [Streptomyces avermitilis MA-4680]	BTC	x	
29609238	>gi|29609238|dbj|BAC73289.1| putative adenosine deaminase [Streptomyces avermitilis MA-4680]	BTC	x	
56679502	>gi|56679502|gb|AAV96168.1| adenosine deaminase [Silicibacter pomeroyi DSS-3]	BTC	x	
8745398	>gi|8745398|gb|AAF78901.1| putative adenosine deaminase [Lutzomyia longipalpis]	SFA	x	
72119527	>gi|72119527|gb|AAZ61790.1| Adenosine deaminase [Ralstonia eutropha JMP134]	BTC	x	
50841312	>gi|50841312|gb|AAT83979.1| adenosine deaminase [Propionibacterium acnes KPA171202]	MFR	x	
77966348	>gi|77966348|gb|ABB07728.1| Adenosine deaminase [Burkholderia sp. 383]	BTC	x	
77969126	>gi|77969126|gb|ABB10505.1| Adenosine deaminase [Burkholderia sp. 383]	BTC	x	
71916694	>gi|71916694|gb|AAZ56596.1| adenosine deaminase [Thermobifida fusca YX]	MFR	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
71916793	>gi|71916793|gb|AAZ56695.1| adenosine deaminase [Thermobifida fusca YX]	BTC	x	
52627853	>gi|52627853|gb|AAU26594.1| adenosine deaminase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]	SFA	x	
52627928	>gi|52627928|gb|AAU26669.1| adenosine deaminase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]	BTC	x	
77386556	>gi|77386556|gb|ABA77741.1| adenosine deaminase [Rhodobacter sphaeroides 2.4.1]	BTC	x	
50950754	>gi|50950754|gb|AAT88455.1| adenosine deaminase protein [Leifsonia xyli subsp. xyli str. CTCB07]	MFR	x	
50951472	>gi|50951472|gb|AAT89173.1| adenosine deaminase protein [Leifsonia xyli subsp. xyli str. CTCB07]	BTC	x	
46916287	>gi|46916287|emb|CAG23056.1| putative adenosine deaminase [Photobacterium profundum SS9]	BTC	x	
46916481	>gi|46916481|emb|CAG23246.1| putative adenosine deaminase [Photobacterium profundum SS9]	BTC	x	
77380902	>gi|77380902|gb|ABA72415.1| Adenosine deaminase [Pseudomonas fluorescens PfO-1]	BTC	x	
48784786	>gi|48784786|ref|ZP_00281091.1| COG1816: Adenosine deaminase [Burkholderia fungorum LB400]	BTC	x	
23495155	>gi|23495155|gb|AAN35486.1| adenosine deaminase, putative [Plasmodium falciparum 3D7]	BTC	x	
34899120	>gi|34899120|ref|NP_910906.1| putative adenosine deaminase [Oryza sativa (japonica cultivar-group)]	BTC	x	
67474174	>gi|67474174|ref|XP_652836.1| adenosine deaminase [Entamoeba histolytica HM-1:IMSS]	SFA	x	
67479401	>gi|67479401|ref|XP_655082.1| adenosine deaminase [Entamoeba histolytica HM-1:IMSS]	MFR	x	
86156527	>gi|86156527|ref|YP_463312.1| adenosine deaminase [Anaeromyxobacter dehalogenans 2CP-C]	MFR	x	
86157675	>gi|86157675|ref|YP_464460.1| Adenosine deaminase [Anaeromyxobacter dehalogenans 2CP-C]	MFR	x	
21111264	>gi|21111264|gb|AAM39613.1| adenosine deaminase [Xanthomonas campestris pv. campestris str. ATCC 33913]	SFA	x	
21106379	>gi|21106379|gb|AAM35200.1| adenosine deaminase [Xanthomonas axonopodis pv. citri str. 306]	SFA	x	
66852887	>gi|66852887|gb|EAL93211.1| adenosine deaminase [Aspergillus fumigatus Af293]	BTC	x	
86739247	>gi|86739247|ref|YP_479647.1| adenosine deaminase [Frankia sp. CcI3]	BTC	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
86739399	>gi|86739399|ref|YP_479799.1| adenosine deaminase [Frankia sp. CcI3]	MFR	x	
86740475	>gi|86740475|ref|YP_480875.1| adenosine deaminase [Frankia sp. CcI3]	MFR	x	
86743133	>gi|86743133|ref|YP_483533.1| adenosine deaminase [Frankia sp. CcI3]	BTC	x	
15419920	>gi|15419920|gb|AAK97208.1| salivary adenosine deaminase [Culex pipiens quinquefasciatus]	SFA	x	
18568326	>gi|18568326|gb|AAL76033.1| putative adenosine deaminase [Aedes aegypti]	SFA	x	
7267246	>gi|7267246|emb|CAB80853.1| putative adenosine deaminase [Arabidopsis thaliana]	BTC	x	
47934208	>gi|47934208|gb|AAT39739.1| adenosine deaminase [Trichinella spiralis]	BTC	x	
56417438	>gi|56417438|gb|AAV90660.1| putative adenosine deaminase [Aedes albopictus]	SFA	x	
66964441	>gi|66964441|ref|ZP_00412011.1| Adenosine deaminase [Arthrobacter sp. FB24]	MFR	x	
67157764	>gi|67157764|ref|ZP_00418959.1| Adenosine deaminase [Azotobacter vinelandii AvOP]	BTC	x	
67546828	>gi|67546828|ref|ZP_00424738.1| Adenosine deaminase [Burkholderia vietnamiensis G4]	BTC	x	
68555572	>gi|68555572|ref|ZP_00594916.1| Adenosine deaminase [Ralstonia metallidurans CH34]	BTC	x	
74018433	>gi|74018433|ref|ZP_00689054.1| N-acyl-D-amino-acid deacylase [Burkholderia ambifaria AMMD]	BTC	x	
74022046	>gi|74022046|ref|ZP_00692631.1| N-acyl-D-amino-acid deacylase [Rhodoferax ferrireducens DSM 15236]	BTC	x	
74023922	>gi|74023922|ref|ZP_00694488.1| N-acyl-D-amino-acid deacylase [Rhodoferax ferrireducens DSM 15236]	BTC	x	
77683559	>gi|77683559|ref|ZP_00799006.1| N-acyl-D-amino-acid deacylase [Alkaliphilus metalliredigenes QYMF]	BTC	x	
77686173	>gi|77686173|ref|ZP_00801539.1| N-acyl-D-amino-acid deacylase [Alkaliphilus metalliredigenes QYMF]	BTC	x	
67655311	>gi|67655311|ref|ZP_00452698.1| N-acyl-D-amino-acid deacylase [Burkholderia cenocepacia AU 1054]	BTC	x	
67663573	>gi|67663573|ref|ZP_00460854.1| N-acyl-D-amino-acid deacylase [Burkholderia cenocepacia HI2424]	BTC	x	
67674685	>gi|67674685|ref|ZP_00471445.1| N-acyl-D-amino-acid deacylase [Chromohalobacter salexigens DSM 3043]	BTC	x	
67930121	>gi|67930121|ref|ZP_00523297.1| N-acyl-D-amino-acid deacylase [Solibacter usitatus Ellin6076]	BTC	x	

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>67932281</td><td>>gi|67932281|ref|ZP_00525428.1| N-acyl-D-amino-acid deacylase [Solibacter usitatus Ellin6076]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>67934147</td><td>>gi|67934147|ref|ZP_00527233.1| N-acyl-D-amino-acid deacylase [Solibacter usitatus Ellin6076]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>67988281</td><td>>gi|67988281|gb|EAM76061.1| N-acyl-D-amino-acid deacylase [Kineococcus radiotolerans SRS30216]</td><td>BTC</td><td>X</td><td></td></tr>
<tr><td>68182035</td><td>>gi|68182035|ref|ZP_00555016.1| N-acyl-D-amino-acid deacylase [Jannaschia sp. CCS1]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>68207945</td><td>>gi|68207945|ref|ZP_00560087.1| N-acyl-D-amino-acid deacylase [Desulfitobacterium hafniense DCB-2]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>68538072</td><td>>gi|68538072|ref|ZP_00577851.1| N-acyl-D-amino-acid deacylase [Sphingopyxis alaskensis RB2256]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>83590149</td><td>>gi|83590149|ref|YP_430158.1| N-acyl-D-amino-acid deacylase [Moorella thermoacetica ATCC 39073]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>78218721</td><td>>gi|78218721|gb|ABB38070.1| N-acyl-D-amino-acid deacylase [Desulfovibrio desulfuricans G20]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>67910973</td><td>>gi|67910973|ref|ZP_00509357.1| N-acyl-D-amino-acid deacylase [Polaromonas sp. JS666]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>67847388</td><td>>gi|67847388|ref|ZP_00502507.1| N-acyl-D-amino-acid deacylase [Polaromonas sp. JS666]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>37545840</td><td>>gi|37545840|gb|AAM96826.1| N-acyl-D-amino acid amidohydrolase [Variovorax paradoxus]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>82748093</td><td>>gi|82748093|ref|ZP_00910582.1| D-aminoacylase (aspartate, glutamate etc) [Clostridium beijerincki NCIMB 8052]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>83950583</td><td>>gi|83950583|ref|ZP_00959316.1| d-aminoacylase (aspartate, glutamate etc) [Roseovarius nubinhibens ISM]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>71068206</td><td>>gi|71068206|gb|AAZ23061.1| probable D-aminoacylase [Streptomyces fradiae]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>78697027</td><td>>gi|78697027|ref|ZP_00861535.1| D-aminoacylase [Bradyrhizobium sp. BTAi1]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>68227645</td><td>>gi|68227645|ref|ZP_00566851.1| putative D-aminoacylase [Frankia sp. EAN1pec]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>58002044</td><td>>gi|58002044|gb|AAW60938.1| D-aminoacylase [Gluconobacter oxydans 621H]</td><td>NSF</td><td>x</td><td></td></tr>
<tr><td>51857994</td><td>>gi|51857994|dbj|BAD42152.1| D-Aminoacylase [Symbiobacterium thermophilum IAM 14863]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>5457574</td><td>>gi|5457574|emb|CAB49065.1| ndaD D-aminoacylase [Pyrococcus abyssi GE5]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>29606933</td><td>>gi|29606933|dbj|BAC70993.1| putative D-aminoacylase [Streptomyces avermitilis MA-4680]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>29607453</td><td>>gi|29607453|dbj|BAC71511.1| putative D-aminoacylase [Streptomyces avermitilis MA-4680]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>32397119</td><td>>gi|32397119|emb|CAD72423.1| D-aminoacylase [Rhodopirellula baltica SH 1]</td><td>BTC</td><td>x</td><td></td></tr>
</table>

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
57228983	>gi|57228983|gb|AAW45417.1| D-aminoacylase, putative [Cryptococcus neoformans var. neoformans JEC21]	BTC	x	
14285280	>gi|14285280|emb|CAC40599.1| putative D-aminoacylase [Streptomyces coelicolor A3(2)]	BTC	x	
48374197	>gi|48374197|gb|AAT41901.1| putative d-aminoacylase [Fremyella diplosiphon]	SFA	x	
79043464	>gi|79043464|ref|ZP_00874026.1| putative D-aminoacylase [Novosphingobium aromaticivorans DSM 12444]	SFA	x	
84386136	>gi|84386136|ref|ZP_00989165.1| probable N-acyl-D-glutamate deacylase protein [Vibrio splendidus 12B01]	BTC	x	
84502478	>gi|84502478|ref|ZP_01000614.1| probable n-acyl-d-glutamate deacylase protein [Oceanicola batsensis HTCC2597]	BTC	x	
71366212	>gi|71366212|ref|ZP_00656757.1| N-acyl-D-glutamate deacylase [Nocardioides sp. JS614]	BTC	x	
37201349	>gi|37201349|dbj|BAC97171.1| probable N-acyl-D-glutamate deacylase protein [Vibrio vulnificus YJ016]	BTC	x	
37201374	>gi|37201374|dbj|BAC97196.1| putative N-acyl-D-glutamate deacylase protein [Vibrio vulnificus YJ016]	SFA	x	
83624999	>gi|83624999|ref|ZP_00935237.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia mallei JHU]	SFA	x	
48784106	>gi|48784106|ref|ZP_00280487.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia fungorum LB400]	SFA	x	
23126238	>gi|23126238|ref|ZP_00108140.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Nostoc punctiforme PCC 73102]	SFA	x	
76783389	>gi|76783389|ref|ZP_00770581.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Mycobacterium tuberculosis F11]	SFA	x	
67639245	>gi|67639245|ref|ZP_00438125.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia mallei GB8 horse 4]	SFA	x	
27358591	>gi|27358591|gb|AAO07540.1| N-acyl-D-aspartate/D-glutamate deacylase [Vibrio vulnificus CMCP6]	BTC	x	
27358685	>gi|27358685|gb|AAO07634.1| N-acyl-D-aspartate/D-glutamate deacylase [Vibrio vulnificus CMCP6]	NSF	x	
67758918	>gi|67758918|ref|ZP_00497667.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia pseudomallei S13]	SFA	x	

Table K-1. GenBank NR data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
67638370	>gi|67638370|ref|ZP_00437306.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia mallei 10399]	SFA	x	
84520150	>gi|84520150|ref|ZP_01007287.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia mallei SAVP1]	SFA	x	
46912894	>gi|46912894|emb|CAG19683.1| Putative N-acyl-D-aspartate/D-glutamate deacylase [Photobacterium profundum SS9]	BTC	x	
67647101	>gi|67647101|ref|ZP_00445348.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia mallei NCTC 10247]	SFA	x	
83716453	>gi|83716453|ref|YP_439486.1| N-acyl-D-glutamate amidohydrolase [Burkholderia thailandensis E264]	SFA	x	
37542814	>gi|37542814|gb|AAL55412.1| L-hydantoinase HyuH [Arthrobacter sp. BT801]	SFA	x	
82748354	>gi|82748354|ref|ZP_00910839.1| D-hydantoinase [Clostridium beijerincki NCIMB 8052]	BTC	x	
71366085	>gi|71366085|ref|ZP_00656632.1| D-hydantoinase [Nocardioides sp. JS614]	SFA	x	
29344533	>gi|29344533|gb|AAO82291.1| D-hydantoinase [Enterococcus faecalis V583]	BTC	x	
15622042	>gi|15622042|dbj|BAB66035.1| 433aa long hypothetical D-hydantoinase [Sulfolobus tokodaii str. 7]	BTC	x	
15622051	>gi|15622051|dbj|BAB66044.1| 413aa long hypothetical D-hydantoinase [Sulfolobus tokodaii str. 7]	SFA	x	
15622159	>gi|15622159|dbj|BAB66151.1| 464aa long hypothetical D-hydantoinase [Sulfolobus tokodaii str. 7]	BTC	x	
83590827	>gi|83590827|ref|YP_430836.1| D-hydantoinase [Moorella thermoacetica ATCC 39073]	BTC	x	
17134148	>gi|17134148|dbj|BAB76709.1| D-hydantoinase [Nostoc sp. PCC 7120]	SFA	x	
67470002	>gi|67470002|ref|XP_650972.1| D-hydantoinase [Entamoeba histolytica HM-1:IMSS]	BTC	x	
84325440	>gi|84325440|ref|ZP_00973475.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Pseudomonas aeruginosa 2192]	NSF	x	
48782486	>gi|48782486|ref|ZP_00279015.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia fungorum LB400]	NSF	x	
23129838	>gi|23129838|ref|ZP_00111661.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Nostoc punctiforme PCC 73102]	NSF	x	
46164408	>gi|46164408|ref|ZP_00137111.2| COG0804: Urea amidohydrolase (urease) alpha subunit [Pseudomonas aeruginosa UCBPP-PA14]	NSF	x	
6690687	>gi|6690687|gb|AAF24255.1| UreC [Rhodobacter sphaeroides]	MFR	x	

Table K-1. GenBank NR data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>71148102</td><td>>gi|71148102|gb|AAZ28575.1| isoaspartyl dipeptidase [Colwellia psychrerythraea 34H]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>10173745</td><td>>gi|10173745|dbj|BAB04848.1| isoaspartyl dipeptidase [Bacillus halodurans C-125]</td><td>BTC</td><td>X</td><td></td></tr>
<tr><td>20515832</td><td>>gi|20515832|gb|AAM24094.1| isoaspartyl dipeptidase [Thermoanaerobacter tengcongensis MB4]</td><td>BTC</td><td>X</td><td></td></tr>
<tr><td>59712116</td><td>>gi|59712116|ref|YP_204892.1| isoaspartyl dipeptidase [Vibrio fischeri ES114]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>18146022</td><td>>gi|18146022|dbj|BAB82062.1| isoaspartyl dipeptidase [Clostridium perfringens str. 13]</td><td>BTC</td><td>X</td><td></td></tr>
<tr><td>46913159</td><td>>gi|46913159|emb|CAG19947.1| hypothetical isoaspartyl dipeptidase [Photobacterium profundum SS9]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>82749209</td><td>>gi|82749209|ref|ZP_00911673.1| Peptidase M38, beta-aspartyl dipeptidase [Clostridium beijerincki NCIMB 8052]</td><td>BTC</td><td>X</td><td></td></tr>
<tr><td>71541505</td><td>>gi|71541505|ref|ZP_00663253.1| Peptidase M38, beta-aspartyl dipeptidase [Syntrophomonas wolfei str. Goettingen]</td><td>BTC</td><td>X</td><td></td></tr>
<tr><td>76795810</td><td>>gi|76795810|ref|ZP_00778181.1| Peptidase M38, beta-aspartyl dipeptidase [Thermoanaerobacter ethanolicus ATCC 33223]</td><td>BTC</td><td>X</td><td></td></tr>
<tr><td>67674966</td><td>>gi|67674966|ref|ZP_00471725.1| Peptidase M38, beta-aspartyl dipeptidase [Chromohalobacter salexigens DSM 3043]</td><td>BTC</td><td>X</td><td></td></tr>
<tr><td>68054545</td><td>>gi|68054545|ref|ZP_00538702.1| Peptidase M38, beta-aspartyl dipeptidase [Exiguobacterium sp. 255-15]</td><td>BTC</td><td>X</td><td></td></tr>
<tr><td>68208959</td><td>>gi|68208959|ref|ZP_00561037.1| Peptidase M38, beta-aspartyl dipeptidase [Desulfitobacterium hafniense DCB-2]</td><td>BTC</td><td>X</td><td></td></tr>
<tr><td>67850704</td><td>>gi|67850704|gb|EAM46278.1| Peptidase M38, beta-aspartyl dipeptidase [Clostridium thermocellum ATCC 27405]</td><td>BTC</td><td>X</td><td></td></tr>
<tr><td>68541856</td><td>>gi|68541856|ref|ZP_00581595.1| Peptidase M38, beta-aspartyl dipeptidase [Shewanella baltica OS155]</td><td>MFR</td><td>x</td><td></td></tr>
<tr><td>68545938</td><td>>gi|68545938|ref|ZP_00585487.1| Peptidase M38, beta-aspartyl dipeptidase [Shewanella amazonensis SB2B]</td><td>MFR</td><td>x</td><td></td></tr>
<tr><td>68195904</td><td>>gi|68195904|gb|EAN10338.1| Peptidase M38, beta-aspartyl dipeptidase [Enterococcus faecium DO]</td><td>BTC</td><td>X</td><td></td></tr>
</table>

K.2. Table K-2 UniProtKB/TrEMBL Data (Chapter 2)

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q4J9V1_SULAC	>gnl|tr|Q4J9V1_SULAC (Q4J9V1) Cytosine deaminase (EC 3.5.4.1)			x
Q97V65_SULSO	>gnl|tr|Q97V65_SULSO (Q97V65) Cytosine deaminase (CodA) (EC 3.5.4.1)			x
Q3JG17_BURP1	>gnl|tr|Q3JG17_BURP1 (Q3JG17) Cytosine deaminase (EC 3.5.4.1)			x
Q3X5C2_9ACTN	>gnl|tr|Q3X5C2_9ACTN (Q3X5C2) Cytosine deaminase (EC 3.5.4.1)			x
Q4AZB6_9BURK	>gnl|tr|Q4AZB6_9BURK (Q4AZB6) Cytosine deaminase (EC 3.5.4.1)			x
Q4J633_AZOVI	>gnl|tr|Q4J633_AZOVI (Q4J633) Cytosine deaminase (EC 3.5.4.1)			x
Q4LTU9_9BURK	>gnl|tr|Q4LTU9_9BURK (Q4LTU9) Cytosine deaminase (EC 3.5.4.1)			x
Q6W266_RHISN	>gnl|tr|Q6W266_RHISN (Q6W266) Cytosine deaminase (EC 3.5.4.1)			x
Q4K9F3_PSEF5	>gnl|tr|Q4K9F3_PSEF5 (Q4K9F3) Cytosine deaminase (EC 3.5.4.1)			x
Q5E7H0_VIBF1	>gnl|tr|Q5E7H0_VIBF1 (Q5E7H0) Cytosine deaminase (EC 3.5.4.1)			x
Q5WAP7_BACSK	>gnl|tr|Q5WAP7_BACSK (Q5WAP7) Cytosine deaminase (EC 3.5.4.1)			x
Q62D65_BURMA	>gnl|tr|Q62D65_BURMA (Q62D65) Cytosine deaminase (EC 3.5.4.1)			x
Q63M99_BURPS	>gnl|tr|Q63M99_BURPS (Q63M99) Cytosine deaminase (EC 3.5.4.1)			x
Q664N0_YERPS	>gnl|tr|Q664N0_YERPS (Q664N0) Cytosine deaminase (EC 3.5.4.1)			x
Q893E4_CLOTE	>gnl|tr|Q893E4_CLOTE (Q893E4) Cytosine deaminase (EC 3.5.4.1)			x
Q8FKG9_ECOL6	>gnl|tr|Q8FKG9_ECOL6 (Q8FKG9) Cytosine deaminase (EC 3.5.4.1)			x
Q8XZ12_RALSO	>gnl|tr|Q8XZ12_RALSO (Q8XZ12) PROBABLE CYTOSINE DEAMINASE (CYTOSINE AMINOHYDROLASE) PROTEIN (EC 3.5.4.1)			x
Q8ZJE7_YERPE	>gnl|tr|Q8ZJE7_YERPE (Q8ZJE7) Cytosine deaminase (EC 3.5.4.1)			x
Q8ZLR0_SALTY	>gnl|tr|Q8ZLR0_SALTY (Q8ZLR0) Putative cytosine deaminase (EC 3.5.4.1)			x
Q92XH0_RHIME	>gnl|tr|Q92XH0_RHIME (Q92XH0) Putative CodA1 cytosine deaminase (EC 3.5.4.1)			x
Q96XW5_SULTO	>gnl|tr|Q96XW5_SULTO (Q96XW5) 412aa long hypothetical cytosine deaminase			x
Q66ZJ3_9CARY	>gnl|tr|Q66ZJ3_9CARY (Q66ZJ3) Cytosine deaminase (Fragment)			x
Q2T4R6_BURTH	>gnl|tr|Q2T4R6_BURTH (Q2T4R6) Cytosine deaminase			x
Q2XIC1_PSEPU	>gnl|tr|Q2XIC1_PSEPU (Q2XIC1) Cytosine deaminase			x
Q3J118_RHOS4	>gnl|tr|Q3J118_RHOS4 (Q3J118) Cytosine deaminase			x
Q3L5C3_BIFBR	>gnl|tr|Q3L5C3_BIFBR (Q3L5C3) Cytosine deaminase			x
Q53ZC8_ECOLI	>gnl|tr|Q53ZC8_ECOLI (Q53ZC8) Cytosine deaminase			x
Q6Q8Q1_ECOLI	>gnl|tr|Q6Q8Q1_ECOLI (Q6Q8Q1) Cytosine deaminase			x
Q57JD4_SALCH	>gnl|tr|Q57JD4_SALCH (Q57JD4) Putative cytosine deaminase			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q5LPP2_SILPO	>gnl|tr|Q5LPP2_SILPO (Q5LPP2) Cytosine deaminase, putative			x
Q5PLF4_SALPA	>gnl|tr|Q5PLF4_SALPA (Q5PLF4) Cytosine deaminase			x
Q6LHI8_PHOPR	>gnl|tr|Q6LHI8_PHOPR (Q6LHI8) Putative cytosine deaminase			x
Q7MCY1_VIBVY	>gnl|tr|Q7MCY1_VIBVY (Q7MCY1) Cytosine deaminase			x
Q7NHK7_GLOVI	>gnl|tr|Q7NHK7_GLOVI (Q7NHK7) Cytosine deaminase			x
Q87GS2_VIBPA	>gnl|tr|Q87GS2_VIBPA (Q87GS2) Putative cytosine deaminase			x
Q88I13_PSEPK	>gnl|tr|Q88I13_PSEPK (Q88I13) Cytosine deaminase			x
Q8D5W3_VIBVU	>gnl|tr|Q8D5W3_VIBVU (Q8D5W3) Cytosine deaminase			x
Q8FLL9_COREF	>gnl|tr|Q8FLL9_COREF (Q8FLL9) Putative cytosine deaminase			x
Q8G870_BIFLO	>gnl|tr|Q8G870_BIFLO (Q8G870) Cytosine deaminase			x
Q8X690_ECO57	>gnl|tr|Q8X690_ECO57 (Q8X690) Cytosine deaminase			x
Q8XMD3_CLOPE	>gnl|tr|Q8XMD3_CLOPE (Q8XMD3) Cytosine deaminase			x
Q8Z3F3_SALTI	>gnl|tr|Q8Z3F3_SALTI (Q8Z3F3) Cytosine deaminase			x
Q9I680_PSEAE	>gnl|tr|Q9I680_PSEAE (Q9I680) Cytosine deaminase			x
Q2WZZ7_9GAMM	>gnl|tr|Q2WZZ7_9GAMM (Q2WZZ7) Adenosine deaminase (EC 3.5.4.4)			x
Q2Z4Z4_9GAMM	>gnl|tr|Q2Z4Z4_9GAMM (Q2Z4Z4) Adenosine deaminase (EC 3.5.4.4)			x
Q2ZM92_SHEPU	>gnl|tr|Q2ZM92_SHEPU (Q2ZM92) Adenosine deaminase (EC 3.5.4.4)			x
Q33P63_9GAMM	>gnl|tr|Q33P63_9GAMM (Q33P63) Adenosine deaminase (EC 3.5.4.4)			x
Q35VI2_9GAMM	>gnl|tr|Q35VI2_9GAMM (Q35VI2) Adenosine deaminase (EC 3.5.4.4)			x
Q365P4_9GAMM	>gnl|tr|Q365P4_9GAMM (Q365P4) Adenosine deaminase (EC 3.5.4.4)			x
Q3NNU5_SHEFR	>gnl|tr|Q3NNU5_SHEFR (Q3NNU5) Adenosine deaminase (EC 3.5.4.4)			x
Q3P429_9GAMM	>gnl|tr|Q3P429_9GAMM (Q3P429) Adenosine deaminase (EC 3.5.4.4)			x
Q3Q260_9GAMM	>gnl|tr|Q3Q260_9GAMM (Q3Q260) Adenosine deaminase (EC 3.5.4.4)			x
Q3QEL7_9GAMM	>gnl|tr|Q3QEL7_9GAMM (Q3QEL7) Adenosine deaminase (EC 3.5.4.4)			x
Q66AF0_YERPS	>gnl|tr|Q66AF0_YERPS (Q66AF0) Adenosine deaminase (EC 3.5.4.4)			x
Q320Y0_SHIBS	>gnl|tr|Q320Y0_SHIBS (Q320Y0) Adenosine deaminase			x
Q32FF0_SHIDS	>gnl|tr|Q32FF0_SHIDS (Q32FF0) Adenosine deaminase			x
Q3E0Q9_CHLAU	>gnl|tr|Q3E0Q9_CHLAU (Q3E0Q9) Adenosine deaminase			x
Q3Z1X8_SHISS	>gnl|tr|Q3Z1X8_SHISS (Q3Z1X8) Adenosine deaminase			x
Q57PH5_SALCH	>gnl|tr|Q57PH5_SALCH (Q57PH5) Adenosine deaminase			x
Q6LLR1_PHOPR	>gnl|tr|Q6LLR1_PHOPR (Q6LLR1) Putative adenosine deaminase			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q39D04_BURS3	>gnl|tr|Q39D04_BURS3 (Q39D04) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)			x
Q3FJ43_9BURK	>gnl|tr|Q3FJ43_9BURK (Q3FJ43) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)			x
Q3JW03_BURP1	>gnl|tr|Q3JW03_BURP1 (Q3JW03) D-aminoacylase (EC 3.5.1.81)			x
Q3RIZ4_RALME	>gnl|tr|Q3RIZ4_RALME (Q3RIZ4) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)			x
Q3RUN2_RALME	>gnl|tr|Q3RUN2_RALME (Q3RUN2) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)			x
Q451H6_9BURK	>gnl|tr|Q451H6_9BURK (Q451H6) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)			x
Q46U08_RALEJ	>gnl|tr|Q46U08_RALEJ (Q46U08) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)			x
Q4BEP1_BURVI	>gnl|tr|Q4BEP1_BURVI (Q4BEP1) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)			x
Q4LJF1_9BURK	>gnl|tr|Q4LJF1_9BURK (Q4LJF1) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)			x
Q4ZZD7_PSEU2	>gnl|tr|Q4ZZD7_PSEU2 (Q4ZZD7) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)			x
Q9AGH8_ALCFA	>gnl|tr|Q9AGH8_ALCFA (Q9AGH8) D-aminoacylase (EC 3.5.1.81)			x
Q63XA6_BURPS	>gnl|tr|Q63XA6_BURPS (Q63XA6) D-aminoacylase (EC 3.5.1.81)			x
Q7VYV0_BORPE	>gnl|tr|Q7VYV0_BORPE (Q7VYV0) N-acyl-D-glutamate deacylase (EC 3.5.1.82)	ESA		x
Q7W9D9_BORPA	>gnl|tr|Q7W9D9_BORPA (Q7W9D9) N-acyl-D-glutamate deacylase (EC 3.5.1.82)	ESA		x
Q7WHC3_BORBR	>gnl|tr|Q7WHC3_BORBR (Q7WHC3) N-acyl-D-glutamate deacylase (EC 3.5.1.82)	ESA		x
Q8XQN5_RALSO	>gnl|tr|Q8XQN5_RALSO (Q8XQN5) PROBABLE N-ACYL-D-GLUTAMATE DEACYLASE PROTEIN (EC 3.5.1.82)			x
Q9F465_ARTAU	>gnl|tr|Q9F465_ARTAU (Q9F465) L-hydantoinase HyuH			x
Q35GJ0_9BRAD	>gnl|tr|Q35GJ0_9BRAD (Q35GJ0) D-hydantoinase (EC 3.5.2.2)			x
Q35K56_9BRAD	>gnl|tr|Q35K56_9BRAD (Q35K56) D-hydantoinase (EC 3.5.2.2)			x
Q35NL8_9BRAD	>gnl|tr|Q35NL8_9BRAD (Q35NL8) D-hydantoinase (EC 3.5.2.2)			x
Q39PA8_BURS3	>gnl|tr|Q39PA8_BURS3 (Q39PA8) D-hydantoinase (EC 3.5.2.2)			x
Q3J1I0_RHOS4	>gnl|tr|Q3J1I0_RHOS4 (Q3J1I0) Putative D-hydantoinase (Dihydropyrimidinase) (EC 3.5.2.2)			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q3KAM5_PSEPF	>gnl|tr|Q3KAM5_PSEPF (Q3KAM5) D-hydantoinase (EC 3.5.2.2)			x
Q477K6_RALEJ	>gnl|tr|Q477K6_RALEJ (Q477K6) D-hydantoinase (EC 3.5.2.2)			x
Q47WW0_COLP3	>gnl|tr|Q47WW0_COLP3 (Q47WW0) D-hydantoinase (EC 3.5.2.2)			x
Q5DLU2_9BACI	>gnl|tr|Q5DLU2_9BACI (Q5DLU2) D-hydantoinase (EC 3.5.2.2)			x
Q5L028_GEOKA	>gnl|tr|Q5L028_GEOKA (Q5L028) Dihydropyrimidinase (D-hydantoinase) (EC 3.5.2.2)			x
Q5LSI5_SILPO	>gnl|tr|Q5LSI5_SILPO (Q5LSI5) D-hydantoinase (EC 3.5.2.2)			x
Q5WBE6_BACSK	>gnl|tr|Q5WBE6_BACSK (Q5WBE6) D-hydantoinase (EC 3.5.2.2)			x
Q893N3_CLOTE	>gnl|tr|Q893N3_CLOTE (Q893N3) D-hydantoinase (EC 3.5.2.2)			x
Q89PZ7_BRAJA	>gnl|tr|Q89PZ7_BRAJA (Q89PZ7) D-hydantoinase (EC 3.5.2.2)			x
Q89Q35_BRAJA	>gnl|tr|Q89Q35_BRAJA (Q89Q35) D-hydantoinase (EC 3.5.2.2)			x
Q8G2P0_BRUSU	>gnl|tr|Q8G2P0_BRUSU (Q8G2P0) D-hydantoinase (EC 3.5.2.2)			x
Q8YF78_BRUME	>gnl|tr|Q8YF78_BRUME (Q8YF78) D-HYDANTOINASE (EC 3.5.2.2)			x
Q92MZ3_RHIME	>gnl|tr|Q92MZ3_RHIME (Q92MZ3) PUTATIVE D-HYDANTOINASE (DIHYDROPYRIMIDINASE) PROTEIN (EC 3.5.2.2)			x
Q2WNG4_CLOBE	>gnl|tr|Q2WNG4_CLOBE (Q2WNG4) D-hydantoinase			x
Q2X8L4_PSEPU	>gnl|tr|Q2X8L4_PSEPU (Q2X8L4) D-hydantoinase			x
Q3IWL8_RHOS4	>gnl|tr|Q3IWL8_RHOS4 (Q3IWL8) Putative D-hydantoinase dihydropyrimidinase			x
Q6TTR0_PSEPU	>gnl|tr|Q6TTR0_PSEPU (Q6TTR0) D-hydantoinase			x
Q84FR6_9MICC	>gnl|tr|Q84FR6_9MICC (Q84FR6) D-hydantoinase			x
Q8VT66_9RHIZ	>gnl|tr|Q8VT66_9RHIZ (Q8VT66) D-hydantoinase			x
Q2MKJ8_9RHIZ	>gnl|tr|Q2MKJ8_9RHIZ (Q2MKJ8) D-hydantoinase			x
Q3IRZ5_NATPD	>gnl|tr|Q3IRZ5_NATPD (Q3IRZ5) Urease (EC 3.5.1.5), alpha subunit (EC 3.5.1.5)			x
Q75ZQ5_HALMA	>gnl|tr|Q75ZQ5_HALMA (Q75ZQ5) Urease alpha subunit UreC (EC 3.5.1.5)			x
O14420_COCPO	>gnl|tr|O14420_COCPO (O14420) Urease (EC 3.5.1.5)			x
Q8W3L6_ORYSA	>gnl|tr|Q8W3L6_ORYSA (Q8W3L6) Urease (EC 3.5.1.5)			x
Q93WI8_SOLTU	>gnl|tr|Q93WI8_SOLTU (Q93WI8) Urease (EC 3.5.1.5)			x
Q93X19_SOLTU	>gnl|tr|Q93X19_SOLTU (Q93X19) Urease (EC 3.5.1.5)			x
Q948Z6_SOLTU	>gnl|tr|Q948Z6_SOLTU (Q948Z6) Urease (EC 3.5.1.5) (Fragment)			x
Q949H4_SOYBN	>gnl|tr|Q949H4_SOYBN (Q949H4) Leaf ubiquitous urease (EC 3.5.1.5)			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
O87402_SYNPV	>gnl|tr|O87402_SYNPV (O87402) Urease alpha subunit (EC 3.5.1.5)			x
Q2SDQ1_9GAMM	>gnl|tr|Q2SDQ1_9GAMM (Q2SDQ1) Urease, alpha subunit (EC 3.5.1.5)			x
Q2SYF7_BURTH	>gnl|tr|Q2SYF7_BURTH (Q2SYF7) Urease, alpha subunit (EC 3.5.1.5)			x
Q2Y9M7_NITMU	>gnl|tr|Q2Y9M7_NITMU (Q2Y9M7) Urease, alpha subunit (EC 3.5.1.5)			x
Q2YYQ6_STAAB	>gnl|tr|Q2YYQ6_STAAB (Q2YYQ6) Urease alpha subunit (EC 3.5.1.5)			x
Q31B49_PROM9	>gnl|tr|Q31B49_PROM9 (Q31B49) Urease, alpha subunit (EC 3.5.1.5)			x
Q34RK6_RHOPA	>gnl|tr|Q34RK6_RHOPA (Q34RK6) Urease (EC 3.5.1.5)			x
Q34XU6_9GAMM	>gnl|tr|Q34XU6_9GAMM (Q34XU6) Urease, alpha subunit (EC 3.5.1.5)			x
Q35JE7_9BRAD	>gnl|tr|Q35JE7_9BRAD (Q35JE7) Urease, alpha subunit (EC 3.5.1.5)			x
Q35P05_9BRAD	>gnl|tr|Q35P05_9BRAD (Q35P05) Urease, alpha subunit (EC 3.5.1.5)			x
Q35RD7_9BRAD	>gnl|tr|Q35RD7_9BRAD (Q35RD7) Urease, alpha subunit (EC 3.5.1.5)			x
Q374G2_RHOPA	>gnl|tr|Q374G2_RHOPA (Q374G2) Urease, alpha subunit (EC 3.5.1.5)			x
Q37N01_RHOPA	>gnl|tr|Q37N01_RHOPA (Q37N01) Urease, alpha subunit (EC 3.5.1.5)			x
Q39IW3_BURS3	>gnl|tr|Q39IW3_BURS3 (Q39IW3) Urease, alpha subunit (EC 3.5.1.5)			x
Q3AGD0_SYNSC	>gnl|tr|Q3AGD0_SYNSC (Q3AGD0) Urease, alpha subunit (EC 3.5.1.5)			x
Q3AVR1_SYNS9	>gnl|tr|Q3AVR1_SYNS9 (Q3AVR1) Urease, alpha subunit (EC 3.5.1.5)			x
Q3FBA4_9BURK	>gnl|tr|Q3FBA4_9BURK (Q3FBA4) Urease (EC 3.5.1.5)			x
Q3FXN9_9BURK	>gnl|tr|Q3FXN9_9BURK (Q3FXN9) Urease (EC 3.5.1.5)			x
Q3GRG7_9GAMM	>gnl|tr|Q3GRG7_9GAMM (Q3GRG7) Urease (EC 3.5.1.5)			x
Q3GSR3_9GAMM	>gnl|tr|Q3GSR3_9GAMM (Q3GSR3) Urease (EC 3.5.1.5)			x
Q3HBC3_TRIER	>gnl|tr|Q3HBC3_TRIER (Q3HBC3) Urease (EC 3.5.1.5)			x
Q3IH68_PSEHT	>gnl|tr|Q3IH68_PSEHT (Q3IH68) Urease, alpha subunit (EC 3.5.1.5)			x
Q3J154_RHOS4	>gnl|tr|Q3J154_RHOS4 (Q3J154) Urea amidohydrolase (Urease) alpha subunit (EC 3.5.1.5)			x
Q3J770_NITOC	>gnl|tr|Q3J770_NITOC (Q3J770) Urease, alpha subunit (EC 3.5.1.5)			x
Q3JPJ6_BURP1	>gnl|tr|Q3JPJ6_BURP1 (Q3JPJ6) Urease, alpha subunit (EC 3.5.1.5)			x
Q3M712_ANAVT	>gnl|tr|Q3M712_ANAVT (Q3M712) Urease, alpha subunit (EC 3.5.1.5)			x
Q3RWB6_RALME	>gnl|tr|Q3RWB6_RALME (Q3RWB6) Urease (EC 3.5.1.5)			x
Q3VZP2_9ACTO	>gnl|tr|Q3VZP2_9ACTO (Q3VZP2) Urease (EC 3.5.1.5)			x
Q3X7H8_METFL	>gnl|tr|Q3X7H8_METFL (Q3X7H8) Urease (EC 3.5.1.5)			x
Q40VS0_KINRA	>gnl|tr|Q40VS0_KINRA (Q40VS0) Urease (EC 3.5.1.5)			x
Q437T6_9ACTO	>gnl|tr|Q437T6_9ACTO (Q437T6) Urease (EC 3.5.1.5)			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q44DF6_CHRSL	>gnl|tr|Q44DF6_CHRSL (Q44DF6) Urease (EC 3.5.1.5)			x
Q454M1_9BURK	>gnl|tr|Q454M1_9BURK (Q454M1) Urease (EC 3.5.1.5)			x
Q46IY3_PROMT	>gnl|tr|Q46IY3_PROMT (Q46IY3) Urease, alpha subunit (EC 3.5.1.5)			x
Q48DE6_PSE14	>gnl|tr|Q48DE6_PSE14 (Q48DE6) Urease, alpha subunit (EC 3.5.1.5)			x
Q4BIH6_BURVI	>gnl|tr|Q4BIH6_BURVI (Q4BIH6) Urease (EC 3.5.1.5)			x
Q4CHE3_CLOTM	>gnl|tr|Q4CHE3_CLOTM (Q4CHE3) Urease (EC 3.5.1.5)			x
Q4IXD2_AZOVI	>gnl|tr|Q4IXD2_AZOVI (Q4IXD2) Urease (EC 3.5.1.5)			x
Q4LNH4_9BURK	>gnl|tr|Q4LNH4_9BURK (Q4LNH4) Urease (EC 3.5.1.5)			x
Q4NKR4_9MICC	>gnl|tr|Q4NKR4_9MICC (Q4NKR4) Urease (EC 3.5.1.5)			x
Q4ZN06_PSEU2	>gnl|tr|Q4ZN06_PSEU2 (Q4ZN06) Urease (EC 3.5.1.5)			x
Q4ZUD2_PSEU2	>gnl|tr|Q4ZUD2_PSEU2 (Q4ZUD2) Urease (EC 3.5.1.5)			x
Q84F75_HELPY	>gnl|tr|Q84F75_HELPY (Q84F75) Urease beta (EC 3.5.1.5)			x
Q9AQT4_RHOCA	>gnl|tr|Q9AQT4_RHOCA (Q9AQT4) Alpha subunit of urease (EC 3.5.1.5)			x
Q4KJ10_PSEF5	>gnl|tr|Q4KJ10_PSEF5 (Q4KJ10) Urease, alpha subunit (EC 3.5.1.5)			x
Q4QN09_HAEI8	>gnl|tr|Q4QN09_HAEI8 (Q4QN09) Urease alpha subunit (EC 3.5.1.5)			x
Q5E728_VIBF1	>gnl|tr|Q5E728_VIBF1 (Q5E728) Urease alpha subunit (EC 3.5.1.5)			x
Q5KYM1_GEOKA	>gnl|tr|Q5KYM1_GEOKA (Q5KYM1) Urease alpha subunit (Urea amidohydrolase) (EC 3.5.1.5)			x
Q5LSQ2_SILPO	>gnl|tr|Q5LSQ2_SILPO (Q5LSQ2) Urease, alpha subunit (EC 3.5.1.5)			x
Q62HS0_BURMA	>gnl|tr|Q62HS0_BURMA (Q62HS0) Urease, alpha subunit (EC 3.5.1.5)			x
Q63RL3_BURPS	>gnl|tr|Q63RL3_BURPS (Q63RL3) Urease alpha subunit (EC 3.5.1.5)			x
Q6FD83_ACIAD	>gnl|tr|Q6FD83_ACIAD (Q6FD83) Urease alpha subunit (EC 3.5.1.5)			x
Q6N3N3_RHOPA	>gnl|tr|Q6N3N3_RHOPA (Q6N3N3) Urease alpha subunit (EC 3.5.1.5)			x
Q733J6_BACC1	>gnl|tr|Q733J6_BACC1 (Q733J6) Urease alpha subunit (EC 3.5.1.5)			x
Q79VJ3_CORGL	>gnl|tr|Q79VJ3_CORGL (Q79VJ3) Urea amidohydrolase (Urease) alpha subunit (EC 3.5.1.5) (UREASE ALPHA SUBUNIT)			x
Q7U3I3_SYNPX	>gnl|tr|Q7U3I3_SYNPX (Q7U3I3) Urease alpha subunit (EC 3.5.1.5)			x
Q7V1B6_PROMP	>gnl|tr|Q7V1B6_PROMP (Q7V1B6) Urease alpha subunit (EC 3.5.1.5)			x
Q7V3V2_PROMM	>gnl|tr|Q7V3V2_PROMM (Q7V3V2) Urease alpha subunit (EC 3.5.1.5)			x
Q7VRS6_BLOFL	>gnl|tr|Q7VRS6_BLOFL (Q7VRS6) Putative urease structural subunit C (Alpha) (EC 3.5.1.5)			x
Q7VUD3_BORPE	>gnl|tr|Q7VUD3_BORPE (Q7VUD3) Urease alpha subunit (EC 3.5.1.5)			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q7W417_BORPA	>gnl|tr|Q7W417_BORPA (Q7W417) Urease alpha subunit (EC 3.5.1.5)			x
Q8FQX2_COREF	>gnl|tr|Q8FQX2_COREF (Q8FQX2) Urease alpha subunit (EC 3.5.1.5)			x
Q8FZW2_BRUSU	>gnl|tr|Q8FZW2_BRUSU (Q8FZW2) Urease, alpha subunit (EC 3.5.1.5)			x
Q8G2P8_BRUSU	>gnl|tr|Q8G2P8_BRUSU (Q8G2P8) Urease, alpha subunit (EC 3.5.1.5)			x
Q8XXT1_RALSO	>gnl|tr|Q8XXT1_RALSO (Q8XXT1) PROBABLE UREASE (ALPHA SUBUNIT) PROTEIN (EC 3.5.1.5)			x
Q8YF72_BRUME	>gnl|tr|Q8YF72_BRUME (Q8YF72) UREASE ALPHA SUBUNIT (EC 3.5.1.5)			x
Q8YHZ8_BRUME	>gnl|tr|Q8YHZ8_BRUME (Q8YHZ8) UREASE ALPHA SUBUNIT (EC 3.5.1.5)			x
Q9KG59_BACHD	>gnl|tr|Q9KG59_BACHD (Q9KG59) Urease alpha subunit (EC 3.5.1.5)			x
Q2YPD5_BRUA2	>gnl|tr|Q2YPD5_BRUA2 (Q2YPD5) Urease:Amidohydrolase (EC 3.5.1.5)			x
Q2YQD8_BRUA2	>gnl|tr|Q2YQD8_BRUA2 (Q2YQD8) Urease:Amidohydrolase (EC 3.5.1.5)			x
Q972W0_SULTO	>gnl|tr|Q972W0_SULTO (Q972W0) 493aa long hypothetical urease alpha subunit			x
Q7SFW8_NEUCR	>gnl|tr|Q7SFW8_NEUCR (Q7SFW8) Hypothetical protein (Probable urease)			x
Q8H6V8_CANEN	>gnl|tr|Q8H6V8_CANEN (Q8H6V8) Urease JBURE-II			x
Q9SR52_ARATH	>gnl|tr|Q9SR52_ARATH (Q9SR52) Putative urease			x
O52305_SYNP2	>gnl|tr|O52305_SYNP2 (O52305) Urease alpha subunit			x
Q2XLA8_PSEPU	>gnl|tr|Q2XLA8_PSEPU (Q2XLA8) Urease, alpha subunit			x
Q2ZGT0_CALSA	>gnl|tr|Q2ZGT0_CALSA (Q2ZGT0) Urease, alpha subunit			x
Q349U1_RHOPA	>gnl|tr|Q349U1_RHOPA (Q349U1) Urease, alpha subunit			x
Q36I62_MARHY	>gnl|tr|Q36I62_MARHY (Q36I62) Urease, alpha subunit			x
Q38Q64_HELPY	>gnl|tr|Q38Q64_HELPY (Q38Q64) Urease B (Fragment)			x
Q3KIT2_PSEPF	>gnl|tr|Q3KIT2_PSEPF (Q3KIT2) Urease, alpha subunit			x
Q3PBN3_PARDE	>gnl|tr|Q3PBN3_PARDE (Q3PBN3) Urease			x
Q3QUL3_9RHOB	>gnl|tr|Q3QUL3_9RHOB (Q3QUL3) Urease			x
Q3S3T8_9STRE	>gnl|tr|Q3S3T8_9STRE (Q3S3T8) Urease alpha subunit			x
Q3WT92_9RHIZ	>gnl|tr|Q3WT92_9RHIZ (Q3WT92) Urease			x
Q3XRS1_9PROT	>gnl|tr|Q3XRS1_9PROT (Q3XRS1) Urease			x
Q40BI2_9RHOB	>gnl|tr|Q40BI2_9RHOB (Q40BI2) Urease			x
Q473Q9_RALEJ	>gnl|tr|Q473Q9_RALEJ (Q473Q9) Urease, alpha subunit			x
Q47G55_DECAR	>gnl|tr|Q47G55_DECAR (Q47G55) Urease, alpha subunit			x
Q492E9_BLOPB	>gnl|tr|Q492E9_BLOPB (Q492E9) Putative urease structural subunit C (Alpha)			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q4A0J5_STAS1	>gnl|tr|Q4A0J5_STAS1 (Q4A0J5) Urease alpha subunit			x
Q5FB23_CAMLA	>gnl|tr|Q5FB23_CAMLA (Q5FB23) Urease B subunit			x
Q6I6H1_CAMLA	>gnl|tr|Q6I6H1_CAMLA (Q6I6H1) Urease beta subunit (Fragment)			x
Q6I6H3_CAMLA	>gnl|tr|Q6I6H3_CAMLA (Q6I6H3) Urease beta subunit (Fragment)			x
Q6I6H5_CAMLA	>gnl|tr|Q6I6H5_CAMLA (Q6I6H5) Urease beta subunit (Fragment)			x
Q6I6H7_CAMLA	>gnl|tr|Q6I6H7_CAMLA (Q6I6H7) Urease beta subunit (Fragment)			x
Q6I6H9_CAMLA	>gnl|tr|Q6I6H9_CAMLA (Q6I6H9) Urease beta subunit (Fragment)			x
Q6I6I1_CAMLA	>gnl|tr|Q6I6I1_CAMLA (Q6I6I1) Urease beta subunit (Fragment)			x
Q6I6I3_CAMLA	>gnl|tr|Q6I6I3_CAMLA (Q6I6I3) Urease beta subunit (Fragment)			x
Q6I6I5_CAMLA	>gnl|tr|Q6I6I5_CAMLA (Q6I6I5) Urease beta subunit (Fragment)			x
Q6I6I9_CAMLA	>gnl|tr|Q6I6I9_CAMLA (Q6I6I9) Urease beta subunit (Fragment)			x
Q6I6J1_CAMLA	>gnl|tr|Q6I6J1_CAMLA (Q6I6J1) Urease beta subunit (Fragment)			x
Q6JHP2_9PSEU	>gnl|tr|Q6JHP2_9PSEU (Q6JHP2) Urease alpha subunit			x
Q6WVG4_9PROT	>gnl|tr|Q6WVG4_9PROT (Q6WVG4) Urease C subunit			x
Q6Y3X2_9PROT	>gnl|tr|Q6Y3X2_9PROT (Q6Y3X2) Urease C			x
Q6Y9S4_9PROT	>gnl|tr|Q6Y9S4_9PROT (Q6Y9S4) Urease subunit C			x
Q7X3W5_HELPY	>gnl|tr|Q7X3W5_HELPY (Q7X3W5) Urease B			x
Q8GH97_HELBI	>gnl|tr|Q8GH97_HELBI (Q8GH97) Urease B			x
Q8KT12_HELPY	>gnl|tr|Q8KT12_HELPY (Q8KT12) Urease UreB (Fragment)			x
Q8KT24_HELFE	>gnl|tr|Q8KT24_HELFE (Q8KT24) Urease UreB (Fragment)			x
Q8KT25_HELBI	>gnl|tr|Q8KT25_HELBI (Q8KT25) Urease UreB (Fragment)			x
Q8KT26_HELBI	>gnl|tr|Q8KT26_HELBI (Q8KT26) Urease UreB (Fragment)			x
Q8KT29_HELHE	>gnl|tr|Q8KT29_HELHE (Q8KT29) Urease UreB (Fragment)			x
Q8KT33_HELPY	>gnl|tr|Q8KT33_HELPY (Q8KT33) Urease UreB (Fragment)			x
Q8RNU6_HELPY	>gnl|tr|Q8RNU6_HELPY (Q8RNU6) Urease B subunit			x
Q9AFB1_HELPY	>gnl|tr|Q9AFB1_HELPY (Q9AFB1) Urease B			x
Q9S0Q5_HELPY	>gnl|tr|Q9S0Q5_HELPY (Q9S0Q5) Urease B			x
Q9S6F6_LACFE	>gnl|tr|Q9S6F6_LACFE (Q9S6F6) Urease alpha subunit			x
Q9Z369_ACTNA	>gnl|tr|Q9Z369_ACTNA (Q9Z369) Urease alpha subunit UreC			x
O86508_STRCO	>gnl|tr|O86508_STRCO (O86508) Urease alpha subunit			x
Q57CE8_BRUAB	>gnl|tr|Q57CE8_BRUAB (Q57CE8) UreC-2, urease, alpha subunit			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q5M1G6_STRT1	>gnl|tr|Q5M1G6_STRT1 (Q5M1G6) Urea amidohydrolase (Urease) alpha subunit			x
Q5M607_STRT2	>gnl|tr|Q5M607_STRT2 (Q5M607) Urea amidohydrolase (Urease) alpha subunit			x
Q5YWR8_NOCFA	>gnl|tr|Q5YWR8_NOCFA (Q5YWR8) Putative urease alpha subunit			x
Q7N4Y7_PHOLL	>gnl|tr|Q7N4Y7_PHOLL (Q7N4Y7) Urease alpha subunit			x
Q826R9_STRAW	>gnl|tr|Q826R9_STRAW (Q826R9) Putative urease alpha subunit			x
Q82JN9_STRAW	>gnl|tr|Q82JN9_STRAW (Q82JN9) Putative urease alpha subunit			x
Q87VP0_PSESM	>gnl|tr|Q87VP0_PSESM (Q87VP0) Urease, alpha subunit			x
Q88J04_PSEPK	>gnl|tr|Q88J04_PSEPK (Q88J04) Urease, alpha subunit			x
Q89UG0_BRAJA	>gnl|tr|Q89UG0_BRAJA (Q89UG0) Urease alpha subunit			x
Q8DMV6_SYNEL	>gnl|tr|Q8DMV6_SYNEL (Q8DMV6) Urease alpha subunit			x
Q8UCT2_AGRT5	>gnl|tr|Q8UCT2_AGRT5 (Q8UCT2) Urease alpha subunit (AGR_C_4357p)			x
Q8XAG0_ECO57	>gnl|tr|Q8XAG0_ECO57 (Q8XAG0) Putative urease structural subunit C (Alpha) (Urease alpha subunit)			x
Q8YQZ0_ANASP	>gnl|tr|Q8YQZ0_ANASP (Q8YQZ0) Urease alpha subunit			x
Q93T81_BRUAB	>gnl|tr|Q93T81_BRUAB (Q93T81) Urease alpha subunit UreC (UreC-1, urease, alpha subunit)			x
Q9FCD3_STRCO	>gnl|tr|Q9FCD3_STRCO (Q9FCD3) Urease alpha subunit			x
Q9HUU5_PSEAE	>gnl|tr|Q9HUU5_PSEAE (Q9HUU5) Urease alpha subunit			x
Q9RYJ4_DEIRA	>gnl|tr|Q9RYJ4_DEIRA (Q9RYJ4) Urease, alpha subunit			x
Q6T368_9PROT	>gnl|tr|Q6T368_9PROT (Q6T368) UreC			x
Q6UB24_STRTR	>gnl|tr|Q6UB24_STRTR (Q6UB24) UreC protein			x
Q6UR33_YERRO	>gnl|tr|Q6UR33_YERRO (Q6UR33) UreC			x
Q6UR42_YERMO	>gnl|tr|Q6UR42_YERMO (Q6UR42) UreC			x
Q6UR51_YERKR	>gnl|tr|Q6UR51_YERKR (Q6UR51) UreC			x
Q6UR60_YERIN	>gnl|tr|Q6UR60_YERIN (Q6UR60) UreC			x
Q6UR68_YERFR	>gnl|tr|Q6UR68_YERFR (Q6UR68) UreC			x
Q6UR76_YERBE	>gnl|tr|Q6UR76_YERBE (Q6UR76) UreC			x
Q6UR84_YERAL	>gnl|tr|Q6UR84_YERAL (Q6UR84) UreC			x
Q84ED2_STRTR	>gnl|tr|Q84ED2_STRTR (Q84ED2) UreC protein			x
Q84I83_STRTR	>gnl|tr|Q84I83_STRTR (Q84I83) UreC			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q8GH75_9PROT	>gnl|tr|Q8GH75_9PROT (Q8GH75) UreC			x
Q8RPY2_RHILV	>gnl|tr|Q8RPY2_RHILV (Q8RPY2) UreC			x
Q9FAS5_VIBPA	>gnl|tr|Q9FAS5_VIBPA (Q9FAS5) UreC			x
Q9L644_PROMA	>gnl|tr|Q9L644_PROMA (Q9L644) UreC			x
Q9RHM4_CORGL	>gnl|tr|Q9RHM4_CORGL (Q9RHM4) UreC			x
Q2UKB4_ASPOR	>gnl|tr|Q2UKB4_ASPOR (Q2UKB4) Urea amidohydrolase			x
Q6YCI8_9PROT	>gnl|tr|Q6YCI8_9PROT (Q6YCI8) Urea amidohydrolase alpha subunit			x
Q8RJJ9_9GAMM	>gnl|tr|Q8RJJ9_9GAMM (Q8RJJ9) Urea amidohydrolase alpha subunit			x
Q64EY3_HELPY	>gnl|tr|Q64EY3_HELPY (Q64EY3) UreB			x
Q31T14_SHIBS	>gnl|tr|Q31T14_SHIBS (Q31T14) Isoaspartyl dipeptidase			x
Q659Y9_ECOLI	>gnl|tr|Q659Y9_ECOLI (Q659Y9) Isoaspartyl dipeptidase yadA			x
Q57G89_SALCH	>gnl|tr|Q57G89_SALCH (Q57G89) Isoaspartyl dipeptidase			x
Q5PM50_SALPA	>gnl|tr|Q5PM50_SALPA (Q5PM50) Probable isoaspartyl dipeptidase			x
Q83P79_SHIFL	>gnl|tr|Q83P79_SHIFL (Q83P79) Isoaspartyl dipeptidase			x
Q8FA99_ECOL6	>gnl|tr|Q8FA99_ECOL6 (Q8FA99) Isoaspartyl dipeptidase (EC 3.4.19.-)			x
Q8XB98_ECO57	>gnl|tr|Q8XB98_ECO57 (Q8XB98) Isoaspartyl dipeptidase			x
Q8Z0X6_SALTI	>gnl|tr|Q8Z0X6_SALTI (Q8Z0X6) Probable isoaspartyl dipeptidase (EC 3.4.19.-)			x
Q8ZJZ8_SALTY	>gnl|tr|Q8ZJZ8_SALTY (Q8ZJZ8) Isoaspartyl dipeptidase (EC 3.4.19.5)			x
Q8WZH4_NEUCR	>gnl|tr|Q8WZH4_NEUCR (Q8WZH4) Probable DELTA3, 5-DELTA2, 4-DIENOYL-COA ISOMERASE (ECH1)			x
Q4WVP0_ASPFU	>gnl|tr|Q4WVP0_ASPFU (Q4WVP0) Mitochondrial 3-hydroxyisobutyryl-CoA hydrolase, putative			x
Q53GA8_HUMAN	>gnl|tr|Q53GA8_HUMAN (Q53GA8) 3-hydroxyisobutyryl-Coenzyme A hydrolase isoform 1 variant (Fragment)			x
Q53GF2_HUMAN	>gnl|tr|Q53GF2_HUMAN (Q53GF2) 3-hydroxyisobutyryl-Coenzyme A hydrolase isoform 1 variant (Fragment)			x
Q6NVY1_HUMAN	>gnl|tr|Q6NVY1_HUMAN (Q6NVY1) 3-hydroxyisobutyryl-Coenzyme A hydrolase, isoform 1			x
Q92931_HUMAN	>gnl|tr|Q92931_HUMAN (Q92931) 3-hydroxyisobutyryl-coenzyme A hydrolase			x
O49330_ARATH	>gnl|tr|O49330_ARATH (O49330) 3-hydroxyisobutyryl-coenzyme A hydrolase			x
O49331_ARATH	>gnl|tr|O49331_ARATH (O49331) 3-hydroxyisobutyryl-coenzyme A hydrolase			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q2QUG3_ORYSA	>gnl|tr|Q2QUG3_ORYSA (Q2QUG3) 3-hydroxyisobutyryl-coenzyme A hydrolase, putative			x
Q2QUG4_ORYSA	>gnl|tr|Q2QUG4_ORYSA (Q2QUG4) 3-hydroxyisobutyryl-coenzyme A hydrolase, putative			x
Q56XU5_ARATH	>gnl|tr|Q56XU5_ARATH (Q56XU5) 3-hydroxyisobutyryl-coenzyme A hydrolase (At1g06550)			x
Q69UF2_ORYSA	>gnl|tr|Q69UF2_ORYSA (Q69UF2) Putative 3-hydroxyisobutyryl-coenzyme A hydrolase			x
Q9LKJ1_ARATH	>gnl|tr|Q9LKJ1_ARATH (Q9LKJ1) CoA-thioester hydrolase CHY1 (3-hydroxyisobutyryl-coenzyme A hydrolase)			x
Q6G3D0_BARHE	>gnl|tr|Q6G3D0_BARHE (Q6G3D0) 3-hydroxyisobutyryl-coenzyme A hydrolase			x
Q81DR3_BACCR	>gnl|tr|Q81DR3_BACCR (Q81DR3) 3-hydroxyisobutyryl-coenzyme A hydrolase (EC 3.1.2.4)			x
Q983C3_RHILO	>gnl|tr|Q983C3_RHILO (Q983C3) 3-hydroxyisobutyryl-Coenzyme A hydrolase			x
Q5XIE6_RAT	>gnl|tr|Q5XIE6_RAT (Q5XIE6) 3-hydroxyisobutyryl-Coenzyme A hydrolase (Predicted)			x
Q58EB4_BRARE	>gnl|tr|Q58EB4_BRARE (Q58EB4) 3-hydroxyisobutyryl-Coenzyme A hydrolase			x
Q7BI35_ARTGO	>gnl|tr|Q7BI35_ARTGO (Q7BI35) 4-chlorobenzoate Co-A dehalogenase			x
O68600_9PROT	>gnl|tr|O68600_9PROT (O68600) 4-chlorobenzoyl CoA dehalogenase			x
O85078_9MICC	>gnl|tr|O85078_9MICC (O85078) 4-chlorobenzoyl CoA dehalogenase			x
Q7BUZ5_9MICC	>gnl|tr|Q7BUZ5_9MICC (Q7BUZ5) 4-chlorobenzoyl CoA dehalogenase			x
Q8GN87_9BURK	>gnl|tr|Q8GN87_9BURK (Q8GN87) 4-chlorobenzoyl CoA dehalogenase			x
Q9LCU3_9MICC	>gnl|tr|Q9LCU3_9MICC (Q9LCU3) 4-chlorobenzoyl CoA dehalogenase			x
Q99QJ6_9MICC	>gnl|tr|Q99QJ6_9MICC (Q99QJ6) 4-CBA-CoA dehalogenase			x
Q33EG2_METHU	>gnl|tr|Q33EG2_METHU (Q33EG2) Enolase (EC 4.2.1.11)			x
Q33G47_METHU	>gnl|tr|Q33G47_METHU (Q33G47) Enolase (EC 4.2.1.11)			x
Q33I06_METHU	>gnl|tr|Q33I06_METHU (Q33I06) Enolase (EC 4.2.1.11)			x
Q3IQT0_NATPD	>gnl|tr|Q3IQT0_NATPD (Q3IQT0) Phosphopyruvate hydratase (EC 4.2.1.11) (Enolase) (EC 4.2.1.11)			x
Q41NP7_METBU	>gnl|tr|Q41NP7_METBU (Q41NP7) Enolase (EC 4.2.1.11)			x
Q648E0_9ARCH	>gnl|tr|Q648E0_9ARCH (Q648E0) Phosphopyruvate hydratase enolase			x
Q703Y8_THETE	>gnl|tr|Q703Y8_THETE (Q703Y8) Enolase (EC 4.2.1.11)			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q2NG02_9EURY	>gnl|tr|Q2NG02_9EURY (Q2NG02) Enolase (EC 4.2.1.11)			x
Q6KZN3_PICTO	>gnl|tr|Q6KZN3_PICTO (Q6KZN3) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x
O93873_PNECA	>gnl|tr|O93873_PNECA (O93873) Enolase			x
Q2UMC4_ASPOR	>gnl|tr|Q2UMC4_ASPOR (Q2UMC4) Enolase			x
Q4IN62_GIBZE	>gnl|tr|Q4IN62_GIBZE (Q4IN62) ENO_ALTAL Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Major allergen Alt a 11) (Alt a XI)			x
Q5B135_EMENI	>gnl|tr|Q5B135_EMENI (Q5B135) ENO_ASPOR Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
Q5KG11_CRYNE	>gnl|tr|Q5KG11_CRYNE (Q5KG11) Enolase 1, putative			x
Q8SUA4_ENCCU	>gnl|tr|Q8SUA4_ENCCU (Q8SUA4) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x
Q7SHD6_NEUCR	>gnl|tr|Q7SHD6_NEUCR (Q7SHD6) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x
Q53FT9_HUMAN	>gnl|tr|Q53FT9_HUMAN (Q53FT9) Enolase 1 variant (Fragment)			x
Q53HR3_HUMAN	>gnl|tr|Q53HR3_HUMAN (Q53HR3) Enolase 1 variant (Fragment)			x
Q6FHV6_HUMAN	>gnl|tr|Q6FHV6_HUMAN (Q6FHV6) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x
O44100_DROPS	>gnl|tr|O44100_DROPS (O44100) Enolase (Fragment)			X
O44101_DROSU	>gnl|tr|O44101_DROSU (O44101) Enolase (Fragment)			X
Q38BV6_9TRYP	>gnl|tr|Q38BV6_9TRYP (Q38BV6) Enolase (EC 4.2.1.11)			x
Q3HL75_LEIME	>gnl|tr|Q3HL75_LEIME (Q3HL75) Enolase (EC 4.2.1.11)			x
Q3SEA7_PARTE	>gnl|tr|Q3SEA7_PARTE (Q3SEA7) Enolase, putative			x
Q3SEB6_PARTE	>gnl|tr|Q3SEB6_PARTE (Q3SEB6) Enolase, putative			x
Q4DZ98_TRYCR	>gnl|tr|Q4DZ98_TRYCR (Q4DZ98) Enolase, putative (EC 4.2.1.11)			x
Q4N1N2_THEPA	>gnl|tr|Q4N1N2_THEPA (Q4N1N2) Enolase, putative (EC 4.2.1.11)			x
Q4QFL8_LEIMA	>gnl|tr|Q4QFL8_LEIMA (Q4QFL8) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x
Q4U8Y7_THEAN	>gnl|tr|Q4U8Y7_THEAN (Q4U8Y7) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x
Q4YQJ5_PLABE	>gnl|tr|Q4YQJ5_PLABE (Q4YQJ5) Enolase, putative			x

Table K-2. TrEMBL data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>Q50QB0_ENTHI</td><td>>gnl|tr|Q50QB0_ENTHI (Q50QB0) Enolase, putative</td><td></td><td></td><td>x</td></tr>
<tr><td>Q56RN2_DROMI</td><td>>gnl|tr|Q56RN2_DROMI (Q56RN2) Enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q56RN9_DROMI</td><td>>gnl|tr|Q56RN9_DROMI (Q56RN9) Enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q56RP2_DROPS</td><td>>gnl|tr|Q56RP2_DROPS (Q56RP2) Enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q5CRP8_CRYPV</td><td>>gnl|tr|Q5CRP8_CRYPV (Q5CRP8) Enolase (2-phosphoglycerate dehydratase) (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q5EFD8_TRIVA</td><td>>gnl|tr|Q5EFD8_TRIVA (Q5EFD8) Enolase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q5XXS5_9HEMI</td><td>>gnl|tr|Q5XXS5_9HEMI (Q5XXS5) Enolase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q6A4N1_CAEEL</td><td>>gnl|tr|Q6A4N1_CAEEL (Q6A4N1) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q6JKT2_9EUKA</td><td>>gnl|tr|Q6JKT2_9EUKA (Q6JKT2) Enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q6JKT3_9EUKA</td><td>>gnl|tr|Q6JKT3_9EUKA (Q6JKT3) Enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q6JKT4_9EUKA</td><td>>gnl|tr|Q6JKT4_9EUKA (Q6JKT4) Enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q6JKT5_9EUKA</td><td>>gnl|tr|Q6JKT5_9EUKA (Q6JKT5) Enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q6JKT6_9EUKA</td><td>>gnl|tr|Q6JKT6_9EUKA (Q6JKT6) Enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q6JKT7_9EUKA</td><td>>gnl|tr|Q6JKT7_9EUKA (Q6JKT7) Enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q6JKT8_9EUKA</td><td>>gnl|tr|Q6JKT8_9EUKA (Q6JKT8) Enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q6JKT9_9EUKA</td><td>>gnl|tr|Q6JKT9_9EUKA (Q6JKT9) Enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q6JKU0_9EUKA</td><td>>gnl|tr|Q6JKU0_9EUKA (Q6JKU0) Enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q6WP07_9EUKA</td><td>>gnl|tr|Q6WP07_9EUKA (Q6WP07) Enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q6WP08_TRIFO</td><td>>gnl|tr|Q6WP08_TRIFO (Q6WP08) Enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q76DW2_9EUKA</td><td>>gnl|tr|Q76DW2_9EUKA (Q76DW2) Enolase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q7YZX3_ONCVO</td><td>>gnl|tr|Q7YZX3_ONCVO (Q7YZX3) Enolase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q8MU59_ANISI</td><td>>gnl|tr|Q8MU59_ANISI (Q8MU59) Enolase (EC 4.2.1.11)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q8MVR9_CLOSI</td><td>>gnl|tr|Q8MVR9_CLOSI (Q8MVR9) Enolase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q8WP40_GIALA</td><td>>gnl|tr|Q8WP40_GIALA (Q8WP40) Enolase (EC 4.2.1.11)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q95WA8_9HYMN</td><td>>gnl|tr|Q95WA8_9HYMN (Q95WA8) Enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q95WA9_TETTH</td><td>>gnl|tr|Q95WA9_TETTH (Q95WA9) Enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q95WB0_9HYMN</td><td>>gnl|tr|Q95WB0_9HYMN (Q95WB0) Enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q95WB1_PARTE</td><td>>gnl|tr|Q95WB1_PARTE (Q95WB1) Enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q967M9_9CUCU</td><td>>gnl|tr|Q967M9_9CUCU (Q967M9) Enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q967N8_9CUCU</td><td>>gnl|tr|Q967N8_9CUCU (Q967N8) Enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
</table>

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q967U0_TRISP	>gnl|tr|Q967U0_TRISP (Q967U0) Enolase			x
Q9NDF5_9TRYP	>gnl|tr|Q9NDF5_9TRYP (Q9NDF5) Enolase (EC 4.2.1.11) (Fragment)			x
Q9NDF6_TRIVA	>gnl|tr|Q9NDF6_TRIVA (Q9NDF6) Enolase 5 (EC 4.2.1.11) (Fragment)			x
Q9NDF7_TRIVA	>gnl|tr|Q9NDF7_TRIVA (Q9NDF7) Enolase 4 (EC 4.2.1.11) (Fragment)			x
Q9NDF8_TRIVA	>gnl|tr|Q9NDF8_TRIVA (Q9NDF8) Enolase 3 (EC 4.2.1.11) (Fragment)			x
Q9NDF9_TRIVA	>gnl|tr|Q9NDF9_TRIVA (Q9NDF9) Enolase 2 (EC 4.2.1.11) (Fragment)			x
Q9NDG0_TRIVA	>gnl|tr|Q9NDG0_TRIVA (Q9NDG0) Enolase 1 (EC 4.2.1.11) (Fragment)			x
Q9NDG2_9EUKA	>gnl|tr|Q9NDG2_9EUKA (Q9NDG2) Enolase 2 (EC 4.2.1.11) (Fragment)			x
Q9NDH8_TRYBB	>gnl|tr|Q9NDH8_TRYBB (Q9NDH8) Enolase (EC 4.2.1.11)			x
Q9NG67_9HEXA	>gnl|tr|Q9NG67_9HEXA (Q9NG67) Enolase (Fragment)			x
Q9NG68_9MYRI	>gnl|tr|Q9NG68_9MYRI (Q9NG68) Enolase (Fragment)			x
Q9NG69_9MYRI	>gnl|tr|Q9NG69_9MYRI (Q9NG69) Enolase (Fragment)			x
Q5ISQ0_MACFA	>gnl|tr|Q5ISQ0_MACFA (Q5ISQ0) Enolase 2 (Fragment)			x
Q5R6Y1_PONPY	>gnl|tr|Q5R6Y1_PONPY (Q5R6Y1) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x
Q33AR3_ORYSA	>gnl|tr|Q33AR3_ORYSA (Q33AR3) Enolase			x
Q33AR4_ORYSA	>gnl|tr|Q33AR4_ORYSA (Q33AR4) Enolase			x
Q4H4A2_9DINO	>gnl|tr|Q4H4A2_9DINO (Q4H4A2) Enolase 3 (Fragment)			x
Q4H4A4_9DINO	>gnl|tr|Q4H4A4_9DINO (Q4H4A4) Enolase 3 (Fragment)			x
Q4H4A5_9DINO	>gnl|tr|Q4H4A5_9DINO (Q4H4A5) Enolase 2 (Fragment)			x
Q4H4A8_KARBR	>gnl|tr|Q4H4A8_KARBR (Q4H4A8) Enolase 3 (Fragment)			x
Q4H4B0_KARBR	>gnl|tr|Q4H4B0_KARBR (Q4H4B0) Enolase 3 (Fragment)			x
Q4H4B1_KARBR	>gnl|tr|Q4H4B1_KARBR (Q4H4B1) Enolase 2 (Fragment)			x
Q4H4B2_KARBR	>gnl|tr|Q4H4B2_KARBR (Q4H4B2) Enolase 2 (Fragment)			x
Q5UU97_HETTR	>gnl|tr|Q5UU97_HETTR (Q5UU97) Enolase 2 (Fragment)			x
Q5VNT9_ORYSA	>gnl|tr|Q5VNT9_ORYSA (Q5VNT9) Putative enolase			x
Q5WQL5_HETTR	>gnl|tr|Q5WQL5_HETTR (Q5WQL5) Enolase (Fragment)			x
Q5WQL6_9STRA	>gnl|tr|Q5WQL6_9STRA (Q5WQL6) Enolase (Fragment)			x
Q5WQL7_9EUKA	>gnl|tr|Q5WQL7_9EUKA (Q5WQL7) Enolase (Fragment)			x
Q5WQL8_9STRA	>gnl|tr|Q5WQL8_9STRA (Q5WQL8) Enolase (Fragment)			x
Q5WQL9_PHATR	>gnl|tr|Q5WQL9_PHATR (Q5WQL9) Enolase (Fragment)			x
Q5WQM1_ISOGA	>gnl|tr|Q5WQM1_ISOGA (Q5WQM1) Enolase (Fragment)			x

Table K-2. TrEMBL data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>Q5WQM2_9STRA</td><td>>gnl|tr|Q5WQM2_9STRA (Q5WQM2) Enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q5WQM3_9STRA</td><td>>gnl|tr|Q5WQM3_9STRA (Q5WQM3) Enolase 2 (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q5WQM4_9STRA</td><td>>gnl|tr|Q5WQM4_9STRA (Q5WQM4) Enolase 1 (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q6W7E7_BRANA</td><td>>gnl|tr|Q6W7E7_BRANA (Q6W7E7) Enolase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q6W7E8_BRACM</td><td>>gnl|tr|Q6W7E8_BRACM (Q6W7E8) Enolase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q6WB92_GOSBA</td><td>>gnl|tr|Q6WB92_GOSBA (Q6WB92) Enolase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q7XBE4_ORYSA</td><td>>gnl|tr|Q7XBE4_ORYSA (Q7XBE4) Enolase (EC 4.2.1.11)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q84RL9_DUNSA</td><td>>gnl|tr|Q84RL9_DUNSA (Q84RL9) Enolase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q8H716_PHYIN</td><td>>gnl|tr|Q8H716_PHYIN (Q8H716) Enolase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q8LM12_ORYSA</td><td>>gnl|tr|Q8LM12_ORYSA (Q8LM12) Putative enolase (2-phospho-D-glycerate hydroylase)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q8RWM8_ARATH</td><td>>gnl|tr|Q8RWM8_ARATH (Q8RWM8) Enolase (2-phospho-D-glycerate hydroylase)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q8VYG4_ARATH</td><td>>gnl|tr|Q8VYG4_ARATH (Q8VYG4) Putative enolase (2-phospho-D-glycerate hydroylase)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q947A0_PRILA</td><td>>gnl|tr|Q947A0_PRILA (Q947A0) Enolase 2 (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q947A1_PRILA</td><td>>gnl|tr|Q947A1_PRILA (Q947A1) Enolase 1 (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q947A2_9FLOR</td><td>>gnl|tr|Q947A2_9FLOR (Q947A2) Enolase 2 (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q947A3_9FLOR</td><td>>gnl|tr|Q947A3_9FLOR (Q947A3) Enolase 1 (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q9C9C4_ARATH</td><td>>gnl|tr|Q9C9C4_ARATH (Q9C9C4) Putative enolase; 31277-33713 (Putative enolase)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q9LEE0_SPIOL</td><td>>gnl|tr|Q9LEE0_SPIOL (Q9LEE0) Enolase (EC 4.2.1.11)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q9LEK6_EUGGR</td><td>>gnl|tr|Q9LEK6_EUGGR (Q9LEK6) Chloroplast enolase precursor (EC 4.2.1.11) (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q9LEK7_EUGGR</td><td>>gnl|tr|Q9LEK7_EUGGR (Q9LEK7) Enolase (EC 4.2.1.11)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q9M434_LUPLU</td><td>>gnl|tr|Q9M434_LUPLU (Q9M434) Enolase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q9ZW34_ARATH</td><td>>gnl|tr|Q9ZW34_ARATH (Q9ZW34) Putative enolase 2-phospho-D-glycerate hydroylase (2-phospho-D-glycerate hydroylase)</td><td></td><td></td><td>X</td></tr>
<tr><td>Q2RLT8_MOOTH</td><td>>gnl|tr|Q2RLT8_MOOTH (Q2RLT8) Enolase (EC 4.2.1.11)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q2SKX0_9GAMM</td><td>>gnl|tr|Q2SKX0_9GAMM (Q2SKX0) Enolase (EC 4.2.1.11)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q2SSR3_MYCCA</td><td>>gnl|tr|Q2SSR3_MYCCA (Q2SSR3) Enolase (EC 4.2.1.11)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q2SXC5_BURTH</td><td>>gnl|tr|Q2SXC5_BURTH (Q2SXC5) Enolase (EC 4.2.1.11)</td><td></td><td></td><td>x</td></tr>
</table>

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q2W698_MAGSA	>gnl|tr|Q2W698_MAGSA (Q2W698) Enolase			x
Q2WQ80_CLOBE	>gnl|tr|Q2WQ80_CLOBE (Q2WQ80) Enolase			x
Q2X6H4_9GAMM	>gnl|tr|Q2X6H4_9GAMM (Q2X6H4) Enolase (EC 4.2.1.11)			x
Q2XF58_PSEPU	>gnl|tr|Q2XF58_PSEPU (Q2XF58) Enolase			x
Q2XG84_PSEPU	>gnl|tr|Q2XG84_PSEPU (Q2XG84) Enolase			x
Q2XUR0_CORGL	>gnl|tr|Q2XUR0_CORGL (Q2XUR0) Enolase			x
Q2Y9P0_NITMU	>gnl|tr|Q2Y9P0_NITMU (Q2Y9P0) Enolase (EC 4.2.1.11)			x
Q2YSE8_STAAB	>gnl|tr|Q2YSE8_STAAB (Q2YSE8) Enolase 2-phosphoglycerate dehydratase (EC 4.2.1.11)			x
Q2Z3H6_9GAMM	>gnl|tr|Q2Z3H6_9GAMM (Q2Z3H6) Enolase (EC 4.2.1.11)			x
Q2ZQF5_SHEPU	>gnl|tr|Q2ZQF5_SHEPU (Q2ZQF5) Enolase (EC 4.2.1.11)			x
Q302C2_STRSU	>gnl|tr|Q302C2_STRSU (Q302C2) Enolase (EC 4.2.1.11) (Fragment)			x
Q316Q0_DESDG	>gnl|tr|Q316Q0_DESDG (Q316Q0) Enolase (EC 4.2.1.11)			x
Q31CX3_PROM9	>gnl|tr|Q31CX3_PROM9 (Q31CX3) Enolase (EC 4.2.1.11)			x
Q31G68_THICR	>gnl|tr|Q31G68_THICR (Q31G68) Enolase (EC 4.2.1.11)			x
Q31QJ8_SYNP7	>gnl|tr|Q31QJ8_SYNP7 (Q31QJ8) Enolase (EC 4.2.1.11)			x
Q31XL1_SHIBS	>gnl|tr|Q31XL1_SHIBS (Q31XL1) Enolase			x
Q32CD6_SHIDS	>gnl|tr|Q32CD6_SHIDS (Q32CD6) Enolase			x
Q33Y02_9GAMM	>gnl|tr|Q33Y02_9GAMM (Q33Y02) Enolase (EC 4.2.1.11)			x
Q34CZ0_RHOPA	>gnl|tr|Q34CZ0_RHOPA (Q34CZ0) Enolase			x
Q34UX9_9GAMM	>gnl|tr|Q34UX9_9GAMM (Q34UX9) Enolase (EC 4.2.1.11)			x
Q35JB8_9BRAD	>gnl|tr|Q35JB8_9BRAD (Q35JB8) Enolase (EC 4.2.1.11)			x
Q35US6_9GAMM	>gnl|tr|Q35US6_9GAMM (Q35US6) Enolase (EC 4.2.1.11)			x
Q36D71_9GAMM	>gnl|tr|Q36D71_9GAMM (Q36D71) Enolase (EC 4.2.1.11)			x
Q36RG6_MARHY	>gnl|tr|Q36RG6_MARHY (Q36RG6) Enolase			x
Q36Y92_RHOPA	>gnl|tr|Q36Y92_RHOPA (Q36Y92) Enolase (EC 4.2.1.11)			x
Q37IT6_RHOPA	>gnl|tr|Q37IT6_RHOPA (Q37IT6) Enolase (EC 4.2.1.11)			x
Q37RX0_SPHAR	>gnl|tr|Q37RX0_SPHAR (Q37RX0) Enolase (EC 4.2.1.11)			x
Q39T27_GEOMG	>gnl|tr|Q39T27_GEOMG (Q39T27) Enolase			x
Q3A578_PELCD	>gnl|tr|Q3A578_PELCD (Q3A578) Enolase			x
Q3AFC8_CARHZ	>gnl|tr|Q3AFC8_CARHZ (Q3AFC8) Enolase (EC 4.2.1.11)			x
Q3AGS4_SYNSC	>gnl|tr|Q3AGS4_SYNSC (Q3AGS4) Enolase (EC 4.2.1.11)			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q3ATQ5_CHLCH	>gnl|tr|Q3ATQ5_CHLCH (Q3ATQ5) Enolase (EC 4.2.1.11)			x
Q3AVW5_SYNS9	>gnl|tr|Q3AVW5_SYNS9 (Q3AVW5) Enolase (EC 4.2.1.11)			x
Q3B1G7_PELLD	>gnl|tr|Q3B1G7_PELLD (Q3B1G7) Enolase (EC 4.2.1.11)			x
Q3BUT0_XANC5	>gnl|tr|Q3BUT0_XANC5 (Q3BUT0) Enolase (EC 4.2.1.11)			x
Q3CFC7_THEET	>gnl|tr|Q3CFC7_THEET (Q3CFC7) Enolase (EC 4.2.1.11)			x
Q3CTJ0_ALTAT	>gnl|tr|Q3CTJ0_ALTAT (Q3CTJ0) Enolase (EC 4.2.1.11)			x
Q3D1D7_STRAG	>gnl|tr|Q3D1D7_STRAG (Q3D1D7) Enolase (EC 4.2.1.11)			x
Q3DFV3_STRAG	>gnl|tr|Q3DFV3_STRAG (Q3DFV3) Enolase (EC 4.2.1.11)			x
Q3DK41_STRAG	>gnl|tr|Q3DK41_STRAG (Q3DK41) Enolase (EC 4.2.1.11)			x
Q3DRQ3_STRAG	>gnl|tr|Q3DRQ3_STRAG (Q3DRQ3) Enolase (EC 4.2.1.11)			x
Q3E6B9_CHLAU	>gnl|tr|Q3E6B9_CHLAU (Q3E6B9) Enolase			x
Q3EMP6_BACTI	>gnl|tr|Q3EMP6_BACTI (Q3EMP6) Enolase (EC 4.2.1.11)			x
Q3F8V7_9BURK	>gnl|tr|Q3F8V7_9BURK (Q3F8V7) Enolase (EC 4.2.1.11)			x
Q3FSQ4_9BURK	>gnl|tr|Q3FSQ4_9BURK (Q3FSQ4) Enolase (EC 4.2.1.11)			x
Q3FZA1_9DELT	>gnl|tr|Q3FZA1_9DELT (Q3FZA1) Enolase (EC 4.2.1.11)			x
Q3GIP3_CHLVI	>gnl|tr|Q3GIP3_CHLVI (Q3GIP3) Enolase (EC 4.2.1.11)			x
Q3GKS6_9GAMM	>gnl|tr|Q3GKS6_9GAMM (Q3GKS6) Enolase (EC 4.2.1.11)			x
Q3GWD8_9ACTO	>gnl|tr|Q3GWD8_9ACTO (Q3GWD8) Enolase (EC 4.2.1.11)			x
Q3HGQ2_TRIER	>gnl|tr|Q3HGQ2_TRIER (Q3HGQ2) Enolase (EC 4.2.1.11)			x
Q3IDM2_PSEHT	>gnl|tr|Q3IDM2_PSEHT (Q3IDM2) Enolase (EC 4.2.1.11)			x
Q3J3H9_RHOS4	>gnl|tr|Q3J3H9_RHOS4 (Q3J3H9) Enolase (EC 4.2.1.11)			x
Q3K2B2_STRA1	>gnl|tr|Q3K2B2_STRA1 (Q3K2B2) Enolase (EC 4.2.1.11)			x
Q3KLB0_CHLTA	>gnl|tr|Q3KLB0_CHLTA (Q3KLB0) Enolase (EC 4.2.1.11)			x
Q3LFH6_PROFR	>gnl|tr|Q3LFH6_PROFR (Q3LFH6) Enolase 2 (EC 4.2.1.11)			x
Q3LFH7_PROFR	>gnl|tr|Q3LFH7_PROFR (Q3LFH7) Enolase 1 (EC 4.2.1.11)			x
Q3M7B2_ANAVT	>gnl|tr|Q3M7B2_ANAVT (Q3M7B2) Enolase (EC 4.2.1.11)			x
Q3MZ86_9DELT	>gnl|tr|Q3MZ86_9DELT (Q3MZ86) Enolase (EC 4.2.1.11)			x
Q3ND54_9PROT	>gnl|tr|Q3ND54_9PROT (Q3ND54) Enolase (EC 4.2.1.11)			x
Q3NL87_SHEFR	>gnl|tr|Q3NL87_SHEFR (Q3NL87) Enolase (EC 4.2.1.11)			x
Q3P3W1_9GAMM	>gnl|tr|Q3P3W1_9GAMM (Q3P3W1) Enolase (EC 4.2.1.11)			x
Q3PK04_PARDE	>gnl|tr|Q3PK04_PARDE (Q3PK04) Enolase (EC 4.2.1.11)			x
Q3PU04_NITHA	>gnl|tr|Q3PU04_NITHA (Q3PU04) Enolase (EC 4.2.1.11)			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q3Q3U6_9GAMM	>gnl|tr|Q3Q3U6_9GAMM (Q3Q3U6) Enolase (EC 4.2.1.11)			x
Q3QH16_9GAMM	>gnl|tr|Q3QH16_9GAMM (Q3QH16) Enolase (EC 4.2.1.11)			x
Q3QVK8_9RHOB	>gnl|tr|Q3QVK8_9RHOB (Q3QVK8) Enolase (EC 4.2.1.11)			x
Q3R8C7_XYLFA	>gnl|tr|Q3R8C7_XYLFA (Q3R8C7) Enolase (EC 4.2.1.11)			x
Q3RGV0_XYLFA	>gnl|tr|Q3RGV0_XYLFA (Q3RGV0) Enolase (EC 4.2.1.11)			x
Q3RVQ1_RALME	>gnl|tr|Q3RVQ1_RALME (Q3RVQ1) Enolase (EC 4.2.1.11)			x
Q3RW22_RALME	>gnl|tr|Q3RW22_RALME (Q3RW22) Enolase (EC 4.2.1.11)			x
Q3SL43_THIDA	>gnl|tr|Q3SL43_THIDA (Q3SL43) Enolase (Phosphopyruvate hydratase) (EC 4.2.1.11)			x
Q3SRK4_NITWN	>gnl|tr|Q3SRK4_NITWN (Q3SRK4) Enolase (EC 4.2.1.11)			x
Q3VBY9_9SPHN	>gnl|tr|Q3VBY9_9SPHN (Q3VBY9) Enolase (EC 4.2.1.11)			x
Q3VI98_9CHLB	>gnl|tr|Q3VI98_9CHLB (Q3VI98) Enolase (EC 4.2.1.11)			x
Q3VWM9_PROAE	>gnl|tr|Q3VWM9_PROAE (Q3VWM9) Enolase (EC 4.2.1.11)			x
Q3W1G4_9ACTO	>gnl|tr|Q3W1G4_9ACTO (Q3W1G4) Enolase (EC 4.2.1.11)			x
Q3WWV7_9RHIZ	>gnl|tr|Q3WWV7_9RHIZ (Q3WWV7) Enolase (EC 4.2.1.11)			x
Q3X3P9_9ACTN	>gnl|tr|Q3X3P9_9ACTN (Q3X3P9) Enolase (EC 4.2.1.11)			x
Q3XBL7_METFL	>gnl|tr|Q3XBL7_METFL (Q3XBL7) Enolase (EC 4.2.1.11)			x
Q3XPP9_9PROT	>gnl|tr|Q3XPP9_9PROT (Q3XPP9) Enolase (EC 4.2.1.11)			x
Q3XX08_ENTFC	>gnl|tr|Q3XX08_ENTFC (Q3XX08) Enolase (EC 4.2.1.11)			x
Q3YRX9_EHRCJ	>gnl|tr|Q3YRX9_EHRCJ (Q3YRX9) Enolase (EC 4.2.1.11)			x
Q3YY77_SHISS	>gnl|tr|Q3YY77_SHISS (Q3YY77) Enolase			x
Q3Z8W4_DEHE1	>gnl|tr|Q3Z8W4_DEHE1 (Q3Z8W4) Enolase (EC 4.2.1.11)			x
Q3ZX11_DEHSC	>gnl|tr|Q3ZX11_DEHSC (Q3ZX11) Enolase (EC 4.2.1.11)			x
Q40BD7_9RHOB	>gnl|tr|Q40BD7_9RHOB (Q40BD7) Enolase (EC 4.2.1.11)			x
Q40JH5_EHRCH	>gnl|tr|Q40JH5_EHRCH (Q40JH5) Enolase (EC 4.2.1.11)			x
Q40LS9_DESAC	>gnl|tr|Q40LS9_DESAC (Q40LS9) Enolase (EC 4.2.1.11)			x
Q415I2_KINRA	>gnl|tr|Q415I2_KINRA (Q415I2) Enolase (EC 4.2.1.11)			x
Q41AA9_9BACI	>gnl|tr|Q41AA9_9BACI (Q41AA9) Enolase (EC 4.2.1.11)			x
Q421L5_DESHA	>gnl|tr|Q421L5_DESHA (Q421L5) Enolase (EC 4.2.1.11)			x
Q438Q7_9ACTO	>gnl|tr|Q438Q7_9ACTO (Q438Q7) Enolase (EC 4.2.1.11)			x
Q43J81_9CHLB	>gnl|tr|Q43J81_9CHLB (Q43J81) Enolase (EC 4.2.1.11)			x
Q43KU5_SOLUS	>gnl|tr|Q43KU5_SOLUS (Q43KU5) Enolase (EC 4.2.1.11)			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q44G15_CHRSL	>gnl|tr|Q44G15_CHRSL (Q44G15) Enolase (EC 4.2.1.11)			x
Q44T71_CHLLI	>gnl|tr|Q44T71_CHLLI (Q44T71) Enolase (EC 4.2.1.11)			x
Q457U5_9BURK	>gnl|tr|Q457U5_9BURK (Q457U5) Enolase (EC 4.2.1.11)			x
Q45RT9_BIFAN	>gnl|tr|Q45RT9_BIFAN (Q45RT9) Alpha-enolase			x
Q46HG5_PROMT	>gnl|tr|Q46HG5_PROMT (Q46HG5) Enolase (EC 4.2.1.11)			x
Q473G4_RALEJ	>gnl|tr|Q473G4_RALEJ (Q473G4) Enolase (EC 4.2.1.11)			x
Q47DI1_DECAR	>gnl|tr|Q47DI1_DECAR (Q47DI1) Enolase			x
Q47SV1_THEFY	>gnl|tr|Q47SV1_THEFY (Q47SV1) Enolase (EC 4.2.1.11)			x
Q47WR1_COLP3	>gnl|tr|Q47WR1_COLP3 (Q47WR1) Enolase (EC 4.2.1.11)			x
Q48F79_PSE14	>gnl|tr|Q48F79_PSE14 (Q48F79) Enolase (EC 4.2.1.11)			x
Q48UF7_STRPM	>gnl|tr|Q48UF7_STRPM (Q48UF7) Enolase (EC 4.2.1.11)			x
Q493N5_BLOPB	>gnl|tr|Q493N5_BLOPB (Q493N5) Enolase			x
Q49W03_STAS1	>gnl|tr|Q49W03_STAS1 (Q49W03) Enolase			x
Q4A740_MYCS5	>gnl|tr|Q4A740_MYCS5 (Q4A740) Enolase (EC 4.2.1.11)			x
Q4A8B5_MYCH7	>gnl|tr|Q4A8B5_MYCH7 (Q4A8B5) Enolase (EC 4.2.1.11)			x
Q4AA88_MYCHJ	>gnl|tr|Q4AA88_MYCHJ (Q4AA88) Enolase (EC 4.2.1.11)			x
Q4AFG0_9CHLB	>gnl|tr|Q4AFG0_9CHLB (Q4AFG0) Enolase (EC 4.2.1.11)			x
Q4AJ21_9CHLB	>gnl|tr|Q4AJ21_9CHLB (Q4AJ21) Enolase (EC 4.2.1.11)			x
Q4ARP8_9BURK	>gnl|tr|Q4ARP8_9BURK (Q4ARP8) Enolase (EC 4.2.1.11)			x
Q4B7M9_BURVI	>gnl|tr|Q4B7M9_BURVI (Q4B7M9) Enolase (EC 4.2.1.11)			x
Q4BXE8_CROWT	>gnl|tr|Q4BXE8_CROWT (Q4BXE8) Enolase (EC 4.2.1.11)			x
Q4EBA7_9RICK	>gnl|tr|Q4EBA7_9RICK (Q4EBA7) Enolase (EC 4.2.1.11)			x
Q4EEP6_LISMO	>gnl|tr|Q4EEP6_LISMO (Q4EEP6) Enolase (EC 4.2.1.11)			x
Q4FM37_PELUB	>gnl|tr|Q4FM37_PELUB (Q4FM37) Enolase (EC 4.2.1.11)			x
Q4FR74_PSYAR	>gnl|tr|Q4FR74_PSYAR (Q4FR74) Enolase (EC 4.2.1.11)			x
Q4H8Q9_9DEIO	>gnl|tr|Q4H8Q9_9DEIO (Q4H8Q9) Enolase (EC 4.2.1.11)			x
Q4HE43_CAMCO	>gnl|tr|Q4HE43_CAMCO (Q4HE43) Enolase (EC 4.2.1.11)			x
Q4HLW3_CAMLA	>gnl|tr|Q4HLW3_CAMLA (Q4HLW3) Enolase (EC 4.2.1.11)			x
Q4HR03_CAMUP	>gnl|tr|Q4HR03_CAMUP (Q4HR03) Enolase (EC 4.2.1.11)			x
Q4IUV7_AZOVI	>gnl|tr|Q4IUV7_AZOVI (Q4IUV7) Enolase precursor (EC 4.2.1.11)			x
Q4IV38_AZOVI	>gnl|tr|Q4IV38_AZOVI (Q4IV38) Enolase (EC 4.2.1.11)			x
Q4IXV2_AZOVI	>gnl|tr|Q4IXV2_AZOVI (Q4IXV2) Enolase (EC 4.2.1.11)			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q4J257_AZOVI	>gnl|tr|Q4J257_AZOVI (Q4J257) Enolase (EC 4.2.1.11)			x
Q4LMD0_9BURK	>gnl|tr|Q4LMD0_9BURK (Q4LMD0) Enolase (EC 4.2.1.11)			x
Q4MQ53_BACCE	>gnl|tr|Q4MQ53_BACCE (Q4MQ53) Enolase (EC 4.2.1.11)			x
Q4NII0_9MICC	>gnl|tr|Q4NII0_9MICC (Q4NII0) Enolase (EC 4.2.1.11)			x
Q4NT46_9DELT	>gnl|tr|Q4NT46_9DELT (Q4NT46) Enolase (EC 4.2.1.11)			x
Q4UTP2_XANC8	>gnl|tr|Q4UTP2_XANC8 (Q4UTP2) Enolase			x
Q4ZWE0_PSEU2	>gnl|tr|Q4ZWE0_PSEU2 (Q4ZWE0) Enolase (EC 4.2.1.11)			x
Q4ZWQ8_PSEU2	>gnl|tr|Q4ZWQ8_PSEU2 (Q4ZWQ8) Enolase (EC 4.2.1.11)			x
Q58WU7_9BACT	>gnl|tr|Q58WU7_9BACT (Q58WU7) Enolase			x
Q5K117_9LACO	>gnl|tr|Q5K117_9LACO (Q5K117) Alpha-enolase (EC 4.2.1.11)			x
Q5NJY7_LACPL	>gnl|tr|Q5NJY7_LACPL (Q5NJY7) Enolase (EC 4.2.1.11)			x
Q5NJZ3_LACSK	>gnl|tr|Q5NJZ3_LACSK (Q5NJZ3) Enolase			x
Q6SET0_9BACT	>gnl|tr|Q6SET0_9BACT (Q6SET0) Enolase (EC 4.2.1.11)			x
Q6SGG1_9BACT	>gnl|tr|Q6SGG1_9BACT (Q6SGG1) Enolase (EC 4.2.1.11)			x
Q7P791_FUSNV	>gnl|tr|Q7P791_FUSNV (Q7P791) Enolase (EC 4.2.1.11)			x
Q845Q5_9STRE	>gnl|tr|Q845Q5_9STRE (Q845Q5) Enolase			x
Q84FY9_METEX	>gnl|tr|Q84FY9_METEX (Q84FY9) Enolase			x
Q8GDZ5_HELMO	>gnl|tr|Q8GDZ5_HELMO (Q8GDZ5) Enolase (EC 4.2.1.11) (Fragment)			x
Q8RP81_STRAG	>gnl|tr|Q8RP81_STRAG (Q8RP81) Enolase			x
Q935W7_STRPN	>gnl|tr|Q935W7_STRPN (Q935W7) Alpha-enolase			x
Q2NAQ1_9SPHN	>gnl|tr|Q2NAQ1_9SPHN (Q2NAQ1) Enolase			x
Q2NJ39_9MOLU	>gnl|tr|Q2NJ39_9MOLU (Q2NJ39) Enolase (EC 4.2.1.11)			x
Q2NVN7_SODGL	>gnl|tr|Q2NVN7_SODGL (Q2NVN7) Enolase			x
Q2P1K8_XANOR	>gnl|tr|Q2P1K8_XANOR (Q2P1K8) Enolase			x
Q4KHF6_PSEF5	>gnl|tr|Q4KHF6_PSEF5 (Q4KHF6) Enolase (EC 4.2.1.11)			x
Q4L4K7_STAHJ	>gnl|tr|Q4L4K7_STAHJ (Q4L4K7) Enolase			x
Q4QLX6_HAEI8	>gnl|tr|Q4QLX6_HAEI8 (Q4QLX6) Enolase (EC 4.2.1.11)			x
Q57D07_BRUAB	>gnl|tr|Q57D07_BRUAB (Q57D07) Enolase			x
Q57KH0_SALCH	>gnl|tr|Q57KH0_SALCH (Q57KH0) Enolase			x
Q5FH95_EHRRG	>gnl|tr|Q5FH95_EHRRG (Q5FH95) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x
Q5GTG4_WOLTR	>gnl|tr|Q5GTG4_WOLTR (Q5GTG4) Enolase			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q5L4S5_CHLAB	>gnl|tr|Q5L4S5_CHLAB (Q5L4S5) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x
Q5LG64_BACFN	>gnl|tr|Q5LG64_BACFN (Q5LG64) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x
Q5PAS6_ANAMM	>gnl|tr|Q5PAS6_ANAMM (Q5PAS6) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x
Q2YPV0_BRUA2	>gnl|tr|Q2YPV0_BRUA2 (Q2YPV0) Enolase (EC 4.2.1.11)			x
Q5HB46_EHRRW	>gnl|tr|Q5HB46_EHRRW (Q5HB46) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x
Q65EN2_BACLD	>gnl|tr|Q65EN2_BACLD (Q65EN2) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x
Q3UJ20_MOUSE	>gnl|tr|Q3UJ20_MOUSE (Q3UJ20) 17 days embryo heart cDNA, RIKEN full-length enriched library, clone:I920038O04 product:enolase 2, gamma neuronal, full insert sequence			x
Q545V3_MOUSE	>gnl|tr|Q545V3_MOUSE (Q545V3) Adult male brain cDNA, RIKEN full-length enriched library, clone:0710008M22 product:enolase 2, gamma neuronal, full insert sequence (Adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1520403G13 product:enolase 2,			x
Q5EB49_RAT	>gnl|tr|Q5EB49_RAT (Q5EB49) Enolase 1, alpha			x
Q5FW97_MOUSE	>gnl|tr|Q5FW97_MOUSE (Q5FW97) Hypothetical protein LOC433182 (Melanocyte cDNA, RIKEN full-length enriched library, clone:G270128I15 product:enolase 1, alpha non-neuron, full insert sequence) (Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone			x
Q5SX58_MOUSE	>gnl|tr|Q5SX58_MOUSE (Q5SX58) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x
Q5XIV3_RAT	>gnl|tr|Q5XIV3_RAT (Q5XIV3) Enolase 3, beta			x
Q568G3_BRARE	>gnl|tr|Q568G3_BRARE (Q568G3) Enolase 3, (Beta, muscle)			x
Q6GQM9_BRARE	>gnl|tr|Q6GQM9_BRARE (Q6GQM9) Enolase 2			x
Q6IQP5_BRARE	>gnl|tr|Q6IQP5_BRARE (Q6IQP5) Enolase 1, (Alpha)			x
Q6P8E1_XENTR	>gnl|tr|Q6P8E1_XENTR (Q6P8E1) Enolase (2-phosphoglycerate dehydratase)			x
Q6PC12_BRARE	>gnl|tr|Q6PC12_BRARE (Q6PC12) Enolase 1, (Alpha)			x
Q6TH14_BRARE	>gnl|tr|Q6TH14_BRARE (Q6TH14) Enolase 1, (Alpha)			x

Table K-2. TrEMBL data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>Q8JFE0_CROPL</td><td>>gnl|tr|Q8JFE0_CROPL (Q8JFE0) Tau-crystallin protein (Alpha-enolase)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q9DDG6_SALTR</td><td>>gnl|tr|Q9DDG6_SALTR (Q9DDG6) Alpha-2 enolase-1 (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q9DDG7_SALTR</td><td>>gnl|tr|Q9DDG7_SALTR (Q9DDG7) Alpha-1 enolase-1 (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q9DDG8_CHIPU</td><td>>gnl|tr|Q9DDG8_CHIPU (Q9DDG8) Beta enolase-1 (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q9DDG9_CHIPU</td><td>>gnl|tr|Q9DDG9_CHIPU (Q9DDG9) Alpha enolase-1 (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q9DDH0_NEOFS</td><td>>gnl|tr|Q9DDH0_NEOFS (Q9DDH0) Beta enolase-1 (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q9DDH1_LEPPA</td><td>>gnl|tr|Q9DDH1_LEPPA (Q9DDH1) Beta enolase-1 (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q9DDH4_LATCH</td><td>>gnl|tr|Q9DDH4_LATCH (Q9DDH4) Alpha enolase-1 (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q9DDH5_AMICA</td><td>>gnl|tr|Q9DDH5_AMICA (Q9DDH5) Beta enolase-1 (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q9DDH6_AMICA</td><td>>gnl|tr|Q9DDH6_AMICA (Q9DDH6) Alpha enolase-1 (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q9PTX5_LAMRE</td><td>>gnl|tr|Q9PTX5_LAMRE (Q9PTX5) Enolase-2 (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q9PTX6_LAMRE</td><td>>gnl|tr|Q9PTX6_LAMRE (Q9PTX6) Enolase-1 (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q9U5F7_EPTBU</td><td>>gnl|tr|Q9U5F7_EPTBU (Q9U5F7) Enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q9W6C9_CAICR</td><td>>gnl|tr|Q9W6C9_CAICR (Q9W6C9) Alpha enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q9W6D0_SPHPU</td><td>>gnl|tr|Q9W6D0_SPHPU (Q9W6D0) Alpha enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q9W6D1_EUMIN</td><td>>gnl|tr|Q9W6D1_EUMIN (Q9W6D1) Alpha enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q9W6D2_TRASC</td><td>>gnl|tr|Q9W6D2_TRASC (Q9W6D2) Alpha enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q9W6D3_9SAUR</td><td>>gnl|tr|Q9W6D3_9SAUR (Q9W6D3) Alpha enolase (Fragment)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q41RU7_FERAC</td><td>>gnl|tr|Q41RU7_FERAC (Q41RU7) Phosphopyruvate hydratase (EC 4.2.1.11)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q468E2_METBA</td><td>>gnl|tr|Q468E2_METBA (Q468E2) Phosphopyruvate hydratase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q5KLA7_CRYNE</td><td>>gnl|tr|Q5KLA7_CRYNE (Q5KLA7) Phosphopyruvate hydratase, putative</td><td></td><td></td><td>x</td></tr>
<tr><td>O96656_PENMO</td><td>>gnl|tr|O96656_PENMO (O96656) Phosphopyruvate hydratase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q54RK5_DICDI</td><td>>gnl|tr|Q54RK5_DICDI (Q54RK5) Phosphopyruvate hydratase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q55F83_DICDI</td><td>>gnl|tr|Q55F83_DICDI (Q55F83) Phosphopyruvate hydratase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q2RT60_RHORU</td><td>>gnl|tr|Q2RT60_RHORU (Q2RT60) Phosphopyruvate hydratase (EC 4.2.1.11)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q2S4F8_9SPHI</td><td>>gnl|tr|Q2S4F8_9SPHI (Q2S4F8) Phosphopyruvate hydratase (EC 4.2.1.11)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q30P06_THIDN</td><td>>gnl|tr|Q30P06_THIDN (Q30P06) Phosphopyruvate hydratase (EC 4.2.1.11)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q34LT3_RHOPA</td><td>>gnl|tr|Q34LT3_RHOPA (Q34LT3) Phosphopyruvate hydratase (EC 4.2.1.11)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q38Y18_LACSS</td><td>>gnl|tr|Q38Y18_LACSS (Q38Y18) Phosphopyruvate hydratase (EC 4.2.1.11)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q39EV9_BURS3</td><td>>gnl|tr|Q39EV9_BURS3 (Q39EV9) Phosphopyruvate hydratase (EC 4.2.1.11)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q3JCT1_NITOC</td><td>>gnl|tr|Q3JCT1_NITOC (Q3JCT1) Phosphopyruvate hydratase (EC 4.2.1.11)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q3JQQ6_BURP1</td><td>>gnl|tr|Q3JQQ6_BURP1 (Q3JQQ6) Phosphopyruvate hydratase (EC 4.2.1.11)</td><td></td><td></td><td>x</td></tr>
</table>

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q3KH92_PSEPF	>gnl|tr|Q3KH92_PSEPF (Q3KH92) Phosphopyruvate hydratase (EC 4.2.1.11)			x
Q6QWP3_9SCOR	>gnl|tr|Q6QWP3_9SCOR (Q6QWP3) 2-phospho-D-glycerate hydrolase (Fragment)			x
Q6QWP4_9CRUS	>gnl|tr|Q6QWP4_9CRUS (Q6QWP4) 2-phospho-D-glycerate hydrolase (Fragment)			x
Q6QWP5_9ANNE	>gnl|tr|Q6QWP5_9ANNE (Q6QWP5) 2-phospho-D-glycerate hydrolase (Fragment)			x
Q6QWP6_CALSI	>gnl|tr|Q6QWP6_CALSI (Q6QWP6) 2-phospho-D-glycerate hydrolase (Fragment)			x
Q6QWP7_9CRUS	>gnl|tr|Q6QWP7_9CRUS (Q6QWP7) 2-phospho-D-glycerate hydrolase (Fragment)			x
Q6QWP8_9CRUS	>gnl|tr|Q6QWP8_9CRUS (Q6QWP8) 2-phospho-D-glycerate hydrolase (Fragment)			x
Q6QWP9_LIMPO	>gnl|tr|Q6QWP9_LIMPO (Q6QWP9) 2-phospho-D-glycerate hydrolase (Fragment)			x
Q6QWQ0_9ARAC	>gnl|tr|Q6QWQ0_9ARAC (Q6QWQ0) 2-phospho-D-glycerate hydrolase (Fragment)			x
Q6QWQ1_9MYRI	>gnl|tr|Q6QWQ1_9MYRI (Q6QWQ1) 2-phospho-D-glycerate hydrolase (Fragment)			x
Q6QWQ2_9MYRI	>gnl|tr|Q6QWQ2_9MYRI (Q6QWQ2) 2-phospho-D-glycerate hydrolase (Fragment)			x
Q7XAS6_CYNDA	>gnl|tr|Q7XAS6_CYNDA (Q7XAS6) Pollen 2-phosphoglycerate dehydrogenase 2			x
Q8VVB4_STRTR	>gnl|tr|Q8VVB4_STRTR (Q8VVB4) 2-phosphoglycerate dehydratase			x
Q4JU51_CORJK	>gnl|tr|Q4JU51_CORJK (Q4JU51) Eno protein (EC 4.2.1.11)			x
Q3BUN6_XANC5	>gnl|tr|Q3BUN6_XANC5 (Q3BUN6) Galactonate dehydratase (EC 4.2.1.6)			x
Q48K93_PSE14	>gnl|tr|Q48K93_PSE14 (Q48K93) Galactonate dehydratase (EC 4.2.1.6)			x
Q57I11_SALCH	>gnl|tr|Q57I11_SALCH (Q57I11) Galactonate dehydratase			x
Q5KYJ6_GEOKA	>gnl|tr|Q5KYJ6_GEOKA (Q5KYJ6) Galactonate dehydratase (EC 4.2.1.6)			x
Q5WKP1_BACSK	>gnl|tr|Q5WKP1_BACSK (Q5WKP1) Galactonate dehydratase (EC 4.2.1.6)			x
Q63X38_BURPS	>gnl|tr|Q63X38_BURPS (Q63X38) Putative galactonate dehydratase protein			x
Q7MC07_VIBVY	>gnl|tr|Q7MC07_VIBVY (Q7MC07) Probable galactonate dehydratase protein			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q8XVS8_RALSO	>gnl|tr|Q8XVS8_RALSO (Q8XVS8) PUTATIVE GALACTONATE DEHYDRATASE PROTEIN (EC 4.2.1.6)			x
Q92W53_RHIME	>gnl|tr|Q92W53_RHIME (Q92W53) Probable galactonate dehydratase protein (EC 4.2.1.6)			x
Q2T252_BURTH	>gnl|tr|Q2T252_BURTH (Q2T252) Glucarate dehydratase (EC 4.2.1.40)			x
Q35KA8_9BRAD	>gnl|tr|Q35KA8_9BRAD (Q35KA8) Glucarate dehydratase (EC 4.2.1.40)			x
Q39KL8_BURS3	>gnl|tr|Q39KL8_BURS3 (Q39KL8) Glucarate dehydratase (EC 4.2.1.40)			x
Q3EIQ9_ACTSC	>gnl|tr|Q3EIQ9_ACTSC (Q3EIQ9) Glucarate dehydratase (EC 4.2.1.40)			x
Q3F2Y9_9BURK	>gnl|tr|Q3F2Y9_9BURK (Q3F2Y9) Glucarate dehydratase (EC 4.2.1.40)			x
Q3RWP4_RALME	>gnl|tr|Q3RWP4_RALME (Q3RWP4) Glucarate dehydratase (EC 4.2.1.40)			x
Q44TQ7_9BURK	>gnl|tr|Q44TQ7_9BURK (Q44TQ7) Glucarate dehydratase (EC 4.2.1.40)			x
Q46UW1_RALEJ	>gnl|tr|Q46UW1_RALEJ (Q46UW1) Glucarate dehydratase (EC 4.2.1.40)			x
Q4AUW2_9BURK	>gnl|tr|Q4AUW2_9BURK (Q4AUW2) Glucarate dehydratase (EC 4.2.1.40)			x
Q4B8L5_BURVI	>gnl|tr|Q4B8L5_BURVI (Q4B8L5) Glucarate dehydratase (EC 4.2.1.40)			x
Q4LLI4_9BURK	>gnl|tr|Q4LLI4_9BURK (Q4LLI4) Glucarate dehydratase (EC 4.2.1.40)			x
Q4ZRS0_PSEU2	>gnl|tr|Q4ZRS0_PSEU2 (Q4ZRS0) Glucarate dehydratase (EC 4.2.1.40)			x
Q6D173_ERWCT	>gnl|tr|Q6D173_ERWCT (Q6D173) Glucarate dehydratase (EC 4.2.1.40)			x
Q6FFQ2_ACIAD	>gnl|tr|Q6FFQ2_ACIAD (Q6FFQ2) D-glucarate dehydratase (EC 4.2.1.40)			x
Q89HW7_BRAJA	>gnl|tr|Q89HW7_BRAJA (Q89HW7) Glucarate dehydratase (EC 4.2.1.40)			x
Q8EMK6_OCEIH	>gnl|tr|Q8EMK6_OCEIH (Q8EMK6) Glucarate dehydratase (EC 4.2.1.40)			x
Q8XRK2_RALSO	>gnl|tr|Q8XRK2_RALSO (Q8XRK2) PROBABLE GLUCARATE DEHYDRATASE PROTEIN (EC 4.2.1.40)			x
Q8Y0G5_RALSO	>gnl|tr|Q8Y0G5_RALSO (Q8Y0G5) PROBABLE GLUCARATE DEHYDRATASE PROTEIN (EC 4.2.1.40)			x
Q8Z443_SALTI	>gnl|tr|Q8Z443_SALTI (Q8Z443) Probable glucarate dehydratase 1 (EC 4.2.1.40)			x
Q8ZMD9_SALTY	>gnl|tr|Q8ZMD9_SALTY (Q8ZMD9) D-glucarate dehydratase (EC 4.2.1.40)			x
Q2X863_PSEPU	>gnl|tr|Q2X863_PSEPU (Q2X863) Glucarate dehydratase			x
Q31XK3_SHIBS	>gnl|tr|Q31XK3_SHIBS (Q31XK3) Putative glucarate dehydratase			x
Q3YY69_SHISS	>gnl|tr|Q3YY69_SHISS (Q3YY69) Putative glucarate dehydratase			x
Q4UY48_XANC8	>gnl|tr|Q4UY48_XANC8 (Q4UY48) Glucarate hydratase			x
Q57KF6_SALCH	>gnl|tr|Q57KF6_SALCH (Q57KF6) D-glucarate dehydratase			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q5PEJ1_SALPA	>gnl|tr|Q5PEJ1_SALPA (Q5PEJ1) Probable glucarate dehydratase 1			x
Q83QD4_SHIFL	>gnl|tr|Q83QD4_SHIFL (Q83QD4) Putative glucarate dehydratase			x
Q87ZY7_PSESM	>gnl|tr|Q87ZY7_PSESM (Q87ZY7) Glucarate dehydratase			x
Q88DR6_PSEPK	>gnl|tr|Q88DR6_PSEPK (Q88DR6) Glucarate dehydratase			x
Q8P5U3_XANCP	>gnl|tr|Q8P5U3_XANCP (Q8P5U3) Glucarate hydratase			x
Q5V465_HALMA	>gnl|tr|Q5V465_HALMA (Q5V465) Methylaspartate ammonia-lyase (EC 4.3.1.2)	SWT		x
Q9HN19_HALSA	>gnl|tr|Q9HN19_HALSA (Q9HN19) Methylaspartate ammonia-lyase			x
O66145_CITAM	>gnl|tr|O66145_CITAM (O66145) 3-methylaspartate ammonia-lyase			x
Q32IJ6_SHIDS	>gnl|tr|Q32IJ6_SHIDS (Q32IJ6) Putative methylaspartate ammonia-lyase			x
Q3AEJ6_CARHZ	>gnl|tr|Q3AEJ6_CARHZ (Q3AEJ6) Methylaspartate ammonia-lyase (EC 4.3.1.2)	SWT		x
Q3AEU2_CARHZ	>gnl|tr|Q3AEU2_CARHZ (Q3AEU2) Methylaspartate ammonia-lyase (EC 4.3.1.2)	SWT		x
Q3CBX0_9CLOT	>gnl|tr|Q3CBX0_9CLOT (Q3CBX0) Methylaspartate ammonia-lyase (EC 4.3.1.2)	SWT		x
Q426I1_DESHA	>gnl|tr|Q426I1_DESHA (Q426I1) Methylaspartate ammonia-lyase (EC 4.3.1.2)			x
Q8KJF8_RHILO	>gnl|tr|Q8KJF8_RHILO (Q8KJF8) PUTATIVE METHYLASPARTATE AMMONIA-LYASE PROTEIN (EC 4.3.1.2)	SWT		x
Q73KI3_TREDE	>gnl|tr|Q73KI3_TREDE (Q73KI3) Methylaspartate ammonia-lyase (EC 4.3.1.2)	SWT		x
Q890S3_CLOTE	>gnl|tr|Q890S3_CLOTE (Q890S3) Methylaspartate ammonia-lyase (EC 4.3.1.2)			x
Q8X990_ECO57	>gnl|tr|Q8X990_ECO57 (Q8X990) Putative methylaspartate ammonia-lyase (3-methylaspartate ammonia-lyase)			x
Q98A98_RHILO	>gnl|tr|Q98A98_RHILO (Q98A98) 3-methylaspartate ammonia-lyase			x
Q85G01_CYAME	>gnl|tr|Q85G01_CYAME (Q85G01) 4-(2'-carboxyphenyl)-4-oxybutyric acid synthase	GSA		x
Q31D06_PROM9	>gnl|tr|Q31D06_PROM9 (Q31D06) Putative O-succinylbenzoate synthase			x
Q3AGW3_SYNSC	>gnl|tr|Q3AGW3_SYNSC (Q3AGW3) Putative O-succinylbenzoate synthase			x
Q3AVZ3_SYNS9	>gnl|tr|Q3AVZ3_SYNS9 (Q3AVZ3) Putative O-succinylbenzoate synthase			x
Q4QLT9_HAEI8	>gnl|tr|Q4QLT9_HAEI8 (Q4QLT9) O-succinylbenzoate synthase (EC 4.2.1.-)			x
Q5E484_VIBF1	>gnl|tr|Q5E484_VIBF1 (Q5E484) O-succinylbenzoate synthase (EC 4.2.1.-)			x
Q632I6_BACCZ	>gnl|tr|Q632I6_BACCZ (Q632I6) Possible N-acylamino acid racemase; possible O-succinylbenzoate synthase (EC 4.2.1.-)			x
Q7MMF3_VIBVY	>gnl|tr|Q7MMF3_VIBVY (Q7MMF3) O-succinylbenzoate synthase			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q7U3X1_SYNPX	>gnl|tr|Q7U3X1_SYNPX (Q7U3X1) Putative O-succinylbenzoate synthase (EC 4.2.1.-)			x
Q7V3A7_PROMP	>gnl|tr|Q7V3A7_PROMP (Q7V3A7) Putative O-succinylbenzoate synthase			x
Q7V4A4_PROMM	>gnl|tr|Q7V4A4_PROMM (Q7V4A4) Putative O-succinylbenzoate synthase (EC 4.2.1.-)			x
Q8D823_VIBVU	>gnl|tr|Q8D823_VIBVU (Q8D823) O-succinylbenzoate synthase			x
Q2S2V3_9SPHI	>gnl|tr|Q2S2V3_9SPHI (Q2S2V3) O-succinylbenzoic acid (OSB) synthetase (EC 4.2.1.-)			x
Q2YTP1_STAAB	>gnl|tr|Q2YTP1_STAAB (Q2YTP1) O-succinylbenzoic acid synthetase (EC 4.2.1.-)			x
Q3M9T7_ANAVT	>gnl|tr|Q3M9T7_ANAVT (Q3M9T7) O-succinylbenzoic acid synthase			x
Q49YM1_STAS1	>gnl|tr|Q49YM1_STAS1 (Q49YM1) O-succinylbenzoic acid synthetase			x
Q4MNA0_BACCE	>gnl|tr|Q4MNA0_BACCE (Q4MNA0) O-succinylbenzoic acid (OSB) synthetase (EC 4.2.1.-)			x
Q53635_STAAU	>gnl|tr|Q53635_STAAU (Q53635) O-succinylbenzoic acid (OSB) synthetase			x
Q4L7D3_STAHJ	>gnl|tr|Q4L7D3_STAHJ (Q4L7D3) O-succinylbenzoic acid (OSB) synthetase			x
Q5HEY3_STAAC	>gnl|tr|Q5HEY3_STAAC (Q5HEY3) O-succinylbenzoic acid (OSB) synthetase, putative			x
Q5HNB3_STAEQ	>gnl|tr|Q5HNB3_STAEQ (Q5HNB3) O-succinylbenzoic acid synthetase, putative			x
Q7A4Z3_STAAN	>gnl|tr|Q7A4Z3_STAAN (Q7A4Z3) O-succinylbenzoic acid synthetase			x
Q8CNT4_STAES	>gnl|tr|Q8CNT4_STAES (Q8CNT4) O-succinylbenzoic acid (OSB) synthetase			x
Q8NVZ5_STAAW	>gnl|tr|Q8NVZ5_STAAW (Q8NVZ5) O-succinylbenzoic acid synthetase			x
Q8Z0Q6_ANASP	>gnl|tr|Q8Z0Q6_ANASP (Q8Z0Q6) O-succinylbenzoic acid synthase			x
Q99T74_STAAM	>gnl|tr|Q99T74_STAAM (Q99T74) O-succinylbenzoic acid synthetase			x
Q8GFH9_ALCXX	>gnl|tr|Q8GFH9_ALCXX (Q8GFH9) Chloromuconate cycloisomerase (EC 5.5.1.7)			x
Q93UZ6_9BURK	>gnl|tr|Q93UZ6_9BURK (Q93UZ6) Chloromuconate cycloisomerase (EC 5.5.1.7)			x
O67985_RHOOP	>gnl|tr|O67985_RHOOP (O67985) Chloromuconate cycloisomerase			x
O87609_PSEAE	>gnl|tr|O87609_PSEAE (O87609) Chloromuconate cycloisomerase			x
P94138_RALEU	>gnl|tr|P94138_RALEU (P94138) Chloromuconate cycloisomerase			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q706U0_PSEPU	>gnl|tr|Q706U0_PSEPU (Q706U0) Chloromuconate cycloisomerase			x
Q7BV50_BURCE	>gnl|tr|Q7BV50_BURCE (Q7BV50) Chloromuconate cycloisomerase			x
Q8G9L1_RHOOP	>gnl|tr|Q8G9L1_RHOOP (Q8G9L1) Chloromuconate cycloisomerase			x
Q9RHQ8_VARPD	>gnl|tr|Q9RHQ8_VARPD (Q9RHQ8) Chloromuconate cycloisomerase			x
Q9RPB4_PSEAE	>gnl|tr|Q9RPB4_PSEAE (Q9RPB4) Chloromuconate cycloisomerase			x
Q9RPF7_PSEAE	>gnl|tr|Q9RPF7_PSEAE (Q9RPF7) Chloromuconate cycloisomerase			x
Q393C7_BURS3	>gnl|tr|Q393C7_BURS3 (Q393C7) Muconate cycloisomerase (EC 5.5.1.1)			x
Q3JJV9_BURP1	>gnl|tr|Q3JJV9_BURP1 (Q3JJV9) Muconate cycloisomerase (EC 5.5.1.1)			x
Q3LHT2_9NOCA	>gnl|tr|Q3LHT2_9NOCA (Q3LHT2) Cis,cis-muconate cycloisomerase (EC 5.5.1.1)	ESA		x
Q3PBR5_PARDE	>gnl|tr|Q3PBR5_PARDE (Q3PBR5) Muconate cycloisomerase (EC 5.5.1.1)			x
Q458I5_9BURK	>gnl|tr|Q458I5_9BURK (Q458I5) Muconate cycloisomerase (EC 5.5.1.1)			x
Q4LPX1_9BURK	>gnl|tr|Q4LPX1_9BURK (Q4LPX1) Muconate cycloisomerase (EC 5.5.1.1)			x
Q76CC6_9MICC	>gnl|tr|Q76CC6_9MICC (Q76CC6) Cis,cis-muconate cycloisomerase (EC 5.5.1.1)	ESA		x
Q9AQS7_9BURK	>gnl|tr|Q9AQS7_9BURK (Q9AQS7) Muconate cycloisomerase (EC 5.5.1.1)			x
Q9EV42_RALEU	>gnl|tr|Q9EV42_RALEU (Q9EV42) Putative muconate cycloisomerase (EC 5.5.1.1)			x
Q9Z9Y1_9GAMM	>gnl|tr|Q9Z9Y1_9GAMM (Q9Z9Y1) Muconate cycloisomerase (EC 5.5.1.1)			x
Q9Z9Y6_9GAMM	>gnl|tr|Q9Z9Y6_9GAMM (Q9Z9Y6) Muconate cycloisomerase (EC 5.5.1.1)			x
Q4K9X1_PSEF5	>gnl|tr|Q4K9X1_PSEF5 (Q4K9X1) Muconate cycloisomerase (EC 5.5.1.1)			x
Q62E51_BURMA	>gnl|tr|Q62E51_BURMA (Q62E51) Muconate cycloisomerase (EC 5.5.1.1)			x
Q63J25_BURPS	>gnl|tr|Q63J25_BURPS (Q63J25) Muconate cycloisomerase I (EC 5.5.1.1)			x
Q2T814_BURTH	>gnl|tr|Q2T814_BURTH (Q2T814) Muconate cycloisomerase			x
Q2XL31_PSEPU	>gnl|tr|Q2XL31_PSEPU (Q2XL31) Muconate cycloisomerase			x
Q51958_PSEPU	>gnl|tr|Q51958_PSEPU (Q51958) Muconate lactonizing enzyme			x
Q5NTR1_9BACT	>gnl|tr|Q5NTR1_9BACT (Q5NTR1) Muconate lactonizing enzyme I			x
Q7WWT7_RALEU	>gnl|tr|Q7WWT7_RALEU (Q7WWT7) Putative muconate cycloisomerase			x
Q7WWU8_RALEU	>gnl|tr|Q7WWU8_RALEU (Q7WWU8) Putative muconate cycloisomerase			x
Q8GAY8_BURST	>gnl|tr|Q8GAY8_BURST (Q8GAY8) Cis,cis-muconate lactonizing enzyme			x
Q8GAZ7_BURST	>gnl|tr|Q8GAZ7_BURST (Q8GAZ7) Cis,cis-muconate lactonizing enzyme			x
Q93SR2_PSEPU	>gnl|tr|Q93SR2_PSEPU (Q93SR2) Putative muconate cycloisomerase I CatB			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q9AEQ3_PSEPU	>gnl|tr|Q9AEQ3_PSEPU (Q9AEQ3) Cis,cis-muconate lactonizing enzyme			x
Q9AQQ3_9PSED	>gnl|tr|Q9AQQ3_9PSED (Q9AQQ3) Cis,cis-muconate cycloisomerase CatB			x
Q88GK6_PSEPK	>gnl|tr|Q88GK6_PSEPK (Q88GK6) Muconate cycloisomerase			x
Q8FN45_COREF	>gnl|tr|Q8FN45_COREF (Q8FN45) Putative muconate cycloisomerase			x
Q9I0X3_PSEAE	>gnl|tr|Q9I0X3_PSEAE (Q9I0X3) Muconate cycloisomerase I			x
Q3EFA0_ACTSC	>gnl|tr|Q3EFA0_ACTSC (Q3EFA0) 3-deoxy-manno-octulosonate-8-phosphatase (EC 3.1.3.45)			x
Q3KI02_PSEPF	>gnl|tr|Q3KI02_PSEPF (Q3KI02) Phosphatase kdsC (EC 3.1.3.45)			x
Q4ZNU9_PSEU2	>gnl|tr|Q4ZNU9_PSEU2 (Q4ZNU9) HAD-superfamily hydrolase, subfamily IIIA:Phosphatase YrbI (EC 3.1.3.45)			x
Q4KI83_PSEF5	>gnl|tr|Q4KI83_PSEF5 (Q4KI83) 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45)			x
Q4QJR5_HAEI8	>gnl|tr|Q4QJR5_HAEI8 (Q4QJR5) 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45)			x
Q4K9L7_PSEF5	>gnl|tr|Q4K9L7_PSEF5 (Q4K9L7) 2-phosphonoacetaldehyde hydrolase (EC 3.11.1.1)			x
Q63E46_BACCZ	>gnl|tr|Q63E46_BACCZ (Q63E46) Possible phosphonoacetaldehyde hydrolase (EC 3.11.1.1)			x
Q6HLM1_BACHK	>gnl|tr|Q6HLM1_BACHK (Q6HLM1) Possible phosphonoacetaldehyde hydrolase (EC 3.11.1.1)			x
Q73BH9_BACC1	>gnl|tr|Q73BH9_BACC1 (Q73BH9) Phosphonoacetaldehyde phosphonohydrolase (EC 3.11.1.1)			x
Q88YN8_LACPL	>gnl|tr|Q88YN8_LACPL (Q88YN8) Phosphonoacetaldehyde hydrolase (EC 3.11.1.1)			x
O31156_BACCE	>gnl|tr|O31156_BACCE (O31156) Phosphonoacetaldehyde hydrolase			X
Q2XEK9_PSEPU	>gnl|tr|Q2XEK9_PSEPU (Q2XEK9) Phosphonoacetaldehyde hydrolase:HAD-superfamily hydrolase subfamily IA, variant 3			x
Q3K9Y2_PSEPF	>gnl|tr|Q3K9Y2_PSEPF (Q3K9Y2) Phosphonoacetaldehyde hydrolase			x
Q51386_PSEAE	>gnl|tr|Q51386_PSEAE (Q51386) 2-phosphonoacetaldehyde hydrolase			x
Q8RSQ3_PSEPU	>gnl|tr|Q8RSQ3_PSEPU (Q8RSQ3) 2-phosphonoacetaldehyde hydrolase			x
Q88KT1_PSEPK	>gnl|tr|Q88KT1_PSEPK (Q88KT1) 2-phosphonoacetaldehyde hydrolase			x
Q9I433_PSEAE	>gnl|tr|Q9I433_PSEAE (Q9I433) 2-phosphonoacetaldehyde hydrolase			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q4MSF0_BACCE	>gnl|tr|Q4MSF0_BACCE (Q4MSF0) Phosphonoacetaldehyde phosphonohydrolase VCA0606			x
Q5PFR1_SALPA	>gnl|tr|Q5PFR1_SALPA (Q5PFR1) Phosphonoacetaldehyde phosphonohydrolase			x
Q7MF46_VIBVY	>gnl|tr|Q7MF46_VIBVY (Q7MF46) Phosphonoacetaldehyde phosphonohydrolase			x
Q81TE1_BACAN	>gnl|tr|Q81TE1_BACAN (Q81TE1) Phosphonoacetaldehyde phosphonohydrolase			x
Q87JL6_VIBPA	>gnl|tr|Q87JL6_VIBPA (Q87JL6) Phosphonoacetaldehyde phosphonohydrolase			x
Q8Z8W5_SALTI	>gnl|tr|Q8Z8W5_SALTI (Q8Z8W5) Phosphonoacetaldehyde phosphonohydrolase			x
Q9KLY5_VIBCH	>gnl|tr|Q9KLY5_VIBCH (Q9KLY5) Phosphonoacetaldehyde phosphonohydrolase			x
Q2SX30_BURTH	>gnl|tr|Q2SX30_BURTH (Q2SX30) Haloacid dehalogenase, type II (EC 3.8.1.2)			x
Q39F12_BURS3	>gnl|tr|Q39F12_BURS3 (Q39F12) Haloacid dehalogenase, type II (EC 3.8.1.2)			x
Q3F8P8_9BURK	>gnl|tr|Q3F8P8_9BURK (Q3F8P8) HAD-superfamily hydrolase, subfamily IA, variant 2 (EC 3.8.1.2)			x
Q3JQZ5_BURP1	>gnl|tr|Q3JQZ5_BURP1 (Q3JQZ5) Haloacid dehalogenase, type II (EC 3.8.1.2)			x
Q3RK08_RALME	>gnl|tr|Q3RK08_RALME (Q3RK08) HAD-superfamily hydrolase, subfamily IA, variant 2 (EC 3.8.1.2)			x
Q3WKR9_9RHIZ	>gnl|tr|Q3WKR9_9RHIZ (Q3WKR9) HAD-superfamily hydrolase, subfamily IA, variant 2 (EC 3.8.1.2)			x
Q450N4_9BURK	>gnl|tr|Q450N4_9BURK (Q450N4) HAD-superfamily hydrolase, subfamily IA, variant 2 (EC 3.8.1.2)			x
Q46ZW7_RALEJ	>gnl|tr|Q46ZW7_RALEJ (Q46ZW7) Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2 (EC 3.8.1.2)			x
Q4ASX7_9BURK	>gnl|tr|Q4ASX7_9BURK (Q4ASX7) HAD-superfamily hydrolase, subfamily IA, variant 2 (EC 3.8.1.2)			x
Q4B1A0_9BURK	>gnl|tr|Q4B1A0_9BURK (Q4B1A0) HAD-superfamily hydrolase, subfamily IA, variant 2 (EC 3.8.1.2)			x
Q4B9E0_BURVI	>gnl|tr|Q4B9E0_BURVI (Q4B9E0) HAD-superfamily hydrolase, subfamily IA, variant 2 (EC 3.8.1.2)			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q4LN60_9BURK	>gnl|tr|Q4LN60_9BURK (Q4LN60) HAD-superfamily hydrolase, subfamily IA, variant 2 (EC 3.8.1.2)			x
Q59I43_9BURK	>gnl|tr|Q59I43_9BURK (Q59I43) L-2-haloacid dehalogenase (EC 3.8.1.2)			x
Q5P813_AZOSE	>gnl|tr|Q5P813_AZOSE (Q5P813) Putative 2-haloalkanoic acid dehalogenase (EC 3.8.1.2)			x
Q62J90_BURMA	>gnl|tr|Q62J90_BURMA (Q62J90) Haloacid dehalogenase, type II (EC 3.8.1.2)			x
Q89D82_BRAJA	>gnl|tr|Q89D82_BRAJA (Q89D82) 2-haloalkanoic acid dehalogenase (EC 3.8.1.2)			x
Q8G1Y6_BRUSU	>gnl|tr|Q8G1Y6_BRUSU (Q8G1Y6) Haloacid dehalogenase, type II (EC 3.8.1.2)			x
Q8XZN3_RALSO	>gnl|tr|Q8XZN3_RALSO (Q8XZN3) PUTATIVE 2-HALOALKANOIC ACID DEHALOGENASE PROTEIN (EC 3.8.1.2)			x
Q3E2N8_CHLAU	>gnl|tr|Q3E2N8_CHLAU (Q3E2N8) Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2			x
Q9ZA67_BURCE	>gnl|tr|Q9ZA67_BURCE (Q9ZA67) Cryptic haloacid dehalogenase 1			x
Q57EG9_BRUAB	>gnl|tr|Q57EG9_BRUAB (Q57EG9) Haloacid dehalogenase			x
Q6N251_RHOPA	>gnl|tr|Q6N251_RHOPA (Q6N251) Putative 2-haloacid halidohydrolase Iva			x
Q985K5_RHILO	>gnl|tr|Q985K5_RHILO (Q985K5) 2-haloacid halidohydrolase Iva			x
Q2W483_MAGSA	>gnl|tr|Q2W483_MAGSA (Q2W483) 2-haloalkanoic acid dehalogenase I			x
Q9Z3Z3_PSEPU	>gnl|tr|Q9Z3Z3_PSEPU (Q9Z3Z3) Haloalkanoic acid dehalogenase			x
Q4EH91_LISMO	>gnl|tr|Q4EH91_LISMO (Q4EH91) Beta-phosphoglucomutase (EC 5.4.2.6)			x
Q4ENF6_LISMO	>gnl|tr|Q4ENF6_LISMO (Q4ENF6) Beta-phosphoglucomutase (EC 5.4.2.6)			x
Q71VT0_LISMF	>gnl|tr|Q71VT0_LISMF (Q71VT0) Beta-phosphoglucomutase (EC 5.4.2.6)			x
Q890F6_LACPL	>gnl|tr|Q890F6_LACPL (Q890F6) Beta-phosphoglucomutase (EC 5.4.2.6)			x
Q890I4_LACPL	>gnl|tr|Q890I4_LACPL (Q890I4) Beta-phosphoglucomutase (EC 5.4.2.6)			x
Q8FHR4_ECOL6	>gnl|tr|Q8FHR4_ECOL6 (Q8FHR4) Putative beta-phosphoglucomutase (EC 5.4.2.6)			x
Q98PT4_MYCPU	>gnl|tr|Q98PT4_MYCPU (Q98PT4) BETA-PHOSPHOGLUCOMUTASE (BETA-PGM) (EC 5.4.2.6)			x
Q9JSW9_NEIMA	>gnl|tr|Q9JSW9_NEIMA (Q9JSW9) Beta-phosphoglucomutase (EC 5.4.2.6)			x
Q9JSX3_NEIMA	>gnl|tr|Q9JSX3_NEIMA (Q9JSX3) Beta-phosphoglucomutase (EC 5.4.2.6)			x
Q9K108_NEIMB	>gnl|tr|Q9K108_NEIMB (Q9K108) Beta-phosphoglucomutase (EC 5.4.2.6)			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
O87773_LACSN	>gnl|tr|O87773_LACSN (O87773) Beta-phosphoglucomutase			x
Q3Z162_SHISS	>gnl|tr|Q3Z162_SHISS (Q3Z162) Putative beta-phosphoglucomutase			x
Q836Y8_ENTFA	>gnl|tr|Q836Y8_ENTFA (Q836Y8) Beta-phosphoglucomutase			x
Q83RK7_SHIFL	>gnl|tr|Q83RK7_SHIFL (Q83RK7) Putative beta-phosphoglucomutase			x
Q8X8K2_ECO57	>gnl|tr|Q8X8K2_ECO57 (Q8X8K2) Putative beta-phosphoglucomutase			x
Q97FW2_CLOAB	>gnl|tr|Q97FW2_CLOAB (Q97FW2) Beta-phosphoglucomutase			x
O81923_CAPAA	>gnl|tr|O81923_CAPAA (O81923) 5-epi-aristolochene synthase	x		x
Q84LF0_9SOLA	>gnl|tr|Q84LF0_9SOLA (Q84LF0) 5-epi-aristolochene synthase 37	x		x
Q84LF1_9SOLA	>gnl|tr|Q84LF1_9SOLA (Q84LF1) 5-epi-aristolochene synthase 34	x		x
Q84LF2_9SOLA	>gnl|tr|Q84LF2_9SOLA (Q84LF2) 5-epi-aristolochene synthase 12	x		x
Q84LG0_9SOLA	>gnl|tr|Q84LG0_9SOLA (Q84LG0) 5-epi-aristolochene synthase	x		x
Q82IY4_STRAW	>gnl|tr|Q82IY4_STRAW (Q82IY4) Pentalenene synthase			x
Q2RYC8_RHORU	>gnl|tr|Q2RYC8_RHORU (Q2RYC8) Terpene synthase, squalene cyclase (EC 5.4.99.17)			x
Q2T2Q3_BURTH	>gnl|tr|Q2T2Q3_BURTH (Q2T2Q3) Squalene-hopene cyclase (EC 5.4.99.17)			x
Q39BM5_BURS3	>gnl|tr|Q39BM5_BURS3 (Q39BM5) Terpene synthase/Squalene cyclase (EC 5.4.99.17)			x
Q39LV3_BURS3	>gnl|tr|Q39LV3_BURS3 (Q39LV3) Terpene synthase/Squalene cyclase (EC 5.4.99.17)			x
Q3F5Y2_9BURK	>gnl|tr|Q3F5Y2_9BURK (Q3F5Y2) Terpene synthase (EC 5.4.99.17)			x
Q3FA06_9BURK	>gnl|tr|Q3FA06_9BURK (Q3FA06) Terpene synthase (EC 5.4.99.17)			x
Q3G6F5_9DELT	>gnl|tr|Q3G6F5_9DELT (Q3G6F5) Terpene synthase (EC 5.4.99.17)			x
Q3JBH8_NITOC	>gnl|tr|Q3JBH8_NITOC (Q3JBH8) Terpene synthase/Squalene cyclase (EC 5.4.99.17)			x
Q3JIF6_BURP1	>gnl|tr|Q3JIF6_BURP1 (Q3JIF6) Squalene-hopene cyclase (EC 5.4.99.17)			x
Q3M418_ANAVT	>gnl|tr|Q3M418_ANAVT (Q3M418) Terpene synthase (EC 5.4.99.17)			x
Q3MYE8_9DELT	>gnl|tr|Q3MYE8_9DELT (Q3MYE8) Terpene synthase (EC 5.4.99.17)			x
Q3MZV5_9DELT	>gnl|tr|Q3MZV5_9DELT (Q3MZV5) Terpene synthase (EC 5.4.99.17)			x
Q3N6T0_9PROT	>gnl|tr|Q3N6T0_9PROT (Q3N6T0) Terpene synthase (EC 5.4.99.17)			x
Q3PXP7_NITHA	>gnl|tr|Q3PXP7_NITHA (Q3PXP7) Terpene synthase (EC 5.4.99.17)			x
Q3RN02_RALME	>gnl|tr|Q3RN02_RALME (Q3RN02) Terpene synthase (EC 5.4.99.17)			x
Q3RZT4_RALME	>gnl|tr|Q3RZT4_RALME (Q3RZT4) Terpene synthase precursor (EC 5.4.99.17)			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q3SQB8_NITWN	>gnl|tr|Q3SQB8_NITWN (Q3SQB8) Terpene synthase/Squalene cyclase (EC 5.4.99.17)			x
Q3W9E9_9ACTO	>gnl|tr|Q3W9E9_9ACTO (Q3W9E9) Terpene synthase (EC 5.4.99.17)			x
Q459N5_9BURK	>gnl|tr|Q459N5_9BURK (Q459N5) Terpene synthase (EC 5.4.99.17)			x
Q45EI7_9BURK	>gnl|tr|Q45EI7_9BURK (Q45EI7) Terpene synthase precursor (EC 5.4.99.17)			x
Q4BML1_BURVI	>gnl|tr|Q4BML1_BURVI (Q4BML1) Terpene synthase (EC 5.4.99.17)			x
Q4J480_AZOVI	>gnl|tr|Q4J480_AZOVI (Q4J480) Terpene synthase (EC 5.4.99.17)			X
Q4LM82_9BURK	>gnl|tr|Q4LM82_9BURK (Q4LM82) Terpene synthase (EC 5.4.99.17)			x
Q4LRR6_9BURK	>gnl|tr|Q4LRR6_9BURK (Q4LRR6) Terpene synthase precursor (EC 5.4.99.17)			x
Q5NM88_ZYMMO	>gnl|tr|Q5NM88_ZYMMO (Q5NM88) Squalene--hopene cyclase (EC 5.4.99.17)			x
Q629M5_BURMA	>gnl|tr|Q629M5_BURMA (Q629M5) Squalene-hopene cyclase (EC 5.4.99.17)			x
Q63HT1_BURPS	>gnl|tr|Q63HT1_BURPS (Q63HT1) Squalene--hopene cyclase (EC 5.4.99.17)			x
Q748E3_GEOSL	>gnl|tr|Q748E3_GEOSL (Q748E3) Squalene-hopene cyclase (EC 5.4.99.17)			x
Q74FC1_GEOSL	>gnl|tr|Q74FC1_GEOSL (Q74FC1) Squalene-hopene cyclase (EC 5.4.99.17)			x
O69446_METCA	>gnl|tr|O69446_METCA (O69446) Squalene-hopene cyclase			x
O69790_RHOPA	>gnl|tr|O69790_RHOPA (O69790) Squalene-hopene cyclase			x
Q3A7E3_PELCD	>gnl|tr|Q3A7E3_PELCD (Q3A7E3) Squalene-hopene cyclase			x
Q59080_9BACL	>gnl|tr|Q59080_9BACL (Q59080) Squalene-hopene cyclase (EC 5.4.99.7)			x
Q5FNQ3_GLUOX	>gnl|tr|Q5FNQ3_GLUOX (Q5FNQ3) Squalene-hopene cyclase			x
Q7NE23_GLOVI	>gnl|tr|Q7NE23_GLOVI (Q7NE23) Squalene-hopene cyclase			x
Q81YD8_BACAN	>gnl|tr|Q81YD8_BACAN (Q81YD8) Squalene-hopene cyclase			x
Q82ML0_STRAW	>gnl|tr|Q82ML0_STRAW (Q82ML0) Squalene-hopene cyclase			x
Q9X7V9_STRCO	>gnl|tr|Q9X7V9_STRCO (Q9X7V9) Putative squalene-hopene cyclase			x
Q2Y5X6_NITMU	>gnl|tr|Q2Y5X6_NITMU (Q2Y5X6) Squalene cyclase			x
Q34E48_RHOPA	>gnl|tr|Q34E48_RHOPA (Q34E48) Terpene synthase:Squalene cyclase			x
Q34RT4_RHOPA	>gnl|tr|Q34RT4_RHOPA (Q34RT4) Squalene-hopene-cyclase			x
Q37GN6_RHOPA	>gnl|tr|Q37GN6_RHOPA (Q37GN6) Terpene synthase:Squalene cyclase			x
Q39RT6_GEOMG	>gnl|tr|Q39RT6_GEOMG (Q39RT6) Terpene synthase:Squalene cyclase			x
Q39YL2_GEOMG	>gnl|tr|Q39YL2_GEOMG (Q39YL2) Terpene synthase:Squalene cyclase			x
Q3A7M9_PELCD	>gnl|tr|Q3A7M9_PELCD (Q3A7M9) Squalene--hopene cyclase			x
Q46RD2_RALEJ	>gnl|tr|Q46RD2_RALEJ (Q46RD2) Terpene synthase:Squalene cyclase			x
Q4MKR1_BACCE	>gnl|tr|Q4MKR1_BACCE (Q4MKR1) Squalene--hopene cyclase			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
P73914_SYNY3	>gnl|tr|P73914_SYNY3 (P73914) Squalene-hopene-cyclase			x
Q8DGK8_SYNEL	>gnl|tr|Q8DGK8_SYNEL (Q8DGK8) Squalene-hopene-cyclase			x
Q8YYS1_ANASP	>gnl|tr|Q8YYS1_ANASP (Q8YYS1) Squalene-hopene-cyclase			x
Q71RX9_STACH	>gnl|tr|Q71RX9_STACH (Q71RX9) Trichodiene synthase			x
Q76PE4_GIBZE	>gnl|tr|Q76PE4_GIBZE (Q76PE4) Trichodiene synthase			x
Q7LJL3_GIBZE	>gnl|tr|Q7LJL3_GIBZE (Q7LJL3) Trichodiene synthase			x
Q7LJL9_FUSAU	>gnl|tr|Q7LJL9_FUSAU (Q7LJL9) Trichodiene synthase			x
Q7LJS4_FUSMI	>gnl|tr|Q7LJS4_FUSMI (Q7LJS4) Trichodiene synthase			x
Q7LJT2_FUSAS	>gnl|tr|Q7LJT2_FUSAS (Q7LJT2) Trichodiene synthase			x
Q7LP67_FUSSP	>gnl|tr|Q7LP67_FUSSP (Q7LP67) Trichodiene synthase			x
Q7Z8B9_FUSPO	>gnl|tr|Q7Z8B9_FUSPO (Q7Z8B9) Trichodiene synthase			x
Q7Z8C0_FUSSP	>gnl|tr|Q7Z8C0_FUSSP (Q7Z8C0) Trichodiene synthase			x
Q8NJH2_FUSLU	>gnl|tr|Q8NJH2_FUSLU (Q8NJH2) Trichodiene synthase			x
Q96W88_GIBZE	>gnl|tr|Q96W88_GIBZE (Q96W88) Trichodiene synthase			x
Q8NJU9_GIBZE	>gnl|tr|Q8NJU9_GIBZE (Q8NJU9) Trichodiene synthetase			x
Q8NJV0_GIBZE	>gnl|tr|Q8NJV0_GIBZE (Q8NJV0) Trichodiene synthetase			x
Q9UR08_ASPTE	>gnl|tr|Q9UR08_ASPTE (Q9UR08) Aristolochene synthase			x
Q8VQN0_PROFR	>gnl|tr|Q8VQN0_PROFR (Q8VQN0) Methylmalonyl CoA epimerase (EC 5.1.99.1)			x
Q977P4_PYRHO	>gnl|tr|Q977P4_PYRHO (Q977P4) Methylmalonyl-CoA epimerase (Fragment)			x
Q6BG80_PARTE	>gnl|tr|Q6BG80_PARTE (Q6BG80) 4-hydroxyphenylpyruvate dioxygenase, putative			x
Q56H33_MEDTR	>gnl|tr|Q56H33_MEDTR (Q56H33) 4-hydroxyphenylpyruvate dioxygenase			x
Q6H4V1_ORYSA	>gnl|tr|Q6H4V1_ORYSA (Q6H4V1) Putative 4-hydroxyphenylpyruvate dioxygenase			x
Q8L7E8_ARATH	>gnl|tr|Q8L7E8_ARATH (Q8L7E8) 4-hydroxyphenylpyruvate dioxygenase HPD			x
Q2S2T7_9SPHI	>gnl|tr|Q2S2T7_9SPHI (Q2S2T7) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q2SND1_9GAMM	>gnl|tr|Q2SND1_9GAMM (Q2SND1) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q2STZ8_BURTH	>gnl|tr|Q2STZ8_BURTH (Q2STZ8) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q2T3K2_BURTH	>gnl|tr|Q2T3K2_BURTH (Q2T3K2) 4-hydroxyphenylpyruvate dioxygenase, putative			x
Q2T5Y1_BURTH	>gnl|tr|Q2T5Y1_BURTH (Q2T5Y1) 4-hydroxyphenylpyruvate dioxygenase			x
Q2X680_9GAMM	>gnl|tr|Q2X680_9GAMM (Q2X680) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q2XKA2_PSEPU	>gnl|tr|Q2XKA2_PSEPU (Q2XKA2) 4-hydroxyphenylpyruvate dioxygenase			x
Q2XM67_PSEPU	>gnl|tr|Q2XM67_PSEPU (Q2XM67) 4-hydroxyphenylpyruvate dioxygenase, putative			x
Q2Z830_9GAMM	>gnl|tr|Q2Z830_9GAMM (Q2Z830) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q2ZNE8_SHEPU	>gnl|tr|Q2ZNE8_SHEPU (Q2ZNE8) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q33PL8_9GAMM	>gnl|tr|Q33PL8_9GAMM (Q33PL8) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q35GS2_9BRAD	>gnl|tr|Q35GS2_9BRAD (Q35GS2) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q35KQ1_9BRAD	>gnl|tr|Q35KQ1_9BRAD (Q35KQ1) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q35TW0_9GAMM	>gnl|tr|Q35TW0_9GAMM (Q35TW0) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q36BK6_9GAMM	>gnl|tr|Q36BK6_9GAMM (Q36BK6) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q37V98_SPHAR	>gnl|tr|Q37V98_SPHAR (Q37V98) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q37XY1_SPHAR	>gnl|tr|Q37XY1_SPHAR (Q37XY1) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q395X2_BURS3	>gnl|tr|Q395X2_BURS3 (Q395X2) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q39AQ2_BURS3	>gnl|tr|Q39AQ2_BURS3 (Q39AQ2) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q39KJ4_BURS3	>gnl|tr|Q39KJ4_BURS3 (Q39KJ4) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x

Table K-2. TrEMBL data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>Q3BYF0_XANC5</td><td>>gnl|tr|Q3BYF0_XANC5 (Q3BYF0) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q3CUY6_ALTAT</td><td>>gnl|tr|Q3CUY6_ALTAT (Q3CUY6) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q3CWI1_ALTAT</td><td>>gnl|tr|Q3CWI1_ALTAT (Q3CWI1) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q3DXR8_CHLAU</td><td>>gnl|tr|Q3DXR8_CHLAU (Q3DXR8) 4-hydroxyphenylpyruvate dioxygenase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q3EW31_BACTI</td><td>>gnl|tr|Q3EW31_BACTI (Q3EW31) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q3F1S4_9BURK</td><td>>gnl|tr|Q3F1S4_9BURK (Q3F1S4) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q3F6R6_9BURK</td><td>>gnl|tr|Q3F6R6_9BURK (Q3F6R6) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q3FD81_9BURK</td><td>>gnl|tr|Q3FD81_9BURK (Q3FD81) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q3GL80_9GAMM</td><td>>gnl|tr|Q3GL80_9GAMM (Q3GL80) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q3H2J4_9ACTO</td><td>>gnl|tr|Q3H2J4_9ACTO (Q3H2J4) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q3IET4_PSEHT</td><td>>gnl|tr|Q3IET4_PSEHT (Q3IET4) 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) (EC 1.13.11.27)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q3JB70_NITOC</td><td>>gnl|tr|Q3JB70_NITOC (Q3JB70) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q3JYB9_BURP1</td><td>>gnl|tr|Q3JYB9_BURP1 (Q3JYB9) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q3K6G2_PSEPF</td><td>>gnl|tr|Q3K6G2_PSEPF (Q3K6G2) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q3KC47_PSEPF</td><td>>gnl|tr|Q3KC47_PSEPF (Q3KC47) 4-hydroxyphenylpyruvate dioxygenase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q3NQQ8_SHEFR</td><td>>gnl|tr|Q3NQQ8_SHEFR (Q3NQQ8) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q3P045_9GAMM</td><td>>gnl|tr|Q3P045_9GAMM (Q3P045) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td></tr>
</table>

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q3PHY1_PARDE	>gnl|tr|Q3PHY1_PARDE (Q3PHY1) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q3Q520_9GAMM	>gnl|tr|Q3Q520_9GAMM (Q3Q520) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q3QEM4_9GAMM	>gnl|tr|Q3QEM4_9GAMM (Q3QEM4) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q3QWK3_9RHOB	>gnl|tr|Q3QWK3_9RHOB (Q3QWK3) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q3RV34_RALME	>gnl|tr|Q3RV34_RALME (Q3RV34) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q3V924_9SPHN	>gnl|tr|Q3V924_9SPHN (Q3V924) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q3W6Y0_9ACTO	>gnl|tr|Q3W6Y0_9ACTO (Q3W6Y0) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q3WKZ6_9RHIZ	>gnl|tr|Q3WKZ6_9RHIZ (Q3WKZ6) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q3WTX8_9RHIZ	>gnl|tr|Q3WTX8_9RHIZ (Q3WTX8) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q40C79_9RHOB	>gnl|tr|Q40C79_9RHOB (Q40C79) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q442A4_SOLUS	>gnl|tr|Q442A4_SOLUS (Q442A4) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q44U09_9BURK	>gnl|tr|Q44U09_9BURK (Q44U09) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q45B07_9BURK	>gnl|tr|Q45B07_9BURK (Q45B07) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q45CM2_9BURK	>gnl|tr|Q45CM2_9BURK (Q45CM2) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q46R51_RALEJ	>gnl|tr|Q46R51_RALEJ (Q46R51) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q46R58_RALEJ	>gnl|tr|Q46R58_RALEJ (Q46R58) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q46SN3_RALEJ	>gnl|tr|Q46SN3_RALEJ (Q46SN3) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q47YG2_COLP3	>gnl|tr|Q47YG2_COLP3 (Q47YG2) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q48GS3_PSE14	>gnl|tr|Q48GS3_PSE14 (Q48GS3) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q48JV3_PSE14	>gnl|tr|Q48JV3_PSE14 (Q48JV3) 4-hydroxyphenylpyruvate dioxygenase, putative			x
Q4AZW6_9BURK	>gnl|tr|Q4AZW6_9BURK (Q4AZW6) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q4B831_BURVI	>gnl|tr|Q4B831_BURVI (Q4B831) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q4BSU0_BURVI	>gnl|tr|Q4BSU0_BURVI (Q4BSU0) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q4BU52_BURVI	>gnl|tr|Q4BU52_BURVI (Q4BU52) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q4IUU1_AZOVI	>gnl|tr|Q4IUU1_AZOVI (Q4IUU1) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q4IY20_AZOVI	>gnl|tr|Q4IY20_AZOVI (Q4IY20) 4-hydroxyphenylpyruvate dioxygenase precursor (EC 1.13.11.27)			x
Q4J186_AZOVI	>gnl|tr|Q4J186_AZOVI (Q4J186) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q4LIA5_9BURK	>gnl|tr|Q4LIA5_9BURK (Q4LIA5) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q4LJW9_9BURK	>gnl|tr|Q4LJW9_9BURK (Q4LJW9) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q4LSN2_9BURK	>gnl|tr|Q4LSN2_9BURK (Q4LSN2) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q4MPU8_BACCE	>gnl|tr|Q4MPU8_BACCE (Q4MPU8) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q4UZJ1_XANC8	>gnl|tr|Q4UZJ1_XANC8 (Q4UZJ1) 4-hydroxyphenylpyruvate dioxygenase			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q4ZR60_PSEU2	>gnl|tr|Q4ZR60_PSEU2 (Q4ZR60) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q4ZUJ9_PSEU2	>gnl|tr|Q4ZUJ9_PSEU2 (Q4ZUJ9) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q7X4L3_9BACT	>gnl|tr|Q7X4L3_9BACT (Q7X4L3) 4-hydroxyphenylpyruvate dioxygenase			x
Q8VQC4_VIBAN	>gnl|tr|Q8VQC4_VIBAN (Q8VQC4) 4-hydroxyphenylpyruvate dioxygenase			x
Q2NAB6_9SPHN	>gnl|tr|Q2NAB6_9SPHN (Q2NAB6) 4-hydroxyphenylpyruvate dioxygenase			x
Q2NYM6_XANOR	>gnl|tr|Q2NYM6_XANOR (Q2NYM6) 4-hydroxyphenylpyruvate dioxygenase			x
Q4K5N0_PSEF5	>gnl|tr|Q4K5N0_PSEF5 (Q4K5N0) 4-hydroxyphenylpyruvate dioxygenase, putative			x
Q4KB91_PSEF5	>gnl|tr|Q4KB91_PSEF5 (Q4KB91) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q5GVE8_XANOR	>gnl|tr|Q5GVE8_XANOR (Q5GVE8) 4-hydroxyphenylpyruvate dioxygenase			x
Q5LTI8_SILPO	>gnl|tr|Q5LTI8_SILPO (Q5LTI8) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q5R0G8_IDILO	>gnl|tr|Q5R0G8_IDILO (Q5R0G8) 4-hydroxyphenylpyruvate dioxygenase			x
Q5WUG4_LEGPL	>gnl|tr|Q5WUG4_LEGPL (Q5WUG4) 4-hydroxyphenylpyruvate dioxygenase (Legiolysin)			x
Q5X304_LEGPA	>gnl|tr|Q5X304_LEGPA (Q5X304) 4-hydroxyphenylpyruvate dioxygenase (Legiolysin)			x
Q5YPF8_NOCFA	>gnl|tr|Q5YPF8_NOCFA (Q5YPF8) Putative 4-hydroxyphenylpyruvate dioxygenase			x
Q62CM9_BURMA	>gnl|tr|Q62CM9_BURMA (Q62CM9) Putative 4-hydroxyphenylpyruvate dioxygenase			x
Q62GQ1_BURMA	>gnl|tr|Q62GQ1_BURMA (Q62GQ1) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q63GY1_BACCZ	>gnl|tr|Q63GY1_BACCZ (Q63GY1) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q63PY5_BURPS	>gnl|tr|Q63PY5_BURPS (Q63PY5) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x
Q6HPF2_BACHK	>gnl|tr|Q6HPF2_BACHK (Q6HPF2) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x

Table K-2. TrEMBL data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>Q6LI28_PHOPR</td><td>>gnl|tr|Q6LI28_PHOPR (Q6LI28) Putative 4-hydroxyphenylpyruvate dioxygenase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q6MHJ8_BDEBA</td><td>>gnl|tr|Q6MHJ8_BDEBA (Q6MHJ8) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q6NDU9_RHOPA</td><td>>gnl|tr|Q6NDU9_RHOPA (Q6NDU9) 4-hydroxyphenylpyruvate dioxygenase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q73EU8_BACC1</td><td>>gnl|tr|Q73EU8_BACC1 (Q73EU8) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q7NZF3_CHRVO</td><td>>gnl|tr|Q7NZF3_CHRVO (Q7NZF3) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q81IU6_BACCR</td><td>>gnl|tr|Q81IU6_BACCR (Q81IU6) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q81VG6_BACAN</td><td>>gnl|tr|Q81VG6_BACAN (Q81VG6) 4-hydroxyphenylpyruvate dioxygenase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q87Q01_VIBPA</td><td>>gnl|tr|Q87Q01_VIBPA (Q87Q01) 4-hydroxyphenylpyruvate dioxygenase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q87Z77_PSESM</td><td>>gnl|tr|Q87Z77_PSESM (Q87Z77) 4-hydroxyphenylpyruvate dioxygenase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q883L0_PSESM</td><td>>gnl|tr|Q883L0_PSESM (Q883L0) 4-hydroxyphenylpyruvate dioxygenase, putative</td><td></td><td></td><td>x</td></tr>
<tr><td>Q88HC7_PSEPK</td><td>>gnl|tr|Q88HC7_PSEPK (Q88HC7) 4-hydroxyphenylpyruvate dioxygenase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q88JU3_PSEPK</td><td>>gnl|tr|Q88JU3_PSEPK (Q88JU3) 4-hydroxyphenylpyruvate dioxygenase, putative</td><td></td><td></td><td>x</td></tr>
<tr><td>Q89XH5_BRAJA</td><td>>gnl|tr|Q89XH5_BRAJA (Q89XH5) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q8EFK9_SHEON</td><td>>gnl|tr|Q8EFK9_SHEON (Q8EFK9) 4-hydroxyphenylpyruvate dioxygenase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q8PDA4_XANCP</td><td>>gnl|tr|Q8PDA4_XANCP (Q8PDA4) 4-hydroxyphenylpyruvate dioxygenase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q8PQ76_XANAC</td><td>>gnl|tr|Q8PQ76_XANAC (Q8PQ76) 4-hydroxyphenylpyruvate dioxygenase</td><td></td><td></td><td>x</td></tr>
<tr><td>Q8XF91_RALSO</td><td>>gnl|tr|Q8XF91_RALSO (Q8XF91) PROBABLE 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE OXIDOREDUCTASE PROTEIN (EC 1.13.11.27)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q8XUT2_RALSO</td><td>>gnl|tr|Q8XUT2_RALSO (Q8XUT2) PROBABLE 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE OXIDOREDUCTASE PROTEIN (EC 1.13.11.27)</td><td></td><td></td><td>x</td></tr>
<tr><td>Q92LT1_RHIME</td><td>>gnl|tr|Q92LT1_RHIME (Q92LT1) PUTATIVE 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE PROTEIN (EC 1.13.11.27)</td><td></td><td></td><td>x</td></tr>
</table>

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q983J0_RHILO	>gnl|tr|Q983J0_RHILO (Q983J0) 4-hydroxyphenylpyruvate dioxygenase			x
Q9A5B7_CAUCR	>gnl|tr|Q9A5B7_CAUCR (Q9A5B7) 4-hydroxyphenylpyruvate dioxygenase			x
Q9I576_PSEAE	>gnl|tr|Q9I576_PSEAE (Q9I576) 4-hydroxyphenylpyruvate dioxygenase			x
Q9RCH2_VIBCH	>gnl|tr|Q9RCH2_VIBCH (Q9RCH2) P-hydroxyphenylpyruvate dioxygenase (4-hydroxyphenylpyruvate dioxygenase)			x
O82449_ARATH	>gnl|tr|O82449_ARATH (O82449) P-hydroxyphenylpyruvate dioxygenase			x
Q6EMJ1_PSEPU	>gnl|tr|Q6EMJ1_PSEPU (Q6EMJ1) P-hydroxyphenylpyruvate dioxygenase			x
Q696X2_PHANO	>gnl|tr|Q696X2_PHANO (Q696X2) Glyoxylase I (EC 4.4.1.5)			x
Q870H6_PARBR	>gnl|tr|Q870H6_PARBR (Q870H6) Glyoxalase I (EC 4.4.1.5)			x
Q6XC06_MAIZE	>gnl|tr|Q6XC06_MAIZE (Q6XC06) Glyoxalase I (EC 4.4.1.5)			x
Q9XGF2_WHEAT	>gnl|tr|Q9XGF2_WHEAT (Q9XGF2) Putative glyoxalase I (EC 4.4.1.5) (Fragment)			x
Q9ZS21_SOYBN	>gnl|tr|Q9ZS21_SOYBN (Q9ZS21) Glyoxalase I (EC 4.4.1.5)			x
Q2SDH5_9GAMM	>gnl|tr|Q2SDH5_9GAMM (Q2SDH5) Lactoylglutathione lyase (EC 4.4.1.5)			x
Q2T112_BURTH	>gnl|tr|Q2T112_BURTH (Q2T112) Lactoylglutathione lyase (EC 4.4.1.5)			x
Q2Y5Q9_NITMU	>gnl|tr|Q2Y5Q9_NITMU (Q2Y5Q9) Glyoxalase I (EC 4.4.1.5)			x
Q31QJ9_SYNP7	>gnl|tr|Q31QJ9_SYNP7 (Q31QJ9) Glyoxalase I (EC 4.4.1.5)			x
Q39D39_BURS3	>gnl|tr|Q39D39_BURS3 (Q39D39) Glyoxalase I (EC 4.4.1.5)			x
Q3BP33_XANC5	>gnl|tr|Q3BP33_XANC5 (Q3BP33) Lactoylglutathione lyase (EC 4.4.1.5)			x
Q3CV50_ALTAT	>gnl|tr|Q3CV50_ALTAT (Q3CV50) Glyoxalase I (EC 4.4.1.5)			x
Q3EF41_ACTSC	>gnl|tr|Q3EF41_ACTSC (Q3EF41) Lactoylglutathione lyase (EC 4.4.1.5)			x
Q3FJ10_9BURK	>gnl|tr|Q3FJ10_9BURK (Q3FJ10) Glyoxalase I (EC 4.4.1.5)			x
Q3H8N5_TRIER	>gnl|tr|Q3H8N5_TRIER (Q3H8N5) Glyoxalase I (EC 4.4.1.5)			x
Q3IGQ9_PSEHT	>gnl|tr|Q3IGQ9_PSEHT (Q3IGQ9) Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase) (EC 4.4.1.5)			x
Q3J7R2_NITOC	>gnl|tr|Q3J7R2_NITOC (Q3J7R2) Glyoxalase I (EC 4.4.1.5)			x
Q3JVW4_BURP1	>gnl|tr|Q3JVW4_BURP1 (Q3JVW4) Lactoylglutathione lyase (EC 4.4.1.5)			x
Q3MGX1_ANAVT	>gnl|tr|Q3MGX1_ANAVT (Q3MGX1) Glyoxalase I (EC 4.4.1.5)			x
Q3N8V3_9PROT	>gnl|tr|Q3N8V3_9PROT (Q3N8V3) Glyoxalase I (EC 4.4.1.5)			x
Q3R2G4_XYLFA	>gnl|tr|Q3R2G4_XYLFA (Q3R2G4) Glyoxalase I (EC 4.4.1.5)			x
Q3RBN2_XYLFA	>gnl|tr|Q3RBN2_XYLFA (Q3RBN2) Glyoxalase I (EC 4.4.1.5)			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q3RH69_XYLFA	>gnl|tr|Q3RH69_XYLFA (Q3RH69) Glyoxalase I (EC 4.4.1.5)			x
Q3XB57_METFL	>gnl|tr|Q3XB57_METFL (Q3XB57) Glyoxalase I (EC 4.4.1.5)			x
Q44K51_CHRSL	>gnl|tr|Q44K51_CHRSL (Q44K51) Glyoxalase I (EC 4.4.1.5)			x
Q451L0_9BURK	>gnl|tr|Q451L0_9BURK (Q451L0) Glyoxalase I (EC 4.4.1.5)			x
Q475P8_RALEJ	>gnl|tr|Q475P8_RALEJ (Q475P8) Glyoxalase I (EC 4.4.1.5)			x
Q48JF2_PSE14	>gnl|tr|Q48JF2_PSE14 (Q48JF2) Lactoylglutathione lyase (EC 4.4.1.5)			x
Q4AT89_9BURK	>gnl|tr|Q4AT89_9BURK (Q4AT89) Glyoxalase I (EC 4.4.1.5)			x
Q4BES9_BURVI	>gnl|tr|Q4BES9_BURVI (Q4BES9) Glyoxalase I (EC 4.4.1.5)			x
Q4C9S5_CROWT	>gnl|tr|Q4C9S5_CROWT (Q4C9S5) Glyoxalase I (EC 4.4.1.5)			x
Q4IWB5_AZOVI	>gnl|tr|Q4IWB5_AZOVI (Q4IWB5) Glyoxalase I (EC 4.4.1.5)			x
Q4LU31_9BURK	>gnl|tr|Q4LU31_9BURK (Q4LU31) Glyoxalase I (EC 4.4.1.5)			x
Q4NTS9_9DELT	>gnl|tr|Q4NTS9_9DELT (Q4NTS9) Glyoxalase I (EC 4.4.1.5)			x
Q4ZS65_PSEU2	>gnl|tr|Q4ZS65_PSEU2 (Q4ZS65) Glyoxalase I (EC 4.4.1.5)			x
Q4KB85_PSEF5	>gnl|tr|Q4KB85_PSEF5 (Q4KB85) Lactoylglutathione lyase (EC 4.4.1.5)			x
Q4QNL6_HAEI8	>gnl|tr|Q4QNL6_HAEI8 (Q4QNL6) Lactoylglutathione lyase (EC 4.4.1.5)			x
Q5E6C3_VIBF1	>gnl|tr|Q5E6C3_VIBF1 (Q5E6C3) Lactoylglutathione lyase (EC 4.4.1.5)			x
Q5P269_AZOSE	>gnl|tr|Q5P269_AZOSE (Q5P269) Lactoylglutathione lyase (EC 4.4.1.5)			x
Q62MM1_BURMA	>gnl|tr|Q62MM1_BURMA (Q62MM1) Lactoylglutathione lyase (EC 4.4.1.5)			x
Q63X74_BURPS	>gnl|tr|Q63X74_BURPS (Q63X74) Lactoylglutathione lyase (EC 4.4.1.5)			x
Q66A37_YERPS	>gnl|tr|Q66A37_YERPS (Q66A37) Lactoylglutathione lyase (EC 4.4.1.5)			x
Q6D5V9_ERWCT	>gnl|tr|Q6D5V9_ERWCT (Q6D5V9) Lactoylglutathione lyase (EC 4.4.1.5)			x
Q6FAA3_ACIAD	>gnl|tr|Q6FAA3_ACIAD (Q6FAA3) Lactoylglutathione lyase (EC 4.4.1.5)			x
Q6MJD2_BDEBA	>gnl|tr|Q6MJD2_BDEBA (Q6MJD2) Lactoylglutathione lyase (EC 4.4.1.5)			x
Q7NXG6_CHRVO	>gnl|tr|Q7NXG6_CHRVO (Q7NXG6) Lactoylglutathione lyase (EC 4.4.1.5)			x
Q7U3T2_SYNPX	>gnl|tr|Q7U3T2_SYNPX (Q7U3T2) Lactoylglutathione lyase (EC 4.4.1.5)			x
Q7W0Q1_BORPE	>gnl|tr|Q7W0Q1_BORPE (Q7W0Q1) Lactoylglutathione lyase (EC 4.4.1.5)			x
Q7W4K1_BORPA	>gnl|tr|Q7W4K1_BORPA (Q7W4K1) Lactoylglutathione lyase (EC 4.4.1.5)			x
Q7WG26_BORBR	>gnl|tr|Q7WG26_BORBR (Q7WG26) Lactoylglutathione lyase (EC 4.4.1.5)			x
Q82UQ5_NITEU	>gnl|tr|Q82UQ5_NITEU (Q82UQ5) Possible gloA; lactoylglutathione lyase (EC 4.4.1.5)			x
Q8FH76_ECOL6	>gnl|tr|Q8FH76_ECOL6 (Q8FH76) Lactoylglutathione lyase (EC 4.4.1.5)			x
Q8ZE09_YERPE	>gnl|tr|Q8ZE09_YERPE (Q8ZE09) Lactoylglutathione lyase (EC 4.4.1.5)			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q59EL0_HUMAN	>gnl|tr|Q59EL0_HUMAN (Q59EL0) Glyoxalase I variant (Fragment)			x
Q4X4Q2_PLACH	>gnl|tr|Q4X4Q2_PLACH (Q4X4Q2) Glyoxalase I, putative			x
Q4YS97_PLABE	>gnl|tr|Q4YS97_PLABE (Q4YS97) Glyoxalase I, putative			x
Q5XQR1_LEIDO	>gnl|tr|Q5XQR1_LEIDO (Q5XQR1) Glyoxalase I	ESA		x
Q71KM3_PLAFA	>gnl|tr|Q71KM3_PLAFA (Q71KM3) Glyoxalase I			x
Q8IIM5_PLAF7	>gnl|tr|Q8IIM5_PLAF7 (Q8IIM5) Glyoxalase I, putative			x
Q6ES23_ORYSA	>gnl|tr|Q6ES23_ORYSA (Q6ES23) Putative glyoxalase I			x
Q8LEY7_ARATH	>gnl|tr|Q8LEY7_ARATH (Q8LEY7) Glyoxalase I, putative			x
Q9AXH1_AVIMR	>gnl|tr|Q9AXH1_AVIMR (Q9AXH1) Glyoxalase I			x
Q2XL87_PSEPU	>gnl|tr|Q2XL87_PSEPU (Q2XL87) Glyoxalase I			x
Q36NB0_MARHY	>gnl|tr|Q36NB0_MARHY (Q36NB0) Glyoxalase I			x
Q3KC41_PSEPF	>gnl|tr|Q3KC41_PSEPF (Q3KC41) Glyoxalase I			x
Q47A63_DECAR	>gnl|tr|Q47A63_DECAR (Q47A63) Glyoxalase I			x
Q57PK1_SALCH	>gnl|tr|Q57PK1_SALCH (Q57PK1) Glyoxalase I, nickel isomerase			x
Q75GB0_ORYSA	>gnl|tr|Q75GB0_ORYSA (Q75GB0) Putative glyoxalase			x
Q7N3W1_PHOLL	>gnl|tr|Q7N3W1_PHOLL (Q7N3W1) Lactoylglutathione lyase (Methylglyoxalase) (S-D-lactolyglutathione methylglyoxal lyase)			x
Q6P696_BRARE	>gnl|tr|Q6P696_BRARE (Q6P696) Glyoxalase 1			x
Q4WN17_ASPFU	>gnl|tr|Q4WN17_ASPFU (Q4WN17) Lactoylglutathione lyase			x
Q7RRI6_PLAYO	>gnl|tr|Q7RRI6_PLAYO (Q7RRI6) Lactoylglutathione lyase, putative			x
Q940A4_ARATH	>gnl|tr|Q940A4_ARATH (Q940A4) Putative lactoylglutathione lyase			x
Q321A6_SHIBS	>gnl|tr|Q321A6_SHIBS (Q321A6) Lactoylglutathione lyase			x
Q32FB9_SHIDS	>gnl|tr|Q32FB9_SHIDS (Q32FB9) Lactoylglutathione lyase			x
Q3Z207_SHISS	>gnl|tr|Q3Z207_SHISS (Q3Z207) Lactoylglutathione lyase			x
Q4UQH4_XANC8	>gnl|tr|Q4UQH4_XANC8 (Q4UQH4) Lactoylglutathione lyase			x
Q8D0L9_YERPE	>gnl|tr|Q8D0L9_YERPE (Q8D0L9) Lactoylglutathione lyase			x
Q2P7N8_XANOR	>gnl|tr|Q2P7N8_XANOR (Q2P7N8) Lactoylglutathione lyase			x
Q5H4W2_XANOR	>gnl|tr|Q5H4W2_XANOR (Q5H4W2) Lactoylglutathione lyase			x
Q5N3P3_SYNP6	>gnl|tr|Q5N3P3_SYNP6 (Q5N3P3) Lactoylglutathione lyase			x
Q5PH08_SALPA	>gnl|tr|Q5PH08_SALPA (Q5PH08) Lactoylglutathione lyase			x
Q5QZJ8_IDILO	>gnl|tr|Q5QZJ8_IDILO (Q5QZJ8) Lactoylglutathione lyase			x
Q7MM88_VIBVY	>gnl|tr|Q7MM88_VIBVY (Q7MM88) Lactoylglutathione lyase			x

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q87DQ2_XYLFT	>gnl|tr|Q87DQ2_XYLFT (Q87DQ2) Lactoylglutathione lyase			x
Q87I32_VIBPA	>gnl|tr|Q87I32_VIBPA (Q87I32) Lactoylglutathione lyase			x
Q880P8_PSESM	>gnl|tr|Q880P8_PSESM (Q880P8) Lactoylglutathione lyase			x
Q88GF8_PSEPK	>gnl|tr|Q88GF8_PSEPK (Q88GF8) Lactoylglutathione lyase			x
Q8PCX6_XANCP	>gnl|tr|Q8PCX6_XANCP (Q8PCX6) Lactoylglutathione lyase			x
Q8PGI4_XANAC	>gnl|tr|Q8PGI4_XANAC (Q8PGI4) Lactoylglutathione lyase			x
Q8YUM0_ANASP	>gnl|tr|Q8YUM0_ANASP (Q8YUM0) Lactoylglutathione lyase			x
Q9HU72_PSEAE	>gnl|tr|Q9HU72_PSEAE (Q9HU72) Lactoylglutathione lyase			x
Q9HY85_PSEAE	>gnl|tr|Q9HY85_PSEAE (Q9HY85) Lactoylglutathione lyase			x
Q9PDI0_XYLFA	>gnl|tr|Q9PDI0_XYLFA (Q9PDI0) Lactoylglutathione lyase			x
Q3EUI1_BACTI	>gnl|tr|Q3EUI1_BACTI (Q3EUI1) Cytosine deaminase (EC 3.5.4.1)	SFA	x	
Q7U5R2_SYNPX	>gnl|tr|Q7U5R2_SYNPX (Q7U5R2) Possible cytosine deaminase (EC 3.5.4.1)	SFA	x	
Q7V0F8_PROMP	>gnl|tr|Q7V0F8_PROMP (Q7V0F8) Possible cytosine deaminase (EC 3.5.4.1)	SFA	x	
Q7V8L5_PROMM	>gnl|tr|Q7V8L5_PROMM (Q7V8L5) Possible cytosine deaminase (EC 3.5.4.1)	SFA	x	
Q817N4_BACCR	>gnl|tr|Q817N4_BACCR (Q817N4) Cytosine deaminase (EC 3.5.4.1)	SFA	x	
Q5V6C0_HALMA	>gnl|tr|Q5V6C0_HALMA (Q5V6C0) Cytosine deaminase	SFA	x	
Q67VW4_ORYSA	>gnl|tr|Q67VW4_ORYSA (Q67VW4) Putative cytosine deaminase	NSF	x	
Q31QR9_SYNP7	>gnl|tr|Q31QR9_SYNP7 (Q31QR9) Cytosine deaminase	SFA	x	
Q3ALB0_SYNSC	>gnl|tr|Q3ALB0_SYNSC (Q3ALB0) Possible cytosine deaminase	SFA	x	
Q46JG7_PROMT	>gnl|tr|Q46JG7_PROMT (Q46JG7) Possible cytosine deaminase	SFA	x	
Q4BC59_BURVI	>gnl|tr|Q4BC59_BURVI (Q4BC59) Cytosine deaminase	SFA	x	
Q936Y0_PSESD	>gnl|tr|Q936Y0_PSESD (Q936Y0) Putative cytosine deaminase	SFA	x	
P73487_SYNY3	>gnl|tr|P73487_SYNY3 (P73487) Cytosine deaminase	BAC	x	
Q5N3H6_SYNP6	>gnl|tr|Q5N3H6_SYNP6 (Q5N3H6) Cytosine deaminase	SFA	x	
Q7MH11_VIBVY	>gnl|tr|Q7MH11_VIBVY (Q7MH11) Cytosine deaminase	SFA	x	
Q7VAS6_PROMA	>gnl|tr|Q7VAS6_PROMA (Q7VAS6) Cytosine deaminase	SFA	x	
Q98J79_RHILO	>gnl|tr|Q98J79_RHILO (Q98J79) Cytosine deaminase	SFA	x	
Q98J79_RHILO	>gnl|tr|Q98J79_RHILO (Q98J79) Cytosine deaminase	BAC	x	
Q98KW4_RHILO	>gnl|tr|Q98KW4_RHILO (Q98KW4) Cytosine deaminase	SFA	x	
Q4FWQ3_LEIMA	>gnl|tr|Q4FWQ3_LEIMA (Q4FWQ3) Adenosine deaminase, putative (EC 3.5.4.4)	BTC	x	
Q86GS5_PLAFA	>gnl|tr|Q86GS5_PLAFA (Q86GS5) Adenosine deaminase (EC 3.5.4.4)	BTC	x	

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q9NC65_LUTLO	>gnl|tr|Q9NC65_LUTLO (Q9NC65) Putative adenosine deaminase (EC 3.5.4.4)	SFA	x	
Q2RWC5_RHORU	>gnl|tr|Q2RWC5_RHORU (Q2RWC5) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q2S4S0_9SPHI	>gnl|tr|Q2S4S0_9SPHI (Q2S4S0) Adenosine deaminase (EC 3.5.4.4)	MFR	x	
Q2SLW3_9GAMM	>gnl|tr|Q2SLW3_9GAMM (Q2SLW3) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q300I6_STRSU	>gnl|tr|Q300I6_STRSU (Q300I6) Adenosine deaminase (EC 3.5.4.4)	MFR	x	
Q38ZJ2_LACSS	>gnl|tr|Q38ZJ2_LACSS (Q38ZJ2) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q39AK6_BURS3	>gnl|tr|Q39AK6_BURS3 (Q39AK6) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q39II8_BURS3	>gnl|tr|Q39II8_BURS3 (Q39II8) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q3B2Q0_PELLD	>gnl|tr|Q3B2Q0_PELLD (Q3B2Q0) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q3BYW5_XANC5	>gnl|tr|Q3BYW5_XANC5 (Q3BYW5) Putative adenosine deaminase (EC 3.5.4.4)	SFA	x	
Q3CLR4_ALTAT	>gnl|tr|Q3CLR4_ALTAT (Q3CLR4) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q3CP14_ALTAT	>gnl|tr|Q3CP14_ALTAT (Q3CP14) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q3D378_STRAG	>gnl|tr|Q3D378_STRAG (Q3D378) Adenosine deaminase (EC 3.5.4.4)	MFR	x	
Q3D947_STRAG	>gnl|tr|Q3D947_STRAG (Q3D947) Adenosine deaminase (EC 3.5.4.4)	MFR	x	
Q3DEK8_STRAG	>gnl|tr|Q3DEK8_STRAG (Q3DEK8) Adenosine deaminase (EC 3.5.4.4)	MFR	x	
Q3DLP4_STRAG	>gnl|tr|Q3DLP4_STRAG (Q3DLP4) Adenosine deaminase (EC 3.5.4.4)	MFR	x	
Q3DTB2_STRAG	>gnl|tr|Q3DTB2_STRAG (Q3DTB2) Adenosine deaminase (EC 3.5.4.4)	MFR	x	
Q3F7I7_9BURK	>gnl|tr|Q3F7I7_9BURK (Q3F7I7) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q3FE67_9BURK	>gnl|tr|Q3FE67_9BURK (Q3FE67) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q3FXC2_9BURK	>gnl|tr|Q3FXC2_9BURK (Q3FXC2) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q3GNC6_9GAMM	>gnl|tr|Q3GNC6_9GAMM (Q3GNC6) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q3H1A0_9ACTO	>gnl|tr|Q3H1A0_9ACTO (Q3H1A0) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q3H1M2_9ACTO	>gnl|tr|Q3H1M2_9ACTO (Q3H1M2) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q3H4Z7_9ACTO	>gnl|tr|Q3H4Z7_9ACTO (Q3H4Z7) Adenosine deaminase (EC 3.5.4.4)	MFR	x	
Q3IF68_PSEHT	>gnl|tr|Q3IF68_PSEHT (Q3IF68) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q3J643_RHOS4	>gnl|tr|Q3J643_RHOS4 (Q3J643) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q3JPV5_BURP1	>gnl|tr|Q3JPV5_BURP1 (Q3JPV5) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q3K2D4_STRA1	>gnl|tr|Q3K2D4_STRA1 (Q3K2D4) Adenosine deaminase (EC 3.5.4.4)	MFR	x	
Q3PDL7_PARDE	>gnl|tr|Q3PDL7_PARDE (Q3PDL7) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q3RWI8_RALME	>gnl|tr|Q3RWI8_RALME (Q3RWI8) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q3VD51_9SPHN	>gnl|tr|Q3VD51_9SPHN (Q3VD51) Adenosine deaminase (EC 3.5.4.4)	BTC	x	

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q3VZ32_9ACTO	>gnl|tr|Q3VZ32_9ACTO (Q3VZ32) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q3WB85_9ACTO	>gnl|tr|Q3WB85_9ACTO (Q3WB85) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q3WDT5_9ACTO	>gnl|tr|Q3WDT5_9ACTO (Q3WDT5) Adenosine deaminase (EC 3.5.4.4)	MFR	x	
Q3WVH6_9RHIZ	>gnl|tr|Q3WVH6_9RHIZ (Q3WVH6) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q407A3_9RHOB	>gnl|tr|Q407A3_9RHOB (Q407A3) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q40WD9_KINRA	>gnl|tr|Q40WD9_KINRA (Q40WD9) Adenosine deaminase (EC 3.5.4.4)	MFR	x	
Q40Y35_KINRA	>gnl|tr|Q40Y35_KINRA (Q40Y35) Adenosine deaminase (EC 3.5.4.4)	SFA	x	
Q412I7_KINRA	>gnl|tr|Q412I7_KINRA (Q412I7) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q413X9_KINRA	>gnl|tr|Q413X9_KINRA (Q413X9) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q415A2_KINRA	>gnl|tr|Q415A2_KINRA (Q415A2) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q416N0_KINRA	>gnl|tr|Q416N0_KINRA (Q416N0) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q42XQ5_9ACTO	>gnl|tr|Q42XQ5_9ACTO (Q42XQ5) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q42XR5_9ACTO	>gnl|tr|Q42XR5_9ACTO (Q42XR5) Adenosine deaminase (EC 3.5.4.4)	MFR	x	
Q437A1_9ACTO	>gnl|tr|Q437A1_9ACTO (Q437A1) Adenosine deaminase (EC 3.5.4.4)	MFR	x	
Q43AD5_9ACTO	>gnl|tr|Q43AD5_9ACTO (Q43AD5) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q43HE1_9CHLB	>gnl|tr|Q43HE1_9CHLB (Q43HE1) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q444T0_SOLUS	>gnl|tr|Q444T0_SOLUS (Q444T0) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q44D76_CHRSL	>gnl|tr|Q44D76_CHRSL (Q44D76) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q44YC4_9BURK	>gnl|tr|Q44YC4_9BURK (Q44YC4) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q45CH8_9BURK	>gnl|tr|Q45CH8_9BURK (Q45CH8) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q46YJ3_RALEJ	>gnl|tr|Q46YJ3_RALEJ (Q46YJ3) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q47LS6_THEFY	>gnl|tr|Q47LS6_THEFY (Q47LS6) Adenosine deaminase (EC 3.5.4.4)	MFR	x	
Q483Q7_COLP3	>gnl|tr|Q483Q7_COLP3 (Q483Q7) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q486B3_COLP3	>gnl|tr|Q486B3_COLP3 (Q486B3) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q48D01_PSE14	>gnl|tr|Q48D01_PSE14 (Q48D01) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q4APG9_9CHLB	>gnl|tr|Q4APG9_9CHLB (Q4APG9) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q4AU08_9BURK	>gnl|tr|Q4AU08_9BURK (Q4AU08) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q4BFP8_BURVI	>gnl|tr|Q4BFP8_BURVI (Q4BFP8) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q4IV28_AZOVI	>gnl|tr|Q4IV28_AZOVI (Q4IV28) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q4LHN2_9BURK	>gnl|tr|Q4LHN2_9BURK (Q4LHN2) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q4LQ39_9BURK	>gnl|tr|Q4LQ39_9BURK (Q4LQ39) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q4NIH8_9MICC	>gnl|tr|Q4NIH8_9MICC (Q4NIH8) Adenosine deaminase precursor (EC 3.5.4.4)	MFR	x	

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q4NVL4_9DELT	>gnl|tr|Q4NVL4_9DELT (Q4NVL4) Adenosine deaminase (EC 3.5.4.4)	MFR	x	
Q4P031_9DELT	>gnl|tr|Q4P031_9DELT (Q4P031) Adenosine deaminase (EC 3.5.4.4)	MFR	x	
Q4ZYP1_PSEU2	>gnl|tr|Q4ZYP1_PSEU2 (Q4ZYP1) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q4JTJ3_CORJK	>gnl|tr|Q4JTJ3_CORJK (Q4JTJ3) Add protein (EC 3.5.4.4)	MFR	x	
Q4KIS2_PSEF5	>gnl|tr|Q4KIS2_PSEF5 (Q4KIS2) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q5FIX0_LACAC	>gnl|tr|Q5FIX0_LACAC (Q5FIX0) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q5FR10_GLUOX	>gnl|tr|Q5FR10_GLUOX (Q5FR10) Adenosine deaminase (EC 3.5.4.4)	SFA	x	
Q5LPC1_SILPO	>gnl|tr|Q5LPC1_SILPO (Q5LPC1) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q5NGB0_FRATT	>gnl|tr|Q5NGB0_FRATT (Q5NGB0) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q5NNW5_ZYMMO	>gnl|tr|Q5NNW5_ZYMMO (Q5NNW5) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q5NPT1_ZYMMO	>gnl|tr|Q5NPT1_ZYMMO (Q5NPT1) Adenosine deaminase (EC 3.5.4.4)	SFA	x	
Q5ZY00_LEGPH	>gnl|tr|Q5ZY00_LEGPH (Q5ZY00) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q62LZ8_BURMA	>gnl|tr|Q62LZ8_BURMA (Q62LZ8) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q63RY2_BURPS	>gnl|tr|Q63RY2_BURPS (Q63RY2) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q6A5I4_PROAC	>gnl|tr|Q6A5I4_PROAC (Q6A5I4) Adenosine deaminase (EC 3.5.4.4)	MFR	x	
Q6D4X4_ERWCT	>gnl|tr|Q6D4X4_ERWCT (Q6D4X4) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q6FCU0_ACIAD	>gnl|tr|Q6FCU0_ACIAD (Q6FCU0) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q6MHR4_BDEBA	>gnl|tr|Q6MHR4_BDEBA (Q6MHR4) Add protein (EC 3.5.4.4)	BTC	x	
Q8EZR9_LEPIN	>gnl|tr|Q8EZR9_LEPIN (Q8EZR9) Adenosine deaminase (EC 3.5.4.4)	BTC	x	
Q4X1Q4_ASPFU	>gnl|tr|Q4X1Q4_ASPFU (Q4X1Q4) Adenosine deaminase	BTC	x	
Q4Y1U6_PLACH	>gnl|tr|Q4Y1U6_PLACH (Q4Y1U6) Adenosine deaminase, putative	BTC	x	
Q4YQ35_PLABE	>gnl|tr|Q4YQ35_PLABE (Q4YQ35) Adenosine deaminase, putative	BTC	x	
Q511D9_ENTHI	>gnl|tr|Q511D9_ENTHI (Q511D9) Adenosine deaminase, putative		x	
Q51A21_ENTHI	>gnl|tr|Q51A21_ENTHI (Q51A21) Adenosine deaminase, putative	MFR	x	
Q54KF3_DICDI	>gnl|tr|Q54KF3_DICDI (Q54KF3) Adenosine deaminase	MFR	x	
Q5MIX2_AEDAL	>gnl|tr|Q5MIX2_AEDAL (Q5MIX2) Putative adenosine deaminase	SFA	x	
Q6IWY7_TRISP	>gnl|tr|Q6IWY7_TRISP (Q6IWY7) Adenosine deaminase	BTC	x	
Q7RMV2_PLAYO	>gnl|tr|Q7RMV2_PLAYO (Q7RMV2) Adenosine deaminase	BTC	x	
Q8IJA9_PLAF7	>gnl|tr|Q8IJA9_PLAF7 (Q8IJA9) Adenosine deaminase, putative	BTC	x	
Q8T9T6_AEDAE	>gnl|tr|Q8T9T6_AEDAE (Q8T9T6) Putative adenosine deaminase	SFA	x	
Q95WT8_CULQU	>gnl|tr|Q95WT8_CULQU (Q95WT8) Salivary adenosine deaminase	SFA	x	
Q8H3U7_ORYSA	>gnl|tr|Q8H3U7_ORYSA (Q8H3U7) Putative adenosine deaminase	BTC	x	

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q8LPL7_ARATH	>gnl|tr|Q8LPL7_ARATH (Q8LPL7) Putative adenosine deaminase	BTC	x	
Q9M0Z1_ARATH	>gnl|tr|Q9M0Z1_ARATH (Q9M0Z1) Putative adenosine deaminase	BTC	x	
Q2SY49_BURTH	>gnl|tr|Q2SY49_BURTH (Q2SY49) Adenosine deaminase	BTC	x	
Q2XGR7_PSEPU	>gnl|tr|Q2XGR7_PSEPU (Q2XGR7) Adenosine deaminase	BTC	x	
Q34BN5_RHOPA	>gnl|tr|Q34BN5_RHOPA (Q34BN5) Adenosine deaminase	BTC	x	
Q3E0F5_CHLAU	>gnl|tr|Q3E0F5_CHLAU (Q3E0F5) Adenosine deaminase	BTC	x	
Q3KIJ1_PSEPF	>gnl|tr|Q3KIJ1_PSEPF (Q3KIJ1) Adenosine deaminase	BTC	x	
Q47LH7_THEFY	>gnl|tr|Q47LH7_THEFY (Q47LH7) Adenosine deaminase	BTC	x	
Q49UM8_STAS1	>gnl|tr|Q49UM8_STAS1 (Q49UM8) Putative adenosine deaminase	MFR	x	
Q4UZY3_XANC8	>gnl|tr|Q4UZY3_XANC8 (Q4UZY3) Adenosine deaminase	SFA	x	
Q5M4W6_STRT2	>gnl|tr|Q5M4W6_STRT2 (Q5M4W6) Adenosine deaminase	MFR	x	
Q5QWC8_IDILO	>gnl|tr|Q5QWC8_IDILO (Q5QWC8) Adenosine deaminase	MFR	x	
Q5Z193_NOCFA	>gnl|tr|Q5Z193_NOCFA (Q5Z193) Putative adenosine deaminase	MFR	x	
Q5ZY75_LEGPH	>gnl|tr|Q5ZY75_LEGPH (Q5ZY75) Adenosine deaminase	SFA	x	
Q64PK0_BACFR	>gnl|tr|Q64PK0_BACFR (Q64PK0) Putative adenosine deaminase	SFA	x	
Q6AEM3_LEIXX	>gnl|tr|Q6AEM3_LEIXX (Q6AEM3) Adenosine deaminase protein	BTC	x	
Q6AGP0_LEIXX	>gnl|tr|Q6AGP0_LEIXX (Q6AGP0) Adenosine deaminase protein	MFR	x	
Q6F1Q1_MESFL	>gnl|tr|Q6F1Q1_MESFL (Q6F1Q1) Adenosine deaminase	SFA	x	
Q6LHI4_PHOPR	>gnl|tr|Q6LHI4_PHOPR (Q6LHI4) Putative adenosine deaminase	BTC	x	
Q6LI24_PHOPR	>gnl|tr|Q6LI24_PHOPR (Q6LI24) Putative adenosine deaminase	BTC	x	
Q72V44_LEPIC	>gnl|tr|Q72V44_LEPIC (Q72V44) Adenosine deaminase	BTC	x	
Q82BX7_STRAW	>gnl|tr|Q82BX7_STRAW (Q82BX7) Putative adenosine deaminase	BTC	x	
Q82DR3_STRAW	>gnl|tr|Q82DR3_STRAW (Q82DR3) Putative adenosine deaminase	BTC	x	
Q82I00_STRAW	>gnl|tr|Q82I00_STRAW (Q82I00) Putative adenosine deaminase	MFR	x	
Q82K09_STRAW	>gnl|tr|Q82K09_STRAW (Q82K09) Putative adenosine deaminase	BTC	x	
Q82NX6_STRAW	>gnl|tr|Q82NX6_STRAW (Q82NX6) Putative adenosine deaminase	MFR	x	
Q8PDP1_XANCP	>gnl|tr|Q8PDP1_XANCP (Q8PDP1) Adenosine deaminase	SFA	x	
Q6FP78_CANGA	>gnl|tr|Q6FP78_CANGA (Q6FP78) Similar to sp|P53909 Saccharomyces cerevisiae YNL141w AAH1 Adenosine aminohydrolase	BTC	x	
Q2RIX4_MOOTH	>gnl|tr|Q2RIX4_MOOTH (Q2RIX4) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)	BTC	x	

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q312S6_DESDG	>gnl|tr|Q312S6_DESDG (Q312S6) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)	BTC	x	
Q3C683_9CLOT	>gnl|tr|Q3C683_9CLOT (Q3C683) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)	BTC	x	
Q3CDG6_9CLOT	>gnl|tr|Q3CDG6_9CLOT (Q3CDG6) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)	BTC	x	
Q3F703_9BURK	>gnl|tr|Q3F703_9BURK (Q3F703) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)	BTC	x	
Q3FMP5_9BURK	>gnl|tr|Q3FMP5_9BURK (Q3FMP5) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)	BTC	x	
Q3FSZ7_9BURK	>gnl|tr|Q3FSZ7_9BURK (Q3FSZ7) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)	BTC	x	
Q3VFC6_9SPHN	>gnl|tr|Q3VFC6_9SPHN (Q3VFC6) N-acyl-D-amino-acid deacylase precursor (EC 3.5.1.81)	BTC	x	
Q40C65_9RHOB	>gnl|tr|Q40C65_9RHOB (Q40C65) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)	BTC	x	
Q415M3_KINRA	>gnl|tr|Q415M3_KINRA (Q415M3) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)	BTC	x	
Q41ZL3_DESHA	>gnl|tr|Q41ZL3_DESHA (Q41ZL3) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)	BTC	x	
Q43LM9_SOLUS	>gnl|tr|Q43LM9_SOLUS (Q43LM9) N-acyl-D-amino-acid deacylase precursor (EC 3.5.1.81)	BTC	x	
Q43RT2_SOLUS	>gnl|tr|Q43RT2_SOLUS (Q43RT2) N-acyl-D-amino-acid deacylase precursor (EC 3.5.1.81)	BTC	x	
Q43XW0_SOLUS	>gnl|tr|Q43XW0_SOLUS (Q43XW0) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)	BTC	x	
Q44KH6_CHRSL	>gnl|tr|Q44KH6_CHRSL (Q44KH6) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)	BTC	x	
Q45D19_9BURK	>gnl|tr|Q45D19_9BURK (Q45D19) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)	BTC	x	
Q4ARC7_9BURK	>gnl|tr|Q4ARC7_9BURK (Q4ARC7) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)	BTC	x	
Q4B5U4_9BURK	>gnl|tr|Q4B5U4_9BURK (Q4B5U4) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)	BTC	x	

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q4LV99_9BURK	>gnl|tr|Q4LV99_9BURK (Q4LV99) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)	BTC	x	
Q5FRQ8_GLUOX	>gnl|tr|Q5FRQ8_GLUOX (Q5FRQ8) D-aminoacylase (EC 3.5.1.81)	NSF	X	
Q633U7_BACCZ	>gnl|tr|Q633U7_BACCZ (Q633U7) Hypothetical protein (EC 3.5.1.81)	SFA	x	
Q7UWE0_RHOBA	>gnl|tr|Q7UWE0_RHOBA (Q7UWE0) D-aminoacylase (EC 3.5.1.81)	BTC	x	
Q6EMR8_VARPD	>gnl|tr|Q6EMR8_VARPD (Q6EMR8) N-acyl-D-amino acid amidohydrolase	BTC	x	
Q9V2D3_PYRAB	>gnl|tr|Q9V2D3_PYRAB (Q9V2D3) NdaD D-aminoacylase	BTC	x	
Q5KC38_CRYNE	>gnl|tr|Q5KC38_CRYNE (Q5KC38) D-aminoacylase, putative	BTC	x	
Q2WL43_CLOBE	>gnl|tr|Q2WL43_CLOBE (Q2WL43) D-aminoacylase (Aspartate, glutamate etc)	SFA	x	
Q35E24_9BRAD	>gnl|tr|Q35E24_9BRAD (Q35E24) D-aminoacylase	BTC	x	
Q37QB2_SPHAR	>gnl|tr|Q37QB2_SPHAR (Q37QB2) Putative D-aminoacylase	SFA	x	
Q3WJ83_9ACTO	>gnl|tr|Q3WJ83_9ACTO (Q3WJ83) Putative D-aminoacylase	SFA	x	
Q45R99_STRFR	>gnl|tr|Q45R99_STRFR (Q45R99) Probable D-aminoacylase	BTC	x	
Q6H068_FREDI	>gnl|tr|Q6H068_FREDI (Q6H068) Putative d-aminoacylase	SFA	x	
Q67JJ8_SYMTH	>gnl|tr|Q67JJ8_SYMTH (Q67JJ8) D-Aminoacylase	BTC	x	
Q82GU7_STRAW	>gnl|tr|Q82GU7_STRAW (Q82GU7) Putative D-aminoacylase	SFA	x	
Q82I76_STRAW	>gnl|tr|Q82I76_STRAW (Q82I76) Putative D-aminoacylase	BTC	x	
Q93JK8_STRCO	>gnl|tr|Q93JK8_STRCO (Q93JK8) Putative D-aminoacylase	BTC	x	
Q3H3B2_9ACTO	>gnl|tr|Q3H3B2_9ACTO (Q3H3B2) N-acyl-D-glutamate deacylase precursor (EC 3.5.1.82)	BTC	x	
Q7MD66_VIBVY	>gnl|tr|Q7MD66_VIBVY (Q7MD66) Putative N-acyl-D-glutamate deacylase protein	SFA	x	
Q7MD91_VIBVY	>gnl|tr|Q7MD91_VIBVY (Q7MD91) Probable N-acyl-D-glutamate deacylase protein	BTC	x	
Q6LSP3_PHOPR	>gnl|tr|Q6LSP3_PHOPR (Q6LSP3) Putative N-acyl-D-aspartate/D-glutamate deacylase	BTC	x	
Q8D645_VIBVU	>gnl|tr|Q8D645_VIBVU (Q8D645) N-acyl-D-aspartate/D-glutamate deacylase	NSF	X	
Q8D6D9_VIBVU	>gnl|tr|Q8D6D9_VIBVU (Q8D6D9) N-acyl-D-aspartate/D-glutamate deacylase	BTC	x	
Q2T5R3_BURTH	>gnl|tr|Q2T5R3_BURTH (Q2T5R3) N-acyl-D-glutamate amidohydrolase	SFA	x	
Q6YNI0_9MICC	>gnl|tr|Q6YNI0_9MICC (Q6YNI0) L-hydantoinase HyuH	BTC	x	
Q2RGZ6_MOOTH	>gnl|tr|Q2RGZ6_MOOTH (Q2RGZ6) D-hydantoinase (EC 3.5.2.2)	BTC	x	
Q972L4_SULTO	>gnl|tr|Q972L4_SULTO (Q972L4) 464aa long hypothetical D-hydantoinase	BTC	x	
Q972W9_SULTO	>gnl|tr|Q972W9_SULTO (Q972W9) 413aa long hypothetical D-hydantoinase	SFA	x	

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q972X8_SULTO	>gnl|tr|Q972X8_SULTO (Q972X8) 433aa long hypothetical D-hydantoinase	BTC	x	
Q50VG8_ENTHI	>gnl|tr|Q50VG8_ENTHI (Q50VG8) D-hydantoinase, putative	BTC	x	
Q2WKD6_CLOBE	>gnl|tr|Q2WKD6_CLOBE (Q2WKD6) D-hydantoinase	BTC	x	
Q3H3N5_9ACTO	>gnl|tr|Q3H3N5_9ACTO (Q3H3N5) D-hydantoinase	SFA	x	
Q831D1_ENTFA	>gnl|tr|Q831D1_ENTFA (Q831D1) D-hydantoinase	BTC	x	
Q8YMC4_ANASP	>gnl|tr|Q8YMC4_ANASP (Q8YMC4) D-hydantoinase	SFA	x	
Q41X18_DESHA	>gnl|tr|Q41X18_DESHA (Q41X18) Urease alpha-subunit, catalytic domain	NSF	x	
Q9RFF2_RHOSH	>gnl|tr|Q9RFF2_RHOSH (Q9RFF2) UreC	MFR	x	
Q484B6_COLP3	>gnl|tr|Q484B6_COLP3 (Q484B6) Isoaspartyl dipeptidase (EC 3.4.19.-)	BTC	X	
Q5E4P2_VIBF1	>gnl|tr|Q5E4P2_VIBF1 (Q5E4P2) Isoaspartyl dipeptidase	BTC	x	
Q6LRX9_PHOPR	>gnl|tr|Q6LRX9_PHOPR (Q6LRX9) Hypothetical isoaspartyl dipeptidase	BTC	x	
Q8RBI0_THETN	>gnl|tr|Q8RBI0_THETN (Q8RBI0) Isoaspartyl dipeptidase	BTC	X	
Q8XHX0_CLOPE	>gnl|tr|Q8XHX0_CLOPE (Q8XHX0) Isoaspartyl dipeptidase	BTC	X	
Q9KDT2_BACHD	>gnl|tr|Q9KDT2_BACHD (Q9KDT2) Isoaspartyl dipeptidase	BTC	X	
Q2WI02_CLOBE	>gnl|tr|Q2WI02_CLOBE (Q2WI02) Peptidase M38, beta-aspartyl dipeptidase	BTC	X	
Q3CJA4_THEET	>gnl|tr|Q3CJA4_THEET (Q3CJA4) Peptidase M38, beta-aspartyl dipeptidase	BTC	X	
Q3GCN1_9FIRM	>gnl|tr|Q3GCN1_9FIRM (Q3GCN1) Peptidase M38, beta-aspartyl dipeptidase	BTC	X	
Q3Q871_9GAMM	>gnl|tr|Q3Q871_9GAMM (Q3Q871) Peptidase M38, beta-aspartyl dipeptidase	MFR	x	
Q3QJN6_9GAMM	>gnl|tr|Q3QJN6_9GAMM (Q3QJN6) Peptidase M38, beta-aspartyl dipeptidase	MFR	x	
Q3Y1L2_ENTFC	>gnl|tr|Q3Y1L2_ENTFC (Q3Y1L2) Peptidase M38, beta-aspartyl dipeptidase	MFR	x	
Q41FJ1_9BACI	>gnl|tr|Q41FJ1_9BACI (Q41FJ1) Peptidase M38, beta-aspartyl dipeptidase	BTC	X	
Q41WX5_DESHA	>gnl|tr|Q41WX5_DESHA (Q41WX5) Peptidase M38, beta-aspartyl dipeptidase	BTC	X	
Q44JN7_CHRSL	>gnl|tr|Q44JN7_CHRSL (Q44JN7) Peptidase M38, beta-aspartyl dipeptidase	BTC	X	
Q4CGV7_CLOTM	>gnl|tr|Q4CGV7_CLOTM (Q4CGV7) Peptidase M38, beta-aspartyl dipeptidase	BTC	X	
Q4CRI1_TRYCR	>gnl|tr|Q4CRI1_TRYCR (Q4CRI1) 3,2-trans-enoyl-CoA isomerase, mitochondrial, putative (EC 5.3.3.8)	BTC	x	
Q4CTQ3_TRYCR	>gnl|tr|Q4CTQ3_TRYCR (Q4CTQ3) 3,2-trans-enoyl-CoA isomerase, mitochondrial, putative (EC 5.3.3.8)	BTC	x	
Q4CXJ3_TRYCR	>gnl|tr|Q4CXJ3_TRYCR (Q4CXJ3) 3,2-trans-enoyl-CoA isomerase, mitochondrial, putative (EC 5.3.3.8)	MFR	x	
Q4Q636_LEIMA	>gnl|tr|Q4Q636_LEIMA (Q4Q636) 3,2-trans-enoyl-CoA isomerase, mitochondrial, putative (EC 5.3.3.8)	BTC	x	

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q57V74_9TRYP	>gnl|tr|Q57V74_9TRYP (Q57V74) 3,2-trans-enoyl-CoA isomerase, mitochondrial, putative (EC 5.3.3.8)	BTC	x	
Q580R2_9TRYP	>gnl|tr|Q580R2_9TRYP (Q580R2) 3,2-trans-enoyl-CoA isomerase, mitochondrial, putative (EC 5.3.3.8)	BTC	x	
Q584L4_9TRYP	>gnl|tr|Q584L4_9TRYP (Q584L4) 3,2-trans-enoyl-CoA isomerase, mitochondrial, putative (EC 5.3.3.8)	BTC	x	
Q64592_RAT	>gnl|tr|Q64592_RAT (Q64592) Delta3, delta2-enoyl-CoA isomerase precursor (EC 5.3.3.8)	BTC	x	
Q5KPF9_CRYNE	>gnl|tr|Q5KPF9_CRYNE (Q5KPF9) 3-hydroxyisobutyryl-CoA hydrolase, putative	BTC	x	
Q3EKW7_BACTI	>gnl|tr|Q3EKW7_BACTI (Q3EKW7) 3-hydroxyisobutyryl-CoA hydrolase (EC 3.1.2.4)	BTC	x	
Q8I523_PLAF7	>gnl|tr|Q8I523_PLAF7 (Q8I523) 3-hydroxyisobutyryl-coenzyme A hydrolase, putative	BTC	x	
Q2QUG2_ORYSA	>gnl|tr|Q2QUG2_ORYSA (Q2QUG2) 3-hydroxyisobutyryl-coenzyme A hydrolase, putative	BTC	x	
Q6LXM2_METMP	>gnl|tr|Q6LXM2_METMP (Q6LXM2) Enolase	NSA	x	
Q8U0E9_PYRFU	>gnl|tr|Q8U0E9_PYRFU (Q8U0E9) Enolase (2-phosphoglycerate dehydratase)	NSA	x	
Q381E5_9TRYP	>gnl|tr|Q381E5_9TRYP (Q381E5) Enolase, putative (EC 4.2.1.11)	NSA	X	
Q4CN28_TRYCR	>gnl|tr|Q4CN28_TRYCR (Q4CN28) Enolase, putative	NSA	x	
Q4DMY6_TRYCR	>gnl|tr|Q4DMY6_TRYCR (Q4DMY6) Enolase, putative	NSA	x	
Q6WP09_9EUKA	>gnl|tr|Q6WP09_9EUKA (Q6WP09) Enolase 2 (Fragment)	BTC	x	
Q6WP10_9EUKA	>gnl|tr|Q6WP10_9EUKA (Q6WP10) Enolase 1 (Fragment)	BTC	x	
Q86M22_BRALA	>gnl|tr|Q86M22_BRALA (Q86M22) Enolase 3 (Fragment)	MFR	x	
Q8I4F9_CAEEL	>gnl|tr|Q8I4F9_CAEEL (Q8I4F9) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)	MFR	x	
Q9NDG1_9EUKA	>gnl|tr|Q9NDG1_9EUKA (Q9NDG1) Enolase 1 (EC 4.2.1.11) (Fragment)	BTC	x	
Q9NDG3_9EUKA	>gnl|tr|Q9NDG3_9EUKA (Q9NDG3) Enolase 1 (EC 4.2.1.11) (Fragment)	BTC	x	
Q9NDG4_9EUKA	>gnl|tr|Q9NDG4_9EUKA (Q9NDG4) Enolase 2 (EC 4.2.1.11) (Fragment)	BTC	x	
Q8BVS9_MOUSE	>gnl|tr|Q8BVS9_MOUSE (Q8BVS9) Adult male testis cDNA, RIKEN full-length enriched library, clone:4930412P13 product:hypothetical Enolase containing protein, full insert sequence	NSA	x	

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q8C042_MOUSE	>gnl|tr|Q8C042_MOUSE (Q8C042) Adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:6430537H07 product:hypothetical Enolase containing protein, full insert sequence	NSA	x	
Q7NSG8_CHRVO	>gnl|tr|Q7NSG8_CHRVO (Q7NSG8) Probable phosphopyruvate hydratase	NSA	x	
Q57I10_SALCH	>gnl|tr|Q57I10_SALCH (Q57I10) Galactonate dehydratase	NSA	x	
Q57M62_SALCH	>gnl|tr|Q57M62_SALCH (Q57M62) Paral putative galactonate dehydratase	SFA	x	
Q5LKY4_SILPO	>gnl|tr|Q5LKY4_SILPO (Q5LKY4) Galactonate dehydratase, putative	SFA	x	
Q8YD21_BRUME	>gnl|tr|Q8YD21_BRUME (Q8YD21) GALACTONATE DEHYDRATASE (EC 4.2.1.6)	NSA	x	
Q8ZNF9_SALTY	>gnl|tr|Q8ZNF9_SALTY (Q8ZNF9) Putative galactonate dehydratase	SFA	x	
Q3JVP3_BURP1	>gnl|tr|Q3JVP3_BURP1 (Q3JVP3) Mandelate racemase (EC 5.1.2.2)	BTC	x	
Q5NN22_ZYMMO	>gnl|tr|Q5NN22_ZYMMO (Q5NN22) Putative mandelate racemase (EC 5.1.2.2)	SFA	x	
Q5NN58_ZYMMO	>gnl|tr|Q5NN58_ZYMMO (Q5NN58) Mandelate racemase (EC 5.1.2.2)	SFA	x	
Q63X15_BURPS	>gnl|tr|Q63X15_BURPS (Q63X15) Putative mandelate racemase (EC 5.1.2.2)	BTC	x	
Q8YF15_BRUME	>gnl|tr|Q8YF15_BRUME (Q8YF15) MANDELATE RACEMASE (EC 5.1.2.2)	BTC	x	
Q8YF20_BRUME	>gnl|tr|Q8YF20_BRUME (Q8YF20) MANDELATE RACEMASE (EC 5.1.2.2)	SFA	x	
Q4J6U9_SULAC	>gnl|tr|Q4J6U9_SULAC (Q4J6U9) Mandelate racemase	SFA	x	
Q972M4_SULTO	>gnl|tr|Q972M4_SULTO (Q972M4) 373aa long hypothetical mandelate racemase	BTC	x	
Q2WPN7_CLOBE	>gnl|tr|Q2WPN7_CLOBE (Q2WPN7) Putative mandelate racemase	SFA	x	
Q2ZJ97_CALSA	>gnl|tr|Q2ZJ97_CALSA (Q2ZJ97) Conserved hypothetical mandelate racemase	BTC, MOF	x	
Q34P21_RHOPA	>gnl|tr|Q34P21_RHOPA (Q34P21) Putative mandelate racemase	SFA	x	
Q35J17_9BRAD	>gnl|tr|Q35J17_9BRAD (Q35J17) Probable mandelate racemase	BTC	x	
Q5PHP6_SALPA	>gnl|tr|Q5PHP6_SALPA (Q5PHP6) Putative mandelate racemase	SFA	x	
Q6D8H6_ERWCT	>gnl|tr|Q6D8H6_ERWCT (Q6D8H6) Putative mandelate racemase	BTC	x	
Q7VYH9_BORPE	>gnl|tr|Q7VYH9_BORPE (Q7VYH9) Putative mandelate racemase	SFA	x	
Q7W747_BORPA	>gnl|tr|Q7W747_BORPA (Q7W747) Putative mandelate racemase	SFA	x	
Q7WEE8_BORBR	>gnl|tr|Q7WEE8_BORBR (Q7WEE8) Putative mandelate racemase	BTC	x	
Q7WIN6_BORBR	>gnl|tr|Q7WIN6_BORBR (Q7WIN6) Putative mandelate racemase	SFA	x	
Q826B1_STRAW	>gnl|tr|Q826B1_STRAW (Q826B1) Putative mandelate racemase	SFA	x	
Q8Z7A7_SALTI	>gnl|tr|Q8Z7A7_SALTI (Q8Z7A7) Putative mandelate racemase	SFA	x	

Table K-2. TrEMBL data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>Q8ZKY6_SALTY</td><td>>gnl|tr|Q8ZKY6_SALTY (Q8ZKY6) Putative mandelate racemase</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q8ZL58_SALTY</td><td>>gnl|tr|Q8ZL58_SALTY (Q8ZL58) Putative mandelate racemase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q986Z4_RHILO</td><td>>gnl|tr|Q986Z4_RHILO (Q986Z4) Mandelate racemase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q44HW8_CHRSL</td><td>>gnl|tr|Q44HW8_CHRSL (Q44HW8) Glucarate dehydratase (EC 4.2.1.40)</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q8FEG5_ECOL6</td><td>>gnl|tr|Q8FEG5_ECOL6 (Q8FEG5) Glucarate dehydratase (EC 4.2.1.40)</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q8Z442_SALTI</td><td>>gnl|tr|Q8Z442_SALTI (Q8Z442) Probable glucarate dehydratase 2 (EC 4.2.1.40)</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q8ZMD8_SALTY</td><td>>gnl|tr|Q8ZMD8_SALTY (Q8ZMD8) Putative d-glucarate dehydratase (EC 4.2.1.40)</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q31XK2_SHIBS</td><td>>gnl|tr|Q31XK2_SHIBS (Q31XK2) Putative glucarate dehydratase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q3EIQ4_ACTSC</td><td>>gnl|tr|Q3EIQ4_ACTSC (Q3EIQ4) Putative d-glucarate dehydratase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q3YY68_SHISS</td><td>>gnl|tr|Q3YY68_SHISS (Q3YY68) Putative glucarate dehydratase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q7AB75_ECO57</td><td>>gnl|tr|Q7AB75_ECO57 (Q7AB75) Putative glucarate dehydratase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q5YTY6_NOCFA</td><td>>gnl|tr|Q5YTY6_NOCFA (Q5YTY6) Putative glucarate dehydratase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q6D8N6_ERWCT</td><td>>gnl|tr|Q6D8N6_ERWCT (Q6D8N6) Putative glucarate dehydratase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q82BX3_STRAW</td><td>>gnl|tr|Q82BX3_STRAW (Q82BX3) Putative glucarate dehydratase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q83QD3_SHIFL</td><td>>gnl|tr|Q83QD3_SHIFL (Q83QD3) Putative glucarate dehydratase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q8UBI7_AGRT5</td><td>>gnl|tr|Q8UBI7_AGRT5 (Q8UBI7) Glucarate dehydratase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q8X6T9_ECO57</td><td>>gnl|tr|Q8X6T9_ECO57 (Q8X6T9) Putative glucarate dehydratase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q4WFW5_ASPFU</td><td>>gnl|tr|Q4WFW5_ASPFU (Q4WFW5) Methylaspartate ammonia-lyase</td><td>BNC</td><td>x</td><td></td></tr>
<tr><td>Q7VUC6_BORPE</td><td>>gnl|tr|Q7VUC6_BORPE (Q7VUC6) Putative methylaspartate ammonia-lyase (EC 4.3.1.2)</td><td>BNC</td><td>x</td><td></td></tr>
<tr><td>Q7VZT1_BORPE</td><td>>gnl|tr|Q7VZT1_BORPE (Q7VZT1) Methylaspartate ammonia-lyase (EC 4.3.1.2)</td><td>BNC</td><td>x</td><td></td></tr>
<tr><td>Q7W411_BORPA</td><td>>gnl|tr|Q7W411_BORPA (Q7W411) Putative methylaspartate ammonia-lyase (EC 4.3.1.2)</td><td>BNC</td><td>x</td><td></td></tr>
<tr><td>Q7W579_BORPA</td><td>>gnl|tr|Q7W579_BORPA (Q7W579) Methylaspartate ammonia-lyase (EC 4.3.1.2)</td><td>BNC</td><td>x</td><td></td></tr>
<tr><td>Q7WCQ9_BORBR</td><td>>gnl|tr|Q7WCQ9_BORBR (Q7WCQ9) Methylaspartate ammonia-lyase (EC 4.3.1.2)</td><td>BNC</td><td>x</td><td></td></tr>
<tr><td>Q7WFE3_BORBR</td><td>>gnl|tr|Q7WFE3_BORBR (Q7WFE3) Putative methylaspartate ammonia-lyase (EC 4.3.1.2)</td><td>BNC</td><td>x</td><td></td></tr>
</table>

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q62R90_BACLD	>gnl|tr|Q62R90_BACLD (Q62R90) O-succinylbenzoate synthase	NSF	x	
Q6MAL2_PARUW	>gnl|tr|Q6MAL2_PARUW (Q6MAL2) Putative o-succinylbenzoate synthase II, menC	SFA	x	
Q6J674_9BURK	>gnl|tr|Q6J674_9BURK (Q6J674) L-alanine-DL-glutamate epimerase	SFA	x	
Q3BNF2_XANC5	>gnl|tr|Q3BNF2_XANC5 (Q3BNF2) Putative chloromuconate cycloisomerase (EC 5.5.1.7)	BAC, MOF	x	
Q7UJR2_RHOBA	>gnl|tr|Q7UJR2_RHOBA (Q7UJR2) Chloromuconate cycloisomerase YkfB1 (EC 5.5.1.7)	SGA	x	
Q5UX71_HALMA	>gnl|tr|Q5UX71_HALMA (Q5UX71) Chloromuconate cycloisomerase	SGA	x	
Q5V3S6_HALMA	>gnl|tr|Q5V3S6_HALMA (Q5V3S6) Chloromuconate cycloisomerase	SGA	x	
Q5V5B0_HALMA	>gnl|tr|Q5V5B0_HALMA (Q5V5B0) Chloromuconate cycloisomerase	BAC, MOF	x	
Q9HP25_HALSA	>gnl|tr|Q9HP25_HALSA (Q9HP25) Chloromuconate cycloisomerase	BAC, MOF	x	
Q9HQN7_HALSA	>gnl|tr|Q9HQN7_HALSA (Q9HQN7) Chloromuconate cycloisomerase	SGA	x	
O34027_BURCE	>gnl|tr|O34027_BURCE (O34027) Putative chloromuconate cycloisomerase	MFR	x	
Q4UPV4_XANC8	>gnl|tr|Q4UPV4_XANC8 (Q4UPV4) Chloromuconate cycloisomerase	BAC, MOF	x	
Q2NYJ4_XANOR	>gnl|tr|Q2NYJ4_XANOR (Q2NYJ4) Chloromuconate cycloisomerase	BAC	x	
Q57NY1_SALCH	>gnl|tr|Q57NY1_SALCH (Q57NY1) Putative chloromuconate cycloisomerase (Muconate cycloisomerase)	SGA	x	
Q5GVB7_XANOR	>gnl|tr|Q5GVB7_XANOR (Q5GVB7) Chloromuconate cycloisomerase	BAC, MOF	x	
Q5SHA6_THET8	>gnl|tr|Q5SHA6_THET8 (Q5SHA6) Chloromuconate cycloisomerase	SGA	x	
Q5ZU52_LEGPH	>gnl|tr|Q5ZU52_LEGPH (Q5ZU52) Chloromuconate cycloisomerase	BAC, MOF	x	
Q607C7_METCA	>gnl|tr|Q607C7_METCA (Q607C7) Putative chloromuconate cycloisomerase	BAC, MOF	x	
Q64WQ7_BACFR	>gnl|tr|Q64WQ7_BACFR (Q64WQ7) Chloromuconate cycloisomerase	SGA	x	
Q8P4A3_XANCP	>gnl|tr|Q8P4A3_XANCP (Q8P4A3) Chloromuconate cycloisomerase	BAC, MOF	x	

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q8PFW0_XANAC	>gnl|tr|Q8PFW0_XANAC (Q8PFW0) Chloromuconate cycloisomerase	BAC, MOF	x	
Q8UJJ9_AGRT5	>gnl|tr|Q8UJJ9_AGRT5 (Q8UJJ9) Chloromuconate cycloisomerase	SGA	x	
Q986H6_RHILO	>gnl|tr|Q986H6_RHILO (Q986H6) Chloromuconate cycloisomerase	MFR	x	
Q9RT94_DEIRA	>gnl|tr|Q9RT94_DEIRA (Q9RT94) Chloromuconate cycloisomerase, putative	BAC	x	
O28181_ARCFU	>gnl|tr|O28181_ARCFU (O28181) Muconate cycloisomerase II (ClcB)	SFA	x	
Q3X638_9ACTN	>gnl|tr|Q3X638_9ACTN (Q3X638) Muconate cycloisomerase (EC 5.5.1.1)	MFR	x	
Q407G0_9RHOB	>gnl|tr|Q407G0_9RHOB (Q407G0) Muconate cycloisomerase (EC 5.5.1.1)	BTC	x	
Q70AN9_RHOER	>gnl|tr|Q70AN9_RHOER (Q70AN9) Muconate cycloisomerase (EC 5.5.1.1)	BTC	x	
Q83XA5_RHOER	>gnl|tr|Q83XA5_RHOER (Q83XA5) Cis,cis-muconate cycloisomerase (EC 5.5.1.1)	BTC	x	
Q5LM96_SILPO	>gnl|tr|Q5LM96_SILPO (Q5LM96) Muconate cycloisomerase I (EC 5.5.1.1)	BTC	x	
Q5WDL3_BACSK	>gnl|tr|Q5WDL3_BACSK (Q5WDL3) Muconate cycloisomerase (EC 5.5.1.1)	SFA	x	
Q6N2T4_RHOPA	>gnl|tr|Q6N2T4_RHOPA (Q6N2T4) Putative muconate cycloisomerase (EC 5.5.1.1)	SGA	x	
Q72HL4_THET2	>gnl|tr|Q72HL4_THET2 (Q72HL4) Muconate cycloisomerase (EC 5.5.1.1)	SGA	x	
Q7UK54_RHOBA	>gnl|tr|Q7UK54_RHOBA (Q7UK54) Muconate cycloisomerase I (EC 5.5.1.1)	SGA	x	
Q8YH38_BRUME	>gnl|tr|Q8YH38_BRUME (Q8YH38) MUCONATE CYCLOISOMERASE I (EC 5.5.1.1)	SGA	x	
Q92YR6_RHIME	>gnl|tr|Q92YR6_RHIME (Q92YR6) Putative muconate cycloisomerase (EC 5.5.1.1)	SGA	x	
Q2XQ17_9NOCA	>gnl|tr|Q2XQ17_9NOCA (Q2XQ17) Cis-muconate cycloisomerase	BTC	x	
Q2ZG10_CALSA	>gnl|tr|Q2ZG10_CALSA (Q2ZG10) Muconate cycloisomerase	SGA	x	
Q34S34_RHOPA	>gnl|tr|Q34S34_RHOPA (Q34S34) Putative muconate cycloisomerase	SGA	x	
Q58LW9_9BURK	>gnl|tr|Q58LW9_9BURK (Q58LW9) Muconate cycloisomerase	BTC	x	
Q7AEG8_ECO57	>gnl|tr|Q7AEG8_ECO57 (Q7AEG8) Putative muconate cycloisomerase I	SGA	x	
Q8GH61_STRSE	>gnl|tr|Q8GH61_STRSE (Q8GH61) Muconate cycloisomerase	SGA	x	
Q5LBR0_BACFN	>gnl|tr|Q5LBR0_BACFN (Q5LBR0) Putative muconate cycloisomerase	SGA	x	
Q5LFS2_BACFN	>gnl|tr|Q5LFS2_BACFN (Q5LFS2) Putative muconate cycloisomerase	SGA	x	
Q5YTX2_NOCFA	>gnl|tr|Q5YTX2_NOCFA (Q5YTX2) Putative muconate cycloisomerase	BTC	x	
Q64SN3_BACFR	>gnl|tr|Q64SN3_BACFR (Q64SN3) Muconate cycloisomerase	SGA	x	
Q6LQX4_PHOPR	>gnl|tr|Q6LQX4_PHOPR (Q6LQX4) Hypothetical muconate cycloisomerase I	SGA	x	

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q83LB1_SHIFL	>gnl|tr|Q83LB1_SHIFL (Q83LB1) Putative muconate cycloisomerase I	SGA	x	
Q87JC4_VIBPA	>gnl|tr|Q87JC4_VIBPA (Q87JC4) Putative muconate cycloisomerase I	SGA	x	
Q8A861_BACTN	>gnl|tr|Q8A861_BACTN (Q8A861) Muconate cycloisomerase	SGA	x	
Q8EM93_OCEIH	>gnl|tr|Q8EM93_OCEIH (Q8EM93) Muconate cycloisomerase	BTC, MOF	x	
Q8EMJ9_OCEIH	>gnl|tr|Q8EMJ9_OCEIH (Q8EMJ9) Muconate cycloisomerase	SFA	x	
Q8FSB7_COREF	>gnl|tr|Q8FSB7_COREF (Q8FSB7) Putative muconate cycloisomerase	SGA	x	
Q8YRB6_ANASP	>gnl|tr|Q8YRB6_ANASP (Q8YRB6) Muconate cycloisomerase	SGA	x	
Q986H5_RHILO	>gnl|tr|Q986H5_RHILO (Q986H5) Muconate lactonizing enzyme	SGA	x	
Q98LZ8_RHILO	>gnl|tr|Q98LZ8_RHILO (Q98LZ8) Probable muconate cycloisomerase	SGA	x	
Q9K8K0_BACHD	>gnl|tr|Q9K8K0_BACHD (Q9K8K0) Muconate cycloisomerase	SGA	x	
Q9WXM1_THEMA	>gnl|tr|Q9WXM1_THEMA (Q9WXM1) Muconate cycloisomerase	SGA	x	
Q2X3Y2_9GAMM	>gnl|tr|Q2X3Y2_9GAMM (Q2X3Y2) HAD-superfamily hydrolase subfamily IIIA:Phosphatase kdsC (EC 3.1.3.45)	BTC	x	
Q2YCX4_NITMU	>gnl|tr|Q2YCX4_NITMU (Q2YCX4) Phosphatase kdsC precursor (EC 3.1.3.45)	BTC	x	
Q2Z8E4_9GAMM	>gnl|tr|Q2Z8E4_9GAMM (Q2Z8E4) HAD-superfamily hydrolase subfamily IIIA:Phosphatase kdsC (EC 3.1.3.45)	BTC	x	
Q31H02_THICR	>gnl|tr|Q31H02_THICR (Q31H02) Phosphatase kdsC (EC 3.1.3.45)	BTC	x	
Q31KV1_SYNP7	>gnl|tr|Q31KV1_SYNP7 (Q31KV1) Phosphatase kdsC (EC 3.1.3.45)	BTC	x	
Q33X06_9GAMM	>gnl|tr|Q33X06_9GAMM (Q33X06) HAD-superfamily hydrolase, subfamily IIIA:Phosphatase YrbI (EC 3.1.3.45)	BTC	x	
Q34XQ2_9GAMM	>gnl|tr|Q34XQ2_9GAMM (Q34XQ2) HAD-superfamily hydrolase subfamily IIIA:Phosphatase kdsC precursor (EC 3.1.3.45)	BTC	x	
Q35XU6_9GAMM	>gnl|tr|Q35XU6_9GAMM (Q35XU6) HAD-superfamily hydrolase subfamily IIIA:Phosphatase kdsC (EC 3.1.3.45)	BTC	x	
Q366V6_9GAMM	>gnl|tr|Q366V6_9GAMM (Q366V6) HAD-superfamily hydrolase subfamily IIIA:Phosphatase kdsC (EC 3.1.3.45)	BTC	x	
Q39CV5_BURS3	>gnl|tr|Q39CV5_BURS3 (Q39CV5) Phosphatase KdsC (EC 3.1.3.45)	BTC	x	
Q39M81_BURS3	>gnl|tr|Q39M81_BURS3 (Q39M81) Phosphatase kdsC (EC 3.1.3.45)	BTC	x	
Q3AP52_CHLCH	>gnl|tr|Q3AP52_CHLCH (Q3AP52) Putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45)	MFR	x	
Q3ARP0_CHLCH	>gnl|tr|Q3ARP0_CHLCH (Q3ARP0) Phosphatase kdsC (EC 3.1.3.45)	BTC	x	

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q3CMC6_ALTAT	>gnl|tr|Q3CMC6_ALTAT (Q3CMC6) Phosphatase YrbI precursor (EC 3.1.3.45)	BTC	x	
Q3FJA0_9BURK	>gnl|tr|Q3FJA0_9BURK (Q3FJA0) Phosphatase YrbI (EC 3.1.3.45)	BTC	x	
Q3IG37_PSEHT	>gnl|tr|Q3IG37_PSEHT (Q3IG37) 3-Deoxy-D-manno-octulosonate 8-phosphate (KDO 8-P) phosphatase (EC 3.1.3.45)	BTC	X	
Q3J7G0_NITOC	>gnl|tr|Q3J7G0_NITOC (Q3J7G0) Phosphatase kdsC (EC 3.1.3.45)	BTC	x	
Q3JP69_BURP1	>gnl|tr|Q3JP69_BURP1 (Q3JP69) 3-deoxy-manno-octulosonate-8-phosphatase (EC 3.1.3.45)	BTC	x	
Q3N5Y5_9DELT	>gnl|tr|Q3N5Y5_9DELT (Q3N5Y5) HAD-superfamily hydrolase, subfamily IIIA:Phosphatase YrbI (EC 3.1.3.45)	BTC	x	
Q40R39_DESAC	>gnl|tr|Q40R39_DESAC (Q40R39) HAD-superfamily hydrolase, subfamily IIIA:Phosphatase kdsC (EC 3.1.3.45)	BTC	x	
Q44DT2_CHRSL	>gnl|tr|Q44DT2_CHRSL (Q44DT2) HAD-superfamily hydrolase, subfamily IIIA:Phosphatase YrbI precursor (EC 3.1.3.45)	BTC	x	
Q451D1_9BURK	>gnl|tr|Q451D1_9BURK (Q451D1) Phosphatase YrbI (EC 3.1.3.45)	BTC	x	
Q4B879_BURVI	>gnl|tr|Q4B879_BURVI (Q4B879) Phosphatase YrbI (EC 3.1.3.45)	BTC	x	
Q5E7W0_VIBF1	>gnl|tr|Q5E7W0_VIBF1 (Q5E7W0) 3-deoxy-manno-octulosonate-8-phosphatase (EC 3.1.3.45)	BTC	x	
Q5E8H4_VIBF1	>gnl|tr|Q5E8H4_VIBF1 (Q5E8H4) 3-deoxy-manno-octulosonate-8-phosphatase (EC 3.1.3.45)	BTC	x	
Q5NG30_FRATT	>gnl|tr|Q5NG30_FRATT (Q5NG30) 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45)	BTC	x	
Q6FC69_ACIAD	>gnl|tr|Q6FC69_ACIAD (Q6FC69) 3-Deoxy-D-manno-octulosonate 8-phosphate (KDO 8-P) phosphatase (EC 3.1.3.45)	BTC	x	
Q2SHM4_9GAMM	>gnl|tr|Q2SHM4_9GAMM (Q2SHM4) Phosphonoacetaldehyde hydrolase (EC 3.11.1.1)	BTC	x	
Q38V12_LACSS	>gnl|tr|Q38V12_LACSS (Q38V12) Phosphonoacetaldehyde hydrolase (EC 3.11.1.1)	BTC	x	
Q81G82_BACCR	>gnl|tr|Q81G82_BACCR (Q81G82) Phosphonoacetaldehyde hydrolase (EC 3.11.1.1)	BTC	x	
Q3MYL4_9DELT	>gnl|tr|Q3MYL4_9DELT (Q3MYL4) Phosphonoacetaldehyde hydrolase	BTC	x	
Q3N6B6_9DELT	>gnl|tr|Q3N6B6_9DELT (Q3N6B6) Phosphonoacetaldehyde hydrolase	BTC	x	
Q3XZA4_ENTFC	>gnl|tr|Q3XZA4_ENTFC (Q3XZA4) Phosphonoacetaldehyde hydrolase	BTC	x	

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q64PZ2_BACFR	>gnl|tr|Q64PZ2_BACFR (Q64PZ2) Phosphonoacetaldehyde hydrolase	BTC	x	
Q6AG44_LEIXX	>gnl|tr|Q6AG44_LEIXX (Q6AG44) Phosphonoacetaldehyde hydrolase	NSF	X	
P95933_SULSO	>gnl|tr|P95933_SULSO (P95933) Orf c01035 protein (2-haloalkanoic acid dehalogenase) (EC 3.8.1.2)	SFA	X	
Q5V5A3_HALMA	>gnl|tr|Q5V5A3_HALMA (Q5V5A3) 2-haloalkanoic acid dehalogenase (EC 3.8.1.2)	BTC	x	
Q97WT6_SULSO	>gnl|tr|Q97WT6_SULSO (Q97WT6) 2-haloalkanoic acid dehalogenase (EC 3.8.1.2)	NSF	X	
Q97X58_SULSO	>gnl|tr|Q97X58_SULSO (Q97X58) 2-haloalkanoic acid dehalogenase (EC 3.8.1.2)	NSF	X	
Q9UXB5_SULSO	>gnl|tr|Q9UXB5_SULSO (Q9UXB5) Hypothetical protein ORF-c10_004 (2-haloalkanoic acid dehalogenase, putative) (EC 3.8.1.2)	NSF	X	
O33563_RHISP	>gnl|tr|O33563_RHISP (O33563) 2-haloacid dehalogenase (EC 3.8.1.2)	NSF	x	
Q2S347_9SPHI	>gnl|tr|Q2S347_9SPHI (Q2S347) Haloacid dehalogenase, type II (EC 3.8.1.2)	SFA	x	
Q2T7Z2_BURTH	>gnl|tr|Q2T7Z2_BURTH (Q2T7Z2) Haloacid dehalogenase, type II (EC 3.8.1.2)	SFA	x	
Q394H6_BURS3	>gnl|tr|Q394H6_BURS3 (Q394H6) Haloacid dehalogenase, type II (EC 3.8.1.2)	BTC	x	
Q3FL85_9BURK	>gnl|tr|Q3FL85_9BURK (Q3FL85) HAD-superfamily hydrolase, subfamily IA, variant 2 (EC 3.8.1.2)	BTC	x	
Q3IHE0_PSEHT	>gnl|tr|Q3IHE0_PSEHT (Q3IHE0) Cryptic haloacid dehalogenase 1 (EC 3.8.1.2) (EC 3.8.1.2)	BTC	x	
Q3JJY3_BURP1	>gnl|tr|Q3JJY3_BURP1 (Q3JJY3) Haloacid dehalogenase, type II (EC 3.8.1.2)	SFA	x	
Q43L46_SOLUS	>gnl|tr|Q43L46_SOLUS (Q43L46) HAD-superfamily hydrolase, subfamily IA, variant 2 (EC 3.8.1.2)	MFR	x	
Q44IP7_CHRSL	>gnl|tr|Q44IP7_CHRSL (Q44IP7) HAD-superfamily hydrolase, subfamily IA, variant 2 (EC 3.8.1.2)	BTC	x	
Q47ZE3_COLP3	>gnl|tr|Q47ZE3_COLP3 (Q47ZE3) Haloacid dehalogenase, type II (EC 3.8.1.2)	BTC	x	
Q48BY1_PSE14	>gnl|tr|Q48BY1_PSE14 (Q48BY1) Haloacid dehalogenase, type II (EC 3.8.1.2)	SFA	x	
Q48KU3_PSE14	>gnl|tr|Q48KU3_PSE14 (Q48KU3) Haloacid dehalogenase, type II (EC 3.8.1.2)	SFA	x	
Q4AW91_9BURK	>gnl|tr|Q4AW91_9BURK (Q4AW91) HAD-superfamily hydrolase, subfamily IA, variant 2 (EC 3.8.1.2)	BTC	x	
Q4FPC8_PELUB	>gnl|tr|Q4FPC8_PELUB (Q4FPC8) (S)-2-haloacid dehalogenase (EC 3.8.1.2)	BTC	x	
Q5LKE4_SILPO	>gnl|tr|Q5LKE4_SILPO (Q5LKE4) Haloacid dehalogenase, type II (EC 3.8.1.2)	BTC	x	

Table K-2. TrEMBL data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>Q62E30_BURMA</td><td>>gnl|tr|Q62E30_BURMA (Q62E30) Haloacid dehalogenase, type II (EC 3.8.1.2)</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q7USD6_RHOBA</td><td>>gnl|tr|Q7USD6_RHOBA (Q7USD6) Cryptic haloacid dehalogenase 1 (EC 3.8.1.2)</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q814M0_BACCR</td><td>>gnl|tr|Q814M0_BACCR (Q814M0) 2-haloalkanoic acid dehalogenase (EC 3.8.1.2)</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q81B55_BACCR</td><td>>gnl|tr|Q81B55_BACCR (Q81B55) 2-haloalkanoic acid dehalogenase (EC 3.8.1.2)</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q81CM4_BACCR</td><td>>gnl|tr|Q81CM4_BACCR (Q81CM4) 2-haloalkanoic acid dehalogenase (EC 3.8.1.2)</td><td>NSF</td><td>x</td><td></td></tr>
<tr><td>Q88TT5_LACPL</td><td>>gnl|tr|Q88TT5_LACPL (Q88TT5) 2-haloacid dehalogenase (Putative) (EC 3.8.1.2)</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q893A5_CLOTE</td><td>>gnl|tr|Q893A5_CLOTE (Q893A5) 2-haloalkanoic acid dehalogenase I (EC 3.8.1.2)</td><td>NSF</td><td>x</td><td></td></tr>
<tr><td>Q8YFS7_BRUME</td><td>>gnl|tr|Q8YFS7_BRUME (Q8YFS7) 2-HALOALKANOIC ACID DEHALOGENASE I (EC 3.8.1.2)</td><td>NSF</td><td>x</td><td></td></tr>
<tr><td>Q8YFZ4_BRUME</td><td>>gnl|tr|Q8YFZ4_BRUME (Q8YFZ4) 2-HALOALKANOIC ACID DEHALOGENASE I (EC 3.8.1.2)</td><td>MFR</td><td>x</td><td></td></tr>
<tr><td>Q92Y68_RHIME</td><td>>gnl|tr|Q92Y68_RHIME (Q92Y68) Putative dehalogenase (EC 3.8.1.2)</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q4WW71_ASPFU</td><td>>gnl|tr|Q4WW71_ASPFU (Q4WW71) Haloacid dehalogenase, type II</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q4X243_ASPFU</td><td>>gnl|tr|Q4X243_ASPFU (Q4X243) Haloacid dehalogenase, type II</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q5KBZ3_CRYNE</td><td>>gnl|tr|Q5KBZ3_CRYNE (Q5KBZ3) Haloacid dehalogenase, putative</td><td>NSF</td><td>x</td><td></td></tr>
<tr><td>Q3CLA3_ALTAT</td><td>>gnl|tr|Q3CLA3_ALTAT (Q3CLA3) Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2:HAD-superfamily hydrolase, subfamily IA, variant 3</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q4FRW4_PSYAR</td><td>>gnl|tr|Q4FRW4_PSYAR (Q4FRW4) Probable Haloacid dehalogenase, type II</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q6W0Y1_RHISN</td><td>>gnl|tr|Q6W0Y1_RHISN (Q6W0Y1) 2-haloacid halidohydrolase Iva</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q6W0Y4_RHISN</td><td>>gnl|tr|Q6W0Y4_RHISN (Q6W0Y4) 2-haloacid halidohydrolase IVa</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q6W115_RHISN</td><td>>gnl|tr|Q6W115_RHISN (Q6W115) 2-haloacid halidohydrolase IVa</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q5LQL5_SILPO</td><td>>gnl|tr|Q5LQL5_SILPO (Q5LQL5) Haloacid dehalogenase, type II, putative</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q7NZQ7_CHRVO</td><td>>gnl|tr|Q7NZQ7_CHRVO (Q7NZQ7) Probable haloacid dehalogenase</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q7VSB2_BORPE</td><td>>gnl|tr|Q7VSB2_BORPE (Q7VSB2) Probable haloacid dehalogenase</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q88AY6_PSESM</td><td>>gnl|tr|Q88AY6_PSESM (Q88AY6) Haloacid dehalogenase, type II</td><td>SFA</td><td>x</td><td></td></tr>
</table>

Table K-2. TrEMBL data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>Q9I5C9_PSEAE</td><td>>gnl|tr|Q9I5C9_PSEAE (Q9I5C9) Probable haloacid dehalogenase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q5QUA4_IDILO</td><td>>gnl|tr|Q5QUA4_IDILO (Q5QUA4) L-2-haloalkanoic acid dehalogenase, HAD superfamily</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q96XE7_SULTO</td><td>>gnl|tr|Q96XE7_SULTO (Q96XE7) 201aa long hypothetical 2-haloalkanoic acid dehalogenase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q96ZJ9_SULTO</td><td>>gnl|tr|Q96ZJ9_SULTO (Q96ZJ9) 200aa long hypothetical 2-haloalkanoic acid dehalogenase</td><td>NSF</td><td>x</td><td></td></tr>
<tr><td>Q4WC33_ASPFU</td><td>>gnl|tr|Q4WC33_ASPFU (Q4WC33) 2-haloalkanoic acid dehalogenase, putative</td><td>NSF</td><td>x</td><td></td></tr>
<tr><td>Q4WL82_ASPFU</td><td>>gnl|tr|Q4WL82_ASPFU (Q4WL82) 2-haloalkanoic acid dehalogenase</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q3A4S3_PELCD</td><td>>gnl|tr|Q3A4S3_PELCD (Q3A4S3) L-2-haloalkanoic acid dehalogenase</td><td>NSF</td><td>x</td><td></td></tr>
<tr><td>Q4A097_STAS1</td><td>>gnl|tr|Q4A097_STAS1 (Q4A097) Putative 2-haloalkanoic acid dehalogenase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q72YT0_BACC1</td><td>>gnl|tr|Q72YT0_BACC1 (Q72YT0) L-2-haloalkanoic acid dehalogenase</td><td>NSF</td><td>x</td><td></td></tr>
<tr><td>Q82PY4_STRAW</td><td>>gnl|tr|Q82PY4_STRAW (Q82PY4) Putative 2-haloalkanoic acid dehalogenase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q89F74_BRAJA</td><td>>gnl|tr|Q89F74_BRAJA (Q89F74) 2-haloalkanoic acid dehalogenase</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q8CQ52_STAES</td><td>>gnl|tr|Q8CQ52_STAES (Q8CQ52) L-2-haloalkanoic acid dehalogenase</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q8CV25_OCEIH</td><td>>gnl|tr|Q8CV25_OCEIH (Q8CV25) L-2-haloalkanoic acid dehalogenase</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q8UAG6_AGRT5</td><td>>gnl|tr|Q8UAG6_AGRT5 (Q8UAG6) 2-haloalkanoic acid dehalogenase (AGR_L_2827p)</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q98DR9_RHILO</td><td>>gnl|tr|Q98DR9_RHILO (Q98DR9) 2-haloalkanoic acid dehalogenase</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q99W01_STAAM</td><td>>gnl|tr|Q99W01_STAAM (Q99W01) L-2-haloalkanoic acid dehalogenase</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q9RJT2_STRCO</td><td>>gnl|tr|Q9RJT2_STRCO (Q9RJT2) Putative 2-haloalkanoic acid dehalogenase</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q8UAG9_AGRT5</td><td>>gnl|tr|Q8UAG9_AGRT5 (Q8UAG9) Haloalkanoic acid dehalogenase</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q8GJ84_PSEPU</td><td>>gnl|tr|Q8GJ84_PSEPU (Q8GJ84) Halocarboxylic acid dehalogenase DehI</td><td>NSF</td><td>x</td><td></td></tr>
<tr><td>Q4JCF8_SULAC</td><td>>gnl|tr|Q4JCF8_SULAC (Q4JCF8) Beta-phosphoglucomutase (EC 5.4.2.6)</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q8PWF4_METMA</td><td>>gnl|tr|Q8PWF4_METMA (Q8PWF4) Beta-phosphoglucomutase (EC 5.4.2.6)</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q8PZ02_METMA</td><td>>gnl|tr|Q8PZ02_METMA (Q8PZ02) Beta-phosphoglucomutase (EC 5.4.2.6)</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q3M459_ANAVT</td><td>>gnl|tr|Q3M459_ANAVT (Q3M459) HAD-superfamily hydrolase subfamily IA, variant 3 (EC 5.4.2.6)</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q3M8K3_ANAVT</td><td>>gnl|tr|Q3M8K3_ANAVT (Q3M8K3) HAD-superfamily hydrolase subfamily IA, variant 3 (EC 5.4.2.6)</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>Q4A6U4_MYCS5</td><td>>gnl|tr|Q4A6U4_MYCS5 (Q4A6U4) Beta-phosphoglucomutase (EC 5.4.2.6)</td><td>BTC</td><td>x</td><td></td></tr>
</table>

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q5FI05_LACAC	>gnl|tr|Q5FI05_LACAC (Q5FI05) Beta-phosphoglucomutase (EC 5.4.2.6)	BTC	x	
Q5ZWJ3_LEGPH	>gnl|tr|Q5ZWJ3_LEGPH (Q5ZWJ3) Beta-phosphoglucomutase (EC 5.4.2.6)	SFA	x	
Q6KHP8_MYCMO	>gnl|tr|Q6KHP8_MYCMO (Q6KHP8) Beta-phosphoglucomutase (EC 5.4.2.6)	BTC	x	
Q7NY78_CHRVO	>gnl|tr|Q7NY78_CHRVO (Q7NY78) Probable beta-phosphoglucomutase (EC 5.4.2.6)	SFA	x	
Q7NY80_CHRVO	>gnl|tr|Q7NY80_CHRVO (Q7NY80) Probable beta-phosphoglucomutase (EC 5.4.2.6)	SFA	x	
Q46EH2_METBA	>gnl|tr|Q46EH2_METBA (Q46EH2) Beta-phosphoglucomutase	SFA	x	
Q46G16_METBA	>gnl|tr|Q46G16_METBA (Q46G16) Beta-phosphoglucomutase	SFA	x	
Q8TTI2_METAC	>gnl|tr|Q8TTI2_METAC (Q8TTI2) Beta-phosphoglucomutase	SFA	x	
Q336Q4_ORYSA	>gnl|tr|Q336Q4_ORYSA (Q336Q4) Beta-phosphoglucomutase, putative	SFA	x	
Q8S7Q2_ORYSA	>gnl|tr|Q8S7Q2_ORYSA (Q8S7Q2) Putative beta-phosphoglucomutase	SFA	x	
Q9ZVJ5_ARATH	>gnl|tr|Q9ZVJ5_ARATH (Q9ZVJ5) Expressed protein (At2g38740/T6A23.6) (Putative beta-phosphoglucomutase)	SFA	x	
Q487N7_COLP3	>gnl|tr|Q487N7_COLP3 (Q487N7) Putative beta-phosphoglucomutase	BTC	x	
Q5M187_STRT1	>gnl|tr|Q5M187_STRT1 (Q5M187) Beta-phosphoglucomutase, putative	SFA	x	
Q5M5S4_STRT2	>gnl|tr|Q5M5S4_STRT2 (Q5M5S4) Beta-phosphoglucomutase, putative	SFA	x	
Q64PM5_BACFR	>gnl|tr|Q64PM5_BACFR (Q64PM5) Putative beta-phosphoglucomutase	SFA	x	
Q74LH1_LACJO	>gnl|tr|Q74LH1_LACJO (Q74LH1) Beta-phosphoglucomutase	BTC	x	
Q8A5V9_BACTN	>gnl|tr|Q8A5V9_BACTN (Q8A5V9) Putative beta-phosphoglucomutase	SFA	x	
Q8DAJ6_VIBVU	>gnl|tr|Q8DAJ6_VIBVU (Q8DAJ6) Beta-phosphoglucomutase	SFA	x	
Q8FQN0_COREF	>gnl|tr|Q8FQN0_COREF (Q8FQN0) Putative beta-phosphoglucomutase	BTC	x	
Q97MN9_CLOAB	>gnl|tr|Q97MN9_CLOAB (Q97MN9) Beta-phosphoglucomutase, putative	BTC	x	
Q9K668_BACHD	>gnl|tr|Q9K668_BACHD (Q9K668) Beta-phosphoglucomutase	BTC	x	
Q3MBN2_ANAVT	>gnl|tr|Q3MBN2_ANAVT (Q3MBN2) Terpene synthase, metal-binding (EC 4.2.3.7)	NSF	x	
Q372B1_RHOPA	>gnl|tr|Q372B1_RHOPA (Q372B1) Terpene synthase:Squalene cyclase (EC 5.4.99.17)	BTC	x	
Q9V0H4_PYRAB	>gnl|tr|Q9V0H4_PYRAB (Q9V0H4) Squalene-hopene cyclase, putative	NSF	x	
Q4WA71_ASPFU	>gnl|tr|Q4WA71_ASPFU (Q4WA71) Squalene-hopene cyclase	BTC	x	
Q2U3C4_ASPOR	>gnl|tr|Q2U3C4_ASPOR (Q2U3C4) Squalene cyclase	BTC	x	
Q35C98_9BRAD	>gnl|tr|Q35C98_9BRAD (Q35C98) Terpene synthase:Squalene cyclase	BTC	x	

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q3EMG8_BACTI	>gnl|tr|Q3EMG8_BACTI (Q3EMG8) Methylmalonyl CoA epimerase (EC 5.1.99.1)	BTC	x	
Q5LUX0_SILPO	>gnl|tr|Q5LUX0_SILPO (Q5LUX0) Methylmalonyl-CoA epimerase (EC 5.1.99.1)	BTC	x	
Q6A8R5_PROAC	>gnl|tr|Q6A8R5_PROAC (Q6A8R5) Methylmalonyl CoA epimerase (EC 5.1.99.1)	BTC	x	
Q81EX4_BACCR	>gnl|tr|Q81EX4_BACCR (Q81EX4) Methylmalonyl CoA epimerase (EC 5.1.99.1)	BTC	x	
Q8YGL6_BRUME	>gnl|tr|Q8YGL6_BRUME (Q8YGL6) Methylmalonyl CoA epimerase (EC 5.1.99.1)	BTC	x	
Q5JG02_PYRKO	>gnl|tr|Q5JG02_PYRKO (Q5JG02) Methylmalonyl-CoA epimerase	BTC	x	
Q9V226_PYRAB	>gnl|tr|Q9V226_PYRAB (Q9V226) Methylmalonyl-coA epimerase	BTC	x	
P90791_CAEEL	>gnl|tr|P90791_CAEEL (P90791) Hypothetical protein mce-1 (Mitochondrial methylmalonyl-CoA epimerase)	BTC	x	
Q553V2_DICDI	>gnl|tr|Q553V2_DICDI (Q553V2) Methylmalonyl-CoA epimerase	BTC	x	
Q84FV9_METEX	>gnl|tr|Q84FV9_METEX (Q84FV9) Methylmalonyl-CoA epimerase	BTC	x	
Q5SLA1_THET8	>gnl|tr|Q5SLA1_THET8 (Q5SLA1) Probable methylmalonyl-CoA epimerase	BTC	x	
Q6NHS4_CORDI	>gnl|tr|Q6NHS4_CORDI (Q6NHS4) Putative methylmalonyl-CoA epimerase	BTC	x	
Q72LN4_THET2	>gnl|tr|Q72LN4_THET2 (Q72LN4) Probable methylmalonyl-coA epimerase	BTC	x	
Q747G3_GEOSL	>gnl|tr|Q747G3_GEOSL (Q747G3) Methylmalonyl-CoA epimerase	BTC	x	
Q41R00_FERAC	>gnl|tr|Q41R00_FERAC (Q41R00) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)	BTC	x	
Q6KZ98_PICTO	>gnl|tr|Q6KZ98_PICTO (Q6KZ98) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)	BTC	x	
Q4W8X8_ASPFU	>gnl|tr|Q4W8X8_ASPFU (Q4W8X8) 4-hydroxyphenylpyruvate dioxygenase, putative	NSF	x	
Q4WF44_ASPFU	>gnl|tr|Q4WF44_ASPFU (Q4WF44) 4-hydroxyphenylpyruvate dioxygenase, putative	NSF	x	
Q4WMT9_ASPFU	>gnl|tr|Q4WMT9_ASPFU (Q4WMT9) 4-hydroxyphenylpyruvate dioxygenase, putative	NSF	x	
Q4WYZ8_ASPFU	>gnl|tr|Q4WYZ8_ASPFU (Q4WYZ8) 4-hydroxyphenylpyruvate dioxygenase, putative	NSF	x	

Table K-2. TrEMBL data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>Q2WBX9_PLADU</td><td>>gnl|tr|Q2WBX9_PLADU (Q2WBX9) 4-hydroxyphenylpyruvate dioxygenase protein (Fragment)</td><td>BTC</td><td>X</td><td></td></tr>
<tr><td>Q45FE8_WHEAT</td><td>>gnl|tr|Q45FE8_WHEAT (Q45FE8) 4-hydroxyphenylpyruvate dioxygenase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q8H1T5_ABUTH</td><td>>gnl|tr|Q8H1T5_ABUTH (Q8H1T5) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (Fragment)</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q35GS3_9BRAD</td><td>>gnl|tr|Q35GS3_9BRAD (Q35GS3) 4-hydroxyphenylpyruvate dioxygenase</td><td>NSF</td><td>X</td><td></td></tr>
<tr><td>Q3HK21_TRIER</td><td>>gnl|tr|Q3HK21_TRIER (Q3HK21) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q3M423_ANAVT</td><td>>gnl|tr|Q3M423_ANAVT (Q3M423) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q430G8_9ACTO</td><td>>gnl|tr|Q430G8_9ACTO (Q430G8) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q44C76_CHRSL</td><td>>gnl|tr|Q44C76_CHRSL (Q44C76) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td>BTC</td><td>X</td><td></td></tr>
<tr><td>Q4AWB1_9BURK</td><td>>gnl|tr|Q4AWB1_9BURK (Q4AWB1) 4-hydroxyphenylpyruvate dioxygenase precursor (EC 1.13.11.27)</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q4AZ09_9BURK</td><td>>gnl|tr|Q4AZ09_9BURK (Q4AZ09) 4-hydroxyphenylpyruvate dioxygenase</td><td>NSF</td><td>x</td><td></td></tr>
<tr><td>Q4C4V8_CROWT</td><td>>gnl|tr|Q4C4V8_CROWT (Q4C4V8) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q4NPL0_9DELT</td><td>>gnl|tr|Q4NPL0_9DELT (Q4NPL0) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q5FTP5_GLUOX</td><td>>gnl|tr|Q5FTP5_GLUOX (Q5FTP5) Putative 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td>NSF</td><td>x</td><td></td></tr>
<tr><td>Q7NC88_GLOVI</td><td>>gnl|tr|Q7NC88_GLOVI (Q7NC88) 4-hydroxyphenylpyruvate dioxygenase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q8YYS5_ANASP</td><td>>gnl|tr|Q8YYS5_ANASP (Q8YYS5) 4-hydroxyphenylpyruvate dioxygenase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q92TL8_RHIME</td><td>>gnl|tr|Q92TL8_RHIME (Q92TL8) Putative 4-hydroxyphenylpyruvate dioxygenase protein (EC 1.13.11.27)</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q70ZL8_CHLRE</td><td>>gnl|tr|Q70ZL8_CHLRE (Q70ZL8) P-hydroxyphenylpyruvate dioxigenase (EC 1.13.11.27) (Fragment)</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>Q9Z4X7_STRCO</td><td>>gnl|tr|Q9Z4X7_STRCO (Q9Z4X7) Putative 4-hydroxyphenylpyruvic acid dioxygenase</td><td>BTC</td><td>x</td><td></td></tr>
</table>

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q736Y5_BACC1	>gnl|tr|Q736Y5_BACC1 (Q736Y5) Fosfomycin resistance protein (Glutathione transferase) BH1778 (EC 2.5.1.18)	SGA	x	
Q8KFS3_CHLTE	>gnl|tr|Q8KFS3_CHLTE (Q8KFS3) Glutathione S-transferase, fosfomycin resistance protein, putative (EC 2.5.1.18)	SFA	x	
Q3AQL5_CHLCH	>gnl|tr|Q3AQL5_CHLCH (Q3AQL5) Glutathione S-transferase, fosfomycin resistance protein, putative	SFA	x	
Q3B206_PELLD	>gnl|tr|Q3B206_PELLD (Q3B206) Glutathione S-transferase, fosfomycin resistance protein, putative	SFA	x	
Q5UZJ5_HALMA	>gnl|tr|Q5UZJ5_HALMA (Q5UZJ5) Putative lactoyglutathione lyase (EC 4.4.1.5)	SFA	x	
Q5V0W9_HALMA	>gnl|tr|Q5V0W9_HALMA (Q5V0W9) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q5V2B4_HALMA	>gnl|tr|Q5V2B4_HALMA (Q5V2B4) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q8PS64_METMA	>gnl|tr|Q8PS64_METMA (Q8PS64) Conserved protein (EC 4.4.1.5)	SFA	x	
Q8PSP8_METMA	>gnl|tr|Q8PSP8_METMA (Q8PSP8) Lactoylglutathione lyase (EC 4.4.1.5)	SFA	x	
Q97W20_SULSO	>gnl|tr|Q97W20_SULSO (Q97W20) Lactoylglutathione lyase (Glyoxalase I), putative (EC 4.4.1.5)	SFA	x	
Q2PYM9_LEIIN	>gnl|tr|Q2PYM9_LEIIN (Q2PYM9) Glyoxalase I (EC 4.4.1.5)	BTC	x	
Q6LFL9_PLAF7	>gnl|tr|Q6LFL9_PLAF7 (Q6LFL9) Glyoxalase I, putative (EC 4.4.1.5)	NSF	x	
Q2RRH9_RHORU	>gnl|tr|Q2RRH9_RHORU (Q2RRH9) Glyoxalase/bleomycin resistance protein/dioxygenase (EC 4.4.1.5)	BTC	x	
Q2SMR0_9GAMM	>gnl|tr|Q2SMR0_9GAMM (Q2SMR0) Lactoylglutathione lyase (EC 4.4.1.5)	SFA	x	
Q2X3I0_9GAMM	>gnl|tr|Q2X3I0_9GAMM (Q2X3I0) Glyoxalase I (EC 4.4.1.5)	BTC	x	
Q2YVH1_STAAB	>gnl|tr|Q2YVH1_STAAB (Q2YVH1) Probable glyoxylase family protein (EC 4.4.1.5)	SFA	x	
Q2ZAU5_9GAMM	>gnl|tr|Q2ZAU5_9GAMM (Q2ZAU5) Glyoxalase I (EC 4.4.1.5)	BTC	x	
Q2ZP50_SHEPU	>gnl|tr|Q2ZP50_SHEPU (Q2ZP50) Glyoxalase I (EC 4.4.1.5)	BTC	x	
Q31BN2_PROM9	>gnl|tr|Q31BN2_PROM9 (Q31BN2) Glyoxalase I (EC 4.4.1.5)	BTC	x	
Q31FE5_THICR	>gnl|tr|Q31FE5_THICR (Q31FE5) Glyoxalase I (EC 4.4.1.5)	BTC	x	
Q33VQ8_9GAMM	>gnl|tr|Q33VQ8_9GAMM (Q33VQ8) Glyoxalase I (EC 4.4.1.5)	BTC	x	
Q35XA3_9GAMM	>gnl|tr|Q35XA3_9GAMM (Q35XA3) Glyoxalase I (EC 4.4.1.5)	BTC	x	
Q36B94_9GAMM	>gnl|tr|Q36B94_9GAMM (Q36B94) Glyoxalase I (EC 4.4.1.5)	BTC	x	
Q3AGS5_SYNSC	>gnl|tr|Q3AGS5_SYNSC (Q3AGS5) Glyoxalase I (EC 4.4.1.5)	BTC	x	
Q3AVW6_SYNS9	>gnl|tr|Q3AVW6_SYNS9 (Q3AVW6) Glyoxalase I (EC 4.4.1.5)	BTC	x	

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q3CT67_ALTAT	>gnl|tr|Q3CT67_ALTAT (Q3CT67) Glyoxalase I (EC 4.4.1.5)	BTC	x	
Q3D407_STRAG	>gnl|tr|Q3D407_STRAG (Q3D407) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q3D918_STRAG	>gnl|tr|Q3D918_STRAG (Q3D918) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q3DG17_STRAG	>gnl|tr|Q3DG17_STRAG (Q3DG17) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q3DKJ5_STRAG	>gnl|tr|Q3DKJ5_STRAG (Q3DKJ5) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q3DVB3_STRAG	>gnl|tr|Q3DVB3_STRAG (Q3DVB3) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q3ELY9_BACTI	>gnl|tr|Q3ELY9_BACTI (Q3ELY9) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q3EV18_BACTI	>gnl|tr|Q3EV18_BACTI (Q3EV18) Lactoylglutathione lyase (EC 4.4.1.5)	SFA	x	
Q3EY13_BACTI	>gnl|tr|Q3EY13_BACTI (Q3EY13) Lactoylglutathione lyase (EC 4.4.1.5)	NSF	x	
Q3FMG8_9BURK	>gnl|tr|Q3FMG8_9BURK (Q3FMG8) Glyoxalase I (EC 4.4.1.5)	BTC	x	
Q3GQN1_9GAMM	>gnl|tr|Q3GQN1_9GAMM (Q3GQN1) Glyoxalase I (EC 4.4.1.5)	BTC	x	
Q3IKD2_PSEHT	>gnl|tr|Q3IKD2_PSEHT (Q3IKD2) Glyoxalase I, nickel isomerase (Lactoylglutathione lyase) (EC 4.4.1.5)	BTC	x	
Q3IX84_RHOS4	>gnl|tr|Q3IX84_RHOS4 (Q3IX84) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q3IZP4_RHOS4	>gnl|tr|Q3IZP4_RHOS4 (Q3IZP4) Glyoxalase I (Lactoylglutathione lyase) (EC 4.4.1.5)	SFA	x	
Q3K038_STRA1	>gnl|tr|Q3K038_STRA1 (Q3K038) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q3NL38_SHEFR	>gnl|tr|Q3NL38_SHEFR (Q3NL38) Glyoxalase I (EC 4.4.1.5)	BTC	x	
Q3NNJ6_SHEFR	>gnl|tr|Q3NNJ6_SHEFR (Q3NNJ6) Glyoxalase I (EC 4.4.1.5)	BTC	x	
Q3NXI1_9GAMM	>gnl|tr|Q3NXI1_9GAMM (Q3NXI1) Glyoxalase I (EC 4.4.1.5)	BTC	x	
Q3Q738_9GAMM	>gnl|tr|Q3Q738_9GAMM (Q3Q738) Glyoxalase I (EC 4.4.1.5)	BTC	x	
Q3QFF7_9GAMM	>gnl|tr|Q3QFF7_9GAMM (Q3QFF7) Glyoxalase I (EC 4.4.1.5)	BTC	x	
Q3RXS7_RALME	>gnl|tr|Q3RXS7_RALME (Q3RXS7) Glyoxalase I (EC 4.4.1.5)	BTC	x	
Q3SGF4_THIDA	>gnl|tr|Q3SGF4_THIDA (Q3SGF4) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q3SS69_NITWN	>gnl|tr|Q3SS69_NITWN (Q3SS69) Glyoxalase/bleomycin resistance protein/dioxygenase (EC 4.4.1.5)	BTC	X	
Q482V1_COLP3	>gnl|tr|Q482V1_COLP3 (Q482V1) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q48TJ7_STRPM	>gnl|tr|Q48TJ7_STRPM (Q48TJ7) Lactoylglutathione lyase (EC 4.4.1.5)	SFA	x	
Q48UT3_STRPM	>gnl|tr|Q48UT3_STRPM (Q48UT3) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q48YS8_STRP1	>gnl|tr|Q48YS8_STRP1 (Q48YS8) Lactoylglutathione lyase (EC 4.4.1.5)	SFA	x	
Q4FMW7_PELUB	>gnl|tr|Q4FMW7_PELUB (Q4FMW7) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q4FV67_PSYAR	>gnl|tr|Q4FV67_PSYAR (Q4FV67) Probable lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q4MXC6_BACCE	>gnl|tr|Q4MXC6_BACCE (Q4MXC6) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q6SF47_9BACT	>gnl|tr|Q6SF47_9BACT (Q6SF47) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q7P5L7_FUSNV	>gnl|tr|Q7P5L7_FUSNV (Q7P5L7) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q7P5W4_FUSNV	>gnl|tr|Q7P5W4_FUSNV (Q7P5W4) Lactoylglutathione lyase (EC 4.4.1.5)	NSF	x	
Q7P6M4_FUSNV	>gnl|tr|Q7P6M4_FUSNV (Q7P6M4) Lactoylglutathione lyase (EC 4.4.1.5)	SFA	x	
Q5DZT6_VIBF1	>gnl|tr|Q5DZT6_VIBF1 (Q5DZT6) Lactoylglutathione lyase (EC 4.4.1.5)	NSF	x	
Q5FPY3_GLUOX	>gnl|tr|Q5FPY3_GLUOX (Q5FPY3) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q5KXF1_GEOKA	>gnl|tr|Q5KXF1_GEOKA (Q5KXF1) Lactoylglutathione lyase (EC 4.4.1.5)	SFA	x	
Q5NFM2_FRATT	>gnl|tr|Q5NFM2_FRATT (Q5NFM2) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q5NLR5_ZYMMO	>gnl|tr|Q5NLR5_ZYMMO (Q5NLR5) Lactoylglutathione lyase (EC 4.4.1.5)	NSF	x	
Q5NPH5_ZYMMO	>gnl|tr|Q5NPH5_ZYMMO (Q5NPH5) Lactoylglutathione lyase (EC 4.4.1.5)	NSF	x	
Q5NRK0_ZYMMO	>gnl|tr|Q5NRK0_ZYMMO (Q5NRK0) Lactoylglutathione lyase (EC 4.4.1.5)	NSF	x	
Q5WH68_BACSK	>gnl|tr|Q5WH68_BACSK (Q5WH68) Lactoylglutathione lyase (EC 4.4.1.5)	SFA	x	
Q5WJT2_BACSK	>gnl|tr|Q5WJT2_BACSK (Q5WJT2) Lactoylglutathione lyase (EC 4.4.1.5)	SFA	x	
Q5XC56_STRP6	>gnl|tr|Q5XC56_STRP6 (Q5XC56) Lactoylglutathione lyase (EC 4.4.1.5)	SFA	x	
Q5XDD0_STRP6	>gnl|tr|Q5XDD0_STRP6 (Q5XDD0) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q5ZUC5_LEGPH	>gnl|tr|Q5ZUC5_LEGPH (Q5ZUC5) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q607V5_METCA	>gnl|tr|Q607V5_METCA (Q607V5) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q631D5_BACCZ	>gnl|tr|Q631D5_BACCZ (Q631D5) Lactoylglutathione lyase (Glyoxalase I) (EC 4.4.1.5)	NSF	x	
Q637I6_BACCZ	>gnl|tr|Q637I6_BACCZ (Q637I6) Glyoxalase/bleomycin resistance protein (EC 4.4.1.5)	SFA	x	
Q637I9_BACCZ	>gnl|tr|Q637I9_BACCZ (Q637I9) Glyoxalase/bleomycin resistance protein (EC 4.4.1.5)	SFA	x	
Q637T9_BACCZ	>gnl|tr|Q637T9_BACCZ (Q637T9) Glyoxalase family protein (EC 4.4.1.5)	NSF	x	
Q638N4_BACCZ	>gnl|tr|Q638N4_BACCZ (Q638N4) Possible glyoxylase family protein (Lactoylglutathione lyase) (EC 4.4.1.5)	SFA	x	
Q638T9_BACCZ	>gnl|tr|Q638T9_BACCZ (Q638T9) Glyoxalase family protein (EC 4.4.1.5)	SFA	x	
Q639C0_BACCZ	>gnl|tr|Q639C0_BACCZ (Q639C0) Lactoylglutathione lyase, glyoxylase family protein (EC 4.4.1.5)	BTC	x	

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q639V0_BACCZ	>gnl|tr|Q639V0_BACCZ (Q639V0) Lactoylglutathione lyase (EC 4.4.1.5)	SFA	x	
Q63C57_BACCZ	>gnl|tr|Q63C57_BACCZ (Q63C57) Lactoylglutathione lyase (EC 4.4.1.5)	NSF	x	
Q63CP2_BACCZ	>gnl|tr|Q63CP2_BACCZ (Q63CP2) Glyoxalase family protein (EC 4.4.1.5)	SFA	x	
Q63FK4_BACCZ	>gnl|tr|Q63FK4_BACCZ (Q63FK4) Lactoylglutathione lyase (EC 4.4.1.5)	NSF	x	
Q63G38_BACCZ	>gnl|tr|Q63G38_BACCZ (Q63G38) Lactoylglutathione lyase (Glyoxylase I) (EC 4.4.1.5)	SFA	x	
Q6HB68_BACHK	>gnl|tr|Q6HB68_BACHK (Q6HB68) Lactoylglutathione lyase (Glyoxalase I) (EC 4.4.1.5)	NSF	x	
Q6HCL8_BACHK	>gnl|tr|Q6HCL8_BACHK (Q6HCL8) Possible glyoxalase/bleomycin resistance protein, dioxygenase superfamily (Lactoylglutathione lyase) (EC 4.4.1.5)	NSF	x	
Q6HDG5_BACHK	>gnl|tr|Q6HDG5_BACHK (Q6HDG5) Glyoxalase family protein (EC 4.4.1.5)	NSF	x	
Q6HFF9_BACHK	>gnl|tr|Q6HFF9_BACHK (Q6HFF9) Glyoxalase/bleomycin resistance protein (EC 4.4.1.5)	SFA	x	
Q6HFG2_BACHK	>gnl|tr|Q6HFG2_BACHK (Q6HFG2) Glyoxalase/bleomycin resistance protein (EC 4.4.1.5)	SFA	x	
Q6HFR4_BACHK	>gnl|tr|Q6HFR4_BACHK (Q6HFR4) Glyoxalase family protein (EC 4.4.1.5)	NSF	x	
Q6HG65_BACHK	>gnl|tr|Q6HG65_BACHK (Q6HG65) Possible glyoxylase family protein (Lactoylglutathione lyase) (EC 4.4.1.5)	SFA	x	
Q6HGC3_BACHK	>gnl|tr|Q6HGC3_BACHK (Q6HGC3) Glyoxalase family protein (EC 4.4.1.5)	SFA	x	
Q6HGM7_BACHK	>gnl|tr|Q6HGM7_BACHK (Q6HGM7) Lactoylglutathione lyase, glyoxylase family protein (EC 4.4.1.5)	BTC	x	
Q6HHA2_BACHK	>gnl|tr|Q6HHA2_BACHK (Q6HHA2) Lactoylglutathione lyase (EC 4.4.1.5)	SFA	x	
Q6HJK5_BACHK	>gnl|tr|Q6HJK5_BACHK (Q6HJK5) Lactoylglutathione lyase (EC 4.4.1.5)	NSF	x	
Q6HK42_BACHK	>gnl|tr|Q6HK42_BACHK (Q6HK42) Glyoxalase family protein (EC 4.4.1.5)	SFA	x	
Q6HN10_BACHK	>gnl|tr|Q6HN10_BACHK (Q6HN10) Lactoylglutathione lyase (EC 4.4.1.5)	NSF	x	
Q6HNK6_BACHK	>gnl|tr|Q6HNK6_BACHK (Q6HNK6) Lactoylglutathione lyase (Glyoxylase I) (EC 4.4.1.5)	SFA	x	
Q6MH83_BDEBA	>gnl|tr|Q6MH83_BDEBA (Q6MH83) Hypothetical protein (EC 4.4.1.5)	NSF	x	
Q6MQL0_BDEBA	>gnl|tr|Q6MQL0_BDEBA (Q6MQL0) Putative lactoylglutathione lyase (EC 4.4.1.5)	SFA	x	
Q6N6U1_RHOPA	>gnl|tr|Q6N6U1_RHOPA (Q6N6U1) Putative lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q6NA09_RHOPA	>gnl|tr|Q6NA09_RHOPA (Q6NA09) Possible glyoxalase (EC 4.4.1.5)	BTC	x	
Q7TUC2_PROMP	>gnl|tr|Q7TUC2_PROMP (Q7TUC2) LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5)	BTC	x	
Q7TUK6_PROMM	>gnl|tr|Q7TUK6_PROMM (Q7TUK6) Lactoylglutathione lyase; Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily (EC 4.4.1.5)	BTC	x	
Q815E1_BACCR	>gnl|tr|Q815E1_BACCR (Q815E1) Lactoylglutathione lyase (EC 4.4.1.5)	NSF	x	
Q81BH9_BACCR	>gnl|tr|Q81BH9_BACCR (Q81BH9) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q81BK1_BACCR	>gnl|tr|Q81BK1_BACCR (Q81BK1) Lactoylglutathione lyase (EC 4.4.1.5)	SFA	x	
Q81BZ3_BACCR	>gnl|tr|Q81BZ3_BACCR (Q81BZ3) Lactoylglutathione lyase (EC 4.4.1.5)	SFA	x	
Q81C30_BACCR	>gnl|tr|Q81C30_BACCR (Q81C30) Lactoylglutathione lyase (EC 4.4.1.5)	SFA	x	
Q81E83_BACCR	>gnl|tr|Q81E83_BACCR (Q81E83) Lactoylglutathione lyase (EC 4.4.1.5)	NSF	x	
Q81HI4_BACCR	>gnl|tr|Q81HI4_BACCR (Q81HI4) Lactoylglutathione lyase (EC 4.4.1.5)	SFA	x	
Q81I16_BACCR	>gnl|tr|Q81I16_BACCR (Q81I16) Lactoylglutathione lyase (EC 4.4.1.5)	SFA	x	
Q8DSZ8_STRMU	>gnl|tr|Q8DSZ8_STRMU (Q8DSZ8) Putative lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q8EQ54_OCEIH	>gnl|tr|Q8EQ54_OCEIH (Q8EQ54) Lactoylglutathione lyase (EC 4.4.1.5)	SFA	x	
Q8F692_LEPIN	>gnl|tr|Q8F692_LEPIN (Q8F692) Lactoylglutathione lyase, putative (EC 4.4.1.5)	SFA	x	
Q8G047_BRUSU	>gnl|tr|Q8G047_BRUSU (Q8G047) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q8NRV1_CORGL	>gnl|tr|Q8NRV1_CORGL (Q8NRV1) Predicted lactoylglutathione lyase (EC 4.4.1.5)	SFA	x	
Q8REP8_FUSNN	>gnl|tr|Q8REP8_FUSNN (Q8REP8) Lactoylglutathione lyase (EC 4.4.1.5)	NSF	x	
Q8REW3_FUSNN	>gnl|tr|Q8REW3_FUSNN (Q8REW3) Lactoylglutathione lyase (EC 4.4.1.5)	SFA	x	
Q8RGE4_FUSNN	>gnl|tr|Q8RGE4_FUSNN (Q8RGE4) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q8Y217_RALSO	>gnl|tr|Q8Y217_RALSO (Q8Y217) PROBABLE LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE) PROTEIN (EC 4.4.1.5)	BTC	x	
Q8YCW3_BRUME	>gnl|tr|Q8YCW3_BRUME (Q8YCW3) LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5)	NSF	x	
Q8YDW0_BRUME	>gnl|tr|Q8YDW0_BRUME (Q8YDW0) LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5)	SFA	x	
Q8YEJ0_BRUME	>gnl|tr|Q8YEJ0_BRUME (Q8YEJ0) LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5)	BTC	x	

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q8YHR6_BRUME	>gnl|tr|Q8YHR6_BRUME (Q8YHR6) LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5)	BTC	x	
Q8YJC2_BRUME	>gnl|tr|Q8YJC2_BRUME (Q8YJC2) PROBABLE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5)	SFA	x	
Q92PM1_RHIME	>gnl|tr|Q92PM1_RHIME (Q92PM1) PROBABLE LACTOYLGLUTATHIONE LYASE METHYLGLYOXALASE PROTEIN (EC 4.4.1.5)	BTC	x	
Q9A121_STRP1	>gnl|tr|Q9A121_STRP1 (Q9A121) Lactoylglutathione lyase (EC 4.4.1.5)	BTC	x	
Q2YM78_BRUA2	>gnl|tr|Q2YM78_BRUA2 (Q2YM78) Glyoxalase/Bleomycin resistance protein/dioxygenase domain:Glyoxalase I (EC 4.4.1.5)	BTC	x	
Q2YNE7_BRUA2	>gnl|tr|Q2YNE7_BRUA2 (Q2YNE7) Glyoxalase/Bleomycin resistance protein/dioxygenase domain (EC 4.4.1.5)	SFA	x	
Q2YPP0_BRUA2	>gnl|tr|Q2YPP0_BRUA2 (Q2YPP0) Glyoxalase/Bleomycin resistance protein/dioxygenase domain:Glyoxalase I (EC 4.4.1.5)	BTC	x	
Q4XX76_PLACH	>gnl|tr|Q4XX76_PLACH (Q4XX76) Glyoxalase I, putative	NSF	x	
Q4YHS2_PLABE	>gnl|tr|Q4YHS2_PLABE (Q4YHS2) Glyoxalase I, putative (Fragment)	NSF	x	
Q2WI72_CLOBE	>gnl|tr|Q2WI72_CLOBE (Q2WI72) Glyoxalase I (Glyoxalase family)	SFA	x	
Q2WRA4_CLOBE	>gnl|tr|Q2WRA4_CLOBE (Q2WRA4) Glyoxalase I	SFA	x	
Q3BZ23_XANC5	>gnl|tr|Q3BZ23_XANC5 (Q3BZ23) Putative glyoxalase I	NSF	x	
Q62NG3_BACLD	>gnl|tr|Q62NG3_BACLD (Q62NG3) Glyoxalase I	NSF	x	
Q5LYN9_STRT1	>gnl|tr|Q5LYN9_STRT1 (Q5LYN9) Glyoxalase I/lactoylglutathione lyase	BTC	x	
Q5M3A3_STRT2	>gnl|tr|Q5M3A3_STRT2 (Q5M3A3) Glyoxalase I/lactoylglutathione lyase	BTC	x	
Q65MB8_BACLD	>gnl|tr|Q65MB8_BACLD (Q65MB8) Glyoxalase I YfiE	NSF	x	
Q97ME9_CLOAB	>gnl|tr|Q97ME9_CLOAB (Q97ME9) Glyoxalase I (Glyoxalase family)	SFA	x	
Q4X0G5_ASPFU	>gnl|tr|Q4X0G5_ASPFU (Q4X0G5) Lactoylglutathione lyase	BTC	x	
Q5KB67_CRYNE	>gnl|tr|Q5KB67_CRYNE (Q5KB67) Lactoylglutathione lyase, putative	BTC	x	
Q54EY7_DICDI	>gnl|tr|Q54EY7_DICDI (Q54EY7) Lactoylglutathione lyase	BTC	x	
Q2S7L6_9GAMM	>gnl|tr|Q2S7L6_9GAMM (Q2S7L6) Lactoylglutathione lyase	NSF	x	
Q2S888_9GAMM	>gnl|tr|Q2S888_9GAMM (Q2S888) Lactoylglutathione lyase	NSF	x	
Q2SA50_9GAMM	>gnl|tr|Q2SA50_9GAMM (Q2SA50) Lactoylglutathione lyase	SFA	x	
Q2SCR0_9GAMM	>gnl|tr|Q2SCR0_9GAMM (Q2SCR0) Lactoylglutathione lyase	NSF	x	
Q2SDC3_9GAMM	>gnl|tr|Q2SDC3_9GAMM (Q2SDC3) Lactoylglutathione lyase	NSF	x	
Q2SEG2_9GAMM	>gnl|tr|Q2SEG2_9GAMM (Q2SEG2) Lactoylglutathione lyase	SFA	x	

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q2SFL6_9GAMM	>gnl|tr|Q2SFL6_9GAMM (Q2SFL6) Lactoylglutathione lyase	NSF	x	
Q2SKG9_9GAMM	>gnl|tr|Q2SKG9_9GAMM (Q2SKG9) Lactoylglutathione lyase	NSF	x	
Q2SLE3_9GAMM	>gnl|tr|Q2SLE3_9GAMM (Q2SLE3) Lactoylglutathione lyase	SFA	x	
Q2SLP6_9GAMM	>gnl|tr|Q2SLP6_9GAMM (Q2SLP6) Lactoylglutathione lyase	SFA	x	
Q2WK94_CLOBE	>gnl|tr|Q2WK94_CLOBE (Q2WK94) Lactoylglutathione lyase	BTC	x	
Q34M94_RHOPA	>gnl|tr|Q34M94_RHOPA (Q34M94) Putative lactoylglutathione lyase	BTC	x	
Q351E9_9GAMM	>gnl|tr|Q351E9_9GAMM (Q351E9) Lactoylglutathione lyase	BTC	x	
Q35ET3_9BRAD	>gnl|tr|Q35ET3_9BRAD (Q35ET3) Lactoylglutathione lyase	BTC	x	
Q35PP5_9BRAD	>gnl|tr|Q35PP5_9BRAD (Q35PP5) Lactoylglutathione lyase	BTC	x	
Q36S03_MARHY	>gnl|tr|Q36S03_MARHY (Q36S03) Lactoylglutathione lyase	BTC	x	
Q37TB7_SPHAR	>gnl|tr|Q37TB7_SPHAR (Q37TB7) Lactoylglutathione lyase, putative	BTC	x	
Q37XC8_SPHAR	>gnl|tr|Q37XC8_SPHAR (Q37XC8) Lactoylglutathione lyase, putative	SFA	x	
Q3A025_PELCD	>gnl|tr|Q3A025_PELCD (Q3A025) Lactoylglutathione lyase	SFA	x	
Q3A4I4_PELCD	>gnl|tr|Q3A4I4_PELCD (Q3A4I4) Lactoylglutathione lyase	BTC	x	
Q3A778_PELCD	>gnl|tr|Q3A778_PELCD (Q3A778) Lactoylglutathione lyase	BTC	x	
Q3B3D2_PELLD	>gnl|tr|Q3B3D2_PELLD (Q3B3D2) Lactoylglutathione lyase	SFA	x	
Q3DRD9_STRAG	>gnl|tr|Q3DRD9_STRAG (Q3DRD9) Lactoylglutathione lyase	NSF	X	
Q3FP24_9BURK	>gnl|tr|Q3FP24_9BURK (Q3FP24) Putative lactoylglutathione lyase	NSF	x	
Q3J0W8_RHOS4	>gnl|tr|Q3J0W8_RHOS4 (Q3J0W8) Probable lactoylglutathione lyase	BTC	x	
Q47JC2_DECAR	>gnl|tr|Q47JC2_DECAR (Q47JC2) Lactoylglutathione lyase	SFA	x	
Q49W22_STAS1	>gnl|tr|Q49W22_STAS1 (Q49W22) Putative lactoylglutathione lyase	NSF	X	
Q4B225_9BURK	>gnl|tr|Q4B225_9BURK (Q4B225) Lactoylglutathione lyase, putative	NSF	x	
Q4ELC3_LISMO	>gnl|tr|Q4ELC3_LISMO (Q4ELC3) Lactoylglutathione lyase, putative	BTC	x	
Q4ESX1_LISMO	>gnl|tr|Q4ESX1_LISMO (Q4ESX1) Lactoylglutathione lyase, putative	BTC	x	
Q4JMK6_9BACT	>gnl|tr|Q4JMK6_9BACT (Q4JMK6) Predicted lactoylglutathione lyase	BTC	x	
Q4MH18_BACCE	>gnl|tr|Q4MH18_BACCE (Q4MH18) Lactoylglutathione lyase, putative	NSF	X	
Q4MWP9_BACCE	>gnl|tr|Q4MWP9_BACCE (Q4MWP9) Lactoylglutathione lyase	SFA	X	
Q4MXA9_BACCE	>gnl|tr|Q4MXA9_BACCE (Q4MXA9) Lactoylglutathione lyase	SFA	x	
Q4MXR2_BACCE	>gnl|tr|Q4MXR2_BACCE (Q4MXR2) Lactoylglutathione lyase	SFA	X	
Q4V084_XANC8	>gnl|tr|Q4V084_XANC8 (Q4V084) Lactoylglutathione lyase	SFA	x	
Q7X2Z9_9BACT	>gnl|tr|Q7X2Z9_9BACT (Q7X2Z9) Putative lactoylglutathione lyase	SFA	x	
Q2NB70_9SPHN	>gnl|tr|Q2NB70_9SPHN (Q2NB70) Lactoylglutathione lyase, putative	SFA	x	

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q2NDA2_9SPHN	>gnl|tr|Q2NDA2_9SPHN (Q2NDA2) Lactoylglutathione lyase, putative	BTC	x	
Q57CM6_BRUAB	>gnl|tr|Q57CM6_BRUAB (Q57CM6) GloA, lactoylglutathione lyase	BTC	x	
Q57JZ9_SALCH	>gnl|tr|Q57JZ9_SALCH (Q57JZ9) Putative lactoylglutathione lyase	SFA	x	
Q57T20_SALCH	>gnl|tr|Q57T20_SALCH (Q57T20) Putative lactoylglutathione lyase	SFA	x	
Q5DZD7_VIBF1	>gnl|tr|Q5DZD7_VIBF1 (Q5DZD7) Lactoylglutathione lyase	SFA	x	
Q5LFJ8_BACFN	>gnl|tr|Q5LFJ8_BACFN (Q5LFJ8) Putative lactoylglutathione lyase	BTC	x	
Q5LTZ0_SILPO	>gnl|tr|Q5LTZ0_SILPO (Q5LTZ0) Lactoylglutathione lyase, putative	BTC	x	
Q5QZT6_IDILO	>gnl|tr|Q5QZT6_IDILO (Q5QZT6) Lactoylglutathione lyase	BTC	x	
Q64WC5_BACFR	>gnl|tr|Q64WC5_BACFR (Q64WC5) Lactoylglutathione lyase	BTC	x	
Q64Y52_BACFR	>gnl|tr|Q64Y52_BACFR (Q64Y52) Putative lactoylglutathione lyase	SFA	x	
Q67Q70_SYMTH	>gnl|tr|Q67Q70_SYMTH (Q67Q70) Putative lactoylglutathione lyase	SFA	x	
Q6LS69_PHOPR	>gnl|tr|Q6LS69_PHOPR (Q6LS69) Putative lactoylglutathione lyase	NSF	x	
Q6MK89_BDEBA	>gnl|tr|Q6MK89_BDEBA (Q6MK89) Putative lactoylglutathione lyase	NSF	x	
Q6N6Z4_RHOPA	>gnl|tr|Q6N6Z4_RHOPA (Q6N6Z4) Putative lactoylglutathione lyase	SFA	x	
Q71XJ8_LISMF	>gnl|tr|Q71XJ8_LISMF (Q71XJ8) Putative lactoylglutathione lyase	BTC	x	
Q72KJ9_THET2	>gnl|tr|Q72KJ9_THET2 (Q72KJ9) Probable lactoylglutathione lyase	SFA	x	
Q72PY7_LEPIC	>gnl|tr|Q72PY7_LEPIC (Q72PY7) Putative lactoylglutathione lyase	SFA	x	
Q7CFD7_STRP3	>gnl|tr|Q7CFD7_STRP3 (Q7CFD7) Putative lactoylglutathione lyase	BTC	x	
Q7CNH1_STRP8	>gnl|tr|Q7CNH1_STRP8 (Q7CNH1) Putative lactoylglutathione lyase	BTC	x	
Q7MD79_VIBVY	>gnl|tr|Q7MD79_VIBVY (Q7MD79) Lactoylglutathione lyase	SFA	x	
Q7MFM3_VIBVY	>gnl|tr|Q7MFM3_VIBVY (Q7MFM3) Lactoylglutathione lyase	SFA	x	
Q7MIW3_VIBVY	>gnl|tr|Q7MIW3_VIBVY (Q7MIW3) Lactoylglutathione lyase	BTC	x	
Q7MJV8_VIBVY	>gnl|tr|Q7MJV8_VIBVY (Q7MJV8) Lactoylglutathione lyase	SFA	x	
Q7MK72_VIBVY	>gnl|tr|Q7MK72_VIBVY (Q7MK72) Lactoylglutathione lyase	SFA	x	
Q7MQ53_VIBVY	>gnl|tr|Q7MQ53_VIBVY (Q7MQ53) Lactoylglutathione lyase	BTC	x	
Q7MW91_PORGI	>gnl|tr|Q7MW91_PORGI (Q7MW91) Lactoylglutathione lyase, putative	BTC	x	
Q7NFG4_GLOVI	>gnl|tr|Q7NFG4_GLOVI (Q7NFG4) Lactoylglutathione lyase	BTC	x	
Q7VND9_HAEDU	>gnl|tr|Q7VND9_HAEDU (Q7VND9) Lactoylglutathione lyase	BTC	x	
Q82CE8_STRAW	>gnl|tr|Q82CE8_STRAW (Q82CE8) Putative lactoylglutathione lyase	SFA	x	
Q836H2_ENTFA	>gnl|tr|Q836H2_ENTFA (Q836H2) Lactoylglutathione lyase	BTC	x	
Q87FJ4_VIBPA	>gnl|tr|Q87FJ4_VIBPA (Q87FJ4) Putative lactoylglutathione lyase	SFA	x	
Q87MR5_VIBPA	>gnl|tr|Q87MR5_VIBPA (Q87MR5) Putative lactoylglutathione lyase	BTC	x	

Table K-2. TrEMBL data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
Q892C0_CLOTE	>gnl|tr|Q892C0_CLOTE (Q892C0) Putative lactoylglutathione lyase	SFA	x	
Q89DF0_BRAJA	>gnl|tr|Q89DF0_BRAJA (Q89DF0) Lactoylglutathione lyase	BTC	x	
Q89LZ4_BRAJA	>gnl|tr|Q89LZ4_BRAJA (Q89LZ4) Lactoylglutathione lyase	BTC	x	
Q8A7E4_BACTN	>gnl|tr|Q8A7E4_BACTN (Q8A7E4) Lactoylglutathione lyase	BTC	x	
Q8D449_VIBVU	>gnl|tr|Q8D449_VIBVU (Q8D449) Lactoylglutathione lyase	SFA	X	
Q8D4M2_VIBVU	>gnl|tr|Q8D4M2_VIBVU (Q8D4M2) Lactoylglutathione lyase	SFA	x	
Q8D6C8_VIBVU	>gnl|tr|Q8D6C8_VIBVU (Q8D6C8) Lactoylglutathione lyase	SFA	x	
Q8D9P5_VIBVU	>gnl|tr|Q8D9P5_VIBVU (Q8D9P5) Lactoylglutathione lyase	SFA	X	
Q8D9U0_VIBVU	>gnl|tr|Q8D9U0_VIBVU (Q8D9U0) Lactoylglutathione lyase	SFA	X	
Q8D9W7_VIBVU	>gnl|tr|Q8D9W7_VIBVU (Q8D9W7) Lactoylglutathione lyase	SFA	X	
Q8DAB4_VIBVU	>gnl|tr|Q8DAB4_VIBVU (Q8DAB4) Lactoylglutathione lyase	SFA	X	
Q8DB12_VIBVU	>gnl|tr|Q8DB12_VIBVU (Q8DB12) Lactoylglutathione lyase	BTC	x	
Q8DQ39_STRR6	>gnl|tr|Q8DQ39_STRR6 (Q8DQ39) Lactoylglutathione lyase	BTC	x	
Q8DYK2_STRA5	>gnl|tr|Q8DYK2_STRA5 (Q8DYK2) Lactoylglutathione lyase	BTC	x	
Q8EFD7_SHEON	>gnl|tr|Q8EFD7_SHEON (Q8EFD7) Lactoylglutathione lyase	BTC	x	
Q8PDZ2_XANCP	>gnl|tr|Q8PDZ2_XANCP (Q8PDZ2) Lactoylglutathione lyase	SFA	x	
Q8PQW0_XANAC	>gnl|tr|Q8PQW0_XANAC (Q8PQW0) Lactoylglutathione lyase	SFA	x	
Q8U9Z6_AGRT5	>gnl|tr|Q8U9Z6_AGRT5 (Q8U9Z6) Lactoylglutathione lyase	SFA	x	
Q8UCM7_AGRT5	>gnl|tr|Q8UCM7_AGRT5 (Q8UCM7) Lactoylglutathione lyase (AGR_C_4460p)	BTC	x	
Q8UCY4_AGRT5	>gnl|tr|Q8UCY4_AGRT5 (Q8UCY4) Lactoylglutathione lyase	SFA	x	
Q8UEF6_AGRT5	>gnl|tr|Q8UEF6_AGRT5 (Q8UEF6) Lactoylglutathione lyase (AGR_C_3314p)	BTC	x	
Q8XN91_CLOPE	>gnl|tr|Q8XN91_CLOPE (Q8XN91) Lactoylglutathione lyase	BTC	x	
Q8ZM36_SALTY	>gnl|tr|Q8ZM36_SALTY (Q8ZM36) Putative lactoylglutathione lyase	SFA	x	
Q8ZRN6_SALTY	>gnl|tr|Q8ZRN6_SALTY (Q8ZRN6) Putative lactoylglutathione lyase	SFA	x	
Q97R67_STRPN	>gnl|tr|Q97R67_STRPN (Q97R67) Lactoylglutathione lyase	BTC	x	
Q98DN5_RHILO	>gnl|tr|Q98DN5_RHILO (Q98DN5) Lactoylglutathione lyase	SFA	x	
Q98IT9_RHILO	>gnl|tr|Q98IT9_RHILO (Q98IT9) Probable lactoylglutathione lyase	NSF	x	
Q98NF2_RHILO	>gnl|tr|Q98NF2_RHILO (Q98NF2) Lactoylglutathione lyase	BTC	x	
Q9A6Z3_CAUCR	>gnl|tr|Q9A6Z3_CAUCR (Q9A6Z3) Lactoylglutathione lyase, putative	SFA	x	
Q9A8N8_CAUCR	>gnl|tr|Q9A8N8_CAUCR (Q9A8N8) Lactoylglutathione lyase, putative	BTC	x	
Q9I5L8_PSEAE	>gnl|tr|Q9I5L8_PSEAE (Q9I5L8) Lactoylglutathione lyase	BTC	x	
Q9RSB7_DEIRA	>gnl|tr|Q9RSB7_DEIRA (Q9RSB7) Lactoylglutathione lyase, putative	SFA	X	

K.3. Table K-3. KEGG Data (Chapter 2)

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
bcl:ABC4032	>gnl|kg|bcl:ABC4032 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
blo:BL0011	>gnl|kg|blo:BL0011 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
bma:BMAA0603	>gnl|kg|bma:BMAA0603 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
bpm:BURPS1710b_A2335	>gnl|kg|bpm:BURPS1710b_A2335 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
bps:BPSS0761	>gnl|kg|bps:BPSS0761 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
cpe:CPE0756	>gnl|kg|cpe:CPE0756 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
ctc:CTC01883	>gnl|kg|ctc:CTC01883 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
cya:CYA_1587	>gnl|kg|cya:CYA_1587 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
cyb:CYB_0393	>gnl|kg|cyb:CYB_0393 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
ecc:c0456	>gnl|kg|ecc:c0456 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
ecj:JW0328	>gnl|kg|ecj:JW0328 codA; Cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
ecs:ECs0390	>gnl|kg|ecs:ECs0390 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
ece:Z0433	>gnl|kg|ece:Z0433 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
eco:b0337	>gnl|kg|eco:b0337 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
gvi:gll2528	>gnl|kg|gvi:gll2528 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
pae:PA0437	>gnl|kg|pae:PA0437 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
pfl:PFL_4033	>gnl|kg|pfl:PFL_4033 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
pmu:PM0565	>gnl|kg|pmu:PM0565 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
ppr:PBPRB1375	>gnl|kg|ppr:PBPRB1375 putative cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
ppu:PP3189	>gnl|kg|ppu:PP3189 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
ret:RHE_PB00107	>gnl|kg|ret:RHE_PB00107 codAb; cytosine deaminase protein [EC:3.5.4.1] [KO:K01485]			x
rso:RSc1594	>gnl|kg|rso:RSc1594 codA, RS03956; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
sai:Saci_1072	>gnl|kg|sai:Saci_1072 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
sec:SC3272	>gnl|kg|sec:SC3272 codA; putative cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
spt:SPA3202	>gnl|kg|spt:SPA3202 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
sme:SMa2371	>gnl|kg|sme:SMa2371 codA1; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
sil:SPO2806	>gnl|kg|sil:SPO2806 cytosine deaminase, putative [EC:3.5.4.1] [KO:K01485]			x
sso:SSO2770	>gnl|kg|sso:SSO2770 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
sto:ST2403	>gnl|kg|sto:ST2403 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
stm:STM3334	>gnl|kg|stm:STM3334 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
sty:STY3514	>gnl|kg|sty:STY3514 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
stt:t3251	>gnl|kg|stt:t3251 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
vfi:VF0531	>gnl|kg|vfi:VF0531 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
vpa:VPA1243	>gnl|kg|vpa:VPA1243 putative cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
vvu:VV20789	>gnl|kg|vvu:VV20789 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
vvy:VVA1255	>gnl|kg|vvy:VVA1255 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
ypk:y3946	>gnl|kg|ypk:y3946 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
ypm:YP0164	>gnl|kg|ypm:YP0164 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
ype:YPO0162	>gnl|kg|ype:YPO0162 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
yps:YPTB3739	>gnl|kg|yps:YPTB3739 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x
bte:BTH_II1639	>gnl|kg|bte:BTH_II1639 cytosine deaminase			x
cef:CE2849	>gnl|kg|cef:CE2849 putative cytosine deaminase			x
rsp:RSP_0341	>gnl|kg|rsp:RSP_0341 cytosine deaminase			x
bta:280712	>gnl|kg|bta:280712 ADA; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x
ecc:c2015	>gnl|kg|ecc:c2015 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x
ecj:JW1615	>gnl|kg|ecj:JW1615 add; Adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x
ecs:ECs2331	>gnl|kg|ecs:ECs2331 adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x
ece:Z2628	>gnl|kg|ece:Z2628 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x
eco:b1623	>gnl|kg|eco:b1623 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x
hsa:100	>gnl|kg|hsa:100 ADA; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
mmu:11486	>gnl|kg|mmu:11486 Ada; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x
ppr:PBPRA3496	>gnl|kg|ppr:PBPRA3496 putative adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x
rno:24165	>gnl|kg|rno:24165 Ada; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x
sec:SC1480	>gnl|kg|sec:SC1480 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x
sfx:S1780	>gnl|kg|sfx:S1780 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x
sfl:SF1648	>gnl|kg|sfl:SF1648 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x
son:SO4731	>gnl|kg|son:SO4731 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x
ssn:SSO_1535	>gnl|kg|ssn:SSO_1535 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x
stm:STM1463	>gnl|kg|stm:STM1463 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x
sty:STY1658	>gnl|kg|sty:STY1658 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x
stt:t1331	>gnl|kg|stt:t1331 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x
vch:VC2751	>gnl|kg|vch:VC2751 adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x
vpa:VP0116	>gnl|kg|vpa:VP0116 adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x
xla:444167	>gnl|kg|xla:444167 MGC80635; MGC80635 protein [EC:3.5.4.4] [KO:K01488]			x
xtr:496434	>gnl|kg|xtr:496434 ada-prov; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x
yps:YPTB2180	>gnl|kg|yps:YPTB2180 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x
sbo:SBO_1511	>gnl|kg|sbo:SBO_1511 add; adenosine deaminase			x
sdy:SDY_1846	>gnl|kg|sdy:SDY_1846 add; adenosine deaminase			x
bma:BMA0178	>gnl|kg|bma:BMA0178 N-acyl-D-amino-acid deacylase family protein [EC:3.5.1.81]			X
bpm:BURPS1710b_0837	>gnl|kg|bpm:BURPS1710b_0837 D-aminoacylase [EC:3.5.1.81]			x
bps:BPSL0630	>gnl|kg|bps:BPSL0630 dan; D-aminoacylase [EC:3.5.1.81]			x
bur:Bcep18194_A6068	>gnl|kg|bur:Bcep18194_A6068 N-acyl-D-amino-acid deacylase [EC:3.5.1.81]			x
reu:Reut_B4020	>gnl|kg|reu:Reut_B4020 N-acyl-D-amino-acid deacylase [EC:3.5.1.81]			x
psb:Psyr_0415	>gnl|kg|psb:Psyr_0415 N-acyl-D-amino-acid deacylase [EC:3.5.1.82]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
pfl:PFL_0775	>gnl|kg|pfl:PFL_0775 N-acyl-D-amino acid deacylase family protein [EC:3.5.1.82]			x
pst:PSPTO5117	>gnl|kg|pst:PSPTO5117 N-acyl-D-amino acid deacylase family protein [EC:3.5.1.82]			x
psp:PSPPH_0405	>gnl|kg|psp:PSPPH_0405 N-acyl-D-amino acid deacylase family protein [EC:3.5.1.82]			x
bbr:BB3285	>gnl|kg|bbr:BB3285 N-acyl-D-glutamate deacylase [EC:3.5.1.82]	ESA		x
bpa:BPP1821	>gnl|kg|bpa:BPP1821 N-acyl-D-glutamate deacylase [EC:3.5.1.82]	ESA		x
bpe:BP1207	>gnl|kg|bpe:BP1207 N-acyl-D-glutamate deacylase [EC:3.5.1.82]	ESA		x
rso:RSp1187	>gnl|kg|rso:RSp1187 ndeD, RS03131; probable N-acyl-D-glutamate deacylase protein [EC:3.5.1.82]			x
bms:BR0278	>gnl|kg|bms:BR0278 dhT; D-hydantoinase [EC:3.5.2.2] [KO:K01464]			x
bur:Bcep18194_C6658	>gnl|kg|bur:Bcep18194_C6658 D-hydantoinase [EC:3.5.2.2] [KO:K01464]			x
pfo:Pfl_3441	>gnl|kg|pfo:Pfl_3441 D-hydantoinase [EC:3.5.2.2] [KO:K01464]			x
reu:Reut_A0045	>gnl|kg|reu:Reut_A0045 D-hydantoinase [EC:3.5.2.2] [KO:K01464]			x
sco:SCO6415	>gnl|kg|sco:SCO6415 SC1A6.04; putative D-hydantoinase [EC:3.5.2.2] [KO:K01464]			x
sil:SPO1783	>gnl|kg|sil:SPO1783 hydA; D-hydantoinase [EC:3.5.2.2] [KO:K01464]			x
aci:ACIAD1091	>gnl|kg|aci:ACIAD1091 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
ana:alr3670	>gnl|kg|ana:alr3670 urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
ath:At1g67550	>gnl|kg|ath:At1g67550 F12B7.10; urease, putative / urea amidohydrolase, putative [EC:3.5.1.5] [KO:K01428 K01429 K01430]			x
atc:AGR_C_4357	>gnl|kg|atc:AGR_C_4357 ureA; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
atu:Atu2401	>gnl|kg|atu:Atu2401 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
ava:Ava_3618	>gnl|kg|ava:Ava_3618 urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x
bmb:BruAb1_0296	>gnl|kg|bmb:BruAb1_0296 ureC-1; UreC-1, urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x
bmb:BruAb1_1355	>gnl|kg|bmb:BruAb1_1355 ureC-2; UreC-2, urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x
bbr:BB4323	>gnl|kg|bbr:BB4323 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
bca:BCE3662	>gnl|kg|bca:BCE3662 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
bfl:Bfl523	>gnl|kg|bfl:Bfl523 ureC; putative urease structural subunit C (alpha) [EC:3.5.1.5] [KO:K01428]			x
bha:BH0254	>gnl|kg|bha:BH0254 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
bja:blr1457	>gnl|kg|bja:blr1457 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
bma:BMA2184	>gnl|kg|bma:BMA2184 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x
bmf:BAB1_0300	>gnl|kg|bmf:BAB1_0300 ureC-1; urease:amidohydrolase [EC:3.5.1.5] [KO:K01427]			x
bmf:BAB1_1378	>gnl|kg|bmf:BAB1_1378 urease:amidohydrolase [EC:3.5.1.5] [KO:K01427]			x
bme:BMEI0647	>gnl|kg|bme:BMEI0647 urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
bme:BMEI1652	>gnl|kg|bme:BMEI1652 urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
bpa:BPP3855	>gnl|kg|bpa:BPP3855 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
bpn:BPEN_542	>gnl|kg|bpn:BPEN_542 ureC; putative urease structural subunit C (alpha) [EC:3.5.1.5] [KO:K01428]			x
bpe:BP3168	>gnl|kg|bpe:BP3168 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
bpm:BURPS1710b_3135	>gnl|kg|bpm:BURPS1710b_3135 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x
bps:BPSL2659	>gnl|kg|bps:BPSL2659 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
bsu:BG11983	>gnl|kg|bsu:BG11983 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
bms:BR0270	>gnl|kg|bms:BR0270 ureC-1; urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x
bms:BR1358	>gnl|kg|bms:BR1358 ureC-2; urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x
bte:BTH_I1496	>gnl|kg|bte:BTH_I1496 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x
bur:Bcep18194_A4006	>gnl|kg|bur:Bcep18194_A4006 urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x
cef:CE0995	>gnl|kg|cef:CE0995 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
cgb:cg0115	>gnl|kg|cgb:cg0115 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
cgl:NCgl0085	>gnl|kg|cgl:NCgl0085 Cgl0086; urea amidohydrolase (urease) alpha subunit [EC:3.5.1.5] [KO:K01428]			x
cne:CNH01900	>gnl|kg|cne:CNH01900 urease [EC:3.5.1.5] [KO:K01428 K01429 K01430]			x
cya:CYA_0603	>gnl|kg|cya:CYA_0603 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x
cyb:CYB_0023	>gnl|kg|cyb:CYB_0023 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x
dar:Daro_1427	>gnl|kg|dar:Daro_1427 urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x
dra:DRA0318	>gnl|kg|dra:DRA0318 urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x
ecs:ECs1324	>gnl|kg|ecs:ECs1324 urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
ece:Z1145	>gnl|kg|ece:Z1145 ureC; putative urease structural subunit C (alpha) [EC:3.5.1.5] [KO:K01428]			x
ece:Z1584	>gnl|kg|ece:Z1584 ureC_2; putative urease structural subunit C (alpha) [EC:3.5.1.5] [KO:K01428]			x
fra:Francci3_0832	>gnl|kg|fra:Francci3_0832 urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x
gka:GK1930	>gnl|kg|gka:GK1930 ureC; urease alpha subunit (urea amidohydrolase) [EC:3.5.1.5] [KO:K01428]			x
hch:HCH_04523	>gnl|kg|hch:HCH_04523 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x
hhe:HH0408	>gnl|kg|hhe:HH0408 ureB; urease [EC:3.5.1.5] [KO:K01428]			x
hit:NTHI0665	>gnl|kg|hit:NTHI0665 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
hin:HI0539	>gnl|kg|hin:HI0539 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
hma:pNG7124	>gnl|kg|hma:pNG7124 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
hpj:jhp0067	>gnl|kg|hpj:jhp0067 ureB; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
hpy:HP0072	>gnl|kg|hpy:HP0072 ureB; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
mbo:Mb1881	>gnl|kg|mbo:Mb1881 ureC; urease alpha subunit UreC (urea amidohydrolase) [EC:3.5.1.5] [KO:K01428]			x
mlo:mll4940	>gnl|kg|mlo:mll4940 urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
mtc:MT1898	>gnl|kg|mtc:MT1898 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
mtu:Rv1850	>gnl|kg|mtu:Rv1850 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
nfa:nfa25260	>gnl|kg|nfa:nfa25260 ureC; putative urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
nmu:Nmul_A1241	>gnl|kg|nmu:Nmul_A1241 urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x
noc:Noc_2880	>gnl|kg|noc:Noc_2880 urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x
nph:NP2010A	>gnl|kg|nph:NP2010A ureA; urease , alpha subunit [EC:3.5.1.5] [KO:K01428]			x
pae:PA4868	>gnl|kg|pae:PA4868 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
pfl:PFL_0631	>gnl|kg|pfl:PFL_0631 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x
pha:PSHAa1759	>gnl|kg|pha:PSHAa1759 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x
plu:plu2173	>gnl|kg|plu:plu2173 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
pmm:PMM0963	>gnl|kg|pmm:PMM0963 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
pmi:PMT9312_0836	>gnl|kg|pmi:PMT9312_0836 urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x
pmt:PMT2236	>gnl|kg|pmt:PMT2236 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
pmn:PMN2A_1055	>gnl|kg|pmn:PMN2A_1055 urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x
ppu:PP2845	>gnl|kg|ppu:PP2845 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x
psb:Psyr_2197	>gnl|kg|psb:Psyr_2197 urease [EC:3.5.1.5] [KO:K01428]			x
psb:Psyr_4436	>gnl|kg|psb:Psyr_4436 urease [EC:3.5.1.5] [KO:K01428]			x
pst:PSPTO4895	>gnl|kg|pst:PSPTO4895 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x
psp:PSPPH_4479	>gnl|kg|psp:PSPPH_4479 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x
ret:RHE_CH03305	>gnl|kg|ret:RHE_CH03305 ureC; urease (UreA amidohydrolase) alpha subunit protein [EC:3.5.1.5] [KO:K01427]			x
reu:Reut_A0995	>gnl|kg|reu:Reut_A0995 urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x
rpb:RPB_1803	>gnl|kg|rpb:RPB_1803 urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x
rpa:RPA3660	>gnl|kg|rpa:RPA3660 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
rso:RSc2032	>gnl|kg|rso:RSc2032 ureC, RS02789; probable urease (alpha subunit) protein [EC:3.5.1.5] [KO:K01428]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
rsp:RSP_6111	>gnl|kg|rsp:RSP_6111 ureC; UreA amidohydrolase (urease) alpha subunit [EC:3.5.1.5] [KO:K01427]			x
sac:SACOL2282	>gnl|kg|sac:SACOL2282 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x
sar:SAR2374	>gnl|kg|sar:SAR2374 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
sas:SAS2180	>gnl|kg|sas:SAS2180 urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
sav:SAV2290	>gnl|kg|sav:SAV2290 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
sam:MW2208	>gnl|kg|sam:MW2208 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
sau:SA2084	>gnl|kg|sau:SA2084 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
sab:SAB2162	>gnl|kg|sab:SAB2162 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01427]			x
saa:SAUSA300_2240	>gnl|kg|saa:SAUSA300_2240 ureC; urease, alpha subunit [EC:3.5.1.5]			x
sma:SAV2715	>gnl|kg|sma:SAV2715 ureC2; putative urease subunit alpha [EC:3.5.1.5] [KO:K01428]			x
sma:SAV7106	>gnl|kg|sma:SAV7106 ureC1; putative urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
sco:SCO1234	>gnl|kg|sco:SCO1234 2SCG1.09c, ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
sco:SCO5526	>gnl|kg|sco:SCO5526 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
sep:SE1863	>gnl|kg|sep:SE1863 urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
ser:SERP1871	>gnl|kg|ser:SERP1871 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x
sme:SMc01837	>gnl|kg|sme:SMc01837 ureC; urease alpha subunit protein [EC:3.5.1.5] [KO:K01428]			x
spo:SPAC1952.11c	>gnl|kg|spo:SPAC1952.11c ure1; urease (EC 3.5.1.5) [EC:3.5.1.5] [KO:K01428 K01429 K01430]			x
sil:SPO1714	>gnl|kg|sil:SPO1714 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x
ssp:SSP0263	>gnl|kg|ssp:SSP0263 urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
stc:str0283	>gnl|kg|stc:str0283 ureC; urea amidohydrolase (urease) alpha subunit [EC:3.5.1.5] [KO:K01428]			x
stl:stu0283	>gnl|kg|stl:stu0283 ureC; urea amidohydrolase (urease) alpha subunit [EC:3.5.1.5] [KO:K01428]			x
sto:ST1028	>gnl|kg|sto:ST1028 urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
syd:Syncc9605_2627	>gnl|kg|syd:Syncc9605_2627 urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x
sye:Syncc9902_2257	>gnl|kg|sye:Syncc9902_2257 urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x
syw:SYNW2449	>gnl|kg|syw:SYNW2449 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
syn:sll1750	>gnl|kg|syn:sll1750 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
tel:tlr0005	>gnl|kg|tel:tlr0005 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
uur:UU432	>gnl|kg|uur:UU432 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
vfi:VF0673	>gnl|kg|vfi:VF0673 urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
ypk:y1239	>gnl|kg|ypk:y1239 ureC; urease (urea amidohydrolase) alpha subunit [EC:3.5.1.5] [KO:K01428]			x
ypm:YP2468	>gnl|kg|ypm:YP2468 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
ype:YPO2667	>gnl|kg|ype:YPO2667 ureC, yeuC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
yps:YPTB2942	>gnl|kg|yps:YPTB2942 ureC, yeuC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x
pfo:Pfl_0580	>gnl|kg|pfo:Pfl_0580 urease, alpha subunit			x
ecc:c5408	>gnl|kg|ecc:c5408 iadA; isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]			x
ecj:JW4291	>gnl|kg|ecj:JW4291 iadA; isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]			x
ecs:ECs5286	>gnl|kg|ecs:ECs5286 isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]			x
ece:Z5927	>gnl|kg|ece:Z5927 iadA; isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]			x
eco:b4328	>gnl|kg|eco:b4328 iadA, yjiF; isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]			x
sbo:SBO_4379	>gnl|kg|sbo:SBO_4379 iadA; isoaspartyl dipeptidase			x
sec:SC4367	>gnl|kg|sec:SC4367 iadA; isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]			x
spt:SPA4332	>gnl|kg|spt:SPA4332 iadA; probable isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]			x
sfx:S4446	>gnl|kg|sfx:S4446 iadA; isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]			x
sfl:SF4190	>gnl|kg|sfl:SF4190 iadA; isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
stm:STM4512	>gnl|kg|stm:STM4512 iadA; isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]			x
sty:STY4868	>gnl|kg|sty:STY4868 iadA; probable isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]			x
stt:t4562	>gnl|kg|stt:t4562 iadA; probable isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]			x
dme:CG4598-PA	>gnl|kg|dme:CG4598-PA CG4598; CG4598 gene product from transcript CG4598-RA [EC:5.3.3.8] [KO:K01825]			x
dme:CG4594-PA	>gnl|kg|dme:CG4594-PA CG4594; CG4594 gene product from transcript CG4594-RA [EC:5.3.3.8] [KO:K01825]			x
hsa:1632	>gnl|kg|hsa:1632 DCI; dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase) [EC:5.3.3.8] [KO:K01825]			x
mmu:13177	>gnl|kg|mmu:13177 Dci; dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase) [EC:5.3.3.8] [KO:K01825]			x
rno:29740	>gnl|kg|rno:29740 Dci; dodecenoyl-coenzyme A delta isomerase [EC:5.3.3.8] [KO:K01825]			x
xla:432103	>gnl|kg|xla:432103 MGC82167; hypothetical protein MGC82167 [EC:5.3.3.8] [KO:K01825]			x
xtr:496654	>gnl|kg|xtr:496654 dci-prov; dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase) [EC:5.3.3.8] [KO:K01825]			x
eco:b2919	>gnl|kg|eco:b2919 ygfG; methylmalonyl-CoA decarboxylase, biotin-independent			x
ath:At2g30650	>gnl|kg|ath:At2g30650 T11J7.4; 3-hydroxyisobutyryl-coenzyme A hydrolase, putative / CoA-thioester hydrolase, putative			x
ath:At2g30660	>gnl|kg|ath:At2g30660 T11J7.5; 3-hydroxyisobutyryl-coenzyme A hydrolase, putative / CoA-thioester hydrolase, putative			x
ath:At5g65940	>gnl|kg|ath:At5g65940 K14B20.11; 3-hydroxyisobutyryl-coenzyme A hydrolase (CoA-thioester hydrolase) (CHY1)			x
hsa:26275	>gnl|kg|hsa:26275 HIBCH; 3-hydroxyisobutyryl-Coenzyme A hydrolase			x
mmu:227095	>gnl|kg|mmu:227095 Hibch; 3-hydroxyisobutyryl-Coenzyme A hydrolase			x
rno:301384	>gnl|kg|rno:301384 Hibch_predicted; 3-hydroxyisobutyryl-Coenzyme A hydrolase (predicted)			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
spo:SPBC2D10.09	>gnl|kg|spo:SPBC2D10.09 3-hydroxyisobutyryl-coenzyme a hydrolase; Enoyl-CoA isomerase family			x
aae:aq_484	>gnl|kg|aae:aq_484 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
aci:ACIAD2001	>gnl|kg|aci:ACIAD2001 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
ago:AER294C	>gnl|kg|ago:AER294C AER294Cp; enolase (ENO2) (ENO1) [EC:4.2.1.11] [KO:K01689]			x
ama:AM600	>gnl|kg|ama:AM600 eno; Enolase 1 (2-phosphoglycerate dehydratase 1) [EC:4.2.1.11] [KO:K01689]			x
ana:all3538	>gnl|kg|ana:all3538 enolase [EC:4.2.1.11] [KO:K01689]			x
ape:APE2458	>gnl|kg|ape:APE2458 enolase [EC:4.2.1.11] [KO:K01689]			x
ath:At1g74030	>gnl|kg|ath:At1g74030 F2P9.10; enolase, putative [EC:4.2.1.11] [KO:K01689]			x
ath:At2g29560	>gnl|kg|ath:At2g29560 F16P2.6; enolase, putative			X
ath:At2g36530	>gnl|kg|ath:At2g36530 F1O11.16; enolase [EC:4.2.1.11] [KO:K01689]			x
atc:AGR_C_2631	>gnl|kg|atc:AGR_C_2631 enolase [EC:4.2.1.11] [KO:K01689]			x
atu:Atu1426	>gnl|kg|atu:Atu1426 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
bmb:BruAb1_1138	>gnl|kg|bmb:BruAb1_1138 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
baa:BA_0223	>gnl|kg|baa:BA_0223 enolase [EC:4.2.1.11] [KO:K01689]			x
bar:GBAA5364	>gnl|kg|bar:GBAA5364 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
ban:BA5364	>gnl|kg|ban:BA5364 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
bat:BAS4985	>gnl|kg|bat:BAS4985 enolase [EC:4.2.1.11] [KO:K01689]			x
bab:bbp377	>gnl|kg|bab:bbp377 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
bas:BUsg400	>gnl|kg|bas:BUsg400 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
bbr:BB3703	>gnl|kg|bbr:BB3703 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
bbu:BB0337	>gnl|kg|bbu:BB0337 eno; enolase (eno) [EC:4.2.1.11] [KO:K01689]			x
bca:BCE5238	>gnl|kg|bca:BCE5238 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
bce:BC5135	>gnl|kg|bce:BC5135 enolase [EC:4.2.1.11] [KO:K01689]			x
bcz:BCZK4824	>gnl|kg|bcz:BCZK4824 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
bcl:ABC3017	>gnl|kg|bcl:ABC3017 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
bfl:Bfl157	>gnl|kg|bfl:Bfl157 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
bfr:BF1188	>gnl|kg|bfr:BF1188 enolase [EC:4.2.1.11] [KO:K01689]			x
bga:BG0338	>gnl|kg|bga:BG0338 eno; enolase [EC:4.2.1.11] [KO:K01689]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
bha:BH3556	>gnl|kg|bha:BH3556 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
bhe:BH05720	>gnl|kg|bhe:BH05720 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
bja:bll4794	>gnl|kg|bja:bll4794 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
bld:BLi03661	>gnl|kg|bld:BLi03661 eno; enolase; RBL03415 [EC:4.2.1.11] [KO:K01689]			x
bli:BL03468	>gnl|kg|bli:BL03468 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
blo:BL1022	>gnl|kg|blo:BL1022 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
bma:BMA1689	>gnl|kg|bma:BMA1689 enolase [EC:4.2.1.11] [KO:K01689]			x
bmf:BAB1_1155	>gnl|kg|bmf:BAB1_1155 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
bme:BMEI0851	>gnl|kg|bme:BMEI0851 enolase [EC:4.2.1.11] [KO:K01689]			x
bpn:BPEN_162	>gnl|kg|bpn:BPEN_162 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
bps:BPSL2270	>gnl|kg|bps:BPSL2270 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
bqu:BQ04880	>gnl|kg|bqu:BQ04880 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
bsu:BG10899	>gnl|kg|bsu:BG10899 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
bms:BR1132	>gnl|kg|bms:BR1132 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
bta:281141	>gnl|kg|bta:281141 ENO1; enolase 1 [EC:4.2.1.11] [KO:K01689]			x
bte:BTH_I1894	>gnl|kg|bte:BTH_I1894 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
bth:BT4572	>gnl|kg|bth:BT4572 enolase [EC:4.2.1.11] [KO:K01689]			x
btk:BT9727_4814	>gnl|kg|btk:BT9727_4814 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
buc:BU417	>gnl|kg|buc:BU417 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
cab:CAB932	>gnl|kg|cab:CAB932 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
cac:CAC0713	>gnl|kg|cac:CAC0713 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
cal:orf19.395	>gnl|kg|cal:orf19.395 ENO1; enolase I [EC:4.2.1.11] [KO:K01689]			x
cbu:CBU_1674	>gnl|kg|cbu:CBU_1674 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
cca:CCA00963	>gnl|kg|cca:CCA00963 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
cch:Cag_0347	>gnl|kg|cch:Cag_0347 enolase [EC:4.2.1.11] [KO:K01689]			x
ccr:CC1724	>gnl|kg|ccr:CC1724 enolase [EC:4.2.1.11] [KO:K01689]			x
cdi:DIP0917	>gnl|kg|cdi:DIP0917 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
cef:CE1042	>gnl|kg|cef:CE1042 putative enolase [EC:4.2.1.11] [KO:K01689]			x
cgl:NCgl0935	>gnl|kg|cgl:NCgl0935 Cgl0974; enolase [EC:4.2.1.11] [KO:K01689]			x
chy:CHY_0284	>gnl|kg|chy:CHY_0284 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
cjk:jk1483	>gnl|kg|cjk:jk1483 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
cje:Cj1672c	>gnl|kg|cje:Cj1672c eno; enolase [EC:4.2.1.11] [KO:K01689]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
cme:CMK131C	>gnl|kg|cme:CMK131C enolase [EC:4.2.1.11] [KO:K01689]			x
cmu:TC0876	>gnl|kg|cmu:TC0876 enolase [EC:4.2.1.11] [KO:K01689]			x
cne:CNE00040	>gnl|kg|cne:CNE00040 enolase 1, putative [EC:4.2.1.11] [KO:K01689]			x
cne:CNE05250	>gnl|kg|cne:CNE05250 enolase 1, putative			x
cpv:cgd5_1960	>gnl|kg|cpv:cgd5_1960 enolase (2-phosphoglycerate dehydratase) [EC:4.2.1.11] [KO:K01689]			x
cpe:CPE1299	>gnl|kg|cpe:CPE1299 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
cpa:CP1071	>gnl|kg|cpa:CP1071 enolase [EC:4.2.1.11] [KO:K01689]			x
cpj:CPj0800	>gnl|kg|cpj:CPj0800 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
cpn:CPn0800	>gnl|kg|cpn:CPn0800 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
cpt:CpB0829	>gnl|kg|cpt:CpB0829 enolase [EC:4.2.1.11] [KO:K01689]			x
cte:CT0145	>gnl|kg|cte:CT0145 eno-2; enolase [EC:4.2.1.11] [KO:K01689]			x
cte:CT1962	>gnl|kg|cte:CT1962 eno-1; enolase [EC:4.2.1.11] [KO:K01689]			x
cta:CTA_0637	>gnl|kg|cta:CTA_0637 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
ctr:CT587	>gnl|kg|ctr:CT587 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
dar:Daro_2364	>gnl|kg|dar:Daro_2364 enolase [EC:4.2.1.11] [KO:K01689]			x
dde:Dde_0295	>gnl|kg|dde:Dde_0295 enolase [EC:4.2.1.11] [KO:K01689]			x
deh:cbdb_A573	>gnl|kg|deh:cbdb_A573 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
det:DET0593	>gnl|kg|det:DET0593 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
dps:DP1799	>gnl|kg|dps:DP1799 probable enolase [EC:4.2.1.11] [KO:K01689]			x
dra:DR2637	>gnl|kg|dra:DR2637 enolase [EC:4.2.1.11] [KO:K01689]			x
dre:334116	>gnl|kg|dre:334116 enolase [EC:4.2.1.11] [KO:K01689]			x
dre:378963	>gnl|kg|dre:378963 eno3; enolase 3, (beta, muscle) [EC:4.2.1.11] [KO:K01689]			x
dre:393668	>gnl|kg|dre:393668 enolase [EC:4.2.1.11] [KO:K01689]			x
dre:402874	>gnl|kg|dre:402874 eno2; enolase 2			x
dvu:DVU0322	>gnl|kg|dvu:DVU0322 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
ecn:Ecaj_0489	>gnl|kg|ecn:Ecaj_0489 enolase [EC:4.2.1.11] [KO:K01689]			x
ecj:JW2750	>gnl|kg|ecj:JW2750 eno; Enolase (2-phosphoglycerate dehydratase) (2-phospho-d- glycerate hydro-lyase). [EC:4.2.1.11] [KO:K01689]			x
ecs:ECs3639	>gnl|kg|ecs:ECs3639 enolase [EC:4.2.1.11] [KO:K01689]			x
ece:Z4094	>gnl|kg|ece:Z4094 eno; enolase [EC:4.2.1.11] [KO:K01689]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
eco:b2779	>gnl|kg|eco:b2779 eno, eno'; enolase [EC:4.2.1.11] [KO:K01689]			x
ecu:ECU10_1690	>gnl|kg|ecu:ECU10_1690 10_1690, ENOLASE, ENO_FASHE, gene found by Glimmer [EC:4.2.1.11] [KO:K01689]			x
efa:EF1961	>gnl|kg|efa:EF1961 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
ehi:337.t00001	>gnl|kg|ehi:337.t00001 enolase, putative [EC:4.2.1.11] [KO:K01689]			x
eli:ELI_05740	>gnl|kg|eli:ELI_05740 enolase			x
erg:ERGA_CDS_04960	>gnl|kg|erg:ERGA_CDS_04960 eno; enolase (2-phosphoglycerate dehydratase) [EC:4.2.1.11] [KO:K01689]			x
eru:Erum4840	>gnl|kg|eru:Erum4840 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
erw:ERWE_CDS_05060	>gnl|kg|erw:ERWE_CDS_05060 eno; enolase (2-phosphoglycerate dehydratase) [EC:4.2.1.11] [KO:K01689]			x
fnu:FN1764	>gnl|kg|fnu:FN1764 enolase [EC:4.2.1.11] [KO:K01689]			x
ftu:FTT0709	>gnl|kg|ftu:FTT0709 eno; enolase (2-phosphoglycerate dehydratase) [EC:4.2.1.11] [KO:K01689]			x
gga:395689	>gnl|kg|gga:395689 LOC395689; gamma-subunit of enolase			x
gga:396016	>gnl|kg|gga:396016 LOC396016; enolase			x
gga:396017	>gnl|kg|gga:396017 LOC396017; enolase [EC:4.2.1.11] [KO:K01689]			x
gme:Gmet_2372	>gnl|kg|gme:Gmet_2372 enolase			x
gox:GOX2279	>gnl|kg|gox:GOX2279 enolase [EC:4.2.1.11] [KO:K01689]			x
gsu:GSU2286	>gnl|kg|gsu:GSU2286 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
gvi:gll2121	>gnl|kg|gvi:gll2121 enolase [EC:4.2.1.11] [KO:K01689]			x
hal:VNG1142G	>gnl|kg|hal:VNG1142G eno; enolase [EC:4.2.1.11] [KO:K01689]			x
hch:HCH_01867	>gnl|kg|hch:HCH_01867 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
hdu:HD0477	>gnl|kg|hdu:HD0477 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
hit:NTHI1103	>gnl|kg|hit:NTHI1103 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
hin:HI0932	>gnl|kg|hin:HI0932 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
hpj:jhp0142	>gnl|kg|hpj:jhp0142 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
hpy:HP0154	>gnl|kg|hpy:HP0154 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
hsa:2023	>gnl|kg|hsa:2023 ENO1; enolase 1, (alpha) [EC:4.2.1.11] [KO:K01689]			x
hsa:2026	>gnl|kg|hsa:2026 ENO2; enolase 2 (gamma, neuronal) [EC:4.2.1.11] [KO:K01689]			x

Table K-3. KEGG Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>hsa:2027</td><td>>gnl|kg|hsa:2027 ENO3; enolase 3 (beta, muscle) [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>ilo:IL0772</td><td>>gnl|kg|ilo:IL0772 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>lic:LIC11954</td><td>>gnl|kg|lic:LIC11954 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>lil:LA1951</td><td>>gnl|kg|lil:LA1951 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>ljo:LJ0875</td><td>>gnl|kg|ljo:LJ0875 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>ljo:LJ1246</td><td>>gnl|kg|ljo:LJ1246 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>ljo:LJ1416</td><td>>gnl|kg|ljo:LJ1416 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>lla:L0007</td><td>>gnl|kg|lla:L0007 enoA; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>lma:LmjF14.1160</td><td>>gnl|kg|lma:LmjF14.1160 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>lmf:LMOf2365_2428</td><td>>gnl|kg|lmf:LMOf2365_2428 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>lmo:lmo2455</td><td>>gnl|kg|lmo:lmo2455 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>lpf:lpl2015</td><td>>gnl|kg|lpf:lpl2015 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>lpp:lpp2020</td><td>>gnl|kg|lpp:lpp2020 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>lpn:lpg2037</td><td>>gnl|kg|lpn:lpg2037 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>lxx:Lxx17200</td><td>>gnl|kg|lxx:Lxx17200 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>mpa:MAP0990</td><td>>gnl|kg|mpa:MAP0990 eno; putative enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>mcp:MCAP_0213</td><td>>gnl|kg|mcp:MCAP_0213 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>mca:MCA1933</td><td>>gnl|kg|mca:MCA1933 eno-1; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>mca:MCA2515</td><td>>gnl|kg|mca:MCA2515 eno-2; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>mfl:Mfl468</td><td>>gnl|kg|mfl:Mfl468 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>mga:MGA_0209</td><td>>gnl|kg|mga:MGA_0209 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>mge:MG407</td><td>>gnl|kg|mge:MG407 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>mja:MJ0232</td><td>>gnl|kg|mja:MJ0232 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>mka:MK1647</td><td>>gnl|kg|mka:MK1647 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>mle:ML0255</td><td>>gnl|kg|mle:ML0255 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>mlo:mlr0378</td><td>>gnl|kg|mlo:mlr0378 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>mag:amb1823</td><td>>gnl|kg|mag:amb1823 enolase</td><td></td><td></td><td>x</td></tr>
<tr><td>mmp:MMP0396</td><td>>gnl|kg|mmp:MMP0396 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>mma:MM2836</td><td>>gnl|kg|mma:MM2836 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>mmu:13806</td><td>>gnl|kg|mmu:13806 Eno1; enolase 1, alpha non-neuron [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
</table>

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
mmu:13807	>gnl|kg|mmu:13807 Eno2; enolase 2, gamma neuronal [EC:4.2.1.11] [KO:K01689]			x
mmu:13808	>gnl|kg|mmu:13808 Eno3; enolase 3, beta muscle [EC:4.2.1.11] [KO:K01689]			x
mpe:MYPE3750	>gnl|kg|mpe:MYPE3750 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
mpn:MPN606	>gnl|kg|mpn:MPN606 eno, C12_orf456; enolase [EC:4.2.1.11] [KO:K01689]			x
mpu:MYPU_5180	>gnl|kg|mpu:MYPU_5180 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
mst:Msp_0862	>gnl|kg|mst:Msp_0862 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
msu:MS0256	>gnl|kg|msu:MS0256 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
mta:Moth_0266	>gnl|kg|mta:Moth_0266 enolase [EC:4.2.1.11] [KO:K01689]			x
mtc:MT1051	>gnl|kg|mtc:MT1051 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
nfa:nfa48590	>gnl|kg|nfa:nfa48590 eno; putative enolase [EC:4.2.1.11] [KO:K01689]			x
ngo:NGO0617	>gnl|kg|ngo:NGO0617 putative enolase (2-phosphoglycerate dehydratase) [EC:4.2.1.11] [KO:K01689]			x
nma:NMA1495	>gnl|kg|nma:NMA1495 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
nme:NMB1285	>gnl|kg|nme:NMB1285 enolase [EC:4.2.1.11] [KO:K01689]			x
nmu:Nmul_A1228	>gnl|kg|nmu:Nmul_A1228 enolase [EC:4.2.1.11] [KO:K01689]			x
nwi:Nwi_1827	>gnl|kg|nwi:Nwi_1827 enolase [EC:4.2.1.11] [KO:K01689]			x
oih:OB2434	>gnl|kg|oih:OB2434 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
pab:PAB1126	>gnl|kg|pab:PAB1126 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
pai:PAE0812	>gnl|kg|pai:PAE0812 enolase [EC:4.2.1.11] [KO:K01689]			x
pae:PA3635	>gnl|kg|pae:PA3635 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
pcu:pc0143	>gnl|kg|pcu:pc0143 eno; probable phosphopyruvate hydratase (enolase) [EC:4.2.1.11] [KO:K01689]			x
par:Psyc_1636	>gnl|kg|par:Psyc_1636 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
pca:Pcar_1230	>gnl|kg|pca:Pcar_1230 enolase			x
pfa:PF10_0155	>gnl|kg|pfa:PF10_0155 enolase [EC:4.2.1.11] [KO:K01689]			x
pfu:PF0215	>gnl|kg|pfu:PF0215 enolase [EC:4.2.1.11] [KO:K01689]			x
pgi:PG1824	>gnl|kg|pgi:PG1824 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
pho:PH1942	>gnl|kg|pho:PH1942 enolase [EC:4.2.1.11] [KO:K01689]			x
ayw:AYWB_437	>gnl|kg|ayw:AYWB_437 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
poy:PAM284	>gnl|kg|poy:PAM284 eno; enolase [EC:4.2.1.11] [KO:K01689]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
plu:plu0913	>gnl|kg|plu:plu0913 eno; enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) [EC:4.2.1.11] [KO:K01689]			x
plt:Plut_1972	>gnl|kg|plt:Plut_1972 enolase [EC:4.2.1.11] [KO:K01689]			x
pmm:PMM0208	>gnl|kg|pmm:PMM0208 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
pmi:PMT9312_0210	>gnl|kg|pmi:PMT9312_0210 enolase [EC:4.2.1.11] [KO:K01689]			x
pmt:PMT2083	>gnl|kg|pmt:PMT2083 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
pmn:PMN2A_1575	>gnl|kg|pmn:PMN2A_1575 enolase [EC:4.2.1.11] [KO:K01689]			x
pma:Pro0235	>gnl|kg|pma:Pro0235 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
pmu:PM1871	>gnl|kg|pmu:PM1871 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
ppr:PBPRA3079	>gnl|kg|ppr:PBPRA3079 eno; putative enolase [EC:4.2.1.11] [KO:K01689]			x
ppu:PP1612	>gnl|kg|ppu:PP1612 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
psb:Psyr_1482	>gnl|kg|psb:Psyr_1482 enolase [EC:4.2.1.11] [KO:K01689]			x
pst:PSPTO1554	>gnl|kg|pst:PSPTO1554 eno-1; enolase [EC:4.2.1.11] [KO:K01689]			x
pst:PSPTO4616	>gnl|kg|pst:PSPTO4616 eno-2; enolase [EC:4.2.1.11] [KO:K01689]			x
psp:PSPPH_3820	>gnl|kg|psp:PSPPH_3820 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
ptr:457913	>gnl|kg|ptr:457913 ENO1; enolase 1			x
pub:SAR11_0939	>gnl|kg|pub:SAR11_0939 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
rba:RB12381	>gnl|kg|rba:RB12381 eno; enolase (2-phosphoglycerate dehydratase) [EC:4.2.1.11] [KO:K01689]			x
ret:RHE_CH01931	>gnl|kg|ret:RHE_CH01931 eno; 2-phosphoglycerate dehydratase (enolase) protein [EC:4.2.1.11] [KO:K01689]			x
reu:Reut_A1091	>gnl|kg|reu:Reut_A1091 enolase [EC:4.2.1.11] [KO:K01689]			x
rno:24333	>gnl|kg|rno:24333 Eno1; enolase 1, alpha [EC:4.2.1.11] [KO:K01689]			x
rno:24334	>gnl|kg|rno:24334 Eno2; enolase 2, gamma [EC:4.2.1.11] [KO:K01689]			x
rno:25438	>gnl|kg|rno:25438 Eno3; enolase 3, beta [EC:4.2.1.11] [KO:K01689]			x
rpb:RPB_2778	>gnl|kg|rpb:RPB_2778 enolase [EC:4.2.1.11] [KO:K01689]			x
rpa:RPA2874	>gnl|kg|rpa:RPA2874 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
rso:RSc1129	>gnl|kg|rso:RSc1129 eno, RS04624; enolase [EC:4.2.1.11] [KO:K01689]			x
rsp:RSP_2491	>gnl|kg|rsp:RSP_2491 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
sai:Saci_1377	>gnl|kg|sai:Saci_1377 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
san:gbs0608	>gnl|kg|san:gbs0608 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
sag:SAG0628	>gnl|kg|sag:SAG0628 eno; enolase [EC:4.2.1.11] [KO:K01689]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
sac:SACOL0842	>gnl|kg|sac:SACOL0842 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
sar:SAR0832	>gnl|kg|sar:SAR0832 eno; putative enolase [EC:4.2.1.11] [KO:K01689]			x
sas:SAS0742	>gnl|kg|sas:SAS0742 putative enolase [EC:4.2.1.11] [KO:K01689]			x
sav:SAV0776	>gnl|kg|sav:SAV0776 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
sam:MW0738	>gnl|kg|sam:MW0738 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
sau:SA0731	>gnl|kg|sau:SA0731 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
sab:SAB0732	>gnl|kg|sab:SAB0732 eno; enolase 2-phosphoglycerate dehydratase [EC:4.2.1.11] [KO:K01689]			x
sma:SAV3533	>gnl|kg|sma:SAV3533 eno; putative enolase [EC:4.2.1.11] [KO:K01689]			x
sbo:SBO_2660	>gnl|kg|sbo:SBO_2660 eno; enolase			x
sce:YGR254W	>gnl|kg|sce:YGR254W ENO1; enolase I [EC:4.2.1.11] [KO:K01689]			x
sce:YHR174W	>gnl|kg|sce:YHR174W ENO2; enolase [EC:4.2.1.11] [KO:K01689]			x
sco:SCO3096	>gnl|kg|sco:SCO3096 eno, SCE41.05c; enolase [EC:4.2.1.11] [KO:K01689]			x
sco:SCO7638	>gnl|kg|sco:SCO7638 eno2, SC10F4.11c; enolase [EC:4.2.1.11] [KO:K01689]			x
sdy:SDY_2996	>gnl|kg|sdy:SDY_2996 eno; enolase			x
sec:SC2886	>gnl|kg|sec:SC2886 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
spt:SPA2809	>gnl|kg|spt:SPA2809 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
sep:SE0561	>gnl|kg|sep:SE0561 enolase [EC:4.2.1.11] [KO:K01689]			x
ser:SERP0446	>gnl|kg|ser:SERP0446 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
sfx:S2988	>gnl|kg|sfx:S2988 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
sfl:SF2794	>gnl|kg|sfl:SF2794 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
sgl:SG0513	>gnl|kg|sgl:SG0513 enolase			x
sha:SH2109	>gnl|kg|sha:SH2109 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
sme:SMc01028	>gnl|kg|sme:SMc01028 eno; probable enolase protein [EC:4.2.1.11] [KO:K01689]			x
son:SO3440	>gnl|kg|son:SO3440 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
spn:SP1128	>gnl|kg|spn:SP1128 enolase [EC:4.2.1.11] [KO:K01689]			x
spr:spr1036	>gnl|kg|spr:spr1036 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
spo:SPBC1815.01	>gnl|kg|spo:SPBC1815.01 eno1; enolase [EC:4.2.1.11] [KO:K01689]			x
sil:SPO2474	>gnl|kg|sil:SPO2474 eno; enolase [EC:4.2.1.11] [KO:K01689]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
spm:spyM18_0798	>gnl|kg|spm:spyM18_0798 eno; putative enolase [EC:4.2.1.11] [KO:K01689]			x
spg:SpyM3_0479	>gnl|kg|spg:SpyM3_0479 eno; putative enolase [EC:4.2.1.11] [KO:K01689]			x
spy:SPy0731	>gnl|kg|spy:SPy0731 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
sps:SPs1375	>gnl|kg|sps:SPs1375 putative enolase [EC:4.2.1.11] [KO:K01689]			x
ssp:SSP1912	>gnl|kg|ssp:SSP1912 enolase [EC:4.2.1.11] [KO:K01689]			x
sso:SSO0913	>gnl|kg|sso:SSO0913 enolase [EC:4.2.1.11] [KO:K01689]			x
ssn:SSO_2936	>gnl|kg|ssn:SSO_2936 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
sth:STH249	>gnl|kg|sth:STH249 enolase [EC:4.2.1.11] [KO:K01689]			x
stc:str0635	>gnl|kg|stc:str0635 eno; 2-phosphoglycerate dehydratase, enolase [EC:4.2.1.11] [KO:K01689]			x
stl:stu0635	>gnl|kg|stl:stu0635 eno; 2-phosphoglycerate dehydratase, enolase [EC:4.2.1.11] [KO:K01689]			x
sto:ST1212	>gnl|kg|sto:ST1212 enolase [EC:4.2.1.11] [KO:K01689]			x
stm:STM2952	>gnl|kg|stm:STM2952 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
sty:STY3081	>gnl|kg|sty:STY3081 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
stt:t2853	>gnl|kg|stt:t2853 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
syd:Syncc9605_2476	>gnl|kg|syd:Syncc9605_2476 enolase [EC:4.2.1.11] [KO:K01689]			x
sye:Syncc9902_2161	>gnl|kg|sye:Syncc9902_2161 enolase [EC:4.2.1.11] [KO:K01689]			x
syc:syc0886_c	>gnl|kg|syc:syc0886_c eno; enolase [EC:4.2.1.11] [KO:K01689]			x
syf:Synpcc7942_0639	>gnl|kg|syf:Synpcc7942_0639 enolase [EC:4.2.1.11] [KO:K01689]			x
syw:SYNW2348	>gnl|kg|syw:SYNW2348 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
syn:slr0752	>gnl|kg|syn:slr0752 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
tac:Ta0882	>gnl|kg|tac:Ta0882 enolase [EC:4.2.1.11] [KO:K01689]			x
tan:TA10425	>gnl|kg|tan:TA10425 enolase, putative			x
tbr:Tb10.70.4740	>gnl|kg|tbr:Tb10.70.4740 enolase [EC:4.2.1.11] [KO:K01689]			x
tcx:Tcr_1260	>gnl|kg|tcx:Tcr_1260 enolase [EC:4.2.1.11] [KO:K01689]			x
tcr:504105.140	>gnl|kg|tcr:504105.140 enolase [EC:4.2.1.11] [KO:K01689]			x
tde:TDE0949	>gnl|kg|tde:TDE0949 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
tel:tlr0658	>gnl|kg|tel:tlr0658 enolase [EC:4.2.1.11] [KO:K01689]			x
tko:TK2106	>gnl|kg|tko:TK2106 enolase [EC:4.2.1.11] [KO:K01689]			x
tma:TM0877	>gnl|kg|tma:TM0877 enolase [EC:4.2.1.11] [KO:K01689]			x

Table K-3. KEGG Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>tpa:TP0817</td><td>>gnl|kg|tpa:TP0817 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>tpv:TP04_0700</td><td>>gnl|kg|tpv:TP04_0700 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>tte:TTE1759</td><td>>gnl|kg|tte:TTE1759 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>ttj:TTHA0002</td><td>>gnl|kg|ttj:TTHA0002 enolase (2-phosphoglycerate dehydratase) [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>tth:TTC1610</td><td>>gnl|kg|tth:TTC1610 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>tvo:TVN0981</td><td>>gnl|kg|tvo:TVN0981 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>twh:TWT783</td><td>>gnl|kg|twh:TWT783 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>tws:TW793</td><td>>gnl|kg|tws:TW793 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>uur:UU184</td><td>>gnl|kg|uur:UU184 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>vch:VC2447</td><td>>gnl|kg|vch:VC2447 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>vpa:VP2561</td><td>>gnl|kg|vpa:VP2561 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>vvu:VV11579</td><td>>gnl|kg|vvu:VV11579 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>vvy:VV2818</td><td>>gnl|kg|vvy:VV2818 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>wbr:WGLp353</td><td>>gnl|kg|wbr:WGLp353 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>wbm:Wbm0119</td><td>>gnl|kg|wbm:Wbm0119 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>wol:WD0494</td><td>>gnl|kg|wol:WD0494 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>xac:XAC1719</td><td>>gnl|kg|xac:XAC1719 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>xcb:XC_2531</td><td>>gnl|kg|xcb:XC_2531 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>xcc:XCC1700</td><td>>gnl|kg|xcc:XCC1700 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>xfa:XF1291</td><td>>gnl|kg|xfa:XF1291 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>xft:PD0543</td><td>>gnl|kg|xft:PD0543 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>xla:380038</td><td>>gnl|kg|xla:380038 eno3-prov; enolase 3, beta muscle [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>xla:380298</td><td>>gnl|kg|xla:380298 eno1-prov; enolase 1, alpha [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>xoo:XOO2963</td><td>>gnl|kg|xoo:XOO2963 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>xtr:394749</td><td>>gnl|kg|xtr:394749 MGC75746; Enolase (2-phosphoglycerate dehydratase) [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>ypk:y0814</td><td>>gnl|kg|ypk:y0814 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>ypm:YP0310</td><td>>gnl|kg|ypm:YP0310 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>ype:YPO3376</td><td>>gnl|kg|ype:YPO3376 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
</table>

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
zma:ENO1	>gnl|kg|zma:ENO1 eno1, pgh1; enolase 1 (2-phosphoglycerate dehydratase 1) (2-phospho- d-glycerate hydro-lyase 1). [EC:4.2.1.11] [SP:ENO1_MAIZE]			x
zma:ENO2	>gnl|kg|zma:ENO2 eno2; enolase 2 (2-phosphoglycerate dehydratase 2) (2-phospho- d-glycerate hydro-lyase 2). [EC:4.2.1.11] [SP:ENO2_MAIZE]			x
zmo:ZMO1608	>gnl|kg|zmo:ZMO1608 eno; enolase [EC:4.2.1.11] [KO:K01689]			x
afu:AF1132	>gnl|kg|afu:AF1132 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
ava:Ava_3517	>gnl|kg|ava:Ava_3517 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
eba:ebA6162	>gnl|kg|eba:ebA6162 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
bba:Bd0796	>gnl|kg|bba:Bd0796 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
bfs:BF1155	>gnl|kg|bfs:BF1155 eno, hupA; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
bpa:BPP3252	>gnl|kg|bpa:BPP3252 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
bpe:BP2386	>gnl|kg|bpe:BP2386 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
bpm:BURPS1710b_2711	>gnl|kg|bpm:BURPS1710b_2711 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
bur:Bcep18194_A5413	>gnl|kg|bur:Bcep18194_A5413 phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
cgb:cg1111	>gnl|kg|cgb:cg1111 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
cjr:CJE1844	>gnl|kg|cjr:CJE1844 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
cne:CNC00160	>gnl|kg|cne:CNC00160 phosphopyruvate hydratase, putative [EC:4.2.1.11] [KO:K01689]			x
cps:CPS_4106	>gnl|kg|cps:CPS_4106 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
ctc:CTC00382	>gnl|kg|ctc:CTC00382 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
cya:CYA_2554	>gnl|kg|cya:CYA_2554 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
cyb:CYB_2531	>gnl|kg|cyb:CYB_2531 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
eca:ECA3566	>gnl|kg|eca:ECA3566 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
ecc:c3344	>gnl|kg|ecc:c3344 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
fra:Francci3_3923	>gnl|kg|fra:Francci3_3923 phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
gka:GK3054	>gnl|kg|gka:GK3054 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
hhe:HH0631	>gnl|kg|hhe:HH0631 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
hma:rrnAC0069	>gnl|kg|hma:rrnAC0069 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
lpl:lp_0792	>gnl|kg|lpl:lp_0792 enoA1; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
lpl:lp_1920	>gnl|kg|lpl:lp_1920 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
lsa:LSA0607	>gnl|kg|lsa:LSA0607 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
mac:MA1672	>gnl|kg|mac:MA1672 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
mba:Mbar_A2850	>gnl|kg|mba:Mbar_A2850 phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
mbo:Mb1051	>gnl|kg|mbo:Mb1051 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
mhp:MHP7448_0250	>gnl|kg|mhp:MHP7448_0250 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
mhj:MHJ_0242	>gnl|kg|mhj:MHJ_0242 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
mhy:mhp129	>gnl|kg|mhy:mhp129 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
mmo:MMOB1800	>gnl|kg|mmo:MMOB1800 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
mmy:MSC_0253	>gnl|kg|mmy:MSC_0253 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
msy:MS53_0009	>gnl|kg|msy:MS53_0009 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
mth:MTH43	>gnl|kg|mth:MTH43 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
mtu:Rv1023	>gnl|kg|mtu:Rv1023 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
nar:Saro_2223	>gnl|kg|nar:Saro_2223 phosphopyruvate hydratase [EC:4.2.1.11]			x
neu:NE1044	>gnl|kg|neu:NE1044 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
noc:Noc_0852	>gnl|kg|noc:Noc_0852 phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
nph:NP2846A	>gnl|kg|nph:NP2846A eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
pac:PPA0545	>gnl|kg|pac:PPA0545 phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
pfl:PFL_1196	>gnl|kg|pfl:PFL_1196 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
pfo:Pfl_1121	>gnl|kg|pfo:Pfl_1121 phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
pha:PSHAa0742	>gnl|kg|pha:PSHAa0742 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
psb:Psyr_1363	>gnl|kg|psb:Psyr_1363 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x
pto:PTO1234	>gnl|kg|pto:PTO1234 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x

Table K-3. KEGG Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>rru:Rru_A1885</td><td>>gnl|kg|rru:Rru_A1885 phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>sak:SAK_0713</td><td>>gnl|kg|sak:SAK_0713 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>saa:SAUSA300_0760</td><td>>gnl|kg|saa:SAUSA300_0760 eno; phosphopyruvate hydratase [EC:4.2.1.11]</td><td></td><td></td><td>x</td></tr>
<tr><td>smu:SMU.1247</td><td>>gnl|kg|smu:SMU.1247 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>spz:M5005_Spy_0556</td><td>>gnl|kg|spz:M5005_Spy_0556 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>spb:M28_Spy0535</td><td>>gnl|kg|spb:M28_Spy0535 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>sru:SRU_0787</td><td>>gnl|kg|sru:SRU_0787 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>tdn:Tmden_2001</td><td>>gnl|kg|tdn:Tmden_2001 phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>tbd:Tbd_0621</td><td>>gnl|kg|tbd:Tbd_0621 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>tfu:Tfu_0428</td><td>>gnl|kg|tfu:Tfu_0428 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>vfi:VF2075</td><td>>gnl|kg|vfi:VF2075 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>wsu:WS1494</td><td>>gnl|kg|wsu:WS1494 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>xcv:XCV1752</td><td>>gnl|kg|xcv:XCV1752 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>yps:YPTB0755</td><td>>gnl|kg|yps:YPTB0755 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>ddi:DDB0231355</td><td>>gnl|kg|ddi:DDB0231355 enoA; 2-phospho-D-glycerate hydrolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
<tr><td>ddi:DDB0231356</td><td>>gnl|kg|ddi:DDB0231356 enoB; 2-phospho-D-glycerate hydrolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td></tr>
</table>

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
lac:LBA0889	>gnl|kg|lac:LBA0889 2-phosphoglycerate dehydratase [EC:4.2.1.11] [KO:K01689]			x
lla:L0008	>gnl|kg|lla:L0008 enoB; 2-phosphoglycerate dehydratase [EC:4.2.1.11] [KO:K01689]			x
cel:T21B10.2a	>gnl|kg|cel:T21B10.2a Hypothetical protein T21B10.2a [EC:4.2.1.11] [KO:K01689]			x
dme:CG17654-PB	>gnl|kg|dme:CG17654-PB CG17654; CG17654 gene product from transcript CG17654-RB CG17654 gene product from transcript CG17654-RC [EC:4.2.1.11] [KO:K01689]			x
dme:CG17654-PA	>gnl|kg|dme:CG17654-PA CG17654; CG17654 gene product from transcript CG17654-RA [EC:4.2.1.11] [KO:K01689]			x
sce:YMR323W	>gnl|kg|sce:YMR323W Hypothetical ORF [EC:4.2.1.11] [KO:K01689]			x
bcl:ABC0524	>gnl|kg|bcl:ABC0524 galactonate dehydratase [EC:4.2.1.6] [KO:K01684]			x
bps:BPSL0699	>gnl|kg|bps:BPSL0699 putative galactonate dehydratase protein [EC:4.2.1.6] [KO:K01684]			x
eco:b4478	>gnl|kg|eco:b4478 dgoD; galactonate dehydratase [EC:4.2.1.6] [KO:K01684]			x
gka:GK1955	>gnl|kg|gka:GK1955 galactonate dehydratase [EC:4.2.1.6] [KO:K01684]			x
oih:OB2215	>gnl|kg|oih:OB2215 putative galactonate dehydratase [EC:4.2.1.6] [KO:K01684]			x
psp:PSPPH_1958	>gnl|kg|psp:PSPPH_1958 dgoD; galactonate dehydratase [EC:4.2.1.6] [KO:K01684]			x
rso:RSc2751	>gnl|kg|rso:RSc2751 dgoAb, RS00103; putative galactonate dehydratase protein [EC:4.2.1.6] [KO:K01684]			x
sco:SCO3475	>gnl|kg|sco:SCO3475 SCE65.11c; putative galactonate dehydratase protein [EC:4.2.1.6] [KO:K01684]			x
sec:SC3745	>gnl|kg|sec:SC3745 dgoA; galactonate dehydratase [EC:4.2.1.6] [KO:K01684]			x
sme:SMb20510	>gnl|kg|sme:SMb20510 dgoA; probable galactonate dehydratase protein [EC:4.2.1.6] [KO:K01684]			x
vvy:VVA1580	>gnl|kg|vvy:VVA1580 probable galactonate dehydratase protein [EC:4.2.1.6] [KO:K01684]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
xcv:XCV1796	>gnl|kg|xcv:XCV1796 dgoD; galactonate dehydratase [EC:4.2.1.6] [KO:K01684]			x
bld:BLi04070	>gnl|kg|bld:BLi04070 hypothetical protein [EC:4.2.1.6] [KO:K01684]			x
aci:ACIAD0128	>gnl|kg|aci:ACIAD0128 gudD; D-glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x
bja:blr5872	>gnl|kg|bja:blr5872 gudD; glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x
bsu:BG11161	>gnl|kg|bsu:BG11161 ycbF; glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x
bte:BTH_I0189	>gnl|kg|bte:BTH_I0189 glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x
bur:Bcep18194_A3396	>gnl|kg|bur:Bcep18194_A3396 glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x
eca:ECA3575	>gnl|kg|eca:ECA3575 gudD; glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x
ecj:JW2758	>gnl|kg|ecj:JW2758 ygcX; Probable glucarate dehydrogenase 1 (GDH) [EC:4.2.1.40] [KO:K01706]			x
ecs:ECs3647	>gnl|kg|ecs:ECs3647 putative glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x
ece:Z4102	>gnl|kg|ece:Z4102 ygcX; putative glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x
eco:b2787	>gnl|kg|eco:b2787 gudD, ygcX, gdh1; (D)-glucarate dehydratase 1 [EC:4.2.1.40] [KO:K01706]			x
oih:OB2836	>gnl|kg|oih:OB2836 glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x
ppu:PP4757	>gnl|kg|ppu:PP4757 glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x
psb:Psyr_3120	>gnl|kg|psb:Psyr_3120 glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x
pst:PSPTO3285	>gnl|kg|pst:PSPTO3285 gudD; glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x
reu:Reut_B3715	>gnl|kg|reu:Reut_B3715 glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x
rso:RSc1079	>gnl|kg|rso:RSc1079 gudD1, RS04108; probable glucarate dehydratase protein [EC:4.2.1.40] [KO:K01706]			x
rso:RSp0829	>gnl|kg|rso:RSp0829 gudD2, RS05366; probable glucarate dehydratase protein [EC:4.2.1.40] [KO:K01706]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
sec:SC2900	>gnl|kg|sec:SC2900 gudD; D-glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x
spt:SPA2825	>gnl|kg|spt:SPA2825 ygcX; probable glucarate dehydratase 1 [EC:4.2.1.40] [KO:K01706]			x
sfx:S2994	>gnl|kg|sfx:S2994 ygcX; putative glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x
sfl:SF2800	>gnl|kg|sfl:SF2800 ygcX; putative glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x
ssn:SSO_2944	>gnl|kg|ssn:SSO_2944 ygcX; putative glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x
stm:STM2960	>gnl|kg|stm:STM2960 gudD; D-glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x
sty:STY3098	>gnl|kg|sty:STY3098 ygcX; probable glucarate dehydratase 1 [EC:4.2.1.40] [KO:K01706]			x
stt:t2869	>gnl|kg|stt:t2869 ygcX; probable glucarate dehydratase 1 [EC:4.2.1.40] [KO:K01706]			x
xcb:XC_0951	>gnl|kg|xcb:XC_0951 glucarate hydratase [EC:4.2.1.40] [KO:K01706]			x
xcc:XCC3242	>gnl|kg|xcc:XCC3242 tcbD; glucarate hydratase [EC:4.2.1.40] [KO:K01706]			x
sbo:SBO_2668	>gnl|kg|sbo:SBO_2668 ygcX; putative glucarate dehydratase			x
ctc:CTC02563	>gnl|kg|ctc:CTC02563 methylaspartate ammonia-lyase [EC:4.3.1.2] [KO:K04835]			x
ecs:ECs0761	>gnl|kg|ecs:ECs0761 3-methylaspartate ammonia-lyase [EC:4.3.1.2] [KO:K04835]			x
ece:Z0892	>gnl|kg|ece:Z0892 putative methylaspartate ammonia-lyase [EC:4.3.1.2] [KO:K04835]			x
hal:VNG2289G	>gnl|kg|hal:VNG2289G mal; methylaspartate ammonia-lyase [EC:4.3.1.2] [KO:K04835]			x
mlo:mlr6095	>gnl|kg|mlo:mlr6095 3-methylaspartate ammonia-lyase [EC:4.3.1.2] [KO:K04835]			x
sdy:SDY_0673	>gnl|kg|sdy:SDY_0673 putative methylaspartate ammonia-lyase			x
cme:CMV117C	>gnl|kg|cme:CMV117C 4-(2'-carboxyphenyl)-4-oxybutyric acid synthase	GSA		x

Table K-3. KEGG Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>ava:Ava_2635</td><td>>gnl|kg|ava:Ava_2635 O-succinylbenzoate synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td></td><td>x</td></tr>
<tr><td>bcz:BCZK4606</td><td>>gnl|kg|bcz:BCZK4606 menC; possible N-acylamino acid racemase; possible O-succinylbenzoate synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td></td><td>x</td></tr>
<tr><td>bsu:BG13847</td><td>>gnl|kg|bsu:BG13847 menC, ytfD; o-succinylbenzoate synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td></td><td>x</td></tr>
<tr><td>cya:CYA_1249</td><td>>gnl|kg|cya:CYA_1249 menC; O-succinylbenzoate synthetase [EC:4.2.1.-]</td><td></td><td></td><td>x</td></tr>
<tr><td>cyb:CYB_0729</td><td>>gnl|kg|cyb:CYB_0729 menC; O-succinylbenzoate synthetase [EC:4.2.1.-]</td><td></td><td></td><td>x</td></tr>
<tr><td>hit:NTHI1142</td><td>>gnl|kg|hit:NTHI1142 menC; O-succinylbenzoate synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td></td><td>x</td></tr>
<tr><td>pmm:PMM0175</td><td>>gnl|kg|pmm:PMM0175 menC; putative O-succinylbenzoate synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td></td><td>x</td></tr>
<tr><td>pmi:PMT9312_0177</td><td>>gnl|kg|pmi:PMT9312_0177 putative O-succinylbenzoate synthase</td><td></td><td></td><td>x</td></tr>
<tr><td>pmt:PMT2058</td><td>>gnl|kg|pmt:PMT2058 menC; putative O-succinylbenzoate synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td></td><td>x</td></tr>
<tr><td>syd:Syncc9605_2437</td><td>>gnl|kg|syd:Syncc9605_2437 putative O-succinylbenzoate synthase</td><td></td><td></td><td>x</td></tr>
<tr><td>sye:Syncc9902_2118</td><td>>gnl|kg|sye:Syncc9902_2118 putative O-succinylbenzoate synthase</td><td></td><td></td><td>x</td></tr>
<tr><td>syw:SYNW2306</td><td>>gnl|kg|syw:SYNW2306 menC; putative O-succinylbenzoate synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td></td><td>x</td></tr>
<tr><td>vfi:VF1667</td><td>>gnl|kg|vfi:VF1667 O-succinylbenzoate synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td></td><td>x</td></tr>
<tr><td>vvy:VV1119</td><td>>gnl|kg|vvy:VV1119 O-succinylbenzoate synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td></td><td>x</td></tr>
<tr><td>ana:alr0034</td><td>>gnl|kg|ana:alr0034 menC; O-succinylbenzoic acid synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td></td><td>x</td></tr>
<tr><td>sac:SACOL1843</td><td>>gnl|kg|sac:SACOL1843 O-succinylbenzoic acid (OSB) synthetase, putative [EC:4.2.1.-] [KO:K02549]</td><td></td><td></td><td>x</td></tr>
<tr><td>sav:SAV1796</td><td>>gnl|kg|sav:SAV1796 menC; o-succinylbenzoic acid synthetase [EC:4.2.1.-] [KO:K02549]</td><td></td><td></td><td>x</td></tr>
<tr><td>sam:MW1734</td><td>>gnl|kg|sam:MW1734 menC; O-succinylbenzoic acid synthetase [EC:4.2.1.-] [KO:K02549]</td><td></td><td></td><td>x</td></tr>
<tr><td>sau:SA1614</td><td>>gnl|kg|sau:SA1614 menC; o-succinylbenzoic acid (OSB) synthetase [EC:4.2.1.-] [KO:K02549]</td><td></td><td></td><td>x</td></tr>
<tr><td>sab:SAB1650c</td><td>>gnl|kg|sab:SAB1650c O-succinylbenzoic acid synthetase [EC:4.2.1.-]</td><td></td><td></td><td>x</td></tr>
</table>

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
saa:SAUSA300_1735	>gnl|kg|saa:SAUSA300_1735 menC; O-succinylbenzoic acid synthetase [EC:4.2.1.-]			x
sep:SE1463	>gnl|kg|sep:SE1463 o-succinylbenzoic acid (OSB) synthetase [EC:4.2.1.-] [KO:K02549]			x
ser:SERP1357	>gnl|kg|ser:SERP1357 O-succinylbenzoic acid synthetase, putative [EC:4.2.1.-] [KO:K02549]			x
sha:SH1133	>gnl|kg|sha:SH1133 menC; O-succinylbenzoic acid (OSB) synthetase [EC:4.2.1.-] [KO:K02549]			x
sru:SRU_1354	>gnl|kg|sru:SRU_1354 menC; O-succinylbenzoic acid (OSB) synthetase [EC:4.2.1.-]			x
ssp:SSP0971	>gnl|kg|ssp:SSP0971 O-succinylbenzoic acid synthetase [EC:4.2.1.-] [KO:K02549]			x
aci:ACIAD1446	>gnl|kg|aci:ACIAD1446 catB; muconate cycloisomerase I (cis,cis-muconate lactonizing enzyme I) (MLE) [EC:5.5.1.1] [KO:K01856]			x
bma:BMAA0200	>gnl|kg|bma:BMAA0200 catB; muconate cycloisomerase [EC:5.5.1.1] [KO:K01856]			x
bpm:BURPS1710b_A0986	>gnl|kg|bpm:BURPS1710b_A0986 catB; muconate cycloisomerase [EC:5.5.1.1] [KO:K01856]			x
bps:BPSS1891	>gnl|kg|bps:BPSS1891 catB; muconate cycloisomerase I [EC:5.5.1.1] [KO:K01856]			x
bur:Bcep18194_B2328	>gnl|kg|bur:Bcep18194_B2328 muconate cycloisomerase [EC:5.5.1.1] [KO:K01856]			x
pfl:PFL_3862	>gnl|kg|pfl:PFL_3862 catB; muconate cycloisomerase [EC:5.5.1.1] [KO:K01856]			x
bte:BTH_II0485	>gnl|kg|bte:BTH_II0485 muconate cycloisomerase			x
cef:CE2303	>gnl|kg|cef:CE2303 putative muconate cycloisomerase			x
ppu:PP3715	>gnl|kg|ppu:PP3715 catB; muconate cycloisomerase			x
aae:aq_2171	>gnl|kg|aae:aq_2171 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]			x
eba:ebD6	>gnl|kg|eba:ebD6 ppcC; phenylphosphate carboxylase, gamma subunit [EC:3.1.3.45] [KO:K03270]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
ecc:c3958	>gnl|kg|ecc:c3958 yrbI; putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	ESA, swissprot		x
ecj:JW3165	>gnl|kg|ecj:JW3165 yrbI; putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	ESA, swissprot		x
ecs:ECs4077	>gnl|kg|ecs:ECs4077 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	ESA, swissprot		x
ece:Z4561	>gnl|kg|ece:Z4561 yrbI; hypothetical protein [EC:3.1.3.45] [KO:K03270]	ESA, swissprot		x
eco:b3198	>gnl|kg|eco:b3198 yrbI, yrbJ; conserved hypothetical protein, phosphatase-like domain [EC:3.1.3.45] [KO:K03270]	ESA, swissprot		x
hit:NTHI1982	>gnl|kg|hit:NTHI1982 yrbI; 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]			x
hin:HI1679	>gnl|kg|hin:HI1679 yrbI; putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]			x
hpj:jhp1478	>gnl|kg|hpj:jhp1478 putative [EC:3.1.3.45] [KO:K03270]			x
hpy:HP1570	>gnl|kg|hpy:HP1570 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]			x
ngo:NGO1608	>gnl|kg|ngo:NGO1608 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (KDO 8-P phosphatase) [EC:3.1.3.45] [KO:K03270]			x
nma:NMA2134	>gnl|kg|nma:NMA2134 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]			x
nme:NMB0353	>gnl|kg|nme:NMB0353 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]			x
pae:PA4458	>gnl|kg|pae:PA4458 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]			x
pfl:PFL_0919	>gnl|kg|pfl:PFL_0919 kdsC; 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]			x
pfo:Pfl_0861	>gnl|kg|pfo:Pfl_0861 kdsC; phosphatase KdsC [EC:3.1.3.45] [KO:K03270]			x
pmu:PM0524	>gnl|kg|pmu:PM0524 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]			x
psb:Psyr_4143	>gnl|kg|psb:Psyr_4143 yrbI; HAD-superfamily hydrolase, subfamily IIIA:phosphatase YrbI [EC:3.1.3.45] [KO:K03270]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
pst:PSPTO4449	>gnl|kg|pst:PSPTO4449 phosphatase, YrbI family [EC:3.1.3.45] [KO:K03270]			X
psp:PSPPH_4147	>gnl|kg|psp:PSPPH_4147 phosphatase, YrbI family [EC:3.1.3.45] [KO:K03270]			X
sfx:S3456	>gnl|kg|sfx:S3456 yrbI; putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	ESA, swissprot		x
sfl:SF3238	>gnl|kg|sfl:SF3238 yrbI; putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	ESA, swissprot		x
ssn:SSO_3346	>gnl|kg|ssn:SSO_3346 yrbI; hypothetical protein [EC:3.1.3.45] [KO:K03270]	ESA, swissprot		x
syw:SYNW0186	>gnl|kg|syw:SYNW0186 possible phosphatase [EC:3.1.3.45] [KO:K03270]			X
xac:XAC2968	>gnl|kg|xac:XAC2968 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]			X
xcb:XC_1315	>gnl|kg|xcb:XC_1315 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (KDO 8-P phosphatase) [EC:3.1.3.45] [KO:K03270]			X
xcc:XCC2798	>gnl|kg|xcc:XCC2798 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]			X
xoo:XOO1288	>gnl|kg|xoo:XOO1288 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (KDO 8-P phosphatase) [EC:3.1.3.45] [KO:K03270]			X
bar:GBAA1340	>gnl|kg|bar:GBAA1340 phnX; phosphonoacetaldehyde phosphonohydrolase [EC:3.11.1.1] [KO:K05306]			x
ban:BA1340	>gnl|kg|ban:BA1340 phnX; phosphonoacetaldehyde phosphonohydrolase [EC:3.11.1.1] [KO:K05306]			x
bat:BAS1239	>gnl|kg|bat:BAS1239 phosphonoacetaldehyde phosphonohydrolase [EC:3.11.1.1] [KO:K05306]			x
bca:BCE1439	>gnl|kg|bca:BCE1439 phnX; phosphonoacetaldehyde phosphonohydrolase [EC:3.11.1.1] [KO:K05306]			x
bcz:BCZK1217	>gnl|kg|bcz:BCZK1217 phnX; possible phosphonoacetaldehyde hydrolase [EC:3.11.1.1] [KO:K05306]			x
btk:BT9727_1215	>gnl|kg|btk:BT9727_1215 phnX; possible phosphonoacetaldehyde hydrolase [EC:3.11.1.1] [KO:K05306]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
lpl:lp_0711	>gnl|kg|lpl:lp_0711 phnX; phosphonoacetaldehyde hydrolase [EC:3.11.1.1] [KO:K05306]			x
pfl:PFL_3966	>gnl|kg|pfl:PFL_3966 phnX; 2-phosphonoacetaldehyde hydrolase [EC:3.11.1.1] [KO:K05306]			x
pae:PA1311	>gnl|kg|pae:PA1311 phnX; 2-phosphonoacetaldehyde hydrolase			x
pfo:Pfl_3684	>gnl|kg|pfo:Pfl_3684 phosphonoacetaldehyde hydrolase			x
ppu:PP2208	>gnl|kg|ppu:PP2208 phnX; 2-phosphonoacetaldehyde hydrolase			x
spt:SPA2291	>gnl|kg|spt:SPA2291 phnX; phosphonoacetaldehyde phosphonohydrolase			x
sty:STY0471	>gnl|kg|sty:STY0471 phnX; phosphonoacetaldehyde phosphonohydrolase			x
stt:t2431	>gnl|kg|stt:t2431 phnX; phosphonoacetaldehyde phosphonohydrolase			x
vch:VCA0606	>gnl|kg|vch:VCA0606 phosphonoacetaldehyde phosphonohydrolase			x
vpa:VPA0233	>gnl|kg|vpa:VPA0233 phosphonoacetaldehyde phosphonohydrolase			x
vvy:VVA0474	>gnl|kg|vvy:VVA0474 phosphonoacetaldehyde phosphonohydrolase			x
eba:ebA812	>gnl|kg|eba:ebA812 putative 2-haloalkanoic acid dehalogenase [EC:3.8.1.2] [KO:K01560]			x
bmb:BruAb1_0587	>gnl|kg|bmb:BruAb1_0587 haloacid dehalogenase [EC:3.8.1.2] [KO:K01560]			x
bja:blr7560	>gnl|kg|bja:blr7560 dhlB; 2-haloalkanoic acid dehalogenase [EC:3.8.1.2] [KO:K01560]			x
bma:BMA1589	>gnl|kg|bma:BMA1589 dheII; haloacid dehalogenase, type II [EC:3.8.1.2] [KO:K01560]			x
bpm:BURPS1710b_2616	>gnl|kg|bpm:BURPS1710b_2616 dehII; haloacid dehalogenase, type II [EC:3.8.1.2] [KO:K01560]			x
bps:BPSL2191	>gnl|kg|bps:BPSL2191 putative dehalogenase [EC:3.8.1.2] [KO:K01560]			x
bms:BR0565	>gnl|kg|bms:BR0565 haloacid dehalogenase, type II [EC:3.8.1.2] [KO:K01560]			x
bte:BTH_I1995	>gnl|kg|bte:BTH_I1995 dehII-1; haloacid dehalogenase, type II [EC:3.8.1.2] [KO:K01560]			x
bur:Bcep18194_A5360	>gnl|kg|bur:Bcep18194_A5360 haloacid dehalogenase, type II [EC:3.8.1.2] [KO:K01560]			x
reu:Reut_A1952	>gnl|kg|reu:Reut_A1952 haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2 [EC:3.8.1.2] [KO:K01560]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
rpa:RPA4199	>gnl|kg|rpa:RPA4199 putative 2-haloacid halidohydrolase Iva [EC:3.8.1.2] [KO:K01560]			x
rso:RSc1362	>gnl|kg|rso:RSc1362 RS04644; putative 2-haloalkanoic acid dehalogenase protein [EC:3.8.1.2] [KO:K01560]			x
mlo:mll7634	>gnl|kg|mlo:mll7634 2-haloacid halidohydrolase Iva			x
mag:amb2538	>gnl|kg|mag:amb2538 2-haloalkanoic acid dehalogenase I			x
bsu:BG12422	>gnl|kg|bsu:BG12422 yvdM; putative beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]			x
cac:CAC2614	>gnl|kg|cac:CAC2614 beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]			x
ecc:c1789	>gnl|kg|ecc:c1789 ycjU; putative beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]			x
ecj:JW1310	>gnl|kg|ecj:JW1310 ycjU; Putative beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]			x
ecs:ECs1896	>gnl|kg|ecs:ECs1896 putative beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]			x
ece:Z2465	>gnl|kg|ece:Z2465 ycjU; putative beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]			x
efa:EF0956	>gnl|kg|efa:EF0956 pgmB; beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]			x
lla:L0001	>gnl|kg|lla:L0001 pgmB; beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]			x
lmf:LMOf2365_2822	>gnl|kg|lmf:LMOf2365_2822 beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]			x
lmo:lmo2831	>gnl|kg|lmo:lmo2831 putative beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]			x
lpl:lp_0027	>gnl|kg|lpl:lp_0027 pgmB1; beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]			x
lpl:lp_0066	>gnl|kg|lpl:lp_0066 pgmB2; beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]			x
mpu:MYPU_6350	>gnl|kg|mpu:MYPU_6350 pgmB; beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]			x

Table K-3. KEGG Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>nma:NMA2093</td><td>>gnl|kg|nma:NMA2093 pgm2; beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td></tr>
<tr><td>nma:NMA2097</td><td>>gnl|kg|nma:NMA2097 pgm1; beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td></tr>
<tr><td>nme:NMB0391</td><td>>gnl|kg|nme:NMB0391 beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td></tr>
<tr><td>sfx:S1406</td><td>>gnl|kg|sfx:S1406 ycjU; putative beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td></tr>
<tr><td>sfl:SF1323</td><td>>gnl|kg|sfl:SF1323 ycjU; putative beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td></tr>
<tr><td>ssn:SSO_1823</td><td>>gnl|kg|ssn:SSO_1823 ycjU; putative beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td></tr>
<tr><td>sma:SAV2998</td><td>>gnl|kg|sma:SAV2998 ptlA; pentalenene synthase [EC:4.2.3.7]</td><td></td><td></td><td>x</td></tr>
<tr><td>ava:Ava_4671</td><td>>gnl|kg|ava:Ava_4671 terpene synthase [EC:5.4.99.17]</td><td></td><td></td><td>x</td></tr>
<tr><td>bma:BMAA2100</td><td>>gnl|kg|bma:BMAA2100 shc; squalene-hopene cyclase [EC:5.4.99.17]</td><td></td><td></td><td>x</td></tr>
<tr><td>bpm:BURPS1710b_A1490</td><td>>gnl|kg|bpm:BURPS1710b_A1490 shc; squalene-hopene cyclase [EC:5.4.99.17]</td><td></td><td></td><td>x</td></tr>
<tr><td>bps:BPSS2339</td><td>>gnl|kg|bps:BPSS2339 shc; squalene--hopene cyclase [EC:5.4.99.17]</td><td></td><td></td><td>x</td></tr>
<tr><td>bte:BTH_II2359</td><td>>gnl|kg|bte:BTH_II2359 shc; squalene-hopene cyclase [EC:5.4.99.17]</td><td></td><td></td><td>x</td></tr>
<tr><td>bur:Bcep18194_B0019</td><td>>gnl|kg|bur:Bcep18194_B0019 terpene synthase/squalene cyclase [EC:5.4.99.17]</td><td></td><td></td><td>x</td></tr>
<tr><td>bur:Bcep18194_C7519</td><td>>gnl|kg|bur:Bcep18194_C7519 terpene synthase/squalene cyclase [EC:5.4.99.17]</td><td></td><td></td><td>x</td></tr>
<tr><td>gox:GOX2260</td><td>>gnl|kg|gox:GOX2260 squalene-hopene cyclase [EC:5.4.99.17]</td><td></td><td></td><td>x</td></tr>
<tr><td>gsu:GSU0688</td><td>>gnl|kg|gsu:GSU0688 shc-1; squalene-hopene cyclase [EC:5.4.99.17]</td><td></td><td></td><td>x</td></tr>
<tr><td>gsu:GSU3061</td><td>>gnl|kg|gsu:GSU3061 shc-2; squalene-hopene cyclase [EC:5.4.99.17]</td><td></td><td></td><td>x</td></tr>
<tr><td>noc:Noc_1320</td><td>>gnl|kg|noc:Noc_1320 terpene synthase/squalene cyclase [EC:5.4.99.17]</td><td></td><td></td><td>x</td></tr>
<tr><td>nwi:Nwi_2269</td><td>>gnl|kg|nwi:Nwi_2269 terpene synthase/squalene cyclase [EC:5.4.99.17]</td><td></td><td></td><td>x</td></tr>
<tr><td>reu:Reut_B4954</td><td>>gnl|kg|reu:Reut_B4954 terpene synthase:squalene cyclase [EC:5.4.99.17]</td><td></td><td></td><td>x</td></tr>
<tr><td>rru:Rru_A0062</td><td>>gnl|kg|rru:Rru_A0062 terpene synthase, squalene cyclase [EC:5.4.99.17]</td><td></td><td></td><td>x</td></tr>
<tr><td>zmo:ZMO0872</td><td>>gnl|kg|zmo:ZMO0872 shc; squalene--hopene cyclase [EC:5.4.99.17]</td><td></td><td></td><td>x</td></tr>
<tr><td>zmo:ZMO1548</td><td>>gnl|kg|zmo:ZMO1548 shc; squalene--hopene cyclase [EC:5.4.99.17]</td><td></td><td></td><td>x</td></tr>
</table>

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
bsu:BG12679	>gnl|kg|bsu:BG12679 sqhC; squalene-hopene cyclase			x
gvi:glr4057	>gnl|kg|gvi:glr4057 shc; squalene-hopene cyclase			x
pca:Pcar_0441	>gnl|kg|pca:Pcar_0441 squalene-hopene cyclase			x
sma:SAV1650	>gnl|kg|sma:SAV1650 hopA; squalene-hopene cyclase			x
sco:SCO6764	>gnl|kg|sco:SCO6764 SC6A5.13; putative squalene-hopene cyclase			x
ana:all0775	>gnl|kg|ana:all0775 squalene-hopene-cyclase			x
fra:Francci3_0823	>gnl|kg|fra:Francci3_0823 squalene cyclase			x
gme:Gmet_0419	>gnl|kg|gme:Gmet_0419 terpene synthase:squalene cyclase			x
gme:Gmet_2820	>gnl|kg|gme:Gmet_2820 terpene synthase:squalene cyclase			x
nmu:Nmul_A2556	>gnl|kg|nmu:Nmul_A2556 squalene cyclase			x
pca:Pcar_0355	>gnl|kg|pca:Pcar_0355 squalene--hopene cyclase			x
rpb:RPB_1726	>gnl|kg|rpb:RPB_1726 squalene cyclase			x
rpa:RPA3740	>gnl|kg|rpa:RPA3740 sqhC; squalene-hopene-cyclase [EC:5.4.99.7] [KO:K01852]			x
syn:slr2089	>gnl|kg|syn:slr2089 shc; squalene-hopene-cyclase			x
tel:tlr2309	>gnl|kg|tel:tlr2309 shc; squalene-hopene-cyclase			x
hsa:84693	>gnl|kg|hsa:84693 MCEE; methylmalonyl CoA epimerase [EC:5.1.99.1] [KO:K05606]			x
mmu:73724	>gnl|kg|mmu:73724 Mcee; methylmalonyl CoA epimerase [EC:5.1.99.1] [KO:K05606]			x
rno:293829	>gnl|kg|rno:293829 Mcee_predicted; methylmalonyl CoA epimerase (predicted) [EC:5.1.99.1] [KO:K05606]			x
ath:At1g06570	>gnl|kg|ath:At1g06570 F12K11.9; 4-hydroxyphenylpyruvate dioxygenase (HPD) [EC:1.13.11.27] [KO:K00457]			x
atc:AGR_L_678	>gnl|kg|atc:AGR_L_678 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
atu:Atu4529	>gnl|kg|atu:Atu4529 putative 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
bar:GBAA0240	>gnl|kg|bar:GBAA0240 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
ban:BA0240	>gnl|kg|ban:BA0240 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
bat:BAS0226	>gnl|kg|bat:BAS0226 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
bba:Bd3543	>gnl|kg|bba:Bd3543 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
bca:BCE0260	>gnl|kg|bca:BCE0260 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
bce:BC0252	>gnl|kg|bce:BC0252 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
bcz:BCZK0215	>gnl|kg|bcz:BCZK0215 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
bja:bll0339	>gnl|kg|bja:bll0339 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
bja:bll1053	>gnl|kg|bja:bll1053 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
bma:BMA2582	>gnl|kg|bma:BMA2582 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
bma:BMAA0848	>gnl|kg|bma:BMAA0848 4-hydroxyphenylpyruvate dioxygenase, putative [EC:1.13.11.27] [KO:K00457]			x
bpm:BURPS1710b_0016	>gnl|kg|bpm:BURPS1710b_0016 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
bps:BPSL3239	>gnl|kg|bps:BPSL3239 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
bta:516058	>gnl|kg|bta:516058 HPD; 4-hydroxyphenylpyruvate dioxygenase			x
bte:BTH_I3106	>gnl|kg|bte:BTH_I3106 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
bte:BTH_II1222	>gnl|kg|bte:BTH_II1222 4-hydroxyphenylpyruvate dioxygenase			x
bte:BTH_II2059	>gnl|kg|bte:BTH_II2059 4-hydroxyphenylpyruvate dioxygenase, putative			x
btk:BT9727_0213	>gnl|kg|btk:BT9727_0213 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
bur:Bcep18194_A3420	>gnl|kg|bur:Bcep18194_A3420 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
bur:Bcep18194_B0343	>gnl|kg|bur:Bcep18194_B0343 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
bur:Bcep18194_B1625	>gnl|kg|bur:Bcep18194_B1625 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
ccr:CC2533	>gnl|kg|ccr:CC2533 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
cme:CMI063C	>gnl|kg|cme:CMI063C 4-hydroxyphenylpyruvate dioxygenase, 4HPPD [EC:1.13.11.27] [KO:K00457]			x
cps:CPS_3484	>gnl|kg|cps:CPS_3484 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
cvi:CV0969	>gnl|kg|cvi:CV0969 hpd; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
eli:ELI_06415	>gnl|kg|eli:ELI_06415 4-hydroxyphenylpyruvate dioxygenase			x
hch:HCH_00955	>gnl|kg|hch:HCH_00955 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
hsa:3242	>gnl|kg|hsa:3242 HPD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
ilo:IL0722	>gnl|kg|ilo:IL0722 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
lpf:lpl2204	>gnl|kg|lpf:lpl2204 lly; 4-hydroxyphenylpyruvate dioxygenase (legiolysin) [EC:1.13.11.27] [KO:K00457]			X
lpp:lpp2232	>gnl|kg|lpp:lpp2232 lly; 4-hydroxyphenylpyruvate dioxygenase (legiolysin) [EC:1.13.11.27] [KO:K00457]			X
lpn:lpg2278	>gnl|kg|lpn:lpg2278 hpd; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
mlo:mll8309	>gnl|kg|mlo:mll8309 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
nar:Saro_0597	>gnl|kg|nar:Saro_0597 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27]			x
nar:Saro_1586	>gnl|kg|nar:Saro_1586 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
nfa:nfa50810	>gnl|kg|nfa:nfa50810 putative 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
noc:Noc_1437	>gnl|kg|noc:Noc_1437 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
pae:PA0242	>gnl|kg|pae:PA0242 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
pae:PA0865	>gnl|kg|pae:PA0865 hpd; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
pfl:PFL_3387	>gnl|kg|pfl:PFL_3387 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
pfl:PFL_5385	>gnl|kg|pfl:PFL_5385 4-hydroxyphenylpyruvate dioxygenase, putative [EC:1.13.11.27] [KO:K00457]			x
pfo:Pfl_2917	>gnl|kg|pfo:Pfl_2917 4-hydroxyphenylpyruvate dioxygenase			x
pfo:Pfl_4905	>gnl|kg|pfo:Pfl_4905 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
pha:PSHAa2168	>gnl|kg|pha:PSHAa2168 melA; 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) [EC:1.13.11.27] [KO:K00457]			x
ppr:PBPRB1180	>gnl|kg|ppr:PBPRB1180 putative 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
ppu:PP2554	>gnl|kg|ppu:PP2554 4-hydroxyphenylpyruvate dioxygenase, putative [EC:1.13.11.27] [KO:K00457]			x
ppu:PP3433	>gnl|kg|ppu:PP3433 hpd; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
psb:Psyr_2130	>gnl|kg|psb:Psyr_2130 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
psb:Psyr_3330	>gnl|kg|psb:Psyr_3330 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
pst:PSPTO2346	>gnl|kg|pst:PSPTO2346 4-hydroxyphenylpyruvate dioxygenase, putative [EC:1.13.11.27] [KO:K00457]			x
pst:PSPTO3553	>gnl|kg|pst:PSPTO3553 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
psp:PSPPH_2105	>gnl|kg|psp:PSPPH_2105 4-hydroxyphenylpyruvate dioxygenase, putative [EC:1.13.11.27] [KO:K00457]			x
psp:PSPPH_3250	>gnl|kg|psp:PSPPH_3250 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
ptr:473296	>gnl|kg|ptr:473296 HPD; 4-hydroxyphenylpyruvate dioxygenase			x
ret:RHE_CH01745	>gnl|kg|ret:RHE_CH01745 probable 4-hydroxyphenylpyruvate dioxygenase protein [EC:1.13.11.27] [KO:K00457]			x
ret:RHE_PC00215	>gnl|kg|ret:RHE_PC00215 putative 4-hydroxyphenylpyruvate dioxygenase protein [EC:1.13.11.27] [KO:K00457]			x
reu:Reut_B4501	>gnl|kg|reu:Reut_B4501 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
reu:Reut_B5028	>gnl|kg|reu:Reut_B5028 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
reu:Reut_B5035	>gnl|kg|reu:Reut_B5035 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
rpa:RPA0005	>gnl|kg|rpa:RPA0005 hpd; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
rso:RSc3103	>gnl|kg|rso:RSc3103 RS00556; probable 4-hydroxyphenylpyruvate dioxygenase oxidoreductase protein [EC:1.13.11.27] [KO:K00457]			x
rso:RS05661	>gnl|kg|rso:RS05661 RSp1316; probable 4-hydroxyphenylpyruvate dioxygenase oxidoreductase protein [EC:1.13.11.27] [KO:K00457]			x
rso:RS04776	>gnl|kg|rso:RS04776 RSp1347; probable 4-hydroxyphenylpyruvate dioxygenase oxidoreductase protein [EC:1.13.11.27] [KO:K00457]			x
rso:RS02058	>gnl|kg|rso:RS02058 RSp1400; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
sma:SAV5149	>gnl|kg|sma:SAV5149 hpd; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
sco:SCO2927	>gnl|kg|sco:SCO2927 SCE19A.27c; putative 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x
sme:SMc03211	>gnl|kg|sme:SMc03211 putative 4-hydroxyphenylpyruvate dioxygenase protein [EC:1.13.11.27] [KO:K00457]			x

Table K-3. KEGG Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>son:SO1962</td><td>>gnl|kg|son:SO1962 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
<tr><td>sil:SPO1426</td><td>>gnl|kg|sil:SPO1426 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
<tr><td>sru:SRU_1370</td><td>>gnl|kg|sru:SRU_1370 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
<tr><td>vch:VC1344</td><td>>gnl|kg|vch:VC1344 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
<tr><td>vpa:VP1349</td><td>>gnl|kg|vpa:VP1349 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
<tr><td>vvu:VV12768</td><td>>gnl|kg|vvu:VV12768 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
<tr><td>xac:XAC0452</td><td>>gnl|kg|xac:XAC0452 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
<tr><td>xcb:XC_0450</td><td>>gnl|kg|xcb:XC_0450 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
<tr><td>xcc:XCC0436</td><td>>gnl|kg|xcc:XCC0436 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
<tr><td>xcv:XCV0482</td><td>>gnl|kg|xcv:XCV0482 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
<tr><td>xoo:XOO4071</td><td>>gnl|kg|xoo:XOO4071 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
<tr><td>mmu:15445</td><td>>gnl|kg|mmu:15445 Hpd; 4-hydroxyphenylpyruvic acid dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
<tr><td>rno:29531</td><td>>gnl|kg|rno:29531 Hpd; 4-hydroxyphenylpyruvic acid dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
<tr><td>ssc:397443</td><td>>gnl|kg|ssc:397443 HPD; 4-hydroxyphenylpyruvic acid dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
<tr><td>bbr:BB4213</td><td>>gnl|kg|bbr:BB4213 bllY; putative hemolysin [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
<tr><td>bpa:BPP3767</td><td>>gnl|kg|bpa:BPP3767 bllY; putative hemolysin [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
<tr><td>bpe:BP3040</td><td>>gnl|kg|bpe:BP3040 bllY; putative hemolysin [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
</table>

Table K-3. KEGG Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>bps:BPSS0339</td><td>>gnl|kg|bps:BPSS0339 putative amino acid dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
<tr><td>cel:T21C12.2</td><td>>gnl|kg|cel:T21C12.2 hpd-1; Hypothetical protein T21C12.2 [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
<tr><td>ddi:DDB0203373</td><td>>gnl|kg|ddi:DDB0203373 hypothetical protein [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
<tr><td>dme:CG11796-PA</td><td>>gnl|kg|dme:CG11796-PA CG11796; CG11796 gene product from transcript CG11796-RA [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
<tr><td>dre:394142</td><td>>gnl|kg|dre:394142 zgc:56326 [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
<tr><td>vvy:VV1495</td><td>>gnl|kg|vvy:VV1495 putitive hemolysin [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
<tr><td>xla:495029</td><td>>gnl|kg|xla:495029 LOC495029; hypothetical LOC495029 [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td></tr>
<tr><td>xtr:594976</td><td>>gnl|kg|xtr:594976 hpd-prov; hpd-prov protein</td><td></td><td></td><td>x</td></tr>
<tr><td>aci:ACIAD2213</td><td>>gnl|kg|aci:ACIAD2213 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>ago:ADR286C</td><td>>gnl|kg|ago:ADR286C ADR286Cp; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>X</td></tr>
<tr><td>ana:alr2321</td><td>>gnl|kg|ana:alr2321 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>ath:At1g08110</td><td>>gnl|kg|ath:At1g08110 T6D22.20; lactoylglutathione lyase, putative / glyoxalase I, putative [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>ath:At1g11840</td><td>>gnl|kg|ath:At1g11840 F12F1.32; lactoylglutathione lyase, putative / glyoxalase I, putative [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>ava:Ava_0139</td><td>>gnl|kg|ava:Ava_0139 glyoxalase I [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>eba:ebB148</td><td>>gnl|kg|eba:ebB148 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>bba:Bd2848</td><td>>gnl|kg|bba:Bd2848 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>bbr:BB4094</td><td>>gnl|kg|bbr:BB4094 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>bma:BMA0213</td><td>>gnl|kg|bma:BMA0213 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>bpa:BPP3659</td><td>>gnl|kg|bpa:BPP3659 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
</table>

Table K-3. KEGG Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>bpe:BP0038</td><td>>gnl|kg|bpe:BP0038 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>bpm:BURPS1710b_0876</td><td>>gnl|kg|bpm:BURPS1710b_0876 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>bps:BPSL0663</td><td>>gnl|kg|bps:BPSL0663 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>bte:BTH_I0580</td><td>>gnl|kg|bte:BTH_I0580 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>bur:Bcep18194_A6033</td><td>>gnl|kg|bur:Bcep18194_A6033 glyoxalase I [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>cal:orf19.6058</td><td>>gnl|kg|cal:orf19.6058 GLO1; glyoxalase I [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>cvi:CV1660</td><td>>gnl|kg|cvi:CV1660 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>cya:CYA_1244</td><td>>gnl|kg|cya:CYA_1244 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>dar:Daro_3539</td><td>>gnl|kg|dar:Daro_3539 glyoxalase I [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>dme:CG1707-PA</td><td>>gnl|kg|dme:CG1707-PA CG1707; CG1707 gene product from transcript CG1707-RA [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>eca:ECA1929</td><td>>gnl|kg|eca:ECA1929 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>ecc:c2044</td><td>>gnl|kg|ecc:c2044 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>ecj:JW1643</td><td>>gnl|kg|ecj:JW1643 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>ecs:ECs2360</td><td>>gnl|kg|ecs:ECs2360 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>ece:Z2669</td><td>>gnl|kg|ece:Z2669 gloA; hypothetical protein [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>eco:b1651</td><td>>gnl|kg|eco:b1651 gloA; glyoxalase I, nickel isomerase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>hch:HCH_04598</td><td>>gnl|kg|hch:HCH_04598 gloA2; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>hit:NTHI0441</td><td>>gnl|kg|hit:NTHI0441 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>hin:HI0323</td><td>>gnl|kg|hin:HI0323 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>hsa:2739</td><td>>gnl|kg|hsa:2739 GLO1; glyoxalase I [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
</table>

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
ilo:IL2633	>gnl|kg|ilo:IL2633 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x
mmu:109801	>gnl|kg|mmu:109801 Glo1; glyoxalase 1 [EC:4.4.1.5] [KO:K01759]			x
msu:MS0703	>gnl|kg|msu:MS0703 gloA; lactoylglutathione lyase and related lyases [EC:4.4.1.5] [KO:K01759]			X
neu:NE1427	>gnl|kg|neu:NE1427 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x
nma:NMA2147	>gnl|kg|nma:NMA2147 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x
nme:NMB0340	>gnl|kg|nme:NMB0340 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x
nmu:Nmul_A2625	>gnl|kg|nmu:Nmul_A2625 glyoxalase I [EC:4.4.1.5] [KO:K01759]			x
noc:Noc_2681	>gnl|kg|noc:Noc_2681 glyoxalase I [EC:4.4.1.5] [KO:K01759]			x
pae:PA3524	>gnl|kg|pae:PA3524 gloA1; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x
pae:PA5111	>gnl|kg|pae:PA5111 gloA3; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x
pfa:PF11_0145	>gnl|kg|pfa:PF11_0145 glyoxalase I, putative [EC:4.4.1.5] [KO:K01759]			x
pfl:PFL_3393	>gnl|kg|pfl:PFL_3393 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x
pha:PSHAa1601	>gnl|kg|pha:PSHAa1601 gloA; lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase) [EC:4.4.1.5] [KO:K01759]			x
plu:plu2602	>gnl|kg|plu:plu2602 gloA; lactoylglutathione lyase (methylglyoxalase) (S-D-lactolyglutathione methylglyoxal lyase) [EC:4.4.1.5] [KO:K01759]			x
pma:Pro0234	>gnl|kg|pma:Pro0234 gloA; lactoylglutathione lyase family enzyme [EC:4.4.1.5] [KO:K01759]			X
pmu:PM0987	>gnl|kg|pmu:PM0987 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x
ppu:PP3766	>gnl|kg|ppu:PP3766 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x
psb:Psyr_2973	>gnl|kg|psb:Psyr_2973 glyoxalase I [EC:4.4.1.5] [KO:K01759]			x
pst:PSPTO3106	>gnl|kg|pst:PSPTO3106 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x

Table K-3. KEGG Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>psp:PSPPH_2267</td><td>>gnl|kg|psp:PSPPH_2267 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>reu:Reut_A0503</td><td>>gnl|kg|reu:Reut_A0503 glyoxalase I [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>sce:YML004C</td><td>>gnl|kg|sce:YML004C GLO1; Regulated by HOG (high osmolarity glycerol)-MAP (mitogen-activated protein) kinase pathway in osmotic stress response [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>sec:SC1454</td><td>>gnl|kg|sec:SC1454 gloA; glyoxalase I, nickel isomerase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>spt:SPA1418</td><td>>gnl|kg|spt:SPA1418 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>sfx:S1810</td><td>>gnl|kg|sfx:S1810 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>sfl:SF1678</td><td>>gnl|kg|sfl:SF1678 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>spo:SPBC12C2.12c</td><td>>gnl|kg|spo:SPBC12C2.12c lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>ssn:SSO_1505</td><td>>gnl|kg|ssn:SSO_1505 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>stm:STM1435</td><td>>gnl|kg|stm:STM1435 gloA; glyoxalase I, nickel isomerase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>sty:STY1687</td><td>>gnl|kg|sty:STY1687 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>stt:t1303</td><td>>gnl|kg|stt:t1303 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>syc:syc0887_d</td><td>>gnl|kg|syc:syc0887_d gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>syf:Synpcc7942_0638</td><td>>gnl|kg|syf:Synpcc7942_0638 glyoxalase I [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>syw:SYNW2347</td><td>>gnl|kg|syw:SYNW2347 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>syn:slr0381</td><td>>gnl|kg|syn:slr0381 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>vch:VC1010</td><td>>gnl|kg|vch:VC1010 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>vfi:VF0928</td><td>>gnl|kg|vfi:VF0928 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>vpa:VP2109</td><td>>gnl|kg|vpa:VP2109 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>vpa:VPA0774</td><td>>gnl|kg|vpa:VPA0774 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>vvy:VV1185</td><td>>gnl|kg|vvy:VV1185 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
</table>

Table K-3. KEGG Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>xac:XAC3632</td><td>>gnl|kg|xac:XAC3632 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>xcb:XC_3658</td><td>>gnl|kg|xcb:XC_3658 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>xcc:XCC0575</td><td>>gnl|kg|xcc:XCC0575 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>xcv:XCV3749</td><td>>gnl|kg|xcv:XCV3749 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>xfa:XF1399</td><td>>gnl|kg|xfa:XF1399 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>xft:PD0629</td><td>>gnl|kg|xft:PD0629 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>xla:446359</td><td>>gnl|kg|xla:446359 MGC82317; MGC82317 protein [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>xla:447401</td><td>>gnl|kg|xla:447401 MGC84827; MGC84827 protein [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>xoo:XOO0754</td><td>>gnl|kg|xoo:XOO0754 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>ypk:y1957</td><td>>gnl|kg|ypk:y1957 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>ypm:YP2167</td><td>>gnl|kg|ypm:YP2167 gloA1; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>ype:YPO2381</td><td>>gnl|kg|ype:YPO2381 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>yps:YPTB2295</td><td>>gnl|kg|yps:YPTB2295 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td></tr>
<tr><td>ath:At1g67280</td><td>>gnl|kg|ath:At1g67280 F1N21.10; lactoylglutathione lyase, putative / glyoxalase I, putative</td><td></td><td></td><td>x</td></tr>
<tr><td>pfo:Pfl_2923</td><td>>gnl|kg|pfo:Pfl_2923 glyoxalase I</td><td></td><td></td><td>x</td></tr>
<tr><td>dre:368213</td><td>>gnl|kg|dre:368213 glo1; glyoxalase 1</td><td></td><td></td><td>x</td></tr>
<tr><td>sbo:SBO_1484</td><td>>gnl|kg|sbo:SBO_1484 gloA; lactoylglutathione lyase</td><td></td><td></td><td>x</td></tr>
<tr><td>sdy:SDY_1877</td><td>>gnl|kg|sdy:SDY_1877 gloA; lactoylglutathione lyase</td><td></td><td></td><td>x</td></tr>
<tr><td>bce:BC4503</td><td>>gnl|kg|bce:BC4503 cytosine deaminase [EC:3.5.4.1] [KO:K01485]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>bja:bll7276</td><td>>gnl|kg|bja:bll7276 putative cytosine deaminase [EC:3.5.4.1] [KO:K01485]</td><td>MFR</td><td>x</td><td></td></tr>
<tr><td>pmm:PMM1304</td><td>>gnl|kg|pmm:PMM1304 codA; possible cytosine deaminase [EC:3.5.4.1] [KO:K01485]</td><td>SFA</td><td>x</td><td></td></tr>
</table>

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
pmt:PMT0326	>gnl|kg|pmt:PMT0326 codA; possible cytosine deaminase [EC:3.5.4.1] [KO:K01485]	SFA	x	
pmn:PMN2A_0870	>gnl|kg|pmn:PMN2A_0870 possible cytosine deaminase [EC:3.5.4.1] [KO:K01485]	SFA	x	
pma:Pro1378	>gnl|kg|pma:Pro1378 ssnA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]	SFA	x	
syc:syc0954_d	>gnl|kg|syc:syc0954_d codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]	SFA	x	
syw:SYNW1638	>gnl|kg|syw:SYNW1638 codA; possible cytosine deaminase [EC:3.5.4.1] [KO:K01485]	SFA	x	
syn:slr1237	>gnl|kg|syn:slr1237 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]	BAC	x	
bar:GBAA4727	>gnl|kg|bar:GBAA4727 cytosine deaminase	SFA	x	
bar:GBAA4728	>gnl|kg|bar:GBAA4728 cytosine deaminase	SFA	x	
ban:BA4727	>gnl|kg|ban:BA4727 cytosine deaminase	SFA	x	
ban:BA4728	>gnl|kg|ban:BA4728 cytosine deaminase	SFA	x	
bat:BAS4388	>gnl|kg|bat:BAS4388 cytosine deaminase	SFA	x	
bat:BAS4389	>gnl|kg|bat:BAS4389 cytosine deaminase	SFA	x	
bca:BCE4628	>gnl|kg|bca:BCE4628 cytosine deaminase	SFA	x	
btk:BT9727_4229	>gnl|kg|btk:BT9727_4229 cytosine deaminase	SFA	x	
ecc:c0445	>gnl|kg|ecc:c0445 yahJ; cytosine deaminase	SFA	x	
ecj:JW0316	>gnl|kg|ecj:JW0316 yahJ; putative cytosine deaminase	SFA	x	
ecs:ECs0373	>gnl|kg|ecs:ECs0373 cytosine deaminase	SFA	x	
ece:Z0413	>gnl|kg|ece:Z0413 yahJ; cytosine deaminase	SFA	x	
efa:EF1061	>gnl|kg|efa:EF1061 cytosine deaminase	SFA	x	
efa:EF1062	>gnl|kg|efa:EF1062 cytosine deaminase	SFA	x	
mlo:mll2061	>gnl|kg|mlo:mll2061 cytosine deaminase	BAC	x	
oih:OB1267	>gnl|kg|oih:OB1267 cytosine deaminase	SFA	x	
ret:RHE_PE00074	>gnl|kg|ret:RHE_PE00074 probable cytosine deaminase protein	SFA	x	
sme:SMc02420	>gnl|kg|sme:SMc02420 cytosine deaminase	SFA	x	
ssn:SSO_0309	>gnl|kg|ssn:SSO_0309 yahJ; cytosine deaminase	SFA	x	
syd:Syncc9605_0854	>gnl|kg|syd:Syncc9605_0854 possible cytosine deaminase	SFA	x	
syf:Synpcc7942_0568	>gnl|kg|syf:Synpcc7942_0568 cytosine deaminase	SFA	x	
vvu:VV11303	>gnl|kg|vvu:VV11303 cytosine deaminase	SFA	x	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
vvy:VV3062	>gnl|kg|vvy:VV3062 cytosine deaminase	SFA	x	
aci:ACIAD1245	>gnl|kg|aci:ACIAD1245 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
atc:AGR_C_218	>gnl|kg|atc:AGR_C_218 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
atu:Atu0136	>gnl|kg|atu:Atu0136 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
bba:Bd3476	>gnl|kg|bba:Bd3476 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
bbr:BB1254	>gnl|kg|bbr:BB1254 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
bma:BMA0461	>gnl|kg|bma:BMA0461 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
bpa:BPP1038	>gnl|kg|bpa:BPP1038 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
bpm:BURPS1710b_3021	>gnl|kg|bpm:BURPS1710b_3021 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
bps:BPSL2539	>gnl|kg|bps:BPSL2539 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
bur:Bcep18194_A4131	>gnl|kg|bur:Bcep18194_A4131 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
bur:Bcep18194_B0389	>gnl|kg|bur:Bcep18194_B0389 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
cac:CAC3005	>gnl|kg|cac:CAC3005 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
cal:orf19.2251	>gnl|kg|cal:orf19.2251 AAH1; adenine aminohydrolase [EC:3.5.4.4] [KO:K01488]	BTC	x	
ccr:CC3180	>gnl|kg|ccr:CC3180 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
cjk:jk1687	>gnl|kg|cjk:jk1687 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
cme:CMH009C	>gnl|kg|cme:CMH009C probable adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
cpe:CPE2506	>gnl|kg|cpe:CPE2506 add; probable adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
cps:CPS_1359	>gnl|kg|cps:CPS_1359 add1; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
cps:CPS_1979	>gnl|kg|cps:CPS_1979 add2; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
ddi:DDB0230171	>gnl|kg|ddi:DDB0230171 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
eca:ECA2266	>gnl|kg|eca:ECA2266 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
efa:EF0171	>gnl|kg|efa:EF0171 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
ehi:37.t00009	>gnl|kg|ehi:37.t00009 adenosine deaminase, putative [EC:3.5.4.4] [KO:K01488]	MFR	x	
ehi:103.t00019	>gnl|kg|ehi:103.t00019 adenosine deaminase, putative [EC:3.5.4.4] [KO:K01488]	SFA	x	
fra:Francci3_0534	>gnl|kg|fra:Francci3_0534 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
fra:Francci3_0686	>gnl|kg|fra:Francci3_0686 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
fra:Francci3_1770	>gnl|kg|fra:Francci3_1770 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
fra:Francci3_4458	>gnl|kg|fra:Francci3_4458 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
ftu:FTT0939c	>gnl|kg|ftu:FTT0939c add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
gox:GOX1436	>gnl|kg|gox:GOX1436 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	SFA	x	
hch:HCH_01503	>gnl|kg|hch:HCH_01503 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
hdu:HD0377	>gnl|kg|hdu:HD0377 add; probable adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
lac:LBA1535	>gnl|kg|lac:LBA1535 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
lic:LIC10459	>gnl|kg|lic:LIC10459 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
lil:LA3783	>gnl|kg|lil:LA3783 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
ljo:LJ1639	>gnl|kg|ljo:LJ1639 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
lla:L87453	>gnl|kg|lla:L87453 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
lma:LmjF35.2160	>gnl|kg|lma:LmjF35.2160 adenosine deaminase, putative [EC:3.5.4.4] [KO:K01488]	BTC	x	
lpf:lpl0615	>gnl|kg|lpf:lpl0615 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
lpp:lpp0631	>gnl|kg|lpp:lpp0631 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
lpn:lpg0580	>gnl|kg|lpn:lpg0580 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
lsa:LSA0086	>gnl|kg|lsa:LSA0086 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
lxx:Lxx04660	>gnl|kg|lxx:Lxx04660 add; adenosine deaminase protein [EC:3.5.4.4] [KO:K01488]	MFR	x	
lxx:Lxx13430	>gnl|kg|lxx:Lxx13430 add; adenosine deaminase protein [EC:3.5.4.4] [KO:K01488]	BTC	x	
mpa:MAP3438c	>gnl|kg|mpa:MAP3438c add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
mbo:Mb3342c	>gnl|kg|mbo:Mb3342c add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
mfl:Mfl215	>gnl|kg|mfl:Mfl215 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	SFA	x	
mle:ML0700	>gnl|kg|mle:ML0700 add; putative adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
mlo:mll3163	>gnl|kg|mlo:mll3163 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
mtu:Rv3313c	>gnl|kg|mtu:Rv3313c add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
nfa:nfa9530	>gnl|kg|nfa:nfa9530 putative adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
pac:PPA2273	>gnl|kg|pac:PPA2273 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
pae:PA0148	>gnl|kg|pae:PA0148 probable adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
pfa:PF10_0289	>gnl|kg|pfa:PF10_0289 adenosine deaminase, putative [EC:3.5.4.4] [KO:K01488]	BTC	x	
pfl:PFL_0719	>gnl|kg|pfl:PFL_0719 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
pha:PSHAa0102	>gnl|kg|pha:PSHAa0102 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
plu:plu2362	>gnl|kg|plu:plu2362 add; adenosine deaminase (adenosine aminohydrolase) [EC:3.5.4.4] [KO:K01488]	BTC	x	
plt:Plut_1524	>gnl|kg|plt:Plut_1524 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
ppr:PBPRB1184	>gnl|kg|ppr:PBPRB1184 putative adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
ppr:PBPRB1379	>gnl|kg|ppr:PBPRB1379 putative adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
ppu:PP0591	>gnl|kg|ppu:PP0591 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
psb:Psyr_0661	>gnl|kg|psb:Psyr_0661 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
pst:PSPTO0757	>gnl|kg|pst:PSPTO0757 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
psp:PSPPH_4636	>gnl|kg|psp:PSPPH_4636 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
ret:RHE_CH00197	>gnl|kg|ret:RHE_CH00197 add; adenosine deaminase protein [EC:3.5.4.4] [KO:K01488]	BTC	x	
reu:Reut_A2428	>gnl|kg|reu:Reut_A2428 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
rru:Rru_A0766	>gnl|kg|rru:Rru_A0766 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
rso:RSc2098	>gnl|kg|rso:RSc2098 add, RS03663; probable adenosine deaminase protein [EC:3.5.4.4] [KO:K01488]	BTC	x	
rsp:RSP_1597	>gnl|kg|rsp:RSP_1597 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
sak:SAK_0688	>gnl|kg|sak:SAK_0688 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
san:gbs0583	>gnl|kg|san:gbs0583 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
sag:SAG0538	>gnl|kg|sag:SAG0538 adenosine deaminase, putative [EC:3.5.4.4] [KO:K01488]	MFR	x	
sma:SAV1165	>gnl|kg|sma:SAV1165 add1; putative adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
sma:SAV2595	>gnl|kg|sma:SAV2595 add2; putative adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
sma:SAV3358	>gnl|kg|sma:SAV3358 add3; putative adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
sma:SAV4906	>gnl|kg|sma:SAV4906 add4; putative adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
sma:SAV5577	>gnl|kg|sma:SAV5577 add5; putative adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
sce:YNL141W	>gnl|kg|sce:YNL141W AAH1; adenine aminohydrolase (adenine deaminase) [EC:3.5.4.4] [KO:K01488]	BTC	x	
sco:SCO2546	>gnl|kg|sco:SCO2546 SCC77.13c; probable adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
sco:SCO4644	>gnl|kg|sco:SCO4644 add, SCD82.15c; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
sco:SCO4901	>gnl|kg|sco:SCO4901 2SCK8.27; putative adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
sco:SCO5662	>gnl|kg|sco:SCO5662 SC6A9.05; putative adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
sco:SCO7268	>gnl|kg|sco:SCO7268 add, SC5H1.24c; putative adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
sme:SMc04120	>gnl|kg|sme:SMc04120 add; putative adenosine deaminase protein [EC:3.5.4.4] [KO:K01488]	BTC	x	
smu:SMU.1295	>gnl|kg|smu:SMU.1295 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
spo:SPBC1683.02	>gnl|kg|spo:SPBC1683.02 putative adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
spo:SPBC1198.02	>gnl|kg|spo:SPBC1198.02 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
sil:SPO2927	>gnl|kg|sil:SPO2927 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
sru:SRU_0673	>gnl|kg|sru:SRU_0673 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
ssp:SSP2398	>gnl|kg|ssp:SSP2398 putative adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
stl:stu0750	>gnl|kg|stl:stu0750 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
tfu:Tfu_2563	>gnl|kg|tfu:Tfu_2563 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
tfu:Tfu_2662	>gnl|kg|tfu:Tfu_2662 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
tpa:TP0045	>gnl|kg|tpa:TP0045 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	NSF	X	
vpa:VPA1292	>gnl|kg|vpa:VPA1292 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
vvu:VV20468	>gnl|kg|vvu:VV20468 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
vvy:VVA1020	>gnl|kg|vvy:VVA1020 adenosine deaminase [EC:3.5.4.4] [KO:K01488]	MFR	x	
wsu:WS0737	>gnl|kg|wsu:WS0737 putative adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
xcv:XCV0317	>gnl|kg|xcv:XCV0317 add; putative adenosine deaminase [EC:3.5.4.4] [KO:K01488]	SFA	x	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
zmo:ZMO0655	>gnl|kg|zmo:ZMO0655 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	SFA	x	
zmo:ZMO0971	>gnl|kg|zmo:ZMO0971 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]	BTC	x	
bfr:BF3839	>gnl|kg|bfr:BF3839 putative adenosine deaminase	SFA	x	
bte:BTH_I1612	>gnl|kg|bte:BTH_I1612 adenosine deaminase	BTC	x	
cya:CYA_1916	>gnl|kg|cya:CYA_1916 putative adenosine deaminase	SFA	x	
cyb:CYB_2006	>gnl|kg|cyb:CYB_2006 adenosine deaminase, putative	SFA	x	
ilo:IL0360	>gnl|kg|ilo:IL0360 add; adenosine deaminase	MFR	x	
lpn:lpg0497	>gnl|kg|lpn:lpg0497 adenosine deaminase	SFA	x	
pfo:Pfl_0671	>gnl|kg|pfo:Pfl_0671 adenosine deaminase	BTC	x	
xac:XAC0308	>gnl|kg|xac:XAC0308 add; adenosine deaminase	SFA	x	
xcb:XC_0304	>gnl|kg|xcb:XC_0304 adenosine deaminase	SFA	x	
xcc:XCC0294	>gnl|kg|xcc:XCC0294 add; adenosine deaminase	SFA	x	
dde:Dde_1269	>gnl|kg|dde:Dde_1269 N-acyl-D-amino-acid deacylase [EC:3.5.1.81]	BTC	x	
gox:GOX1177	>gnl|kg|gox:GOX1177 D-glutamate deacylase [EC:3.5.1.81]	NSF	X	
mta:Moth_1302	>gnl|kg|mta:Moth_1302 N-acyl-D-amino-acid deacylase [EC:3.5.1.81]	BTC	x	
rba:RB2098	>gnl|kg|rba:RB2098 ndaD; D-aminoacylase [EC:3.5.1.81]	BTC	x	
cne:CNI00370	>gnl|kg|cne:CNI00370 D-aminoacylase, putative	BTC	x	
gvi:gll1307	>gnl|kg|gvi:gll1307 probable D-aminoacylase	BTC	x	
pab:PAB0090	>gnl|kg|pab:PAB0090 ndaD; D-aminoacylase (aspartate, glutamate etc)	BTC	x	
sma:SAV3282	>gnl|kg|sma:SAV3282 putative D-aminoacylase	BTC	x	
sma:SAV3799	>gnl|kg|sma:SAV3799 putative D-aminoacylase	SFA	x	
sco:SCO4986	>gnl|kg|sco:SCO4986 2SCK36.09c; putative D-aminoacylase	BTC	x	
sth:STH3170	>gnl|kg|sth:STH3170 D-Aminoacylase	BTC	x	
vvy:VVA1145	>gnl|kg|vvy:VVA1145 probable N-acyl-D-glutamate deacylase protein [EC:3.5.1.82]	BTC	x	
ppr:PBPRA1272	>gnl|kg|ppr:PBPRA1272 putative N-acyl-D-aspartate/D-glutamate deacylase [EC:3.5.1.82]	BTC	x	
vvu:VV20594	>gnl|kg|vvu:VV20594 N-acyl-D-aspartate/D-glutamate deacylase [EC:3.5.1.82]	BTC	x	
bte:BTH_II1290	>gnl|kg|bte:BTH_II1290 N-acyl-D-glutamate amidohydrolase	SFA	x	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
efa:EF2580	>gnl|kg|efa:EF2580 D-hydantoinase [EC:3.5.2.2] [KO:K01464]	BTC	x	
mta:Moth_1997	>gnl|kg|mta:Moth_1997 D-hydantoinase [EC:3.5.2.2] [KO:K01464]	BTC	x	
sto:ST1011	>gnl|kg|sto:ST1011 hypothetical D-hydantoinase	BTC	x	
sto:ST1118	>gnl|kg|sto:ST1118 hypothetical D-hydantoinase [EC:3.5.2.-]	BTC	x	
hhe:HH0407	>gnl|kg|hhe:HH0407 ureA; urease [EC:3.5.1.5] [KO:K01429 K01430]	NSF	x	
noc:Noc_2881	>gnl|kg|noc:Noc_2881 urease [EC:3.5.1.5] [KO:K01427]	NSF	x	
noc:Noc_2882	>gnl|kg|noc:Noc_2882 urease [EC:3.5.1.5] [KO:K01427]	NSF	x	
pfo:Pfl_0584	>gnl|kg|pfo:Pfl_0584 urease [EC:3.5.1.5] [KO:K01427]	NSF	x	
bha:BH1129	>gnl|kg|bha:BH1129 isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]	BTC	X	
cpe:CPE2356	>gnl|kg|cpe:CPE2356 isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]	BTC	X	
cps:CPS_1869	>gnl|kg|cps:CPS_1869 iadA; isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]	BTC	x	
ppr:PBPRA1536	>gnl|kg|ppr:PBPRA1536 hypothetical isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]	BTC	x	
tte:TTE0837	>gnl|kg|tte:TTE0837 isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]	BTC	x	
vfi:VF1509	>gnl|kg|vfi:VF1509 isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]		x	
cel:R06F6.9	>gnl|kg|cel:R06F6.9 ech-4; Hypothetical protein R06F6.9 [EC:5.3.3.8] [KO:K01825]	SFA	x	
dme:CG4592-PA	>gnl|kg|dme:CG4592-PA CG4592; CG4592 gene product from transcript CG4592-RA [EC:5.3.3.8] [KO:K01825]	MFR	x	
dme:CG13890-PA	>gnl|kg|dme:CG13890-PA CG13890; CG13890 gene product from transcript CG13890-RA [EC:5.3.3.8] [KO:K01825]	SFA	x	
lma:LmjF31.2250	>gnl|kg|lma:LmjF31.2250 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor, putative [EC:5.3.3.8] [KO:K01825]	BTC	x	
tbr:Tb927.4.4910	>gnl|kg|tbr:Tb927.4.4910 Tb04.3M17.150; 3,2-trans-enoyl-CoA isomerase [EC:5.3.3.8] [KO:K01825]	BTC	x	
tbr:Tb927.3.5630	>gnl|kg|tbr:Tb927.3.5630 Tb03.5L5.870; 3,2-trans-enoyl-CoA isomerase mitochondrial precursor [EC:5.3.3.8] [KO:K01825]	BTC	x	
tbr:Tb927.8.7530	>gnl|kg|tbr:Tb927.8.7530 Tb08.30P3.50; 3,2-trans-enoyl-CoA isomerase mitochondrial precursor [EC:5.3.3.8] [KO:K01825]	BTC	x	
tcr:509261.30	>gnl|kg|tcr:509261.30 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor, putative [EC:5.3.3.8] [KO:K01825]	BTC	x	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
tcr:507107.40	>gnl|kg|tcr:507107.40 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor, putative [EC:5.3.3.8] [KO:K01825]	BTC	x	
tcr:510645.30	>gnl|kg|tcr:510645.30 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor, putative [EC:5.3.3.8] [KO:K01825]	MFR	x	
sce:YOR180C	>gnl|kg|sce:YOR180C DCI1, ECI2; Peroxisomal delta(3,5)-delta(2,4)-dienoyl-CoA isomerase, involved in fatty acid metabolism, contains peroxisome targeting signals at amino and carboxy termini	SFA	x	
cne:CNA02940	>gnl|kg|cne:CNA02940 3-hydroxyisobutyryl-CoA hydrolase, putative	BTC	x	
pfa:PFL1940w	>gnl|kg|pfa:PFL1940w 3-hydroxyisobutyryl-coenzyme A hydrolase, putative [EC:3.1.2.4] [KO:K05605]	BTC	x	
mmp:MMP1328	>gnl|kg|mmp:MMP1328 enolase	NSA	x	
pfu:PF1641	>gnl|kg|pfu:PF1641 enolase (2-phosphoglycerate dehydratase)	NSA	x	
spo:SPAPB1A10.02	>gnl|kg|spo:SPAPB1A10.02 putative alpha enolase	NSA	x	
tbr:Tb11.01.8100	>gnl|kg|tbr:Tb11.01.8100 enolase [EC:4.2.1.11] [KO:K01689]	NSA	x	
tcr:511029.10	>gnl|kg|tcr:511029.10 enolase	NSA	x	
tcr:511529.90	>gnl|kg|tcr:511529.90 enolase	NSA	x	
cvi:CV3458	>gnl|kg|cvi:CV3458 probable phosphopyruvate hydratase	NSA	x	
eli:ELI_05735	>gnl|kg|eli:ELI_05735 probable phosphopyruvate hydratase	NSA	x	
ret:RHE_PE00096	>gnl|kg|ret:RHE_PE00096 putative galactonate dehydratase protein	BTC	x	
sec:SC2294	>gnl|kg|sec:SC2294 yfaW; paral putative galactonate dehydratase	SFA	x	
sec:SC3746	>gnl|kg|sec:SC3746 dgoA; galactonate dehydratase [EC:4.1.2.21] [KO:K01631]	NSA	x	
sil:SPOA0245	>gnl|kg|sil:SPOA0245 galactonate dehydratase, putative	SFA	x	
stm:STM2291	>gnl|kg|stm:STM2291 yfaW; putative galactonate dehydratase	SFA	x	
tac:Ta0085m	>gnl|kg|tac:Ta0085m dgoA-2; galactonate dehydratase	BTC, MOF	x	
tvo:TVN0168	>gnl|kg|tvo:TVN0168 galactonate dehydratase	BTC, MOF	x	
tvo:TVN1194	>gnl|kg|tvo:TVN1194 galactonate dehydratase	BTC, MOF	x	
atc:AGR_L_1470	>gnl|kg|atc:AGR_L_1470 putative racemase [EC:5.1.2.2] [KO:K01781]	SFA	x	
atu:Atu4120	>gnl|kg|atu:Atu4120 mandelate racemase [EC:5.1.2.2] [KO:K01781]	SFA	x	

Table K-3. KEGG Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>bbr:BB2683</td><td>>gnl|kg|bbr:BB2683 putative racemase [EC:5.1.2.2] [KO:K01781]</td><td>BTC, MOF</td><td>x</td><td></td></tr>
<tr><td>bja:blr7625</td><td>>gnl|kg|bja:blr7625 probable mandelate racemase [EC:5.1.2.2] [KO:K01781]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>bme:BMEI1707</td><td>>gnl|kg|bme:BMEI1707 mandelate racemase [EC:5.1.2.2] [KO:K01781]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>bme:BMEI1712</td><td>>gnl|kg|bme:BMEI1712 mandelate racemase [EC:5.1.2.2] [KO:K01781]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>bpe:BP1161</td><td>>gnl|kg|bpe:BP1161 putative racemase [EC:5.1.2.2] [KO:K01781]</td><td>BTC, MOF</td><td>x</td><td></td></tr>
<tr><td>bpm:BURPS1710b_0947</td><td>>gnl|kg|bpm:BURPS1710b_0947 mandelate racemase [EC:5.1.2.2] [KO:K01781]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>bps:BPSL0725</td><td>>gnl|kg|bps:BPSL0725 putative mandelate racemase [EC:5.1.2.2] [KO:K01781]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>eca:ECA0998</td><td>>gnl|kg|eca:ECA0998 putative mandelate racemase [EC:5.1.2.2] [KO:K01781]</td><td>BTC, MOF</td><td>x</td><td></td></tr>
<tr><td>mpa:MAP1382c</td><td>>gnl|kg|mpa:MAP1382c putative mandelate racemase [EC:5.1.2.2] [KO:K01781]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>mlo:mll7149</td><td>>gnl|kg|mlo:mll7149 mandelate racemase [EC:5.1.2.2] [KO:K01781]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>sco:SCO3480</td><td>>gnl|kg|sco:SCO3480 SCE65.16c; putative racemase [EC:5.1.2.2] [KO:K01781]</td><td>BTC, MOF</td><td>x</td><td></td></tr>
<tr><td>spt:SPA3549</td><td>>gnl|kg|spt:SPA3549 putative racemase [EC:5.1.2.2] [KO:K01781]</td><td>BTC, MOF</td><td>x</td><td></td></tr>
<tr><td>sty:STY4099</td><td>>gnl|kg|sty:STY4099 putative racemase [EC:5.1.2.2] [KO:K01781]</td><td>BTC, MOF</td><td>x</td><td></td></tr>
<tr><td>stt:t3822</td><td>>gnl|kg|stt:t3822 putative racemase [EC:5.1.2.2] [KO:K01781]</td><td>BTC, MOF</td><td>x</td><td></td></tr>
<tr><td>tfu:Tfu_1717</td><td>>gnl|kg|tfu:Tfu_1717 putative racemase [EC:5.1.2.2] [KO:K01781]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>zmo:ZMO1228</td><td>>gnl|kg|zmo:ZMO1228 ykfB; mandelate racemase [EC:5.1.2.2] [KO:K01781]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>zmo:ZMO1264</td><td>>gnl|kg|zmo:ZMO1264 rspA; putative mandelate racemase [EC:5.1.2.2] [KO:K01781]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>bbr:BB2815</td><td>>gnl|kg|bbr:BB2815 putative mandelate racemase</td><td>SFA</td><td>x</td><td></td></tr>
</table>

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
bbr:BB4687	>gnl|kg|bbr:BB4687 putative mandelate racemase	BTC, MOF	x	
bja:bll6349	>gnl|kg|bja:bll6349 putative mandelate racemase	SFA	x	
bpa:BPP2687	>gnl|kg|bpa:BPP2687 putative mandelate racemase	SFA	x	
bpe:BP1359	>gnl|kg|bpe:BP1359 putative mandelate racemase	SFA	x	
ret:RHE_PE00430	>gnl|kg|ret:RHE_PE00430 probable mandelate racemase protein	SFA	x	
ret:RHE_PF00381	>gnl|kg|ret:RHE_PF00381 putative mandelate racemase protein	BTC, MOF	x	
sai:Saci_2196	>gnl|kg|sai:Saci_2196 mandelate racemase [EC:5.5.1.7] [KO:K01860]	SFA	x	
sma:SAV7282	>gnl|kg|sma:SAV7282 menC; putative mandelate racemase	SFA	x	
spt:SPA1203	>gnl|kg|spt:SPA1203 ycjG; putative mandelate racemase	SFA	x	
sto:ST1108	>gnl|kg|sto:ST1108 hypothetical mandelate racemase	BTC, MOF	x	
stm:STM3833	>gnl|kg|stm:STM3833 putative mandelate racemase	SFA	x	
atc:AGR_L_3551	>gnl|kg|atc:AGR_L_3551 glucarate dehydratase [EC:4.2.1.40] [KO:K01706]	BTC	x	
atu:Atu3029	>gnl|kg|atu:Atu3029 gudD; glucarate dehydratase [EC:4.2.1.40] [KO:K01706]	BTC	x	
eca:ECA3576	>gnl|kg|eca:ECA3576 gudX; probable glucarate dehydratase [EC:4.2.1.40] [KO:K01706]	BTC	x	
ecc:c3350	>gnl|kg|ecc:c3350 ygcX; glucarate dehydratase [EC:4.2.1.40] [KO:K01706]	BTC	x	
ecj:JW2759	>gnl|kg|ecj:JW2759 gud2; Probable glucarate dehydratase (gdh) [EC:4.2.1.40] [KO:K01706]	BTC	x	
ecs:ECs3648	>gnl|kg|ecs:ECs3648 putative glucarate dehydratase [EC:4.2.1.40] [KO:K01706]	BTC	x	
ece:Z4103	>gnl|kg|ece:Z4103 ygcY; putative glucarate dehydratase [EC:4.2.1.40] [KO:K01706]	BTC	x	
eco:b2788	>gnl|kg|eco:b2788 gudX, ygcY, gdh2; putative (D)-glucarate dehydratase 2 [EC:4.2.1.40] [KO:K01706]	BTC	x	
nfa:nfa35070	>gnl|kg|nfa:nfa35070 putative glucarate dehydratase [EC:4.2.1.40] [KO:K01706]	BTC	x	
sma:SAV5581	>gnl|kg|sma:SAV5581 gudD; putative glucarate dehydratase [EC:4.2.1.40] [KO:K01706]	BTC	x	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
sco:SCO2542	>gnl|kg|sco:SCO2542 SCC77.09c; putative glucarate dehydratase [EC:4.2.1.40] [KO:K01706]	BTC	x	
sfx:S2995	>gnl|kg|sfx:S2995 ygcY; putative glucarate dehydratase [EC:4.2.1.40] [KO:K01706]	BTC	x	
sfl:SF2801	>gnl|kg|sfl:SF2801 ygcY; putative glucarate dehydratase [EC:4.2.1.40] [KO:K01706]	BTC	x	
ssn:SSO_2945	>gnl|kg|ssn:SSO_2945 ygcY; putative glucarate dehydratase [EC:4.2.1.40] [KO:K01706]	BTC	x	
stm:STM2961	>gnl|kg|stm:STM2961 ygcY; putative D-glucarate dehydratase [EC:4.2.1.40] [KO:K01706]	BTC	x	
sty:STY3099	>gnl|kg|sty:STY3099 ygcY; probable glucarate dehydratase 2 [EC:4.2.1.40] [KO:K01706]	BTC	x	
stt:t2870	>gnl|kg|stt:t2870 ygcY; probable glucarate dehydratase 2 [EC:4.2.1.40] [KO:K01706]	BTC	x	
eca:ECA0936	>gnl|kg|eca:ECA0936 putative glucarate dehydratase	BTC	x	
sbo:SBO_2669	>gnl|kg|sbo:SBO_2669 ygcY; putative glucarate dehydratase	BTC	x	
bbr:BB3872	>gnl|kg|bbr:BB3872 methylaspartate ammonia-lyase [EC:4.3.1.2] [KO:K04835]	BTC	x	
bbr:BB4337	>gnl|kg|bbr:BB4337 putative methylaspartate ammonia-lyase [EC:4.3.1.2] [KO:K04835]	BTC	x	
bpa:BPP3422	>gnl|kg|bpa:BPP3422 methylaspartate ammonia-lyase [EC:4.3.1.2] [KO:K04835]	BTC	x	
bpa:BPP3864	>gnl|kg|bpa:BPP3864 putative methylaspartate ammonia-lyase [EC:4.3.1.2] [KO:K04835]	BTC	x	
bpe:BP0806	>gnl|kg|bpe:BP0806 methylaspartate ammonia-lyase [EC:4.3.1.2] [KO:K04835]	BTC	x	
bpe:BP3177	>gnl|kg|bpe:BP3177 putative methylaspartate ammonia-lyase [EC:4.3.1.2] [KO:K04835]	BTC	x	
chy:CHY_0484	>gnl|kg|chy:CHY_0484 methylaspartate ammonia-lyase [EC:4.3.1.2] [KO:K04835]	BTC	x	
chy:CHY_0582	>gnl|kg|chy:CHY_0582 methylaspartate ammonia-lyase [EC:4.3.1.2] [KO:K04835]	BTC	x	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
hma:rrnAC0687	>gnl|kg|hma:rrnAC0687 mal; methylaspartate ammonia-lyase [EC:4.3.1.2] [KO:K04835]	BTC	x	
tde:TDE2235	>gnl|kg|tde:TDE2235 methylaspartate ammonia-lyase [EC:4.3.1.2] [KO:K04835]	BTC	x	
bli:BL02407	>gnl|kg|bli:BL02407 menHA; O-succinylbenzoate synthase	NSF	x	
pcu:pc1663	>gnl|kg|pcu:pc1663 menC; putative o-succinylbenzoate synthase II, menC [EC:4.2.1.-] [KO:K02549]	SFA	x	
afu:AF2099	>gnl|kg|afu:AF2099 clcB; muconate cycloisomerase II (ClcB) [EC:5.5.1.7] [KO:K01860]	SFA	x	
cgb:cg2635	>gnl|kg|cgb:cg2635 catB; chloromuconate cycloisomerase [EC:5.5.1.7] [KO:K01860]	BAC, MOF	x	
ddi:DDB0186151	>gnl|kg|ddi:DDB0186151 hypothetical protein [EC:5.5.1.7] [KO:K01860]	SGA	x	
rba:RB8686	>gnl|kg|rba:RB8686 ykfB; chloromuconate cycloisomerase YkfB1 [EC:5.5.1.7] [KO:K01860]	SGA	x	
rba:RB11118	>gnl|kg|rba:RB11118 chloromuconate cycloisomerase YkfB1 [EC:5.5.1.7] [KO:K01860]	SGA	x	
xcv:XCV3980	>gnl|kg|xcv:XCV3980 tcbD; putative chloromuconate cycloisomerase [EC:5.5.1.7] [KO:K01860]	BAC, MOF	x	
atc:AGR_pAT_707	>gnl|kg|atc:AGR_pAT_707 chloromuconate cycloisomerase homolog YkfB	SGA	x	
atu:Atu5478	>gnl|kg|atu:Atu5478 chloromuconate cycloisomerase	SGA	x	
bfr:BF1319	>gnl|kg|bfr:BF1319 chloromuconate cycloisomerase	SGA	x	
bth:BT4703	>gnl|kg|bth:BT4703 chloromuconate cycloisomerase	SGA	x	
cgl:NCgl2318	>gnl|kg|cgl:NCgl2318 Cgl2401; putative chloromuconate cycloisomerase	BAC, MOF	x	
dra:DR1871	>gnl|kg|dra:DR1871 chloromuconate cycloisomerase, putative	BAC	x	
hma:rrnAC0233	>gnl|kg|hma:rrnAC0233 ykfB2; chloromuconate cycloisomerase	BAC, MOF	x	
hma:rrnAC0844	>gnl|kg|hma:rrnAC0844 ykfB1; chloromuconate cycloisomerase	SGA	x	
hma:rrnAC3455	>gnl|kg|hma:rrnAC3455 ykfB3; chloromuconate cycloisomerase	SGA	x	
lpn:lpg1956	>gnl|kg|lpn:lpg1956 chloromuconate cycloisomerase	BAC, MOF	x	

Table K-3. KEGG Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>mca:MCA1834</td><td>>gnl|kg|mca:MCA1834 chloromuconate cycloisomerase, putative</td><td>BAC, MOF</td><td>x</td><td></td></tr>
<tr><td>mlo:mll7352</td><td>>gnl|kg|mlo:mll7352 chloromuconate cycloisomerase</td><td>MSF</td><td>x</td><td></td></tr>
<tr><td>ttj:TTHA1824</td><td>>gnl|kg|ttj:TTHA1824 chloromuconate cycloisomerase</td><td>SGA</td><td>x</td><td></td></tr>
<tr><td>xac:XAC3862</td><td>>gnl|kg|xac:XAC3862 tcbD; chloromuconate cycloisomerase</td><td>BAC, MOF</td><td>x</td><td></td></tr>
<tr><td>xcb:XC_3879</td><td>>gnl|kg|xcb:XC_3879 chloromuconate cycloisomerase</td><td>BAC, MOF</td><td>x</td><td></td></tr>
<tr><td>xcc:XCC3807</td><td>>gnl|kg|xcc:XCC3807 tcbD; chloromuconate cycloisomerase</td><td>BAC, MOF</td><td>x</td><td></td></tr>
<tr><td>xoo:XOO4102</td><td>>gnl|kg|xoo:XOO4102 tcbD; chloromuconate cycloisomerase</td><td>BAC, MOF</td><td>x</td><td></td></tr>
<tr><td>bcl:ABC3013</td><td>>gnl|kg|bcl:ABC3013 muconate cycloisomerase [EC:5.5.1.1] [KO:K01856]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>bme:BMEI0966</td><td>>gnl|kg|bme:BMEI0966 muconate cycloisomerase I [EC:5.5.1.1] [KO:K01856]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>rba:RB10855</td><td>>gnl|kg|rba:RB10855 muconate cycloisomerase I [EC:5.5.1.1] [KO:K01856]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>reu:Reut_D6474</td><td>>gnl|kg|reu:Reut_D6474 muconate cycloisomerase [EC:5.5.1.1] [KO:K01856]</td><td>BAC</td><td>x</td><td></td></tr>
<tr><td>rpa:RPA3964</td><td>>gnl|kg|rpa:RPA3964 putative muconate cycloisomerase [EC:5.5.1.1] [KO:K01856]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>sme:SMa1461</td><td>>gnl|kg|sme:SMa1461 putative muconate cycloisomerase [EC:5.5.1.1] [KO:K01856]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>sil:SPO3667</td><td>>gnl|kg|sil:SPO3667 catB; muconate cycloisomerase I [EC:5.5.1.1] [KO:K01856]</td><td>BAC</td><td>x</td><td></td></tr>
<tr><td>tth:TTC1473</td><td>>gnl|kg|tth:TTC1473 muconate cycloisomerase [EC:5.5.1.1] [KO:K01856]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>atc:AGR_C_3037</td><td>>gnl|kg|atc:AGR_C_3037 putative muconate cycloisomerase I</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>bfs:BF1304</td><td>>gnl|kg|bfs:BF1304 putative muconate cycloisomerase</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>bfr:BF2746</td><td>>gnl|kg|bfr:BF2746 muconate cycloisomerase</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>bha:BH3006</td><td>>gnl|kg|bha:BH3006 muconate cycloisomerase</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>bli:BL03765</td><td>>gnl|kg|bli:BL03765 putative muconate cycloisomerase</td><td>BAC</td><td>x</td><td></td></tr>
<tr><td>bth:BT1313</td><td>>gnl|kg|bth:BT1313 muconate cycloisomerase</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>ecs:ECs1904</td><td>>gnl|kg|ecs:ECs1904 putative muconate cycloisomerase I</td><td>SFA</td><td>x</td><td></td></tr>
</table>

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
ece:Z2450	>gnl|kg|ece:Z2450 ycjG; putative muconate cycloisomerase I	SFA	x	
mlo:mlr0803	>gnl|kg|mlo:mlr0803 probable muconate cycloisomerase	SFA	x	
mlo:mll7353	>gnl|kg|mlo:mll7353 muconate lactonizing enzyme	SFA	x	
nfa:nfa35210	>gnl|kg|nfa:nfa35210 putative muconate cycloisomerase	BAC	x	
oih:OB2843	>gnl|kg|oih:OB2843 muconate cycloisomerase	SFA	x	
oih:OB2965	>gnl|kg|oih:OB2965 muconate cycloisomerase	MFR	x	
ppr:PBPRA1898	>gnl|kg|ppr:PBPRA1898 hypothetical muconate cycloisomerase I	SFA	x	
ret:RHE_CH02350	>gnl|kg|ret:RHE_CH02350 probable muconate cycloisomerase I protein	SFA	x	
sfx:S1414	>gnl|kg|sfx:S1414 ycjG; putative muconate cycloisomerase I	SFA	x	
ssn:SSO_1813	>gnl|kg|ssn:SSO_1813 ycjG; putative muconate cycloisomerase I	SFA	x	
vpa:VPA0329	>gnl|kg|vpa:VPA0329 putative muconate cycloisomerase I	SFA	x	
aci:ACIAD1483	>gnl|kg|aci:ACIAD1483 kdsC; 3-Deoxy-D-manno-octulosonate 8-phosphate (KDO 8-P) phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	
eba:ebA1316	>gnl|kg|eba:ebA1316 conserved hypothetical protein, predicted phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	
bba:Bd0827	>gnl|kg|bba:Bd0827 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	
bfs:BF3121	>gnl|kg|bfs:BF3121 putative lipopolysaccharide biosynthesis-related protein [EC:3.1.3.45] [KO:K03270]	BTC	x	
bma:BMA3103	>gnl|kg|bma:BMA3103 phosphatase, YrbI family [EC:3.1.3.45] [KO:K03270]	BTC	X	
bpm:BURPS1710b_3263	>gnl|kg|bpm:BURPS1710b_3263 3-deoxy-manno-octulosonate-8-phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	
bps:BPSL0537	>gnl|kg|bps:BPSL0537 hypothetical protein [EC:3.1.3.45] [KO:K03270]	BTC	x	
bur:Bcep18194_A6117	>gnl|kg|bur:Bcep18194_A6117 kdsC; phosphatase KdsC [EC:3.1.3.45] [KO:K03270]	BTC	x	
bur:Bcep18194_C7391	>gnl|kg|bur:Bcep18194_C7391 kdsC; phosphatase KdsC [EC:3.1.3.45] [KO:K03270]	BTC	x	
cbu:CBU_0749	>gnl|kg|cbu:CBU_0749 hydrolase, HAD-superfamily, subfamily IIIA [EC:3.1.3.45] [KO:K03270]	BTC	X	
cch:Cag_1073	>gnl|kg|cch:Cag_1073 kdsC; phosphatase KdsC [EC:3.1.3.45] [KO:K03270]	BTC	x	
cch:Cag_1975	>gnl|kg|cch:Cag_1975 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	MFR	x	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
cje:Cj0647	>gnl|kg|cje:Cj0647 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	
cjr:CJE0750	>gnl|kg|cjr:CJE0750 phosphatase, YrbI family [EC:3.1.3.45] [KO:K03270]	BTC	X	
cps:CPS_4539	>gnl|kg|cps:CPS_4539 phosphatase, YrbI family [EC:3.1.3.45] [KO:K03270]	BTC	X	
cte:CT0087	>gnl|kg|cte:CT0087 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	MFR	x	
cvi:CV3328	>gnl|kg|cvi:CV3328 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	X	
dar:Daro_3419	>gnl|kg|dar:Daro_3419 kdsC; HAD-superfamily hydrolase subfamily IIIA:phosphatase KdsC [EC:3.1.3.45] [KO:K03270]	BTC	x	
dvu:DVU1625	>gnl|kg|dvu:DVU1625 phosphatase, YrbI family [EC:3.1.3.45] [KO:K03270]	BTC	X	
eca:ECA0292	>gnl|kg|eca:ECA0292 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	
ftu:FTT1027c	>gnl|kg|ftu:FTT1027c yrbI; 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	
gsu:GSU1892	>gnl|kg|gsu:GSU1892 phosphatase, YrbI family [EC:3.1.3.45] [KO:K03270]	BTC	X	
hdu:HD0297	>gnl|kg|hdu:HD0297 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	
hhe:HH1326	>gnl|kg|hhe:HH1326 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	
ilo:IL0400	>gnl|kg|ilo:IL0400 predicted phosphatase, HAD superfamily [EC:3.1.3.45] [KO:K03270]	BTC	X	
lpf:lpl0870	>gnl|kg|lpf:lpl0870 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (KDO 8-P phosphatase) [EC:3.1.3.45] [KO:K03270]	BTC	x	
lpp:lpp0901	>gnl|kg|lpp:lpp0901 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (KDO 8-P phosphatase) [EC:3.1.3.45] [KO:K03270]	BTC	x	
lpn:lpg0839	>gnl|kg|lpn:lpg0839 hydrolase, HAD superfamily, subfamily III A [EC:3.1.3.45] [KO:K03270]	BTC	X	
mca:MCA0745	>gnl|kg|mca:MCA0745 phosphatase, YrbI family [EC:3.1.3.45] [KO:K03270]	BTC	X	
nmu:Nmul_A0088	>gnl|kg|nmu:Nmul_A0088 kdsC; phosphatase KdsC [EC:3.1.3.45] [KO:K03270]	BTC	x	
noc:Noc_2789	>gnl|kg|noc:Noc_2789 kdsC; phosphatase KdsC [EC:3.1.3.45] [KO:K03270]	BTC	x	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
par:Psyc_0923	>gnl|kg|par:Psyc_0923 probable phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	X	
pgi:PG0658	>gnl|kg|pgi:PG0658 phosphatase, YrbI family [EC:3.1.3.45] [KO:K03270]	BTC	X	
pha:PSHAa2547	>gnl|kg|pha:PSHAa2547 kdsC; 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	
pmt:PMT1912	>gnl|kg|pmt:PMT1912 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	
ppr:PBPRA3251	>gnl|kg|ppr:PBPRA3251 putative low specificity phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	X	
ppu:PP0956	>gnl|kg|ppu:PP0956 phosphatase, YrbI family [EC:3.1.3.45] [KO:K03270]	BTC	X	
rba:RB9821	>gnl|kg|rba:RB9821 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	
rso:RSc0412	>gnl|kg|rso:RSc0412 RS03380; putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	
spt:SPA3183	>gnl|kg|spt:SPA3183 yrbI; hypothetical protein [EC:3.1.3.45] [KO:K03270]	BTC	x	
son:SO3957	>gnl|kg|son:SO3957 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	
sty:STY3495	>gnl|kg|sty:STY3495 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	
stt:t3233	>gnl|kg|stt:t3233 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	
syc:syc1812_d	>gnl|kg|syc:syc1812_d putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	
syf:Synpcc7942_2288	>gnl|kg|syf:Synpcc7942_2288 kdsC; phosphatase KdsC [EC:3.1.3.45] [KO:K03270]	BTC	x	
tcx:Tcr_0976	>gnl|kg|tcx:Tcr_0976 kdsC; phosphatase KdsC [EC:3.1.3.45] [KO:K03270]	BTC	x	
tbd:Tbd_0537	>gnl|kg|tbd:Tbd_0537 kdsC; phosphatase KdsC [EC:3.1.3.45] [KO:K03270]	BTC	x	
vch:VC2524	>gnl|kg|vch:VC2524 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	
vfi:VF0177	>gnl|kg|vfi:VF0177 3-deoxy-manno-octulosonate-8-phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	
vfi:VF0391	>gnl|kg|vfi:VF0391 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
vvu:VV10688	>gnl|kg|vvu:VV10688 low specificity phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	X	
vvy:VV0452	>gnl|kg|vvy:VV0452 low specificity phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	X	
wsu:WS2069	>gnl|kg|wsu:WS2069 conserved hypothetical protein-predicted HAD supefamily proteins [EC:3.1.3.45] [KO:K03270]	BTC	X	
xfa:XF1412	>gnl|kg|xfa:XF1412 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	
xft:PD0641	>gnl|kg|xft:PD0641 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	
ypk:y0150	>gnl|kg|ypk:y0150 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	
ype:YPO3578	>gnl|kg|ype:YPO3578 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]	BTC	x	
yps:YPTB3522	>gnl|kg|yps:YPTB3522 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (KDO 8-P phosphatase) [EC:3.1.3.45] [KO:K03270]	BTC	x	
bce:BC1326	>gnl|kg|bce:BC1326 phosphonoacetaldehyde hydrolase [EC:3.11.1.1] [KO:K05306]	BTC	x	
bfr:BF3696	>gnl|kg|bfr:BF3696 phosphonoacetaldehyde hydrolase [EC:3.11.1.1] [KO:K05306]	BTC	x	
hch:HCH_03084	>gnl|kg|hch:HCH_03084 phnX; phosphonoacetaldehyde hydrolase [EC:3.11.1.1] [KO:K05306]	BTC	x	
lsa:LSA1665	>gnl|kg|lsa:LSA1665 phnX; phosphonoacetaldehyde hydrolase [EC:3.11.1.1] [KO:K05306]	BTC	x	
lxx:Lxx07220	>gnl|kg|lxx:Lxx07220 phosphonoacetaldehyde hydrolase	NSF	X	
bce:BC3334	>gnl|kg|bce:BC3334 2-haloalkanoic acid dehalogenase [EC:3.8.1.2] [KO:K01560]	SFA	x	
bce:BC5408	>gnl|kg|bce:BC5408 2-haloalkanoic acid dehalogenase [EC:3.8.1.2] [KO:K01560]	SFA	x	
bma:BMAA0223	>gnl|kg|bma:BMAA0223 dehII; haloacid dehalogenase, type II [EC:3.8.1.2] [KO:K01560]	SFA	x	
bme:BMEI1368	>gnl|kg|bme:BMEI1368 2-haloalkanoic acid dehalogenase I [EC:3.8.1.2] [KO:K01560]	MFR	x	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
bme:BMEI1443	>gnl|kg|bme:BMEI1443 2-haloalkanoic acid dehalogenase I [EC:3.8.1.2] [KO:K01560]	NSF	x	
bpm:BURPS1710b_A0962	>gnl|kg|bpm:BURPS1710b_A0962 dehII; haloacid dehalogenase, type II [EC:3.8.1.2] [KO:K01560]	SFA	x	
bte:BTH_II0507	>gnl|kg|bte:BTH_II0507 dehII-2; haloacid dehalogenase, type II [EC:3.8.1.2] [KO:K01560]	SFA	x	
bur:Bcep18194_B2027	>gnl|kg|bur:Bcep18194_B2027 haloacid dehalogenase, type II [EC:3.8.1.2] [KO:K01560]	BTC	x	
bur:Bcep18194_B2556	>gnl|kg|bur:Bcep18194_B2556 HAD-superfamily hydrolase, subfamily IA, variant 1 [EC:3.8.1.2] [KO:K01560]	SFA	x	
cps:CPS_3130	>gnl|kg|cps:CPS_3130 dehII; haloacid dehalogenase, type II [EC:3.8.1.2] [KO:K01560]	BTC	x	
ctc:CTC01925	>gnl|kg|ctc:CTC01925 2-haloalkanoic acid dehalogenase I [EC:3.8.1.2] [KO:K01560]	NSF	x	
hma:rrnAC0241	>gnl|kg|hma:rrnAC0241 hadL; 2-haloalkanoic acid dehalogenase [EC:3.8.1.2] [KO:K01560]	BTC	x	
ilo:IL1575	>gnl|kg|ilo:IL1575 hadL; L-2-haloalkanoic acid dehalogenase, HAD superfamily [EC:3.8.1.2] [KO:K01560]	BTC	x	
lic:LIC12279	>gnl|kg|lic:LIC12279 haloacid dehalogenase-like hydrolase [EC:3.8.1.2] [KO:K01560]	NSF	X	
lpl:lp_2835	>gnl|kg|lpl:lp_2835 2-haloacid dehalogenase (putative) [EC:3.8.1.2] [KO:K01560]	SFA	x	
mja:MJ1437	>gnl|kg|mja:MJ1437 L-2-haloalkanoic acid dehalogenase isolog [EC:3.8.1.2] [KO:K01560]	NSF	x	
pab:PAB1316	>gnl|kg|pab:PAB1316 2-haloalkanoic acid dehalogenase [EC:3.8.1.2] [KO:K01560]	SFA	x	
pha:PSHAa1832	>gnl|kg|pha:PSHAa1832 cryptic haloacid dehalogenase 1 (partial) [EC:3.8.1.2] [KO:K01560]	BTC	x	
pho:PH0459	>gnl|kg|pho:PH0459 putative 2-haloalkanoic acid dehalogenase [EC:3.8.1.2] [KO:K01560]	SFA	x	
psp:PSPPH_1747	>gnl|kg|psp:PSPPH_1747 dehII1; haloacid dehalogenase, type II [EC:3.8.1.2] [KO:K01560]	SFA	x	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
psp:PSPPH_5028	>gnl|kg|psp:PSPPH_5028 dehII2; haloacid dehalogenase, type II [EC:3.8.1.2] [KO:K01560]	SFA	x	
pub:SAR11_0137	>gnl|kg|pub:SAR11_0137 dhlB; (S)-2-haloacid dehalogenase [EC:3.8.1.2] [KO:K01560]	BTC	x	
rba:RB4567	>gnl|kg|rba:RB4567 chd1; cryptic haloacid dehalogenase 1 [EC:3.8.1.2] [KO:K01560]	BTC	x	
sai:Saci_0018	>gnl|kg|sai:Saci_0018 putative 2-haloalkanoic acid dehalogenase ; K01560 2-haloacid dehalogenase [EC:3.8.1.2] [KO:K01560]	NSF	x	
sme:SMa1851	>gnl|kg|sme:SMa1851 putative dehalogenase [EC:3.8.1.2] [KO:K01560]	SFA	x	
sil:SPOA0437	>gnl|kg|sil:SPOA0437 dehII; haloacid dehalogenase, type II [EC:3.8.1.2] [KO:K01560]	BTC	x	
sru:SRU_1260	>gnl|kg|sru:SRU_1260 dehII; haloacid dehalogenase type II [EC:3.8.1.2] [KO:K01560]	SFA	x	
ssp:SSP0367	>gnl|kg|ssp:SSP0367 putative 2-haloalkanoic acid dehalogenase [EC:3.8.1.2] [KO:K01560]	BTC	x	
sso:SSO0726	>gnl|kg|sso:SSO0726 2-haloalkanoic acid dehalogenase, putative [EC:3.8.1.2] [KO:K01560]	NSF	x	
sso:SSO1896	>gnl|kg|sso:SSO1896 2-haloalkanoic acid dehalogenase [EC:3.8.1.2] [KO:K01560]	NSF	x	
sso:SSO2028	>gnl|kg|sso:SSO2028 2-haloalkanoic acid dehalogenase [EC:3.8.1.2] [KO:K01560]	NSF	x	
sso:SSO2159	>gnl|kg|sso:SSO2159 2-haloalkanoic acid dehalogenase [EC:3.8.1.2] [KO:K01560]	NSF	x	
sto:ST0436	>gnl|kg|sto:ST0436 2-haloalkanoic acid dehalogenase [EC:3.8.1.2] [KO:K01560]	NSF	x	
sto:ST2145	>gnl|kg|sto:ST2145 2-haloalkanoic acid dehalogenase [EC:3.8.1.2] [KO:K01560]	NSF	x	
sto:ST2620	>gnl|kg|sto:ST2620 2-haloalkanoic acid dehalogenase [EC:3.8.1.2] [KO:K01560]	NSF	x	
tko:TK0058	>gnl|kg|tko:TK0058 hydrolase, HAD superfamily [EC:3.8.1.2] [KO:K01560]	SFA	x	
pae:PA0810	>gnl|kg|pae:PA0810 probable haloacid dehalogenase	BTC	x	
par:Psyc_1396	>gnl|kg|par:Psyc_1396 probable haloacid dehalogenase, type II	BTC	x	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
pfo:Pfl_3802	>gnl|kg|pfo:Pfl_3802 haloacid dehalogenase, type II	SFA	x	
pst:PSPTO0247	>gnl|kg|pst:PSPTO0247 dehII; haloacid dehalogenase, type II	SFA	x	
reu:Reut_B5659	>gnl|kg|reu:Reut_B5659 haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2	SFA	x	
reu:Reut_B5662	>gnl|kg|reu:Reut_B5662 haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2	SFA	x	
rpb:RPB_2963	>gnl|kg|rpb:RPB_2963 haloacid dehalogenase, type II	SFA	x	
sil:SPO2473	>gnl|kg|sil:SPO2473 haloacid dehalogenase, type II, putative	BTC	x	
tcr:511153.50	>gnl|kg|tcr:511153.50 haloacid dehalogenase hydrolase	NSF	x	
tcr:506779.170	>gnl|kg|tcr:506779.170 haloacid dehalogenase hydrolase	NSF	x	
atu:Atu3405	>gnl|kg|atu:Atu3405 hadL; haloalkanoic acid dehalogenase	SFA	x	
atu:Atu3408	>gnl|kg|atu:Atu3408 hadL; 2-haloalkanoic acid dehalogenase	SFA	x	
bja:bll6827	>gnl|kg|bja:bll6827 hadL; 2-haloalkanoic acid dehalogenase	SFA	x	
bca:BCE4940	>gnl|kg|bca:BCE4940 L-2-haloalkanoic acid dehalogenase	NSF	x	
bce:BC2730	>gnl|kg|bce:BC2730 2-haloalkanoic acid dehalogenase	NSF	x	
mlo:mll4579	>gnl|kg|mlo:mll4579 2-haloalkanoic acid dehalogenase	SFA	x	
oih:OB0932	>gnl|kg|oih:OB0932 L-2-haloalkanoic acid dehalogenase	SFA	x	
pca:Pcar_1388	>gnl|kg|pca:Pcar_1388 L-2-haloalkanoic acid dehalogenase	NSF	x	
ret:RHE_PF00350	>gnl|kg|ret:RHE_PF00350 putative 2-haloalkanoic acid dehalogenase protein	SFA	x	
sav:SAV0611	>gnl|kg|sav:SAV0611 L-2-haloalkanoic acid dehalogenase	SFA	x	
sma:SAV737	>gnl|kg|sma:SAV737 putative 2-haloalkanoic acid dehalogenase	BTC	x	
sco:SCO0404	>gnl|kg|sco:SCO0404 SCF51.03; putative 2-haloalkanoic acid dehalogenase	SFA	x	
sep:SE0385	>gnl|kg|sep:SE0385 L-2-haloalkanoic acid dehalogenase	SFA	x	
sto:ST1836	>gnl|kg|sto:ST1836 hypothetical 2-haloalkanoic acid dehalogenase	NSF	x	
ana:alr3528	>gnl|kg|ana:alr3528 putative beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]	BTC	x	
ava:Ava_3074	>gnl|kg|ava:Ava_3074 HAD-superfamily hydrolase subfamily IA, variant 3 [EC:5.4.2.6] [KO:K01838]	SFA	x	
ava:Ava_4630	>gnl|kg|ava:Ava_4630 HAD-superfamily hydrolase subfamily IA, variant 3 [EC:5.4.2.6] [KO:K01838]	SFA	x	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
bha:BH3864	>gnl|kg|bha:BH3864 beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]	BTC	x	
cps:CPS_0979	>gnl|kg|cps:CPS_0979 putative beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]	BTC	x	
cvi:CV1394	>gnl|kg|cvi:CV1394 probable beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]	SFA	x	
cvi:CV1397	>gnl|kg|cvi:CV1397 probable beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]	SFA	X	
efa:EF3158	>gnl|kg|efa:EF3158 hydrolase, haloacid dehalogenase-like family [EC:5.4.2.6] [KO:K01838]	BTC	X	
gsu:GSU1839	>gnl|kg|gsu:GSU1839 hydrolase, haloacid dehalogenase-like family [EC:5.4.2.6] [KO:K01838]	SFA	X	
gvi:glr3176	>gnl|kg|gvi:glr3176 putative beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]	BTC	x	
lac:LBA1869	>gnl|kg|lac:LBA1869 pgmB; beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]	BTC	x	
ljo:LJ0214	>gnl|kg|ljo:LJ0214 beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]	BTC	x	
lpf:lpl1096	>gnl|kg|lpf:lpl1096 beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]	SFA	x	
lpp:lpp1093	>gnl|kg|lpp:lpp1093 beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]	SFA	x	
lpn:lpg1092	>gnl|kg|lpn:lpg1092 beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]	SFA	x	
mac:MA0451	>gnl|kg|mac:MA0451 beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]	SFA	x	
mba:Mbar_A0742	>gnl|kg|mba:Mbar_A0742 beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]	SFA	x	
mga:MGA_1263	>gnl|kg|mga:MGA_1263 beta-pgm; beta-phosphoglucomutase (beta-PGM) [EC:5.4.2.6] [KO:K01838]	BTC	x	
mma:MM0696	>gnl|kg|mma:MM0696 beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]	SFA	x	
mma:MM1635	>gnl|kg|mma:MM1635 beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]	SFA	x	
mmo:MMOB3960	>gnl|kg|mmo:MMOB3960 pgmB; beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]	BTC	x	
msy:MS53_0106	>gnl|kg|msy:MS53_0106 pgmB; beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]	BTC	x	

Table K-3. KEGG Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>sai:Saci_0094</td><td>>gnl|kg|sai:Saci_0094 pgmB; beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>spa:M6_Spy0549</td><td>>gnl|kg|spa:M6_Spy0549 beta-phosphoglucomutase [EC:5.4.2.6 2.7.1.41] [KO:K05344 K01838]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>tel:tll0697</td><td>>gnl|kg|tel:tll0697 putative beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>tma:TM1254</td><td>>gnl|kg|tma:TM1254 beta-phosphoglucomutase, putative [EC:5.4.2.6] [KO:K01838]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>bfr:BF3814</td><td>>gnl|kg|bfr:BF3814 putative beta-phosphoglucomutase</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>bth:BT2127</td><td>>gnl|kg|bth:BT2127 putative beta-phosphoglucomutase</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>cac:CAC0153</td><td>>gnl|kg|cac:CAC0153 beta-phosphoglucomutase, putative</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>cef:CE1089</td><td>>gnl|kg|cef:CE1089 putative beta-phosphoglucomutase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>mba:Mbar_A0192</td><td>>gnl|kg|mba:Mbar_A0192 beta-phosphoglucomutase</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>stc:str0379</td><td>>gnl|kg|stc:str0379 beta-phosphoglucomutase, putative</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>tfu:Tfu_3043</td><td>>gnl|kg|tfu:Tfu_3043 HAD-superfamily hydrolase subfamily IA, variant 3:beta-phosphoglucomutase hydrolase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>vvu:VV12198</td><td>>gnl|kg|vvu:VV12198 beta-phosphoglucomutase</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>ava:Ava_1982</td><td>>gnl|kg|ava:Ava_1982 terpene synthase, metal-binding [EC:4.2.3.7]</td><td>NSF</td><td>x</td><td></td></tr>
<tr><td>bce:BC1837</td><td>>gnl|kg|bce:BC1837 methylmalonyl CoA epimerase [EC:5.1.99.1] [KO:K05606]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>pac:PPA1104</td><td>>gnl|kg|pac:PPA1104 methylmalonyl CoA epimerase [EC:5.1.99.1] [KO:K05606]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>sil:SPO0932</td><td>>gnl|kg|sil:SPO0932 methylmalonyl-CoA epimerase [EC:5.1.99.1] [KO:K05606]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>cdi:DIP1057</td><td>>gnl|kg|cdi:DIP1057 putative methylmalonyl-CoA epimerase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>gsu:GSU3303</td><td>>gnl|kg|gsu:GSU3303 methylmalonyl-CoA epimerase [EC:4.4.1.5] [KO:K01759]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>tko:TK0330</td><td>>gnl|kg|tko:TK0330 methylmalonyl-CoA epimerase [EC:4.4.1.5] [KO:K01759]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>ttj:TTHA0392</td><td>>gnl|kg|ttj:TTHA0392 probable methylmalonyl-CoA epimerase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>tth:TTC0024</td><td>>gnl|kg|tth:TTC0024 coa; probable methylmalonyl-coA epimerase</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>ddi:DDB0231097</td><td>>gnl|kg|ddi:DDB0231097 methylmalonyl coenzyme A racemase</td><td>BTC</td><td>x</td><td></td></tr>
</table>

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
ana:all0771	>gnl|kg|ana:all0771 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]	BTC	x	
ava:Ava_4666	>gnl|kg|ava:Ava_4666 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]	BTC	x	
cal:orf19.5499	>gnl|kg|cal:orf19.5499 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]	BTC	x	
cya:CYA_0478	>gnl|kg|cya:CYA_0478 putative 4-hydroxyphenylpyruvate dioxygenase	BTC	x	
cyb:CYB_0246	>gnl|kg|cyb:CYB_0246 4-hydroxyphenylpyruvate dioxygenase, putative	BTC	x	
fra:Francci3_2454	>gnl|kg|fra:Francci3_2454 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]	BTC	x	
gox:GOX0471	>gnl|kg|gox:GOX0471 putative 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]	NSS	X	
gvi:glr3091	>gnl|kg|gvi:glr3091 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]	BTC	X	
pto:PTO1369	>gnl|kg|pto:PTO1369 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]	BTC	x	
sma:SAV1776	>gnl|kg|sma:SAV1776 putative 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]	BTC	x	
sme:SMb20581	>gnl|kg|sme:SMb20581 putative 4-hydroxyphenylpyruvate dioxygenase protein [EC:1.13.11.27] [KO:K00457]	BTC	x	
syn:slr0090	>gnl|kg|syn:slr0090 ppd; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]	BTC	x	
sco:SCO3229	>gnl|kg|sco:SCO3229 SCE63.04; putative 4-hydroxyphenylpyruvic acid dioxygenase	BTC	x	
dme:CG11796-PB	>gnl|kg|dme:CG11796-PB CG11796; CG11796 gene product from transcript CG11796-RB [EC:1.13.11.27] [KO:K00457]	BTC	x	
xla:398893	>gnl|kg|xla:398893 MGC68535; hypothetical protein MGC68535 [EC:1.13.11.27] [KO:K00457]	BTC	x	
bca:BCE2765	>gnl|kg|bca:BCE2765 fosfomycin resistance protein (glutathione transferase) BH1778 [imported] [EC:2.5.1.18] [KO:K00799]	SFA	x	
cch:Cag_1454	>gnl|kg|cch:Cag_1454 glutathione S-transferase, fosfomycin resistance protein, putative	SFA	x	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
cte:CT0249	>gnl|kg|cte:CT0249 glutathione S-transferase, fosfomycin resistance protein, putative	SFA	x	
plt:Plut_1771	>gnl|kg|plt:Plut_1771 glutathione S-transferase, fosfomycin resistance protein, putative	SFA	x	
ago:ADR285W	>gnl|kg|ago:ADR285W ADR285Wp; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	NSF	x	
atc:AGR_C_3314	>gnl|kg|atc:AGR_C_3314 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
atc:AGR_C_4460	>gnl|kg|atc:AGR_C_4460 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
atu:Atu1802	>gnl|kg|atu:Atu1802 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
atu:Atu2456	>gnl|kg|atu:Atu2456 lguL; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
eba:ebA3749	>gnl|kg|eba:ebA3749 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	NSF	x	
bmb:BruAb1_0056	>gnl|kg|bmb:BruAb1_0056 glyoxalase family protein [EC:4.4.1.5] [KO:K01759]	BTC	X	
bmb:BruAb1_1270	>gnl|kg|bmb:BruAb1_1270 gloA; GloA, lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
bmb:BruAb2_0029	>gnl|kg|bmb:BruAb2_0029 glyoxalase family protein [EC:4.4.1.5] [KO:K01759]	SFA	X	
baa:BA_2606	>gnl|kg|baa:BA_2606 glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily [EC:4.4.1.5] [KO:K01759]	NSF	X	
baa:BA_3519	>gnl|kg|baa:BA_3519 glyoxalase/bleomycin resistance protein/dioxygenase superfamily [EC:4.4.1.5] [KO:K01759]	SFA	X	
baa:BA_3720	>gnl|kg|baa:BA_3720 glyoxalase/bleomycin resistance protein/dioxygenase superfamily [EC:4.4.1.5] [KO:K01759]	BTC	X	
baa:BA_3898	>gnl|kg|baa:BA_3898 glyoxalase/bleomycin resistance protein/dioxygenase superfamily [EC:4.4.1.5] [KO:K01759]	SFA	X	
bar:GBAA0607	>gnl|kg|bar:GBAA0607 glyoxylase family protein [EC:4.4.1.5] [KO:K01759]	SFA	X	
bar:GBAA2111	>gnl|kg|bar:GBAA2111 glyoxalase family protein [EC:4.4.1.5] [KO:K01759]	SFA	X	
bar:GBAA3011	>gnl|kg|bar:GBAA3011 glyoxalase family protein [EC:4.4.1.5] [KO:K01759]	NSF	X	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
bar:GBAA3208	>gnl|kg|bar:GBAA3208 glyoxylase family protein [EC:4.4.1.5] [KO:K01759]	BTC	X	
ban:BA0607	>gnl|kg|ban:BA0607 glyoxylase family protein [EC:4.4.1.5] [KO:K01759]	SFA	X	
ban:BA2111	>gnl|kg|ban:BA2111 glyoxalase family protein [EC:4.4.1.5] [KO:K01759]	SFA	X	
ban:BA3011	>gnl|kg|ban:BA3011 glyoxalase family protein [EC:4.4.1.5] [KO:K01759]	NSF	X	
ban:BA3208	>gnl|kg|ban:BA3208 glyoxylase family protein [EC:4.4.1.5] [KO:K01759]	BTC	X	
ban:BA3399	>gnl|kg|ban:BA3399 glyoxylase family protein [EC:4.4.1.5] [KO:K01759]	SFA	X	
bat:BAS0574	>gnl|kg|bat:BAS0574 glyoxylase family protein [EC:4.4.1.5] [KO:K01759]	SFA	X	
bat:BAS1963	>gnl|kg|bat:BAS1963 glyoxalase family protein [EC:4.4.1.5] [KO:K01759]	NSF	X	
bat:BAS2799	>gnl|kg|bat:BAS2799 glyoxalase family protein [EC:4.4.1.5] [KO:K01759]	SFA	X	
bat:BAS2983	>gnl|kg|bat:BAS2983 glyoxylase family protein [EC:4.4.1.5] [KO:K01759]	BTC	X	
bat:BAS3152	>gnl|kg|bat:BAS3152 glyoxylase family protein [EC:4.4.1.5] [KO:K01759]	SFA	X	
bba:Bd0456	>gnl|kg|bba:Bd0456 putative lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	SFA	x	
bca:BCE0675	>gnl|kg|bca:BCE0675 glyoxylase family protein [EC:4.4.1.5] [KO:K01759]	SFA	X	
bca:BCE2192	>gnl|kg|bca:BCE2192 glyoxalase family protein [EC:4.4.1.5] [KO:K01759]	NSF	X	
bca:BCE3047	>gnl|kg|bca:BCE3047 glyoxalase family protein [EC:4.4.1.5] [KO:K01759]	SFA	X	
bca:BCE3232	>gnl|kg|bca:BCE3232 glyoxylase family protein [EC:4.4.1.5] [KO:K01759]	BTC	X	
bce:BC0609	>gnl|kg|bce:BC0609 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	SFA	X	
bce:BC2105	>gnl|kg|bce:BC2105 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	NSF	X	
bce:BC2954	>gnl|kg|bce:BC2954 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	SFA	X	
bce:BC2993	>gnl|kg|bce:BC2993 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	SFA	X	
bce:BC3178	>gnl|kg|bce:BC3178 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	SFA	x	
bce:BC3178	>gnl|kg|bce:BC3178 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
bce:BC5220	>gnl|kg|bce:BC5220 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	NSF	X	
bcz:BCZK0518	>gnl|kg|bcz:BCZK0518 gloA; lactoylglutathione lyase (glyoxylase I) [EC:4.4.1.5] [KO:K01759]	SFA	X	
bcz:BCZK0704	>gnl|kg|bcz:BCZK0704 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	NSF	X	
bcz:BCZK1730	>gnl|kg|bcz:BCZK1730 glyoxalase family protein [EC:4.4.1.5] [KO:K01759]	SFA	X	
bcz:BCZK1918	>gnl|kg|bcz:BCZK1918 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	NSF	X	
bcz:BCZK2730	>gnl|kg|bcz:BCZK2730 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	SFA	X	
bcz:BCZK2900	>gnl|kg|bcz:BCZK2900 lactoylglutathione lyase, glyoxalase family protein [EC:4.4.1.5] [KO:K01759]	SFA	X	

Table K-3. KEGG Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>bcz:BCZK2910</td><td>>gnl|kg|bcz:BCZK2910 gloA; lactoylglutathione lyase, glyoxylase family protein [EC:4.4.1.5] [KO:K01759]</td><td>BTC</td><td>X</td><td></td></tr>
<tr><td>bcz:BCZK2991</td><td>>gnl|kg|bcz:BCZK2991 glyoxalase family protein [EC:4.4.1.5] [KO:K01759]</td><td>SFA</td><td>X</td><td></td></tr>
<tr><td>bcz:BCZK3046</td><td>>gnl|kg|bcz:BCZK3046 possible glyoxylase family protein (lactoylglutathione lyase) [EC:4.4.1.5] [KO:K01759]</td><td>SFA</td><td>X</td><td></td></tr>
<tr><td>bcz:BCZK3242</td><td>>gnl|kg|bcz:BCZK3242 glyoxalase family protein [EC:4.4.1.5] [KO:K01759]</td><td>NSF</td><td>X</td><td></td></tr>
<tr><td>bcz:BCZK3343</td><td>>gnl|kg|bcz:BCZK3343 glyoxalase/bleomycin resistance protein [EC:4.4.1.5] [KO:K01759]</td><td>SFA</td><td>X</td><td></td></tr>
<tr><td>bcz:BCZK3346</td><td>>gnl|kg|bcz:BCZK3346 glyoxalase/bleomycin resistance protein [EC:4.4.1.5] [KO:K01759]</td><td>SFA</td><td>X</td><td></td></tr>
<tr><td>bcz:BCZK4912</td><td>>gnl|kg|bcz:BCZK4912 glxI; lactoylglutathione lyase (glyoxalase I) [EC:4.4.1.5] [KO:K01759]</td><td>NSF</td><td>X</td><td></td></tr>
<tr><td>bcl:ABC0834</td><td>>gnl|kg|bcl:ABC0834 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td>SFA</td><td>X</td><td></td></tr>
<tr><td>bcl:ABC1752</td><td>>gnl|kg|bcl:ABC1752 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>bfs:BF1382</td><td>>gnl|kg|bfs:BF1382 putative lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>bfs:BF2471</td><td>>gnl|kg|bfs:BF2471 glyoxalase family protein [EC:4.4.1.5] [KO:K01759]</td><td>SFA</td><td>X</td><td></td></tr>
<tr><td>bfs:BF3127</td><td>>gnl|kg|bfs:BF3127 hypothetical protein [EC:4.4.1.5] [KO:K01759]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>bfr:BF1450</td><td>>gnl|kg|bfr:BF1450 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>bfr:BF2387</td><td>>gnl|kg|bfr:BF2387 hypothetical protein [EC:4.4.1.5] [KO:K01759]</td><td>SFA</td><td>X</td><td></td></tr>
<tr><td>bfr:BF3288</td><td>>gnl|kg|bfr:BF3288 lactoylglutathione lyase and related protein [EC:4.4.1.5] [KO:K01759]</td><td>SFA</td><td>X</td><td></td></tr>
<tr><td>bja:bll4399</td><td>>gnl|kg|bja:bll4399 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>bja:blr7489</td><td>>gnl|kg|bja:blr7489 lguL; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>bld:BLi01307</td><td>>gnl|kg|bld:BLi01307 yyaH; similar to proteins; RBL00537 [EC:4.4.1.5] [KO:K01759]</td><td>SFA</td><td>X</td><td></td></tr>
<tr><td>bli:BL01952</td><td>>gnl|kg|bli:BL01952 yyaH; glyoxalase/bleomycin resistance protein/dioxygenase domain [EC:4.4.1.5] [KO:K01759]</td><td>SFA</td><td>X</td><td></td></tr>
<tr><td>bmf:BAB1_0053</td><td>>gnl|kg|bmf:BAB1_0053 glyoxalase/bleomycin resistance protein/dioxygenase domain:glyoxalase I [EC:4.4.1.5] [KO:K01759]</td><td>BTC</td><td>X</td><td></td></tr>
</table>

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
bmf:BAB1_0838	>gnl|kg|bmf:BAB1_0838 glyoxalase/bleomycin resistance protein/dioxygenase domain [EC:4.4.1.5] [KO:K01759]	SFA	X	
bmf:BAB1_1286	>gnl|kg|bmf:BAB1_1286 gloA; glyoxalase/bleomycin resistance protein/dioxygenase domain:glyoxalase I [EC:4.4.1.5] [KO:K01759]	BTC	X	
bme:BMEI0164	>gnl|kg|bme:BMEI0164 probable lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	SFA	x	
bme:BMEI0730	>gnl|kg|bme:BMEI0730 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
bme:BMEI1142	>gnl|kg|bme:BMEI1142 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	SFA	x	
bme:BMEI1888	>gnl|kg|bme:BMEI1888 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
bme:BMEII0064	>gnl|kg|bme:BMEII0064 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	SFA	x	
bme:BMEII0415	>gnl|kg|bme:BMEII0415 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	NSF	X	
bms:BR0056	>gnl|kg|bms:BR0056 glyoxalase family protein [EC:4.4.1.5] [KO:K01759]	BTC	X	
bms:BR1268	>gnl|kg|bms:BR1268 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
bth:BT1580	>gnl|kg|bth:BT1580 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
bth:BT1685	>gnl|kg|bth:BT1685 lactoylglutathione lyase and related protein [EC:4.4.1.5] [KO:K01759]	SFA	X	
btk:BT9727_0518	>gnl|kg|btk:BT9727_0518 gloA; lactoylglutathione lyase (glyoxylase I) [EC:4.4.1.5] [KO:K01759]	SFA	X	
btk:BT9727_0717	>gnl|kg|btk:BT9727_0717 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	NSF	X	
btk:BT9727_1752	>gnl|kg|btk:BT9727_1752 glyoxalase family protein [EC:4.4.1.5] [KO:K01759]	SFA	X	
btk:BT9727_1942	>gnl|kg|btk:BT9727_1942 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	NSF	X	
btk:BT9727_2750	>gnl|kg|btk:BT9727_2750 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	SFA	X	
btk:BT9727_2965	>gnl|kg|btk:BT9727_2965 lactoylglutathione lyase, glyoxalase family protein [EC:4.4.1.5] [KO:K01759]	SFA	X	
btk:BT9727_2976	>gnl|kg|btk:BT9727_2976 gloA; lactoylglutathione lyase, glyoxylase family protein [EC:4.4.1.5] [KO:K01759]	BTC	X	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
btk:BT9727_3080	>gnl|kg|btk:BT9727_3080 glyoxalase family protein [EC:4.4.1.5] [KO:K01759]	SFA	X	
btk:BT9727_3138	>gnl|kg|btk:BT9727_3138 possible glyoxylase family protein (lactoylglutathione lyase) [EC:4.4.1.5] [KO:K01759]	SFA	X	
btk:BT9727_3395	>gnl|kg|btk:BT9727_3395 glyoxalase/bleomycin resistance protein [EC:4.4.1.5] [KO:K01759]	SFA	X	
btk:BT9727_4899	>gnl|kg|btk:BT9727_4899 glxI; lactoylglutathione lyase (glyoxalase I) [EC:4.4.1.5] [KO:K01759]	NSF	X	
ccr:CC1315	>gnl|kg|ccr:CC1315 lactoylglutathione lyase, putative [EC:4.4.1.5] [KO:K01759]	BTC	x	
cgl:NCgl0903	>gnl|kg|cgl:NCgl0903 Cgl0940; predicted lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	SFA	x	
cme:CMD108C	>gnl|kg|cme:CMD108C probable lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
cne:CNI03610	>gnl|kg|cne:CNI03610 lactoylglutathione lyase, putative [EC:4.4.1.5] [KO:K01759]	BTC	x	
cpe:CPE0447	>gnl|kg|cpe:CPE0447 lguL; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
cps:CPS_1846	>gnl|kg|cps:CPS_1846 glyoxalase family protein [EC:4.4.1.5] [KO:K01759]	SFA	X	
cps:CPS_2191	>gnl|kg|cps:CPS_2191 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
dar:Daro_0300	>gnl|kg|dar:Daro_0300 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	SFA	x	
ddi:DDB0230987	>gnl|kg|ddi:DDB0230987 gloA; glyoxylase I [EC:4.4.1.5] [KO:K01759]	BTC	x	
eca:ECA2168	>gnl|kg|eca:ECA2168 conserved hypothetical protein [EC:4.4.1.5] [KO:K01759]	SFA	X	
efa:EF1140	>gnl|kg|efa:EF1140 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
fnu:FN0356	>gnl|kg|fnu:FN0356 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
fnu:FN1050	>gnl|kg|fnu:FN1050 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	NSF	X	
ftu:FTT1212c	>gnl|kg|ftu:FTT1212c gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
gka:GK1362	>gnl|kg|gka:GK1362 hypothetical protein [EC:4.4.1.5] [KO:K01759]	SFA	X	

Table K-3. KEGG Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>gka:GK2350</td><td>>gnl|kg|gka:GK2350 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>gox:GOX1824</td><td>>gnl|kg|gox:GOX1824 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>gvi:gll3561</td><td>>gnl|kg|gvi:gll3561 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>hch:HCH_01189</td><td>>gnl|kg|hch:HCH_01189 gloA1; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>hdu:HD0610</td><td>>gnl|kg|hdu:HD0610 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>hma:rrnAC1409</td><td>>gnl|kg|hma:rrnAC1409 gloA1; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>hma:rrnAC1966</td><td>>gnl|kg|hma:rrnAC1966 gloA3; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>hma:rrnAC2504</td><td>>gnl|kg|hma:rrnAC2504 lgl; putative lactoyglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>ilo:IL1434</td><td>>gnl|kg|ilo:IL1434 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>lin:lin0429</td><td>>gnl|kg|lin:lin0429 similar to B. subtilis YyaH protein [EC:4.4.1.5] [KO:K01759]</td><td>SFA</td><td>X</td><td></td></tr>
<tr><td>lin:lin2271</td><td>>gnl|kg|lin:lin2271 similar to glyoxalase I [EC:4.4.1.5] [KO:K01759]</td><td>BTC</td><td>X</td><td></td></tr>
<tr><td>lic:LIC12328</td><td>>gnl|kg|lic:LIC12328 putative lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>lil:LA1417</td><td>>gnl|kg|lil:LA1417 gloA; lactoylglutathione lyase, putative [EC:4.4.1.5] [KO:K01759]</td><td>SFA</td><td>x</td><td></td></tr>
<tr><td>lma:LmjF35.3010</td><td>>gnl|kg|lma:LmjF35.3010 glyoxalase i [EC:4.4.1.5] [KO:K01759]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>lmf:LMOf2365_0426</td><td>>gnl|kg|lmf:LMOf2365_0426 glyoxalase family protein [EC:4.4.1.5] [KO:K01759]</td><td>SFA</td><td>X</td><td></td></tr>
<tr><td>lmf:LMOf2365_2200</td><td>>gnl|kg|lmf:LMOf2365_2200 lactoylglutathione lyase, putative [EC:4.4.1.5] [KO:K01759]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>lmo:lmo0406</td><td>>gnl|kg|lmo:lmo0406 similar to B. subtilis YyaH protein [EC:4.4.1.5] [KO:K01759]</td><td>SFA</td><td>X</td><td></td></tr>
<tr><td>lmo:lmo2168</td><td>>gnl|kg|lmo:lmo2168 similar to glyoxalase I [EC:4.4.1.5] [KO:K01759]</td><td>BTC</td><td>X</td><td></td></tr>
<tr><td>lpf:lpl1843</td><td>>gnl|kg|lpf:lpl1843 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td>BTC</td><td>x</td><td></td></tr>
<tr><td>lpp:lpp1846</td><td>>gnl|kg|lpp:lpp1846 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td>BTC</td><td>x</td><td></td></tr>
</table>

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
lpn:lpg1882	>gnl|kg|lpn:lpg1882 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
mca:MCA1648	>gnl|kg|mca:MCA1648 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
mlo:mll0167	>gnl|kg|mlo:mll0167 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
mma:MM3029	>gnl|kg|mma:MM3029 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	SFA	x	
msu:MS0597	>gnl|kg|msu:MS0597 gloA; lactoylglutathione lyase and related lyases [EC:4.4.1.5] [KO:K01759]	SFA	X	
msu:MS0611	>gnl|kg|msu:MS0611 gloA; lactoylglutathione lyase and related lyases [EC:4.4.1.5] [KO:K01759]	SFA	X	
mth:MTH758	>gnl|kg|mth:MTH758 S-D-lactoylglutathione methylglyoxal lyase [EC:4.4.1.5] [KO:K01759]	SFA	X	
oih:OB1861	>gnl|kg|oih:OB1861 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	SFA	x	
pab:PAB2438	>gnl|kg|pab:PAB2438 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	SFA	x	
pae:PA0710	>gnl|kg|pae:PA0710 gloA2; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
par:Psyc_0218	>gnl|kg|par:Psyc_0218 gloA; probable lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
pfa:MAL6P1.50	>gnl|kg|pfa:MAL6P1.50 glyoxalase I, putative [EC:4.4.1.5] [KO:K01759]	NSF	x	
pfu:PF1948	>gnl|kg|pfu:PF1948 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	SFA	x	
pgi:PG0745	>gnl|kg|pgi:PG0745 lactoylglutathione lyase, putative [EC:4.4.1.5] [KO:K01759]	BTC	x	
pgi:PG1613	>gnl|kg|pgi:PG1613 glyoxalase family protein [EC:4.4.1.5] [KO:K01759]	SFA	X	
pha:PSHAa1091	>gnl|kg|pha:PSHAa1091 gloA; glyoxalase I, nickel isomerase (lactoylglutathione lyase) [EC:4.4.1.5] [KO:K01759]	BTC	x	
pmm:PMM0653	>gnl|kg|pmm:PMM0653 gloA; glyoxalase/bleomycin resistance protein/dioxygenase superfami... [EC:4.4.1.5] [KO:K01759]	BTC	X	
pmi:PMT9312_0652	>gnl|kg|pmi:PMT9312_0652 glyoxalase I [EC:4.4.1.5] [KO:K01759]	BTC	x	
pmt:PMT2084	>gnl|kg|pmt:PMT2084 gloA; glyoxalase/bleomycin resistance protein/dioxygenase superfamily [EC:4.4.1.5] [KO:K01759]	BTC	X	
ppr:PBPRB0895	>gnl|kg|ppr:PBPRB0895 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
pub:SAR11_0652	>gnl|kg|pub:SAR11_0652 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
ret:RHE_CH01884	>gnl|kg|ret:RHE_CH01884 gloA; lactoylglutathione lyase methylglyoxalase protein [EC:4.4.1.5] [KO:K01759]	BTC	x	
rpa:RPA2523	>gnl|kg|rpa:RPA2523 putative lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
rso:RSc0520	>gnl|kg|rso:RSc0520 gloA, RS04961; probable lactoylglutathione lyase (methylglyoxalase) protein [EC:4.4.1.5] [KO:K01759]	BTC	x	
rsp:RSP_0812	>gnl|kg|rsp:RSP_0812 glyoxalase I (lactoylglutathione lyase) [EC:4.4.1.5] [KO:K01759]	SFA	x	
rsp:RSP_3237	>gnl|kg|rsp:RSP_3237 lguL; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
sai:Saci_0923	>gnl|kg|sai:Saci_0923 hypothetical protein [EC:4.4.1.5] [KO:K01759]	SFA	x	
sak:SAK_1508	>gnl|kg|sak:SAK_1508 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
san:gbs1544	>gnl|kg|san:gbs1544 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
sag:SAG1478	>gnl|kg|sag:SAG1478 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
sab:SAB0287	>gnl|kg|sab:SAB0287 probable glyoxylase family protein [EC:4.4.1.5] [KO:K01759]	SFA	X	
saa:SAUSA300_1088	>gnl|kg|saa:SAUSA300_1088 glyoxalase family protein [EC:4.4.1.5]	NSF	X	
saa:SAUSA300_1458	>gnl|kg|saa:SAUSA300_1458 glyoxalase family protein [EC:4.4.1.5]	NSF	X	
sma:SAV5402	>gnl|kg|sma:SAV5402 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	SFA	x	
sme:SMc00290	>gnl|kg|sme:SMc00290 gloA; probable lactoylglutathione lyase methylglyoxalase protein [EC:4.4.1.5] [KO:K01759]	BTC	x	
smu:SMU.1603	>gnl|kg|smu:SMU.1603 lguL; putative lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
son:SO2044	>gnl|kg|son:SO2044 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
spn:SP0962	>gnl|kg|spn:SP0962 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
spr:spr0864	>gnl|kg|spr:spr0864 lguL; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
sil:SPO0917	>gnl|kg|sil:SPO0917 glyoxalase family protein [EC:4.4.1.5] [KO:K01759]	NSF	X	
sil:SPO1270	>gnl|kg|sil:SPO1270 lactoylglutathione lyase, putative [EC:4.4.1.5] [KO:K01759]	BTC	x	
spm:spyM18_0569	>gnl|kg|spm:spyM18_0569 putative lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
spg:SpyM3_0359	>gnl|kg|spg:SpyM3_0359 gloA; putative lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
spa:M6_Spy0448	>gnl|kg|spa:M6_Spy0448 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
spa:M6_Spy0872	>gnl|kg|spa:M6_Spy0872 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	SFA	x	
spz:M5005_Spy_0421	>gnl|kg|spz:M5005_Spy_0421 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
spz:M5005_Spy_0876	>gnl|kg|spz:M5005_Spy_0876 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	SFA	x	
spb:M28_Spy0409	>gnl|kg|spb:M28_Spy0409 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
spb:M28_Spy0850	>gnl|kg|spb:M28_Spy0850 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	SFA	x	
spy:SPy0511	>gnl|kg|spy:SPy0511 gloA; putative lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
sps:SPs1494	>gnl|kg|sps:SPs1494 putative lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
sso:SSO2426	>gnl|kg|sso:SSO2426 lactoylglutathione lyase (glyoxalase I), putative [EC:4.4.1.5] [KO:K01759]	SFA	x	
sth:STH1188	>gnl|kg|sth:STH1188 putative lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	SFA	x	
stc:str1532	>gnl|kg|stc:str1532 gloA; glyoxalase I/lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
stl:stu1532	>gnl|kg|stl:stu1532 gloA; glyoxalase I/lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
sto:ST0554	>gnl|kg|sto:ST0554 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	SFA	x	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
syd:Syncc9605_2475	>gnl|kg|syd:Syncc9605_2475 glyoxalase I [EC:4.4.1.5] [KO:K01759]	BTC	x	
sye:Syncc9902_2160	>gnl|kg|sye:Syncc9902_2160 glyoxalase I [EC:4.4.1.5] [KO:K01759]	BTC	x	
tcx:Tcr_1536	>gnl|kg|tcx:Tcr_1536 glyoxalase I [EC:4.4.1.5] [KO:K01759]	BTC	x	
tcr:510743.70	>gnl|kg|tcr:510743.70 lactoylglutathione lyase-like protein [EC:4.4.1.5] [KO:K01759]	BTC	X	
tcr:510659.240	>gnl|kg|tcr:510659.240 lactoylglutathione lyase-like protein [EC:4.4.1.5] [KO:K01759]	BTC	X	
tbd:Tbd_2343	>gnl|kg|tbd:Tbd_2343 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
tte:TTE2386	>gnl|kg|tte:TTE2386 gloA3; lactoylglutathione lyase and related lyases [EC:4.4.1.5] [KO:K01759]	SFA	X	
vfi:VF1212	>gnl|kg|vfi:VF1212 putative lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
vfi:VFA0640	>gnl|kg|vfi:VFA0640 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	NSF	x	
vpa:VP2166	>gnl|kg|vpa:VP2166 putative lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
vvu:VV12016	>gnl|kg|vvu:VV12016 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
vvy:VV0155	>gnl|kg|vvy:VV0155 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
vvy:VV2400	>gnl|kg|vvy:VV2400 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	BTC	x	
zmo:ZMO0030	>gnl|kg|zmo:ZMO0030 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	NSF	x	
zmo:ZMO0761	>gnl|kg|zmo:ZMO0761 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	NSF	x	
zmo:ZMO1721	>gnl|kg|zmo:ZMO1721 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]	NSF	X	
ath:At1g11840_1	>gnl|kg|ath:At1g11840_1 F12F1.32; lactoylglutathione lyase, putative / glyoxalase I, putative	BTC	x	
ctc:CTC02185	>gnl|kg|ctc:CTC02185 glyoxalase I	SFA	x	
xcv:XCV0259	>gnl|kg|xcv:XCV0259 putative glyoxalase I	NSF	X	
aci:ACIAD1805	>gnl|kg|aci:ACIAD1805 putative glyoxalase (dioxygenase domain)	NSF	X	
bmb:BruAb2_0742	>gnl|kg|bmb:BruAb2_0742 hypothetical glyoxalase	SFA	x	
atc:AGR_C_4259	>gnl|kg|atc:AGR_C_4259 probable lactoylglutathione lyase	SFA	x	
atu:Atu2344	>gnl|kg|atu:Atu2344 lactoylglutathione lyase	SFA	x	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
atu:Atu3579	>gnl|kg|atu:Atu3579 gloA; lactoylglutathione lyase	SFA	x	
bba:Bd2520	>gnl|kg|bba:Bd2520 putative lactoylglutathione lyase	NSF	X	
bce:BC0824	>gnl|kg|bce:BC0824 lactoylglutathione lyase	SFA	X	
bce:BC3154	>gnl|kg|bce:BC3154 lactoylglutathione lyase	SFA	x	
bfr:BF0823	>gnl|kg|bfr:BF0823 putative lactoylglutathione lyase	SFA	x	
cac:CAC2192	>gnl|kg|cac:CAC2192 lactoylglutathione lyase, YQJC B.subtilis ortholog	SFA	X	
ccr:CC1933	>gnl|kg|ccr:CC1933 lactoylglutathione lyase, putative	SFA	x	
cgb:cg1073	>gnl|kg|cgb:cg1073 predicted lactoylglutathione lyase	SFA	x	
cgl:NCgl1170	>gnl|kg|cgl:NCgl1170 Cgl1217; lactoylglutathione lyase	SFA	x	
cme:CMP124C	>gnl|kg|cme:CMP124C probable lactoylglutathione lyase	NSF	x	
dra:DR2208	>gnl|kg|dra:DR2208 lactoylglutathione lyase, putative	SFA	X	
eli:ELI_01235	>gnl|kg|eli:ELI_01235 lactoylglutathione lyase, putative	BTC	x	
eli:ELI_04895	>gnl|kg|eli:ELI_04895 lactoylglutathione lyase, putative	SFA	x	
fnu:FN0974	>gnl|kg|fnu:FN0974 lactoylglutathione lyase	SFA	x	
hch:HCH_01571	>gnl|kg|hch:HCH_01571 lactoylglutathione lyase	SFA	x	
hch:HCH_01678	>gnl|kg|hch:HCH_01678 lactoylglutathione lyase	SFA	x	
hch:HCH_02021	>gnl|kg|hch:HCH_02021 lactoylglutathione lyase	NSF	X	
hch:HCH_03828	>gnl|kg|hch:HCH_03828 lactoylglutathione lyase	NSF	X	
hch:HCH_04255	>gnl|kg|hch:HCH_04255 lactoylglutathione lyase	SFA	x	
hch:HCH_04652	>gnl|kg|hch:HCH_04652 lactoylglutathione lyase	NSF	x	
hch:HCH_04873	>gnl|kg|hch:HCH_04873 lactoylglutathione lyase	NSF	x	
hch:HCH_05824	>gnl|kg|hch:HCH_05824 lactoylglutathione lyase	SFA	X	
hch:HCH_06495	>gnl|kg|hch:HCH_06495 lactoylglutathione lyase	NSF	X	
hch:HCH_06732	>gnl|kg|hch:HCH_06732 lactoylglutathione lyase	NSF	x	
mlo:mll2252	>gnl|kg|mlo:mll2252 probable lactoylglutathione lyase	NSF	x	
mlo:mlr4624	>gnl|kg|mlo:mlr4624 lactoylglutathione lyase	SFA	x	
pca:Pcar_0506	>gnl|kg|pca:Pcar_0506 lactoylglutathione lyase	BTC	x	
pca:Pcar_1477	>gnl|kg|pca:Pcar_1477 lactoylglutathione lyase	BTC	x	
pca:Pcar_3047	>gnl|kg|pca:Pcar_3047 lactoylglutathione lyase	SFA	x	
plt:Plut_1289	>gnl|kg|plt:Plut_1289 lactoylglutathione lyase	SFA	x	
ppr:PBPRA1446	>gnl|kg|ppr:PBPRA1446 putative lactoylglutathione lyase	NSF	x	
ret:RHE_CH00362	>gnl|kg|ret:RHE_CH00362 probable lactoylglutathione lyase protein	SFA	x	

Table K-3. KEGG Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
ret:RHE_CH00791	>gnl|kg|ret:RHE_CH00791 putative lactoylglutathione lyase protein	NSF	X	
ret:RHE_CH01266	>gnl|kg|ret:RHE_CH01266 probable lactoylglutathione lyase protein	NSF	X	
ret:RHE_CH01621	>gnl|kg|ret:RHE_CH01621 putative lactoylglutathione lyase protein	SFA	x	
ret:RHE_CH02623	>gnl|kg|ret:RHE_CH02623 probable lactoylglutathione lyase protein	SFA	X	
ret:RHE_CH03999	>gnl|kg|ret:RHE_CH03999 probable lactoylglutathione lyase protein	NSF	X	
rpa:RPA2469	>gnl|kg|rpa:RPA2469 putative lactoylglutathione lyase	SFA	x	
rsp:RSP_0392	>gnl|kg|rsp:RSP_0392 probable lactoylglutathione lyase	BTC	x	
sec:SC0235	>gnl|kg|sec:SC0235 yaeR; putative lactoylglutathione lyase	SFA	X	
sec:SC3057	>gnl|kg|sec:SC3057 agl; putative lactoylglutathione lyase	SFA	x	
ssp:SSP1892	>gnl|kg|ssp:SSP1892 putative lactoylglutathione lyase	NSF	X	
stm:STM0235	>gnl|kg|stm:STM0235 yaeR; putative lactoylglutathione lyase	SFA	X	
stm:STM3117	>gnl|kg|stm:STM3117 putative lactoylglutathione lyase	SFA	x	
tth:TTC0449	>gnl|kg|tth:TTC0449 probable lactoylglutathione lyase	SFA	x	
vfi:VFA0789	>gnl|kg|vfi:VFA0789 lactoylglutathione lyase	SFA	x	
vpa:VPA1685	>gnl|kg|vpa:VPA1685 putative lactoylglutathione lyase	SFA	x	
vvu:VV12294	>gnl|kg|vvu:VV12294 lactoylglutathione lyase	SFA	X	
vvu:VV12461	>gnl|kg|vvu:VV12461 lactoylglutathione lyase	SFA	X	
vvu:VV12494	>gnl|kg|vvu:VV12494 lactoylglutathione lyase	SFA	X	
vvu:VV12549	>gnl|kg|vvu:VV12549 lactoylglutathione lyase	SFA	X	
vvu:VV20606	>gnl|kg|vvu:VV20606 lactoylglutathione lyase	SFA	x	
vvu:VV21271	>gnl|kg|vvu:VV21271 lactoylglutathione lyase	SFA	x	
vvu:VV21477	>gnl|kg|vvu:VV21477 lactoylglutathione lyase	SFA	X	
vvy:VV1937	>gnl|kg|vvy:VV1937 lactoylglutathione lyase	SFA	x	
vvy:VV2052	>gnl|kg|vvy:VV2052 lactoylglutathione lyase	SFA	x	
vvy:VVA0297	>gnl|kg|vvy:VVA0297 lactoylglutathione lyase	SFA	X	
vvy:VVA1157	>gnl|kg|vvy:VVA1157 lactoylglutathione lyase	SFA	x	
xac:XAC0211	>gnl|kg|xac:XAC0211 gloA; lactoylglutathione lyase	SFA	x	
xcb:XC_0202	>gnl|kg|xcb:XC_0202 lactoylglutathione lyase	SFA	x	
xcc:XCC0192	>gnl|kg|xcc:XCC0192 gloA; lactoylglutathione lyase	SFA	x	

K.4. Table K-4. UniProtKB/Swiss-Prot Data (Chapter 2)

Table K-4. Swiss-Prot Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>CODA_ECOLI</td><td>>gnl|sp|CODA_ECOLI (P25524) Cytosine deaminase (EC 3.5.4.1) (Cytosine aminohydrolase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ADA_BOVIN</td><td>>gnl|sp|ADA_BOVIN (P56658) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ADA_HUMAN</td><td>>gnl|sp|ADA_HUMAN (P00813) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ADA_MOUSE</td><td>>gnl|sp|ADA_MOUSE (P03958) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ADA_RAT</td><td>>gnl|sp|ADA_RAT (Q920P6) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ADA_XENLA</td><td>>gnl|sp|ADA_XENLA (Q6GP70) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ADA_XENTR</td><td>>gnl|sp|ADA_XENTR (Q63ZU0) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ADD1_VIBPA</td><td>>gnl|sp|ADD1_VIBPA (Q87TF3) Adenosine deaminase 1 (EC 3.5.4.4) (Adenosine aminohydrolase 1)</td><td></td><td></td><td>x</td></tr>
<tr><td>ADD_ECO57</td><td>>gnl|sp|ADD_ECO57 (Q8X661) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ADD_ECOL6</td><td>>gnl|sp|ADD_ECOL6 (Q8FH99) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ADD_ECOLI</td><td>>gnl|sp|ADD_ECOLI (P22333) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ADD_SALTI</td><td>>gnl|sp|ADD_SALTI (Q8Z6R2) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ADD_SALTY</td><td>>gnl|sp|ADD_SALTY (Q8ZPL9) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ADD_SHEON</td><td>>gnl|sp|ADD_SHEON (Q8E8D4) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ADD_SHIFL</td><td>>gnl|sp|ADD_SHIFL (Q83RC0) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ADD_VIBCH</td><td>>gnl|sp|ADD_VIBCH (Q9KNI7) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)</td><td></td><td></td><td>x</td></tr>
</table>

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
NDAD_ALCXX	>gnl|sp|NDAD_ALCXX (P72349) D-aminoacylase (EC 3.5.1.81) (N-acyl-D-amino-acid deacylase)			x
NDDD_ALCXX	>gnl|sp|NDDD_ALCXX (P94212) N-acyl-D-aspartate deacylase (EC 3.5.1.83) (N-acyl-D-aspartate amidohydrolase)			x
NDED_ALCXX	>gnl|sp|NDED_ALCXX (P94211) N-acyl-D-glutamate deacylase (EC 3.5.1.82) (N-acyl-D-glutamate amidohydrolase)			x
HYDL_ARTAU	>gnl|sp|HYDL_ARTAU (P81006) Non-ATP-dependent L-selective hydantoinase (EC 3.5.2.2)			x
URE1_ACTPL	>gnl|sp|URE1_ACTPL (O54420) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_BACPA	>gnl|sp|URE1_BACPA (P41020) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_BACSB	>gnl|sp|URE1_BACSB (Q07397) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_BACSU	>gnl|sp|URE1_BACSU (P77837) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_BORBR	>gnl|sp|URE1_BORBR (O08400) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_CLOPE	>gnl|sp|URE1_CLOPE (P94669) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_HAEIN	>gnl|sp|URE1_HAEIN (P44391) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_KLEAE	>gnl|sp|URE1_KLEAE (P18314) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_LACFE	>gnl|sp|URE1_LACFE (P26929) Acid urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_MYCBO	>gnl|sp|URE1_MYCBO (P0A661) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_MYCTU	>gnl|sp|URE1_MYCTU (P0A660) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_PROMI	>gnl|sp|URE1_PROMI (P17086) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
URE1_PROVU	>gnl|sp|URE1_PROVU (P16122) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_RHIME	>gnl|sp|URE1_RHIME (P42885) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_STAAC	>gnl|sp|URE1_STAAC (Q5HDR8) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_STAAM	>gnl|sp|URE1_STAAM (P67403) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_STAAN	>gnl|sp|URE1_STAAN (P67404) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_STAAR	>gnl|sp|URE1_STAAR (Q6GEE4) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_STAAS	>gnl|sp|URE1_STAAS (Q6G732) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_STAAW	>gnl|sp|URE1_STAAW (P67405) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_STAEQ	>gnl|sp|URE1_STAEQ (Q5HLW1) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_STAES	>gnl|sp|URE1_STAES (Q8CNC9) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_STAXY	>gnl|sp|URE1_STAXY (P42873) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_STRSL	>gnl|sp|URE1_STRSL (P50047) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_SYNY3	>gnl|sp|URE1_SYNY3 (P73061) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_UREPA	>gnl|sp|URE1_UREPA (Q60058) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_UREUR	>gnl|sp|URE1_UREUR (P17272) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_YEREN	>gnl|sp|URE1_YEREN (P31494) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
URE1_YERPE	>gnl|sp|URE1_YERPE (Q9ZFR9) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE1_YERPS	>gnl|sp|URE1_YERPS (P52313) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE2_HELFE	>gnl|sp|URE2_HELFE (Q08716) Urease beta subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE2_HELHE	>gnl|sp|URE2_HELHE (P42823) Urease beta subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE2_HELPJ	>gnl|sp|URE2_HELPJ (P69997) Urease beta subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
URE2_HELPY	>gnl|sp|URE2_HELPY (P69996) Urease beta subunit (EC 3.5.1.5) (Urea amidohydrolase)	x		x
UREA_ASPFU	>gnl|sp|UREA_ASPFU (Q6A3P9) Urease (EC 3.5.1.5) (Urea amidohydrolase)	x		x
UREA_CANEN	>gnl|sp|UREA_CANEN (P07374) Urease (EC 3.5.1.5) (Urea amidohydrolase)	x		x
UREA_CRYNE	>gnl|sp|UREA_CRYNE (Q5KCQ6) Urease (EC 3.5.1.5) (Urea amidohydrolase)	x		x
UREA_CRYNV	>gnl|sp|UREA_CRYNV (O13465) Urease (EC 3.5.1.5) (Urea amidohydrolase)	x		x
UREA_SCHPO	>gnl|sp|UREA_SCHPO (O00084) Urease (EC 3.5.1.5) (Urea amidohydrolase)	x		x
IADA_ECOLI	>gnl|sp|IADA_ECOLI (P39377) Isoaspartyl dipeptidase (EC 3.4.19.-)			x
D3D2_HUMAN	>gnl|sp|D3D2_HUMAN (P42126) 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor (EC 5.3.3.8) (Dodecenoyl-CoA isomerase) (Delta(3),delta(2)-enoyl-CoA isomerase) (D3,D2-enoyl-CoA isomerase)			x
D3D2_MOUSE	>gnl|sp|D3D2_MOUSE (P42125) 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor (EC 5.3.3.8) (Dodecenoyl-CoA isomerase) (Delta(3),delta(2)-enoyl-CoA isomerase) (D3,D2-enoyl-CoA isomerase)			x
D3D2_RAT	>gnl|sp|D3D2_RAT (P23965) 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor (EC 5.3.3.8) (Dodecenoyl-CoA isomerase) (Delta(3),delta(2)-enoyl-CoA isomerase) (D3,D2-enoyl-CoA isomerase)			x
ECI1_YEAST	>gnl|sp|ECI1_YEAST (Q05871) 3,2-trans-enoyl-CoA isomerase (EC 5.3.3.8) (Dodecenoyl-CoA isomerase) (Delta(3),delta(2)-enoyl-CoA isomerase) (D3,D2-enoyl-CoA isomerase)			x
ECH1_HUMAN	>gnl|sp|ECH1_HUMAN (Q13011) Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor (EC 5.3.3.-)			x

Table K-4. Swiss-Prot Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>ECH1_MOUSE</td><td>>gnl|sp|ECH1_MOUSE (O35459) Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor (EC 5.3.3.-)</td><td></td><td></td><td>x</td></tr>
<tr><td>ECH1_PONPY</td><td>>gnl|sp|ECH1_PONPY (Q5RFG0) Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor (EC 5.3.3.-)</td><td></td><td></td><td>x</td></tr>
<tr><td>ECH1_RAT</td><td>>gnl|sp|ECH1_RAT (Q62651) Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor (EC 5.3.3.-)</td><td></td><td></td><td>x</td></tr>
<tr><td>MMCD_ECOLI</td><td>>gnl|sp|MMCD_ECOLI (P52045) Methylmalonyl-CoA decarboxylase (EC 4.1.1.41) (Transcarboxylase) (MMCD)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO11_SCHPO</td><td>>gnl|sp|ENO11_SCHPO (P40370) Enolase 1-1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1-1) (2-phospho-D-glycerate hydro-lyase 1-1)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO12_SCHPO</td><td>>gnl|sp|ENO12_SCHPO (Q8NKC2) Enolase 1-2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1-2) (2-phospho-D-glycerate hydro-lyase 1-2)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO1B_HUMAN</td><td>>gnl|sp|ENO1B_HUMAN (Q05524) Alpha-enolase, lung specific (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (HLE1)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO1_CANAL</td><td>>gnl|sp|ENO1_CANAL (P30575) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO1_CANGA</td><td>>gnl|sp|ENO1_CANGA (Q6FTW6) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO1_CHLTE</td><td>>gnl|sp|ENO1_CHLTE (Q8KB35) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO1_DEBHA</td><td>>gnl|sp|ENO1_DEBHA (Q6BTB1) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO1_ENTHI</td><td>>gnl|sp|ENO1_ENTHI (P51555) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO1_HEVBR</td><td>>gnl|sp|ENO1_HEVBR (Q9LEJ0) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1) (Allergen Hev b 9)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO1_LACJO</td><td>>gnl|sp|ENO1_LACJO (Q74K78) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO1_LACLA</td><td>>gnl|sp|ENO1_LACLA (Q9CHS7) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)</td><td></td><td></td><td>x</td></tr>
</table>

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
ENO1_LACPL	>gnl|sp|ENO1_LACPL (Q88YH3) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x
ENO1_MAIZE	>gnl|sp|ENO1_MAIZE (P26301) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x
ENO1_METCA	>gnl|sp|ENO1_METCA (Q606T2) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x
ENO1_PSESM	>gnl|sp|ENO1_PSESM (Q886M3) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x
ENO1_STRCO	>gnl|sp|ENO1_STRCO (Q9F2Q3) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x
ENO1_TOXGO	>gnl|sp|ENO1_TOXGO (Q9UAE6) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x
ENO1_YEAST	>gnl|sp|ENO1_YEAST (P00924) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x
ENO2_CANGA	>gnl|sp|ENO2_CANGA (Q6FQY4) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x
ENO2_CHLTE	>gnl|sp|ENO2_CHLTE (Q8KG25) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x
ENO2_DEBHA	>gnl|sp|ENO2_DEBHA (Q6BI20) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x
ENO2_HEVBR	>gnl|sp|ENO2_HEVBR (Q9LEI9) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2) (Allergen Hev b 9)			x
ENO2_LACJO	>gnl|sp|ENO2_LACJO (Q74J64) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x
ENO2_LACLA	>gnl|sp|ENO2_LACLA (Q9CIT0) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x
ENO2_LACPL	>gnl|sp|ENO2_LACPL (Q88VW2) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x
ENO2_MAIZE	>gnl|sp|ENO2_MAIZE (P42895) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x
ENO2_METCA	>gnl|sp|ENO2_METCA (Q604M4) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
ENO2_PSESM	>gnl|sp|ENO2_PSESM (Q87WD5) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x
ENO2_STRCO	>gnl|sp|ENO2_STRCO (Q9F3P9) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x
ENO2_TOXGO	>gnl|sp|ENO2_TOXGO (Q9BPL7) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x
ENO2_YEAST	>gnl|sp|ENO2_YEAST (P00925) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x
ENO3_LACJO	>gnl|sp|ENO3_LACJO (Q74IV0) Enolase 3 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 3)			x
ENOA_ALLMI	>gnl|sp|ENOA_ALLMI (Q9PVK2) Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Phosphopyruvate hydratase)			x
ENOA_ANAPL	>gnl|sp|ENOA_ANAPL (P19140) Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Tau-crystallin)			x
ENOA_BOVIN	>gnl|sp|ENOA_BOVIN (Q9XSJ4) Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1) (Phosphopyruvate hydratase) (HAP47)			x
ENOA_CHICK	>gnl|sp|ENOA_CHICK (P51913) Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Phosphopyruvate hydratase)			x
ENOA_HUMAN	>gnl|sp|ENOA_HUMAN (P06733) Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1) (Phosphopyruvate hydratase) (C-myc promoter-binding protein) (MBP-1) (MPB-1) (Plasminogen-binding protein)			x
ENOA_MOUSE	>gnl|sp|ENOA_MOUSE (P17182) Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1)			x
ENOA_PYTRG	>gnl|sp|ENOA_PYTRG (Q9W7L0) Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Phosphopyruvate hydratase)			x
ENOA_RAT	>gnl|sp|ENOA_RAT (P04764) Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1)			x
ENOA_SCEUN	>gnl|sp|ENOA_SCEUN (Q9W7L2) Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Phosphopyruvate hydratase)			x
ENOA_XENLA	>gnl|sp|ENOA_XENLA (P08734) Alpha-enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
ENOB_CHICK	>gnl|sp|ENOB_CHICK (P07322) Beta-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Phosphopyruvate hydratase)			x
ENOB_HUMAN	>gnl|sp|ENOB_HUMAN (P13929) Beta-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase) (Enolase 3)			x
ENOB_MOUSE	>gnl|sp|ENOB_MOUSE (P21550) Beta-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase) (Enolase 3)			x
ENOB_RABIT	>gnl|sp|ENOB_RABIT (P25704) Beta-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase) (Enolase 3)			x
ENOB_RAT	>gnl|sp|ENOB_RAT (P15429) Beta-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase) (Enolase 3)			x
ENOG_CHICK	>gnl|sp|ENOG_CHICK (O57391) Gamma-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Neural enolase) (NSE)			x
ENOG_HUMAN	>gnl|sp|ENOG_HUMAN (P09104) Gamma-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Neural enolase) (Neuron-specific enolase) (NSE) (Enolase 2)			x
ENOG_MOUSE	>gnl|sp|ENOG_MOUSE (P17183) Gamma-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Neural enolase) (Neuron-specific enolase) (NSE) (Enolase 2)			x
ENOG_RAT	>gnl|sp|ENOG_RAT (P07323) Gamma-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Neural enolase) (Neuron-specific enolase) (NSE) (Enolase 2)			x
ENO_ACIAD	>gnl|sp|ENO_ACIAD (Q6FAT9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_AERHY	>gnl|sp|ENO_AERHY (Q8GE63) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_AERPE	>gnl|sp|ENO_AERPE (Q9Y927) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_AGRT5	>gnl|sp|ENO_AGRT5 (Q8UFH1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_ALLMI	>gnl|sp|ENO_ALLMI (P42897) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Fragment)			x
ENO_ALNGL	>gnl|sp|ENO_ALNGL (Q43321) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x

Table K-4. Swiss-Prot Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>ENO_ALTAL</td><td>>gnl|sp|ENO_ALTAL (Q9HDT3) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Major allergen Alt a 6) (Alt a 11) (Alt a XI)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_ANASP</td><td>>gnl|sp|ENO_ANASP (Q8YRB0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_AQUAE</td><td>>gnl|sp|ENO_AQUAE (O66778) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_ARATH</td><td>>gnl|sp|ENO_ARATH (P25696) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_ARCFU</td><td>>gnl|sp|ENO_ARCFU (O29133) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_ASHGO</td><td>>gnl|sp|ENO_ASHGO (Q756H2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_ASPFU</td><td>>gnl|sp|ENO_ASPFU (Q96X30) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Allergen Asp f 22)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_ASPOR</td><td>>gnl|sp|ENO_ASPOR (Q12560) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_AZOSE</td><td>>gnl|sp|ENO_AZOSE (Q5NZ69) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_BACAN</td><td>>gnl|sp|ENO_BACAN (Q81X78) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_BACC1</td><td>>gnl|sp|ENO_BACC1 (Q72XY5) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_BACCR</td><td>>gnl|sp|ENO_BACCR (Q815K8) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_BACCZ</td><td>>gnl|sp|ENO_BACCZ (Q631M2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_BACFR</td><td>>gnl|sp|ENO_BACFR (Q8KNX9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Heme uptake protein A)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_BACHD</td><td>>gnl|sp|ENO_BACHD (Q9K717) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
</table>

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
ENO_BACHK	>gnl|sp|ENO_BACHK (Q6HBF3) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_BACSK	>gnl|sp|ENO_BACSK (Q5WDK9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_BACSU	>gnl|sp|ENO_BACSU (P37869) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_BACTN	>gnl|sp|ENO_BACTN (Q89Z05) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_BARHE	>gnl|sp|ENO_BARHE (Q8L202) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_BARQU	>gnl|sp|ENO_BARQU (Q6G173) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_BDEBA	>gnl|sp|ENO_BDEBA (Q6MPQ2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_BIFLO	>gnl|sp|ENO_BIFLO (Q8G5I9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_BLOFL	>gnl|sp|ENO_BLOFL (Q7VQH3) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_BORBR	>gnl|sp|ENO_BORBR (Q7WD75) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_BORBU	>gnl|sp|ENO_BORBU (O51312) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_BORGA	>gnl|sp|ENO_BORGA (Q661T0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_BORPA	>gnl|sp|ENO_BORPA (Q7W5N9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_BORPE	>gnl|sp|ENO_BORPE (Q7VW79) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_BRAJA	>gnl|sp|ENO_BRAJA (Q89KV6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_BRUME	>gnl|sp|ENO_BRUME (Q8YHF0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x

Table K-4. Swiss-Prot Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>ENO_BRUSU</td><td>>gnl|sp|ENO_BRUSU (Q8G0G3) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_BUCAI</td><td>>gnl|sp|ENO_BUCAI (P57492) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_BUCAP</td><td>>gnl|sp|ENO_BUCAP (Q8K9E0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_BUCBP</td><td>>gnl|sp|ENO_BUCBP (P59566) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_BURMA</td><td>>gnl|sp|ENO_BURMA (Q62J10) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_BURPS</td><td>>gnl|sp|ENO_BURPS (Q63SQ0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_CAEEL</td><td>>gnl|sp|ENO_CAEEL (Q27527) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_CAMJE</td><td>>gnl|sp|ENO_CAMJE (P42448) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_CAMJR</td><td>>gnl|sp|ENO_CAMJR (Q5HSC1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_CAUCR</td><td>>gnl|sp|ENO_CAUCR (Q9A7J9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_CHLCV</td><td>>gnl|sp|ENO_CHLCV (Q821H7) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_CHLMU</td><td>>gnl|sp|ENO_CHLMU (Q9PJF3) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_CHLPN</td><td>>gnl|sp|ENO_CHLPN (Q9Z7A6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_CHLTR</td><td>>gnl|sp|ENO_CHLTR (O84591) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_CLAHE</td><td>>gnl|sp|ENO_CLAHE (P42040) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Allergen Cla h 6) (Cla h VI)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_CLOAB</td><td>>gnl|sp|ENO_CLOAB (Q97L52) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
</table>

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
ENO_CLOPE	>gnl|sp|ENO_CLOPE (Q8XKU4) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_CLOTE	>gnl|sp|ENO_CLOTE (Q898R0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_CORDI	>gnl|sp|ENO_CORDI (Q6NI61) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_COREF	>gnl|sp|ENO_COREF (Q8FQS7) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_CORGL	>gnl|sp|ENO_CORGL (Q8NRS1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_COXBU	>gnl|sp|ENO_COXBU (Q83B44) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_CRYPA	>gnl|sp|ENO_CRYPA (Q6RG04) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_CUNEL	>gnl|sp|ENO_CUNEL (O74286) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Fragment)			x
ENO_CURLU	>gnl|sp|ENO_CURLU (Q96VP4) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_DEIRA	>gnl|sp|ENO_DEIRA (Q9RR60) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_DESPS	>gnl|sp|ENO_DESPS (Q6AM97) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_DESVH	>gnl|sp|ENO_DESVH (Q72F92) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_DESVM	>gnl|sp|ENO_DESVM (O32513) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_DROME	>gnl|sp|ENO_DROME (P15007) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_ECO57	>gnl|sp|ENO_ECO57 (P0A6Q1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_ECOL6	>gnl|sp|ENO_ECOL6 (P0A6Q0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x

Table K-4. Swiss-Prot Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>ENO_ECOLI</td><td>>gnl|sp|ENO_ECOLI (P0A6P9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_EIMTE</td><td>>gnl|sp|ENO_EIMTE (Q967Y8) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_ENTFA</td><td>>gnl|sp|ENO_ENTFA (Q9K596) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_ENTHR</td><td>>gnl|sp|ENO_ENTHR (Q8GR70) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_ERWCT</td><td>>gnl|sp|ENO_ERWCT (Q6D182) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_FASHE</td><td>>gnl|sp|ENO_FASHE (Q27655) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_FRATT</td><td>>gnl|sp|ENO_FRATT (Q5NGW8) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_FUSNN</td><td>>gnl|sp|ENO_FUSNN (Q8RI55) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_GEOKA</td><td>>gnl|sp|ENO_GEOKA (Q5KVE7) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_GEOSL</td><td>>gnl|sp|ENO_GEOSL (Q74AR6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_GLOVI</td><td>>gnl|sp|ENO_GLOVI (Q7NIR1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_GLUOX</td><td>>gnl|sp|ENO_GLUOX (Q5FNN5) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_HAEDU</td><td>>gnl|sp|ENO_HAEDU (Q7VNM6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_HAEIN</td><td>>gnl|sp|ENO_HAEIN (P43806) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_HALMA</td><td>>gnl|sp|ENO_HALMA (P29201) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_HALSA</td><td>>gnl|sp|ENO_HALSA (Q9HQI9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
</table>

Table K-4. Swiss-Prot Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>ENO_HELHP</td><td>>gnl|sp|ENO_HELHP (Q7VIH4) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_HELPJ</td><td>>gnl|sp|ENO_HELPJ (Q9ZMS6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_HELPY</td><td>>gnl|sp|ENO_HELPY (P48285) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_HOMGA</td><td>>gnl|sp|ENO_HOMGA (P56252) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_IDILO</td><td>>gnl|sp|ENO_IDILO (Q5R143) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_KLULA</td><td>>gnl|sp|ENO_KLULA (Q70CP7) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_LACAC</td><td>>gnl|sp|ENO_LACAC (Q5FKM6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_LEGPA</td><td>>gnl|sp|ENO_LEGPA (Q5X3L4) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_LEGPH</td><td>>gnl|sp|ENO_LEGPH (Q5ZTX1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_LEGPL</td><td>>gnl|sp|ENO_LEGPL (Q5WV02) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_LEIXX</td><td>>gnl|sp|ENO_LEIXX (Q6ADR6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_LEPIC</td><td>>gnl|sp|ENO_LEPIC (Q72QZ8) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_LEPIN</td><td>>gnl|sp|ENO_LEPIN (Q8F4T8) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_LISIN</td><td>>gnl|sp|ENO_LISIN (P64075) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_LISMF</td><td>>gnl|sp|ENO_LISMF (Q71WX1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_LISMO</td><td>>gnl|sp|ENO_LISMO (P64074) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
</table>

Table K-4. Swiss-Prot Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>ENO_LOLPE</td><td>>gnl|sp|ENO_LOLPE (O02654) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_LYCES</td><td>>gnl|sp|ENO_LYCES (P26300) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_MANSM</td><td>>gnl|sp|ENO_MANSM (Q65VZ7) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_MASBA</td><td>>gnl|sp|ENO_MASBA (Q9U615) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_MESCR</td><td>>gnl|sp|ENO_MESCR (Q43130) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_MESFL</td><td>>gnl|sp|ENO_MESFL (Q6F0Z7) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_METAC</td><td>>gnl|sp|ENO_METAC (Q8TQ79) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_METJA</td><td>>gnl|sp|ENO_METJA (Q60173) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_METKA</td><td>>gnl|sp|ENO_METKA (Q8TUV6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_METMA</td><td>>gnl|sp|ENO_METMA (Q8PT81) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_METMP</td><td>>gnl|sp|ENO_METMP (Q6M075) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_METTH</td><td>>gnl|sp|ENO_METTH (O26149) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_MYCBO</td><td>>gnl|sp|ENO_MYCBO (Q7U0U6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_MYCGA</td><td>>gnl|sp|ENO_MYCGA (Q7NAY0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_MYCGE</td><td>>gnl|sp|ENO_MYCGE (P47647) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_MYCH2</td><td>>gnl|sp|ENO_MYCH2 (Q601S2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
</table>

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
ENO_MYCLE	>gnl|sp|ENO_MYCLE (Q9CD42) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_MYCMO	>gnl|sp|ENO_MYCMO (Q6KIB0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_MYCMS	>gnl|sp|ENO_MYCMS (Q6MTZ2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_MYCPA	>gnl|sp|ENO_MYCPA (Q741U7) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_MYCPE	>gnl|sp|ENO_MYCPE (Q8EW32) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_MYCPN	>gnl|sp|ENO_MYCPN (P75189) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_MYCPU	>gnl|sp|ENO_MYCPU (Q98Q50) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_MYCTU	>gnl|sp|ENO_MYCTU (P96377) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_NEIG1	>gnl|sp|ENO_NEIG1 (Q5F8Z2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_NEIMA	>gnl|sp|ENO_NEIMA (Q9JU46) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_NEIMB	>gnl|sp|ENO_NEIMB (Q9JZ53) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_NEOFR	>gnl|sp|ENO_NEOFR (P42894) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_NEUCR	>gnl|sp|ENO_NEUCR (Q7RV85) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_NITEU	>gnl|sp|ENO_NITEU (O85348) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_NOCFA	>gnl|sp|ENO_NOCFA (Q5YQ30) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_OCEIH	>gnl|sp|ENO_OCEIH (Q8ENP5) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
ENO_ONYPE	>gnl|sp|ENO_ONYPE (Q6YQT9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_ORYSA	>gnl|sp|ENO_ORYSA (Q42971) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (OSE1)			x
ENO_PARUW	>gnl|sp|ENO_PARUW (Q6MEY2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_PASMU	>gnl|sp|ENO_PASMU (P57975) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_PENCH	>gnl|sp|ENO_PENCH (Q76KF9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_PENCI	>gnl|sp|ENO_PENCI (Q96X46) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Allergen Pen c 22)			x
ENO_PHOLL	>gnl|sp|ENO_PHOLL (Q7N835) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_PHOPR	>gnl|sp|ENO_PHOPR (Q6LMT1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_PLAF7	>gnl|sp|ENO_PLAF7 (Q8IJN7) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_PLAFA	>gnl|sp|ENO_PLAFA (Q27727) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_PLAFG	>gnl|sp|ENO_PLAFG (Q9UAL5) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_PLAYO	>gnl|sp|ENO_PLAYO (Q7RA60) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_PORGI	>gnl|sp|ENO_PORGI (Q7MTV8) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_PROAC	>gnl|sp|ENO_PROAC (Q6AAB8) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_PROMA	>gnl|sp|ENO_PROMA (Q7VDY0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_PROMM	>gnl|sp|ENO_PROMM (Q7V483) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
ENO_PROMP	>gnl|sp|ENO_PROMP (Q7V377) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_PSEAE	>gnl|sp|ENO_PSEAE (Q9HXZ5) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_PSEPK	>gnl|sp|ENO_PSEPK (Q88MF9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_PYRAB	>gnl|sp|ENO_PYRAB (Q9UXZ0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_PYRAE	>gnl|sp|ENO_PYRAE (Q8ZYE7) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_PYRFU	>gnl|sp|ENO_PYRFU (Q8U477) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_PYRHO	>gnl|sp|ENO_PYRHO (O59605) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_PYRKO	>gnl|sp|ENO_PYRKO (Q5JEV6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_RALSO	>gnl|sp|ENO_RALSO (Q8Y0B5) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_RHILO	>gnl|sp|ENO_RHILO (Q98MZ3) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_RHIME	>gnl|sp|ENO_RHIME (Q92Q98) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_RHOBA	>gnl|sp|ENO_RHOBA (Q7UIR2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_RHOPA	>gnl|sp|ENO_RHOPA (Q6N5U6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_RHORB	>gnl|sp|ENO_RHORB (Q870B9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Allergen Rho m 1)			x
ENO_RICCO	>gnl|sp|ENO_RICCO (P42896) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_SALPA	>gnl|sp|ENO_SALPA (Q5PEH4) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
ENO_SALTI	>gnl|sp|ENO_SALTI (P64077) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_SALTY	>gnl|sp|ENO_SALTY (P64076) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_SCHJA	>gnl|sp|ENO_SCHJA (P33676) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_SCHMA	>gnl|sp|ENO_SCHMA (Q27877) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_SHEON	>gnl|sp|ENO_SHEON (Q8EBR0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_SHIFL	>gnl|sp|ENO_SHIFL (P0A6Q2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_SILPO	>gnl|sp|ENO_SILPO (Q5LQL4) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_STAAC	>gnl|sp|ENO_STAAC (Q5HHP1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_STAAM	>gnl|sp|ENO_STAAM (P64078) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_STAAN	>gnl|sp|ENO_STAAN (P99088) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_STAAR	>gnl|sp|ENO_STAAR (Q6GIL4) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_STAAS	>gnl|sp|ENO_STAAS (Q6GB54) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_STAAU	>gnl|sp|ENO_STAAU (O69174) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Laminin binding protein)			x
ENO_STAAW	>gnl|sp|ENO_STAAW (P64079) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_STAEQ	>gnl|sp|ENO_STAEQ (Q5HQV0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_STAES	>gnl|sp|ENO_STAES (Q8CPY3) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x

Table K-4. Swiss-Prot Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>ENO_STRA3</td><td>>gnl|sp|ENO_STRA3 (P64080) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_STRA5</td><td>>gnl|sp|ENO_STRA5 (P64081) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_STRAW</td><td>>gnl|sp|ENO_STRAW (Q82HH5) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_STRIT</td><td>>gnl|sp|ENO_STRIT (Q9XDS7) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_STRMU</td><td>>gnl|sp|ENO_STRMU (Q8DTS9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_STRP1</td><td>>gnl|sp|ENO_STRP1 (P69949) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_STRP3</td><td>>gnl|sp|ENO_STRP3 (P69950) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_STRP6</td><td>>gnl|sp|ENO_STRP6 (Q5XD01) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_STRP8</td><td>>gnl|sp|ENO_STRP8 (P69951) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_STRPN</td><td>>gnl|sp|ENO_STRPN (Q97QS2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_STRR6</td><td>>gnl|sp|ENO_STRR6 (Q8DPS0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_STRT1</td><td>>gnl|sp|ENO_STRT1 (Q5M0M5) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_STRT2</td><td>>gnl|sp|ENO_STRT2 (Q5M561) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_STRTR</td><td>>gnl|sp|ENO_STRTR (O52191) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_SULAC</td><td>>gnl|sp|ENO_SULAC (Q4J920) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
<tr><td>ENO_SULSO</td><td>>gnl|sp|ENO_SULSO (Q97ZJ3) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td></tr>
</table>

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
ENO_SULTO	>gnl|sp|ENO_SULTO (Q972B6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_SYMTH	>gnl|sp|ENO_SYMTH (Q67SV9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_SYNEL	>gnl|sp|ENO_SYNEL (Q8DL40) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_SYNP6	>gnl|sp|ENO_SYNP6 (Q5N3P4) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_SYNPX	>gnl|sp|ENO_SYNPX (Q7U3T1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_SYNY3	>gnl|sp|ENO_SYNY3 (P77972) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_THEAC	>gnl|sp|ENO_THEAC (Q9HJT1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_THEMA	>gnl|sp|ENO_THEMA (P42848) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_THET2	>gnl|sp|ENO_THET2 (Q72H85) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_THET8	>gnl|sp|ENO_THET8 (Q5SME1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_THETN	>gnl|sp|ENO_THETN (Q8R967) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_THEVO	>gnl|sp|ENO_THEVO (Q979Z9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_TREDE	>gnl|sp|ENO_TREDE (Q73P50) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_TREPA	>gnl|sp|ENO_TREPA (P74934) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_TROW8	>gnl|sp|ENO_TROW8 (Q83H73) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_TROWT	>gnl|sp|ENO_TROWT (Q83FF7) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
ENO_TUBBO	>gnl|sp|ENO_TUBBO (Q6W3C0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_UREPA	>gnl|sp|ENO_UREPA (Q9PQV9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_VIBCH	>gnl|sp|ENO_VIBCH (Q9KPC5) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_VIBF1	>gnl|sp|ENO_VIBF1 (Q5E326) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_VIBPA	>gnl|sp|ENO_VIBPA (Q87LQ0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_VIBVU	>gnl|sp|ENO_VIBVU (Q8DC62) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_VIBVY	>gnl|sp|ENO_VIBVY (Q7MHQ1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_WIGBR	>gnl|sp|ENO_WIGBR (Q8D2K1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_WOLPM	>gnl|sp|ENO_WOLPM (Q73HQ2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_WOLSU	>gnl|sp|ENO_WOLSU (Q7M8Q0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_XANAC	>gnl|sp|ENO_XANAC (Q8PLS0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_XANCP	>gnl|sp|ENO_XANCP (Q8P9Z3) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_XANOR	>gnl|sp|ENO_XANOR (Q5GYK4) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_XYLFA	>gnl|sp|ENO_XYLFA (Q9PDT8) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_XYLFT	>gnl|sp|ENO_XYLFT (Q87DY6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_YARLI	>gnl|sp|ENO_YARLI (Q6C1F3) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
ENO_YERPE	>gnl|sp|ENO_YERPE (Q8ZBN2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_YERPS	>gnl|sp|ENO_YERPS (Q66ED8) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
ENO_ZYMMO	>gnl|sp|ENO_ZYMMO (P33675) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x
DGOD_ECOLI	>gnl|sp|DGOD_ECOLI (Q6BF17) Galactonate dehydratase (EC 4.2.1.6)			x
MANR_PSEPU	>gnl|sp|MANR_PSEPU (P11444) Mandelate racemase (EC 5.1.2.2) (MR)			x
GUDH_BACSU	>gnl|sp|GUDH_BACSU (P42238) Probable glucarate dehydratase (EC 4.2.1.40) (GDH) (GlucD)			x
GUDH_ECO57	>gnl|sp|GUDH_ECO57 (P0AES3) Glucarate dehydratase (EC 4.2.1.40) (GDH) (GlucD)			x
GUDH_ECOLI	>gnl|sp|GUDH_ECOLI (P0AES2) Glucarate dehydratase (EC 4.2.1.40) (GDH) (GlucD)			x
GUDH_PSEPU	>gnl|sp|GUDH_PSEPU (P42206) Glucarate dehydratase (EC 4.2.1.40) (GDH) (GlucD)			x
MAAL_CLOTT	>gnl|sp|MAAL_CLOTT (Q05514) Methylaspartate ammonia-lyase (EC 4.3.1.2) (Beta-methylaspartase)			x
MENC_BACSU	>gnl|sp|MENC_BACSU (O34514) O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x
MENC_ECO57	>gnl|sp|MENC_ECO57 (P58484) O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x
MENC_ECOLI	>gnl|sp|MENC_ECOLI (P29208) O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x
MENC_HAEIN	>gnl|sp|MENC_HAEIN (P44961) O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x
MENC_MYCBO	>gnl|sp|MENC_MYCBO (P65426) Probable O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
MENC_MYCLE	>gnl|sp|MENC_MYCLE (Q9CBB2) Probable O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x
MENC_MYCTU	>gnl|sp|MENC_MYCTU (P65425) Probable O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x
MENC_PASMU	>gnl|sp|MENC_PASMU (Q9CLV7) O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x
MENC_SALTI	>gnl|sp|MENC_SALTI (P58485) O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x
MENC_SALTY	>gnl|sp|MENC_SALTY (P58486) O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x
MENC_SYNY3	>gnl|sp|MENC_SYNY3 (Q55117) Probable O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x
MENC_VIBCH	>gnl|sp|MENC_VIBCH (Q9KQM6) O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x
MENC_YERPE	>gnl|sp|MENC_YERPE (P58487) O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x
CBNB_RALEU	>gnl|sp|CBNB_RALEU (P83763) Chloromuconate cycloisomerase cbnB (EC 5.5.1.7) (Muconate cycloisomerase II cbnB)			x
CLCB_PSEPU	>gnl|sp|CLCB_PSEPU (P11452) Chloromuconate cycloisomerase (EC 5.5.1.7) (Muconate cycloisomerase II)			x
TCBD_PSESQ	>gnl|sp|TCBD_PSESQ (P27099) Chloromuconate cycloisomerase (EC 5.5.1.7) (Muconate cycloisomerase II)			x
TFDD1_RALEJ	>gnl|sp|TFDD1_RALEJ (P05404) Chloromuconate cycloisomerase (EC 5.5.1.7) (Muconate cycloisomerase II)			x

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
TFDD_COMAC	>gnl|sp|TFDD_COMAC (Q9RNZ9) Chloromuconate cycloisomerase (EC 5.5.1.7)			x
CATB1_ACILW	>gnl|sp|CATB1_ACILW (O33946) Muconate cycloisomerase I 1 (EC 5.5.1.1) (Cis,cis-muconate lactonizing enzyme I 1) (MLE 1)			x
CATB_ACIAD	>gnl|sp|CATB_ACIAD (Q43931) Muconate cycloisomerase I (EC 5.5.1.1) (Cis,cis-muconate lactonizing enzyme I) (MLE)			x
CATB_PSEPU	>gnl|sp|CATB_PSEPU (P08310) Muconate cycloisomerase I (EC 5.5.1.1) (Cis,cis-muconate lactonizing enzyme I) (MLE)			x
CATB_RHOOP	>gnl|sp|CATB_RHOOP (P95608) Muconate cycloisomerase I (EC 5.5.1.1) (Cis,cis-muconate lactonizing enzyme I) (MLE)			x
KDOP_HAEIN	>gnl|sp|KDOP_HAEIN (P45314) 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45) (KDO 8-P phosphatase)			x
KDSC_ECO57	>gnl|sp|KDSC_ECO57 (P0ABZ5) 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45) (KDO 8-P phosphatase)	ESA, BTC		x
KDSC_ECOL6	>gnl|sp|KDSC_ECOL6 (P67653) 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45) (KDO 8-P phosphatase)	ESA, BTC		x
KDSC_ECOLI	>gnl|sp|KDSC_ECOLI (P0ABZ4) 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45) (KDO 8-P phosphatase)	ESA, BTC		x
KDSC_SHIFL	>gnl|sp|KDSC_SHIFL (P67654) 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45) (KDO 8-P phosphatase)	ESA, BTC		x
HAD1_PSEUC	>gnl|sp|HAD1_PSEUC (P24069) (S)-2-haloacid dehalogenase I (EC 3.8.1.2) (2-haloalkanoic acid dehalogenase I) (L-2-haloacid dehalogenase I) (Halocarboxylic acid halidohydrolase I) (DEHCI)			x
HAD2_PSEUC	>gnl|sp|HAD2_PSEUC (P24070) (S)-2-haloacid dehalogenase II (EC 3.8.1.2) (2-haloalkanoic acid dehalogenase II) (L-2-haloacid dehalogenase II) (Halocarboxylic acid halidohydrolase II) (DEHCII)			x
HAD4_BURCE	>gnl|sp|HAD4_BURCE (Q51645) (S)-2-haloacid dehalogenase IVA (EC 3.8.1.2) (2-haloalkanoic acid dehalogenase IVA) (L-2-haloacid dehalogenase IVA) (Halocarboxylic acid halidohydrolase IVA)			x
HAD9_PSEPU	>gnl|sp|HAD9_PSEPU (Q59728) (S)-2-haloacid dehalogenase H-109 (EC 3.8.1.2) (2-haloalkanoic acid dehalogenase H-109) (L-2-haloacid dehalogenase H-109) (Halocarboxylic acid halidohydrolase H-109)			x

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
HADL_PSEPU	>gnl|sp|HADL_PSEPU (Q52087) (S)-2-haloacid dehalogenase (EC 3.8.1.2) (2-haloalkanoic acid dehalogenase) (L-2-haloacid dehalogenase) (Halocarboxylic acid halidohydrolase)			x
HAD_AGRTR	>gnl|sp|HAD_AGRTR (P60527) 2-haloalkanoic acid dehalogenase (EC 3.8.1.2) (L-2-haloacid dehalogenase) (Halocarboxylic acid halidohydrolase) (L-DEX) (Cryptic L-isomer-specific dehalogenase) (DhlS5I)			x
HAD_PSEFL	>gnl|sp|HAD_PSEFL (Q59666) (S)-2-haloacid dehalogenase (EC 3.8.1.2) (2-haloalkanoic acid dehalogenase) (L-2-haloacid dehalogenase) (Halocarboxylic acid halidohydrolase)			x
HAD_PSEUY	>gnl|sp|HAD_PSEUY (Q53464) (S)-2-haloacid dehalogenase (EC 3.8.1.2) (2-haloalkanoic acid dehalogenase) (L-2-haloacid dehalogenase) (Halocarboxylic acid halidohydrolase) (L-DEX)			x
HAD_XANAU	>gnl|sp|HAD_XANAU (Q60099) (S)-2-haloacid dehalogenase (EC 3.8.1.2) (2-haloalkanoic acid dehalogenase) (L-2-haloacid dehalogenase) (Halocarboxylic acid halidohydrolase)			x
PGMB_BACSU	>gnl|sp|PGMB_BACSU (O06995) Putative beta-phosphoglucomutase (EC 5.4.2.6) (Beta-PGM)			x
PGMB_ECOLI	>gnl|sp|PGMB_ECOLI (P77366) Putative beta-phosphoglucomutase (EC 5.4.2.6) (Beta-PGM)			x
PGMB_LACLA	>gnl|sp|PGMB_LACLA (P71447) Beta-phosphoglucomutase (EC 5.4.2.6) (Beta-PGM)			x
BPPS_SALOF	>gnl|sp|BPPS_SALOF (O81192) (+)-bornyl diphosphate synthase, chloroplast precursor (EC 5.5.1.8) (SBS) (BPPS)			x
PTLS_STRS3	>gnl|sp|PTLS_STRS3 (Q55012) Pentalenene synthase (EC 4.2.3.7)			x
SQHC_ALIAC	>gnl|sp|SQHC_ALIAC (P33247) Squalene--hopene cyclase (EC 5.4.99.17)			x
SQHC_BRAJA	>gnl|sp|SQHC_BRAJA (P54924) Squalene--hopene cyclase (EC 5.4.99.17)			x
SQHC_RHISN	>gnl|sp|SQHC_RHISN (P55348) Probable squalene--hopene cyclase (EC 5.4.99.17)			x
SQHC_ZYMMO	>gnl|sp|SQHC_ZYMMO (P33990) Squalene--hopene cyclase (EC 5.4.99.17)			x
TRI5_FUSAC	>gnl|sp|TRI5_FUSAC (Q7LJR6) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x
TRI5_FUSAS	>gnl|sp|TRI5_FUSAS (Q8NIH6) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
TRI5_FUSAU	>gnl|sp|TRI5_FUSAU (Q8NIH0) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x
TRI5_FUSBO	>gnl|sp|TRI5_FUSBO (Q8NIH3) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x
TRI5_FUSCE	>gnl|sp|TRI5_FUSCE (Q8NIC1) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x
TRI5_FUSCO	>gnl|sp|TRI5_FUSCO (Q7LJF8) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x
TRI5_FUSCU	>gnl|sp|TRI5_FUSCU (Q8NIG9) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x
TRI5_FUSME	>gnl|sp|TRI5_FUSME (Q8NIC8) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x
TRI5_FUSMI	>gnl|sp|TRI5_FUSMI (Q8NJA1) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x
TRI5_FUSPO	>gnl|sp|TRI5_FUSPO (Q00835) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x
TRI5_FUSPS	>gnl|sp|TRI5_FUSPS (Q8NID7) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x
TRI5_FUSSP	>gnl|sp|TRI5_FUSSP (P13513) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x
TRI5_GIBPU	>gnl|sp|TRI5_GIBPU (P27679) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x
TRI5_GIBZE	>gnl|sp|TRI5_GIBZE (Q00909) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x
TRI5_MYRRO	>gnl|sp|TRI5_MYRRO (O13489) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x
TRI5_STACH	>gnl|sp|TRI5_STACH (O59947) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x
ARIS_PENRO	>gnl|sp|ARIS_PENRO (Q03471) Aristolochene synthase (EC 4.2.3.9) (Sesquiterpene cyclase) (AS)			x
MCEE_HUMAN	>gnl|sp|MCEE_HUMAN (Q96PE7) Methylmalonyl-CoA epimerase, mitochondrial precursor (EC 5.1.99.1) (DL-methylmalonyl-CoA racemase)			x

Table K-4. Swiss-Prot Data (Chapter 2)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Misan. Code</th><th>Incorrect</th><th>Correct</th></tr>
<tr><td>MCEE_MOUSE</td><td>>gnl|sp|MCEE_MOUSE (Q9D1I5) Methylmalonyl-CoA epimerase, mitochondrial precursor (EC 5.1.99.1) (DL-methylmalonyl-CoA racemase)</td><td></td><td></td><td>x</td></tr>
<tr><td>HPPD1_ASPFU</td><td>>gnl|sp|HPPD1_ASPFU (Q4WHU1) Probable 4-hydroxyphenylpyruvate dioxygenase 1 (EC 1.13.11.27) (4HPPD 1) (HPD 1) (HPPDase 1)</td><td></td><td></td><td>x</td></tr>
<tr><td>HPPD2_ASPFU</td><td>>gnl|sp|HPPD2_ASPFU (Q4WPV8) Probable 4-hydroxyphenylpyruvate dioxygenase 2 (EC 1.13.11.27) (4HPPD 2) (HPD 2) (HPPDase 2)</td><td></td><td></td><td>x</td></tr>
<tr><td>HPPD_ARATH</td><td>>gnl|sp|HPPD_ARATH (P93836) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acide oxidase)</td><td></td><td></td><td>x</td></tr>
<tr><td>HPPD_BOVIN</td><td>>gnl|sp|HPPD_BOVIN (Q5EA20) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acide oxidase)</td><td></td><td></td><td>x</td></tr>
<tr><td>HPPD_BRARE</td><td>>gnl|sp|HPPD_BRARE (Q6TGZ5) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acide oxidase)</td><td></td><td></td><td>x</td></tr>
<tr><td>HPPD_CAEBR</td><td>>gnl|sp|HPPD_CAEBR (Q60Y65) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acide oxidase)</td><td></td><td></td><td>x</td></tr>
<tr><td>HPPD_CAEEL</td><td>>gnl|sp|HPPD_CAEEL (Q22633) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acide oxidase)</td><td></td><td></td><td>x</td></tr>
<tr><td>HPPD_COCIM</td><td>>gnl|sp|HPPD_COCIM (Q00415) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (T-cell reactive protein)</td><td></td><td></td><td>x</td></tr>
<tr><td>HPPD_DAUCA</td><td>>gnl|sp|HPPD_DAUCA (O23920) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acide oxidase)</td><td></td><td></td><td>x</td></tr>
<tr><td>HPPD_HUMAN</td><td>>gnl|sp|HPPD_HUMAN (P32754) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acide oxidase)</td><td></td><td></td><td>x</td></tr>
<tr><td>HPPD_MAGGR</td><td>>gnl|sp|HPPD_MAGGR (Q96X22) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase)</td><td></td><td></td><td>x</td></tr>
<tr><td>HPPD_MOUSE</td><td>>gnl|sp|HPPD_MOUSE (P49429) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (4-hydroxyphenylpyruvic acide oxidase) (HPPDase) (F protein) (F Alloantigen)</td><td></td><td></td><td>x</td></tr>
<tr><td>HPPD_MYCGR</td><td>>gnl|sp|HPPD_MYCGR (O42764) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase)</td><td></td><td></td><td>x</td></tr>
<tr><td>HPPD_NEUCR</td><td>>gnl|sp|HPPD_NEUCR (Q872T7) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase)</td><td></td><td></td><td>x</td></tr>
</table>

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
HPPD_PIG	>gnl|sp|HPPD_PIG (Q02110) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acide oxidase)			x
HPPD_PSEUJ	>gnl|sp|HPPD_PSEUJ (P80064) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase)			x
HPPD_RAT	>gnl|sp|HPPD_RAT (P32755) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (4-hydroxyphenylpyruvic acide oxidase) (HPPDase) (F protein) (F Alloantigen)			x
HPPD_SOLSC	>gnl|sp|HPPD_SOLSC (Q9ARF9) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acide oxidase)			x
HPPD_STRAW	>gnl|sp|HPPD_STRAW (Q53586) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase)			x
HPPD_STRCO	>gnl|sp|HPPD_STRCO (Q9S2F4) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase)			x
HPPD_TETTH	>gnl|sp|HPPD_TETTH (Q27203) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acide oxidase) (F-antigen homolog) (TF-AG)			x
HPPD_XENTR	>gnl|sp|HPPD_XENTR (Q5BKL0) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acide oxidase)			x
HPPD_YARLI	>gnl|sp|HPPD_YARLI (Q6CDR5) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase)			x
LLY_LEGPH	>gnl|sp|LLY_LEGPH (Q5ZT84) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (Legiolysin)			x
LLY_LEGPN	>gnl|sp|LLY_LEGPN (P69053) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (Legiolysin)			x
FOSA_PSEAE	>gnl|sp|FOSA_PSEAE (Q9I4K6) Glutathione transferase fosA (EC 2.5.1.18) (Fosfomycin resistance protein)			x
FOSA_SERMA	>gnl|sp|FOSA_SERMA (Q56415) Glutathione transferase fosA (EC 2.5.1.18) (Fosfomycin resistance protein)			x
LGUL_ARATH	>gnl|sp|LGUL_ARATH (Q8H0V3) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
LGUL_BRAJU	>gnl|sp|LGUL_BRAJU (O04885) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x
LGUL_BRAOG	>gnl|sp|LGUL_BRAOG (Q39366) Putative lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x
LGUL_CICAR	>gnl|sp|LGUL_CICAR (O49818) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x
LGUL_ECO57	>gnl|sp|LGUL_ECO57 (P0AC82) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x
LGUL_ECOLI	>gnl|sp|LGUL_ECOLI (P0AC81) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x
LGUL_HAEIN	>gnl|sp|LGUL_HAEIN (P44638) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x
LGUL_HUMAN	>gnl|sp|LGUL_HUMAN (Q04760) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x
LGUL_LYCES	>gnl|sp|LGUL_LYCES (Q42891) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x
LGUL_MACFA	>gnl|sp|LGUL_MACFA (Q4R5F2) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x
LGUL_MOUSE	>gnl|sp|LGUL_MOUSE (Q9CPU0) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
LGUL_NEIMA	>gnl|sp|LGUL_NEIMA (P0A0T2) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x
LGUL_NEIMB	>gnl|sp|LGUL_NEIMB (P0A0T3) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x
LGUL_ORYSA	>gnl|sp|LGUL_ORYSA (Q948T6) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase) (Allergen Ory s ?) (Allergen Glb33) (PP33)			x
LGUL_PSEPU	>gnl|sp|LGUL_PSEPU (P16635) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x
LGUL_RAT	>gnl|sp|LGUL_RAT (Q6P7Q4) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x
LGUL_SALTI	>gnl|sp|LGUL_SALTI (P0A1Q3) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x
LGUL_SALTY	>gnl|sp|LGUL_SALTY (P0A1Q2) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x
LGUL_SCHPO	>gnl|sp|LGUL_SCHPO (Q09751) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x
LGUL_SHIFL	>gnl|sp|LGUL_SHIFL (P0AC83) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x
LGUL_SYNY3	>gnl|sp|LGUL_SYNY3 (Q55595) Probable lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
LGUL_VIBCH	>gnl|sp|LGUL_VIBCH (Q9KT93) Probable lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x
LGUL_VIBPA	>gnl|sp|LGUL_VIBPA (P46235) Probable lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x
LGUL_YEAST	>gnl|sp|LGUL_YEAST (P50107) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x
ADA_BRARE	>gnl|sp|ADA_BRARE (Q6DG22) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	BTC	x	
ADA_CHICK	>gnl|sp|ADA_CHICK (Q5ZKP6) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	BTC	x	
ADA_YEAST	>gnl|sp|ADA_YEAST (P53909) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	BTC	x	
ADD1_STRCO	>gnl|sp|ADD1_STRCO (O86737) Probable adenosine deaminase 1 (EC 3.5.4.4) (Adenosine aminohydrolase 1)	BTC	x	
ADD2_STRCO	>gnl|sp|ADD2_STRCO (Q9X7T2) Probable adenosine deaminase 2 (EC 3.5.4.4) (Adenosine aminohydrolase 2)	MFR	x	
ADD2_VIBPA	>gnl|sp|ADD2_VIBPA (Q87GM3) Adenosine deaminase 2 (EC 3.5.4.4) (Adenosine aminohydrolase 2)	BTC	x	
ADD3_STRCO	>gnl|sp|ADD3_STRCO (Q9RDE5) Probable adenosine deaminase 3 (EC 3.5.4.4) (Adenosine aminohydrolase 3)	BTC	x	
ADD4_STRCO	>gnl|sp|ADD4_STRCO (Q9L0L6) Probable adenosine deaminase 4 (EC 3.5.4.4) (Adenosine aminohydrolase 4)	BTC	x	
ADD5_STRCO	>gnl|sp|ADD5_STRCO (Q9AK25) Probable adenosine deaminase 5 (EC 3.5.4.4) (Adenosine aminohydrolase 5)	MFR	x	
ADD_AGRT5	>gnl|sp|ADD_AGRT5 (Q8UJ05) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	BTC	x	
ADD_BORBR	>gnl|sp|ADD_BORBR (Q7WMY6) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	BTC	x	

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
ADD_BORPA	>gnl|sp|ADD_BORPA (Q7WBG5) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	BTC	x	
ADD_CAUCR	>gnl|sp|ADD_CAUCR (Q9A3M3) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	BTC	x	
ADD_CLOAB	>gnl|sp|ADD_CLOAB (Q97EV1) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	MFR	x	
ADD_CLOPE	>gnl|sp|ADD_CLOPE (Q8XHH8) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	MFR	x	
ADD_ENTFA	>gnl|sp|ADD_ENTFA (Q839J4) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	MFR	x	
ADD_HAEDU	>gnl|sp|ADD_HAEDU (Q7VNV1) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	MFR	x	
ADD_LACLA	>gnl|sp|ADD_LACLA (Q9CIR9) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	MFR	x	
ADD_MYCBO	>gnl|sp|ADD_MYCBO (P63908) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	MFR	x	
ADD_MYCLE	>gnl|sp|ADD_MYCLE (Q9CCL9) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	MFR	x	
ADD_MYCTU	>gnl|sp|ADD_MYCTU (P63907) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	MFR	x	
ADD_PHOLL	>gnl|sp|ADD_PHOLL (Q7N4H5) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	BTC	x	
ADD_PSEAE	>gnl|sp|ADD_PSEAE (Q9I6Y4) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	BTC	x	
ADD_PSEPK	>gnl|sp|ADD_PSEPK (Q88QA3) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	BTC	x	
ADD_PSESM	>gnl|sp|ADD_PSESM (Q889J2) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	BTC	x	
ADD_RALSO	>gnl|sp|ADD_RALSO (Q8XXL5) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	BTC	x	
ADD_RHILO	>gnl|sp|ADD_RHILO (Q98GV2) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	BTC	x	

Table K-4. Swiss-Prot Data (Chapter 2)

Accession	Annotation	Misan. Code	Incorrect	Correct
ADD_RHIME	>gnl|sp|ADD_RHIME (Q92T48) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	BTC	x	
ADD_STRA3	>gnl|sp|ADD_STRA3 (P63909) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	MFR	x	
ADD_STRA5	>gnl|sp|ADD_STRA5 (P63910) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	MFR	x	
ADD_STRMU	>gnl|sp|ADD_STRMU (Q8DTN8) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	MFR	x	
ADD_STRVG	>gnl|sp|ADD_STRVG (P53984) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	BTC	x	
ADD_VIBVU	>gnl|sp|ADD_VIBVU (Q8D6Q8) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	MFR	x	
ADD_VIBVY	>gnl|sp|ADD_VIBVY (Q7MDL6) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	MFR	x	
ADD_WOLSU	>gnl|sp|ADD_WOLSU (Q7M9R5) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	BTC	x	
ENOA_TRASC	>gnl|sp|ENOA_TRASC (Q9W7L1) Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Phosphopyruvate hydratase)	MFR	x	
GUDH_STRCO	>gnl|sp|GUDH_STRCO (Q9RDE9) Probable glucarate dehydratase (EC 4.2.1.40) (GDH) (GlucD)	BAC	x	
TFDD2_RALEJ	>gnl|sp|TFDD2_RALEJ (P42428) Chloromuconate cycloisomerase (EC 5.5.1.7) (Muconate cycloisomerase II)	BAC	x	
KDSC_SALTI	>gnl|sp|KDSC_SALTI (Q8Z3G5) 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45) (KDO 8-P phosphatase)	BTC	x	
KDSC_SALTY	>gnl|sp|KDSC_SALTY (Q8ZLS0) 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45) (KDO 8-P phosphatase)	BTC	x	
KDSC_YERPE	>gnl|sp|KDSC_YERPE (Q8ZB47) 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45) (KDO 8-P phosphatase)	BTC	x	
TRI5_TRIHA	>gnl|sp|TRI5_TRIHA (Q6A1B7) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)	BTC	x	
HPPD_HORVU	>gnl|sp|HPPD_HORVU (O48604) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acide oxidase)	BTC	x	

Appendix L. Data, Similarity-Based Annotation Analysis (Chapter 3)

L.1. Table L-1. GenBank NR Data (Chapter 3)

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
68556473	>gi|68556473|ref|ZP_00595816.1| Amidohydrolase [Ralstonia metallidurans CH34]			x	x
68529646	>gi|68529646|gb|EAN52609.1| Amidohydrolase [Ralstonia metallidurans CH34]			x	x
73992038	>gi|73992038|ref|XP_534428.2| PREDICTED: similar to Adenosine deaminase (Adenosine aminohydrolase) isoform 1 [Canis familiaris]			x	x
73992040	>gi|73992040|ref|XP_866253.1| PREDICTED: similar to Adenosine deaminase (Adenosine aminohydrolase) isoform 2 [Canis familiaris]			x	x
74019554	>gi|74019554|ref|ZP_00690169.1| Amidohydrolase [Burkholderia ambifaria AMMD]			x	x
72607770	>gi|72607770|gb|EAO43727.1| Amidohydrolase [Burkholderia ambifaria AMMD]			x	x
67542664	>gi|67542664|ref|ZP_00420599.1| Amidohydrolase [Burkholderia vietnamiensis G4]			x	x
67535877	>gi|67535877|gb|EAM32601.1| Amidohydrolase [Burkholderia vietnamiensis G4]			x	x
67659616	>gi|67659616|ref|ZP_00456976.1| Amidohydrolase [Burkholderia cenocepacia AU 1054]			x	x
67092835	>gi|67092835|gb|EAM10384.1| Amidohydrolase [Burkholderia cenocepacia AU 1054]			x	x
75196826	>gi|75196826|ref|ZP_00706896.1| COG0044: Dihydroorotase and related cyclic amidohydrolases [Escherichia coli HS]			x	x
75234602	>gi|75234602|ref|ZP_00718933.1| COG0044: Dihydroorotase and related cyclic amidohydrolases [Escherichia coli E110019]			x	x
75230847	>gi|75230847|ref|ZP_00717305.1| COG0044: Dihydroorotase and related cyclic amidohydrolases [Escherichia coli B7A]			x	x
75239218	>gi|75239218|ref|ZP_00723191.1| COG0044: Dihydroorotase and related cyclic amidohydrolases [Escherichia coli F11]			x	x
2623168	>gi|2623168|gb|AAB86485.1| putative dienoyl-CoA isomerase [Homo sapiens]			x	x
24985728	>gi|24985728|gb|AAN69622.1| enoyl-CoA hydratase/isomerase family protein [Pseudomonas putida KT2440]			x	x

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>82739940</td><td>>gi|82739940|ref|ZP_00902717.1| enoyl-CoA hydratase/isomerase family protein [Pseudomonas putida F1]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>82712992</td><td>>gi|82712992|gb|EAP48129.1| enoyl-CoA hydratase/isomerase family protein [Pseudomonas putida F1]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>28853151</td><td>>gi|28853151|gb|AAO56220.1| enoyl-CoA hydratase/isomerase family protein [Pseudomonas syringae pv. tomato str. DC3000]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>68344930</td><td>>gi|68344930|gb|AAY92536.1| enoyl-CoA hydratase/isomerase family protein [Pseudomonas fluorescens Pf-5]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>71557578</td><td>>gi|71557578|gb|AAZ36789.1| enoyl-CoA hydratase/isomerase family protein [Pseudomonas syringae pv. phaseolicola 1448A]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>71737025</td><td>>gi|71737025|ref|YP_274802.1| enoyl-CoA hydratase/isomerase family protein [Pseudomonas syringae pv. phaseolicola 1448A]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>13421504</td><td>>gi|13421504|gb|AAK22340.1| enoyl-CoA hydratase/isomerase family protein [Caulobacter crescentus CB15]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>16124608</td><td>>gi|16124608|ref|NP_419172.1| enoyl-CoA hydratase/isomerase family protein [Caulobacter crescentus CB15]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>13883763</td><td>>gi|13883763|gb|AAK48248.1| enoyl-CoA hydratase/isomerase family protein [Mycobacterium tuberculosis CDC1551]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>66851811</td><td>>gi|66851811|gb|EAL92136.1| enoyl-CoA hydratase/isomerase family protein [Aspergillus fumigatus Af293]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>77953360</td><td>>gi|77953360|ref|ZP_00817769.1| enoyl-CoA hydratase/isomerase family protein [Marinobacter aquaeolei VT8]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>77867780</td><td>>gi|77867780|gb|EAO99054.1| enoyl-CoA hydratase/isomerase family protein [Marinobacter aquaeolei VT8]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>54013855</td><td>>gi|54013855|dbj|BAD55225.1| putative enoyl-CoA hydratase/isomerase family protein [Nocardia farcinica IFM 10152]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>86165533</td><td>>gi|86165533|gb|EAQ66800.1| enoyl-CoA hydratase/isomerase family protein [Marinomonas sp. MED121]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>1789286</td><td>>gi|1789286|gb|AAC75956.1| putative enzyme [Escherichia coli K12]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>13363261</td><td>>gi|13363261|dbj|BAB37212.1| putative enzyme [Escherichia coli O157:H7]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>12517451</td><td>>gi|12517451|gb|AAG58045.1| putative enzyme [Escherichia coli O157:H7 EDL933]</td><td></td><td></td><td>x</td><td>x</td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
15803453	>gi|15803453|ref|NP_289486.1| putative enzyme [Escherichia coli O157:H7 EDL933]			x	x
56383754	>gi|56383754|gb|AAN44387.2| putative enzyme [Shigella flexneri 2a str. 301]			x	x
30042485	>gi|30042485|gb|AAP18209.1| putative enzyme [Shigella flexneri 2a str. 2457T]			x	x
82545462	>gi|82545462|ref|YP_409409.1| putative enzyme [Shigella boydii Sb227]			x	x
30064228	>gi|30064228|ref|NP_838399.1| putative enzyme [Shigella flexneri 2a str. 2457T]			x	x
56480203	>gi|56480203|ref|NP_708680.2| putative enzyme [Shigella flexneri 2a str. 301]			x	x
81246873	>gi|81246873|gb|ABB67581.1| putative enzyme [Shigella boydii Sb227]			x	x
74313475	>gi|74313475|ref|YP_311894.1| putative enzyme [Shigella sonnei Ss046]			x	x
73856952	>gi|73856952|gb|AAZ89659.1| putative enzyme [Shigella sonnei Ss046]			x	x
74005032	>gi|74005032|ref|XP_848689.1| PREDICTED: similar to 3-hydroxyisobutyryl-Coenzyme A hydrolase isoform 1 [Canis familiaris]			x	x
72105061	>gi|72105061|ref|XP_791196.1| PREDICTED: similar to 3-hydroxyisobutyryl-Coenzyme A hydrolase isoform 1 [Strongylocentrotus purpuratus]			x	x
8572760	>gi|8572760|gb|AAF77193.1| CoA-thioester hydrolase CHY1 [Arabidopsis thaliana]			x	x
76609336	>gi|76609336|ref|XP_615997.2| PREDICTED: similar to 3-hydroxyisobutyryl-Coenzyme A hydrolase isoform 1 [Bos taurus]			x	x
42569479	>gi|42569479|ref|NP_180624.2| catalytic [Arabidopsis thaliana]			x	x
42569477	>gi|42569477|ref|NP_180623.2| catalytic [Arabidopsis thaliana]			x	x
42566089	>gi|42566089|ref|NP_191610.3| catalytic [Arabidopsis thaliana]			x	x
79473201	>gi|79473201|ref|NP_193072.2| catalytic [Arabidopsis thaliana]			x	x
11994698	>gi|11994698|dbj|BAB02936.1| 3-hydroxyisobutyryl-coenzyme A hydrolase-like protein [Arabidopsis thaliana]			x	x
7268039	>gi|7268039|emb|CAB78378.1| 3-hydroxyisobutyryl-coenzyme A hydrolase-like protein [Arabidopsis thaliana]			x	x

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>4584541</td><td>>gi|4584541|emb|CAB40771.1| 3-hydroxyisobutyryl-coenzyme A hydrolase-like protein [Arabidopsis thaliana]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>21536517</td><td>>gi|21536517|gb|AAM60849.1| 3-hydroxyisobutyryl-coenzyme A hydrolase-like protein [Arabidopsis thaliana]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>52209887</td><td>>gi|52209887|emb|CAH35859.1| putative hydratase [Burkholderia pseudomallei K96243]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>38199742</td><td>>gi|38199742|emb|CAE49402.1| Putative hydrolase [Corynebacterium diphtheriae]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>76616437</td><td>>gi|76616437|ref|XP_869949.1| PREDICTED: similar to Gamma enolase (2-phospho-D-glycerate hydro-lyase) (Neural enolase) (Neuron-specific enolase) (NSE) (Enolase 2) isoform 2 [Bos taurus]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>73997297</td><td>>gi|73997297|ref|XP_534902.2| PREDICTED: similar to Gamma enolase (2-phospho-D-glycerate hydro-lyase) (Neural enolase) (Neuron-specific enolase) (NSE) (Enolase 2) isoform 2 [Canis familiaris]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>73955314</td><td>>gi|73955314|ref|XP_536606.2| PREDICTED: similar to Beta enolase (2-phospho-D-glycerate hydro-lyase) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase) (Enolase 3) isoform 1 [Canis familiaris]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>73955316</td><td>>gi|73955316|ref|XP_856204.1| PREDICTED: similar to Beta enolase (2-phospho-D-glycerate hydro-lyase) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase) (Enolase 3) isoform 2 [Canis familiaris]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>73997301</td><td>>gi|73997301|ref|XP_867312.1| PREDICTED: similar to Gamma enolase (2-phospho-D-glycerate hydro-lyase) (Neural enolase) (Neuron-specific enolase) (NSE) (Enolase 2) isoform 4 [Canis familiaris]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>76616435</td><td>>gi|76616435|ref|XP_604365.2| PREDICTED: similar to Gamma enolase (2-phospho-D-glycerate hydro-lyase) (Neural enolase) (Neuron-specific enolase) (NSE) (Enolase 2) isoform 1 [Bos taurus]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>2281464</td><td>>gi|2281464|gb|AAC46289.1| enolase homolog [Borrelia burgdorferi]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>73997303</td><td>>gi|73997303|ref|XP_867321.1| PREDICTED: similar to Gamma enolase (2-phospho-D-glycerate hydro-lyase) (Neural enolase) (Neuron-specific enolase) (NSE) (Enolase 2) isoform 5 [Canis familiaris]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>73997299</td><td>>gi|73997299|ref|XP_867303.1| PREDICTED: similar to Gamma enolase (2-phospho-D-glycerate hydro-lyase) (Neural enolase) (Neuron-specific enolase) (NSE) (Enolase 2) isoform 3 [Canis familiaris]</td><td></td><td></td><td>x</td><td>x</td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
72004519	>gi|72004519|ref|XP_784476.1| PREDICTED: similar to enolase 1, (alpha) [Strongylocentrotus purpuratus]			x	x
6323985	>gi|6323985|ref|NP_014056.1| Protein of unknown function, has similarity to enolases; Err3p [Saccharomyces cerevisiae]			x	x
1706698	>gi|1706698|sp|P42222|ERR3_YEAST Enolase-related protein 3			x	x
6324974	>gi|6324974|ref|NP_015042.1| Protein of unknown function, has similarity to enolases; Err2p [Saccharomyces cerevisiae]			x	x
6324969	>gi|6324969|ref|NP_015038.1| Protein of unknown function, has similarity to enolases; Err1p [Saccharomyces cerevisiae]			x	x
51827777	>gi|51827777|sp|Q12007|ERR1_YEAST Enolase-related protein 1/2			x	x
55644845	>gi|55644845|ref|XP_511294.1| PREDICTED: similar to enolase 3; enolase-3, beta, muscle; muscle specific enolase; beta enolase; skeletal muscle enolase; 2-phospho-D-glycerate hydrolyase [Pan troglodytes]			x	x
10640159	>gi|10640159|emb|CAC12011.1| enolase related protein [Thermoplasma acidophilum]			x	x
48785058	>gi|48785058|ref|ZP_00281363.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia fungorum LB400]			x	x
28869382	>gi|28869382|ref|NP_792001.1| mandelate racemase/muconate lactonizing enzyme family protein [Pseudomonas syringae pv. tomato str. DC3000]			x	x
28852623	>gi|28852623|gb|AAO55696.1| mandelate racemase/muconate lactonizing enzyme family protein [Pseudomonas syringae pv. tomato str. DC3000]			x	x
84362795	>gi|84362795|ref|ZP_00987408.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia dolosa AUO158]			x	x
84355722	>gi|84355722|ref|ZP_00980597.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia cenocepacia PC184]			x	x
67669556	>gi|67669556|ref|ZP_00466386.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia pseudomallei 1655]			x	x

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
82536379	>gi|82536379|ref|ZP_00895386.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia pseudomallei 1106b]			x	x
82528410	>gi|82528410|ref|ZP_00887686.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia pseudomallei 1106a]			x	x
67739119	>gi|67739119|ref|ZP_00489725.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia pseudomallei 668]			x	x
67753215	>gi|67753215|ref|ZP_00492159.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia pseudomallei Pasteur]			x	x
67684280	>gi|67684280|ref|ZP_00478280.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia pseudomallei 1710a]			x	x
83676063	>gi|83676063|ref|ZP_00937864.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia pseudomallei 406e]			x	x
67760958	>gi|67760958|ref|ZP_00499673.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia pseudomallei S13]			x	x
67639301	>gi|67639301|ref|ZP_00438173.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia mallei GB8 horse 4]			x	x
67645063	>gi|67645063|ref|ZP_00443375.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia mallei NCTC 10247]			x	x
85066625	>gi|85066625|ref|ZP_01027478.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia mallei 10229]			x	x
84521886	>gi|84521886|ref|ZP_01009022.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia mallei SAVP1]			x	x

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
83622215	>gi|83622215|ref|ZP_00932549.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia mallei JHU]			x	x
83617215	>gi|83617215|ref|ZP_00927738.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia mallei FMH]			x	x
67634196	>gi|67634196|ref|ZP_00433179.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia mallei 10399]			x	x
75242518	>gi|75242518|ref|ZP_00726262.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli F11]			x	x
75514245	>gi|75514245|ref|ZP_00736553.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli 53638]			x	x
75258232	>gi|75258232|ref|ZP_00729680.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli E22]			x	x
75236416	>gi|75236416|ref|ZP_00720512.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli E110019]			x	x
75231038	>gi|75231038|ref|ZP_00717473.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli B7A]			x	x
75210696	>gi|75210696|ref|ZP_00710837.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli B171]			x	x
75188449	>gi|75188449|ref|ZP_00701716.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli E24377A]			x	x
83588442	>gi|83588442|ref|ZP_00927066.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli 101-1]			x	x

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
75197590	>gi|75197590|ref|ZP_00707660.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli HS]			x	x
77978070	>gi|77978070|ref|ZP_00833504.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Yersinia intermedia ATCC 29909]			x	x
71915919	>gi|71915919|gb|AAZ55821.1| mandelate racemase/muconate lactonizing enzyme family [Thermobifida fusca YX]			x	x
72162187	>gi|72162187|ref|YP_289844.1| mandelate racemase/muconate lactonizing enzyme family [Thermobifida fusca YX]			x	x
55379642	>gi|55379642|ref|YP_137492.1| mandelate racemase/muconate lactonizing enzyme family [Haloarcula marismortui ATCC 43049]			x	x
55232367	>gi|55232367|gb|AAV47786.1| mandelate racemase/muconate lactonizing enzyme family [Haloarcula marismortui ATCC 43049]			x	x
66847933	>gi|66847933|gb|EAL88263.1| mandelate racemase/muconate lactonizing enzyme family protein [Aspergillus fumigatus Af293]			x	x
48789123	>gi|48789123|ref|ZP_00285102.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia fungorum LB400]			x	x
48788775	>gi|48788775|ref|ZP_00284754.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia fungorum LB400]			x	x
84361237	>gi|84361237|ref|ZP_00985914.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia dolosa AUO158]			x	x
47572881	>gi|47572881|ref|ZP_00242922.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Rubrivivax gelatinosus PM1]			x	x
75256874	>gi|75256874|ref|ZP_00728468.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli E22]			x	x

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
75233987	>gi|75233987|ref|ZP_00718436.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli E110019]			x	x
75187515	>gi|75187515|ref|ZP_00700782.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli E24377A]			x	x
75511930	>gi|75511930|ref|ZP_00734533.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli 53638]			x	x
75228252	>gi|75228252|ref|ZP_00714909.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli B7A]			x	x
75196758	>gi|75196758|ref|ZP_00706828.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli HS]			x	x
83584957	>gi|83584957|ref|ZP_00923613.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli 101-1]			x	x
75212593	>gi|75212593|ref|ZP_00712617.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli B171]			x	x
75241823	>gi|75241823|ref|ZP_00725642.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli F11]			x	x
75176351	>gi|75176351|ref|ZP_00696495.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Shigella boydii BS512]			x	x
75429736	>gi|75429736|ref|ZP_00732398.1| O-succinylbenzoate synthase and related enzymes [Actinobacillus succinogenes 130Z]			x	x
74276944	>gi|74276944|gb|EAO50531.1| O-succinylbenzoate synthase and related enzymes [Actinobacillus succinogenes 130Z]			x	x

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
49330345	>gi|49330345|gb|AAT60991.1| enolase superfamily protein; possible N-acylamino acid racemase, mandelate racemase/muconate lactonizing enzyme, or o-succinylbenzoate synthase [Bacillus thuringiensis serovar konkukian str. 97-27]			x	x
49478789	>gi|49478789|ref|YP_038896.1| enolase superfamily protein; possible N-acylamino acid racemase, mandelate racemase/muconate lactonizing enzyme, or o-succinylbenzoate synthase [Bacillus thuringiensis serovar konkukian str. 97-27]			x	x
65322219	>gi|65322219|ref|ZP_00395178.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Bacillus anthracis str. A2012]			x	x
58177235	>gi|58177235|pdb|1WUE|B Chain B, Crystal Structure Of Protein Gi:29375081, Unknown Member Of Enolase Superfamily From Enterococcus Faecalis V583			x	x
58177234	>gi|58177234|pdb|1WUE|A Chain A, Crystal Structure Of Protein Gi:29375081, Unknown Member Of Enolase Superfamily From Enterococcus Faecalis V583			x	x
21323231	>gi|21323231|dbj|BAB97859.1| O-succinylbenzoate synthase and related enzymes [Corynebacterium glutamicum ATCC 13032]			x	x
29342540	>gi|29342540|gb|AAO80305.1| mandelate racemase/muconate lactonizing enzyme family protein [Enterococcus faecalis V583]			x	x
29375081	>gi|29375081|ref|NP_814234.1| mandelate racemase/muconate lactonizing enzyme family protein [Enterococcus faecalis V583]			x	x
50875140	>gi|50875140|emb|CAG34980.1| related to N-acylamino acid racemase (MenC) [Desulfotalea psychrophila LSv54]			x	x
51244103	>gi|51244103|ref|YP_063987.1| similar to N-acylamino acid racemase (MenC) [Desulfotalea psychrophila LSv54]			x	x
34541184	>gi|34541184|ref|NP_905663.1| mandelate racemase/muconate lactonizing enzyme family protein [Porphyromonas gingivalis W83]			x	x
34397500	>gi|34397500|gb|AAQ66562.1| mandelate racemase/muconate lactonizing enzyme family protein [Porphyromonas gingivalis W83]			x	x

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
62463998	>gi|62463998|ref|ZP_00383303.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Lactococcus lactis subsp. cremoris SK11]			x	x
76785842	>gi|76785842|ref|ZP_00773006.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Mycobacterium tuberculosis F11]			x	x
81255566	>gi|81255566|ref|ZP_00880040.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Mycobacterium tuberculosis C]			x	x
23124230	>gi|23124230|ref|ZP_00106232.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Nostoc punctiforme PCC 73102]			x	x
53689596	>gi|53689596|ref|ZP_00346114.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]			x	x
71673678	>gi|71673678|ref|ZP_00671426.1| similar to L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Trichodesmium erythraeum IMS101]			x	x
71672926	>gi|71672926|gb|EAO29588.1| similar to L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Trichodesmium erythraeum IMS101]			x	x
58177237	>gi|58177237|pdb|1WUF|B Chain B, Crystal Structure Of Protein Gi:16801725, Member Of Enolase Superfamily From Listeria Innocua Clip11262			x	x
58177236	>gi|58177236|pdb|1WUF|A Chain A, Crystal Structure Of Protein Gi:16801725, Member Of Enolase Superfamily From Listeria Innocua Clip11262			x	x
23347839	>gi|23347839|gb|AAN29940.1| mandelate racemase/muconate lactonizing enzyme family protein [Brucella suis 1330]			x	x
62289941	>gi|62289941|ref|YP_221734.1| mandelate racemase/muconate lactonizing enzyme family protein [Brucella abortus biovar 1 str. 9-941]			x	x
62196073	>gi|62196073|gb|AAX74373.1| mandelate racemase/muconate lactonizing enzyme family protein [Brucella abortus biovar 1 str. 9-941]			x	x

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
23501898	>gi|23501898|ref|NP_698025.1| mandelate racemase/muconate lactonizing enzyme family protein [Brucella suis 1330]			x	x
17740080	>gi|17740080|gb|AAL42649.1| mandelate racemase/muconate lactonizing enzyme family protein [Agrobacterium tumefaciens str. C58]			x	x
17935543	>gi|17935543|ref|NP_532333.1| mandelate racemase/muconate lactonizing enzyme family protein [Agrobacterium tumefaciens str. C58]			x	x
78218629	>gi|78218629|gb|ABB37978.1| L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily-like [Desulfovibrio desulfuricans G20]			x	x
78356224	>gi|78356224|ref|YP_387673.1| L-alanine-DL-glutamate epimerase and related enzyme of enolase superfamily-like [Desulfovibrio desulfuricans G20]			x	x
83370196	>gi|83370196|ref|ZP_00915040.1| mandelate racemase/muconate lactonizing enzyme family protein [Rhodobacter sphaeroides ATCC 17025]			x	x
83360087	>gi|83360087|gb|EAP63619.1| mandelate racemase/muconate lactonizing enzyme family protein [Rhodobacter sphaeroides ATCC 17025]			x	x
83371865	>gi|83371865|ref|ZP_00916645.1| mandelate racemase/muconate lactonizing enzyme family protein [Rhodobacter sphaeroides ATCC 17029]			x	x
83366187	>gi|83366187|gb|EAP69673.1| mandelate racemase/muconate lactonizing enzyme family protein [Rhodobacter sphaeroides ATCC 17029]			x	x
48783179	>gi|48783179|ref|ZP_00279641.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia fungorum LB400]			x	x
16502501	>gi|16502501|emb|CAD01649.1| putative mandelate racemase / muconate lactonizing enzyme family protein [Salmonella enterica subsp. enterica serovar Typhi]			x	x
16760206	>gi|16760206|ref|NP_455823.1| putative mandelate racemase / muconate lactonizing enzyme family protein [Salmonella enterica subsp. enterica serovar Typhi str. CT18]			x	x

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
29142025	>gi|29142025|ref|NP_805367.1| muconate lactonizing enzyme family protein [Salmonella enterica subsp. enterica serovar Typhi Ty2]			x	x
25292762	>gi|25292762|pir||AH0659 probable mandelate racemase / muconate lactonizing enzyme family protein STY1382 [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)			x	x
75242125	>gi|75242125|ref|ZP_00725919.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli F11]			x	x
23124447	>gi|23124447|ref|ZP_00106436.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Nostoc punctiforme PCC 73102]			x	x
75190411	>gi|75190411|ref|ZP_00703678.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli E24377A]			x	x
75195474	>gi|75195474|ref|ZP_00705544.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli HS]			x	x
83587466	>gi|83587466|ref|ZP_00926094.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli 101-1]			x	x
75259437	>gi|75259437|ref|ZP_00730756.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli E22]			x	x
75212765	>gi|75212765|ref|ZP_00712763.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli B171]			x	x
75179027	>gi|75179027|ref|ZP_00699045.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Shigella boydii BS512]			x	x
75240029	>gi|75240029|ref|ZP_00723990.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli E110019]			x	x

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
75231877	>gi|75231877|ref|ZP_00718218.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli B7A]			x	x
75515055	>gi|75515055|ref|ZP_00737259.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Escherichia coli 53638]			x	x
77629331	>gi|77629331|ref|ZP_00791917.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Yersinia pseudotuberculosis IP 31758]			x	x
77634477	>gi|77634477|ref|ZP_00796577.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Yersinia pestis Angola]			x	x
83953326	>gi|83953326|ref|ZP_00962048.1| mandelate racemase/muconate lactonizing enzyme family protein [Sulfitobacter sp. NAS-14.1]			x	x
83842294	>gi|83842294|gb|EAP81462.1| mandelate racemase/muconate lactonizing enzyme family protein [Sulfitobacter sp. NAS-14.1]			x	x
84684109	>gi|84684109|ref|ZP_01012011.1| mandelate racemase/muconate lactonizing enzyme family protein [Rhodobacterales bacterium HTCC2654]			x	x
84667862	>gi|84667862|gb|EAQ14330.1| mandelate racemase/muconate lactonizing enzyme family protein [Rhodobacterales bacterium HTCC2654]			x	x
83944285	>gi|83944285|ref|ZP_00956740.1| mandelate racemase/muconate lactonizing enzyme family protein [Sulfitobacter sp. EE-36]			x	x
83844829	>gi|83844829|gb|EAP82711.1| mandelate racemase/muconate lactonizing enzyme family protein [Sulfitobacter sp. EE-36]			x	x
77979523	>gi|77979523|ref|ZP_00834941.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Yersinia intermedia ATCC 29909]			x	x
77958047	>gi|77958047|ref|ZP_00822088.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Yersinia bercovieri ATCC 43970]			x	x

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>13424773</td><td>>gi|13424773|gb|AAK25075.1| mandelate racemase/muconate lactonizing enzyme family protein [Caulobacter crescentus CB15]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>16127343</td><td>>gi|16127343|ref|NP_421907.1| mandelate racemase/muconate lactonizing enzyme family protein [Caulobacter crescentus CB15]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>29896521</td><td>>gi|29896521|gb|AAP09800.1| Mandelate racemase/muconate lactonizing enzyme family protein [Bacillus cereus ATCC 14579]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>30020968</td><td>>gi|30020968|ref|NP_832599.1| Mandelate racemase/muconate lactonizing enzyme family protein [Bacillus cereus ATCC 14579]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>77961680</td><td>>gi|77961680|ref|ZP_00825512.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Yersinia mollaretii ATCC 43969]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>86140220</td><td>>gi|86140220|ref|ZP_01058782.1| mandelate racemase/muconate lactonizing enzyme family protein [Roseobacter sp. MED193]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>85823157</td><td>>gi|85823157|gb|EAQ43370.1| mandelate racemase/muconate lactonizing enzyme family protein [Roseobacter sp. MED193]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>77975347</td><td>>gi|77975347|ref|ZP_00830883.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Yersinia frederiksenii ATCC 33641]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>85705676</td><td>>gi|85705676|ref|ZP_01036773.1| mandelate racemase/muconate lactonizing enzyme family protein [Roseovarius sp. 217]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>85669666</td><td>>gi|85669666|gb|EAQ24530.1| mandelate racemase/muconate lactonizing enzyme family protein [Roseovarius sp. 217]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>84501274</td><td>>gi|84501274|ref|ZP_00999479.1| mandelate racemase/muconate lactonizing enzyme family protein [Oceanicola batsensis HTCC2597]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>84390565</td><td>>gi|84390565|gb|EAQ03053.1| mandelate racemase/muconate lactonizing enzyme family protein [Oceanicola batsensis HTCC2597]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>47503291</td><td>>gi|47503291|gb|AAT31967.1| mandelate racemase/muconate lactonizing enzyme family protein [Bacillus anthracis str. 'Ames Ancestor']</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>49179593</td><td>>gi|49179593|gb|AAT54969.1| mandelate racemase/muconate lactonizing enzyme family protein [Bacillus anthracis str. Sterne]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>49185666</td><td>>gi|49185666|ref|YP_028918.1| mandelate racemase/muconate lactonizing enzyme family protein [Bacillus anthracis str. Sterne]</td><td></td><td></td><td>x</td><td>x</td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>30257450</td><td>>gi|30257450|gb|AAP26680.1| mandelate racemase/muconate lactonizing enzyme family protein [Bacillus anthracis str. Ames]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>47528143</td><td>>gi|47528143|ref|YP_019492.1| mandelate racemase/muconate lactonizing enzyme family protein [Bacillus anthracis str. 'Ames Ancestor']</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>30262817</td><td>>gi|30262817|ref|NP_845194.1| mandelate racemase/muconate lactonizing enzyme family protein [Bacillus anthracis str. Ames]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>65320143</td><td>>gi|65320143|ref|ZP_00393102.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Bacillus anthracis str. A2012]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>56680164</td><td>>gi|56680164|gb|AAV96830.1| mandelate racemase/muconate lactonizing enzyme family protein [Silicibacter pomeroyi DSS-3]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>56698427</td><td>>gi|56698427|ref|YP_168801.1| mandelate racemase/muconate lactonizing enzyme family protein [Silicibacter pomeroyi DSS-3]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>42781935</td><td>>gi|42781935|ref|NP_979182.1| mandelate racemase/muconate lactonizing enzyme family protein [Bacillus cereus ATCC 10987]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>42737859</td><td>>gi|42737859|gb|AAS41790.1| mandelate racemase/muconate lactonizing enzyme family protein [Bacillus cereus ATCC 10987]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>83951112</td><td>>gi|83951112|ref|ZP_00959845.1| mandelate racemase/muconate lactonizing enzyme family protein [Roseovarius nubinhibens ISM]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>83839011</td><td>>gi|83839011|gb|EAP78307.1| mandelate racemase/muconate lactonizing enzyme family protein [Roseovarius nubinhibens ISM]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>47567668</td><td>>gi|47567668|ref|ZP_00238378.1| mandelate racemase/muconate lactonizing enzyme family protein [Bacillus cereus G9241]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>47555645</td><td>>gi|47555645|gb|EAL13986.1| mandelate racemase/muconate lactonizing enzyme family protein [Bacillus cereus G9241]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>75857840</td><td>>gi|75857840|ref|ZP_00765452.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Vibrio sp. Ex25]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>49609626</td><td>>gi|49609626|emb|CAG73059.1| putative mandelate racemase / muconate lactonizing enzyme family protein [Erwinia carotovora subsp. atroseptica SCRI1043]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>50119100</td><td>>gi|50119100|ref|YP_048267.1| putative mandelate racemase / muconate lactonizing enzyme family protein [Erwinia carotovora subsp. atroseptica SCRI1043]</td><td></td><td></td><td>x</td><td>x</td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
48788203	>gi|48788203|ref|ZP_00284182.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia fungorum LB400]			x	x
48784065	>gi|48784065|ref|ZP_00280446.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia fungorum LB400]			x	x
46163636	>gi|46163636|ref|ZP_00135767.2| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Pseudomonas aeruginosa UCBPP-PA14]			x	x
84320738	>gi|84320738|ref|ZP_00969107.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Pseudomonas aeruginosa C3719]			x	x
84326835	>gi|84326835|ref|ZP_00974859.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Pseudomonas aeruginosa 2192]			x	x
84353826	>gi|84353826|ref|ZP_00978746.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia cenocepacia PC184]			x	x
67647913	>gi|67647913|ref|ZP_00446149.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia mallei NCTC 10247]			x	x
67641750	>gi|67641750|ref|ZP_00440518.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia mallei GB8 horse 4]			x	x
67636965	>gi|67636965|ref|ZP_00435907.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia mallei 10399]			x	x
85064052	>gi|85064052|ref|ZP_01024906.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia mallei 10229]			x	x
84521164	>gi|84521164|ref|ZP_01008301.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia mallei SAVP1]			x	x

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
83624267	>gi|83624267|ref|ZP_00934518.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia mallei JHU]			x	x
83620360	>gi|83620360|ref|ZP_00930781.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia mallei FMH]			x	x
67740097	>gi|67740097|ref|ZP_00490598.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia pseudomallei 668]			x	x
67754538	>gi|67754538|ref|ZP_00493445.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia pseudomallei Pasteur]			x	x
67763500	>gi|67763500|ref|ZP_00502196.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia pseudomallei S13]			x	x
67682431	>gi|67682431|ref|ZP_00476662.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia pseudomallei 1710a]			x	x
67674151	>gi|67674151|ref|ZP_00470914.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia pseudomallei 1655]			x	x
83677234	>gi|83677234|ref|ZP_00938989.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia pseudomallei 406e]			x	x
82538237	>gi|82538237|ref|ZP_00897231.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia pseudomallei 1106b]			x	x
82530183	>gi|82530183|ref|ZP_00889418.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia pseudomallei 1106a]			x	x
67546464	>gi|67546464|ref|ZP_00424377.1| Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Burkholderia vietnamiensis G4]			x	x

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
67532188	>gi|67532188|gb|EAM28980.1| Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Burkholderia vietnamiensis G4]			x	x
21325172	>gi|21325172|dbj|BAB99794.1| O-succinylbenzoate synthase and related enzymes [Corynebacterium glutamicum ATCC 13032]			x	x
84352742	>gi|84352742|ref|ZP_00977691.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia cenocepacia PC184]			x	x
84359310	>gi|84359310|ref|ZP_00984058.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia dolosa AUO158]			x	x
77634427	>gi|77634427|ref|ZP_00796528.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Yersinia pestis Angola]			x	x
77628795	>gi|77628795|ref|ZP_00791381.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Yersinia pseudotuberculosis IP 31758]			x	x
62289215	>gi|62289215|ref|YP_221008.1| mandelate racemase/muconate lactonizing enzyme domain protein [Brucella abortus biovar 1 str. 9-941]			x	x
62195347	>gi|62195347|gb|AAX73647.1| mandelate racemase/muconate lactonizing enzyme domain protein [Brucella abortus biovar 1 str. 9-941]			x	x
82735350	>gi|82735350|ref|ZP_00898213.1| mandelate racemase/muconate lactonizing enzyme family protein [Pseudomonas putida F1]			x	x
82718025	>gi|82718025|gb|EAP53076.1| mandelate racemase/muconate lactonizing enzyme family protein [Pseudomonas putida F1]			x	x
48785521	>gi|48785521|ref|ZP_00281771.1| COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Burkholderia fungorum LB400]			x	x
26989550	>gi|26989550|ref|NP_744975.1| mandelate racemase/muconate lactonizing enzyme family protein [Pseudomonas putida KT2440]			x	x
24984426	>gi|24984426|gb|AAN68439.1| mandelate racemase/muconate lactonizing enzyme family protein [Pseudomonas putida KT2440]			x	x

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
66852952	>gi|66852952|gb|EAL93276.1| mandelate racemase/muconate lactonizing enzyme family protein [Aspergillus fumigatus Af293]			x	x
71554284	>gi|71554284|gb|AAZ33495.1| phosphatase, YrbI family [Pseudomonas syringae pv. phaseolicola 1448A]			x	x
71733731	>gi|71733731|ref|YP_276269.1| phosphatase, YrbI family [Pseudomonas syringae pv. phaseolicola 1448A]			x	x
28871584	>gi|28871584|ref|NP_794203.1| phosphatase, YrbI family [Pseudomonas syringae pv. tomato str. DC3000]			x	x
28854836	>gi|28854836|gb|AAO57898.1| phosphatase, YrbI family [Pseudomonas syringae pv. tomato str. DC3000]			x	x
16273566	>gi|16273566|ref|NP_439821.1| phosphatase [Haemophilus influenzae Rd KW20]			x	x
77381091	>gi|77381091|gb|ABA72604.1| Phosphatase kdsC [Pseudomonas fluorescens PfO-1]			x	x
77457088	>gi|77457088|ref|YP_346593.1| Phosphatase kdsC [Pseudomonas fluorescens PfO-1]			x	x
26987692	>gi|26987692|ref|NP_743117.1| phosphatase, YrbI family [Pseudomonas putida KT2440]			x	x
24982378	>gi|24982378|gb|AAN66581.1| phosphatase, YrbI family [Pseudomonas putida KT2440]			x	x
82735971	>gi|82735971|ref|ZP_00898832.1| HAD-superfamily hydrolase subfamily IIIA:Phosphatase kdsC [Pseudomonas putida F1]			x	x
82716958	>gi|82716958|gb|EAP52011.1| HAD-superfamily hydrolase subfamily IIIA:Phosphatase kdsC [Pseudomonas putida F1]			x	x
67156187	>gi|67156187|ref|ZP_00417813.1| HAD-superfamily hydrolase, subfamily IIIA:Phosphatase YrbI [Azotobacter vinelandii AvOP]			x	x
67086517	>gi|67086517|gb|EAM05986.1| HAD-superfamily hydrolase, subfamily IIIA:Phosphatase YrbI [Azotobacter vinelandii AvOP]			x	x
66047370	>gi|66047370|ref|YP_237211.1| HAD-superfamily hydrolase, subfamily IIIA:Phosphatase YrbI [Pseudomonas syringae pv. syringae B728a]			x	x
63258077	>gi|63258077|gb|AAY39173.1| HAD-superfamily hydrolase, subfamily IIIA:Phosphatase YrbI [Pseudomonas syringae pv. syringae B728a]			x	x

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
33632245	>gi|33632245|emb|CAE06701.1| possible phosphatase [Synechococcus sp. WH 8102]			x	x
33864722	>gi|33864722|ref|NP_896281.1| possible phosphatase [Synechococcus sp. WH 8102]			x	x
78196193	>gi|78196193|gb|ABB33958.1| phosphatase kdsC [Synechococcus sp. CC9605]			x	x
78211734	>gi|78211734|ref|YP_380513.1| phosphatase kdsC [Synechococcus sp. CC9605]			x	x
78168088	>gi|78168088|gb|ABB25185.1| Phosphatase kdsC [Synechococcus sp. CC9902]			x	x
78183794	>gi|78183794|ref|YP_376228.1| Phosphatase kdsC [Synechococcus sp. CC9902]			x	x
48787727	>gi|48787727|ref|ZP_00283706.1| COG1011: Predicted hydrolase (HAD superfamily) [Burkholderia fungorum LB400]			x	x
68559621	>gi|68559621|ref|ZP_00598953.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Ralstonia metallidurans CH34]			x	x
68526065	>gi|68526065|gb|EAN49039.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Ralstonia metallidurans CH34]			x	x
67680298	>gi|67680298|ref|ZP_00474869.1| COG1011: Predicted hydrolase (HAD superfamily) [Burkholderia pseudomallei 1710a]			x	x
52210214	>gi|52210214|emb|CAH36193.1| putative dehalogenase [Burkholderia pseudomallei K96243]			x	x
53719800	>gi|53719800|ref|YP_108786.1| putative dehalogenase [Burkholderia pseudomallei K96243]			x	x
3108343	>gi|3108343|gb|AAC61260.1| sesquiterpene cyclase [Capsicum annuum]			x	x
75704592	>gi|75704592|gb|ABA24268.1| Terpene synthase [Anabaena variabilis ATCC 29413]			x	x
75910867	>gi|75910867|ref|YP_325163.1| Terpene synthase [Anabaena variabilis ATCC 29413]			x	x
69926775	>gi|69926775|ref|ZP_00624246.1| Terpene synthase [Nitrobacter hamburgensis X14]			x	x
69144438	>gi|69144438|gb|EAN62925.1| Terpene synthase [Nitrobacter hamburgensis X14]			x	x

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
67920371	>gi|67920371|ref|ZP_00513891.1| Terpene synthase [Crocosphaera watsonii WH 8501]			x	x
67664823	>gi|67664823|ref|ZP_00462093.1| Terpene synthase [Burkholderia cenocepacia HI2424]			x	x
67654865	>gi|67654865|ref|ZP_00452252.1| Terpene synthase [Burkholderia cenocepacia AU 1054]			x	x
67101530	>gi|67101530|gb|EAM18670.1| Terpene synthase [Burkholderia cenocepacia HI2424]			x	x
67097003	>gi|67097003|gb|EAM14525.1| Terpene synthase [Burkholderia cenocepacia AU 1054]			x	x
71676599	>gi|71676599|ref|ZP_00674340.1| Terpene synthase [Trichodesmium erythraeum IMS101]			x	x
71670279	>gi|71670279|gb|EAO26948.1| Terpene synthase [Trichodesmium erythraeum IMS101]			x	x
74018822	>gi|74018822|ref|ZP_00689442.1| Terpene synthase [Burkholderia ambifaria AMMD]			x	x
72608755	>gi|72608755|gb|EAO44707.1| Terpene synthase [Burkholderia ambifaria AMMD]			x	x
67544402	>gi|67544402|ref|ZP_00422330.1| Terpene synthase [Burkholderia vietnamiensis G4]			x	x
67534159	>gi|67534159|gb|EAM30906.1| Terpene synthase [Burkholderia vietnamiensis G4]			x	x
68554434	>gi|68554434|ref|ZP_00593779.1| Terpene synthase [Ralstonia metallidurans CH34]			x	x
68531108	>gi|68531108|gb|EAN54069.1| Terpene synthase [Ralstonia metallidurans CH34]			x	x
71838437	>gi|71838437|ref|ZP_00678196.1| Terpene synthase [Pelobacter propionicus DSM 2379]			x	x
71741010	>gi|71741010|gb|EAO36169.1| Terpene synthase [Pelobacter propionicus DSM 2379]			x	x
71546746	>gi|71546746|ref|ZP_00667512.1| Terpene synthase [Syntrophobacter fumaroxidans MPOB]			x	x

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
71487530	>gi|71487530|gb|EAO19978.1| Terpene synthase [Syntrophobacter fumaroxidans MPOB]			x	x
71551144	>gi|71551144|ref|ZP_00671141.1| Terpene synthase [Nitrosomonas eutropha C71]			x	x
71483744	>gi|71483744|gb|EAO16327.1| Terpene synthase [Nitrosomonas eutropha C71]			x	x
68231600	>gi|68231600|ref|ZP_00570765.1| Terpene synthase [Frankia sp. EAN1pec]			x	x
68200793	>gi|68200793|gb|EAN15000.1| Terpene synthase [Frankia sp. EAN1pec]			x	x
68231155	>gi|68231155|ref|ZP_00570328.1| Terpene synthase [Frankia sp. EAN1pec]			x	x
68201242	>gi|68201242|gb|EAN15441.1| Terpene synthase [Frankia sp. EAN1pec]			x	x
68558757	>gi|68558757|ref|ZP_00598094.1| Terpene synthase [Ralstonia metallidurans CH34]			x	x
68527124	>gi|68527124|gb|EAN50093.1| Terpene synthase [Ralstonia metallidurans CH34]			x	x
74017366	>gi|74017366|ref|ZP_00687990.1| Terpene synthase [Burkholderia ambifaria AMMD]			x	x
72609994	>gi|72609994|gb|EAO45942.1| Terpene synthase [Burkholderia ambifaria AMMD]			x	x
67666427	>gi|67666427|ref|ZP_00463675.1| Terpene synthase [Burkholderia cenocepacia HI2424]			x	x
67656569	>gi|67656569|ref|ZP_00453951.1| Terpene synthase [Burkholderia cenocepacia AU 1054]			x	x
67100039	>gi|67100039|gb|EAM17201.1| Terpene synthase [Burkholderia cenocepacia HI2424]			x	x
67095754	>gi|67095754|gb|EAM13281.1| Terpene synthase [Burkholderia cenocepacia AU 1054]			x	x
71546164	>gi|71546164|ref|ZP_00667005.1| Terpene synthase [Syntrophobacter fumaroxidans MPOB]			x	x
71488020	>gi|71488020|gb|EAO20454.1| Terpene synthase [Syntrophobacter fumaroxidans MPOB]			x	x

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
76676331	>gi|76676331|ref|XP_584912.2| PREDICTED: similar to methylmalonyl-CoA epimerase [Bos taurus]			x	x
62640426	>gi|62640426|ref|XP_215213.2| PREDICTED: similar to Methylmalonyl-CoA epimerase, mitochondrial precursor (DL-methylmalonyl-CoA racemase) [Rattus norvegicus]			x	x
28374346	>gi|28374346|gb|AAH46075.1| Similar to 4-hydroxyphenylpyruvate dioxygenase [Danio rerio]			x	x
72024564	>gi|72024564|ref|XP_798672.1| PREDICTED: similar to 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) [Strongylocentrotus purpuratus]			x	x
154989	>gi|154989|gb|AAA98399.1| fosfomycin-resistance protein [Serratia marcescens]			x	x
46014944	>gi|46014944|pdb|1NPB|F Chain F, Crystal Structure Of The Fosfomycin Resistance Protein From Transposon Tn2921			x	x
46014943	>gi|46014943|pdb|1NPB|E Chain E, Crystal Structure Of The Fosfomycin Resistance Protein From Transposon Tn2921			x	x
46014942	>gi|46014942|pdb|1NPB|D Chain D, Crystal Structure Of The Fosfomycin Resistance Protein From Transposon Tn2921			x	x
46014941	>gi|46014941|pdb|1NPB|C Chain C, Crystal Structure Of The Fosfomycin Resistance Protein From Transposon Tn2921			x	x
46014940	>gi|46014940|pdb|1NPB|B Chain B, Crystal Structure Of The Fosfomycin Resistance Protein From Transposon Tn2921			x	x
46014939	>gi|46014939|pdb|1NPB|A Chain A, Crystal Structure Of The Fosfomycin Resistance Protein From Transposon Tn2921			x	x
320413	>gi|320413|pir||A60635 glutathione transferase (EC 2.5.1.18), fosfomycin-modifying - Escherichia coli plasmid pSU961 transposon Tn2921			x	x
9947049	>gi|9947049|gb|AAG04518.1| probable fosfomycin resistance protein [Pseudomonas aeruginosa PAO1]			x	x
15596326	>gi|15596326|ref|NP_249820.1| probable fosfomycin resistance protein [Pseudomonas aeruginosa PAO1]			x	x
42543104	>gi|42543104|pdb|1NNR|B Chain B, Crystal Structure Of A Probable Fosfomycin Resistance Protein (Pa1129) From Pseudomonas Aeruginosa With Sulfate Present In The Active Site			x	x

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
42543103	>gi|42543103|pdb|1NNR|A Chain A, Crystal Structure Of A Probable Fosfomycin Resistance Protein (Pa1129) From Pseudomonas Aeruginosa With Sulfate Present In The Active Site			x	x
50740506	>gi|50740506|ref|XP_419481.1| PREDICTED: similar to glyoxylase 1; glyoxalase 1 [Gallus gallus]			x	x
79317664	>gi|79317664|ref|NP_001031025.1| ATGLX1 (GLYOXALASE I HOMOLOG); lactoylglutathione lyase [Arabidopsis thaliana]			x	x
79587736	>gi|79587736|ref|NP_849644.2| ATGLX1 (GLYOXALASE I HOMOLOG); lactoylglutathione lyase [Arabidopsis thaliana]			x	x
30682443	>gi|30682443|ref|NP_849643.1| ATGLX1 (GLYOXALASE I HOMOLOG); lactoylglutathione lyase [Arabidopsis thaliana]			x	x
15221116	>gi|15221116|ref|NP_172648.1| ATGLX1 (GLYOXALASE I HOMOLOG); lactoylglutathione lyase [Arabidopsis thaliana]			x	x
21593459	>gi|21593459|gb|AAM65426.1| lactoylglutathione lyase-like protein [Arabidopsis thaliana]			x	x
11094299	>gi|11094299|dbj|BAB17665.1| Glyoxalase I homolog [Arabidopsis thaliana]			x	x
73972779	>gi|73972779|ref|XP_532129.2| PREDICTED: similar to glyoxylase 1 [Canis familiaris]			x	x
84323805	>gi|84323805|ref|ZP_00971872.1| COG0346: Lactoylglutathione lyase and related lyases [Pseudomonas aeruginosa 2192]			x	x
84317645	>gi|84317645|ref|ZP_00966083.1| COG0346: Lactoylglutathione lyase and related lyases [Pseudomonas aeruginosa C3719]			x	x
53726632	>gi|53726632|ref|ZP_00141583.2| COG0346: Lactoylglutathione lyase and related lyases [Pseudomonas aeruginosa UCBPP-PA14]			x	x
72014470	>gi|72014470|ref|XP_782938.1| PREDICTED: similar to Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase) [Strongylocentrotus purpuratus]			x	x
47573157	>gi|47573157|ref|ZP_00243196.1| COG0346: Lactoylglutathione lyase and related lyases [Rubrivivax gelatinosus PM1]			x	x
84362813	>gi|84362813|ref|ZP_00987425.1| COG0346: Lactoylglutathione lyase and related lyases [Burkholderia dolosa AUO158]			x	x

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
84355685	>gi|84355685|ref|ZP_00980560.1| COG0346: Lactoylglutathione lyase and related lyases [Burkholderia cenocepacia PC184]			x	x
75829851	>gi|75829851|ref|ZP_00759141.1| COG0346: Lactoylglutathione lyase and related lyases [Vibrio cholerae MO10]			x	x
75826317	>gi|75826317|ref|ZP_00755752.1| COG0346: Lactoylglutathione lyase and related lyases [Vibrio cholerae O395]			x	x
75814530	>gi|75814530|ref|ZP_00745106.1| COG0346: Lactoylglutathione lyase and related lyases [Vibrio cholerae V52]			x	x
23128141	>gi|23128141|ref|ZP_00109995.1| COG0346: Lactoylglutathione lyase and related lyases [Nostoc punctiforme PCC 73102]			x	x
48863527	>gi|48863527|ref|ZP_00317421.1| COG0346: Lactoylglutathione lyase and related lyases [Microbulbifer degradans 2-40]			x	x
67647704	>gi|67647704|ref|ZP_00445943.1| COG0346: Lactoylglutathione lyase and related lyases [Burkholderia mallei NCTC 10247]			x	x
67641456	>gi|67641456|ref|ZP_00440234.1| COG0346: Lactoylglutathione lyase and related lyases [Burkholderia mallei GB8 horse 4]			x	x
85066589	>gi|85066589|ref|ZP_01027442.1| COG0346: Lactoylglutathione lyase and related lyases [Burkholderia mallei 10229]			x	x
84521850	>gi|84521850|ref|ZP_01008986.1| COG0346: Lactoylglutathione lyase and related lyases [Burkholderia mallei SAVP1]			x	x
83676948	>gi|83676948|ref|ZP_00938713.1| COG0346: Lactoylglutathione lyase and related lyases [Burkholderia pseudomallei 406e]			x	x
83625910	>gi|83625910|ref|ZP_00936138.1| COG0346: Lactoylglutathione lyase and related lyases [Burkholderia mallei JHU]			x	x
83620971	>gi|83620971|ref|ZP_00931385.1| COG0346: Lactoylglutathione lyase and related lyases [Burkholderia mallei FMH]			x	x
82532706	>gi|82532706|ref|ZP_00891916.1| COG0346: Lactoylglutathione lyase and related lyases [Burkholderia pseudomallei 1106a]			x	x
75190690	>gi|75190690|ref|ZP_00703957.1| COG0346: Lactoylglutathione lyase and related lyases [Escherichia coli E24377A]			x	x
75257069	>gi|75257069|ref|ZP_00728629.1| COG0346: Lactoylglutathione lyase and related lyases [Escherichia coli E22]			x	x

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>75234962</td><td>>gi|75234962|ref|ZP_00719241.1| COG0346: Lactoylglutathione lyase and related lyases [Escherichia coli E110019]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>75230901</td><td>>gi|75230901|ref|ZP_00717350.1| COG0346: Lactoylglutathione lyase and related lyases [Escherichia coli B7A]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>75212987</td><td>>gi|75212987|ref|ZP_00712985.1| COG0346: Lactoylglutathione lyase and related lyases [Escherichia coli B171]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>75195730</td><td>>gi|75195730|ref|ZP_00705800.1| COG0346: Lactoylglutathione lyase and related lyases [Escherichia coli HS]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>83587985</td><td>>gi|83587985|ref|ZP_00926611.1| COG0346: Lactoylglutathione lyase and related lyases [Escherichia coli 101-1]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>12515646</td><td>>gi|12515646|gb|AAG56640.1| enzyme; Central intermediary metabolism: Pool, multipurpose conversions of intermed. met'm [Escherichia coli O157:H7 EDL933]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>46164285</td><td>>gi|46164285|ref|ZP_00136888.2| COG0346: Lactoylglutathione lyase and related lyases [Pseudomonas aeruginosa UCBPP-PA14]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>84325798</td><td>>gi|84325798|ref|ZP_00973830.1| COG0346: Lactoylglutathione lyase and related lyases [Pseudomonas aeruginosa 2192]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>84319750</td><td>>gi|84319750|ref|ZP_00968140.1| COG0346: Lactoylglutathione lyase and related lyases [Pseudomonas aeruginosa C3719]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>75238789</td><td>>gi|75238789|ref|ZP_00722773.1| COG0346: Lactoylglutathione lyase and related lyases [Escherichia coli F11]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>72014468</td><td>>gi|72014468|ref|XP_782882.1| PREDICTED: similar to glyoxylase 1 [Strongylocentrotus purpuratus]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>48786604</td><td>>gi|48786604|ref|ZP_00282738.1| COG0346: Lactoylglutathione lyase and related lyases [Burkholderia fungorum LB400]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>75178453</td><td>>gi|75178453|ref|ZP_00698499.1| COG0346: Lactoylglutathione lyase and related lyases [Shigella boydii BS512]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>53692250</td><td>>gi|53692250|ref|ZP_00123583.2| COG0346: Lactoylglutathione lyase and related lyases [Haemophilus somnus 129PT]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>77975304</td><td>>gi|77975304|ref|ZP_00830840.1| COG0346: Lactoylglutathione lyase and related lyases [Yersinia frederiksenii ATCC 33641]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>32029379</td><td>>gi|32029379|ref|ZP_00132412.1| COG0346: Lactoylglutathione lyase and related lyases [Haemophilus somnus 2336]</td><td></td><td></td><td>x</td><td>x</td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
33237211	>gi|33237211|gb|AAP99280.1| Lactoylglutathione lyase family enzyme [Prochlorococcus marinus subsp. marinus str. CCMP1375]			x	x
33239686	>gi|33239686|ref|NP_874628.1| Lactoylglutathione lyase family enzyme [Prochlorococcus marinus subsp. marinus str. CCMP1375]			x	x
77629366	>gi|77629366|ref|ZP_00791952.1| COG0346: Lactoylglutathione lyase and related lyases [Yersinia pseudotuberculosis IP 31758]			x	x
77633722	>gi|77633722|ref|ZP_00795841.1| COG0346: Lactoylglutathione lyase and related lyases [Yersinia pestis Angola]			x	x
77959188	>gi|77959188|ref|ZP_00823210.1| COG0346: Lactoylglutathione lyase and related lyases [Yersinia bercovieri ATCC 43970]			x	x
42630624	>gi|42630624|ref|ZP_00156163.1| COG0346: Lactoylglutathione lyase and related lyases [Haemophilus influenzae R2866]			x	x
68057128	>gi|68057128|gb|AAX87381.1| lactoylglutathione lyase [Haemophilus influenzae 86-028NP]			x	x
68248929	>gi|68248929|ref|YP_248041.1| lactoylglutathione lyase [Haemophilus influenzae 86-028NP]			x	x
16272276	>gi|16272276|ref|NP_438488.1| lactoylglutathione lyase [Haemophilus influenzae Rd KW20]			x	x
1573292	>gi|1573292|gb|AAC21986.1| lactoylglutathione lyase (gloA) [Haemophilus influenzae Rd KW20]			x	x
1246363	>gi|1246363|gb|AAA93512.1| cytosine deaminase:uracil phosphoribosyltransferase fusion protein			x	
1246360	>gi|1246360|gb|AAA93510.1| cytosine deaminase:uracil phosphoribosyltransferase fusion protein			x	
1246357	>gi|1246357|gb|AAA93508.1| cytosine deaminase:uracil phosphoribosyltransferase fusion protein			x	
1246354	>gi|1246354|gb|AAA93506.1| cytosine deaminase:uracil phosphoribosyltransferase fusion protein			x	
75211133	>gi|75211133|ref|ZP_00711240.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Escherichia coli B171]			x	
1657533	>gi|1657533|gb|AAB18061.1| cytosine deaminase [Escherichia coli]			x	
55669650	>gi|55669650|pdb|1RAK|A Chain A, Bacterial Cytosine Deaminase D314s Mutant Bound To 5-Fluoro- 4-(S)-Hydroxyl-3,4-Dihydropyrimidine.			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
55669647	>gi|55669647|pdb|1R9Z|A Chain A, Bacterial Cytosine Deaminase D314s Mutant			x	
26106750	>gi|26106750|gb|AAN78935.1| Cytosine deaminase [Escherichia coli CFT073]			x	
26246352	>gi|26246352|ref|NP_752391.1| cytosine deaminase [Escherichia coli CFT073]			x	
75257636	>gi|75257636|ref|ZP_00729127.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Escherichia coli E22]			x	
75194561	>gi|75194561|ref|ZP_00704631.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Escherichia coli HS]			x	
75231104	>gi|75231104|ref|ZP_00717526.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Escherichia coli B7A]			x	
75189411	>gi|75189411|ref|ZP_00702678.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Escherichia coli E24377A]			x	
55669649	>gi|55669649|pdb|1RA5|A Chain A, Bacterial Cytosine Deaminase D314a Mutant Bound To 5-Fluoro- 4-(S)-Hydroxyl-3,4-Dihydropyrimidine.			x	
55669646	>gi|55669646|pdb|1R9Y|A Chain A, Bacterial Cytosine Deaminase D314a Mutant			x	
55669648	>gi|55669648|pdb|1RA0|A Chain A, Bacterial Cytosine Deaminase D314g Mutant Bound To 5-Fluoro- 4-(S)-Hydroxy-3,4-Dihydropyrimidine.			x	
55669645	>gi|55669645|pdb|1R9X|A Chain A, Bacterial Cytosine Deaminase D314g Mutant			x	
581052	>gi|581052|emb|CAA45196.1| cytosine deaminase [Escherichia coli]			x	
1786531	>gi|1786531|gb|AAC73440.1| cytosine deaminase [Escherichia coli K12]			x	
85674479	>gi|85674479|dbj|BAE76119.1| cytosine deaminase [Escherichia coli W3110]			x	
33087247	>gi|33087247|gb|AAP92816.1| cytosine deaminase [Escherichia coli]			x	
7239817	>gi|7239817|gb|AAB25761.2| cytosine deaminase; CD [Escherichia coli]			x	
16128322	>gi|16128322|ref|NP_414871.1| cytosine deaminase [Escherichia coli K12]			x	
83586373	>gi|83586373|ref|ZP_00925008.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Escherichia coli 101-1]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
116845	>gi|116845|sp|P25524|CODA_ECOLI Cytosine deaminase (Cytosine aminohydrolase)			x	
75238478	>gi|75238478|ref|ZP_00722472.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Escherichia coli F11]			x	
18655482	>gi|18655482|pdb|1K70|A Chain A, The Structure Of Escherichia Coli Cytosine Deaminase Bound To 4-Hydroxy-3,4-Dihydro-1h-Pyrimidin-2-One			x	
18655481	>gi|18655481|pdb|1K6W|A Chain A, The Structure Of Escherichia Coli Cytosine Deaminase			x	
62181842	>gi|62181842|ref|YP_218259.1| cytosine deaminase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]			x	
62129475	>gi|62129475|gb|AAX67178.1| putative cytosine deaminase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]			x	
13359847	>gi|13359847|dbj|BAB33813.1| cytosine deaminase [Escherichia coli O157:H7]			x	
15829644	>gi|15829644|ref|NP_308417.1| cytosine deaminase [Escherichia coli O157:H7]			x	
12513168	>gi|12513168|gb|AAG54686.1| cytosine deaminase [Escherichia coli O157:H7 EDL933]			x	
15800066	>gi|15800066|ref|NP_286078.1| cytosine deaminase [Escherichia coli O157:H7 EDL933]			x	
77634604	>gi|77634604|ref|ZP_00796701.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Yersinia pestis Angola]			x	
77631143	>gi|77631143|ref|ZP_00793729.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Yersinia pseudotuberculosis IP 31758]			x	
45434881	>gi|45434881|gb|AAS60442.1| cytosine deaminase [Yersinia pestis biovar Medievalis str. 91001]			x	
15978267	>gi|15978267|emb|CAC89025.1| cytosine deaminase [Yersinia pestis CO92]			x	
21960948	>gi|21960948|gb|AAM87490.1| cytosine deaminase [Yersinia pestis KIM]			x	
22127816	>gi|22127816|ref|NP_671239.1| cytosine deaminase [Yersinia pestis KIM]			x	
45440026	>gi|45440026|ref|NP_991565.1| cytosine deaminase [Yersinia pestis biovar Medievalis str. 91001]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
16120505	>gi|16120505|ref|NP_403818.1| cytosine deaminase [Yersinia pestis CO92]			x	
56129520	>gi|56129520|gb|AAV79026.1| cytosine deaminase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]			x	
56415263	>gi|56415263|ref|YP_152338.1| cytosine deaminase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]			x	
16504399	>gi|16504399|emb|CAD07851.1| cytosine deaminase [Salmonella enterica subsp. enterica serovar Typhi]			x	
29139220	>gi|29139220|gb|AAO70787.1| cytosine deaminase [Salmonella enterica subsp. enterica serovar Typhi Ty2]			x	
16762096	>gi|16762096|ref|NP_457713.1| cytosine deaminase [Salmonella enterica subsp. enterica serovar Typhi str. CT18]			x	
29143585	>gi|29143585|ref|NP_806927.1| cytosine deaminase [Salmonella enterica subsp. enterica serovar Typhi Ty2]			x	
25512543	>gi|25512543|pir||AE0907 cytosine deaminase [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)			x	
45356869	>gi|45356869|gb|AAS58473.1| cytosine deaminase [Escherichia coli]			x	
16421892	>gi|16421892|gb|AAL22203.1| putative cytosine deaminase [Salmonella typhimurium LT2]			x	
16766629	>gi|16766629|ref|NP_462244.1| cytosine deaminase [Salmonella typhimurium LT2]			x	
77978185	>gi|77978185|ref|ZP_00833617.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Yersinia intermedia ATCC 29909]			x	
51591311	>gi|51591311|emb|CAH22977.1| cytosine deaminase [Yersinia pseudotuberculosis IP 32953]			x	
51598029	>gi|51598029|ref|YP_072220.1| cytosine deaminase [Yersinia pseudotuberculosis IP 32953]			x	
77975030	>gi|77975030|ref|ZP_00830567.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Yersinia frederiksenii ATCC 33641]			x	
51493749	>gi|51493749|gb|AAU04862.1| cytosine deaminase [Tamarix chinensis]			x	
15602430	>gi|15602430|ref|NP_245502.1| cytosine deaminase [Pasteurella multocida subsp. multocida str. Pm70]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
77958279	>gi|77958279|ref|ZP_00822315.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Yersinia bercovieri ATCC 43970]			x	
53727142	>gi|53727142|ref|ZP_00347786.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Pseudomonas aeruginosa UCBPP-PA14]			x	
9946295	>gi|9946295|gb|AAG03826.1| cytosine deaminase [Pseudomonas aeruginosa PAO1]			x	
15595634	>gi|15595634|ref|NP_249128.1| cytosine deaminase [Pseudomonas aeruginosa PAO1]			x	
84324317	>gi|84324317|ref|ZP_00972376.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Pseudomonas aeruginosa 2192]			x	
77962698	>gi|77962698|ref|ZP_00826515.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Yersinia mollaretii ATCC 43969]			x	
14524455	>gi|14524455|gb|AAK65940.1| putative CodA1 cytosine deaminase [Sinorhizobium meliloti 1021]			x	
16263735	>gi|16263735|ref|NP_436528.1| cytosine deaminase [Sinorhizobium meliloti 1021]			x	
59711138	>gi|59711138|ref|YP_203914.1| cytosine deaminase [Vibrio fischeri ES114]			x	
59479239	>gi|59479239|gb|AAW85026.1| cytosine deaminase [Vibrio fischeri ES114]			x	
28809611	>gi|28809611|dbj|BAC62586.1| putative cytosine deaminase [Vibrio parahaemolyticus RIMD 2210633]			x	
28901098	>gi|28901098|ref|NP_800753.1| cytosine deaminase [Vibrio parahaemolyticus RIMD 2210633]			x	
48787837	>gi|48787837|ref|ZP_00283816.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Burkholderia fungorum LB400]			x	
86144452	>gi|86144452|ref|ZP_01062784.1| cytosine deaminase [Vibrio sp. MED222]			x	
85837351	>gi|85837351|gb|EAQ55463.1| cytosine deaminase [Vibrio sp. MED222]			x	
75854832	>gi|75854832|ref|ZP_00762503.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Vibrio sp. Ex25]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
27358767	>gi|27358767|gb|AAO07716.1| Cytosine deaminase [Vibrio vulnificus CMCP6]			x	
27367199	>gi|27367199|ref|NP_762726.1| cytosine deaminase [Vibrio vulnificus CMCP6]			x	
37201459	>gi|37201459|dbj|BAC97281.1| cytosine deaminase [Vibrio vulnificus YJ016]			x	
37676915	>gi|37676915|ref|NP_937311.1| cytosine deaminase [Vibrio vulnificus YJ016]			x	
46916477	>gi|46916477|emb|CAG23242.1| putative cytosine deaminase [Photobacterium profundum SS9]			x	
54303049	>gi|54303049|ref|YP_133042.1| cytosine deaminase [Photobacterium profundum SS9]			x	
84387544	>gi|84387544|ref|ZP_00990562.1| cytosine deaminase [Vibrio splendidus 12B01]			x	
84377592	>gi|84377592|gb|EAP94457.1| cytosine deaminase [Vibrio splendidus 12B01]			x	
17428610	>gi|17428610|emb|CAD15296.1| PROBABLE CYTOSINE DEAMINASE (CYTOSINE AMINOHYDROLASE) PROTEIN [Ralstonia solanacearum]			x	
17546313	>gi|17546313|ref|NP_519715.1| cytosine deaminase [Ralstonia solanacearum GMI1000]			x	
73537826	>gi|73537826|ref|YP_298193.1| cytosine deaminase [Ralstonia eutropha JMP134]			x	
14025224	>gi|14025224|dbj|BAB51825.1| creatinine deaminase [Mesorhizobium loti MAFF303099]			x	
13474471	>gi|13474471|ref|NP_106039.1| cytosine deaminase [Mesorhizobium loti MAFF303099]			x	
83745851	>gi|83745851|ref|ZP_00942908.1| Cytosine deaminase [Ralstonia solanacearum UW551]			x	
83727541	>gi|83727541|gb|EAP74662.1| Cytosine deaminase [Ralstonia solanacearum UW551]			x	
18144416	>gi|18144416|dbj|BAB80462.1| cytosine deaminase [Clostridium perfringens str. 13]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
18309738	>gi|18309738|ref|NP_561672.1| cytosine deaminase [Clostridium perfringens str. 13]			x	
67153359	>gi|67153359|ref|ZP_00415104.1| Cytosine deaminase [Azotobacter vinelandii AvOP]			x	
67087492	>gi|67087492|gb|EAM06958.1| Cytosine deaminase [Azotobacter vinelandii AvOP]			x	
36958684	>gi|36958684|gb|AAQ87152.1| Cytosine deaminase [Rhizobium sp. NGR234]			x	
23336356	>gi|23336356|ref|ZP_00121577.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Bifidobacterium longum DJO10A]			x	
23464639	>gi|23464639|ref|NP_695242.1| cytosine deaminase [Bifidobacterium longum NCC2705]			x	
23325197	>gi|23325197|gb|AAN23878.1| cytosine deaminase [Bifidobacterium longum NCC2705]			x	
86359986	>gi|86359986|ref|YP_471876.1| cytosine deaminase protein [Rhizobium etli CFN 42]			x	
86284088	>gi|86284088|gb|ABC93149.1| cytosine deaminase protein [Rhizobium etli CFN 42]			x	
84318643	>gi|84318643|ref|ZP_00967064.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Pseudomonas aeruginosa C3719]			x	
77388331	>gi|77388331|gb|ABA79516.1| Cytosine deaminase [Rhodobacter sphaeroides 2.4.1]			x	
77463913	>gi|77463913|ref|YP_353417.1| cytosine deaminase [Rhodobacter sphaeroides 2.4.1]			x	
57339189	>gi|57339189|gb|AAW49583.1| cytosine deaminase [Bifidobacterium breve]			x	
28203958	>gi|28203958|gb|AAO36398.1| cytosine deaminase [Clostridium tetani E88]			x	
28211517	>gi|28211517|ref|NP_782461.1| cytosine deaminase [Clostridium tetani E88]			x	
86606249	>gi|86606249|ref|YP_475012.1| cytosine deaminase [Cyanobacteria bacterium Yellowstone A-Prime]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
68345688	>gi|68345688|gb|AAY93294.1| cytosine deaminase [Pseudomonas fluorescens Pf-5]			x	
70731389	>gi|70731389|ref|YP_261130.1| cytosine deaminase [Pseudomonas fluorescens Pf-5]			x	
56912036	>gi|56912036|dbj|BAD66563.1| cytosine deaminase [Bacillus clausii KSM-K16]			x	
56965790	>gi|56965790|ref|YP_177524.1| cytosine deaminase [Bacillus clausii KSM-K16]			x	
86607889	>gi|86607889|ref|YP_476651.1| cytosine deaminase [Cyanobacteria bacterium Yellowstone B-Prime]			x	
85705815	>gi|85705815|ref|ZP_01036912.1| cytosine deaminase [Roseovarius sp. 217]			x	
85669805	>gi|85669805|gb|EAQ24669.1| cytosine deaminase [Roseovarius sp. 217]			x	
15623524	>gi|15623524|dbj|BAB67512.1| 412aa long hypothetical cytosine deaminase [Sulfolobus tokodaii str. 7]			x	
15922734	>gi|15922734|ref|NP_378403.1| hypothetical cytosine deaminase [Sulfolobus tokodaii str. 7]			x	
86135886	>gi|86135886|ref|ZP_01054465.1| Cytosine deaminase [Roseobacter sp. MED193]			x	
85826760	>gi|85826760|gb|EAQ46956.1| Cytosine deaminase [Roseobacter sp. MED193]			x	
84714350	>gi|84714350|ref|ZP_01021815.1| codA, RSc1594; probable cytosine deaminase (cytosine aminohydrolase) protein [Polaromonas naphthalenivorans CJ2]			x	
84693949	>gi|84693949|gb|EAQ19746.1| codA, RSc1594; probable cytosine deaminase (cytosine aminohydrolase) protein [Polaromonas naphthalenivorans CJ2]			x	
82736446	>gi|82736446|ref|ZP_00899304.1| cytosine deaminase [Pseudomonas putida F1]			x	
82716465	>gi|82716465|gb|EAP51521.1| cytosine deaminase [Pseudomonas putida F1]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
67779564	>gi|67779564|gb|EAM39182.1| Cytosine deaminase [Polaromonas sp. JS666]			x	
67908164	>gi|67908164|ref|ZP_00506564.1| Cytosine deaminase [Polaromonas sp. JS666]			x	
26989908	>gi|26989908|ref|NP_745333.1| cytosine deaminase [Pseudomonas putida KT2440]			x	
24984820	>gi|24984820|gb|AAN68797.1| cytosine deaminase [Pseudomonas putida KT2440]			x	
84359748	>gi|84359748|ref|ZP_00984478.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Burkholderia dolosa AUO158]			x	
83952722	>gi|83952722|ref|ZP_00961452.1| cytosine deaminase [Roseovarius nubinhibens ISM]			x	
83835857	>gi|83835857|gb|EAP75156.1| cytosine deaminase [Roseovarius nubinhibens ISM]			x	
13816107	>gi|13816107|gb|AAK42880.1| Cytosine deaminase (codA) [Sulfolobus solfataricus P2]			x	
15899485	>gi|15899485|ref|NP_344090.1| Cytosine deaminase (codA) [Sulfolobus solfataricus P2]			x	
84354363	>gi|84354363|ref|ZP_00979270.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Burkholderia cenocepacia PC184]			x	
67756409	>gi|67756409|ref|ZP_00495293.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Burkholderia pseudomallei Pasteur]			x	
67740000	>gi|67740000|ref|ZP_00490536.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Burkholderia pseudomallei 668]			x	
67682684	>gi|67682684|ref|ZP_00476891.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Burkholderia pseudomallei 1710a]			x	
67673244	>gi|67673244|ref|ZP_00470012.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Burkholderia pseudomallei 1655]			x	
76582641	>gi|76582641|gb|ABA52115.1| cytosine deaminase [Burkholderia pseudomallei 1710b]			x	
76818168	>gi|76818168|ref|YP_337486.1| cytosine deaminase [Burkholderia pseudomallei 1710b]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
83680421	>gi|83680421|ref|ZP_00942127.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Burkholderia pseudomallei 406e]			x	
82537539	>gi|82537539|ref|ZP_00896536.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Burkholderia pseudomallei 1106b]			x	
82531872	>gi|82531872|ref|ZP_00891087.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Burkholderia pseudomallei 1106a]			x	
67664077	>gi|67664077|ref|ZP_00461354.1| Cytosine deaminase [Burkholderia cenocepacia HI2424]			x	
67102341	>gi|67102341|gb|EAM19474.1| Cytosine deaminase [Burkholderia cenocepacia HI2424]			x	
67762588	>gi|67762588|ref|ZP_00501288.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Burkholderia pseudomallei S13]			x	
67649224	>gi|67649224|ref|ZP_00447449.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Burkholderia mallei NCTC 10247]			x	
67643675	>gi|67643675|ref|ZP_00442419.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Burkholderia mallei GB8 horse 4]			x	
67638557	>gi|67638557|ref|ZP_00437493.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Burkholderia mallei 10399]			x	
52212201	>gi|52212201|emb|CAH38221.1| cytosine deaminase [Burkholderia pseudomallei K96243]			x	
85063486	>gi|85063486|ref|ZP_01024340.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Burkholderia mallei 10229]			x	
52423266	>gi|52423266|gb|AAU46836.1| cytosine deaminase [Burkholderia mallei ATCC 23344]			x	
53721787	>gi|53721787|ref|YP_110772.1| cytosine deaminase [Burkholderia pseudomallei K96243]			x	
53717296	>gi|53717296|ref|YP_105363.1| cytosine deaminase [Burkholderia mallei ATCC 23344]			x	
83626280	>gi|83626280|ref|ZP_00936505.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Burkholderia mallei JHU]			x	
83619304	>gi|83619304|ref|ZP_00929742.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Burkholderia mallei FMH]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
83717088	>gi|83717088|ref|YP_439833.1| cytosine deaminase [Burkholderia thailandensis E264]			x	
83650913	>gi|83650913|gb|ABC34977.1| cytosine deaminase [Burkholderia thailandensis E264]			x	
83647817	>gi|83647817|ref|YP_436252.1| Cytosine deaminase and related metal-dependent Hydrolase [Hahella chejuensis KCTC 2396]			x	
83635860	>gi|83635860|gb|ABC31827.1| Cytosine deaminase and related metal-dependent Hydrolase [Hahella chejuensis KCTC 2396]			x	
56679381	>gi|56679381|gb|AAV96047.1| cytosine deaminase, putative [Silicibacter pomeroyi DSS-3]			x	
56697644	>gi|56697644|ref|YP_168014.1| cytosine deaminase [Silicibacter pomeroyi DSS-3]			x	
41324304	>gi|41324304|emb|CAF18644.1| CREATININE DEAMINASE [Corynebacterium glutamicum ATCC 13032]			x	
62388971	>gi|62388971|ref|YP_224373.1| CREATININE DEAMINASE [Corynebacterium glutamicum ATCC 13032]			x	
21322840	>gi|21322840|dbj|BAB97469.1| Cytosine deaminase and related metal-dependent hydrolases [Corynebacterium glutamicum ATCC 13032]			x	
19551325	>gi|19551325|ref|NP_599327.1| cytosine deaminase or related metal-dependent hydrolase [Corynebacterium glutamicum ATCC 13032]			x	
35213096	>gi|35213096|dbj|BAC90469.1| cytosine deaminase [Gloeobacter violaceus PCC 7421]			x	
37522097	>gi|37522097|ref|NP_925474.1| cytosine deaminase [Gloeobacter violaceus PCC 7421]			x	
68560577	>gi|68560577|ref|ZP_00599889.1| Cytosine deaminase [Rubrobacter xylanophilus DSM 9941]			x	
68513294	>gi|68513294|gb|EAN37089.1| Cytosine deaminase [Rubrobacter xylanophilus DSM 9941]			x	
68567500	>gi|68567500|gb|AAY80429.1| cytosine deaminase [Sulfolobus acidocaldarius DSM 639]			x	
70606852	>gi|70606852|ref|YP_255722.1| cytosine deaminase [Sulfolobus acidocaldarius DSM 639]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
23494693	>gi|23494693|dbj|BAC19659.1| putative cytosine deaminase [Corynebacterium efficiens YS-314]			x	
25029405	>gi|25029405|ref|NP_739459.1| putative cytosine deaminase [Corynebacterium efficiens YS-314]			x	
86163518	>gi|86163518|gb|EAQ64793.1| cytosine deaminase [Marinomonas sp. MED121]			x	
2443394	>gi|2443394|dbj|BAA22413.1| creatinine deaminase [Bacillus sp.]			x	
27806933	>gi|27806933|ref|NP_776312.1| adenosine deaminase [Bos taurus]			x	
9652182	>gi|9652182|gb|AAF91430.1| adenosine deaminase; adenosine aminohydrolase; ADA [Bos taurus]			x	
20141178	>gi|20141178|sp|P56658|ADA_BOVIN Adenosine deaminase (Adenosine aminohydrolase)			x	
25955532	>gi|25955532|gb|AAH40226.1| Adenosine deaminase [Homo sapiens]			x	
14043373	>gi|14043373|gb|AAH07678.1| Adenosine deaminase [Homo sapiens]			x	
56208527	>gi|56208527|emb|CAB09782.2| adenosine deaminase [Homo sapiens]			x	
55662027	>gi|55662027|emb|CAH73885.1| adenosine deaminase [Homo sapiens]			x	
28380	>gi|28380|emb|CAA26734.1| adenosine deaminase [Homo sapiens]			x	
47078295	>gi|47078295|ref|NP_000013.2| adenosine deaminase [Homo sapiens]			x	
113339	>gi|113339|sp|P00813|ADA_HUMAN Adenosine deaminase (Adenosine aminohydrolase)			x	
178077	>gi|178077|gb|AAA78791.1| adenosine deaminase			x	
62898355	>gi|62898355|dbj|BAD97117.1| adenosine deaminase variant [Homo sapiens]			x	
224877	>gi|224877|prf||1203203A deaminase a,adenosine			x	
55670514	>gi|55670514|pdb|1W1I|H Chain H, Crystal Structure Of Dipeptidyl Peptidase Iv (Dppiv Or Cd26) In Complex With Adenosine Deaminase			x	
55670513	>gi|55670513|pdb|1W1I|G Chain G, Crystal Structure Of Dipeptidyl Peptidase Iv (Dppiv Or Cd26) In Complex With Adenosine Deaminase			x	
55670512	>gi|55670512|pdb|1W1I|F Chain F, Crystal Structure Of Dipeptidyl Peptidase Iv (Dppiv Or Cd26) In Complex With Adenosine Deaminase			x	
55670511	>gi|55670511|pdb|1W1I|E Chain E, Crystal Structure Of Dipeptidyl Peptidase Iv (Dppiv Or Cd26) In Complex With Adenosine Deaminase			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
75765416	>gi|75765416|pdb|1WXZ|A Chain A, Crystal Structure Of Adenosine Deaminase Ligated With A Potent Inhibitor			x	
75765415	>gi|75765415|pdb|1WXY|A Chain A, Crystal Structure Of Adenosine Deaminase Ligated With A Potent Inhibitor			x	
75765310	>gi|75765310|pdb|1VFL|A Chain A, Adenosine Deaminase			x	
58177005	>gi|58177005|pdb|1V7A|A Chain A, Crystal Structures Of Adenosine Deaminase Complexed With Potent Inhibitors			x	
58177004	>gi|58177004|pdb|1V79|A Chain A, Crystal Structures Of Adenosine Deaminase Complexed With Potent Inhibitors			x	
58177003	>gi|58177003|pdb|1V78|A Chain A, Crystal Structures Of Adenosine Deaminase Complexed With Potent Inhibitors			x	
40889137	>gi|40889137|pdb|1NDZ|A Chain A, Crystal Structure Of Adenosine Deaminase Complexed With Fr235999			x	
40889136	>gi|40889136|pdb|1NDY|A Chain A, Crystal Structure Of Adenosine Deaminase Complexed With Fr230513			x	
40889135	>gi|40889135|pdb|1NDW|A Chain A, Crystal Structure Of Adenosine Deaminase Complexed With Fr221647			x	
40889134	>gi|40889134|pdb|1NDV|A Chain A, Crystal Structure Of Adenosine Deaminase Complexed With Fr117016			x	
55670343	>gi|55670343|pdb|1UML|A Chain A, Crystal Structure Of Adenosine Deaminase Complexed With A Potent Inhibitor Fr233624			x	
55669530	>gi|55669530|pdb|1O5R|A Chain A, Crystal Structure Of Adenosine Deaminase Complexed With A Potent Inhibitor			x	
55669583	>gi|55669583|pdb|1QXL|A Chain A, Crystal Structure Of Adenosine Deaminase Complexed With Fr235380			x	
28373486	>gi|28373486|pdb|1KRM|A Chain A, Crystal Structure Of Bovine Adenosine Deaminase Complexed With 6-Hydroxyl-1,6-Dihydropurine Riboside			x	
19548716	>gi|19548716|gb|AAL90755.1| adenosine deaminase [Mus musculus]			x	
19548714	>gi|19548714|gb|AAL90754.1| adenosine deaminase [Mus musculus]			x	
1657629	>gi|1657629|gb|AAC08442.1| adenosine deaminase [Mus musculus]			x	
6680636	>gi|6680636|ref|NP_031424.1| adenosine deaminase [Mus musculus]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
113340	>gi|113340|sp|P03958|ADA_MOUSE Adenosine deaminase (Adenosine aminohydrolase)			x	
309091	>gi|309091|gb|AAA37173.1| adenosine deaminase (EC 3.5.4.4)			x	
999767	>gi|999767|pdb|2ADA| Adenosine Deaminase (E.C.3.5.4.4) Complexed With 6-Hydroxyl-1,6-Dihydropurine Ribonucleoside			x	
1518868	>gi|1518868|gb|AAB07142.1| adenosine deaminase (ADA) [Mus musculus]			x	
3892031	>gi|3892031|pdb|1A4M|D Chain D, Ada Structure Complexed With Purine Riboside At Ph 7.0			x	
3892030	>gi|3892030|pdb|1A4M|C Chain C, Ada Structure Complexed With Purine Riboside At Ph 7.0			x	
3892029	>gi|3892029|pdb|1A4M|B Chain B, Ada Structure Complexed With Purine Riboside At Ph 7.0			x	
3892028	>gi|3892028|pdb|1A4M|A Chain A, Ada Structure Complexed With Purine Riboside At Ph 7.0			x	
3892027	>gi|3892027|pdb|1A4L|D Chain D, Ada Structure Complexed With Deoxycoformycin At Ph 7.0			x	
3892026	>gi|3892026|pdb|1A4L|C Chain C, Ada Structure Complexed With Deoxycoformycin At Ph 7.0			x	
3892025	>gi|3892025|pdb|1A4L|B Chain B, Ada Structure Complexed With Deoxycoformycin At Ph 7.0			x	
3892024	>gi|3892024|pdb|1A4L|A Chain A, Ada Structure Complexed With Deoxycoformycin At Ph 7.0			x	
493801	>gi|493801|pdb|1ADD| Adenosine Deaminase (E.C.3.5.4.4) Complexed With 1-Deaza-Adenosine (Daa)			x	
56789878	>gi|56789878|gb|AAH88116.1| Adenosine deaminase [Rattus norvegicus]			x	
18426812	>gi|18426812|ref|NP_569083.1| adenosine deaminase [Rattus norvegicus]			x	
20137184	>gi|20137184|sp|Q920P6|ADA_RAT Adenosine deaminase (Adenosine aminohydrolase)			x	
16040979	>gi|16040979|dbj|BAB69691.1| adenosine deaminase [Rattus norvegicus]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
75822633	>gi|75822633|ref|ZP_00752223.1| COG1816: Adenosine deaminase [Vibrio cholerae RC385]			x	
75830675	>gi|75830675|ref|ZP_00759949.1| COG1816: Adenosine deaminase [Vibrio cholerae MO10]			x	
75827993	>gi|75827993|ref|ZP_00757428.1| COG1816: Adenosine deaminase [Vibrio cholerae O395]			x	
75815380	>gi|75815380|ref|ZP_00745892.1| COG1816: Adenosine deaminase [Vibrio cholerae V52]			x	
9657350	>gi|9657350|gb|AAF95890.1| adenosine deaminase [Vibrio cholerae O1 biovar eltor str. N16961]			x	
15642744	>gi|15642744|ref|NP_232377.1| adenosine deaminase [Vibrio cholerae O1 biovar eltor str. N16961]			x	
11266260	>gi|11266260|pir||F82038 adenosine deaminase VC2751 [imported] - Vibrio cholerae (strain N16961 serogroup O1)			x	
20137242	>gi|20137242|sp|Q9KNI7|ADD_VIBCH Adenosine deaminase (Adenosine aminohydrolase)			x	
75820650	>gi|75820650|ref|ZP_00750693.1| COG1816: Adenosine deaminase [Vibrio cholerae V51]			x	
16502746	>gi|16502746|emb|CAD01904.1| adenosine deaminase [Salmonella enterica subsp. enterica serovar Typhi]			x	
29137418	>gi|29137418|gb|AAO68981.1| adenosine deaminase [Salmonella enterica subsp. enterica serovar Typhi Ty2]			x	
16760450	>gi|16760450|ref|NP_456067.1| adenosine deaminase [Salmonella enterica subsp. enterica serovar Typhi str. CT18]			x	
29141790	>gi|29141790|ref|NP_805132.1| adenosine deaminase [Salmonella enterica subsp. enterica serovar Typhi Ty2]			x	
25290246	>gi|25290246|pir||AG0691 adenosine deaminase [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)			x	
20137212	>gi|20137212|sp|Q8Z6R2|ADD_SALTI Adenosine deaminase (Adenosine aminohydrolase)			x	
74312050	>gi|74312050|ref|YP_310469.1| adenosine deaminase [Shigella sonnei Ss046]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>73855527</td><td>>gi|73855527|gb|AAZ88234.1| adenosine deaminase [Shigella sonnei Ss046]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>62180050</td><td>>gi|62180050|ref|YP_216467.1| adenosine deaminase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>62127683</td><td>>gi|62127683|gb|AAX65386.1| adenosine deaminase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>75238816</td><td>>gi|75238816|ref|ZP_00722800.1| COG1816: Adenosine deaminase [Escherichia coli F11]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>26108273</td><td>>gi|26108273|gb|AAN80475.1| Adenosine deaminase [Escherichia coli CFT073]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>26247870</td><td>>gi|26247870|ref|NP_753910.1| adenosine deaminase [Escherichia coli CFT073]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>29839245</td><td>>gi|29839245|sp|Q8FH99|ADD_ECOL6 Adenosine deaminase (Adenosine aminohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>75512944</td><td>>gi|75512944|ref|ZP_00735425.1| COG1816: Adenosine deaminase [Escherichia coli 53638]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>75234936</td><td>>gi|75234936|ref|ZP_00719215.1| COG1816: Adenosine deaminase [Escherichia coli E110019]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>75230928</td><td>>gi|75230928|ref|ZP_00717377.1| COG1816: Adenosine deaminase [Escherichia coli B7A]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>75212960</td><td>>gi|75212960|ref|ZP_00712958.1| COG1816: Adenosine deaminase [Escherichia coli B171]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>75195703</td><td>>gi|75195703|ref|ZP_00705773.1| COG1816: Adenosine deaminase [Escherichia coli HS]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>75190663</td><td>>gi|75190663|ref|ZP_00703930.1| COG1816: Adenosine deaminase [Escherichia coli E24377A]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1787910</td><td>>gi|1787910|gb|AAC74695.1| adenosine deaminase [Escherichia coli K12]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1742677</td><td>>gi|1742677|dbj|BAA15374.1| adenosine deaminase [Escherichia coli W3110]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>16129581</td><td>>gi|16129581|ref|NP_416140.1| adenosine deaminase [Escherichia coli K12]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
83587958	>gi|83587958|ref|ZP_00926584.1| COG1816: Adenosine deaminase [Escherichia coli 101-1]			x	
2506342	>gi|2506342|sp|P22333|ADD_ECOLI Adenosine deaminase (Adenosine aminohydrolase)			x	
16419984	>gi|16419984|gb|AAL20385.1| adenosine deaminase [Salmonella typhimurium LT2]			x	
16764811	>gi|16764811|ref|NP_460426.1| adenosine deaminase [Salmonella typhimurium LT2]			x	
20137214	>gi|20137214|sp|Q8ZPL9|ADD_SALTY Adenosine deaminase (Adenosine aminohydrolase)			x	
13361798	>gi|13361798|dbj|BAB35754.1| adenosine deaminase [Escherichia coli O157:H7]			x	
15831585	>gi|15831585|ref|NP_310358.1| adenosine deaminase [Escherichia coli O157:H7]			x	
12515612	>gi|12515612|gb|AAG56612.1| adenosine deaminase [Escherichia coli O157:H7 EDL933]			x	
20137203	>gi|20137203|sp|Q8X661|ADD_ECO57 Adenosine deaminase (Adenosine aminohydrolase)			x	
15802037	>gi|15802037|ref|NP_288059.1| adenosine deaminase [Escherichia coli O157:H7 EDL933]			x	
24051977	>gi|24051977|gb|AAN43230.1| adenosine deaminase [Shigella flexneri 2a str. 301]			x	
30041387	>gi|30041387|gb|AAP17116.1| adenosine deaminase [Shigella flexneri 2a str. 2457T]			x	
30063138	>gi|30063138|ref|NP_837309.1| adenosine deaminase [Shigella flexneri 2a str. 2457T]			x	
24113013	>gi|24113013|ref|NP_707523.1| adenosine deaminase [Shigella flexneri 2a str. 301]			x	
41688435	>gi|41688435|sp|Q83RC0|ADD_SHIFL Adenosine deaminase (Adenosine aminohydrolase)			x	
82777097	>gi|82777097|ref|YP_403446.1| adenosine deaminase [Shigella dysenteriae Sd197]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
81241245	>gi|81241245|gb|ABB61955.1| adenosine deaminase [Shigella dysenteriae Sd197]			x	
75257042	>gi|75257042|ref|ZP_00728602.1| COG1816: Adenosine deaminase [Escherichia coli E22]			x	
83571009	>gi|83571009|ref|ZP_00922451.1| COG1816: Adenosine deaminase [Shigella dysenteriae 1012]			x	
75178481	>gi|75178481|ref|ZP_00698527.1| COG1816: Adenosine deaminase [Shigella boydii BS512]			x	
82544009	>gi|82544009|ref|YP_407956.1| adenosine deaminase [Shigella boydii Sb227]			x	
81245420	>gi|81245420|gb|ABB66128.1| adenosine deaminase [Shigella boydii Sb227]			x	
78688097	>gi|78688097|ref|ZP_00852819.1| Adenosine deaminase [Shewanella sp. ANA-3]			x	
78504159	>gi|78504159|gb|EAP17730.1| Adenosine deaminase [Shewanella sp. ANA-3]			x	
76259953	>gi|76259953|ref|ZP_00767596.1| Adenosine deaminase [Chloroflexus aurantiacus J-10-fl]			x	
76165205	>gi|76165205|gb|EAO59342.1| Adenosine deaminase [Chloroflexus aurantiacus J-10-fl]			x	
24376203	>gi|24376203|ref|NP_720247.1| adenosine deaminase [Shewanella oneidensis MR-1]			x	
24351258	>gi|24351258|gb|AAN57690.1| adenosine deaminase [Shewanella oneidensis MR-1]			x	
29839241	>gi|29839241|sp|Q8E8D4|ADD_SHEON Adenosine deaminase (Adenosine aminohydrolase)			x	
78691154	>gi|78691154|ref|ZP_00855782.1| Adenosine deaminase [Shewanella sp. MR-7]			x	
78509428	>gi|78509428|gb|EAP22822.1| Adenosine deaminase [Shewanella sp. MR-7]			x	
145201	>gi|145201|gb|AAA23419.1| adenosine deaminase			x	
82497819	>gi|82497819|ref|ZP_00883345.1| Adenosine deaminase [Shewanella sp. MR-4]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>82404205</td><td>>gi|82404205|gb|EAP44900.1| Adenosine deaminase [Shewanella sp. MR-4]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>28805098</td><td>>gi|28805098|dbj|BAC58379.1| adenosine deaminase [Vibrio parahaemolyticus RIMD 2210633]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>28896890</td><td>>gi|28896890|ref|NP_796495.1| adenosine deaminase [Vibrio parahaemolyticus RIMD 2210633]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>31339969</td><td>>gi|31339969|sp|Q87TF3|ADD1_VIBPA Adenosine deaminase 1 (Adenosine aminohydrolase 1)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77816434</td><td>>gi|77816434|ref|ZP_00815623.1| Adenosine deaminase [Shewanella putrefaciens CN-32]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77808608</td><td>>gi|77808608|gb|EAO93038.1| Adenosine deaminase [Shewanella putrefaciens CN-32]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>82743060</td><td>>gi|82743060|ref|ZP_00905728.1| Adenosine deaminase [Shewanella sp. W3-18-1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>82719594</td><td>>gi|82719594|gb|EAP54492.1| Adenosine deaminase [Shewanella sp. W3-18-1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>75855670</td><td>>gi|75855670|ref|ZP_00763315.1| COG1816: Adenosine deaminase [Vibrio sp. Ex25]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78368950</td><td>>gi|78368950|ref|ZP_00839137.1| Adenosine deaminase [Shewanella sp. PV-4]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78359019</td><td>>gi|78359019|gb|EAP00907.1| Adenosine deaminase [Shewanella sp. PV-4]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68544028</td><td>>gi|68544028|ref|ZP_00583706.1| Adenosine deaminase [Shewanella baltica OS155]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68518274</td><td>>gi|68518274|gb|EAN41857.1| Adenosine deaminase [Shewanella baltica OS155]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>46914992</td><td>>gi|46914992|emb|CAG21767.1| putative adenosine deaminase [Photobacterium profundum SS9]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>54310549</td><td>>gi|54310549|ref|YP_131569.1| adenosine deaminase [Photobacterium profundum SS9]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>69159081</td><td>>gi|69159081|gb|EAN71219.1| Adenosine deaminase [Shewanella denitrificans OS217]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>69942473</td><td>>gi|69942473|ref|ZP_00634260.1| Adenosine deaminase [Shewanella denitrificans OS-217]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68547729</td><td>>gi|68547729|ref|ZP_00587259.1| Adenosine deaminase [Shewanella amazonensis SB2B]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68514544</td><td>>gi|68514544|gb|EAN38275.1| Adenosine deaminase [Shewanella amazonensis SB2B]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>69951986</td><td>>gi|69951986|ref|ZP_00639598.1| Adenosine deaminase [Shewanella frigidimarina NCIMB 400]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>69164637</td><td>>gi|69164637|gb|EAN73697.1| Adenosine deaminase [Shewanella frigidimarina NCIMB 400]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77976844</td><td>>gi|77976844|ref|ZP_00832313.1| COG1816: Adenosine deaminase [Yersinia intermedia ATCC 29909]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>52354740</td><td>>gi|52354740|gb|AAH82820.1| Adenosine deaminase [Xenopus tropicalis]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>58332372</td><td>>gi|58332372|ref|NP_001011025.1| adenosine deaminase [Xenopus tropicalis]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>81167691</td><td>>gi|81167691|sp|Q63ZU0|ADA_XENTR Adenosine deaminase (Adenosine aminohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77629257</td><td>>gi|77629257|ref|ZP_00791843.1| COG1816: Adenosine deaminase [Yersinia pseudotuberculosis IP 31758]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>51589788</td><td>>gi|51589788|emb|CAH21418.1| adenosine deaminase [Yersinia pseudotuberculosis IP 32953]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>51596506</td><td>>gi|51596506|ref|YP_070697.1| adenosine deaminase [Yersinia pseudotuberculosis IP 32953]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77973198</td><td>>gi|77973198|ref|ZP_00828749.1| COG1816: Adenosine deaminase [Yersinia frederiksenii ATCC 33641]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>81167690</td><td>>gi|81167690|sp|Q6GP70|ADA_XENLA Adenosine deaminase (Adenosine aminohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77956975</td><td>>gi|77956975|ref|ZP_00821045.1| COG1816: Adenosine deaminase [Yersinia bercovieri ATCC 43970]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77963273</td><td>>gi|77963273|ref|ZP_00827084.1| COG1816: Adenosine deaminase [Yersinia mollaretii ATCC 43969]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1197210</td><td>>gi|1197210|emb|CAA26130.1| adenosine deaminase [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>66043682</td><td>>gi|66043682|ref|YP_233523.1| N-acyl-D-amino-acid deacylase [Pseudomonas syringae pv. syringae B728a]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>63254389</td><td>>gi|63254389|gb|AAY35485.1| N-acyl-D-amino-acid deacylase [Pseudomonas syringae pv. syringae B728a]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>48786563</td><td>>gi|48786563|ref|ZP_00282697.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia fungorum LB400]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77380954</td><td>>gi|77380954|gb|ABA72467.1| Amidohydrolase [Pseudomonas fluorescens PfO-1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77456951</td><td>>gi|77456951|ref|YP_346456.1| Amidohydrolase [Pseudomonas fluorescens PfO-1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>71554883</td><td>>gi|71554883|gb|AAZ34094.1| N-acyl-D-amino acid deacylase family protein [Pseudomonas syringae pv. phaseolicola 1448A]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>71734330</td><td>>gi|71734330|ref|YP_272708.1| N-acyl-D-amino acid deacylase family protein [Pseudomonas syringae pv. phaseolicola 1448A]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>17431661</td><td>>gi|17431661|emb|CAD18338.1| PROBABLE N-ACYL-D-GLUTAMATE DEACYLASE PROTEIN [Ralstonia solanacearum]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>17549408</td><td>>gi|17549408|ref|NP_522748.1| PROBABLE N-ACYL-D-GLUTAMATE DEACYLASE PROTEIN [Ralstonia solanacearum GMI1000]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68556229</td><td>>gi|68556229|ref|ZP_00595572.1| N-acyl-D-amino-acid deacylase [Ralstonia metallidurans CH34]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68529402</td><td>>gi|68529402|gb|EAN52365.1| N-acyl-D-amino-acid deacylase [Ralstonia metallidurans CH34]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>28872230</td><td>>gi|28872230|ref|NP_794849.1| N-acyl-D-amino acid deacylase family protein [Pseudomonas syringae pv. tomato str. DC3000]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>28855484</td><td>>gi|28855484|gb|AAO58544.1| N-acyl-D-amino acid deacylase family protein [Pseudomonas syringae pv. tomato str. DC3000]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>83745626</td><td>>gi|83745626|ref|ZP_00942684.1| D-aminoacylase [Ralstonia solanacearum UW551]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>83727703</td><td>>gi|83727703|gb|EAP74823.1| D-aminoacylase [Ralstonia solanacearum UW551]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>48425876</td><td>>gi|48425876|pdb|1V51|A Chain A, The Functional Role Of The Binuclear Metal Center In D- Aminoacylase. One-Metal Activation And Second-Metal Attenuation</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>48425349</td><td>>gi|48425349|pdb|1RK6|A Chain A, The Enzyme In Complex With 50mm Cdcl2</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>48425342</td><td>>gi|48425342|pdb|1RJP|A Chain A, Crystal Structure Of D-Aminoacylase In Complex With 100mm Cucl2</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>13194736</td><td>>gi|13194736|gb|AAK15530.1| D-aminoacylase [Alcaligenes faecalis]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>28948588</td><td>>gi|28948588|pdb|1M7J|A Chain A, Crystal Structure Of D-Aminoacylase Defines A Novel Subset Of Amidohydrolases</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>83719564</td><td>>gi|83719564|ref|YP_441103.1| N-acyl-D-amino-acid deacylase family protein [Burkholderia thailandensis E264]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>83653389</td><td>>gi|83653389|gb|ABC37452.1| N-acyl-D-amino-acid deacylase family protein [Burkholderia thailandensis E264]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84362911</td><td>>gi|84362911|ref|ZP_00987522.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia dolosa AUO158]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67757137</td><td>>gi|67757137|ref|ZP_00496015.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia pseudomallei Pasteur]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67739050</td><td>>gi|67739050|ref|ZP_00489656.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia pseudomallei 668]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67683515</td><td>>gi|67683515|ref|ZP_00477603.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia pseudomallei 1710a]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>76578107</td><td>>gi|76578107|gb|ABA47582.1| D-aminoacylase [Burkholderia pseudomallei 1710b]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>76808654</td><td>>gi|76808654|ref|YP_332250.1| D-aminoacylase [Burkholderia pseudomallei 1710b]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>83677451</td><td>>gi|83677451|ref|ZP_00939200.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia pseudomallei 406e]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>82535656</td><td>>gi|82535656|ref|ZP_00894670.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia pseudomallei 1106b]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>82532673</td><td>>gi|82532673|ref|ZP_00891883.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia pseudomallei 1106a]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67670108</td><td>>gi|67670108|ref|ZP_00466921.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia pseudomallei 1655]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1488357</td><td>>gi|1488357|gb|AAB35881.1| D-aminoacylase; N-acyl-D-amino acid amidohydrolase [Achromobacter xylosoxidans]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
3287876	>gi|3287876|sp|P72349|NDAD_ALCXX D-aminoacylase (N-acyl-D-amino-acid deacylase)			x	
1881397	>gi|1881397|dbj|BAA08349.1| N-acyl-D-amino acid amidohydrolase [Achromobacter xylosoxidans]			x	
67762107	>gi|67762107|ref|ZP_00500810.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia pseudomallei S13]			x	
52208687	>gi|52208687|emb|CAH34623.1| D-aminoacylase [Burkholderia pseudomallei K96243]			x	
53718273	>gi|53718273|ref|YP_107259.1| D-aminoacylase [Burkholderia pseudomallei K96243]			x	
3287879	>gi|3287879|sp|P94212|NDDD_ALCXX N-acyl-D-aspartate deacylase (N-acyl-D-aspartate amidohydrolase)			x	
1800111	>gi|1800111|dbj|BAA08350.1| N-acyl-D-amino acid amidohydrolase [Achromobacter xylosoxidans]			x	
67547194	>gi|67547194|ref|ZP_00425100.1| N-acyl-D-amino-acid deacylase [Burkholderia vietnamiensis G4]			x	
67531513	>gi|67531513|gb|EAM28324.1| N-acyl-D-amino-acid deacylase [Burkholderia vietnamiensis G4]			x	
68348571	>gi|68348571|gb|AAY96177.1| N-acyl-D-amino acid deacylase family protein [Pseudomonas fluorescens Pf-5]			x	
70734272	>gi|70734272|ref|YP_257912.1| N-acyl-D-amino acid deacylase family protein [Pseudomonas fluorescens Pf-5]			x	
74014202	>gi|74014202|ref|ZP_00684831.1| N-acyl-D-amino-acid deacylase [Burkholderia ambifaria AMMD]			x	
72612804	>gi|72612804|gb|EAO48747.1| N-acyl-D-amino-acid deacylase [Burkholderia ambifaria AMMD]			x	
72121190	>gi|72121190|gb|AAZ63376.1| N-acyl-D-amino-acid deacylase [Ralstonia eutropha JMP134]			x	
73537853	>gi|73537853|ref|YP_298220.1| N-acyl-D-amino-acid deacylase [Ralstonia eutropha JMP134]			x	
84355751	>gi|84355751|ref|ZP_00980625.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia cenocepacia PC184]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
67667435	>gi|67667435|ref|ZP_00464658.1| N-acyl-D-amino-acid deacylase [Burkholderia cenocepacia HI2424]			x	
67658643	>gi|67658643|ref|ZP_00456013.1| N-acyl-D-amino-acid deacylase [Burkholderia cenocepacia AU 1054]			x	
67098999	>gi|67098999|gb|EAM16186.1| N-acyl-D-amino-acid deacylase [Burkholderia cenocepacia HI2424]			x	
67093731	>gi|67093731|gb|EAM11270.1| N-acyl-D-amino-acid deacylase [Burkholderia cenocepacia AU 1054]			x	
77968282	>gi|77968282|gb|ABB09662.1| N-acyl-D-amino-acid deacylase [Burkholderia sp. 383]			x	
78067537	>gi|78067537|ref|YP_370306.1| N-acyl-D-amino-acid deacylase [Burkholderia sp. 383]			x	
67647671	>gi|67647671|ref|ZP_00445910.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia mallei NCTC 10247]			x	
67642485	>gi|67642485|ref|ZP_00441241.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia mallei GB8 horse 4]			x	
67636680	>gi|67636680|ref|ZP_00435624.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia mallei 10399]			x	
52428407	>gi|52428407|gb|AAU49000.1| N-acyl-D-amino-acid deacylase family protein [Burkholderia mallei ATCC 23344]			x	
85066556	>gi|85066556|ref|ZP_01027409.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia mallei 10229]			x	
84521817	>gi|84521817|ref|ZP_01008953.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia mallei SAVP1]			x	
83625877	>gi|83625877|ref|ZP_00936105.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia mallei JHU]			x	
83620938	>gi|83620938|ref|ZP_00931352.1| COG3653: N-acyl-D-aspartate/D-glutamate deacylase [Burkholderia mallei FMH]			x	
68559991	>gi|68559991|ref|ZP_00599319.1| N-acyl-D-amino-acid deacylase [Ralstonia metallidurans CH34]			x	
68525736	>gi|68525736|gb|EAN48714.1| N-acyl-D-amino-acid deacylase [Ralstonia metallidurans CH34]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
1707291	>gi|1707291|dbj|BAA08778.1| N-acyl-D-amino acids amidohydrolase [Achromobacter xylosoxidans]			x	
3287878	>gi|3287878|sp|P94211|NDED_ALCXX N-acyl-D-glutamate deacylase (N-acyl-D-glutamate amidohydrolase)			x	
1581022	>gi|1581022|prf||2116330A N-acyl-D-Glu amidohydrolase			x	
9931313	>gi|9931313|gb|AAG02130.1| L-hydantoinase HyuH [Arthrobacter aurescens]			x	
3122243	>gi|3122243|sp|P81006|HYDL_ARTAU Non-ATP-dependent L-selective hydantoinase			x	
15075477	>gi|15075477|emb|CAC47033.1| PUTATIVE D-HYDANTOINASE (DIHYDROPYRIMIDINASE) PROTEIN [Sinorhizobium meliloti]			x	
15966207	>gi|15966207|ref|NP_386560.1| dihydropyrimidinase [Sinorhizobium meliloti 1021]			x	
77388169	>gi|77388169|gb|ABA79354.1| putative D-hydantoinase (dihydropyrimidinase) [Rhodobacter sphaeroides 2.4.1]			x	
77463751	>gi|77463751|ref|YP_353255.1| dihydropyrimidinase [Rhodobacter sphaeroides 2.4.1]			x	
83374693	>gi|83374693|ref|ZP_00919463.1| D-hydantoinase [Rhodobacter sphaeroides ATCC 17029]			x	
83364064	>gi|83364064|gb|EAP67557.1| D-hydantoinase [Rhodobacter sphaeroides ATCC 17029]			x	
14022349	>gi|14022349|dbj|BAB48959.1| dihydropyrimidinase [Mesorhizobium loti MAFF303099]			x	
13471607	>gi|13471607|ref|NP_103173.1| dihydropyrimidinase [Mesorhizobium loti MAFF303099]			x	
17740870	>gi|17740870|gb|AAL43374.1| dihydropyrimidinase [Agrobacterium tumefaciens str. C58]			x	
17936268	>gi|17936268|ref|NP_533058.1| dihydropyrimidinase [Agrobacterium tumefaciens str. C58]			x	
15889657	>gi|15889657|ref|NP_355338.1| dihydropyrimidinase [Agrobacterium tumefaciens str. C58]			x	
83369112	>gi|83369112|ref|ZP_00913970.1| D-hydantoinase [Rhodobacter sphaeroides ATCC 17025]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>83361224</td><td>>gi|83361224|gb|EAP64742.1| D-hydantoinase [Rhodobacter sphaeroides ATCC 17025]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>86358891</td><td>>gi|86358891|ref|YP_470783.1| dihydropyrimidinase protein [Rhizobium etli CFN 42]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>86282993</td><td>>gi|86282993|gb|ABC92056.1| dihydropyrimidinase protein [Rhizobium etli CFN 42]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>86137291</td><td>>gi|86137291|ref|ZP_01055868.1| dihydropyrimidinase [Roseobacter sp. MED193]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>85825626</td><td>>gi|85825626|gb|EAQ45824.1| dihydropyrimidinase [Roseobacter sp. MED193]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>69297560</td><td>>gi|69297560|ref|ZP_00619856.1| Dihydropyrimidinase [Silicibacter sp. TM1040]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>69135097</td><td>>gi|69135097|gb|EAN58291.1| Dihydropyrimidinase [Silicibacter sp. TM1040]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>23347063</td><td>>gi|23347063|gb|AAN29227.1| D-hydantoinase [Brucella suis 1330]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>23501185</td><td>>gi|23501185|ref|NP_697312.1| dihydropyrimidinase [Brucella suis 1330]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>56678396</td><td>>gi|56678396|gb|AAV95062.1| D-hydantoinase [Silicibacter pomeroyi DSS-3]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>56696659</td><td>>gi|56696659|ref|YP_167020.1| dihydropyrimidinase [Silicibacter pomeroyi DSS-3]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>17983665</td><td>>gi|17983665|gb|AAL52825.1| D-HYDANTOINASE [Brucella melitensis 16M]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>17987927</td><td>>gi|17987927|ref|NP_540561.1| dihydropyrimidinase [Brucella melitensis 16M]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84514677</td><td>>gi|84514677|ref|ZP_01002041.1| dihydropyrimidinase [Loktanella vestfoldensis SKA53]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84511728</td><td>>gi|84511728|gb|EAQ08181.1| dihydropyrimidinase [Loktanella vestfoldensis SKA53]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>3334230</td><td>>gi|3334230|sp|Q59699|HYDA_PSEPU D-hydantoinase (Dihydropyrimidinase) (DHPase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>2828803</td><td>>gi|2828803|gb|AAC00209.1| D-hydantoinase [Pseudomonas putida]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77383666</td><td>>gi|77383666|gb|ABA75179.1| D-hydantoinase [Pseudomonas fluorescens PfO-1]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
77459663	>gi|77459663|ref|YP_349170.1| dihydropyrimidinase [Pseudomonas fluorescens PfO-1]			x	
68344215	>gi|68344215|gb|AAY91821.1| dihydropyrimidinase [Pseudomonas fluorescens Pf-5]			x	
70729916	>gi|70729916|ref|YP_259655.1| dihydropyrimidinase [Pseudomonas fluorescens Pf-5]			x	
84686022	>gi|84686022|ref|ZP_01013918.1| D-hydantoinase [Rhodobacterales bacterium HTCC2654]			x	
84666115	>gi|84666115|gb|EAQ12589.1| D-hydantoinase [Rhodobacterales bacterium HTCC2654]			x	
82739934	>gi|82739934|ref|ZP_00902711.1| D-hydantoinase [Pseudomonas putida F1]			x	
82712986	>gi|82712986|gb|EAP48123.1| D-hydantoinase [Pseudomonas putida F1]			x	
37222601	>gi|37222601|gb|AAQ90019.1| D-hydantoinase [Pseudomonas putida]			x	
53727146	>gi|53727146|ref|ZP_00140892.2| COG0044: Dihydroorotase and related cyclic amidohydrolases [Pseudomonas aeruginosa UCBPP-PA14]			x	
9946299	>gi|9946299|gb|AAG03830.1| dihydropyrimidinase [Pseudomonas aeruginosa PAO1]			x	
15595638	>gi|15595638|ref|NP_249132.1| dihydropyrimidinase [Pseudomonas aeruginosa PAO1]			x	
84318639	>gi|84318639|ref|ZP_00967060.1| COG0044: Dihydroorotase and related cyclic amidohydrolases [Pseudomonas aeruginosa C3719]			x	
84324321	>gi|84324321|ref|ZP_00972380.1| COG0044: Dihydroorotase and related cyclic amidohydrolases [Pseudomonas aeruginosa 2192]			x	
48787929	>gi|48787929|ref|ZP_00283908.1| COG0044: Dihydroorotase and related cyclic amidohydrolases [Burkholderia fungorum LB400]			x	
34909108	>gi|34909108|ref|NP_915901.1| putative dihydropyrimidinase [Oryza sativa (japonica cultivar-group)]			x	
13872973	>gi|13872973|dbj|BAB44078.1| putative dihydropyrimidine amidohydrolase [Oryza sativa (japonica cultivar-group)]			x	
56379800	>gi|56379800|dbj|BAD75708.1| dihydropyrimidinase (D-hydantoinase) [Geobacillus kaustophilus HTA426]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>56419958</td><td>>gi|56419958|ref|YP_147276.1| dihydropyrimidinase [Geobacillus kaustophilus HTA426]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>688288</td><td>>gi|688288|gb|AAC60487.1| hydantoinase [Bacillus stearothermophilus]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>3122249</td><td>>gi|3122249|sp|Q45515|HYDA_BACST D-hydantoinase (Dihydropyrimidinase) (DHPase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1090997</td><td>>gi|1090997|prf||2020276A hydantoinase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>69936761</td><td>>gi|69936761|ref|ZP_00631516.1| Dihydropyrimidinase [Paracoccus denitrificans PD1222]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>69151784</td><td>>gi|69151784|gb|EAN64966.1| Dihydropyrimidinase [Paracoccus denitrificans PD1222]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>73912501</td><td>>gi|73912501|dbj|BAE20330.1| hydantoinase [Pseudomonas sp. KNK003A]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84351753</td><td>>gi|84351753|ref|ZP_00976734.1| COG0044: Dihydroorotase and related cyclic amidohydrolases [Burkholderia cenocepacia PC184]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77964327</td><td>>gi|77964327|gb|ABB05708.1| D-hydantoinase [Burkholderia sp. 383]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78059777</td><td>>gi|78059777|ref|YP_366352.1| dihydropyrimidinase [Burkholderia sp. 383]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67667893</td><td>>gi|67667893|ref|ZP_00465099.1| Dihydropyrimidinase [Burkholderia cenocepacia HI2424]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67098552</td><td>>gi|67098552|gb|EAM15756.1| Dihydropyrimidinase [Burkholderia cenocepacia HI2424]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68192370</td><td>>gi|68192370|gb|EAN07024.1| Dihydropyrimidinase [Mesorhizobium sp. BNC1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>69276464</td><td>>gi|69276464|ref|ZP_00612058.1| Dihydropyrimidinase [Mesorhizobium sp. BNC1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>42567801</td><td>>gi|42567801|ref|NP_568258.2| dihydropyrimidinase/ hydrolase [Arabidopsis thaliana]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>28194047</td><td>>gi|28194047|gb|AAO33381.1| dihydropyrimidine amidohydrolase [Arabidopsis thaliana]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>9759387</td><td>>gi|9759387|dbj|BAB10038.1| dihydropyrimidinase [Arabidopsis thaliana]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>27355898</td><td>>gi|27355898|dbj|BAC52880.1| dihydropyrimidinase [Bradyrhizobium japonicum USDA 110]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
27382726	>gi|27382726|ref|NP_774255.1| dihydropyrimidinase [Bradyrhizobium japonicum USDA 110]			x	
71146703	>gi|71146703|gb|AAZ27176.1| D-hydantoinase [Colwellia psychrerythraea 34H]			x	
71280963	>gi|71280963|ref|YP_270711.1| dihydropyrimidinase [Colwellia psychrerythraea 34H]			x	
62871419	>gi|62871419|gb|AAY18594.1| dihydropyrimidinase [Bacillus sp. TS-23]			x	
52631436	>gi|52631436|gb|AAU85146.1| dihydropyrimidinase [Bacillus sp. TS-23]			x	
71725082	>gi|71725082|dbj|BAE16757.1| hydantoinase [Bacillus sp. KNK245]			x	
78696155	>gi|78696155|ref|ZP_00860665.1| D-hydantoinase [Bradyrhizobium sp. BTAi1]			x	
78515733	>gi|78515733|gb|EAP29034.1| D-hydantoinase [Bradyrhizobium sp. BTAi1]			x	
85707413	>gi|85707413|ref|ZP_01038494.1| dihydropyrimidinase [Roseovarius sp. 217]			x	
85668069	>gi|85668069|gb|EAQ22949.1| dihydropyrimidinase [Roseovarius sp. 217]			x	
84503015	>gi|84503015|ref|ZP_01001117.1| dihydropyrimidinase [Oceanicola batsensis HTCC2597]			x	
84388760	>gi|84388760|gb|EAQ01631.1| dihydropyrimidinase [Oceanicola batsensis HTCC2597]			x	
84711150	>gi|84711150|ref|ZP_01019452.1| D-hydantoinase [Polaromonas naphthalenivorans CJ2]			x	
84696375	>gi|84696375|gb|EAQ22161.1| D-hydantoinase [Polaromonas naphthalenivorans CJ2]			x	
83953423	>gi|83953423|ref|ZP_00962145.1| dihydropyrimidinase [Sulfitobacter sp. NAS-14.1]			x	
83842391	>gi|83842391|gb|EAP81559.1| dihydropyrimidinase [Sulfitobacter sp. NAS-14.1]			x	
83951604	>gi|83951604|ref|ZP_00960336.1| dihydropyrimidinase [Roseovarius nubinhibens ISM]			x	
83836610	>gi|83836610|gb|EAP75907.1| dihydropyrimidinase [Roseovarius nubinhibens ISM]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
68183017	>gi|68183017|ref|ZP_00555994.1| Dihydropyrimidinase [Jannaschia sp. CCS1]			x	
67976723	>gi|67976723|gb|EAM66348.1| Dihydropyrimidinase [Jannaschia sp. CCS1]			x	
48782314	>gi|48782314|ref|ZP_00278866.1| COG0044: Dihydroorotase and related cyclic amidohydrolases [Burkholderia fungorum LB400]			x	
3127836	>gi|3127836|emb|CAA18902.1| putative D-hydantoinase [Streptomyces coelicolor A3(2)]			x	
21224722	>gi|21224722|ref|NP_630501.1| dihydropyrimidinase [Streptomyces coelicolor A3(2)]			x	
21362598	>gi|21362598|sp|O69809|HYDA_STRCO D-hydantoinase (Dihydropyrimidinase) (DHPase)			x	
68558493	>gi|68558493|ref|ZP_00597831.1| Dihydropyrimidinase [Ralstonia metallidurans CH34]			x	
68527434	>gi|68527434|gb|EAN50402.1| Dihydropyrimidinase [Ralstonia metallidurans CH34]			x	
1296441	>gi|1296441|emb|CAA62549.1| D-hydantoinase [Agrobacterium tumefaciens]			x	
3122248	>gi|3122248|sp|Q44184|HYDA_AGRTU D-hydantoinase (Dihydropyrimidinase) (DHPase)			x	
29605594	>gi|29605594|dbj|BAC69660.1| putative dihydropyrimidinase [Streptomyces avermitilis MA-4680]			x	
29828491	>gi|29828491|ref|NP_823125.1| dihydropyrimidinase [Streptomyces avermitilis MA-4680]			x	
75515343	>gi|75515343|ref|ZP_00737527.1| COG0044: Dihydroorotase and related cyclic amidohydrolases [Escherichia coli 53638]			x	
75258473	>gi|75258473|ref|ZP_00729895.1| COG0044: Dihydroorotase and related cyclic amidohydrolases [Escherichia coli E22]			x	
75187590	>gi|75187590|ref|ZP_00700857.1| COG0044: Dihydroorotase and related cyclic amidohydrolases [Escherichia coli E24377A]			x	
83587731	>gi|83587731|ref|ZP_00926358.1| COG0044: Dihydroorotase and related cyclic amidohydrolases [Escherichia coli 101-1]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
83569892	>gi|83569892|ref|ZP_00921340.1| COG0044: Dihydroorotase and related cyclic amidohydrolases [Shigella dysenteriae 1012]			x	
38704124	>gi|38704124|ref|NP_311773.2| dihydropyrimidinase [Escherichia coli O157:H7]			x	
15803410	>gi|15803410|ref|NP_289443.1| dihydropyrimidinase [Escherichia coli O157:H7 EDL933]			x	
75212512	>gi|75212512|ref|ZP_00712536.1| COG0044: Dihydroorotase and related cyclic amidohydrolases [Escherichia coli B171]			x	
55794125	>gi|55794125|gb|AAV65953.1| D-hydantoinase [Bacillus sp. AR9]			x	
61680757	>gi|61680757|pdb|1YNY|B Chain B, Molecular Structure Of D-Hydantoinase From A Bacillus Sp. Ar9: Evidence For Mercury Inhibition			x	
61680756	>gi|61680756|pdb|1YNY|A Chain A, Molecular Structure Of D-Hydantoinase From A Bacillus Sp. Ar9: Evidence For Mercury Inhibition			x	
85675686	>gi|85675686|dbj|BAE76939.1| D-stereospecific phenylhydantoinase [Escherichia coli W3110]			x	
49176277	>gi|49176277|ref|NP_417349.3| dihydropyrimidinase [Escherichia coli K12]			x	
77389882	>gi|77389882|gb|ABA81066.1| putative D-hydantoinase dihydropyrimidinase [Rhodobacter sphaeroides 2.4.1]			x	
77465464	>gi|77465464|ref|YP_354967.1| dihydropyrimidinase [Rhodobacter sphaeroides 2.4.1]			x	
83374826	>gi|83374826|ref|ZP_00919594.1| D-hydantoinase [Rhodobacter sphaeroides ATCC 17029]			x	
83363898	>gi|83363898|gb|EAP67392.1| D-hydantoinase [Rhodobacter sphaeroides ATCC 17029]			x	
86165787	>gi|86165787|gb|EAQ67054.1| dihydropyrimidinase [Marinomonas sp. MED121]			x	
26249286	>gi|26249286|ref|NP_755326.1| dihydropyrimidinase [Escherichia coli CFT073]			x	
56911787	>gi|56911787|dbj|BAD66314.1| D-hydantoinase [Bacillus clausii KSM-K16]			x	
56965541	>gi|56965541|ref|YP_177275.1| dihydropyrimidinase [Bacillus clausii KSM-K16]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
83368213	>gi|83368213|ref|ZP_00913078.1| D-hydantoinase [Rhodobacter sphaeroides ATCC 17025]			x	
83362273	>gi|83362273|gb|EAP65784.1| D-hydantoinase [Rhodobacter sphaeroides ATCC 17025]			x	
73912499	>gi|73912499|dbj|BAE20329.1| hydantoinase [Agrobacterium sp. KNK712]			x	
17224959	>gi|17224959|gb|AAL37185.1| D-hydantoinase [Ralstonia pickettii]			x	
84180861	>gi|84180861|gb|ABC54847.1| D-hydantoinase [Ensifer adhaerens]			x	
21362600	>gi|21362600|sp|Q8VTT5|HYDA_BURPI D-hydantoinase (Dihydropyrimidinase) (DHPase)			x	
29170610	>gi|29170610|gb|AAO66292.1| dihydropyrimidinase [Brevibacillus agri]			x	
18478562	>gi|18478562|gb|AAL73199.1| D-hydantoinase [Agrobacterium sp. IP I-671]			x	
72117164	>gi|72117164|gb|AAZ59427.1| D-hydantoinase [Ralstonia eutropha JMP134]			x	
73539751	>gi|73539751|ref|YP_294271.1| dihydropyrimidinase [Ralstonia eutropha JMP134]			x	
67910946	>gi|67910946|ref|ZP_00509331.1| Dihydropyrimidinase [Polaromonas sp. JS666]			x	
67776956	>gi|67776956|gb|EAM36589.1| Dihydropyrimidinase [Polaromonas sp. JS666]			x	
68562369	>gi|68562369|ref|ZP_00601633.1| Dihydropyrimidinase [Rubrobacter xylanophilus DSM 9941]			x	
68511484	>gi|68511484|gb|EAN35327.1| Dihydropyrimidinase [Rubrobacter xylanophilus DSM 9941]			x	
67933555	>gi|67933555|ref|ZP_00526668.1| Dihydropyrimidinase [Solibacter usitatus Ellin6076]			x	
67859206	>gi|67859206|gb|EAM54287.1| Dihydropyrimidinase [Solibacter usitatus Ellin6076]			x	
57095288	>gi|57095288|ref|XP_532301.1| PREDICTED: similar to Dihydropyrimidinase (DHPase) (Hydantoinase) (DHP) isoform 1 [Canis familiaris]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
50731830	>gi|50731830|ref|XP_418377.1| PREDICTED: similar to dihydropyrimidinase [Gallus gallus]			x	
28194051	>gi|28194051|gb|AAO33383.1| dihydropyrimidine amidohydrolase [Dictyostelium discoideum]			x	
21707927	>gi|21707927|gb|AAH34395.1| Dihydropyrimidinase [Homo sapiens]			x	
4503375	>gi|4503375|ref|NP_001376.1| dihydropyrimidinase [Homo sapiens]			x	
3608122	>gi|3608122|dbj|BAA33067.1| dihydropyrimidinase [Homo sapiens]			x	
3122049	>gi|3122049|sp|Q14117|DPYS_HUMAN Dihydropyrimidinase (DHPase) (Hydantoinase) (DHP)			x	
1330236	>gi|1330236|dbj|BAA11189.1| dihydropyrimidinase [Homo sapiens]			x	
28203869	>gi|28203869|gb|AAO36309.1| D-hydantoinase [Clostridium tetani E88]			x	
28211428	>gi|28211428|ref|NP_782372.1| dihydropyrimidinase [Clostridium tetani E88]			x	
51980286	>gi|51980286|gb|AAH81768.1| Dihydropyrimidinase [Rattus norvegicus]			x	
57015267	>gi|57015267|sp|Q63150|DPYS_RAT Dihydropyrimidinase (DHPase) (Hydantoinase) (DHP)			x	
21362535	>gi|21362535|sp|Q9EQF5|DPYS_MOUSE Dihydropyrimidinase (DHPase) (Hydantoinase) (DHP)			x	
11559534	>gi|11559534|gb|AAG37999.1| dihydropyrimidinase [Mus musculus]			x	
13928984	>gi|13928984|ref|NP_113893.1| dihydropyrimidinase [Rattus norvegicus]			x	
1378019	>gi|1378019|dbj|BAA09833.1| dihydropyrimidinase [Rattus norvegicus]			x	
31981241	>gi|31981241|ref|NP_073559.2| dihydropyrimidinase [Mus musculus]			x	
54309176	>gi|54309176|ref|YP_130196.1| dihydropyrimidinase [Photobacterium profundum SS9]			x	
12655894	>gi|12655894|gb|AAK00644.1| dihydropyrimidinase [Mus musculus]			x	
76660414	>gi|76660414|ref|XP_586165.2| PREDICTED: similar to Dihydropyrimidinase (DHPase) (Hydantoinase) (DHP) [Bos taurus]			x	
83952550	>gi|83952550|ref|ZP_00961281.1| dihydropyrimidinase [Roseovarius nubinhibens ISM]			x	
83836223	>gi|83836223|gb|EAP75521.1| dihydropyrimidinase [Roseovarius nubinhibens ISM]			x	
68560573	>gi|68560573|ref|ZP_00599885.1| Dihydropyrimidinase [Rubrobacter xylanophilus DSM 9941]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
68513290	>gi|68513290|gb|EAN37085.1| Dihydropyrimidinase [Rubrobacter xylanophilus DSM 9941]			x	
57012655	>gi|57012655|sp|Q61YQ1|DHP2_CAEBR Dihydropyrimidinase 2			x	
66545426	>gi|66545426|ref|XP_392228.2| PREDICTED: similar to dihydropyrimidine amidohydrolase [Apis mellifera]			x	
17539558	>gi|17539558|ref|NP_501797.1| DiHydroPyrimidinase family member (dhp-2) [Caenorhabditis elegans]			x	
3122032	>gi|3122032|sp|Q18677|DHP2_CAEEL Dihydropyrimidinase 2 (CeCRMP/DHP-2) (UlipA)			x	
67986401	>gi|67986401|gb|EAM74224.1| Dihydropyrimidinase [Kineococcus radiotolerans SRS30216]			x	
69287725	>gi|69287725|ref|ZP_00618009.1| Dihydropyrimidinase [Kineococcus radiotolerans SRS30216]			x	
78694838	>gi|78694838|ref|ZP_00859351.1| D-hydantoinase [Bradyrhizobium sp. BTAi1]			x	
78517954	>gi|78517954|gb|EAP31252.1| D-hydantoinase [Bradyrhizobium sp. BTAi1]			x	
69934956	>gi|69934956|ref|ZP_00629987.1| Dihydropyrimidinase [Paracoccus denitrificans PD1222]			x	
69153771	>gi|69153771|gb|EAN66904.1| Dihydropyrimidinase [Paracoccus denitrificans PD1222]			x	
27351554	>gi|27351554|dbj|BAC48560.1| D-hydantoinase [Bradyrhizobium japonicum USDA 110]			x	
27378406	>gi|27378406|ref|NP_769935.1| dihydropyrimidinase [Bradyrhizobium japonicum USDA 110]			x	
67910797	>gi|67910797|ref|ZP_00509184.1| Dihydropyrimidinase [Polaromonas sp. JS666]			x	
67777111	>gi|67777111|gb|EAM36742.1| Dihydropyrimidinase [Polaromonas sp. JS666]			x	
84517193	>gi|84517193|ref|ZP_01004548.1| dihydropyrimidinase [Loktanella vestfoldensis SKA53]			x	
84508868	>gi|84508868|gb|EAQ05330.1| dihydropyrimidinase [Loktanella vestfoldensis SKA53]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
68231582	>gi|68231582|ref|ZP_00570747.1| Amidohydrolase [Frankia sp. EAN1pec]			x	
68200775	>gi|68200775|gb|EAN14982.1| Amidohydrolase [Frankia sp. EAN1pec]			x	
57012654	>gi|57012654|sp|Q60Q85|DHP1_CAEBR Dihydropyrimidinase 1			x	
28194049	>gi|28194049|gb|AAO33382.1| dihydropyrimidine amidohydrolase [Drosophila melanogaster]			x	
25992878	>gi|25992878|sp|Q21773|DHP1_CAEEL Dihydropyrimidinase 1 (CeCRMP/DHP-1) (UlipB)			x	
67662393	>gi|67662393|ref|ZP_00459682.1| Dihydropyrimidinase [Burkholderia cenocepacia HI2424]			x	
67655837	>gi|67655837|ref|ZP_00453222.1| Dihydropyrimidinase [Burkholderia cenocepacia AU 1054]			x	
67104090	>gi|67104090|gb|EAM21211.1| Dihydropyrimidinase [Burkholderia cenocepacia HI2424]			x	
67096537	>gi|67096537|gb|EAM14061.1| Dihydropyrimidinase [Burkholderia cenocepacia AU 1054]			x	
82747261	>gi|82747261|ref|ZP_00909760.1| D-hydantoinase [Clostridium beijerincki NCIMB 8052]			x	
82724944	>gi|82724944|gb|EAP59694.1| D-hydantoinase [Clostridium beijerincki NCIMB 8052]			x	
78693606	>gi|78693606|ref|ZP_00858120.1| D-hydantoinase [Bradyrhizobium sp. BTAi1]			x	
78519161	>gi|78519161|gb|EAP32458.1| D-hydantoinase [Bradyrhizobium sp. BTAi1]			x	
55631094	>gi|55631094|ref|XP_519900.1| PREDICTED: dihydropyrimidinase [Pan troglodytes]			x	
27351592	>gi|27351592|dbj|BAC48598.1| D-hydantoinase [Bradyrhizobium japonicum USDA 110]			x	
27378444	>gi|27378444|ref|NP_769973.1| dihydropyrimidinase [Bradyrhizobium japonicum USDA 110]			x	
27903506	>gi|27903506|gb|AAO24771.1| D-hydantoinase [Arthrobacter crystallopoietes]			x	
14599161	>gi|14599161|emb|CAC43845.1| urease [Glycine max]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
32170831	>gi|32170831|gb|AAO85883.1| leaf ubiquitous urease [Glycine max]			x	
14599435	>gi|14599435|emb|CAC43859.1| urease [Solanum tuberosum]			x	
17402589	>gi|17402589|dbj|BAB78715.1| urease [Oryza sativa (indica cultivar-group)]			x	
15220459	>gi|15220459|ref|NP_176922.1| hydrolase/ nickel ion binding / urease [Arabidopsis thaliana]			x	
12324683	>gi|12324683|gb|AAG52306.1| putative urease [Arabidopsis thaliana]			x	
14599413	>gi|14599413|emb|CAC43857.1| urease [Solanum tuberosum]			x	
14599437	>gi|14599437|emb|CAC43860.1| urease [Solanum tuberosum]			x	
465008	>gi|465008|sp|P07374|UREA_CANEN Urease (Urea amidohydrolase)			x	
225714	>gi|225714|prf||1311327A urease			x	
224797	>gi|224797|prf||1201293A urease			x	
167228	>gi|167228|gb|AAA83831.1| urease			x	
32170829	>gi|32170829|gb|AAO85884.1| embryo-specific urease [Glycine max]			x	
60280325	>gi|60280325|gb|AAC49868.3| urease [Coccidioides posadasii]			x	
2501620	>gi|2501620|sp|O00084|UREA_SCHPO Urease (Urea amidohydrolase)			x	
85541984	>gi|85541984|sp|Q6A3P9|UREA_ASPFU Urease (Urea amidohydrolase)			x	
50788080	>gi|50788080|emb|CAE17672.1| putative urease [Aspergillus fumigatus]			x	
38567277	>gi|38567277|emb|CAE76567.1| probable urease [Neurospora crassa]			x	
57228623	>gi|57228623|gb|AAW45058.1| urease [Cryptococcus neoformans var. neoformans JEC21]			x	
58270418	>gi|58270418|ref|XP_572365.1| urease [Cryptococcus neoformans var. neoformans JEC21]			x	
68053035	>gi|68053035|sp|Q5KCQ6|UREA_CRYNE Urease (Urea amidohydrolase)			x	
3688063	>gi|3688063|gb|AAC62257.1| urease [Cryptococcus neoformans var. grubii]			x	
23822289	>gi|23822289|sp|O13465|UREA_CRYNV Urease (Urea amidohydrolase)			x	
66847836	>gi|66847836|gb|EAL88166.1| urease [Aspergillus fumigatus Af293]			x	
70990710	>gi|70990710|ref|XP_750204.1| urease [Aspergillus fumigatus Af293]			x	
14599415	>gi|14599415|emb|CAC43858.1| urease [Solanum tuberosum]			x	
22831365	>gi|22831365|gb|AAN08919.1| urease JBURE-II [Canavalia ensiformis]			x	
86163898	>gi|86163898|gb|EAQ65170.1| urease, alpha subunit [Marinomonas sp. MED121]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
68246713	>gi|68246713|gb|EAN28807.1| Urease [Magnetococcus sp. MC-1]			x	
69257830	>gi|69257830|ref|ZP_00606748.1| Urease [Magnetococcus sp. MC-1]			x	
66047663	>gi|66047663|ref|YP_237504.1| Urease [Pseudomonas syringae pv. syringae B728a]			x	
63258370	>gi|63258370|gb|AAY39466.1| Urease [Pseudomonas syringae pv. syringae B728a]			x	
71556913	>gi|71556913|gb|AAZ36124.1| urease, alpha subunit [Pseudomonas syringae pv. phaseolicola 1448A]			x	
71736360	>gi|71736360|ref|YP_276595.1| urease, alpha subunit [Pseudomonas syringae pv. phaseolicola 1448A]			x	
28872010	>gi|28872010|ref|NP_794629.1| urease, alpha subunit [Pseudomonas syringae pv. tomato str. DC3000]			x	
28855263	>gi|28855263|gb|AAO58324.1| urease, alpha subunit [Pseudomonas syringae pv. tomato str. DC3000]			x	
2708800	>gi|2708800|gb|AAC26155.1| urease alpha subunit [Synechococcus sp. PCC 7002]			x	
67156658	>gi|67156658|ref|ZP_00418155.1| Urease [Azotobacter vinelandii AvOP]			x	
67085847	>gi|67085847|gb|EAM05318.1| Urease [Azotobacter vinelandii AvOP]			x	
75703548	>gi|75703548|gb|ABA23224.1| Urease, alpha subunit [Anabaena variabilis ATCC 29413]			x	
75909823	>gi|75909823|ref|YP_324119.1| Urease, alpha subunit [Anabaena variabilis ATCC 29413]			x	
68348432	>gi|68348432|gb|AAY96038.1| urease, alpha subunit [Pseudomonas fluorescens Pf-5]			x	
70734133	>gi|70734133|ref|YP_257773.1| urease, alpha subunit [Pseudomonas fluorescens Pf-5]			x	
17132803	>gi|17132803|dbj|BAB75369.1| urease alpha subunit [Nostoc sp. PCC 7120]			x	
17231162	>gi|17231162|ref|NP_487710.1| urease alpha subunit [Nostoc sp. PCC 7120]			x	
77380811	>gi|77380811|gb|ABA72324.1| Urease, alpha subunit [Pseudomonas fluorescens PfO-1]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
77456808	>gi|77456808|ref|YP_346313.1| Urease, alpha subunit [Pseudomonas fluorescens PfO-1]			x	
586164	>gi|586164|sp|Q07397|URE1_BACSB Urease alpha subunit (Urea amidohydrolase)			x	
216362	>gi|216362|dbj|BAA03325.1| urease alpha subunit [Bacillus sp.]			x	
1652159	>gi|1652159|dbj|BAA17083.1| urease alpha subunit [Synechocystis sp. PCC 6803]			x	
16329675	>gi|16329675|ref|NP_440403.1| urease alpha subunit [Synechocystis sp. PCC 6803]			x	
2501624	>gi|2501624|sp|P73061|URE1_SYNY3 Urease alpha subunit (Urea amidohydrolase)			x	
48864341	>gi|48864341|ref|ZP_00318234.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Microbulbifer degradans 2-40]			x	
74016945	>gi|74016945|ref|ZP_00687570.1| Urease [Burkholderia ambifaria AMMD]			x	
72610416	>gi|72610416|gb|EAO46363.1| Urease [Burkholderia ambifaria AMMD]			x	
67665979	>gi|67665979|ref|ZP_00463234.1| Urease [Burkholderia cenocepacia HI2424]			x	
67657836	>gi|67657836|ref|ZP_00455212.1| Urease [Burkholderia cenocepacia AU 1054]			x	
67100398	>gi|67100398|gb|EAM17553.1| Urease [Burkholderia cenocepacia HI2424]			x	
67094572	>gi|67094572|gb|EAM12105.1| Urease [Burkholderia cenocepacia AU 1054]			x	
53687606	>gi|53687606|ref|ZP_00107943.2| COG0804: Urea amidohydrolase (urease) alpha subunit [Nostoc punctiforme PCC 73102]			x	
68555641	>gi|68555641|ref|ZP_00594985.1| Urease [Ralstonia metallidurans CH34]			x	
68530111	>gi|68530111|gb|EAN53073.1| Urease [Ralstonia metallidurans CH34]			x	
77966223	>gi|77966223|gb|ABB07603.1| Urease, alpha subunit [Burkholderia sp. 383]			x	
78065478	>gi|78065478|ref|YP_368247.1| Urease, alpha subunit [Burkholderia sp. 383]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
22293726	>gi|22293726|dbj|BAC07558.1| urease alpha subunit [Thermosynechococcus elongatus BP-1]			x	
22297549	>gi|22297549|ref|NP_680796.1| urease alpha subunit [Thermosynechococcus elongatus BP-1]			x	
71676622	>gi|71676622|ref|ZP_00674363.1| Urease [Trichodesmium erythraeum IMS101]			x	
71670302	>gi|71670302|gb|EAO26971.1| Urease [Trichodesmium erythraeum IMS101]			x	
2340847	>gi|2340847|emb|CAA74065.1| urease, structural subunit [Cupriavidus necator]			x	
10172866	>gi|10172866|dbj|BAB03973.1| urease alpha subunit [Bacillus halodurans C-125]			x	
15612817	>gi|15612817|ref|NP_241120.1| urease alpha subunit [Bacillus halodurans C-125]			x	
67545844	>gi|67545844|ref|ZP_00423763.1| Urease [Burkholderia vietnamiensis G4]			x	
67532913	>gi|67532913|gb|EAM29689.1| Urease [Burkholderia vietnamiensis G4]			x	
72118111	>gi|72118111|gb|AAZ60374.1| Urease, alpha subunit [Ralstonia eutropha JMP134]			x	
73540698	>gi|73540698|ref|YP_295218.1| Urease, alpha subunit [Ralstonia eutropha JMP134]			x	
15075493	>gi|15075493|emb|CAC47049.1| UREASE ALPHA SUBUNIT PROTEIN [Sinorhizobium meliloti]			x	
7404480	>gi|7404480|sp|P42885|URE1_RHIME Urease alpha subunit (Urea amidohydrolase)			x	
15966223	>gi|15966223|ref|NP_386576.1| UREASE ALPHA SUBUNIT PROTEIN [Sinorhizobium meliloti 1021]			x	
84357037	>gi|84357037|ref|ZP_00981867.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia cenocepacia PC184]			x	
83748047	>gi|83748047|ref|ZP_00945076.1| Urease alpha subunit [Ralstonia solanacearum UW551]			x	
83725233	>gi|83725233|gb|EAP72382.1| Urease alpha subunit [Ralstonia solanacearum UW551]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
78701765	>gi|78701765|ref|ZP_00866213.1| Urease, alpha subunit [Alkalilimnicola ehrlichei MLHE-1]			x	
78520847	>gi|78520847|gb|EAP34106.1| Urease, alpha subunit [Alkalilimnicola ehrlichei MLHE-1]			x	
17429050	>gi|17429050|emb|CAD15734.1| PROBABLE UREASE (ALPHA SUBUNIT) PROTEIN [Ralstonia solanacearum]			x	
17546751	>gi|17546751|ref|NP_520153.1| PROBABLE UREASE (ALPHA SUBUNIT) PROTEIN [Ralstonia solanacearum GMI1000]			x	
83647213	>gi|83647213|ref|YP_435648.1| urease, alpha subunit [Hahella chejuensis KCTC 2396]			x	
83635256	>gi|83635256|gb|ABC31223.1| urease, alpha subunit [Hahella chejuensis KCTC 2396]			x	
52210683	>gi|52210683|emb|CAH36667.1| urease alpha subunit [Burkholderia pseudomallei K96243]			x	
53720269	>gi|53720269|ref|YP_109255.1| urease alpha subunit [Burkholderia pseudomallei K96243]			x	
52429706	>gi|52429706|gb|AAU50299.1| urease, alpha subunit [Burkholderia mallei ATCC 23344]			x	
9951141	>gi|9951141|gb|AAG08253.1| urease alpha subunit [Pseudomonas aeruginosa PAO1]			x	
15600061	>gi|15600061|ref|NP_253555.1| urease alpha subunit [Pseudomonas aeruginosa PAO1]			x	
84323470	>gi|84323470|ref|ZP_00971539.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Pseudomonas aeruginosa 2192]			x	
68192333	>gi|68192333|gb|EAN06987.1| Urease [Mesorhizobium sp. BNC1]			x	
69276427	>gi|69276427|ref|ZP_00612021.1| Urease [Mesorhizobium sp. BNC1]			x	
71846680	>gi|71846680|gb|AAZ46176.1| Urease, alpha subunit [Dechloromonas aromatica RCB]			x	
71907059	>gi|71907059|ref|YP_284646.1| Urease, alpha subunit [Dechloromonas aromatica RCB]			x	
86358904	>gi|86358904|ref|YP_470796.1| urease (urea amidohydrolase) alpha subunit protein [Rhizobium etli CFN 42]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>86283006</td><td>>gi|86283006|gb|ABC92069.1| urease (urea amidohydrolase) alpha subunit protein [Rhizobium etli CFN 42]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>86607525</td><td>>gi|86607525|ref|YP_476287.1| urease, alpha subunit [Cyanobacteria bacterium Yellowstone B-Prime]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>76884645</td><td>>gi|76884645|gb|ABA59326.1| Urease, alpha subunit [Nitrosococcus oceani ATCC 19707]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77166331</td><td>>gi|77166331|ref|YP_344856.1| Urease, alpha subunit [Nitrosococcus oceani ATCC 19707]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>14024880</td><td>>gi|14024880|dbj|BAB51482.1| urease alpha subunit [Mesorhizobium loti MAFF303099]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>13474128</td><td>>gi|13474128|ref|NP_105696.1| urease alpha subunit [Mesorhizobium loti MAFF303099]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78170118</td><td>>gi|78170118|gb|ABB27215.1| Urease, alpha subunit [Synechococcus sp. CC9902]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78185824</td><td>>gi|78185824|ref|YP_378258.1| Urease, alpha subunit [Synechococcus sp. CC9902]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>76579628</td><td>>gi|76579628|gb|ABA49103.1| urease, alpha subunit [Burkholderia pseudomallei 1710b]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>76810175</td><td>>gi|76810175|ref|YP_334507.1| urease, alpha subunit [Burkholderia pseudomallei 1710b]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>17740887</td><td>>gi|17740887|gb|AAL43389.1| urease alpha subunit [Agrobacterium tumefaciens str. C58]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>17936283</td><td>>gi|17936283|ref|NP_533073.1| urease alpha subunit [Agrobacterium tumefaciens str. C58]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>33641280</td><td>>gi|33641280|emb|CAE22410.1| Urease alpha subunit [Prochlorococcus marinus str. MIT 9313]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>33864500</td><td>>gi|33864500|ref|NP_896060.1| Urease alpha subunit [Prochlorococcus marinus str. MIT 9313]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78198587</td><td>>gi|78198587|gb|ABB36352.1| urease, alpha subunit [Synechococcus sp. CC9605]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78214128</td><td>>gi|78214128|ref|YP_382907.1| urease, alpha subunit [Synechococcus sp. CC9605]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
83720169	>gi|83720169|ref|YP_442042.1| urease, alpha subunit [Burkholderia thailandensis E264]			x	
83653994	>gi|83653994|gb|ABC38057.1| urease, alpha subunit [Burkholderia thailandensis E264]			x	
77740711	>gi|77740711|ref|ZP_00809197.1| Urease, alpha subunit [Rhodopseudomonas palustris BisA53]			x	
77699272	>gi|77699272|gb|EAO90417.1| Urease, alpha subunit [Rhodopseudomonas palustris BisA53]			x	
56380307	>gi|56380307|dbj|BAD76215.1| urease alpha subunit (urea amidohydrolase) [Geobacillus kaustophilus HTA426]			x	
56420465	>gi|56420465|ref|YP_147783.1| urease alpha subunit (urea amidohydrolase) [Geobacillus kaustophilus HTA426]			x	
68187175	>gi|68187175|gb|EAN01866.1| Urease [Methylobacillus flagellatus KT]			x	
68214390	>gi|68214390|ref|ZP_00566213.1| Urease [Methylobacillus flagellatus KT]			x	
77955793	>gi|77955793|ref|ZP_00820133.1| Urease, alpha subunit [Marinobacter aquaeolei VT8]			x	
77865326	>gi|77865326|gb|EAO96669.1| Urease, alpha subunit [Marinobacter aquaeolei VT8]			x	
33639580	>gi|33639580|emb|CAE08964.1| urease alpha subunit [Synechococcus sp. WH 8102]			x	
33866979	>gi|33866979|ref|NP_898538.1| urease alpha subunit [Synechococcus sp. WH 8102]			x	
27349709	>gi|27349709|dbj|BAC46722.1| urease alpha subunit [Bradyrhizobium japonicum USDA 110]			x	
27376568	>gi|27376568|ref|NP_768097.1| urease alpha subunit [Bradyrhizobium japonicum USDA 110]			x	
84387642	>gi|84387642|ref|ZP_00990659.1| urease, alpha subunit [Vibrio splendidus 12B01]			x	
84377487	>gi|84377487|gb|EAP94353.1| urease, alpha subunit [Vibrio splendidus 12B01]			x	
86169120	>gi|86169120|gb|EAQ70376.1| urease, alpha subunit [Synechococcus sp. RS9917]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
78692690	>gi|78692690|ref|ZP_00857204.1| Urease, alpha subunit [Bradyrhizobium sp. BTAi1]			x	
78518245	>gi|78518245|gb|EAP31542.1| Urease, alpha subunit [Bradyrhizobium sp. BTAi1]			x	
3659633	>gi|3659633|gb|AAC61502.1| urease alpha subunit [Synechococcus sp. WH 7805]			x	
72002743	>gi|72002743|gb|AAZ58545.1| urease, alpha subunit [Prochlorococcus marinus str. NATL2A]			x	
72382893	>gi|72382893|ref|YP_292248.1| urease, alpha subunit [Prochlorococcus marinus str. NATL2A]			x	
78494014	>gi|78494014|ref|ZP_00846244.1| Urease, alpha subunit [Rhodopseudomonas palustris BisB18]			x	
78388717	>gi|78388717|gb|EAP11618.1| Urease, alpha subunit [Rhodopseudomonas palustris BisB18]			x	
48782084	>gi|48782084|ref|ZP_00278657.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia fungorum LB400]			x	
67850889	>gi|67850889|gb|EAM46460.1| Urease [Clostridium thermocellum ATCC 27405]			x	
67874953	>gi|67874953|ref|ZP_00504504.1| Urease [Clostridium thermocellum ATCC 27405]			x	
67677174	>gi|67677174|ref|ZP_00473914.1| Urease [Chromohalobacter salexigens DSM 3043]			x	
67518775	>gi|67518775|gb|EAM22737.1| Urease [Chromohalobacter salexigens DSM 3043]			x	
13959023	>gi|13959023|gb|AAK51069.1| urease alpha subunit UreC [Brucella melitensis biovar Abortus]			x	
82699197	>gi|82699197|ref|YP_413771.1| Urease:Amidohydrolase [Brucella melitensis biovar Abortus 2308]			x	
62289267	>gi|62289267|ref|YP_221060.1| UreC-1, urease, alpha subunit [Brucella abortus biovar 1 str. 9-941]			x	
62195399	>gi|62195399|gb|AAX73699.1| UreC-1, urease, alpha subunit [Brucella abortus biovar 1 str. 9-941]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
82615298	>gi|82615298|emb|CAJ10256.1| Urease:Amidohydrolase [Brucella melitensis biovar Abortus]			x	
23347054	>gi|23347054|gb|AAN29219.1| urease, alpha subunit [Brucella suis 1330]			x	
23501177	>gi|23501177|ref|NP_697304.1| urease, alpha subunit [Brucella suis 1330]			x	
33634096	>gi|33634096|emb|CAE19422.1| Urease alpha subunit [Prochlorococcus marinus subsp. pastoris str. CCMP1986]			x	
7839375	>gi|7839375|gb|AAF70248.1| UreC [Prochlorococcus marinus]			x	
33861519	>gi|33861519|ref|NP_893080.1| Urease alpha subunit [Prochlorococcus marinus subsp. pastoris str. CCMP1986]			x	
137070	>gi|137070|sp|P18314|URE1_KLEAE Urease alpha subunit (Urea amidohydrolase)			x	
96626	>gi|96626|pir||C36138 urease (EC 3.5.1.5) 62K chain [validated] - Klebsiella pneumoniae			x	
1065194	>gi|1065194|pdb|2KAU|C Chain C, Molecule: Klebsiella Aerogenes Urease; Ec: 3.5.1.5; Synonyms: Urea Amidohydrolase, Urease; Engineered			x	
1311333	>gi|1311333|pdb|1KRA|C Chain C, Apoenzyme, Nickel Metalloenzyme Mol_id: 1; Molecule: Urease; Chain: A, B, C; Ec: 3.5.1.5			x	
149338	>gi|149338|gb|AAA25151.1| urease subunit C			x	
49530264	>gi|49530264|emb|CAG67976.1| urease alpha subunit [Acinetobacter sp. ADP1]			x	
50084288	>gi|50084288|ref|YP_045798.1| urease alpha subunit [Acinetobacter sp. ADP1]			x	
84499667	>gi|84499667|ref|ZP_00997955.1| urease, alpha subunit [Oceanicola batsensis HTCC2597]			x	
84392811	>gi|84392811|gb|EAQ05022.1| urease, alpha subunit [Oceanicola batsensis HTCC2597]			x	
78712719	>gi|78712719|gb|ABB49896.1| urease, alpha subunit [Prochlorococcus marinus str. MIT 9312]			x	
78779220	>gi|78779220|ref|YP_397332.1| urease, alpha subunit [Prochlorococcus marinus str. MIT 9312]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
39650578	>gi|39650578|emb|CAE29101.1| urease alpha subunit [Rhodopseudomonas palustris CGA009]			x	
39936722	>gi|39936722|ref|NP_948998.1| urease alpha subunit [Rhodopseudomonas palustris CGA009]			x	
56678330	>gi|56678330|gb|AAV94996.1| urease, alpha subunit [Silicibacter pomeroyi DSS-3]			x	
56696593	>gi|56696593|ref|YP_166953.1| urease, alpha subunit [Silicibacter pomeroyi DSS-3]			x	
17983673	>gi|17983673|gb|AAL52833.1| UREASE ALPHA SUBUNIT [Brucella melitensis 16M]			x	
17987935	>gi|17987935|ref|NP_540569.1| UREASE ALPHA SUBUNIT [Brucella melitensis 16M]			x	
12313641	>gi|12313641|dbj|BAB21067.1| alpha subunit of urease [Rhodobacter capsulatus]			x	
77688020	>gi|77688020|ref|ZP_00803205.1| Urease, alpha subunit [Rhodopseudomonas palustris BisB5]			x	
77655295	>gi|77655295|gb|EAO86936.1| Urease, alpha subunit [Rhodopseudomonas palustris BisB5]			x	
84361059	>gi|84361059|ref|ZP_00985743.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia dolosa AUO158]			x	
77388295	>gi|77388295|gb|ABA79480.1| Urea amidohydrolase (urease) alpha subunit [Rhodobacter sphaeroides 2.4.1]			x	
77463877	>gi|77463877|ref|YP_353381.1| Urea amidohydrolase (urease) alpha subunit [Rhodobacter sphaeroides 2.4.1]			x	
83373265	>gi|83373265|ref|ZP_00918044.1| Urease, alpha subunit [Rhodobacter sphaeroides ATCC 17029]			x	
83365737	>gi|83365737|gb|EAP69224.1| Urease, alpha subunit [Rhodobacter sphaeroides ATCC 17029]			x	
13360784	>gi|13360784|dbj|BAB34747.1| urease alpha subunit [Escherichia coli O157:H7]			x	
15830578	>gi|15830578|ref|NP_309351.1| urease alpha subunit [Escherichia coli O157:H7]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
12514464	>gi|12514464|gb|AAG55699.1| putative urease structural subunit C (alpha) [Escherichia coli O157:H7 EDL933]			x	
12513947	>gi|12513947|gb|AAG55290.1| putative urease structural subunit C (alpha) [Escherichia coli O157:H7 EDL933]			x	
15801072	>gi|15801072|ref|NP_287088.1| putative urease structural subunit C (alpha) [Escherichia coli O157:H7 EDL933]			x	
15800666	>gi|15800666|ref|NP_286680.1| putative urease structural subunit C (alpha) [Escherichia coli O157:H7 EDL933]			x	
1311330	>gi|1311330|pdb|1KRB|C Chain C, Active Site Mutant, Nickel Metalloenzyme Mol_id: 1; Molecule: Urease; Chain: A, B, C; Ec: 3.5.1.5; Mutation: H(C 219)a; Heterogen: Carbon Dioxide; Heterogen: Nickel			x	
1311327	>gi|1311327|pdb|1KRC|C Chain C, Active Site Mutant, Nickel Metalloenzyme Mol_id: 1; Molecule: Urease; Chain: A, B, C; Ec: 3.5.1.5; Mutation: H(C 320)a; Heterogen: Carbon Dioxide; Heterogen: Nickel			x	
83680720	>gi|83680720|ref|ZP_00942424.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia pseudomallei 406e]			x	
67739644	>gi|67739644|ref|ZP_00490204.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia pseudomallei 668]			x	
67674341	>gi|67674341|ref|ZP_00471103.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia pseudomallei 1655]			x	
67644011	>gi|67644011|ref|ZP_00442754.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia mallei GB8 horse 4]			x	
67638047	>gi|67638047|ref|ZP_00436984.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia mallei 10399]			x	
85066783	>gi|85066783|ref|ZP_01027636.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia mallei 10229]			x	
84523498	>gi|84523498|ref|ZP_01010634.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia mallei SAVP1]			x	
83626602	>gi|83626602|ref|ZP_00936826.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia mallei JHU]			x	
83621747	>gi|83621747|ref|ZP_00932155.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia mallei FMH]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
32044238	>gi|32044238|ref|ZP_00141339.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Pseudomonas aeruginosa UCBPP-PA14]			x	
67686103	>gi|67686103|ref|ZP_00479859.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia pseudomallei 1710a]			x	
67761072	>gi|67761072|ref|ZP_00499785.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia pseudomallei S13]			x	
82538472	>gi|82538472|ref|ZP_00897465.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia pseudomallei 1106b]			x	
82530467	>gi|82530467|ref|ZP_00889698.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia pseudomallei 1106a]			x	
86571954	>gi|86571954|gb|ABD06511.1| urease, alpha subunit [Rhodopseudomonas palustris HaA2]			x	
67648604	>gi|67648604|ref|ZP_00446833.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia mallei NCTC 10247]			x	
84515944	>gi|84515944|ref|ZP_01003305.1| urease, alpha subunit [Loktanella vestfoldensis SKA53]			x	
84510386	>gi|84510386|gb|EAQ06842.1| urease, alpha subunit [Loktanella vestfoldensis SKA53]			x	
69298861	>gi|69298861|ref|ZP_00620990.1| Urease [Silicibacter sp. TM1040]			x	
69134095	>gi|69134095|gb|EAN57328.1| Urease [Silicibacter sp. TM1040]			x	
67757584	>gi|67757584|ref|ZP_00496460.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Burkholderia pseudomallei Pasteur]			x	
59711280	>gi|59711280|ref|YP_204056.1| urease alpha subunit [Vibrio fischeri ES114]			x	
59479381	>gi|59479381|gb|AAW85168.1| urease alpha subunit [Vibrio fischeri ES114]			x	
83368250	>gi|83368250|ref|ZP_00913114.1| Urease, alpha subunit [Rhodobacter sphaeroides ATCC 17025]			x	
83361963	>gi|83361963|gb|EAP65475.1| Urease, alpha subunit [Rhodobacter sphaeroides ATCC 17025]			x	
71362355	>gi|71362355|ref|ZP_00653514.1| Urease [Psychrobacter cryohalolentis K5]			x	
71161924	>gi|71161924|gb|EAO11716.1| Urease [Psychrobacter cryohalolentis K5]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>83953306</td><td>>gi|83953306|ref|ZP_00962028.1| urease, alpha subunit [Sulfitobacter sp. NAS-14.1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>83842274</td><td>>gi|83842274|gb|EAP81442.1| urease, alpha subunit [Sulfitobacter sp. NAS-14.1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>86137786</td><td>>gi|86137786|ref|ZP_01056362.1| urease, alpha subunit [Roseobacter sp. MED193]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>85825378</td><td>>gi|85825378|gb|EAQ45577.1| urease, alpha subunit [Roseobacter sp. MED193]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>83944265</td><td>>gi|83944265|ref|ZP_00956720.1| urease, alpha subunit [Sulfitobacter sp. EE-36]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>83844809</td><td>>gi|83844809|gb|EAP82691.1| urease, alpha subunit [Sulfitobacter sp. EE-36]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84685183</td><td>>gi|84685183|ref|ZP_01013082.1| urease, alpha subunit [Rhodobacterales bacterium HTCC2654]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84666915</td><td>>gi|84666915|gb|EAQ13386.1| urease, alpha subunit [Rhodobacterales bacterium HTCC2654]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>137073</td><td>>gi|137073|sp|P17086|URE1_PROMI Urease alpha subunit (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>150918</td><td>>gi|150918|gb|AAA25669.1| urease subunit C</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>42782712</td><td>>gi|42782712|ref|NP_979959.1| urease alpha subunit [Bacillus cereus ATCC 10987]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>42738638</td><td>>gi|42738638|gb|AAS42567.1| urease alpha subunit [Bacillus cereus ATCC 10987]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84714992</td><td>>gi|84714992|ref|ZP_01022214.1| Urease, alpha subunit [Polaromonas naphthalenivorans CJ2]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84693457</td><td>>gi|84693457|gb|EAQ19257.1| Urease, alpha subunit [Polaromonas naphthalenivorans CJ2]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>53729261</td><td>>gi|53729261|ref|ZP_00133792.2| COG0804: Urea amidohydrolase (urease) alpha subunit [Actinobacillus pleuropneumoniae serovar 1 str. 4074]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>137074</td><td>>gi|137074|sp|P16122|URE1_PROVU Urease alpha subunit (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
19310948	>gi|19310948|gb|AAL86691.1| urea amidohydrolase alpha subunit [Nitrosococcus oceani]			x	
66963659	>gi|66963659|ref|ZP_00411230.1| Urease [Arthrobacter sp. FB24]			x	
66870107	>gi|66870107|gb|EAL97472.1| Urease [Arthrobacter sp. FB24]			x	
68182273	>gi|68182273|ref|ZP_00555253.1| Urease [Jannaschia sp. CCS1]			x	
67977377	>gi|67977377|gb|EAM66997.1| Urease [Jannaschia sp. CCS1]			x	
68057335	>gi|68057335|gb|AAX87588.1| Urease alpha subunit [Haemophilus influenzae 86-028NP]			x	
68249136	>gi|68249136|ref|YP_248248.1| Urease alpha subunit [Haemophilus influenzae 86-028NP]			x	
26989564	>gi|26989564|ref|NP_744989.1| urease, alpha subunit [Pseudomonas putida KT2440]			x	
24984442	>gi|24984442|gb|AAN68453.1| urease, alpha subunit [Pseudomonas putida KT2440]			x	
227457	>gi|227457|prf||1704174C urease alpha			x	
53733072	>gi|53733072|ref|ZP_00155532.2| COG0804: Urea amidohydrolase (urease) alpha subunit [Haemophilus influenzae R2846]			x	
82702370	>gi|82702370|ref|YP_411936.1| urease, alpha subunit [Nitrosospira multiformis ATCC 25196]			x	
82410435	>gi|82410435|gb|ABB74544.1| urease, alpha subunit [Nitrosospira multiformis ATCC 25196]			x	
2636189	>gi|2636189|emb|CAB15681.1| urease (alpha subunit) [Bacillus subtilis subsp. subtilis str. 168]			x	
1592696	>gi|1592696|emb|CAA69859.1| urease [Bacillus subtilis]			x	
2501621	>gi|2501621|sp|P77837|URE1_BACSU Urease alpha subunit (Urea amidohydrolase)			x	
16080717	>gi|16080717|ref|NP_391545.1| urease (alpha subunit) [Bacillus subtilis subsp. subtilis str. 168]			x	
16272483	>gi|16272483|ref|NP_438697.1| urease alpha subunit [Haemophilus influenzae Rd KW20]			x	
1573524	>gi|1573524|gb|AAC22197.1| urease, alpha subunit (ureC) [Haemophilus influenzae Rd KW20]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>1174884</td><td>>gi|1174884|sp|P44391|URE1_HAEIN Urease alpha subunit (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>37731823</td><td>>gi|37731823|gb|AAO63582.1| urease C [Nitrosomonas cryotolerans]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>82735364</td><td>>gi|82735364|ref|ZP_00898227.1| Urease, alpha subunit [Pseudomonas putida F1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>82718039</td><td>>gi|82718039|gb|EAP53090.1| Urease, alpha subunit [Pseudomonas putida F1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>3915207</td><td>>gi|3915207|sp|O54420|URE1_ACTPL Urease alpha subunit (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>74020417</td><td>>gi|74020417|ref|ZP_00691006.1| Urease [Rhodoferax ferrireducens DSM 15236]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>72606431</td><td>>gi|72606431|gb|EAO42414.1| Urease [Rhodoferax ferrireducens DSM 15236]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>6460756</td><td>>gi|6460756|gb|AAF12461.1| urease, alpha subunit [Deinococcus radiodurans R1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15807978</td><td>>gi|15807978|ref|NP_285641.1| urease, alpha subunit [Deinococcus radiodurans R1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>85704480</td><td>>gi|85704480|ref|ZP_01035582.1| urease, alpha subunit [Roseovarius sp. 217]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>85670888</td><td>>gi|85670888|gb|EAQ25747.1| urease, alpha subunit [Roseovarius sp. 217]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>32966209</td><td>>gi|32966209|gb|AAP92141.1| urease C subunit [Nitrosospira multiformis]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>37726861</td><td>>gi|37726861|gb|AAO38226.1| urease subunit C [Nitrosospira multiformis]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>71361909</td><td>>gi|71361909|ref|ZP_00653069.1| Urease [Psychrobacter cryohalolentis K5]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>71162027</td><td>>gi|71162027|gb|EAO11818.1| Urease [Psychrobacter cryohalolentis K5]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>14579320</td><td>>gi|14579320|gb|AAK69199.1| urease beta subunit UreB [Helicobacter hepaticus]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>32261956</td><td>>gi|32261956|gb|AAP77005.1| urease [Helicobacter hepaticus ATCC 51449]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>32265907</td><td>>gi|32265907|ref|NP_859939.1| urease [Helicobacter hepaticus ATCC 51449]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
67909315	>gi|67909315|ref|ZP_00507711.1| Peptidase M38, urease [Polaromonas sp. JS666]			x	
67778379	>gi|67778379|gb|EAM38001.1| Peptidase M38, urease [Polaromonas sp. JS666]			x	
75234470	>gi|75234470|ref|ZP_00718825.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Escherichia coli E110019]			x	
76875610	>gi|76875610|emb|CAI86831.1| urease, alpha subunit [Pseudoalteromonas haloplanktis TAC125]			x	
77360699	>gi|77360699|ref|YP_340274.1| urease, alpha subunit [Pseudoalteromonas haloplanktis TAC125]			x	
47574669	>gi|47574669|ref|ZP_00244705.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Rubrivivax gelatinosus PM1]			x	
37724518	>gi|37724518|gb|AAO17783.1| urea amidohydrolase alpha subunit [Nitrosospira briensis]			x	
86605319	>gi|86605319|ref|YP_474082.1| urease, alpha subunit [Cyanobacteria bacterium Yellowstone A-Prime]			x	
2130642	>gi|2130642|gb|AAC46128.1| urease structural subunit C [Bordetella bronchiseptica]			x	
33564160	>gi|33564160|emb|CAE43436.1| urease alpha subunit [Bordetella pertussis Tohama I]			x	
33594086	>gi|33594086|ref|NP_881730.1| urease alpha subunit [Bordetella pertussis Tohama I]			x	
33574493	>gi|33574493|emb|CAE39138.1| urease alpha subunit [Bordetella parapertussis]			x	
33598364	>gi|33598364|ref|NP_886007.1| urease alpha subunit [Bordetella parapertussis 12822]			x	
33577421	>gi|33577421|emb|CAE34686.1| urease alpha subunit [Bordetella bronchiseptica RB50]			x	
33603297	>gi|33603297|ref|NP_890857.1| urease alpha subunit [Bordetella bronchiseptica RB50]			x	
34978388	>gi|34978388|sp|O08400|URE1_BORBR Urease alpha subunit (Urea amidohydrolase)			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>71796401</td><td>>gi|71796401|gb|AAZ41152.1| putative urease structural subunit C (alpha) [Candidatus Blochmannia pennsylvanicus str. BPEN]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>71892295</td><td>>gi|71892295|ref|YP_278029.1| putative urease structural subunit C (alpha) [Candidatus Blochmannia pennsylvanicus str. BPEN]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>27462198</td><td>>gi|27462198|gb|AAO15374.1| urease B [Helicobacter bizzozeronii]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>5913962</td><td>>gi|5913962|dbj|BAA84533.1| urease B [Helicobacter pylori]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>4154576</td><td>>gi|4154576|gb|AAD05651.1| UREASE BETA SUBUNIT [Helicobacter pylori J99]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15644702</td><td>>gi|15644702|ref|NP_206872.1| urease beta subunit (urea amidohydrolase) (ureB) [Helicobacter pylori 26695]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>2313153</td><td>>gi|2313153|gb|AAD07143.1| urease beta subunit (urea amidohydrolase) (ureB) [Helicobacter pylori 26695]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>57014162</td><td>>gi|57014162|sp|P69996|URE2_HELPY Urease beta subunit (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>57014163</td><td>>gi|57014163|sp|P69997|URE2_HELPJ Urease beta subunit (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15611138</td><td>>gi|15611138|ref|NP_222789.1| UREASE BETA SUBUNIT [Helicobacter pylori J99]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77543439</td><td>>gi|77543439|gb|ABA87133.1| urease B [Helicobacter pylori]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>31580721</td><td>>gi|31580721|gb|AAP51176.1| urease B [Helicobacter pylori]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>396162</td><td>>gi|396162|emb|CAA48826.1| urease beta-6 subunit [Helicobacter felis]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>586167</td><td>>gi|586167|sp|Q08716|URE2_HELFE Urease beta subunit (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>13605430</td><td>>gi|13605430|gb|AAK32714.1| urease B [Helicobacter pylori]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>4249613</td><td>>gi|4249613|gb|AAD13732.1| urease alpha subunit UreC [Actinomyces naeslundii]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>4249601</td><td>>gi|4249601|gb|AAD13725.1| urease alpha-subunit [Actinomyces naeslundii]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>33504317</td><td>>gi|33504317|emb|CAD83209.1| putative urease structural subunit C (alpha) [Candidatus Blochmannia floridanus]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>33519971</td><td>>gi|33519971|ref|NP_878803.1| putative urease structural subunit C (alpha) [Candidatus Blochmannia floridanus]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>48855146</td><td>>gi|48855146|ref|ZP_00309306.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Cytophaga hutchinsonii]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>28372407</td><td>>gi|28372407|gb|AAO34403.1| urease beta; urease subunit B; urease large subunit [Helicobacter pylori]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1174891</td><td>>gi|1174891|sp|P42823|URE2_HELHE Urease beta subunit (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>529424</td><td>>gi|529424|gb|AAA65723.1| urease</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>580821</td><td>>gi|580821|emb|CAA55175.1| urease [Sporosarcina pasteurii]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>731075</td><td>>gi|731075|sp|P41020|URE1_BACPA Urease alpha subunit (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>69936847</td><td>>gi|69936847|ref|ZP_00631602.1| Urease [Paracoccus denitrificans PD1222]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>69151870</td><td>>gi|69151870|gb|EAN65052.1| Urease [Paracoccus denitrificans PD1222]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>49245514</td><td>>gi|49245514|emb|CAG43991.1| urease alpha subunit [Staphylococcus aureus subsp. aureus MSSA476]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>14248063</td><td>>gi|14248063|dbj|BAB58452.1| urease alpha subunit [Staphylococcus aureus subsp. aureus Mu50]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>21205379</td><td>>gi|21205379|dbj|BAB96073.1| urease alpha subunit [Staphylococcus aureus subsp. aureus MW2]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>57286408</td><td>>gi|57286408|gb|AAW38502.1| urease, alpha subunit [Staphylococcus aureus subsp. aureus COL]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>13702090</td><td>>gi|13702090|dbj|BAB43382.1| urease alpha subunit [Staphylococcus aureus subsp. aureus N315]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15927870</td><td>>gi|15927870|ref|NP_375403.1| urease alpha subunit [Staphylococcus aureus subsp. aureus N315]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15925280</td><td>>gi|15925280|ref|NP_372814.1| urease alpha subunit [Staphylococcus aureus subsp. aureus Mu50]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>57652222</td><td>>gi|57652222|ref|YP_187089.1| urease, alpha subunit [Staphylococcus aureus subsp. aureus COL]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>54039829</td><td>>gi|54039829|sp|P67405|URE1_STAAW Urease alpha subunit (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>54039828</td><td>>gi|54039828|sp|P67404|URE1_STAAN Urease alpha subunit (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>54042748</td><td>>gi|54042748|sp|P67403|URE1_STAAM Urease alpha subunit (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>81648799</td><td>>gi|81648799|sp|Q6G732|URE1_STAAS Urease alpha subunit (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>81693924</td><td>>gi|81693924|sp|Q5HDR8|URE1_STAAC Urease alpha subunit (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>49487071</td><td>>gi|49487071|ref|YP_044292.1| urease alpha subunit [Staphylococcus aureus subsp. aureus MSSA476]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>21283937</td><td>>gi|21283937|ref|NP_647025.1| urease alpha subunit [Staphylococcus aureus subsp. aureus MW2]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>25290144</td><td>>gi|25290144|pir||E90027 urease alpha subunit [imported] - Staphylococcus aureus (strain N315)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>9967061</td><td>>gi|9967061|gb|AAD28133.2| urease complex component UreC [Ureaplasma urealyticum serovar 13]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>9967054</td><td>>gi|9967054|gb|AAD28130.2| urease complex component UreC [Ureaplasma urealyticum serovar 12]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>9967047</td><td>>gi|9967047|gb|AAD28127.2| urease complex component UreC [Ureaplasma urealyticum serovar 11]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>9967040</td><td>>gi|9967040|gb|AAD28124.2| urease complex component UreC [Ureaplasma urealyticum serovar 10]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>9967033</td><td>>gi|9967033|gb|AAD28121.2| urease complex component UreC [Ureaplasma urealyticum serovar 9]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>9967026</td><td>>gi|9967026|gb|AAD28118.2| urease complex component UreC [Ureaplasma urealyticum serovar 8]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>9967019</td><td>>gi|9967019|gb|AAD28115.2| urease complex component UreC [Ureaplasma urealyticum serovar 7]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>9967012</td><td>>gi|9967012|gb|AAD28112.2| urease complex component UreC [Ureaplasma urealyticum serovar 5]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>9967005</td><td>>gi|9967005|gb|AAD28109.2| urease complex component UreC [Ureaplasma urealyticum serovar 4]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
9966998	>gi|9966998|gb|AAD28106.2| urease complex component UreC [Ureaplasma urealyticum serovar 2]			x	
19856524	>gi|19856524|sp|P17272|URE1_UREUR Urease alpha subunit (Urea amidohydrolase)			x	
57867797	>gi|57867797|ref|YP_189432.1| urease, alpha subunit [Staphylococcus epidermidis RP62A]			x	
57638455	>gi|57638455|gb|AAW55243.1| urease, alpha subunit [Staphylococcus epidermidis RP62A]			x	
27316329	>gi|27316329|gb|AAO05504.1| urease alpha subunit [Staphylococcus epidermidis ATCC 12228]			x	
38605272	>gi|38605272|sp|Q8CNC9|URE1_STAES Urease alpha subunit (Urea amidohydrolase)			x	
27468781	>gi|27468781|ref|NP_765418.1| urease alpha subunit [Staphylococcus epidermidis ATCC 12228]			x	
81673505	>gi|81673505|sp|Q5HLW1|URE1_STAEQ Urease alpha subunit (Urea amidohydrolase)			x	
49242634	>gi|49242634|emb|CAG41355.1| urease alpha subunit [Staphylococcus aureus subsp. aureus MRSA252]			x	
81650552	>gi|81650552|sp|Q6GEE4|URE1_STAAR Urease alpha subunit (Urea amidohydrolase)			x	
49484505	>gi|49484505|ref|YP_041729.1| urease alpha subunit [Staphylococcus aureus subsp. aureus MRSA252]			x	
72494087	>gi|72494087|dbj|BAE17408.1| urease alpha subunit [Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305]			x	
73661572	>gi|73661572|ref|YP_300353.1| urease alpha subunit [Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305]			x	
82751878	>gi|82751878|ref|YP_417619.1| urease alpha subunit [Staphylococcus aureus RF122]			x	
82657409	>gi|82657409|emb|CAI81851.1| urease alpha subunit [Staphylococcus aureus RF122]			x	
9967085	>gi|9967085|gb|AAD28145.2| urease complex component UreC [Ureaplasma parvum serovar 14]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>6899423</td><td>>gi|6899423|gb|AAF30844.1| urease complex component [Ureaplasma parvum serovar 3 str. ATCC 700970]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>12643778</td><td>>gi|12643778|sp|Q60058|URE1_UREPA Urease alpha subunit (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>13357995</td><td>>gi|13357995|ref|NP_078269.1| urease complex component [Ureaplasma parvum serovar 3 str. ATCC 700970]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>19338960</td><td>>gi|19338960|gb|AAL86896.1| urease B subunit [Helicobacter pylori]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>9967077</td><td>>gi|9967077|gb|AAD28139.2| urease complex component UreC [Ureaplasma parvum serovar 1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>9967069</td><td>>gi|9967069|gb|AAD28136.2| urease complex component UreC [Ureaplasma parvum serovar 6]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>410516</td><td>>gi|410516|emb|CAA52680.1| urease alpha subunit [Staphylococcus xylosus]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1174887</td><td>>gi|1174887|sp|P42873|URE1_STAXY Urease alpha subunit (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>23492833</td><td>>gi|23492833|dbj|BAC17805.1| urease alpha subunit [Corynebacterium efficiens YS-314]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>25027551</td><td>>gi|25027551|ref|NP_737605.1| urease alpha subunit [Corynebacterium efficiens YS-314]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>54016003</td><td>>gi|54016003|dbj|BAD57373.1| putative urease alpha subunit [Nocardia farcinica IFM 10152]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>54024495</td><td>>gi|54024495|ref|YP_118737.1| putative urease alpha subunit [Nocardia farcinica IFM 10152]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>7272374</td><td>>gi|7272374|gb|AAA89189.2| UreC [Ureaplasma urealyticum]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>41324314</td><td>>gi|41324314|emb|CAF18654.1| UREASE ALPHA SUBUNIT [Corynebacterium glutamicum ATCC 13032]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>7320802</td><td>>gi|7320802|emb|CAB81937.1| urease alpha subunit [Corynebacterium glutamicum]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>21322850</td><td>>gi|21322850|dbj|BAB97479.1| Urea amidohydrolase (urease) alpha subunit [Corynebacterium glutamicum ATCC 13032]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>62388981</td><td>>gi|62388981|ref|YP_224383.1| UREASE ALPHA SUBUNIT [Corynebacterium glutamicum ATCC 13032]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>19551336</td><td>>gi|19551336|ref|NP_599338.1| urea amidohydrolase (urease) alpha subunit [Corynebacterium glutamicum ATCC 13032]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>76784366</td><td>>gi|76784366|ref|ZP_00771551.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Mycobacterium tuberculosis F11]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>13881549</td><td>>gi|13881549|gb|AAK46169.1| urease, alpha subunit [Mycobacterium tuberculosis CDC1551]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1781197</td><td>>gi|1781197|emb|CAB06137.1| Urease alpha subunit ureC (Urea amidohydrolase) [Mycobacterium tuberculosis H37Rv]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>31618631</td><td>>gi|31618631|emb|CAD94584.1| Urease alpha subunit ureC (Urea amidohydrolase) [Mycobacterium bovis AF2122/97]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>31793040</td><td>>gi|31793040|ref|NP_855533.1| Urease alpha subunit ureC (Urea amidohydrolase) [Mycobacterium bovis AF2122/97]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15608987</td><td>>gi|15608987|ref|NP_216366.1| Urease alpha subunit ureC (Urea amidohydrolase) [Mycobacterium tuberculosis H37Rv]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15841318</td><td>>gi|15841318|ref|NP_336355.1| urease, alpha subunit [Mycobacterium tuberculosis CDC1551]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>61249511</td><td>>gi|61249511|sp|P0A660|URE1_MYCTU Urease alpha subunit (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>61249512</td><td>>gi|61249512|sp|P0A661|URE1_MYCBO Urease alpha subunit (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>81254045</td><td>>gi|81254045|ref|ZP_00878572.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Mycobacterium tuberculosis C]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1016692</td><td>>gi|1016692|gb|AAC43475.1| urease structural subunit C</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>58801243</td><td>>gi|58801243|dbj|BAD89502.1| urease B subunit [Campylobacter lari]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1780784</td><td>>gi|1780784|emb|CAA71385.1| urease catalytic subunit [Clostridium perfringens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>2501623</td><td>>gi|2501623|sp|P94669|URE1_CLOPE Urease alpha subunit (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>74099907</td><td>>gi|74099907|gb|AAZ99164.1| urease alpha subunit [Streptococcus vestibularis]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>38489172</td><td>>gi|38489172|gb|AAR21273.1| UreC protein [Streptococcus thermophilus]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>55738254</td><td>>gi|55738254|gb|AAV61895.1| urea amidohydrolase (urease) alpha subunit [Streptococcus thermophilus CNRZ1066]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>55822269</td><td>>gi|55822269|ref|YP_140710.1| urea amidohydrolase (urease) alpha subunit [Streptococcus thermophilus CNRZ1066]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>55820378</td><td>>gi|55820378|ref|YP_138820.1| urea amidohydrolase (urease) alpha subunit [Streptococcus thermophilus LMG 18311]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>55736363</td><td>>gi|55736363|gb|AAV60005.1| urea amidohydrolase (urease) alpha subunit [Streptococcus thermophilus LMG 18311]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77961632</td><td>>gi|77961632|ref|ZP_00825465.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Yersinia mollaretii ATCC 43969]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1167544</td><td>>gi|1167544|gb|AAC43564.1| urease alpha subunit [Streptococcus salivarius]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>2507522</td><td>>gi|2507522|sp|P50047|URE1_STRSL Urease alpha subunit (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77973096</td><td>>gi|77973096|ref|ZP_00828648.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Yersinia frederiksenii ATCC 33641]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77978460</td><td>>gi|77978460|ref|ZP_00833889.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Yersinia intermedia ATCC 29909]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77957751</td><td>>gi|77957751|ref|ZP_00821799.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Yersinia bercovieri ATCC 43970]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1174889</td><td>>gi|1174889|sp|P31494|URE1_YEREN Urease alpha subunit (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>431752</td><td>>gi|431752|gb|AAA50996.1| urease alpha subunit</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>29610772</td><td>>gi|29610772|dbj|BAC74817.1| putative urease alpha subunit [Streptomyces avermitilis MA-4680]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>29833648</td><td>>gi|29833648|ref|NP_828282.1| putative urease alpha subunit [Streptomyces avermitilis MA-4680]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77635026</td><td>>gi|77635026|ref|ZP_00797116.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Yersinia pestis Angola]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77629975</td><td>>gi|77629975|ref|ZP_00792561.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Yersinia pseudotuberculosis IP 31758]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>45437116</td><td>>gi|45437116|gb|AAS62668.1| urease alpha subunit [Yersinia pestis biovar Medievalis str. 91001]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
51590539	>gi|51590539|emb|CAH22180.1| urease alpha subunit [Yersinia pseudotuberculosis IP 32953]			x	
15980647	>gi|15980647|emb|CAC92906.1| urease alpha subunit [Yersinia pestis CO92]			x	
3901298	>gi|3901298|gb|AAC78634.1| urease alpha subunit UreC [Yersinia pestis]			x	
51597257	>gi|51597257|ref|YP_071448.1| urease alpha subunit [Yersinia pseudotuberculosis IP 32953]			x	
45442252	>gi|45442252|ref|NP_993791.1| urease alpha subunit [Yersinia pestis biovar Medievalis str. 91001]			x	
16122873	>gi|16122873|ref|NP_406186.1| urease alpha subunit [Yersinia pestis CO92]			x	
55977804	>gi|55977804|sp|P52313|URE1_YERPS Urease alpha subunit (Urea amidohydrolase)			x	
6686077	>gi|6686077|sp|Q9ZFR9|URE1_YERPE Urease alpha subunit (Urea amidohydrolase)			x	
9716120	>gi|9716120|emb|CAC01458.1| urease alpha subunit [Streptomyces coelicolor A3(2)]			x	
21219743	>gi|21219743|ref|NP_625522.1| urease alpha subunit [Streptomyces coelicolor A3(2)]			x	
62527922	>gi|62527922|ref|ZP_00389185.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Streptococcus thermophilus LMD-9]			x	
85700461	>gi|85700461|gb|ABC74584.1| urease structural subunit [Yersinia enterocolitica]			x	
1185472	>gi|1185472|gb|AAA87854.1| urease alpha subunit [Yersinia pseudotuberculosis]			x	
82500240	>gi|82500240|ref|ZP_00885663.1| Urease, alpha subunit [Caldicellulosiruptor saccharolyticus DSM 8903]			x	
82401777	>gi|82401777|gb|EAP42575.1| Urease, alpha subunit [Caldicellulosiruptor saccharolyticus DSM 8903]			x	
36785519	>gi|36785519|emb|CAE14466.1| urease alpha subunit [Photorhabdus luminescens subsp. laumondii TTO1]			x	
37526089	>gi|37526089|ref|NP_929433.1| urease alpha subunit [Photorhabdus luminescens subsp. laumondii TTO1]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
68234677	>gi|68234677|ref|ZP_00573744.1| Urease [Frankia sp. EAN1pec]			x	
68197709	>gi|68197709|gb|EAN12014.1| Urease [Frankia sp. EAN1pec]			x	
914897	>gi|914897|emb|CAA35697.1| urease alpha subunit [Ureaplasma urealyticum]			x	
86739545	>gi|86739545|ref|YP_479945.1| urease, alpha subunit [Frankia sp. CcI3]			x	
86566407	>gi|86566407|gb|ABD10216.1| urease, alpha subunit [Frankia sp. CcI3]			x	
23348201	>gi|23348201|gb|AAN30272.1| urease, alpha subunit [Brucella suis 1330]			x	
23502230	>gi|23502230|ref|NP_698357.1| urease, alpha subunit [Brucella suis 1330]			x	
17982574	>gi|17982574|gb|AAL51828.1| UREASE ALPHA SUBUNIT [Brucella melitensis 16M]			x	
17986930	>gi|17986930|ref|NP_539564.1| UREASE ALPHA SUBUNIT [Brucella melitensis 16M]			x	
137071	>gi|137071|sp|P26929|URE1_LACFE Acid urease alpha subunit (Urea amidohydrolase)			x	
216744	>gi|216744|dbj|BAA01460.1| acid urease, alpha subunit [Lactobacillus fermentum]			x	
62290254	>gi|62290254|ref|YP_222047.1| UreC-2, urease, alpha subunit [Brucella abortus biovar 1 str. 9-941]			x	
62196386	>gi|62196386|gb|AAX74686.1| UreC-2, urease, alpha subunit [Brucella abortus biovar 1 str. 9-941]			x	
82616278	>gi|82616278|emb|CAJ11334.1| Urease:Amidohydrolase [Brucella melitensis biovar Abortus]			x	
4545295	>gi|4545295|gb|AAD22480.1| urease alpha subunit [Lactobacillus fermentum]			x	
66045437	>gi|66045437|ref|YP_235278.1| Urease [Pseudomonas syringae pv. syringae B728a]			x	
63256144	>gi|63256144|gb|AAY37240.1| Urease [Pseudomonas syringae pv. syringae B728a]			x	
84317527	>gi|84317527|ref|ZP_00965968.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Pseudomonas aeruginosa C3719]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
84503105	>gi|84503105|ref|ZP_01001201.1| Urease [Oceanicola batsensis HTCC2597]			x	
84388649	>gi|84388649|gb|EAQ01521.1| Urease [Oceanicola batsensis HTCC2597]			x	
21958000	>gi|21958000|gb|AAM84814.1| urease (urea amidohydrolase) alpha subunit [Yersinia pestis KIM]			x	
22125140	>gi|22125140|ref|NP_668563.1| urease (urea amidohydrolase) alpha subunit [Yersinia pestis KIM]			x	
85705527	>gi|85705527|ref|ZP_01036625.1| Urease [Roseovarius sp. 217]			x	
85669952	>gi|85669952|gb|EAQ24815.1| Urease [Roseovarius sp. 217]			x	
78693475	>gi|78693475|ref|ZP_00857989.1| Urease, alpha subunit [Bradyrhizobium sp. BTAi1]			x	
78519030	>gi|78519030|gb|EAP32327.1| Urease, alpha subunit [Bradyrhizobium sp. BTAi1]			x	
76557515	>gi|76557515|emb|CAI49096.1| urease (EC 3.5.1.5), alpha subunit [Natronomonas pharaonis DSM 2160]			x	
76801650	>gi|76801650|ref|YP_326658.1| urease , alpha subunit [Natronomonas pharaonis DSM 2160]			x	
55229415	>gi|55229415|gb|AAV44835.1| urease alpha subunit [Haloarcula marismortui ATCC 43049]			x	
34419197	>gi|34419197|dbj|BAC84958.1| urease alpha subunit UreC [Haloarcula marismortui]			x	
55376690	>gi|55376690|ref|YP_134541.1| urease alpha subunit [Haloarcula marismortui ATCC 43049]			x	
41350153	>gi|41350153|gb|AAS00415.1| urease alpha subunit [Saccharopolyspora spinosa]			x	
48958373	>gi|48958373|dbj|BAD23932.1| urease beta subunit [Campylobacter lari]			x	
48958364	>gi|48958364|dbj|BAD23926.1| urease beta subunit [Campylobacter lari]			x	
48958388	>gi|48958388|dbj|BAD23942.1| urease beta subunit [Campylobacter lari]			x	
48958361	>gi|48958361|dbj|BAD23924.1| urease beta subunit [Campylobacter lari]			x	
48958358	>gi|48958358|dbj|BAD23922.1| urease beta subunit [Campylobacter lari]			x	
48958385	>gi|48958385|dbj|BAD23940.1| urease beta subunit [Campylobacter lari]			x	
48958370	>gi|48958370|dbj|BAD23930.1| urease beta subunit [Campylobacter lari]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>48958382</td><td>>gi|48958382|dbj|BAD23938.1| urease beta subunit [Campylobacter lari]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>48958376</td><td>>gi|48958376|dbj|BAD23934.1| urease beta subunit [Campylobacter lari]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>48958391</td><td>>gi|48958391|dbj|BAD23944.1| urease beta subunit [Campylobacter lari]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15622060</td><td>>gi|15622060|dbj|BAB66053.1| 493aa long hypothetical urease alpha subunit [Sulfolobus tokodaii str. 7]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15921275</td><td>>gi|15921275|ref|NP_376944.1| hypothetical urease alpha subunit [Sulfolobus tokodaii str. 7]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>48958379</td><td>>gi|48958379|dbj|BAD23936.1| urease beta subunit [Campylobacter lari]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>3355674</td><td>>gi|3355674|emb|CAA19974.1| urease alpha subunit [Streptomyces coelicolor A3(2)]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>21223881</td><td>>gi|21223881|ref|NP_629660.1| urease alpha subunit [Streptomyces coelicolor A3(2)]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>29606364</td><td>>gi|29606364|dbj|BAC70426.1| putative urease alpha subunit [Streptomyces avermitilis MA-4680]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>29829257</td><td>>gi|29829257|ref|NP_823891.1| putative urease alpha subunit [Streptomyces avermitilis MA-4680]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78695136</td><td>>gi|78695136|ref|ZP_00859648.1| Urease, alpha subunit [Bradyrhizobium sp. BTAi1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78516810</td><td>>gi|78516810|gb|EAP30109.1| Urease, alpha subunit [Bradyrhizobium sp. BTAi1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67985209</td><td>>gi|67985209|gb|EAM73168.1| Urease [Kineococcus radiotolerans SRS30216]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>69290762</td><td>>gi|69290762|ref|ZP_00619084.1| Urease [Kineococcus radiotolerans SRS30216]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>21637205</td><td>>gi|21637205|gb|AAM70384.1| urease UreB [Helicobacter bizzozeronii]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>21637208</td><td>>gi|21637208|gb|AAM70386.1| urease UreB [Helicobacter felis]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>21637244</td><td>>gi|21637244|gb|AAM70410.1| urease UreB [Helicobacter pylori SS1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>21637179</td><td>>gi|21637179|gb|AAM70367.1| urease UreB [Helicobacter pylori 26695]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>21637192</td><td>>gi|21637192|gb|AAM70375.1| urease UreB [Candidatus Helicobacter heilmannii]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>21637202</td><td>>gi|21637202|gb|AAM70382.1| urease UreB [Helicobacter bizzozeronii]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>23005331</td><td>>gi|23005331|ref|ZP_00048203.1| COG0804: Urea amidohydrolase (urease) alpha subunit [Magnetospirillum magnetotacticum MS-1]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
1790784	>gi|1790784|gb|AAC77284.1| isoaspartyl dipeptidase [Escherichia coli K12]			x	
85677071	>gi|85677071|dbj|BAE78321.1| isoaspartyl dipeptidase [Escherichia coli W3110]			x	
16132149	>gi|16132149|ref|NP_418748.1| isoaspartyl dipeptidase [Escherichia coli K12]			x	
640031	>gi|640031|gb|AAC43299.1| isoaspartyl dipeptidase			x	
732085	>gi|732085|sp|P39377|IADA_ECOLI Isoaspartyl dipeptidase			x	
13364764	>gi|13364764|dbj|BAB38709.1| isoaspartyl dipeptidase [Escherichia coli O157:H7]			x	
15834540	>gi|15834540|ref|NP_313313.1| isoaspartyl dipeptidase [Escherichia coli O157:H7]			x	
12519339	>gi|12519339|gb|AAG59511.1| isoaspartyl dipeptidase [Escherichia coli O157:H7 EDL933]			x	
15804904	>gi|15804904|ref|NP_290945.1| isoaspartyl dipeptidase [Escherichia coli O157:H7 EDL933]			x	
24054703	>gi|24054703|gb|AAN45611.1| isoaspartyl dipeptidase [Shigella flexneri 2a str. 301]			x	
30043677	>gi|30043677|gb|AAP19397.1| isoaspartyl dipeptidase [Shigella flexneri 2a str. 2457T]			x	
30065415	>gi|30065415|ref|NP_839586.1| isoaspartyl dipeptidase [Shigella flexneri 2a str. 2457T]			x	
24115394	>gi|24115394|ref|NP_709904.1| isoaspartyl dipeptidase [Shigella flexneri 2a str. 301]			x	
52420926	>gi|52420926|emb|CAH55805.1| isoaspartyl dipeptidase yadA [Escherichia coli]			x	
82546675	>gi|82546675|ref|YP_410622.1| isoaspartyl dipeptidase [Shigella boydii Sb227]			x	
81248086	>gi|81248086|gb|ABB68794.1| isoaspartyl dipeptidase [Shigella boydii Sb227]			x	
26111649	>gi|26111649|gb|AAN83830.1| Isoaspartyl dipeptidase [Escherichia coli CFT073]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>26251216</td><td>>gi|26251216|ref|NP_757256.1| Isoaspartyl dipeptidase [Escherichia coli CFT073]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>62182937</td><td>>gi|62182937|ref|YP_219354.1| isoaspartyl dipeptidase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>62130570</td><td>>gi|62130570|gb|AAX68273.1| isoaspartyl dipeptidase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>56130553</td><td>>gi|56130553|gb|AAV80059.1| probable isoaspartyl dipeptidase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>56416296</td><td>>gi|56416296|ref|YP_153371.1| probable isoaspartyl dipeptidase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>16423078</td><td>>gi|16423078|gb|AAL23330.1| isoaspartyl dipeptidase [Salmonella typhimurium LT2]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>16767756</td><td>>gi|16767756|ref|NP_463371.1| isoaspartyl dipeptidase [Salmonella typhimurium LT2]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>16505629</td><td>>gi|16505629|emb|CAD03357.1| probable isoaspartyl dipeptidase [Salmonella enterica subsp. enterica serovar Typhi]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>29140437</td><td>>gi|29140437|gb|AAO72000.1| probable isoaspartyl dipeptidase [Salmonella enterica subsp. enterica serovar Typhi Ty2]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>16763320</td><td>>gi|16763320|ref|NP_458937.1| probable isoaspartyl dipeptidase [Salmonella enterica subsp. enterica serovar Typhi str. CT18]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>29144798</td><td>>gi|29144798|ref|NP_808140.1| probable isoaspartyl dipeptidase [Salmonella enterica subsp. enterica serovar Typhi Ty2]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>25290194</td><td>>gi|25290194|pir||AF1067 probable isoaspartyl dipeptidase (EC 3.4.19.-) [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>31981810</td><td>>gi|31981810|ref|NP_034153.2| dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase) [Mus musculus]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>18490960</td><td>>gi|18490960|gb|AAH22712.1| Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase) [Mus musculus]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>51260621</td><td>>gi|51260621|gb|AAH78705.1| Dodecenoyl-coenzyme A delta isomerase [Rattus norvegicus]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>62530384</td><td>>gi|62530384|ref|NP_001910.2| dodecenoyl-Coenzyme A delta isomerase precursor [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>1169204</td><td>>gi|1169204|sp|P42126|D3D2_HUMAN 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor (Dodecenoyl-CoA isomerase) (Delta(3),delta(2)-enoyl-CoA isomerase) (D3,D2-enoyl-CoA isomerase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>825689</td><td>>gi|825689|emb|CAA81066.1| dodecenoyl-CoA delta-isomerase [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>8393243</td><td>>gi|8393243|ref|NP_059002.1| dodecenoyl-coenzyme A delta isomerase [Rattus norvegicus]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>57333</td><td>>gi|57333|emb|CAA43488.1| 3-2trans-enoyl-CoA isomerase [Rattus norvegicus]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>118210</td><td>>gi|118210|sp|P23965|D3D2_RAT 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor (Dodecenoyl-CoA isomerase) (Delta(3),delta(2)-enoyl-CoA isomerase) (D3,D2-enoyl-CoA isomerase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1169205</td><td>>gi|1169205|sp|P42125|D3D2_MOUSE 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor (Dodecenoyl-CoA isomerase) (Delta(3),delta(2)-enoyl-CoA isomerase) (D3,D2-enoyl-CoA isomerase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>817974</td><td>>gi|817974|emb|CAA78418.1| dodecenoyl-CoA delta isomerase [Mus musculus]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>414902</td><td>>gi|414902|emb|CAA78417.1| dodecenoyl-CoA delta-isomerase [Mus musculus]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>17939654</td><td>>gi|17939654|gb|AAH19316.1| Dodecenoyl-Coenzyme A delta isomerase, precursor [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>12653937</td><td>>gi|12653937|gb|AAH00762.1| Dodecenoyl-Coenzyme A delta isomerase, precursor [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>472987</td><td>>gi|472987|emb|CAA81065.1| dodecenoyl-CoA delta-isomerase [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>203900</td><td>>gi|203900|gb|AAA41073.1| delta-3,delta-2-enoyl-CoA isomerase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>73959489</td><td>>gi|73959489|ref|XP_547179.2| PREDICTED: similar to 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor (Dodecenoyl-CoA delta-isomerase) (D3,D2-enoyl-CoA isomerase) [Canis familiaris]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>56967286</td><td>>gi|56967286|pdb|1XX4|A Chain A, Crystal Structure Of Rat Mitochondrial 3,2-Enoyl-Coa</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>56556524</td><td>>gi|56556524|gb|AAH87779.1| Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase) [Xenopus tropicalis]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
58332142	>gi|58332142|ref|NP_001011219.1| dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase) [Xenopus tropicalis]			x	
76652799	>gi|76652799|ref|XP_615184.2| PREDICTED: similar to 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor (Dodecenoyl-CoA isomerase) (Delta(3),delta(2)-enoyl-CoA isomerase) (D3,D2-enoyl-CoA isomerase) isoform 1 [Bos taurus]			x	
511635	>gi|511635|gb|AAA35485.1| delta3, delta2-enoyl-CoA isomerase			x	
60593481	>gi|60593481|pdb|1SG4|C Chain C, Crystal Structure Of Human Mitochondrial Delta3-Delta2- Enoyl-Coa Isomerase			x	
60593480	>gi|60593480|pdb|1SG4|B Chain B, Crystal Structure Of Human Mitochondrial Delta3-Delta2- Enoyl-Coa Isomerase			x	
60593479	>gi|60593479|pdb|1SG4|A Chain A, Crystal Structure Of Human Mitochondrial Delta3-Delta2- Enoyl-Coa Isomerase			x	
82654933	>gi|82654933|sp|Q13011|ECH1_HUMAN Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor			x	
6015047	>gi|6015047|sp|Q62651|ECH1_RAT Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor			x	
3122065	>gi|3122065|sp|O35459|ECH1_MOUSE Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor			x	
75055278	>gi|75055278|sp|Q5RFG0|ECH1_PONPY Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor			x	
4699609	>gi|4699609|pdb|1DCI|C Chain C, Dienoyl-Coa Isomerase			x	
4699608	>gi|4699608|pdb|1DCI|B Chain B, Dienoyl-Coa Isomerase			x	
4699607	>gi|4699607|pdb|1DCI|A Chain A, Dienoyl-Coa Isomerase			x	
18307432	>gi|18307432|emb|CAD21495.1| probable DELTA3, 5-DELTA2, 4-DIENOYL-COA ISOMERASE PRECURSOR (ECH1) [Neurospora crassa]			x	
49176283	>gi|49176283|ref|NP_417394.3| methylmalonyl-CoA decarboxylase, biotin-independent [Escherichia coli K12]			x	
85675730	>gi|85675730|dbj|BAE76983.1| methylmalonyl-CoA decarboxylase, biotin-independent [Escherichia coli W3110]			x	
1723839	>gi|1723839|sp|P52045|MMCD_ECOLI Methylmalonyl-CoA decarboxylase (Transcarboxylase) (MMCD)			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>8569417</td><td>>gi|8569417|pdb|1EF9|A Chain A, The Crystal Structure Of Methylmalonyl Coa Decarboxylase Complexed With 2s-Carboxypropyl Coa</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>8569416</td><td>>gi|8569416|pdb|1EF8|C Chain C, Crystal Structure Of Methylmalonyl Coa Decarboxylase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>8569415</td><td>>gi|8569415|pdb|1EF8|B Chain B, Crystal Structure Of Methylmalonyl Coa Decarboxylase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>8569414</td><td>>gi|8569414|pdb|1EF8|A Chain A, Crystal Structure Of Methylmalonyl Coa Decarboxylase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>62897607</td><td>>gi|62897607|dbj|BAD96743.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase isoform 1 variant [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>37594471</td><td>>gi|37594471|ref|NP_055177.2| 3-hydroxyisobutyryl-Coenzyme A hydrolase isoform 1 [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>62897519</td><td>>gi|62897519|dbj|BAD96699.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase isoform 1 variant [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>45767881</td><td>>gi|45767881|gb|AAH67822.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase, isoform 1 [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>22122625</td><td>>gi|22122625|ref|NP_666220.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase [Mus musculus]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>20071741</td><td>>gi|20071741|gb|AAH26437.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase [Mus musculus]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>61403546</td><td>>gi|61403546|gb|AAH91995.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase [Danio rerio]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>62122813</td><td>>gi|62122813|ref|NP_001014338.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase [Danio rerio]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>3320120</td><td>>gi|3320120|gb|AAC52114.1| 3-hydroxyisobutyryl-coenzyme A hydrolase [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>71895123</td><td>>gi|71895123|ref|NP_001026414.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase [Gallus gallus]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15239206</td><td>>gi|15239206|ref|NP_201395.1| CHY1 (BETA-HYDROXYISOBUTYRYL-COA HYDROLASE 1); 3-hydroxyisobutyryl-CoA hydrolase [Arabidopsis thaliana]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
24030391	>gi|24030391|gb|AAN41356.1| putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]			x	
9759578	>gi|9759578|dbj|BAB11141.1| 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]			x	
17428312	>gi|17428312|emb|CAD15000.1| PROBABLE ENOYL(3-HYDROXYISOBUTYRYL)-COENZYME A HYDRATASE PROTEIN [Ralstonia solanacearum]			x	
83749668	>gi|83749668|ref|ZP_00946649.1| 3-hydroxyisobutyryl-CoA hydrolase [Ralstonia solanacearum UW551]			x	
83723670	>gi|83723670|gb|EAP70867.1| 3-hydroxyisobutyryl-CoA hydrolase [Ralstonia solanacearum UW551]			x	
2880043	>gi|2880043|gb|AAC02737.1| 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]			x	
83747299	>gi|83747299|ref|ZP_00944340.1| 3-hydroxyisobutyryl-CoA hydrolase [Ralstonia solanacearum UW551]			x	
83725999	>gi|83725999|gb|EAP73136.1| 3-hydroxyisobutyryl-CoA hydrolase [Ralstonia solanacearum UW551]			x	
2880042	>gi|2880042|gb|AAC02736.1| 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]			x	
29895975	>gi|29895975|gb|AAP09256.1| 3-hydroxyisobutyryl-coenzyme A hydrolase [Bacillus cereus ATCC 14579]			x	
51976589	>gi|51976589|gb|AAU18139.1| 3-hydroxyisobutyryl-coenzyme A hydrolase [Bacillus cereus E33L]			x	
49329189	>gi|49329189|gb|AAT59835.1| 3-hydroxyisobutyryl-coenzyme A hydrolase [Bacillus thuringiensis serovar konkukian str. 97-27]			x	
14027690	>gi|14027690|dbj|BAB54283.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase [Mesorhizobium loti MAFF303099]			x	
22329062	>gi|22329062|ref|NP_194909.2| 3-hydroxyisobutyryl-CoA hydrolase/ catalytic [Arabidopsis thaliana]			x	
42565158	>gi|42565158|ref|NP_189079.2| 3-hydroxyisobutyryl-CoA hydrolase/ catalytic [Arabidopsis thaliana]			x	
66851010	>gi|66851010|gb|EAL91336.1| mitochondrial 3-hydroxyisobutyryl-CoA hydrolase, putative [Aspergillus fumigatus Af293]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>70997244</td><td>>gi|70997244|ref|XP_753374.1| mitochondrial 3-hydroxyisobutyryl-CoA hydrolase [Aspergillus fumigatus Af293]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>30679729</td><td>>gi|30679729|ref|NP_172142.2| 3-hydroxyisobutyryl-CoA hydrolase/ catalytic [Arabidopsis thaliana]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>62320504</td><td>>gi|62320504|dbj|BAD95058.1| 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77554202</td><td>>gi|77554202|gb|ABA96998.1| 3-hydroxyisobutyryl-coenzyme A hydrolase, putative [Oryza sativa (japonica cultivar-group)]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77554203</td><td>>gi|77554203|gb|ABA96999.1| 3-hydroxyisobutyryl-coenzyme A hydrolase, putative [Oryza sativa (japonica cultivar-group)]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>37594469</td><td>>gi|37594469|ref|NP_932164.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase isoform 2 [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>52628217</td><td>>gi|52628217|gb|AAU26958.1| 3-hydroxyisobutyryl Coenzyme A hydrolase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>52841106</td><td>>gi|52841106|ref|YP_094905.1| 3-hydroxyisobutyryl Coenzyme A hydrolase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>79332547</td><td>>gi|79332547|ref|NP_001032155.1| CHY1 (BETA-HYDROXYISOBUTYRYL-COA HYDROLASE 1); 3-hydroxyisobutyryl-CoA hydrolase [Arabidopsis thaliana]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>50725651</td><td>>gi|50725651|dbj|BAD33117.1| putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Oryza sativa (japonica cultivar-group)]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>50725401</td><td>>gi|50725401|dbj|BAD32875.1| putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Oryza sativa (japonica cultivar-group)]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84717486</td><td>>gi|84717486|ref|ZP_01023545.1| probable enoyl(3-hydroxyisobutyryl)-coenzyme A hydratase protein [Polaromonas naphthalenivorans CJ2]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84692147</td><td>>gi|84692147|gb|EAQ17970.1| probable enoyl(3-hydroxyisobutyryl)-coenzyme A hydratase protein [Polaromonas naphthalenivorans CJ2]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>49238423</td><td>>gi|49238423|emb|CAF27650.1| 3-hydroxyisobutyryl-coenzyme A hydrolase [Bartonella henselae str. Houston-1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>53733532</td><td>>gi|53733532|gb|AAH83737.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase (predicted) [Rattus norvegicus]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>61556993</td><td>>gi|61556993|ref|NP_001013130.1| 3-hydroxyisobutyryl-Coenzyme A hydrolase (predicted) [Rattus norvegicus]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>2392484</td><td>>gi|2392484|pdb|1NZY|C Chain C, 4-Chlorobenzoyl Coenzyme A Dehalogenase From Pseudomonas Sp. Strain Cbs-3</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>2392482</td><td>>gi|2392482|pdb|1NZY|A Chain A, 4-Chlorobenzoyl Coenzyme A Dehalogenase From Pseudomonas Sp. Strain Cbs-3</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>4584855</td><td>>gi|4584855|gb|AAD25164.1| 4-chlorobenzoyl CoA dehalogenase [Arthrobacter sp. SU]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>8517279</td><td>>gi|8517279|gb|AAF76241.1| 4-chlorobenzoyl CoA dehalogenase [Arthrobacter sp. TM1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>11991170</td><td>>gi|11991170|gb|AAG42236.1| 4-chlorobenzoate Co-A dehalogenase [Arthrobacter globiformis]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>142207</td><td>>gi|142207|gb|AAC80223.1| 4-chlorobenzoyl CoA dehalogenase [Arthrobacter sp. SU]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>477389</td><td>>gi|477389|pir||A48956 4-chlorobenzoate-CoA dehalogenase - Arthrobacter sp</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>13516855</td><td>>gi|13516855|dbj|BAB40580.1| 4-CBA-CoA dehalogenase [Arthrobacter sp. FHP1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>13516852</td><td>>gi|13516852|dbj|BAB40577.1| 4-CBA-CoA dehalogenase [Arthrobacter sp. FHP1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>419529</td><td>>gi|419529|pir||A42560 4-chlorobenzoate dehalogenase (EC 3.8.1.6), 30K chain - Pseudomonas sp. (strain CBS-3)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>8712875</td><td>>gi|8712875|gb|AAF78820.1| 4-chlorobenzoyl CoA dehalogenase [Arthrobacter sp. TM1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>2952540</td><td>>gi|2952540|gb|AAC05576.1| 4-chlorobenzoyl CoA dehalogenase [Pseudomonas sp. DJ-12]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>2392483</td><td>>gi|2392483|pdb|1NZY|B Chain B, 4-Chlorobenzoyl Coenzyme A Dehalogenase From Pseudomonas Sp. Strain Cbs-3</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>22901870</td><td>>gi|22901870|gb|AAN10108.1| 4-chlorobenzoyl CoA dehalogenase [Alcaligenes sp. AL3007]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>56381431</td><td>>gi|56381431|dbj|BAD77339.1| enolase (2-phosphoglycerate dehydratase) [Geobacillus kaustophilus HTA426]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
56421589	>gi|56421589|ref|YP_148907.1| phosphopyruvate hydratase [Geobacillus kaustophilus HTA426]			x	
68053527	>gi|68053527|sp|Q5KVE7|ENO_GEOKA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
21646048	>gi|21646048|gb|AAM71393.1| enolase [Chlorobium tepidum TLS]			x	
29839350	>gi|29839350|sp|Q8KG25|ENO2_CHLTE Enolase 2 (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x	
21672986	>gi|21672986|ref|NP_661051.1| enolase [Chlorobium tepidum TLS]			x	
46048768	>gi|46048768|ref|NP_990451.1| enolase 1 [Gallus gallus]			x	
1706653	>gi|1706653|sp|P51913|ENOA_CHICK Alpha-enolase (2-phospho-D-glycerate hydro-lyase) (Phosphopyruvate hydratase)			x	
974176	>gi|974176|dbj|BAA07132.1| enolase [Gallus gallus]			x	
68067447	>gi|68067447|sp|P15007|ENO_DROME Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
50363841	>gi|50363841|gb|AAT75826.1| enolase [Mesoplasma florum L1]			x	
59797546	>gi|59797546|sp|Q6F0Z7|ENO_MESFL Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
50365285	>gi|50365285|ref|YP_053710.1| enolase [Mesoplasma florum L1]			x	
23495020	>gi|23495020|gb|AAN35353.1| enolase [Plasmodium falciparum 3D7]			x	
23507959	>gi|23507959|ref|NP_700629.1| enolase [Plasmodium falciparum 3D7]			x	
50400239	>gi|50400239|sp|Q8IJN7|ENO_PLAF7 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
29650775	>gi|29650775|gb|AAO86694.1| enolase [Dunaliella salina]			x	
20516770	>gi|20516770|gb|AAM24953.1| Enolase [Thermoanaerobacter tengcongensis MB4]			x	
23814070	>gi|23814070|sp|Q8R967|ENO_THETN Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
20808178	>gi|20808178|ref|NP_623349.1| Enolase [Thermoanaerobacter tengcongensis MB4]			x	
1363309	>gi|1363309|pir||JC1039 phosphopyruvate hydratase (EC 4.2.1.11) - rat			x	
32880095	>gi|32880095|gb|AAP88878.1| enolase 2, (gamma, neuronal) [synthetic construct]			x	
60652679	>gi|60652679|gb|AAX29034.1| enolase 2 [synthetic construct]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
60652677	>gi|60652677|gb|AAX29033.1| enolase 2 [synthetic construct]			x	
31165	>gi|31165|emb|CAA36215.1| human gamma enolase [Homo sapiens]			x	
30583605	>gi|30583605|gb|AAP36047.1| enolase 2, (gamma, neuronal) [Homo sapiens]			x	
1732416	>gi|1732416|gb|AAB51320.1| neuron specific gamma-enolase [Homo sapiens]			x	
60655773	>gi|60655773|gb|AAX32450.1| enolase 2 [synthetic construct]			x	
60655771	>gi|60655771|gb|AAX32449.1| enolase 2 [synthetic construct]			x	
60820629	>gi|60820629|gb|AAX36542.1| enolase 2 [synthetic construct]			x	
12803811	>gi|12803811|gb|AAH02745.1| Enolase 2 [Homo sapiens]			x	
20981682	>gi|20981682|sp|P09104|ENOG_HUMAN Gamma-enolase (2-phospho-D-glycerate hydro-lyase) (Neural enolase) (Neuron-specific enolase) (NSE) (Enolase 2)			x	
182116	>gi|182116|gb|AAB59554.1| enolase			x	
5803011	>gi|5803011|ref|NP_001966.1| enolase 2 [Homo sapiens]			x	
37805239	>gi|37805239|gb|AAH60310.1| Enolase 2, gamma [Rattus norvegicus]			x	
119349	>gi|119349|sp|P07323|ENOG_RAT Gamma-enolase (2-phospho-D-glycerate hydro-lyase) (Neural enolase) (Neuron-specific enolase) (NSE) (Enolase 2)			x	
2465396	>gi|2465396|gb|AAB72088.1| neuron-specific enolase [Rattus norvegicus]			x	
26023949	>gi|26023949|ref|NP_647541.1| enolase 2, gamma [Rattus norvegicus]			x	
204042	>gi|204042|gb|AAA41119.1| neuron-specific enolase			x	
225406	>gi|225406|prf||1302225A enolase gamma,neuron specific			x	
56496865	>gi|56496865|emb|CAH99714.1| enolase, putative [Plasmodium berghei]			x	
68070065	>gi|68070065|ref|XP_676944.1| enolase [Plasmodium berghei strain ANKA]			x	
45382393	>gi|45382393|ref|NP_990207.1| enolase 2 (gamma, neuronal) [Gallus gallus]			x	
6015090	>gi|6015090|sp|O57391|ENOG_CHICK Gamma-enolase (2-phospho-D-glycerate hydro-lyase) (Neural enolase) (NSE)			x	
2842531	>gi|2842531|dbj|BAA24680.1| gamma-subunit of enolase [Gallus gallus]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
3023709	>gi|3023709|sp|Q27727|ENO_PLAFA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
392027	>gi|392027|gb|AAA18634.1| enolase			x	
76797225	>gi|76797225|ref|ZP_00779559.1| Enolase [Thermoanaerobacter ethanolicus ATCC 33223]			x	
76587403	>gi|76587403|gb|EAO63841.1| Enolase [Thermoanaerobacter ethanolicus ATCC 33223]			x	
55669907	>gi|55669907|pdb|1TE6|B Chain B, Crystal Structure Of Human Neuron Specific Enolase At 1.8 Angstrom			x	
55669906	>gi|55669906|pdb|1TE6|A Chain A, Crystal Structure Of Human Neuron Specific Enolase At 1.8 Angstrom			x	
19281	>gi|19281|emb|CAA41115.1| enolase [Lycopersicon esculentum]			x	
119354	>gi|119354|sp|P26300|ENO_LYCES Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
930101	>gi|930101|emb|CAA32505.1| gamma enolase [Homo sapiens]			x	
930063	>gi|930063|emb|CAA31512.1| neurone-specific enolase [Homo sapiens]			x	
5305421	>gi|5305421|gb|AAD41643.1| alpha enolase [Alligator mississippiensis]			x	
17367042	>gi|17367042|sp|Q9PVK2|ENOA_ALLMI Alpha-enolase (2-phospho-D-glycerate hydro-lyase) (Phosphopyruvate hydratase)			x	
21618816	>gi|21618816|gb|AAH31739.1| Enolase 2, gamma neuronal [Mus musculus]			x	
7305027	>gi|7305027|ref|NP_038537.1| enolase 2, gamma neuronal [Mus musculus]			x	
119348	>gi|119348|sp|P17183|ENOG_MOUSE Gamma-enolase (2-phospho-D-glycerate hydro-lyase) (Neural enolase) (Neuron-specific enolase) (NSE) (Enolase 2)			x	
50400247	>gi|50400247|sp|Q9UAL5|ENO_PLAFG Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
4589933	>gi|4589933|dbj|BAA76924.1| enolase [Plasmodium falciparum]			x	
28270478	>gi|28270478|emb|CAD63380.1| phosphopyruvate hydratase [Lactobacillus plantarum WCFS1]			x	
56711116	>gi|56711116|emb|CAD99191.1| enolase [Lactobacillus plantarum]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>28377645</td><td>>gi|28377645|ref|NP_784537.1| phosphopyruvate hydratase [Lactobacillus plantarum WCFS1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>38257528</td><td>>gi|38257528|sp|Q88YH3|ENO1_LACPL Enolase 1 (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>56757324</td><td>>gi|56757324|sp|P04764|ENOA_RAT Alpha-enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>30583767</td><td>>gi|30583767|gb|AAP36132.1| Homo sapiens enolase 1, (alpha) [synthetic construct]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>61373094</td><td>>gi|61373094|gb|AAX43977.1| enolase 1 [synthetic construct]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>61364993</td><td>>gi|61364993|gb|AAX42637.1| enolase 1 [synthetic construct]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>60824596</td><td>>gi|60824596|gb|AAX36686.1| enolase 1 [synthetic construct]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>4503571</td><td>>gi|4503571|ref|NP_001419.1| enolase 1 [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1167843</td><td>>gi|1167843|emb|CAA34360.1| alpha-enolase [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>13325287</td><td>>gi|13325287|gb|AAH04458.1| Enolase 1 [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15990505</td><td>>gi|15990505|gb|AAH15641.1| Enolase 1 [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>12804749</td><td>>gi|12804749|gb|AAH01810.1| Enolase 1 [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>14530765</td><td>>gi|14530765|emb|CAC42425.1| enolase 1, (alpha) [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>18490320</td><td>>gi|18490320|gb|AAH22545.1| Enolase 1 [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>30583165</td><td>>gi|30583165|gb|AAP35827.1| enolase 1, (alpha) [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>66268795</td><td>>gi|66268795|gb|AAY43128.1| enolase 1, (alpha) [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>60655647</td><td>>gi|60655647|gb|AAX32387.1| enolase 1 [synthetic construct]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>60655645</td><td>>gi|60655645|gb|AAX32386.1| enolase 1 [synthetic construct]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>61354812</td><td>>gi|61354812|gb|AAX41062.1| enolase 1 [synthetic construct]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>60812591</td><td>>gi|60812591|gb|AAX36218.1| enolase 1 [synthetic construct]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>14602814</td><td>>gi|14602814|gb|AAH09912.1| Enolase 1 [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>20379496</td><td>>gi|20379496|gb|AAH27725.1| Enolase 1 [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15029814</td><td>>gi|15029814|gb|AAH11130.1| Enolase 1 [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>182114</td><td>>gi|182114|gb|AAA52387.1| alpha enolase (EC 4.2.1.11)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>62897945</td><td>>gi|62897945|dbj|BAD96912.1| enolase 1 variant [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>5305427</td><td>>gi|5305427|gb|AAD41646.1| alpha enolase [Python regius]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>17367183</td><td>>gi|17367183|sp|Q9W7L0|ENOA_PYTRG Alpha-enolase (2-phospho-D-glycerate hydro-lyase) (Phosphopyruvate hydratase)</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
82752500	>gi|82752500|ref|XP_727327.1| enolase [Plasmodium yoelii yoelii str. 17XNL]			x	
23483115	>gi|23483115|gb|EAA18892.1| enolase [Plasmodium yoelii yoelii]			x	
54673814	>gi|54673814|gb|AAH85098.1| Enolase 1, alpha non-neuron [Mus musculus]			x	
19353272	>gi|19353272|gb|AAH24644.1| Enolase 1, alpha non-neuron [Mus musculus]			x	
14715046	>gi|14715046|gb|AAH10685.1| Enolase 1, alpha non-neuron [Mus musculus]			x	
13278078	>gi|13278078|gb|AAH03891.1| Enolase 1, alpha non-neuron [Mus musculus]			x	
13637776	>gi|13637776|sp|P17182|ENOA_MOUSE Alpha-enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1)			x	
21325986	>gi|21325986|gb|AAM47554.1| alpha-enolase [Crocodylus palustris]			x	
21325984	>gi|21325984|gb|AAM47553.1| alpha-enolase [Crocodylus palustris]			x	
21325982	>gi|21325982|gb|AAM47552.1| alpha-enolase [Crocodylus palustris]			x	
693933	>gi|693933|emb|CAA59331.1| 2-phosphopyruvate-hydratase alpha-enolase; carbonate dehydratase [Homo sapiens]			x	
62896593	>gi|62896593|dbj|BAD96237.1| enolase 1 variant [Homo sapiens]			x	
31167	>gi|31167|emb|CAA40163.1| muscle specific enolase [Homo sapiens]			x	
416950	>gi|416950|sp|P13929|ENOB_HUMAN Beta-enolase (2-phospho-D-glycerate hydro-lyase) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase) (Enolase 3)			x	
59808815	>gi|59808815|gb|AAH90069.1| Enolase 1, alpha [Rattus norvegicus]			x	
34789	>gi|34789|emb|CAA36216.1| muscle-specific enolase [Homo sapiens]			x	
16554592	>gi|16554592|ref|NP_443739.1| enolase 3 [Homo sapiens]			x	
4503573	>gi|4503573|ref|NP_001967.1| enolase 3 [Homo sapiens]			x	
23003759	>gi|23003759|ref|ZP_00047409.1| COG0148: Enolase [Lactobacillus gasseri]			x	
16878083	>gi|16878083|gb|AAH17249.1| Enolase 3 [Homo sapiens]			x	
37222051	>gi|37222051|gb|AAQ17040.2| pollen 2-phosphoglycerate dehydrogenase 2 precursor [Cynodon dactylon]			x	
602253	>gi|602253|gb|AAD04187.1| enolase [Zea mays]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
1169528	>gi|1169528|sp|P42895|ENO2_MAIZE Enolase 2 (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x	
54035288	>gi|54035288|gb|AAH83566.1| Enolase 3, beta [Rattus norvegicus]			x	
83319528	>gi|83319528|ref|YP_424200.1| enolase [Mycoplasma capricolum subsp. capricolum ATCC 27343]			x	
83283414	>gi|83283414|gb|ABC01346.1| enolase [Mycoplasma capricolum subsp. capricolum ATCC 27343]			x	
8919602	>gi|8919602|emb|CAB96126.1| chloroplast enolase [Euglena gracilis]			x	
42518800	>gi|42518800|ref|NP_964730.1| enolase [Lactobacillus johnsonii NCC 533]			x	
41583086	>gi|41583086|gb|AAS08696.1| enolase [Lactobacillus johnsonii NCC 533]			x	
59797825	>gi|59797825|sp|Q74K78|ENO1_LACJO Enolase 1 (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x	
77994855	>gi|77994855|gb|ABB13754.1| enolase [Carboxydothermus hydrogenoformans Z-2901]			x	
78042740	>gi|78042740|ref|YP_359156.1| enolase [Carboxydothermus hydrogenoformans Z-2901]			x	
68194237	>gi|68194237|gb|EAN08760.1| Enolase [Enterococcus faecium DO]			x	
69249235	>gi|69249235|ref|ZP_00604912.1| Enolase [Enterococcus faecium DO]			x	
50400235	>gi|50400235|sp|Q7RA60|ENO_PLAYO Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
5305423	>gi|5305423|gb|AAD41644.1| alpha enolase [Sceloporus undulatus]			x	
17367189	>gi|17367189|sp|Q9W7L2|ENOA_SCEUN Alpha-enolase (2-phospho-D-glycerate hydro-lyase) (Phosphopyruvate hydratase)			x	
12963491	>gi|12963491|ref|NP_075608.1| enolase 1, alpha non-neuron [Mus musculus]			x	
2635903	>gi|2635903|emb|CAB15395.1| enolase [Bacillus subtilis subsp. subtilis str. 168]			x	
6166147	>gi|6166147|sp|P37869|ENO_BACSU Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
16080443	>gi|16080443|ref|NP_391270.1| phosphopyruvate hydratase [Bacillus subtilis subsp. subtilis str. 168]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
6679651	>gi|6679651|ref|NP_031959.1| enolase 3, beta muscle [Mus musculus]			x	
15488630	>gi|15488630|gb|AAH13460.1| Enolase 3, beta muscle [Mus musculus]			x	
50144	>gi|50144|emb|CAA44540.1| beta-enolase [Mus musculus]			x	
50849	>gi|50849|emb|CAA43797.1| enolase [Mus musculus]			x	
50847	>gi|50847|emb|CAA40913.1| enolase [Mus musculus]			x	
56206033	>gi|56206033|emb|CAI25173.1| enolase 3, beta muscle [Mus musculus]			x	
119344	>gi|119344|sp|P21550|ENOB_MOUSE Beta-enolase (2-phospho-D-glycerate hydro-lyase) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase) (Enolase 3)			x	
119356	>gi|119356|sp|P08734|ENOA_XENLA Alpha-enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
33113259	>gi|33113259|gb|AAP94211.1| enolase [Oryza sativa (japonica cultivar-group)]			x	
18175728	>gi|18175728|gb|AAL59917.1| putative enolase (2-phospho-D-glycerate hydroylase) [Arabidopsis thaliana]			x	
22852211	>gi|22852211|dbj|BAC16223.1| enolase [Enterococcus hirae]			x	
29839250	>gi|29839250|sp|Q8GR70|ENO_ENTHR Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
34810922	>gi|34810922|pdb|1IYX|B Chain B, Crystal Structure Of Enolase From Enterococcus Hirae			x	
34810921	>gi|34810921|pdb|1IYX|A Chain A, Crystal Structure Of Enolase From Enterococcus Hirae			x	
51973903	>gi|51973903|gb|AAU15453.1| enolase [Bacillus cereus E33L]			x	
59797506	>gi|59797506|sp|Q631M2|ENO_BACCZ Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
52140434	>gi|52140434|ref|YP_086395.1| enolase [Bacillus cereus E33L]			x	
55590655	>gi|55590655|ref|XP_514354.1| PREDICTED: enolase 1 [Pan troglodytes]			x	
52005169	>gi|52005169|gb|AAU25111.1| enolase [Bacillus licheniformis ATCC 14580]			x	
52081958	>gi|52081958|ref|YP_080749.1| phosphopyruvate hydratase [Bacillus licheniformis ATCC 14580]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
52787346	>gi|52787346|ref|YP_093175.1| phosphopyruvate hydratase [Bacillus licheniformis ATCC 14580]			x	
10176180	>gi|10176180|dbj|BAB07275.1| enolase (2-phosphoglycerate dehydratase) [Bacillus halodurans C-125]			x	
13124133	>gi|13124133|sp|Q9K717|ENO_BACHD Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
15616118	>gi|15616118|ref|NP_244423.1| enolase (2-phosphoglycerate dehydratase) [Bacillus halodurans C-125]			x	
15227987	>gi|15227987|ref|NP_181192.1| LOS2; phosphopyruvate hydratase [Arabidopsis thaliana]			x	
16271	>gi|16271|emb|CAA41114.1| enolase [Arabidopsis thaliana]			x	
23297411	>gi|23297411|gb|AAN12963.1| enolase (2-phospho-D-glycerate hydroylase) [Arabidopsis thaliana]			x	
4581151	>gi|4581151|gb|AAD24635.1| enolase (2-phospho-D-glycerate hydroylase) [Arabidopsis thaliana]			x	
119350	>gi|119350|sp|P25696|ENO_ARATH Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
65317107	>gi|65317107|ref|ZP_00390066.1| COG0148: Enolase [Bacillus anthracis str. A2012]			x	
49333355	>gi|49333355|gb|AAT64001.1| enolase [Bacillus thuringiensis serovar konkukian str. 97-27]			x	
47505822	>gi|47505822|gb|AAT34498.1| enolase [Bacillus anthracis str. 'Ames Ancestor']			x	
49181898	>gi|49181898|gb|AAT57274.1| enolase [Bacillus anthracis str. Sterne]			x	
49187971	>gi|49187971|ref|YP_031224.1| enolase [Bacillus anthracis str. Sterne]			x	
49481799	>gi|49481799|ref|YP_039123.1| enolase [Bacillus thuringiensis serovar konkukian str. 97-27]			x	
30259838	>gi|30259838|gb|AAP29024.1| enolase [Bacillus anthracis str. Ames]			x	
59797557	>gi|59797557|sp|Q6HBF3|ENO_BACHK Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
59797626	>gi|59797626|sp|Q81X78|ENO_BACAN Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
47530674	>gi|47530674|ref|YP_022023.1| enolase [Bacillus anthracis str. 'Ames Ancestor']			x	
30265161	>gi|30265161|ref|NP_847538.1| enolase [Bacillus anthracis str. Ames]			x	
47567341	>gi|47567341|ref|ZP_00238054.1| enolase [Bacillus cereus G9241]			x	
47555962	>gi|47555962|gb|EAL14300.1| enolase [Bacillus cereus G9241]			x	
8670811	>gi|8670811|emb|CAB94910.1| enolase [Enterococcus faecalis]			x	
29343947	>gi|29343947|gb|AAO81707.1| enolase [Enterococcus faecalis V583]			x	
13124132	>gi|13124132|sp|Q9K596|ENO_ENTFA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
29376483	>gi|29376483|ref|NP_815637.1| enolase [Enterococcus faecalis V583]			x	
14141143	>gi|14141143|gb|AAF71925.2| beta beta enolase [Oryctolagus cuniculus]			x	
20141354	>gi|20141354|sp|P25704|ENOB_RABIT Beta-enolase (2-phospho-D-glycerate hydro-lyase) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase) (Enolase 3)			x	
460259	>gi|460259|gb|AAA21681.1| enolase			x	
42784284	>gi|42784284|ref|NP_981531.1| enolase [Bacillus cereus ATCC 10987]			x	
42740215	>gi|42740215|gb|AAS44139.1| enolase [Bacillus cereus ATCC 10987]			x	
59797591	>gi|59797591|sp|Q72XY5|ENO_BACC1 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
65304337	>gi|65304337|emb|CAI76716.1| enolase, putative [Theileria annulata]			x	
84997239	>gi|84997239|ref|XP_953341.1| enolase [Theileria annulata strain Ankara]			x	
42492297	>gi|42492297|emb|CAE76894.1| phosphopyruvate hydratase [Mycoplasma mycoides subsp. mycoides SC]			x	
42560801	>gi|42560801|ref|NP_975252.1| phosphopyruvate hydratase [Mycoplasma mycoides subsp. mycoides SC str. PG1]			x	
59797570	>gi|59797570|sp|Q6MTZ2|ENO_MYCMS Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
37590349	>gi|37590349|gb|AAH59511.1| Enolase 1, (alpha) [Danio rerio]			x	
48865594	>gi|48865594|ref|ZP_00319453.1| COG0148: Enolase [Oenococcus oeni PSU-1]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
62513221	>gi|62513221|ref|ZP_00384782.1| COG0148: Enolase [Lactobacillus casei ATCC 334]			x	
48762657	>gi|48762657|ref|NP_997887.1| enolase 1, (alpha) [Danio rerio]			x	
47939355	>gi|47939355|gb|AAH71359.1| Enolase 1, (alpha) [Danio rerio]			x	
83589135	>gi|83589135|ref|YP_429144.1| enolase [Moorella thermoacetica ATCC 39073]			x	
83572049	>gi|83572049|gb|ABC18601.1| enolase [Moorella thermoacetica ATCC 39073]			x	
8919731	>gi|8919731|emb|CAB96173.1| enolase [Spinacia oleracea]			x	
780372	>gi|780372|gb|AAC49173.1| enolase			x	
3023713	>gi|3023713|sp|Q42971|ENO_ORYSA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (OSE1)			x	
29898732	>gi|29898732|gb|AAP12004.1| Enolase [Bacillus cereus ATCC 14579]			x	
59797625	>gi|59797625|sp|Q815K8|ENO_BACCR Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
30023172	>gi|30023172|ref|NP_834803.1| enolase [Bacillus cereus ATCC 14579]			x	
75763414	>gi|75763414|ref|ZP_00743143.1| Enolase [Bacillus thuringiensis serovar israelensis ATCC 35646]			x	
74489099	>gi|74489099|gb|EAO52586.1| Enolase [Bacillus thuringiensis serovar israelensis ATCC 35646]			x	
38511762	>gi|38511762|gb|AAH61287.1| Enolase (2-phosphoglycerate dehydratase) [Xenopus tropicalis]			x	
45361015	>gi|45361015|ref|NP_989144.1| Enolase (2-phosphoglycerate dehydratase) [Xenopus tropicalis]			x	
433609	>gi|433609|emb|CAA82232.1| enolase [Ricinus communis]			x	
1169534	>gi|1169534|sp|P42896|ENO_RICCO Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
6978809	>gi|6978809|ref|NP_036686.1| enolase 1, alpha [Rattus norvegicus]			x	
68351290	>gi|68351290|gb|EAN32053.1| enolase, putative [Theileria parva]			x	
71029386	>gi|71029386|ref|XP_764336.1| enolase [Theileria parva strain Muguga]			x	
533474	>gi|533474|gb|AAA21277.1| 2-phospho-D-glycerate hydrolase			x	
8919600	>gi|8919600|emb|CAB96125.1| enolase [Euglena gracilis]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
6226608	>gi|6226608|sp|P42848|ENO_THEMA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
55297212	>gi|55297212|dbj|BAD68886.1| putative enolase [Oryza sativa (japonica cultivar-group)]			x	
55296986	>gi|55296986|dbj|BAD68461.1| putative enolase [Oryza sativa (japonica cultivar-group)]			x	
33415263	>gi|33415263|gb|AAQ18140.1| enolase [Gossypium barbadense]			x	
4981411	>gi|4981411|gb|AAD35958.1| enolase [Thermotoga maritima MSB8]			x	
15643639	>gi|15643639|ref|NP_228685.1| enolase [Thermotoga maritima MSB8]			x	
20260174	>gi|20260174|gb|AAM12985.1| enolase (2-phospho-D-glycerate hydroylase) [Arabidopsis thaliana]			x	
37681795	>gi|37681795|gb|AAQ97775.1| enolase 1, (alpha) [Danio rerio]			x	
47551317	>gi|47551317|ref|NP_999888.1| enolase 3, (beta, muscle) [Danio rerio]			x	
56911024	>gi|56911024|dbj|BAD65551.1| enolase [Bacillus clausii KSM-K16]			x	
59797489	>gi|59797489|sp|Q5WDK9|ENO_BACSK Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
56964781	>gi|56964781|ref|YP_176512.1| enolase [Bacillus clausii KSM-K16]			x	
78170524	>gi|78170524|gb|ABB27620.1| Enolase [Chlorobium chlorochromatii CaD3]			x	
78188325	>gi|78188325|ref|YP_378663.1| Enolase [Chlorobium chlorochromatii CaD3]			x	
1087071	>gi|1087071|gb|AAB34986.1| 2-phospho-D-glycerate hydrolase; enolase [Mesembryanthemum crystallinum]			x	
3023714	>gi|3023714|sp|Q43130|ENO_MESCR Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
78194830	>gi|78194830|gb|ABB32597.1| Enolase [Geobacter metallireducens GS-15]			x	
78223575	>gi|78223575|ref|YP_385322.1| Enolase [Geobacter metallireducens GS-15]			x	
12619316	>gi|12619316|gb|AAG60329.1| enolase [Toxoplasma gondii]			x	
37359340	>gi|37359340|gb|AAP24057.1| enolase 2 [Toxoplasma gondii]			x	
50400628	>gi|50400628|sp|Q9BPL7|ENO2_TOXGO Enolase 2 (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
27262298	>gi|27262298|gb|AAN87430.1| Enolase [Heliobacillus mobilis]			x	
9581744	>gi|9581744|emb|CAC00532.1| enolase, isoform 1 [Hevea brasiliensis]			x	
14423688	>gi|14423688|sp|Q9LEJ0|ENO1_HEVBR Enolase 1 (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1) (Allergen Hev b 9)			x	
51573166	>gi|51573166|gb|AAU07191.1| enolase [Borrelia garinii PBi]			x	
59797519	>gi|59797519|sp|Q661T0|ENO_BORGA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
51598595	>gi|51598595|ref|YP_072783.1| enolase [Borrelia garinii PBi]			x	
2983135	>gi|2983135|gb|AAC06738.1| enolase [Aquifex aeolicus VF5]			x	
6015091	>gi|6015091|sp|O66778|ENO_AQUAE Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
15605961	>gi|15605961|ref|NP_213338.1| enolase [Aquifex aeolicus VF5]			x	
39984275	>gi|39984275|gb|AAR35662.1| enolase [Geobacter sulfurreducens PCA]			x	
39997384	>gi|39997384|ref|NP_953335.1| enolase [Geobacter sulfurreducens PCA]			x	
59797601	>gi|59797601|sp|Q74AR6|ENO_GEOSL Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
68551301	>gi|68551301|ref|ZP_00590717.1| Enolase [Pelodictyon phaeoclathratiforme BU-1]			x	
68241814	>gi|68241814|gb|EAN24059.1| Enolase [Pelodictyon phaeoclathratiforme BU-1]			x	
6996529	>gi|6996529|emb|CAB75428.1| enolase [Lupinus luteus]			x	
68086449	>gi|68086449|gb|AAH92869.2| Enolase 3, (beta, muscle) [Danio rerio]			x	
29349980	>gi|29349980|ref|NP_813483.1| phosphopyruvate hydratase [Bacteroides thetaiotaomicron VPI-5482]			x	
29341891	>gi|29341891|gb|AAO79677.1| enolase [Bacteroides thetaiotaomicron VPI-5482]			x	
59797633	>gi|59797633|sp|Q89Z05|ENO_BACTN Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
28202574	>gi|28202574|gb|AAO35019.1| enolase [Clostridium tetani E88]			x	
28210138	>gi|28210138|ref|NP_781082.1| phosphopyruvate hydratase [Clostridium tetani E88]			x	
59797631	>gi|59797631|sp|Q898R0|ENO_CLOTE Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
81428222	>gi|81428222|ref|YP_395222.1| Phosphopyruvate hydratase [Lactobacillus sakei subsp. sakei 23K]			x	
78609864	>gi|78609864|emb|CAI54911.1| Phosphopyruvate hydratase [Lactobacillus sakei subsp. sakei 23K]			x	
55846716	>gi|55846716|gb|AAV67362.1| enolase 2 [Macaca fascicularis]			x	
71481429	>gi|71481429|ref|ZP_00661136.1| Enolase [Prosthecochloris vibrioformis DSM 265]			x	
71283904	>gi|71283904|gb|EAO15726.1| Enolase [Prosthecochloris vibrioformis DSM 265]			x	
21901927	>gi|21901927|emb|CAD42362.1| alpha-enolase protein [Bacteroides fragilis]			x	
52215345	>gi|52215345|dbj|BAD47938.1| enolase [Bacteroides fragilis YCH46]			x	
53712480	>gi|53712480|ref|YP_098472.1| phosphopyruvate hydratase [Bacteroides fragilis YCH46]			x	
60680680	>gi|60680680|ref|YP_210824.1| phosphopyruvate hydratase [Bacteroides fragilis NCTC 9343]			x	
2688240	>gi|2688240|gb|AAC66719.1| enolase (eno) [Borrelia burgdorferi B31]			x	
3913583	>gi|3913583|sp|O51312|ENO_BORBU Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
15594682	>gi|15594682|ref|NP_212471.1| enolase (eno) [Borrelia burgdorferi B31]			x	
34597330	>gi|34597330|gb|AAQ77240.1| enolase [Brassica rapa]			x	
68056418	>gi|68056418|ref|ZP_00540539.1| Enolase [Exiguobacterium sp. 255-15]			x	
68006980	>gi|68006980|gb|EAM86270.1| Enolase [Exiguobacterium sp. 255-15]			x	
78167716	>gi|78167716|gb|ABB24814.1| Enolase [Pelodictyon luteolum DSM 273]			x	
78187814	>gi|78187814|ref|YP_375857.1| Enolase [Pelodictyon luteolum DSM 273]			x	
66797943	>gi|66797943|ref|ZP_00396700.1| Enolase [Deinococcus geothermalis DSM 11300]			x	
66781652	>gi|66781652|gb|EAL82619.1| Enolase [Deinococcus geothermalis DSM 11300]			x	
15023593	>gi|15023593|gb|AAK78690.1| Enolase [Clostridium acetobutylicum ATCC 824]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>15894001</td><td>>gi|15894001|ref|NP_347350.1| phosphopyruvate hydratase [Clostridium acetobutylicum ATCC 824]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>21263598</td><td>>gi|21263598|sp|Q97L52|ENO_CLOAB Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>48855292</td><td>>gi|48855292|ref|ZP_00309451.1| COG0148: Enolase [Cytophaga hutchinsonii]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>48869740</td><td>>gi|48869740|ref|ZP_00322483.1| COG0148: Enolase [Pediococcus pentosaceus ATCC 25745]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>13937125</td><td>>gi|13937125|gb|AAK50056.1| enolase [Trichinella spiralis]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68245979</td><td>>gi|68245979|gb|EAN28087.1| Enolase [Magnetococcus sp. MC-1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>69259295</td><td>>gi|69259295|ref|ZP_00607469.1| Enolase [Magnetococcus sp. MC-1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>46399418</td><td>>gi|46399418|emb|CAF22867.1| probable phosphopyruvate hydratase (enolase) [Parachlamydia sp. UWE25]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>46445777</td><td>>gi|46445777|ref|YP_007142.1| probable phosphopyruvate hydratase (enolase) [Candidatus Protochlamydia amoebophila UWE25]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>59797567</td><td>>gi|59797567|sp|Q6MEY2|ENO_PARUW Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>42521309</td><td>>gi|42521309|gb|AAS18240.1| enolase [Glycine max]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>54040759</td><td>>gi|54040759|sp|P64074|ENO_LISMO Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>54037038</td><td>>gi|54037038|sp|P64075|ENO_LISIN Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>46908628</td><td>>gi|46908628|ref|YP_015017.1| enolase [Listeria monocytogenes str. 4b F2365]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>47094180</td><td>>gi|47094180|ref|ZP_00231897.1| enolase [Listeria monocytogenes str. 4b H7858]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>47017442</td><td>>gi|47017442|gb|EAL08258.1| enolase [Listeria monocytogenes str. 4b H7858]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>59797577</td><td>>gi|59797577|sp|Q71WX1|ENO_LISMF Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>46881900</td><td>>gi|46881900|gb|AAT05194.1| enolase [Listeria monocytogenes str. 4b F2365]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>232054</td><td>>gi|232054|sp|P30575|ENO1_CANAL Enolase 1 (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>170861</td><td>>gi|170861|gb|AAB46358.1| enolase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>170863</td><td>>gi|170863|gb|AAA71939.1| enolase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>170865</td><td>>gi|170865|gb|AAA34341.1| enolase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>50839631</td><td>>gi|50839631|gb|AAT82298.1| enolase [Propionibacterium acnes KPA171202]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>50842029</td><td>>gi|50842029|ref|YP_055256.1| phosphopyruvate hydratase [Propionibacterium acnes KPA171202]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>59797531</td><td>>gi|59797531|sp|Q6AAB8|ENO_PROAC Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>74693378</td><td>>gi|74693378|sp|Q756H2|ENO_ASHGO Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67917474</td><td>>gi|67917474|ref|ZP_00511080.1| Enolase [Chlorobium limicola DSM 245]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67784777</td><td>>gi|67784777|gb|EAM44150.1| Enolase [Chlorobium limicola DSM 245]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>627094</td><td>>gi|627094|pir||A53665 phosphopyruvate hydratase (EC 4.2.1.11) - liver fluke</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>42526461</td><td>>gi|42526461|ref|NP_971559.1| enolase [Treponema denticola ATCC 35405]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>41816654</td><td>>gi|41816654|gb|AAS11440.1| enolase [Treponema denticola ATCC 35405]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>59797597</td><td>>gi|59797597|sp|Q73P50|ENO_TREDE Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>9581746</td><td>>gi|9581746|emb|CAC00533.1| enolase, isoform 2 [Hevea brasiliensis]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>14423687</td><td>>gi|14423687|sp|Q9LEI9|ENO2_HEVBR Enolase 2 (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2) (Allergen Hev b 9)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>515827</td><td>>gi|515827|emb|CAA56645.1| enolase [Neocallimastix frontalis]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1169533</td><td>>gi|1169533|sp|P42894|ENO_NEOFR Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>71839487</td><td>>gi|71839487|ref|ZP_00679235.1| Enolase [Pelobacter propionicus DSM 2379]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
71740070	>gi|71740070|gb|EAO35240.1| Enolase [Pelobacter propionicus DSM 2379]			x	
51855076	>gi|51855076|dbj|BAD39234.1| enolase [Symbiobacterium thermophilum IAM 14863]			x	
59797528	>gi|59797528|sp|Q67SV9|ENO_SYMTH Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
51891387	>gi|51891387|ref|YP_074078.1| enolase [Symbiobacterium thermophilum IAM 14863]			x	
37693129	>gi|37693129|emb|CAE51943.1| enolase [Kluyveromyces lactis]			x	
74662255	>gi|74662255|sp|Q70CP7|ENO_KLULA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
22273	>gi|22273|emb|CAA39454.1| enolase [Zea mays]			x	
119355	>gi|119355|sp|P26301|ENO1_MAIZE Enolase 1 (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x	
56711110	>gi|56711110|emb|CAD98929.1| enolase [Lactobacillus sakei]			x	
14089932	>gi|14089932|emb|CAC13691.1| ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) [Mycoplasma pulmonis]			x	
15828989	>gi|15828989|ref|NP_326349.1| phosphopyruvate hydratase [Mycoplasma pulmonis UAB CTIP]			x	
21263603	>gi|21263603|sp|Q98Q50|ENO_MYCPU Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
74830161	>gi|74830161|emb|CAI39017.1| enolase, putative [Paramecium tetraurelia]			x	
13774515	>gi|13774515|gb|AAK38886.1| enolase [Eimeria tenella]			x	
50400241	>gi|50400241|sp|Q967Y8|ENO_EIMTE Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
22778120	>gi|22778120|dbj|BAC14390.1| enolase (2-phosphoglycerate dehydratase) [Oceanobacillus iheyensis HTE831]			x	
29839242	>gi|29839242|sp|Q8ENP5|ENO_OCEIH Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
23099889	>gi|23099889|ref|NP_693355.1| enolase [Oceanobacillus iheyensis HTE831]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
60280039	>gi|60280039|gb|AAX16379.1| enolase [uncultured murine large bowel bacterium BAC 31B]			x	
68551717	>gi|68551717|ref|ZP_00591111.1| Enolase [Prosthecochloris aestuarii DSM 271]			x	
68241214	>gi|68241214|gb|EAN23481.1| Enolase [Prosthecochloris aestuarii DSM 271]			x	
34597332	>gi|34597332|gb|AAQ77241.1| enolase [Brassica napus]			x	
67154735	>gi|67154735|ref|ZP_00416480.1| Enolase [Azotobacter vinelandii AvOP]			x	
67088868	>gi|67088868|gb|EAM08334.1| Enolase [Azotobacter vinelandii AvOP]			x	
46578738	>gi|46578738|ref|YP_009546.1| enolase [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]			x	
46448150	>gi|46448150|gb|AAS94805.1| enolase [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]			x	
59797581	>gi|59797581|sp|Q72F92|ENO_DESVH Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
499267	>gi|499267|gb|AAA57450.1| enolase [Fasciola hepatica]			x	
3023708	>gi|3023708|sp|Q27655|ENO_FASHE Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
119336	>gi|119336|sp|P00924|ENO1_YEAST Enolase 1 (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x	
171455	>gi|171455|gb|AAA88712.1| enolase			x	
6321693	>gi|6321693|ref|NP_011770.1| Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2-phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p [Saccharomyces cerevisiae]			x	
77544917	>gi|77544917|gb|ABA88479.1| enolase [Pelobacter carbinolicus DSM 2380]			x	
77918834	>gi|77918834|ref|YP_356649.1| enolase [Pelobacter carbinolicus DSM 2380]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
5459136	>gi|5459136|emb|CAB50622.1| eno enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (EC 4.2.1.11) [Pyrococcus abyssi GE5]			x	
14521916	>gi|14521916|ref|NP_127393.1| phosphopyruvate hydratase [Pyrococcus abyssi GE5]			x	
7436884	>gi|7436884|pir||H75022 phosphopyruvate hydratase (EC 4.2.1.11) PAB1126 - Pyrococcus abyssi (strain Orsay)			x	
49257392	>gi|49257392|gb|AAH72713.1| Enolase 2 [Danio rerio]			x	
51467931	>gi|51467931|ref|NP_001003848.1| enolase 2 [Danio rerio]			x	
74316639	>gi|74316639|ref|YP_314379.1| phosphopyruvate hydratase [Thiobacillus denitrificans ATCC 25259]			x	
74056134	>gi|74056134|gb|AAZ96574.1| enolase (phosphopyruvate hydratase) [Thiobacillus denitrificans ATCC 25259]			x	
83593220	>gi|83593220|ref|YP_426972.1| Phosphopyruvate hydratase [Rhodospirillum rubrum ATCC 11170]			x	
83576134	>gi|83576134|gb|ABC22685.1| Phosphopyruvate hydratase [Rhodospirillum rubrum ATCC 11170]			x	
74661257	>gi|74661257|sp|Q6FQY4|ENO2_CANGA Enolase 2 (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x	
2494354	>gi|2494354|sp|Q27527|ENO_CAEEL Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
23024413	>gi|23024413|ref|ZP_00063626.1| COG0148: Enolase [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]			x	
67157908	>gi|67157908|ref|ZP_00419053.1| Enolase [Azotobacter vinelandii AvOP]			x	
67085177	>gi|67085177|gb|EAM04653.1| Enolase [Azotobacter vinelandii AvOP]			x	
55771384	>gi|55771384|dbj|BAD69825.1| enolase (2-phosphoglycerate dehydratase) [Thermus thermophilus HB8]			x	
46199912	>gi|46199912|ref|YP_005579.1| enolase [Thermus thermophilus HB27]			x	
46197539	>gi|46197539|gb|AAS81952.1| enolase [Thermus thermophilus HB27]			x	
68053536	>gi|68053536|sp|Q5SME1|ENO_THET8 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
59797582	>gi|59797582|sp|Q72H85|ENO_THET2 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
55979971	>gi|55979971|ref|YP_143268.1| enolase (2-phosphoglycerate dehydratase) [Thermus thermophilus HB8]			x	
78217747	>gi|78217747|gb|ABB37096.1| enolase [Desulfovibrio desulfuricans G20]			x	
78355342	>gi|78355342|ref|YP_386791.1| enolase [Desulfovibrio desulfuricans G20]			x	
74830117	>gi|74830117|emb|CAI39008.1| enolase, putative [Paramecium tetraurelia]			x	
76792445	>gi|76792445|ref|ZP_00774944.1| Enolase [Pseudoalteromonas atlantica T6c]			x	
76592227	>gi|76592227|gb|EAO68418.1| Enolase [Pseudoalteromonas atlantica T6c]			x	
67157754	>gi|67157754|ref|ZP_00418949.1| Enolase [Azotobacter vinelandii AvOP]			x	
67085336	>gi|67085336|gb|EAM04811.1| Enolase [Azotobacter vinelandii AvOP]			x	
2914550	>gi|2914550|pdb|2ONE|B Chain B, Asymmetric Yeast Enolase Dimer Complexed With Resolved 2'-Phosphoglycerate And Phosphoenolpyruvate			x	
2914549	>gi|2914549|pdb|2ONE|A Chain A, Asymmetric Yeast Enolase Dimer Complexed With Resolved 2'-Phosphoglycerate And Phosphoenolpyruvate			x	
1942653	>gi|1942653|pdb|1ONE|B Chain B, Yeast Enolase Complexed With An Equilibrium Mixture Of 2'-Phosphoglyceate And Phosphoenolpyruvate			x	
1942652	>gi|1942652|pdb|1ONE|A Chain A, Yeast Enolase Complexed With An Equilibrium Mixture Of 2'-Phosphoglyceate And Phosphoenolpyruvate			x	
1065029	>gi|1065029|pdb|1EBH|B Chain B, Enolase (E.C.4.2.1.11) (2-Phospho-D-Glycerate Hydrolase) Complexed With Mg 2+			x	
1065028	>gi|1065028|pdb|1EBH|A Chain A, Enolase (E.C.4.2.1.11) (2-Phospho-D-Glycerate Hydrolase) Complexed With Mg 2+			x	
1065026	>gi|1065026|pdb|1EBG|B Chain B, Enolase (E.C.4.2.1.11) (2-Phospho-D-Glycerate Hydrolase) (Apo Form)			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
1065025	>gi|1065025|pdb|1EBG|A Chain A, Enolase (E.C.4.2.1.11) (2-Phospho-D-Glycerate Hydrolase) (Apo Form)			x	
3885968	>gi|3885968|gb|AAC78141.1| phosphopyruvate hydratase [Penaeus monodon]			x	
6978811	>gi|6978811|ref|NP_037081.1| enolase 3, beta [Rattus norvegicus]			x	
119346	>gi|119346|sp|P15429|ENOB_RAT Beta-enolase (2-phospho-D-glycerate hydro-lyase) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase) (Enolase 3)			x	
231253	>gi|231253|pdb|7ENL| Enolase (E.C.4.2.1.11) (2-Phospho-D-Glycerate Hydrolase) Complex With 2-Phospho-D-Glyceric Acid And Magnesium			x	
231208	>gi|231208|pdb|6ENL| Enolase (E.C.4.2.1.11) (2-Phospho-D-Glycerate Hydrolase) Complex With Phosphoglycolic Acid And Zinc			x	
231132	>gi|231132|pdb|5ENL| Enolase (E.C.4.2.1.11) (2-Phospho-D-Glycerate Hydrolase) Complex With 2-Phospho-D-Glyceric Acid And Calcium			x	
230999	>gi|230999|pdb|4ENL| Enolase (E.C.4.2.1.11) (2-Phospho-D-Glycerate Hydrolase) (Holo)			x	
230846	>gi|230846|pdb|3ENL| Enolase (E.C.4.2.1.11) (2-Phospho-D-Glycerate Hydrolase) (Apo)			x	
494413	>gi|494413|pdb|1NEL| Enolase (E.C.4.2.1.11) (2-Phospho-D-Glycerate Hydrolase) Complex With Orthophosphate, Fluoride And Magnesium			x	
576098	>gi|576098|pdb|1ELS| Enolase (E.C.4.2.1.11) (2-Phospho-D-Glycerate Hydrolase) Complexed With Phosphonoacetohydroxamate And Manganese			x	
68179394	>gi|68179394|ref|ZP_00552459.1| Enolase [Desulfuromonas acetoxidans DSM 684]			x	
67980540	>gi|67980540|gb|EAM70039.1| Enolase [Desulfuromonas acetoxidans DSM 684]			x	
67935050	>gi|67935050|ref|ZP_00528074.1| Enolase [Chlorobium phaeobacteroides DSM 266]			x	
67775945	>gi|67775945|gb|EAM35607.1| Enolase [Chlorobium phaeobacteroides DSM 266]			x	
53830714	>gi|53830714|gb|AAU95200.1| enolase [Oncometopia nigricans]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
75765318	>gi|75765318|pdb|1W6T|B Chain B, Crystal Structure Of Octameric Enolase From Streptococcus Pneumoniae			x	
75765317	>gi|75765317|pdb|1W6T|A Chain A, Crystal Structure Of Octameric Enolase From Streptococcus Pneumoniae			x	
67924949	>gi|67924949|ref|ZP_00518338.1| Enolase [Crocosphaera watsonii WH 8501]			x	
67853210	>gi|67853210|gb|EAM48580.1| Enolase [Crocosphaera watsonii WH 8501]			x	
462011	>gi|462011|sp|P33676|ENO_SCHJA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
349802	>gi|349802|gb|AAA29874.1| enolase			x	
13124159	>gi|13124159|sp|Q9UXZ0|ENO_PYRAB Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
67941827	>gi|67941827|ref|ZP_00533828.1| Enolase [Chlorobium phaeobacteroides BS1]			x	
67911958	>gi|67911958|gb|EAM61806.1| Enolase [Chlorobium phaeobacteroides BS1]			x	
68536569	>gi|68536569|ref|YP_251274.1| phosphopyruvate hydratase [Corynebacterium jeikeium K411]			x	
6460466	>gi|6460466|gb|AAF12173.1| enolase [Deinococcus radiodurans R1]			x	
13124156	>gi|13124156|sp|Q9RR60|ENO_DEIRA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
15807616	>gi|15807616|ref|NP_296355.1| enolase [Deinococcus radiodurans R1]			x	
82746640	>gi|82746640|ref|ZP_00909145.1| Enolase [Clostridium beijerincki NCIMB 8052]			x	
82725598	>gi|82725598|gb|EAP60342.1| Enolase [Clostridium beijerincki NCIMB 8052]			x	
59802545	>gi|59802545|sp|P33675|ENO_ZYMMO Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
56552504	>gi|56552504|ref|YP_163343.1| enolase [Zymomonas mobilis subsp. mobilis ZM4]			x	
56544078	>gi|56544078|gb|AAV90232.1| enolase [Zymomonas mobilis subsp. mobilis ZM4]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
66964439	>gi|66964439|ref|ZP_00412009.1| Enolase [Arthrobacter sp. FB24]			x	
66869966	>gi|66869966|gb|EAL97332.1| Enolase [Arthrobacter sp. FB24]			x	
38199773	>gi|38199773|emb|CAE49433.1| Enolase [Corynebacterium diphtheriae]			x	
59797574	>gi|59797574|sp|Q6NI61|ENO_CORDI Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
38233513	>gi|38233513|ref|NP_939280.1| phosphopyruvate hydratase [Corynebacterium diphtheriae NCTC 13129]			x	
458897	>gi|458897|gb|AAB68019.1| Eno2p: Enolase 2; 2-phosphoglycerate dehydratase [Saccharomyces cerevisiae]			x	
6321968	>gi|6321968|ref|NP_012044.1| Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2-phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p [Saccharomyces cerevisiae]			x	
119337	>gi|119337|sp|P00925|ENO2_YEAST Enolase 2 (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x	
171457	>gi|171457|gb|AAA88713.1| enolase			x	
23492880	>gi|23492880|dbj|BAC17852.1| putative enolase [Corynebacterium efficiens YS-314]			x	
29839246	>gi|29839246|sp|Q8FQS7|ENO_COREF Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
25027598	>gi|25027598|ref|NP_737652.1| phosphopyruvate hydratase [Corynebacterium efficiens YS-314]			x	
71546423	>gi|71546423|ref|ZP_00667224.1| Enolase [Syntrophobacter fumaroxidans MPOB]			x	
71487780	>gi|71487780|gb|EAO20220.1| Enolase [Syntrophobacter fumaroxidans MPOB]			x	
1590967	>gi|1590967|gb|AAB98220.1| enolase (eno) [Methanocaldococcus jannaschii DSM 2661]			x	
15668407	>gi|15668407|ref|NP_247203.1| enolase (eno) [Methanocaldococcus jannaschii DSM 2661]			x	
2118303	>gi|2118303|pir||A64329 phosphopyruvate hydratase (EC 4.2.1.11) - Methanococcus jannaschii			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
23465590	>gi|23465590|ref|NP_696193.1| enolase [Bifidobacterium longum NCC2705]			x	
29839248	>gi|29839248|sp|Q8G5I9|ENO_BIFLO Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
23326258	>gi|23326258|gb|AAN24829.1| enolase [Bifidobacterium longum NCC2705]			x	
13569595	>gi|13569595|gb|AAK31161.1| enolase [Mastigamoeba balamuthi]			x	
6469814	>gi|6469814|gb|AAF13454.1| enolase [Mastigamoeba balamuthi]			x	
21542033	>gi|21542033|sp|Q9U615|ENO_MASBA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
67940099	>gi|67940099|ref|ZP_00532567.1| Enolase [Chlorobium phaeobacteroides BS1]			x	
67913681	>gi|67913681|gb|EAM63061.1| Enolase [Chlorobium phaeobacteroides BS1]			x	
39654416	>gi|39654416|pdb|1P43|B Chain B, Reverse Protonation Is The Key To General Acid-Base Catalysis In Enolase			x	
39654415	>gi|39654415|pdb|1P43|A Chain A, Reverse Protonation Is The Key To General Acid-Base Catalysis In Enolase			x	
74659032	>gi|74659032|sp|Q6BI20|ENO2_DEBHA Enolase 2 (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x	
46133204	>gi|46133204|ref|ZP_00156796.2| COG0148: Enolase [Haemophilus influenzae R2866]			x	
66879038	>gi|66879038|ref|ZP_00404072.1| COG0148: Enolase [Streptococcus pneumoniae TIGR4]			x	
14972605	>gi|14972605|gb|AAK75238.1| enolase [Streptococcus pneumoniae TIGR4]			x	
15900994	>gi|15900994|ref|NP_345598.1| phosphopyruvate hydratase [Streptococcus pneumoniae TIGR4]			x	
21263599	>gi|21263599|sp|Q97QS2|ENO_STRPN Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
1041245	>gi|1041245|emb|CAA63121.1| enolase [Alnus glutinosa]			x	
3023685	>gi|3023685|sp|Q43321|ENO_ALNGL Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
1911573	>gi|1911573|gb|AAB50731.1| enolase [Loligo pealei]			x	
3023702	>gi|3023702|sp|O02654|ENO_LOLPE Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
16272869	>gi|16272869|ref|NP_439092.1| phosphopyruvate hydratase [Haemophilus influenzae Rd KW20]			x	
1573953	>gi|1573953|gb|AAC22590.1| enolase (eno) [Haemophilus influenzae Rd KW20]			x	
1169532	>gi|1169532|sp|P43806|ENO_HAEIN Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
79042712	>gi|79042712|ref|ZP_00873466.1| Enolase [Novosphingobium aromaticivorans DSM 12444]			x	
78772757	>gi|78772757|gb|EAP36449.1| Enolase [Novosphingobium aromaticivorans DSM 12444]			x	
57015278	>gi|57015278|sp|Q5XD01|ENO_STRP6 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
15458655	>gi|15458655|gb|AAK99840.1| Enolase [Streptococcus pneumoniae R6]			x	
15903080	>gi|15903080|ref|NP_358630.1| phosphopyruvate hydratase [Streptococcus pneumoniae R6]			x	
29839236	>gi|29839236|sp|Q8DPS0|ENO_STRR6 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
18144961	>gi|18144961|dbj|BAB81005.1| enolase [Clostridium perfringens str. 13]			x	
18310281	>gi|18310281|ref|NP_562215.1| phosphopyruvate hydratase [Clostridium perfringens str. 13]			x	
21263576	>gi|21263576|sp|Q8XKU4|ENO_CLOPE Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
68057718	>gi|68057718|gb|AAX87971.1| enolase [Haemophilus influenzae 86-028NP]			x	
68249519	>gi|68249519|ref|YP_248631.1| phosphopyruvate hydratase [Haemophilus influenzae 86-028NP]			x	
59797517	>gi|59797517|sp|Q65VZ7|ENO_MANSM Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
52424311	>gi|52424311|ref|YP_087448.1| phosphopyruvate hydratase [Mannheimia succiniciproducens MBEL55E]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
57160365	>gi|57160365|dbj|BAD86295.1| enolase [Thermococcus kodakarensis KOD1]			x	
57642041	>gi|57642041|ref|YP_184519.1| phosphopyruvate hydratase [Thermococcus kodakarensis KOD1]			x	
68053526	>gi|68053526|sp|Q5JEV6|ENO_PYRKO Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
13621912	>gi|13621912|gb|AAK33680.1| putative enolase [Streptococcus pyogenes M1 GAS]			x	
71802296	>gi|71802296|gb|AAX71649.1| enolase [Streptococcus pyogenes MGAS6180]			x	
19747973	>gi|19747973|gb|AAL97462.1| putative enolase [Streptococcus pyogenes MGAS8232]			x	
21904205	>gi|21904205|gb|AAM79086.1| putative enolase [Streptococcus pyogenes MGAS315]			x	
28811538	>gi|28811538|dbj|BAC64470.1| putative enolase [Streptococcus pyogenes SSI-1]			x	
21910015	>gi|21910015|ref|NP_664283.1| phosphopyruvate hydratase [Streptococcus pyogenes MGAS315]			x	
28896287	>gi|28896287|ref|NP_802637.1| phosphopyruvate hydratase [Streptococcus pyogenes SSI-1]			x	
19745827	>gi|19745827|ref|NP_606963.1| phosphopyruvate hydratase [Streptococcus pyogenes MGAS8232]			x	
15674785	>gi|15674785|ref|NP_268959.1| phosphopyruvate hydratase [Streptococcus pyogenes M1 GAS]			x	
57013833	>gi|57013833|sp|P69951|ENO_STRP8 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
57013832	>gi|57013832|sp|P69950|ENO_STRP3 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
57013831	>gi|57013831|sp|P69949|ENO_STRP1 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
71903201	>gi|71903201|ref|YP_280004.1| phosphopyruvate hydratase [Streptococcus pyogenes MGAS6180]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
77411108	>gi|77411108|ref|ZP_00787461.1| enolase [Streptococcus agalactiae CJB111]			x	
77162831	>gi|77162831|gb|EAO73789.1| enolase [Streptococcus agalactiae CJB111]			x	
85089455	>gi|85089455|ref|XP_957959.1| ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) [Neurospora crassa N150]			x	
74662419	>gi|74662419|sp|Q7RV85|ENO_NEUCR Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
32405096	>gi|32405096|ref|XP_323161.1| ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) [Neurospora crassa]			x	
28919250	>gi|28919250|gb|EAA28723.1| ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) [Neurospora crassa]			x	
71847604	>gi|71847604|gb|AAZ47100.1| Enolase [Dechloromonas aromatica RCB]			x	
71907983	>gi|71907983|ref|YP_285570.1| phosphopyruvate hydratase [Dechloromonas aromatica RCB]			x	
41325200	>gi|41325200|emb|CAF19681.1| ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE [Corynebacterium glutamicum ATCC 13032]			x	
21323741	>gi|21323741|dbj|BAB98367.1| Enolase [Corynebacterium glutamicum ATCC 13032]			x	
62389865	>gi|62389865|ref|YP_225267.1| phosphopyruvate hydratase [Corynebacterium glutamicum ATCC 13032]			x	
19552199	>gi|19552199|ref|NP_600201.1| phosphopyruvate hydratase [Corynebacterium glutamicum ATCC 13032]			x	
23814062	>gi|23814062|sp|Q8NRS1|ENO_CORGL Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
80973065	>gi|80973065|gb|ABB53261.1| enolase [Corynebacterium glutamicum]			x	
77406132	>gi|77406132|ref|ZP_00783205.1| enolase [Streptococcus agalactiae H36B]			x	
77175255	>gi|77175255|gb|EAO78051.1| enolase [Streptococcus agalactiae H36B]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
76798989	>gi|76798989|ref|ZP_00781188.1| enolase [Streptococcus agalactiae 18RS21]			x	
76585660	>gi|76585660|gb|EAO62219.1| enolase [Streptococcus agalactiae 18RS21]			x	
76563415	>gi|76563415|gb|ABA45999.1| enolase [Streptococcus agalactiae A909]			x	
23095026	>gi|23095026|emb|CAD46252.1| enolase [Streptococcus agalactiae NEM316]			x	
22533646	>gi|22533646|gb|AAM99524.1| enolase [Streptococcus agalactiae 2603V/R]			x	
22536801	>gi|22536801|ref|NP_687652.1| phosphopyruvate hydratase [Streptococcus agalactiae 2603V/R]			x	
76788358	>gi|76788358|ref|YP_329341.1| phosphopyruvate hydratase [Streptococcus agalactiae A909]			x	
25010672	>gi|25010672|ref|NP_735067.1| phosphopyruvate hydratase [Streptococcus agalactiae NEM316]			x	
54037041	>gi|54037041|sp|P64081|ENO_STRA5 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
54040762	>gi|54040762|sp|P64080|ENO_STRA3 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
27806645	>gi|27806645|ref|NP_776474.1| enolase 1 [Bos taurus]			x	
4927286	>gi|4927286|gb|AAD33073.1| alpha enolase [Bos taurus]			x	
13124248	>gi|13124248|sp|Q9XSJ4|ENOA_BOVIN Alpha-enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1) (Phosphopyruvate hydratase) (HAP47)			x	
77952809	>gi|77952809|ref|ZP_00817222.1| Enolase [Marinobacter aquaeolei VT8]			x	
77868366	>gi|77868366|gb|EAO99636.1| Enolase [Marinobacter aquaeolei VT8]			x	
13092594	>gi|13092594|emb|CAC29763.1| putative enolase [Mycobacterium leprae]			x	
15827047	>gi|15827047|ref|NP_301310.1| phosphopyruvate hydratase [Mycobacterium leprae TN]			x	
25291616	>gi|25291616|pir||G86940 probable enolase [imported] - Mycobacterium leprae			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>1311141</td><td>>gi|1311141|pdb|1PDZ| Mol_id: 1; Molecule: Enolase; Chain: Null; Synonym: 2-Phospho-D-Glycerate Dehydratase; Ec: 4.2.1.11; Heterogen: Phosphoglycolate; Heterogen: Mn 2+</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1311142</td><td>>gi|1311142|pdb|1PDY| Mol_id: 1; Molecule: Enolase; Chain: Null; Synonym: 2-Phospho-D-Glycerate Dehydratase; Ec: 4.2.1.11</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>49531112</td><td>>gi|49531112|emb|CAG68824.1| enolase [Acinetobacter sp. ADP1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>50085136</td><td>>gi|50085136|ref|YP_046646.1| enolase [Acinetobacter sp. ADP1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>59797548</td><td>>gi|59797548|sp|Q6FAT9|ENO_ACIAD Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>55738590</td><td>>gi|55738590|gb|AAV62231.1| 2-phosphoglycerate dehydratase, enolase [Streptococcus thermophilus CNRZ1066]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>55822605</td><td>>gi|55822605|ref|YP_141046.1| phosphopyruvate hydratase [Streptococcus thermophilus CNRZ1066]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>55820714</td><td>>gi|55820714|ref|YP_139156.1| phosphopyruvate hydratase [Streptococcus thermophilus LMG 18311]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68053530</td><td>>gi|68053530|sp|Q5M561|ENO_STRT2 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68053529</td><td>>gi|68053529|sp|Q5M0M5|ENO_STRT1 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>55736699</td><td>>gi|55736699|gb|AAV60341.1| 2-phosphoglycerate dehydratase, enolase [Streptococcus thermophilus LMG 18311]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>19171969</td><td>>gi|19171969|gb|AAL85688.1| enolase [Streptococcus agalactiae]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>49244091</td><td>>gi|49244091|emb|CAG42517.1| putative enolase [Staphylococcus aureus subsp. aureus MSSA476]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>49241163</td><td>>gi|49241163|emb|CAG39841.1| putative enolase [Staphylococcus aureus subsp. aureus MRSA252]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>14246545</td><td>>gi|14246545|dbj|BAB56938.1| enolase [Staphylococcus aureus subsp. aureus Mu50]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>21203904</td><td>>gi|21203904|dbj|BAB94603.1| enolase [Staphylococcus aureus subsp. aureus MW2]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>57284304</td><td>>gi|57284304|gb|AAW36398.1| enolase [Staphylococcus aureus subsp. aureus COL]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>13700667</td><td>>gi|13700667|dbj|BAB41964.1| enolase [Staphylococcus aureus subsp. aureus N315]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>82750484</td><td>>gi|82750484|ref|YP_416225.1| enolase 2-phosphoglycerate dehydratase [Staphylococcus aureus RF122]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15926453</td><td>>gi|15926453|ref|NP_373986.1| enolase [Staphylococcus aureus subsp. aureus N315]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15923766</td><td>>gi|15923766|ref|NP_371300.1| enolase [Staphylococcus aureus subsp. aureus Mu50]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>57650118</td><td>>gi|57650118|ref|YP_185716.1| enolase [Staphylococcus aureus subsp. aureus COL]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>56748913</td><td>>gi|56748913|sp|Q6GB54|ENO_STAAS Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>56748924</td><td>>gi|56748924|sp|Q6GIL4|ENO_STAAR Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68053523</td><td>>gi|68053523|sp|Q5HHP1|ENO_STAAC Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>82656015</td><td>>gi|82656015|emb|CAI80420.1| enolase 2-phosphoglycerate dehydratase [Staphylococcus aureus RF122]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>54037040</td><td>>gi|54037040|sp|P64079|ENO_STAAW Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>54037045</td><td>>gi|54037045|sp|P99088|ENO_STAAN Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>54040761</td><td>>gi|54040761|sp|P64078|ENO_STAAM Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>49485648</td><td>>gi|49485648|ref|YP_042869.1| putative enolase [Staphylococcus aureus subsp. aureus MSSA476]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>49483034</td><td>>gi|49483034|ref|YP_040258.1| putative enolase [Staphylococcus aureus subsp. aureus MRSA252]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>21282467</td><td>>gi|21282467|ref|NP_645555.1| enolase (2-phosphoglycerate dehydrogenase) [Staphylococcus aureus subsp. aureus MW2]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>3023703</td><td>>gi|3023703|sp|P56252|ENO_HOMGA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
13124709	>gi|13124709|sp|O32513|ENO_DESVM Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
9695277	>gi|9695277|dbj|BAB07786.1| enolase [Desulfovibrio vulgaris]			x	
13431506	>gi|13431506|sp|P57975|ENO_PASMU Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
15603736	>gi|15603736|ref|NP_246810.1| phosphopyruvate hydratase [Pasteurella multocida subsp. multocida str. Pm70]			x	
16151617	>gi|16151617|emb|CAC83091.1| alpha-enolase [Streptococcus pneumoniae]			x	
17066742	>gi|17066742|gb|AAL35382.1| 2-phosphoglycerate dehydratase [Streptococcus thermophilus]			x	
24377625	>gi|24377625|gb|AAN58930.1| putative enolase [Streptococcus mutans UA159]			x	
29839238	>gi|29839238|sp|Q8DTS9|ENO_STRMU Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
24379669	>gi|24379669|ref|NP_721624.1| phosphopyruvate hydratase [Streptococcus mutans UA159]			x	
14021357	>gi|14021357|dbj|BAB47970.1| enolase [Mesorhizobium loti MAFF303099]			x	
21263602	>gi|21263602|sp|Q98MZ3|ENO_RHILO Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
13470615	>gi|13470615|ref|NP_102184.1| enolase [Mesorhizobium loti MAFF303099]			x	
3023710	>gi|3023710|sp|Q27877|ENO_SCHMA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
1002616	>gi|1002616|gb|AAC46886.1| enolase			x	
1002610	>gi|1002610|gb|AAC46884.1| enolase			x	
76556211	>gi|76556211|emb|CAD48738.1| enolase 1 [Propionibacterium freudenreichii subsp. shermanii]			x	
76257976	>gi|76257976|ref|ZP_00765633.1| Enolase [Chloroflexus aurantiacus J-10-fl]			x	
76167062	>gi|76167062|gb|EAO61185.1| Enolase [Chloroflexus aurantiacus J-10-fl]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
78363890	>gi|78363890|gb|ABB41855.1| enolase [Thiomicrospira crunogena XCL-2]			x	
78485604	>gi|78485604|ref|YP_391529.1| enolase [Thiomicrospira crunogena XCL-2]			x	
46164345	>gi|46164345|ref|ZP_00137024.2| COG0148: Enolase [Pseudomonas aeruginosa UCBPP-PA14]			x	
9949794	>gi|9949794|gb|AAG07023.1| enolase [Pseudomonas aeruginosa PAO1]			x	
15598831	>gi|15598831|ref|NP_252325.1| phosphopyruvate hydratase [Pseudomonas aeruginosa PAO1]			x	
84325641	>gi|84325641|ref|ZP_00973675.1| COG0148: Enolase [Pseudomonas aeruginosa 2192]			x	
13124125	>gi|13124125|sp|Q9HXZ5|ENO_PSEAE Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
21263608	>gi|21263608|sp|Q9CD42|ENO_MYCLE Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
68447834	>gi|68447834|dbj|BAE05418.1| enolase [Staphylococcus haemolyticus JCSC1435]			x	
70727110	>gi|70727110|ref|YP_254024.1| enolase [Staphylococcus haemolyticus JCSC1435]			x	
77414276	>gi|77414276|ref|ZP_00790435.1| enolase [Streptococcus agalactiae 515]			x	
77159655	>gi|77159655|gb|EAO70807.1| enolase [Streptococcus agalactiae 515]			x	
84497843	>gi|84497843|ref|ZP_00996640.1| phosphopyruvate hydratase [Janibacter sp. HTCC2649]			x	
84381343	>gi|84381343|gb|EAP97226.1| phosphopyruvate hydratase [Janibacter sp. HTCC2649]			x	
13124712	>gi|13124712|sp|Q60173|ENO_METJA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
3152725	>gi|3152725|gb|AAC17130.1| enolase [Staphylococcus aureus]			x	
6015099	>gi|6015099|sp|O69174|ENO_STAAU Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Laminin binding protein)			x	
40806812	>gi|40806812|gb|AAR92205.1| enolase [Cryphonectria parasitica]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
74661880	>gi|74661880|sp|Q6RG04|ENO_CRYPA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
82737565	>gi|82737565|ref|ZP_00900413.1| Enolase [Pseudomonas putida F1]			x	
82715369	>gi|82715369|gb|EAP50435.1| Enolase [Pseudomonas putida F1]			x	
3258386	>gi|3258386|dbj|BAA31069.1| 428aa long hypothetical phosphoglycerate dehydratase [Pyrococcus horikoshii OT3]			x	
6015098	>gi|6015098|sp|O59605|ENO_PYRHO Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
14591684	>gi|14591684|ref|NP_143772.1| phosphopyruvate hydratase [Pyrococcus horikoshii OT3]			x	
68188665	>gi|68188665|gb|EAN03344.1| Enolase [Methylobacillus flagellatus KT]			x	
68212975	>gi|68212975|ref|ZP_00564810.1| Enolase [Methylobacillus flagellatus KT]			x	
57866440	>gi|57866440|ref|YP_188039.1| enolase [Staphylococcus epidermidis RP62A]			x	
57637098	>gi|57637098|gb|AAW53886.1| enolase [Staphylococcus epidermidis RP62A]			x	
27315022	>gi|27315022|gb|AAO04158.1| enolase [Staphylococcus epidermidis ATCC 12228]			x	
27467479	>gi|27467479|ref|NP_764116.1| enolase [Staphylococcus epidermidis ATCC 12228]			x	
29839232	>gi|29839232|sp|Q8CPY3|ENO_STAES Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
68053524	>gi|68053524|sp|Q5HQV0|ENO_STAEQ Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
39721879	>gi|39721879|dbj|BAD04369.1| enolase [Onion yellows phytoplasma OY-M]			x	
59797575	>gi|59797575|sp|Q6YQT9|ENO_ONYPE Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
39938770	>gi|39938770|ref|NP_950536.1| enolase [Onion yellows phytoplasma OY-M]			x	
24053192	>gi|24053192|gb|AAN44282.1| enolase [Shigella flexneri 2a str. 301]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
75511922	>gi|75511922|ref|ZP_00734525.1| COG0148: Enolase [Escherichia coli 53638]			x	
75256986	>gi|75256986|ref|ZP_00728562.1| COG0148: Enolase [Escherichia coli E22]			x	
75241831	>gi|75241831|ref|ZP_00725650.1| COG0148: Enolase [Escherichia coli F11]			x	
75196750	>gi|75196750|ref|ZP_00706820.1| COG0148: Enolase [Escherichia coli HS]			x	
75187507	>gi|75187507|ref|ZP_00700774.1| COG0148: Enolase [Escherichia coli E24377A]			x	
75176359	>gi|75176359|ref|ZP_00696503.1| COG0148: Enolase [Shigella boydii BS512]			x	
1789141	>gi|1789141|gb|AAC75821.1| enolase [Escherichia coli K12]			x	
85675598	>gi|85675598|dbj|BAE76853.1| enolase [Escherichia coli W3110]			x	
30042382	>gi|30042382|gb|AAP18107.1| enolase [Shigella flexneri 2a str. 2457T]			x	
13363110	>gi|13363110|dbj|BAB37062.1| enolase [Escherichia coli O157:H7]			x	
26109589	>gi|26109589|gb|AAN81792.1| Enolase [Escherichia coli CFT073]			x	
82545078	>gi|82545078|ref|YP_409025.1| enolase [Shigella boydii Sb227]			x	
82778161	>gi|82778161|ref|YP_404510.1| enolase [Shigella dysenteriae Sd197]			x	
30064126	>gi|30064126|ref|NP_838297.1| phosphopyruvate hydratase [Shigella flexneri 2a str. 2457T]			x	
24114065	>gi|24114065|ref|NP_708575.1| phosphopyruvate hydratase [Shigella flexneri 2a str. 301]			x	
16130686	>gi|16130686|ref|NP_417259.1| phosphopyruvate hydratase [Escherichia coli K12]			x	
882673	>gi|882673|gb|AAA69289.1| enolase [Escherichia coli]			x	
15832893	>gi|15832893|ref|NP_311666.1| phosphopyruvate hydratase [Escherichia coli O157:H7]			x	
68053519	>gi|68053519|sp|P0A6Q2|ENO_SHIFL Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
68566315	>gi|68566315|sp|P0A6P9|ENO_ECOLI Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
68053517	>gi|68053517|sp|P0A6Q0|ENO_ECOL6 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
68053518	>gi|68053518|sp|P0A6Q1|ENO_ECO57 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
26249182	>gi|26249182|ref|NP_755222.1| phosphopyruvate hydratase [Escherichia coli CFT073]			x	
81242309	>gi|81242309|gb|ABB63019.1| enolase [Shigella dysenteriae Sd197]			x	
81246489	>gi|81246489|gb|ABB67197.1| enolase [Shigella boydii Sb227]			x	
59801045	>gi|59801045|ref|YP_207757.1| phosphopyruvate hydratase [Neisseria gonorrhoeae FA 1090]			x	
59717940	>gi|59717940|gb|AAW89345.1| putative enolase (2-phosphoglycerate dehydratase) [Neisseria gonorrhoeae FA 1090]			x	
66774125	>gi|66774125|sp|Q5F8Z2|ENO_NEIG1 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
74659376	>gi|74659376|sp|Q6BTB1|ENO1_DEBHA Enolase 1 (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x	
21112791	>gi|21112791|gb|AAM40994.1| enolase [Xanthomonas campestris pv. campestris str. ATCC 33913]			x	
66574171	>gi|66574171|gb|AAY49581.1| enolase [Xanthomonas campestris pv. campestris str. 8004]			x	
66768839	>gi|66768839|ref|YP_243601.1| phosphopyruvate hydratase [Xanthomonas campestris pv. campestris str. 8004]			x	
23814064	>gi|23814064|sp|Q8P9Z3|ENO_XANCP Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
21231153	>gi|21231153|ref|NP_637070.1| phosphopyruvate hydratase [Xanthomonas campestris pv. campestris str. ATCC 33913]			x	
41407088	>gi|41407088|ref|NP_959924.1| phosphopyruvate hydratase [Mycobacterium avium subsp. paratuberculosis K-10]			x	
59797600	>gi|59797600|sp|Q741U7|ENO_MYCPA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
56752615	>gi|56752615|gb|AAW24521.1| SJCHGC00471 protein [Schistosoma japonicum]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>42545184</td><td>>gi|42545184|gb|EAA68027.1| ENO_ALTAL Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Major allergen Alt a 11) (Alt a XI) [Gibberella zeae PH-1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>46108928</td><td>>gi|46108928|ref|XP_381522.1| ENO_ALTAL Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Major allergen Alt a 11) (Alt a XI) [Gibberella zeae PH-1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>62528387</td><td>>gi|62528387|ref|ZP_00389641.1| COG0148: Enolase [Streptococcus thermophilus LMD-9]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>58582586</td><td>>gi|58582586|ref|YP_201602.1| phosphopyruvate hydratase [Xanthomonas oryzae pv. oryzae KACC10331]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>58427180</td><td>>gi|58427180|gb|AAW76217.1| enolase [Xanthomonas oryzae pv. oryzae KACC10331]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>6015094</td><td>>gi|6015094|sp|P42040|ENO_CLAHE Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Allergen Cla h 6) (Cla h VI)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>21107915</td><td>>gi|21107915|gb|AAM36586.1| enolase [Xanthomonas axonopodis pv. citri str. 306]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>21242468</td><td>>gi|21242468|ref|NP_642050.1| phosphopyruvate hydratase [Xanthomonas axonopodis pv. citri str. 306]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>23814066</td><td>>gi|23814066|sp|Q8PLS0|ENO_XANAC Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>46129115</td><td>>gi|46129115|ref|ZP_00202000.1| COG0148: Enolase [Haemophilus influenzae R2846]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>83856594</td><td>>gi|83856594|ref|ZP_00950123.1| enolase [Croceibacter atlanticus HTCC2559]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>83850394</td><td>>gi|83850394|gb|EAP88262.1| enolase [Croceibacter atlanticus HTCC2559]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77635114</td><td>>gi|77635114|ref|ZP_00797203.1| COG0148: Enolase [Yersinia pestis Angola]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>45435025</td><td>>gi|45435025|gb|AAS60585.1| enolase [Yersinia pestis biovar Medievalis str. 91001]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15981302</td><td>>gi|15981302|emb|CAC92606.1| enolase [Yersinia pestis CO92]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>21957544</td><td>>gi|21957544|gb|AAM84401.1| enolase [Yersinia pestis KIM]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
22124727	>gi|22124727|ref|NP_668150.1| phosphopyruvate hydratase [Yersinia pestis KIM]			x	
45440169	>gi|45440169|ref|NP_991708.1| phosphopyruvate hydratase [Yersinia pestis biovar Medievalis str. 91001]			x	
16123525	>gi|16123525|ref|NP_406838.1| phosphopyruvate hydratase [Yersinia pestis CO92]			x	
21263586	>gi|21263586|sp|Q8ZBN2|ENO_YERPE Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
77631732	>gi|77631732|ref|ZP_00794318.1| COG0148: Enolase [Yersinia pseudotuberculosis IP 31758]			x	
51588387	>gi|51588387|emb|CAH19995.1| enolase [Yersinia pseudotuberculosis IP 32953]			x	
51595105	>gi|51595105|ref|YP_069296.1| phosphopyruvate hydratase [Yersinia pseudotuberculosis IP 32953]			x	
59797522	>gi|59797522|sp|Q66ED8|ENO_YERPS Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
37199752	>gi|37199752|dbj|BAC95582.1| enolase [Vibrio vulnificus YJ016]			x	
37681002	>gi|37681002|ref|NP_935611.1| phosphopyruvate hydratase [Vibrio vulnificus YJ016]			x	
46914618	>gi|46914618|emb|CAG21395.1| putative enolase [Photobacterium profundum SS9]			x	
54310177	>gi|54310177|ref|YP_131197.1| phosphopyruvate hydratase [Photobacterium profundum SS9]			x	
59797562	>gi|59797562|sp|Q6LMT1|ENO_PHOPR Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
86132574	>gi|86132574|ref|ZP_01051167.1| enolase [Cellulophaga sp. MED134]			x	
85816816	>gi|85816816|gb|EAQ38001.1| enolase [Cellulophaga sp. MED134]			x	
7380143	>gi|7380143|emb|CAB84728.1| enolase [Neisseria meningitidis Z2491]			x	
15794395	>gi|15794395|ref|NP_284217.1| phosphopyruvate hydratase [Neisseria meningitidis Z2491]			x	
13124126	>gi|13124126|sp|Q9JU46|ENO_NEIMA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
32029561	>gi|32029561|ref|ZP_00132564.1| COG0148: Enolase [Haemophilus somnus 2336]			x	
23467876	>gi|23467876|ref|ZP_00123453.1| COG0148: Enolase [Haemophilus somnus 129PT]			x	
3367647	>gi|3367647|emb|CAA76735.1| enolase [Cunninghamella elegans]			x	
12230023	>gi|12230023|sp|O74286|ENO_CUNEL Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
7226525	>gi|7226525|gb|AAF41661.1| enolase [Neisseria meningitidis MC58]			x	
15677152	>gi|15677152|ref|NP_274305.1| phosphopyruvate hydratase [Neisseria meningitidis MC58]			x	
13124130	>gi|13124130|sp|Q9JZ53|ENO_NEIMB Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
12517248	>gi|12517248|gb|AAG57892.1| enolase [Escherichia coli O157:H7 EDL933]			x	
15803300	>gi|15803300|ref|NP_289333.1| phosphopyruvate hydratase [Escherichia coli O157:H7 EDL933]			x	
25291627	>gi|25291627|pir||H85928 enolase [imported] - Escherichia coli (strain O157:H7, substrain EDL933)			x	
74659668	>gi|74659668|sp|Q6C1F3|ENO_YARLI Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
56178891	>gi|56178891|gb|AAV81613.1| Enolase [Idiomarina loihiensis L2TR]			x	
68053535	>gi|68053535|sp|Q5R143|ENO_IDILO Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
56459881	>gi|56459881|ref|YP_155162.1| Enolase [Idiomarina loihiensis L2TR]			x	
13124161	>gi|13124161|sp|Q9XDS7|ENO_STRIT Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
5263171	>gi|5263171|dbj|BAA81815.1| enolase [Streptococcus intermedius]			x	
46048765	>gi|46048765|ref|NP_990450.1| enolase [Gallus gallus]			x	
1706654	>gi|1706654|sp|P07322|ENOB_CHICK Beta-enolase (2-phospho-D-glycerate hydro-lyase) (Phosphopyruvate hydratase)			x	
1616990	>gi|1616990|dbj|BAA07133.1| enolase [Gallus gallus]			x	
18892150	>gi|18892150|gb|AAL80339.1| enolase (2-phosphoglycerate dehydratase) [Pyrococcus furiosus DSM 3638]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
23814077	>gi|23814077|sp|Q8U477|ENO_PYRFU Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
18976587	>gi|18976587|ref|NP_577944.1| phosphopyruvate hydratase [Pyrococcus furiosus DSM 3638]			x	
83644694	>gi|83644694|ref|YP_433129.1| enolase [Hahella chejuensis KCTC 2396]			x	
83632737	>gi|83632737|gb|ABC28704.1| enolase [Hahella chejuensis KCTC 2396]			x	
9106280	>gi|9106280|gb|AAF84100.1| enolase [Xylella fastidiosa 9a5c]			x	
15837892	>gi|15837892|ref|NP_298580.1| phosphopyruvate hydratase [Xylella fastidiosa 9a5c]			x	
11268953	>gi|11268953|pir||F82700 enolase XF1291 [imported] - Xylella fastidiosa (strain 9a5c)			x	
36784331	>gi|36784331|emb|CAE13208.1| Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) [Photorhabdus luminescens subsp. laumondii TTO1]			x	
59797610	>gi|59797610|sp|Q7N835|ENO_PHOLL Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
37524905	>gi|37524905|ref|NP_928249.1| phosphopyruvate hydratase [Photorhabdus luminescens subsp. laumondii TTO1]			x	
10241779	>gi|10241779|emb|CAC09537.1| enolase [Streptomyces coelicolor A3(2)]			x	
21221535	>gi|21221535|ref|NP_627314.1| phosphopyruvate hydratase [Streptomyces coelicolor A3(2)]			x	
23814098	>gi|23814098|sp|Q9F2Q3|ENO1_STRCO Enolase 1 (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x	
28866546	>gi|28866546|emb|CAD60544.1| enolase [Streptococcus sobrinus]			x	
77976028	>gi|77976028|ref|ZP_00831561.1| COG0148: Enolase [Yersinia frederiksenii ATCC 33641]			x	
3323125	>gi|3323125|gb|AAC65781.1| enolase (eno) [Treponema pallidum subsp. pallidum str. Nichols]			x	
4033380	>gi|4033380|sp|P74934|ENO_TREPA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
15639803	>gi|15639803|ref|NP_219253.1| enolase (eno) [Treponema pallidum subsp. pallidum str. Nichols]			x	
1575361	>gi|1575361|gb|AAB39979.1| 2-phospho-D-glycerate hydrolase [Treponema pallidum]			x	
73660149	>gi|73660149|emb|CAI82756.1| enolase [Dehalococcoides sp. CBDB1]			x	
73748433	>gi|73748433|ref|YP_307672.1| enolase [Dehalococcoides sp. CBDB1]			x	
74313351	>gi|74313351|ref|YP_311770.1| phosphopyruvate hydratase [Shigella sonnei Ss046]			x	
73856828	>gi|73856828|gb|AAZ89535.1| enolase [Shigella sonnei Ss046]			x	
78035738	>gi|78035738|emb|CAJ23429.1| Enolase [Xanthomonas campestris pv. vesicatoria str. 85-10]			x	
78047308	>gi|78047308|ref|YP_363483.1| phosphopyruvate hydratase [Xanthomonas campestris pv. vesicatoria str. 85-10]			x	
22035897	>gi|22035897|emb|CAD43170.1| enolase [Anisakis simplex]			x	
86135551	>gi|86135551|ref|ZP_01054132.1| enolase [Tenacibaculum sp. MED152]			x	
85819724	>gi|85819724|gb|EAQ40881.1| enolase [Tenacibaculum sp. MED152]			x	
71557144	>gi|71557144|gb|AAZ36355.1| enolase [Pseudomonas syringae pv. phaseolicola 1448A]			x	
71736591	>gi|71736591|ref|YP_275958.1| enolase [Pseudomonas syringae pv. phaseolicola 1448A]			x	
68555733	>gi|68555733|ref|ZP_00595077.1| Enolase [Ralstonia metallidurans CH34]			x	
68530203	>gi|68530203|gb|EAN53165.1| Enolase [Ralstonia metallidurans CH34]			x	
50876688	>gi|50876688|emb|CAG36528.1| probable enolase [Desulfotalea psychrophila LSv54]			x	
59797536	>gi|59797536|sp|Q6AM97|ENO_DESPS Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
51245651	>gi|51245651|ref|YP_065535.1| enolase [Desulfotalea psychrophila LSv54]			x	
34392443	>gi|34392443|dbj|BAC82549.1| enolase [Penicillium chrysogenum]			x	
74662366	>gi|74662366|sp|Q76KF9|ENO_PENCH Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
86141170	>gi|86141170|ref|ZP_01059716.1| enolase [Flavobacterium sp. MED217]			x	
85831729	>gi|85831729|gb|EAQ50184.1| enolase [Flavobacterium sp. MED217]			x	
66044611	>gi|66044611|ref|YP_234452.1| phosphopyruvate hydratase [Pseudomonas syringae pv. syringae B728a]			x	
63255318	>gi|63255318|gb|AAY36414.1| Enolase [Pseudomonas syringae pv. syringae B728a]			x	
67156392	>gi|67156392|ref|ZP_00417985.1| Enolase [Azotobacter vinelandii AvOP]			x	
67086151	>gi|67086151|gb|EAM05621.1| Enolase [Azotobacter vinelandii AvOP]			x	
67539152	>gi|67539152|ref|XP_663350.1| enolase [Aspergillus nidulans FGSC A4]			x	
40743649	>gi|40743649|gb|EAA62839.1| ENO_ASPOR Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) [Aspergillus nidulans FGSC A4]			x	
16975440	>gi|16975440|pdb|1E9I|D Chain D, Enolase From E.Coli			x	
16975439	>gi|16975439|pdb|1E9I|C Chain C, Enolase From E.Coli			x	
16975438	>gi|16975438|pdb|1E9I|B Chain B, Enolase From E.Coli			x	
16975437	>gi|16975437|pdb|1E9I|A Chain A, Enolase From E.Coli			x	
71850822	>gi|71850822|gb|AAZ43431.1| enolase [Mycoplasma synoviae 53]			x	
71894034	>gi|71894034|ref|YP_278142.1| phosphopyruvate hydratase [Mycoplasma synoviae 53]			x	
59797608	>gi|59797608|sp|Q7MHQ1|ENO_VIBVY Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
28807571	>gi|28807571|dbj|BAC60824.1| enolase [Vibrio parahaemolyticus RIMD 2210633]			x	
31340054	>gi|31340054|sp|Q87LQ0|ENO_VIBPA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
28899335	>gi|28899335|ref|NP_798940.1| phosphopyruvate hydratase [Vibrio parahaemolyticus RIMD 2210633]			x	
6579195	>gi|6579195|gb|AAA51399.2| phosphopyruvate hydratase [Schizosaccharomyces pombe]			x	
12644257	>gi|12644257|sp|P40370|ENO11_SCHPO Enolase 1-1 (2-phosphoglycerate dehydratase 1-1) (2-phospho-D-glycerate hydro-lyase 1-1)			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
71914564	>gi|71914564|gb|AAZ54466.1| enolase [Thermobifida fusca YX]			x	
72160832	>gi|72160832|ref|YP_288489.1| phosphopyruvate hydratase [Thermobifida fusca YX]			x	
30314940	>gi|30314940|gb|AAP30720.1| enolase [Rhodotorula mucilaginosa]			x	
37078092	>gi|37078092|sp|Q870B9|ENO_RHORB Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Allergen Rho m 1)			x	
77962820	>gi|77962820|ref|ZP_00826636.1| COG0148: Enolase [Yersinia mollaretii ATCC 43969]			x	
77956800	>gi|77956800|ref|ZP_00820878.1| COG0148: Enolase [Yersinia bercovieri ATCC 43970]			x	
71064151	>gi|71064151|gb|AAZ22544.1| alpha-enolase [Bifidobacterium animalis subsp. lactis]			x	
57225057	>gi|57225057|gb|AAW40114.1| enolase [Dehalococcoides ethenogenes 195]			x	
57234609	>gi|57234609|ref|YP_181335.1| enolase [Dehalococcoides ethenogenes 195]			x	
32448033	>gi|32448033|emb|CAD77550.1| enolase (2-phosphoglycerate dehydratase) [Rhodopirellula baltica SH 1]			x	
32477479	>gi|32477479|ref|NP_870473.1| enolase (2-phosphoglycerate dehydratase) [Rhodopirellula baltica SH 1]			x	
59797615	>gi|59797615|sp|Q7UIR2|ENO_RHOBA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
68342877	>gi|68342877|gb|AAY90483.1| enolase [Pseudomonas fluorescens Pf-5]			x	
70728578	>gi|70728578|ref|YP_258327.1| phosphopyruvate hydratase [Pseudomonas fluorescens Pf-5]			x	
76365089	>gi|76365089|gb|AAR00929.2| enolase [Davidiella tassiana]			x	
67676250	>gi|67676250|ref|ZP_00473001.1| Enolase [Chromohalobacter salexigens DSM 3043]			x	
67519787	>gi|67519787|gb|EAM23736.1| Enolase [Chromohalobacter salexigens DSM 3043]			x	
68543414	>gi|68543414|ref|ZP_00583120.1| Enolase [Shewanella baltica OS155]			x	
68518887	>gi|68518887|gb|EAN42440.1| Enolase [Shewanella baltica OS155]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>29607186</td><td>>gi|29607186|dbj|BAC71245.1| putative enolase [Streptomyces avermitilis MA-4680]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>29830076</td><td>>gi|29830076|ref|NP_824710.1| phosphopyruvate hydratase [Streptomyces avermitilis MA-4680]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>59797627</td><td>>gi|59797627|sp|Q82HH5|ENO_STRAW Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>76785279</td><td>>gi|76785279|ref|ZP_00772451.1| COG0148: Enolase [Mycobacterium tuberculosis F11]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>13880623</td><td>>gi|13880623|gb|AAK45302.1| enolase [Mycobacterium tuberculosis CDC1551]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1870005</td><td>>gi|1870005|emb|CAB06856.1| PROBABLE ENOLASE ENO [Mycobacterium tuberculosis H37Rv]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15608163</td><td>>gi|15608163|ref|NP_215539.1| phosphopyruvate hydratase [Mycobacterium tuberculosis H37Rv]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15840451</td><td>>gi|15840451|ref|NP_335488.1| phosphopyruvate hydratase [Mycobacterium tuberculosis CDC1551]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>81255030</td><td>>gi|81255030|ref|ZP_00879522.1| COG0148: Enolase [Mycobacterium tuberculosis C]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>3023706</td><td>>gi|3023706|sp|P96377|ENO_MYCTU Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>13242907</td><td>>gi|13242907|gb|AAG42022.2| enolase [Alternaria alternata]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>14423684</td><td>>gi|14423684|sp|Q9HDT3|ENO_ALTAL Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Major allergen Alt a 6) (Alt a 11) (Alt a XI)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>23814079</td><td>>gi|23814079|sp|Q8UFH1|ENO_AGRT5 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84319615</td><td>>gi|84319615|ref|ZP_00968009.1| COG0148: Enolase [Pseudomonas aeruginosa C3719]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67934468</td><td>>gi|67934468|ref|ZP_00527517.1| Enolase [Solibacter usitatus Ellin6076]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67858300</td><td>>gi|67858300|gb|EAM53445.1| Enolase [Solibacter usitatus Ellin6076]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84368411</td><td>>gi|84368411|dbj|BAE69569.1| enolase [Xanthomonas oryzae pv. oryzae MAFF 311018]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
84624471	>gi|84624471|ref|YP_451843.1| enolase [Xanthomonas oryzae pv. oryzae MAFF 311018]			x	
68053522	>gi|68053522|sp|Q5GYK4|ENO_XANOR Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
72118206	>gi|72118206|gb|AAZ60469.1| Enolase [Ralstonia eutropha JMP134]			x	
73540793	>gi|73540793|ref|YP_295313.1| phosphopyruvate hydratase [Ralstonia eutropha JMP134]			x	
19888365	>gi|19888365|gb|AAM02860.1| Enolase [Methanopyrus kandleri AV19]			x	
23814075	>gi|23814075|sp|Q8TUV6|ENO_METKA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
20095083	>gi|20095083|ref|NP_614930.1| Enolase [Methanopyrus kandleri AV19]			x	
33147912	>gi|33147912|gb|AAP95433.1| enolase [Haemophilus ducreyi 35000HP]			x	
59797620	>gi|59797620|sp|Q7VNM6|ENO_HAEDU Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
33151691	>gi|33151691|ref|NP_873044.1| phosphopyruvate hydratase [Haemophilus ducreyi 35000HP]			x	
71368692	>gi|71368692|ref|ZP_00659180.1| Enolase [Nocardioides sp. JS614]			x	
71155576	>gi|71155576|gb|EAO06015.1| Enolase [Nocardioides sp. JS614]			x	
16504025	>gi|16504025|emb|CAD06058.1| enolase [Salmonella enterica subsp. enterica serovar Typhi]			x	
16421503	>gi|16421503|gb|AAL21832.1| enolase [Salmonella typhimurium LT2]			x	
62181456	>gi|62181456|ref|YP_217873.1| phosphopyruvate hydratase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]			x	
56129153	>gi|56129153|gb|AAV78659.1| enolase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]			x	
29138841	>gi|29138841|gb|AAO70410.1| enolase [Salmonella enterica subsp. enterica serovar Typhi Ty2]			x	
62129089	>gi|62129089|gb|AAX66792.1| enolase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]			x	
16766258	>gi|16766258|ref|NP_461873.1| phosphopyruvate hydratase [Salmonella typhimurium LT2]			x	
68053534	>gi|68053534|sp|Q5PEH4|ENO_SALPA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>54040760</td><td>>gi|54040760|sp|P64076|ENO_SALTY Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>54037039</td><td>>gi|54037039|sp|P64077|ENO_SALTI Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>56414896</td><td>>gi|56414896|ref|YP_151971.1| phosphopyruvate hydratase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>16761724</td><td>>gi|16761724|ref|NP_457341.1| phosphopyruvate hydratase [Salmonella enterica subsp. enterica serovar Typhi str. CT18]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>29143208</td><td>>gi|29143208|ref|NP_806550.1| phosphopyruvate hydratase [Salmonella enterica subsp. enterica serovar Typhi Ty2]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>25291631</td><td>>gi|25291631|pir||AC0859 enolase [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>85057717</td><td>>gi|85057717|ref|YP_456633.1| enolase [Aster yellows witches'-broom phytoplasma AYWB]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84789822</td><td>>gi|84789822|gb|ABC65554.1| enolase [Aster yellows witches'-broom phytoplasma AYWB]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77381351</td><td>>gi|77381351|gb|ABA72864.1| Phosphopyruvate hydratase [Pseudomonas fluorescens PfO-1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77457348</td><td>>gi|77457348|ref|YP_346853.1| phosphopyruvate hydratase [Pseudomonas fluorescens PfO-1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68182317</td><td>>gi|68182317|ref|ZP_00555297.1| Enolase [Jannaschia sp. CCS1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67977421</td><td>>gi|67977421|gb|EAM67041.1| Enolase [Jannaschia sp. CCS1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>49613013</td><td>>gi|49613013|emb|CAG76464.1| enolase [Erwinia carotovora subsp. atroseptica SCRI1043]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>59797542</td><td>>gi|59797542|sp|Q6D182|ENO_ERWCT Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>50122487</td><td>>gi|50122487|ref|YP_051654.1| phosphopyruvate hydratase [Erwinia carotovora subsp. atroseptica SCRI1043]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68546866</td><td>>gi|68546866|ref|ZP_00586410.1| Enolase [Shewanella amazonensis SB2B]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68515455</td><td>>gi|68515455|gb|EAN39172.1| Enolase [Shewanella amazonensis SB2B]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>83942542</td><td>>gi|83942542|ref|ZP_00955003.1| enolase [Sulfitobacter sp. EE-36]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
83846635	>gi|83846635|gb|EAP84511.1| enolase [Sulfitobacter sp. EE-36]			x	
77815272	>gi|77815272|ref|ZP_00814510.1| Enolase [Shewanella putrefaciens CN-32]			x	
77809746	>gi|77809746|gb|EAO94138.1| Enolase [Shewanella putrefaciens CN-32]			x	
82740715	>gi|82740715|ref|ZP_00903451.1| Enolase [Shewanella sp. W3-18-1]			x	
82721935	>gi|82721935|gb|EAP56765.1| Enolase [Shewanella sp. W3-18-1]			x	
13124145	>gi|13124145|sp|Q9PDT8|ENO_XYLFA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
74022142	>gi|74022142|ref|ZP_00692726.1| Enolase [Rhodoferax ferrireducens DSM 15236]			x	
72605139	>gi|72605139|gb|EAO41127.1| Enolase [Rhodoferax ferrireducens DSM 15236]			x	
563868	>gi|563868|emb|CAA57795.1| enolase; phosphopyruvate hydratase [Escherichia coli]			x	
59797611	>gi|59797611|sp|Q7NAY0|ENO_MYCGA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
31544709	>gi|31544709|ref|NP_853287.1| phosphopyruvate hydratase [Mycoplasma gallisepticum R]			x	
31617802	>gi|31617802|emb|CAD93911.1| PROBABLE ENOLASE ENO [Mycobacterium bovis AF2122/97]			x	
31792214	>gi|31792214|ref|NP_854707.1| phosphopyruvate hydratase [Mycobacterium bovis AF2122/97]			x	
59797613	>gi|59797613|sp|Q7U0U6|ENO_MYCBO Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
86166241	>gi|86166241|gb|EAQ67507.1| phosphopyruvate hydratase [Marinomonas sp. MED121]			x	
78492903	>gi|78492903|ref|ZP_00845138.1| Enolase [Rhodopseudomonas palustris BisB18]			x	
78390034	>gi|78390034|gb|EAP12824.1| Enolase [Rhodopseudomonas palustris BisB18]			x	
77979609	>gi|77979609|ref|ZP_00835026.1| COG0148: Enolase [Yersinia intermedia ATCC 29909]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>27361094</td><td>>gi|27361094|gb|AAO10003.1| Enolase [Vibrio vulnificus CMCP6]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>29839234</td><td>>gi|29839234|sp|Q8DC62|ENO_VIBVU Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>27364948</td><td>>gi|27364948|ref|NP_760476.1| phosphopyruvate hydratase [Vibrio vulnificus CMCP6]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>66848203</td><td>>gi|66848203|gb|EAL88532.1| enolase [Aspergillus fumigatus Af293]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>70991443</td><td>>gi|70991443|ref|XP_750570.1| enolase [Aspergillus fumigatus Af293]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>83288046</td><td>>gi|83288046|sp|Q96X30|ENO_ASPFU Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Allergen Asp f 22)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>75828720</td><td>>gi|75828720|ref|ZP_00758069.1| COG0148: Enolase [Vibrio cholerae MO10]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>75827712</td><td>>gi|75827712|ref|ZP_00757147.1| COG0148: Enolase [Vibrio cholerae O395]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>75814347</td><td>>gi|75814347|ref|ZP_00744949.1| COG0148: Enolase [Vibrio cholerae V52]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>9657023</td><td>>gi|9657023|gb|AAF95589.1| enolase [Vibrio cholerae O1 biovar eltor str. N16961]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15642443</td><td>>gi|15642443|ref|NP_232076.1| phosphopyruvate hydratase [Vibrio cholerae O1 biovar eltor str. N16961]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>13124138</td><td>>gi|13124138|sp|Q9KPC5|ENO_VIBCH Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>71853151</td><td>>gi|71853151|gb|AAZ51174.1| enolase [Streptococcus pyogenes MGAS5005]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>71910369</td><td>>gi|71910369|ref|YP_281919.1| phosphopyruvate hydratase [Streptococcus pyogenes MGAS5005]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>27353058</td><td>>gi|27353058|dbj|BAC50059.1| enolase [Bradyrhizobium japonicum USDA 110]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>59797632</td><td>>gi|59797632|sp|Q89KV6|ENO_BRAJA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>27379905</td><td>>gi|27379905|ref|NP_771434.1| enolase [Bradyrhizobium japonicum USDA 110]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>69298335</td><td>>gi|69298335|ref|ZP_00620615.1| Enolase [Silicibacter sp. TM1040]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>69134682</td><td>>gi|69134682|gb|EAN57897.1| Enolase [Silicibacter sp. TM1040]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
57225611	>gi|57225611|gb|AAW42072.1| phosphopyruvate hydratase, putative [Cryptococcus neoformans var. neoformans JEC21]			x	
58264446	>gi|58264446|ref|XP_569379.1| phosphopyruvate hydratase [Cryptococcus neoformans var. neoformans JEC21]			x	
25989631	>gi|25989631|gb|AAN28926.1| enolase [Aeromonas hydrophila]			x	
29839249	>gi|29839249|sp|Q8GE63|ENO_AERHY Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
21647988	>gi|21647988|gb|AAM73181.1| enolase [Chlorobium tepidum TLS]			x	
29839349	>gi|29839349|sp|Q8KB35|ENO1_CHLTE Enolase 1 (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x	
21674774	>gi|21674774|ref|NP_662839.1| enolase [Chlorobium tepidum TLS]			x	
15074376	>gi|15074376|emb|CAC46022.1| PROBABLE ENOLASE PROTEIN [Sinorhizobium meliloti]			x	
21263593	>gi|21263593|sp|Q92Q98|ENO_RHIME Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
15965196	>gi|15965196|ref|NP_385549.1| PROBABLE ENOLASE PROTEIN [Sinorhizobium meliloti 1021]			x	
71274918	>gi|71274918|ref|ZP_00651206.1| Enolase [Xylella fastidiosa Dixon]			x	
71164650	>gi|71164650|gb|EAO14364.1| Enolase [Xylella fastidiosa Dixon]			x	
84787058	>gi|84787058|gb|ABC63240.1| enolase [Erythrobacter litoralis HTCC2594]			x	
85373975	>gi|85373975|ref|YP_458037.1| enolase [Erythrobacter litoralis HTCC2594]			x	
54018341	>gi|54018341|dbj|BAD59711.1| putative enolase [Nocardia farcinica IFM 10152]			x	
59797496	>gi|59797496|sp|Q5YQ30|ENO_NOCFA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
54026833	>gi|54026833|ref|YP_121075.1| phosphopyruvate hydratase [Nocardia farcinica IFM 10152]			x	
78685818	>gi|78685818|ref|ZP_00850593.1| Enolase [Shewanella sp. ANA-3]			x	
78506503	>gi|78506503|gb|EAP20021.1| Enolase [Shewanella sp. ANA-3]			x	
86138676	>gi|86138676|ref|ZP_01057249.1| enolase [Roseobacter sp. MED193]			x	
85824736	>gi|85824736|gb|EAQ44938.1| enolase [Roseobacter sp. MED193]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
13925873	>gi|13925873|gb|AAK49451.1| enolase [Aspergillus fumigatus]			x	
37359341	>gi|37359341|gb|AAP24058.1| enolase 1 [Toxoplasma gondii]			x	
5764087	>gi|5764087|gb|AAD51128.1| enolase [Toxoplasma gondii]			x	
50400687	>gi|50400687|sp|Q9UAE6|ENO1_TOXGO Enolase 1 (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x	
84390114	>gi|84390114|ref|ZP_00991376.1| phosphopyruvate hydratase [Vibrio splendidus 12B01]			x	
84376768	>gi|84376768|gb|EAP93643.1| phosphopyruvate hydratase [Vibrio splendidus 12B01]			x	
4154655	>gi|4154655|gb|AAD05723.1| ENOLASE [Helicobacter pylori J99]			x	
9296935	>gi|9296935|sp|Q9ZMS6|ENO_HELPJ Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
15611212	>gi|15611212|ref|NP_222863.1| phosphopyruvate hydratase [Helicobacter pylori J99]			x	
59712682	>gi|59712682|ref|YP_205458.1| phosphopyruvate hydratase [Vibrio fischeri ES114]			x	
59480783	>gi|59480783|gb|AAW86570.1| enolase [Vibrio fischeri ES114]			x	
66774123	>gi|66774123|sp|Q5E326|ENO_VIBF1 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
85858513	>gi|85858513|ref|YP_460715.1| enolase [Syntrophus aciditrophicus SB]			x	
85721604	>gi|85721604|gb|ABC76547.1| enolase [Syntrophus aciditrophicus SB]			x	
19713005	>gi|19713005|gb|AAL93877.1| Enolase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]			x	
23814071	>gi|23814071|sp|Q8RI55|ENO_FUSNN Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
19705083	>gi|19705083|ref|NP_602578.1| Enolase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]			x	
83953763	>gi|83953763|ref|ZP_00962484.1| enolase [Sulfitobacter sp. NAS-14.1]			x	
83841708	>gi|83841708|gb|EAP80877.1| enolase [Sulfitobacter sp. NAS-14.1]			x	
50951779	>gi|50951779|gb|AAT89480.1| enolase [Leifsonia xyli subsp. xyli str. CTCB07]			x	
50955297	>gi|50955297|ref|YP_062585.1| phosphopyruvate hydratase [Leifsonia xyli subsp. xyli str. CTCB07]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
59797534	>gi|59797534|sp|Q6ADR6|ENO_LEIXX Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
83952177	>gi|83952177|ref|ZP_00960909.1| enolase [Roseovarius nubinhibens ISM]			x	
83837183	>gi|83837183|gb|EAP76480.1| enolase [Roseovarius nubinhibens ISM]			x	
78691419	>gi|78691419|ref|ZP_00856036.1| Enolase [Shewanella sp. MR-7]			x	
78509167	>gi|78509167|gb|EAP22572.1| Enolase [Shewanella sp. MR-7]			x	
82498363	>gi|82498363|ref|ZP_00883864.1| Enolase [Shewanella sp. MR-4]			x	
82403627	>gi|82403627|gb|EAP44347.1| Enolase [Shewanella sp. MR-4]			x	
467660	>gi|467660|emb|CAA55070.1| enolase; phosphopyruvate hydratase [Davidiella tassiana]			x	
1086120	>gi|1086120|pir||S43113 phosphopyruvate hydratase (EC 4.2.1.11) - fungus (Cladosporium herbarum)			x	
66811048	>gi|66811048|ref|XP_639231.1| 2-phospho-D-glycerate hydrolase [Dictyostelium discoideum]			x	
60467884	>gi|60467884|gb|EAL65898.1| phosphopyruvate hydratase [Dictyostelium discoideum]			x	
29839366	>gi|29839366|sp|Q8NKC2|ENO12_SCHPO Enolase 1-2 (2-phosphoglycerate dehydratase 1-2) (2-phospho-D-glycerate hydro-lyase 1-2)			x	
34541443	>gi|34541443|ref|NP_905922.1| phosphopyruvate hydratase [Porphyromonas gingivalis W83]			x	
34397760	>gi|34397760|gb|AAQ66821.1| enolase [Porphyromonas gingivalis W83]			x	
59797609	>gi|59797609|sp|Q7MTV8|ENO_PORGI Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
28198453	>gi|28198453|ref|NP_778767.1| phosphopyruvate hydratase [Xylella fastidiosa Temecula1]			x	
28056537	>gi|28056537|gb|AAO28416.1| enolase [Xylella fastidiosa Temecula1]			x	
32129518	>gi|32129518|sp|Q87DY6|ENO_XYLFT Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
78365755	>gi|78365755|ref|ZP_00836040.1| Enolase [Shewanella sp. PV-4]			x	
78362291	>gi|78362291|gb|EAP04110.1| Enolase [Shewanella sp. PV-4]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
26988344	>gi|26988344|ref|NP_743769.1| phosphopyruvate hydratase [Pseudomonas putida KT2440]			x	
24983094	>gi|24983094|gb|AAN67233.1| enolase [Pseudomonas putida KT2440]			x	
82737180	>gi|82737180|ref|ZP_00900032.1| Enolase [Pseudomonas putida F1]			x	
82715779	>gi|82715779|gb|EAP50841.1| Enolase [Pseudomonas putida F1]			x	
38372167	>gi|38372167|sp|Q88MF9|ENO_PSEPK Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
78695164	>gi|78695164|ref|ZP_00859676.1| Enolase [Bradyrhizobium sp. BTAi1]			x	
78516838	>gi|78516838|gb|EAP30137.1| Enolase [Bradyrhizobium sp. BTAi1]			x	
44920716	>gi|44920716|emb|CAF29952.1| Enolase [Methanococcus maripaludis S2]			x	
45357959	>gi|45357959|ref|NP_987516.1| Enolase [Methanococcus maripaludis S2]			x	
28868760	>gi|28868760|ref|NP_791379.1| phosphopyruvate hydratase [Pseudomonas syringae pv. tomato str. DC3000]			x	
38372195	>gi|38372195|sp|Q886M3|ENO1_PSESM Enolase 1 (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x	
28851999	>gi|28851999|gb|AAO55074.1| enolase [Pseudomonas syringae pv. tomato str. DC3000]			x	
77407751	>gi|77407751|ref|ZP_00784505.1| enolase [Streptococcus agalactiae COH1]			x	
77173617	>gi|77173617|gb|EAO76732.1| enolase [Streptococcus agalactiae COH1]			x	
46191081	>gi|46191081|ref|ZP_00120494.2| COG0148: Enolase [Bifidobacterium longum DJO10A]			x	
23015298	>gi|23015298|ref|ZP_00055078.1| COG0148: Enolase [Magnetospirillum magnetotacticum MS-1]			x	
23394379	>gi|23394379|gb|AAN31479.1| enolase [Phytophthora infestans]			x	
72495736	>gi|72495736|dbj|BAE19057.1| enolase [Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305]			x	
73663221	>gi|73663221|ref|YP_302002.1| enolase [Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
24195632	>gi|24195632|gb|AAN49150.1| Enolase [Leptospira interrogans serovar Lai str. 56601]			x	
45657813	>gi|45657813|ref|YP_001899.1| enolase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]			x	
45601053	>gi|45601053|gb|AAS70536.1| enolase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]			x	
29839244	>gi|29839244|sp|Q8F4T8|ENO_LEPIN Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
59797585	>gi|59797585|sp|Q72QZ8|ENO_LEPIC Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
24214651	>gi|24214651|ref|NP_712132.1| Enolase [Leptospira interrogans serovar Lai str. 56601]			x	
17428142	>gi|17428142|emb|CAD14831.1| PROBABLE ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) PROTEIN [Ralstonia solanacearum]			x	
17545848	>gi|17545848|ref|NP_519250.1| phosphopyruvate hydratase [Ralstonia solanacearum GMI1000]			x	
21263577	>gi|21263577|sp|Q8Y0B5|ENO_RALSO Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
27902665	>gi|27902665|gb|AAO24625.1| enolase [Methylobacterium extorquens]			x	
23128142	>gi|23128142|ref|ZP_00109996.1| COG0148: Enolase [Nostoc punctiforme PCC 73102]			x	
56679062	>gi|56679062|gb|AAV95728.1| enolase [Silicibacter pomeroyi DSS-3]			x	
56697325	>gi|56697325|ref|YP_167691.1| enolase [Silicibacter pomeroyi DSS-3]			x	
68053528	>gi|68053528|sp|Q5LQL4|ENO_SILPO Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
30315823	>gi|30315823|sp|Q8EBR0|ENO_SHEON Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
69953339	>gi|69953339|ref|ZP_00640506.1| Enolase [Shewanella frigidimarina NCIMB 400]			x	
69163601	>gi|69163601|gb|EAN72732.1| Enolase [Shewanella frigidimarina NCIMB 400]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>12723548</td><td>>gi|12723548|gb|AAK04742.1| enolase (EC 4.2.1.11) [Lactococcus lactis subsp. lactis Il1403]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15672626</td><td>>gi|15672626|ref|NP_266800.1| phosphopyruvate hydratase [Lactococcus lactis subsp. lactis Il1403]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>21263619</td><td>>gi|21263619|sp|Q9CHS7|ENO1_LACLA Enolase 1 (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>83748260</td><td>>gi|83748260|ref|ZP_00945286.1| Enolase [Ralstonia solanacearum UW551]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>83725101</td><td>>gi|83725101|gb|EAP72253.1| Enolase [Ralstonia solanacearum UW551]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>32035526</td><td>>gi|32035526|ref|ZP_00135469.1| COG0148: Enolase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>8979174</td><td>>gi|8979174|dbj|BAA99008.1| enolase [Chlamydophila pneumoniae J138]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>7189985</td><td>>gi|7189985|gb|AAF38843.1| enolase [Chlamydophila pneumoniae AR39]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15836333</td><td>>gi|15836333|ref|NP_300857.1| phosphopyruvate hydratase [Chlamydophila pneumoniae J138]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>16752240</td><td>>gi|16752240|ref|NP_445608.1| phosphopyruvate hydratase [Chlamydophila pneumoniae AR39]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>12644033</td><td>>gi|12644033|sp|Q9Z7A6|ENO_CHLPN Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>85703404</td><td>>gi|85703404|ref|ZP_01034508.1| enolase [Roseovarius sp. 217]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>85672332</td><td>>gi|85672332|gb|EAQ27189.1| enolase [Roseovarius sp. 217]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>74017775</td><td>>gi|74017775|ref|ZP_00688398.1| Enolase [Burkholderia ambifaria AMMD]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>72609660</td><td>>gi|72609660|gb|EAO45609.1| Enolase [Burkholderia ambifaria AMMD]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>56604320</td><td>>gi|56604320|emb|CAG45342.1| Enolase (2-phosphoglycerate dehydratase) [Francisella tularensis subsp. tularensis SCHU S4]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>56707828</td><td>>gi|56707828|ref|YP_169724.1| Enolase (2-phosphoglycerate dehydratase) [Francisella tularensis subsp. tularensis SCHU S4]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68053532</td><td>>gi|68053532|sp|Q5NGW8|ENO_FRATT Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
84779011	>gi|84779011|dbj|BAE73788.1| enolase [Sodalis glossinidius str. 'morsitans']			x	
85058491	>gi|85058491|ref|YP_454193.1| enolase [Sodalis glossinidius str. 'morsitans']			x	
77967627	>gi|77967627|gb|ABB09007.1| Phosphopyruvate hydratase [Burkholderia sp. 383]			x	
78066882	>gi|78066882|ref|YP_369651.1| phosphopyruvate hydratase [Burkholderia sp. 383]			x	
47574355	>gi|47574355|ref|ZP_00244391.1| COG0148: Enolase [Rubrivivax gelatinosus PM1]			x	
71898806	>gi|71898806|ref|ZP_00680974.1| Enolase [Xylella fastidiosa Ann-1]			x	
71731392	>gi|71731392|gb|EAO33455.1| Enolase [Xylella fastidiosa Ann-1]			x	
155581	>gi|155581|gb|AAA27686.1| enolase			x	
84714102	>gi|84714102|ref|ZP_01021631.1| Enolase [Polaromonas naphthalenivorans CJ2]			x	
84694080	>gi|84694080|gb|EAQ19876.1| Enolase [Polaromonas naphthalenivorans CJ2]			x	
77689478	>gi|77689478|ref|ZP_00804659.1| Enolase [Rhodopseudomonas palustris BisB5]			x	
77653845	>gi|77653845|gb|EAO85619.1| Enolase [Rhodopseudomonas palustris BisB5]			x	
67657013	>gi|67657013|ref|ZP_00454393.1| Enolase [Burkholderia cenocepacia AU 1054]			x	
67666378	>gi|67666378|ref|ZP_00463627.1| Enolase [Burkholderia cenocepacia HI2424]			x	
67100104	>gi|67100104|gb|EAM17265.1| Enolase [Burkholderia cenocepacia HI2424]			x	
67095281	>gi|67095281|gb|EAM12810.1| Enolase [Burkholderia cenocepacia AU 1054]			x	
84362206	>gi|84362206|ref|ZP_00986839.1| COG0148: Enolase [Burkholderia dolosa AUO158]			x	
84355108	>gi|84355108|ref|ZP_00979998.1| COG0148: Enolase [Burkholderia cenocepacia PC184]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
33236671	>gi|33236671|gb|AAP98758.1| enolase [Chlamydophila pneumoniae TW-183]			x	
33242160	>gi|33242160|ref|NP_877101.1| phosphopyruvate hydratase [Chlamydophila pneumoniae TW-183]			x	
67549711	>gi|67549711|ref|ZP_00427562.1| Enolase [Burkholderia vietnamiensis G4]			x	
67528985	>gi|67528985|gb|EAM25871.1| Enolase [Burkholderia vietnamiensis G4]			x	
4377111	>gi|4377111|gb|AAD18938.1| Enolase [Chlamydophila pneumoniae CWL029]			x	
15618709	>gi|15618709|ref|NP_224995.1| phosphopyruvate hydratase [Chlamydophila pneumoniae CWL029]			x	
86357552	>gi|86357552|ref|YP_469444.1| 2-phosphoglycerate dehydratase (enolase) protein [Rhizobium etli CFN 42]			x	
86281654	>gi|86281654|gb|ABC90717.1| 2-phosphoglycerate dehydratase (enolase) protein [Rhizobium etli CFN 42]			x	
86146349	>gi|86146349|ref|ZP_01064673.1| phosphopyruvate hydratase [Vibrio sp. MED222]			x	
85835828	>gi|85835828|gb|EAQ53962.1| phosphopyruvate hydratase [Vibrio sp. MED222]			x	
67910846	>gi|67910846|ref|ZP_00509232.1| Enolase [Polaromonas sp. JS666]			x	
67777007	>gi|67777007|gb|EAM36639.1| Enolase [Polaromonas sp. JS666]			x	
71364941	>gi|71364941|ref|ZP_00655507.1| Enolase [Psychrobacter cryohalolentis K5]			x	
71159860	>gi|71159860|gb|EAO09695.1| Enolase [Psychrobacter cryohalolentis K5]			x	
86158067	>gi|86158067|ref|YP_464852.1| enolase [Anaeromyxobacter dehalogenans 2CP-C]			x	
85774578	>gi|85774578|gb|ABC81415.1| enolase [Anaeromyxobacter dehalogenans 2CP-C]			x	
59797564	>gi|59797564|sp|Q6M075|ENO_METMP Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
34762728	>gi|34762728|ref|ZP_00143718.1| Enolase [Fusobacterium nucleatum subsp. vincentii ATCC 49256]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
27887627	>gi|27887627|gb|EAA24706.1| Enolase [Fusobacterium nucleatum subsp. vincentii ATCC 49256]			x	
66357920	>gi|66357920|ref|XP_626138.1| enolase (2-phosphoglycerate dehydratase) [Cryptosporidium parvum]			x	
46227284	>gi|46227284|gb|EAK88234.1| enolase (2-phosphoglycerate dehydratase) [Cryptosporidium parvum]			x	
3023683	>gi|3023683|sp|Q12560|ENO_ASPOR Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
1217828	>gi|1217828|dbj|BAA09973.1| enolase [Aspergillus oryzae]			x	
2665456	>gi|2665456|dbj|BAA23760.1| enolase [Aspergillus oryzae]			x	
1586931	>gi|1586931|prf||2205241A enolase			x	
23347962	>gi|23347962|gb|AAN30052.1| enolase [Brucella suis 1330]			x	
82699972	>gi|82699972|ref|YP_414546.1| Enolase [Brucella melitensis biovar Abortus 2308]			x	
62290045	>gi|62290045|ref|YP_221838.1| enolase [Brucella abortus biovar 1 str. 9-941]			x	
62196177	>gi|62196177|gb|AAX74477.1| enolase [Brucella abortus biovar 1 str. 9-941]			x	
29839247	>gi|29839247|sp|Q8G0G3|ENO_BRUSU Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
82616073	>gi|82616073|emb|CAJ11111.1| Enolase [Brucella melitensis biovar Abortus]			x	
23502010	>gi|23502010|ref|NP_698137.1| enolase [Brucella suis 1330]			x	
17132671	>gi|17132671|dbj|BAB75237.1| enolase [Nostoc sp. PCC 7120]			x	
17231030	>gi|17231030|ref|NP_487578.1| phosphopyruvate hydratase [Nostoc sp. PCC 7120]			x	
21263582	>gi|21263582|sp|Q8YRB0|ENO_ANASP Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
49238171	>gi|49238171|emb|CAF27380.1| Enolase [Bartonella henselae str. Houston-1]			x	
20465193	>gi|20465193|gb|AAL74281.1| enolase [Bartonella henselae]			x	
29839252	>gi|29839252|sp|Q8L202|ENO_BARHE Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
49475365	>gi|49475365|ref|YP_033406.1| Enolase [Bartonella henselae str. Houston-1]			x	
15644783	>gi|15644783|ref|NP_206953.1| phosphopyruvate hydratase [Helicobacter pylori 26695]			x	
2313236	>gi|2313236|gb|AAD07219.1| enolase (eno) [Helicobacter pylori 26695]			x	
2506387	>gi|2506387|sp|P48285|ENO_HELPY Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
48787796	>gi|48787796|ref|ZP_00283775.1| COG0148: Enolase [Burkholderia fungorum LB400]			x	
69933446	>gi|69933446|ref|ZP_00628648.1| Enolase [Paracoccus denitrificans PD1222]			x	
69155082	>gi|69155082|gb|EAN68185.1| Enolase [Paracoccus denitrificans PD1222]			x	
39649793	>gi|39649793|emb|CAE28315.1| enolase [Rhodopseudomonas palustris CGA009]			x	
39935939	>gi|39935939|ref|NP_948215.1| enolase [Rhodopseudomonas palustris CGA009]			x	
59797572	>gi|59797572|sp|Q6N5U6|ENO_RHOPA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
30749888	>gi|30749888|pdb|1OEP|A Chain A, Structure Of Trypanosoma Brucei Enolase Reveals The Inhibitory Divalent Metal Site			x	
77742416	>gi|77742416|ref|ZP_00810894.1| Enolase [Rhodopseudomonas palustris BisA53]			x	
77697805	>gi|77697805|gb|EAO88963.1| Enolase [Rhodopseudomonas palustris BisA53]			x	
85708563	>gi|85708563|ref|ZP_01039629.1| enolase [Erythrobacter sp. NAP1]			x	
85690097	>gi|85690097|gb|EAQ30100.1| enolase [Erythrobacter sp. NAP1]			x	
33577120	>gi|33577120|emb|CAE35677.1| enolase [Bordetella bronchiseptica RB50]			x	
33574205	>gi|33574205|emb|CAE38537.1| enolase [Bordetella parapertussis]			x	
33572731	>gi|33572731|emb|CAE42657.1| enolase [Bordetella pertussis Tohama I]			x	
33593375	>gi|33593375|ref|NP_881019.1| phosphopyruvate hydratase [Bordetella pertussis Tohama I]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
33597776	>gi|33597776|ref|NP_885419.1| phosphopyruvate hydratase [Bordetella parapertussis 12822]			x	
33602678	>gi|33602678|ref|NP_890238.1| phosphopyruvate hydratase [Bordetella bronchiseptica RB50]			x	
59797622	>gi|59797622|sp|Q7VW79|ENO_BORPE Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
59797623	>gi|59797623|sp|Q7W5N9|ENO_BORPA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
59797624	>gi|59797624|sp|Q7WD75|ENO_BORBR Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
49239628	>gi|49239628|emb|CAF25987.1| Enolase [Bartonella quintana str. Toulouse]			x	
59797553	>gi|59797553|sp|Q6G173|ENO_BARQU Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
49474124	>gi|49474124|ref|YP_032166.1| Enolase [Bartonella quintana str. Toulouse]			x	
67466006	>gi|67466006|ref|XP_649161.1| enolase [Entamoeba histolytica HM-1:IMSS]			x	
56465529	>gi|56465529|gb|EAL43773.1| enolase, putative [Entamoeba histolytica HM-1:IMSS]			x	
1706652	>gi|1706652|sp|P51555|ENO1_ENTHI Enolase 1 (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
498862	>gi|498862|gb|AAA80166.1| enolase			x	
37147852	>gi|37147852|gb|AAQ88397.1| enolase [Tuber borchii]			x	
74612186	>gi|74612186|sp|Q6W3C0|ENO_TUBBO Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
62424027	>gi|62424027|ref|ZP_00379179.1| COG0148: Enolase [Brevibacterium linens BL2]			x	
17982798	>gi|17982798|gb|AAL52032.1| ENOLASE [Brucella melitensis 16M]			x	
21263581	>gi|21263581|sp|Q8YHF0|ENO_BRUME Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
17987134	>gi|17987134|ref|NP_539768.1| ENOLASE [Brucella melitensis 16M]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
78702809	>gi|78702809|ref|ZP_00867233.1| Enolase [Alkalilimnicola ehrlichei MLHE-1]			x	
78519732	>gi|78519732|gb|EAP33015.1| Enolase [Alkalilimnicola ehrlichei MLHE-1]			x	
68193510	>gi|68193510|gb|EAN08162.1| Enolase [Mesorhizobium sp. BNC1]			x	
69275070	>gi|69275070|ref|ZP_00610982.1| Enolase [Mesorhizobium sp. BNC1]			x	
68539232	>gi|68539232|ref|ZP_00579005.1| Enolase [Sphingopyxis alaskensis RB2256]			x	
68523356	>gi|68523356|gb|EAN46485.1| Enolase [Sphingopyxis alaskensis RB2256]			x	
86742602	>gi|86742602|ref|YP_483002.1| Phosphopyruvate hydratase [Frankia sp. CcI3]			x	
86569464	>gi|86569464|gb|ABD13273.1| Phosphopyruvate hydratase [Frankia sp. CcI3]			x	
84684859	>gi|84684859|ref|ZP_01012759.1| enolase [Rhodobacterales bacterium HTCC2654]			x	
84667194	>gi|84667194|gb|EAQ13664.1| enolase [Rhodobacterales bacterium HTCC2654]			x	
71039176	>gi|71039176|gb|AAZ19484.1| enolase [Psychrobacter arcticus 273-4]			x	
71066191	>gi|71066191|ref|YP_264918.1| enolase [Psychrobacter arcticus 273-4]			x	
82945763	>gi|82945763|dbj|BAE50627.1| Enolase [Magnetospirillum magneticum AMB-1]			x	
83310922	>gi|83310922|ref|YP_421186.1| Enolase [Magnetospirillum magneticum AMB-1]			x	
75703448	>gi|75703448|gb|ABA23124.1| Enolase [Anabaena variabilis ATCC 29413]			x	
75909723	>gi|75909723|ref|YP_324019.1| phosphopyruvate hydratase [Anabaena variabilis ATCC 29413]			x	
84515610	>gi|84515610|ref|ZP_01002972.1| enolase [Loktanella vestfoldensis SKA53]			x	
84510893	>gi|84510893|gb|EAQ07348.1| enolase [Loktanella vestfoldensis SKA53]			x	
67642981	>gi|67642981|ref|ZP_00441731.1| COG0148: Enolase [Burkholderia mallei GB8 horse 4]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
67634803	>gi|67634803|ref|ZP_00433769.1| COG0148: Enolase [Burkholderia mallei 10399]			x	
52427207	>gi|52427207|gb|AAU47800.1| enolase [Burkholderia mallei ATCC 23344]			x	
76580900	>gi|76580900|gb|ABA50375.1| phosphopyruvate hydratase [Burkholderia pseudomallei 1710b]			x	
52210294	>gi|52210294|emb|CAH36273.1| enolase [Burkholderia pseudomallei K96243]			x	
76811447	>gi|76811447|ref|YP_334097.1| phosphopyruvate hydratase [Burkholderia pseudomallei 1710b]			x	
83623653	>gi|83623653|ref|ZP_00933918.1| COG0148: Enolase [Burkholderia mallei JHU]			x	
83618747	>gi|83618747|ref|ZP_00929199.1| COG0148: Enolase [Burkholderia mallei FMH]			x	
59797510	>gi|59797510|sp|Q63SQ0|ENO_BURPS Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
59797504	>gi|59797504|sp|Q62J10|ENO_BURMA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
53719880	>gi|53719880|ref|YP_108866.1| phosphopyruvate hydratase [Burkholderia pseudomallei K96243]			x	
13991101	>gi|13991101|gb|AAK51201.1| enolase [Penicillium citrinum]			x	
74664773	>gi|74664773|sp|Q96X46|ENO_PENCI Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Allergen Pen c 22)			x	
11323224	>gi|11323224|emb|CAC16971.1| enolase [Streptomyces coelicolor A3(2)]			x	
21225899	>gi|21225899|ref|NP_631678.1| enolase [Streptomyces coelicolor A3(2)]			x	
23814099	>gi|23814099|sp|Q9F3P9|ENO2_STRCO Enolase 2 (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x	
13423140	>gi|13423140|gb|AAK23700.1| enolase [Caulobacter crescentus CB15]			x	
16125968	>gi|16125968|ref|NP_420532.1| enolase [Caulobacter crescentus CB15]			x	
21263607	>gi|21263607|sp|Q9A7J9|ENO_CAUCR Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
35212688	>gi|35212688|dbj|BAC90062.1| enolase [Gloeobacter violaceus PCC 7421]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
59797612	>gi|59797612|sp|Q7NIR1|ENO_GLOVI Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
37521690	>gi|37521690|ref|NP_925067.1| enolase [Gloeobacter violaceus PCC 7421]			x	
69159144	>gi|69159144|gb|EAN71282.1| Enolase [Shewanella denitrificans OS217]			x	
69942536	>gi|69942536|ref|ZP_00634323.1| Enolase [Shewanella denitrificans OS-217]			x	
71145813	>gi|71145813|gb|AAZ26286.1| enolase [Colwellia psychrerythraea 34H]			x	
71280073	>gi|71280073|ref|YP_270761.1| phosphopyruvate hydratase [Colwellia psychrerythraea 34H]			x	
70832210	>gi|70832210|gb|EAN77714.1| enolase [Trypanosoma brucei]			x	
71746974	>gi|71746974|ref|XP_822542.1| enolase [Trypanosoma brucei]			x	
8132069	>gi|8132069|gb|AAF73201.1| enolase [Trypanosoma brucei brucei]			x	
22294379	>gi|22294379|dbj|BAC08209.1| enolase [Thermosynechococcus elongatus BP-1]			x	
29839235	>gi|29839235|sp|Q8DL40|ENO_SYNEL Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
22298200	>gi|22298200|ref|NP_681447.1| phosphopyruvate hydratase [Thermosynechococcus elongatus BP-1]			x	
76874604	>gi|76874604|emb|CAI85825.1| enolase [Pseudoalteromonas haloplanktis TAC125]			x	
77359693	>gi|77359693|ref|YP_339268.1| phosphopyruvate hydratase [Pseudoalteromonas haloplanktis TAC125]			x	
83721440	>gi|83721440|ref|YP_442424.1| enolase [Burkholderia thailandensis E264]			x	
83655265	>gi|83655265|gb|ABC39328.1| enolase [Burkholderia thailandensis E264]			x	
83751193	>gi|83751193|ref|ZP_00947607.1| COG0148: Enolase [Bartonella bacilliformis KC583]			x	
68234022	>gi|68234022|ref|ZP_00573122.1| Enolase [Frankia sp. EAN1pec]			x	
68198365	>gi|68198365|gb|EAN12637.1| Enolase [Frankia sp. EAN1pec]			x	
182118	>gi|182118|gb|AAA52388.1| gamma enolase			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
15221107	>gi|15221107|ref|NP_177543.1| phosphopyruvate hydratase [Arabidopsis thaliana]			x	
17065640	>gi|17065640|gb|AAL33814.1| putative enolase [Arabidopsis thaliana]			x	
14334610	>gi|14334610|gb|AAK59483.1| putative enolase [Arabidopsis thaliana]			x	
12325134	>gi|12325134|gb|AAG52510.1| putative enolase; 31277-33713 [Arabidopsis thaliana]			x	
48861278	>gi|48861278|ref|ZP_00315181.1| COG0148: Enolase [Microbulbifer degradans 2-40]			x	
56685854	>gi|56685854|dbj|BAD79076.1| enolase [Synechococcus elongatus PCC 6301]			x	
56750895	>gi|56750895|ref|YP_171596.1| phosphopyruvate hydratase [Synechococcus elongatus PCC 6301]			x	
81299450	>gi|81299450|ref|YP_399658.1| enolase [Synechococcus elongatus PCC 7942]			x	
68053531	>gi|68053531|sp|Q5N3P4|ENO_SYNP6 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
81168331	>gi|81168331|gb|ABB56671.1| enolase [Synechococcus elongatus PCC 7942]			x	
40063045	>gi|40063045|gb|AAR37901.1| enolase [uncultured bacterium 560]			x	
58003118	>gi|58003118|gb|AAW62012.1| Enolase [Gluconobacter oxydans 621H]			x	
68053521	>gi|68053521|sp|Q5FNN5|ENO_GLUOX Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
58040704	>gi|58040704|ref|YP_192668.1| Enolase [Gluconobacter oxydans 621H]			x	
53757045	>gi|53757045|gb|AAU91336.1| enolase [Methylococcus capsulatus str. Bath]			x	
53803284	>gi|53803284|ref|YP_114926.1| enolase [Methylococcus capsulatus str. Bath]			x	
59797673	>gi|59797673|sp|Q604M4|ENO2_METCA Enolase 2 (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x	
71674738	>gi|71674738|ref|ZP_00672484.1| Enolase [Trichodesmium erythraeum IMS101]			x	
71671714	>gi|71671714|gb|EAO28378.1| Enolase [Trichodesmium erythraeum IMS101]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
86572923	>gi|86572923|gb|ABD07480.1| enolase [Rhodopseudomonas palustris HaA2]			x	
68561157	>gi|68561157|ref|ZP_00600460.1| Enolase [Rubrobacter xylanophilus DSM 9941]			x	
68512646	>gi|68512646|gb|EAN36450.1| Enolase [Rubrobacter xylanophilus DSM 9941]			x	
69928271	>gi|69928271|ref|ZP_00625432.1| Enolase [Nitrobacter hamburgensis X14]			x	
69143275	>gi|69143275|gb|EAN61803.1| Enolase [Nitrobacter hamburgensis X14]			x	
77387470	>gi|77387470|gb|ABA78655.1| Enolase [Rhodobacter sphaeroides 2.4.1]			x	
77463052	>gi|77463052|ref|YP_352556.1| Enolase [Rhodobacter sphaeroides 2.4.1]			x	
83374072	>gi|83374072|ref|ZP_00918848.1| Enolase [Rhodobacter sphaeroides ATCC 17029]			x	
83364615	>gi|83364615|gb|EAP68105.1| Enolase [Rhodobacter sphaeroides ATCC 17029]			x	
67988318	>gi|67988318|gb|EAM76098.1| Enolase [Kineococcus radiotolerans SRS30216]			x	
69284254	>gi|69284254|ref|ZP_00616202.1| Enolase [Kineococcus radiotolerans SRS30216]			x	
26453833	>gi|26453833|dbj|BAC44164.1| enolase [Mycoplasma penetrans HF-2]			x	
26553826	>gi|26553826|ref|NP_757760.1| phosphopyruvate hydratase [Mycoplasma penetrans HF-2]			x	
29839243	>gi|29839243|sp|Q8EW32|ENO_MYCPE Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
1653839	>gi|1653839|dbj|BAA18749.1| enolase [Synechocystis sp. PCC 6803]			x	
16332209	>gi|16332209|ref|NP_442937.1| phosphopyruvate hydratase [Synechocystis sp. PCC 6803]			x	
3023705	>gi|3023705|sp|P77972|ENO_SYNY3 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
1169529	>gi|1169529|sp|P42897|ENO_ALLMI Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
472797	>gi|472797|gb|AAA53671.1| alpha-enolase			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
70885013	>gi|70885013|gb|EAN97849.1| enolase, putative [Trypanosoma cruzi]			x	
71665461	>gi|71665461|ref|XP_819700.1| enolase [Trypanosoma cruzi strain CL Brener]			x	
40949688	>gi|40949688|gb|AAR97555.1| enolase [Heterocapsa triquetra]			x	
83371294	>gi|83371294|ref|ZP_00916109.1| Enolase [Rhodobacter sphaeroides ATCC 17025]			x	
83359037	>gi|83359037|gb|EAP62598.1| Enolase [Rhodobacter sphaeroides ATCC 17025]			x	
47458343	>gi|47458343|gb|AAT27666.1| enolase [Mycoplasma mobile 163K]			x	
59797560	>gi|59797560|sp|Q6KIB0|ENO_MYCMO Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
47459015	>gi|47459015|ref|YP_015877.1| phosphopyruvate hydratase [Mycoplasma mobile 163K]			x	
83816221	>gi|83816221|ref|YP_444923.1| phosphopyruvate hydratase [Salinibacter ruber DSM 13855]			x	
83757615	>gi|83757615|gb|ABC45728.1| phosphopyruvate hydratase [Salinibacter ruber DSM 13855]			x	
74661357	>gi|74661357|sp|Q6FTW6|ENO1_CANGA Enolase 1 (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x	
56315000	>gi|56315000|emb|CAI09645.1| Enolase [Azoarcus sp. EbN1]			x	
56478957	>gi|56478957|ref|YP_160546.1| phosphopyruvate hydratase [Azoarcus sp. EbN1]			x	
68053533	>gi|68053533|sp|Q5NZ69|ENO_AZOSE Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
38636433	>gi|38636433|emb|CAE81969.1| probable enolase [Neurospora crassa]			x	
13508345	>gi|13508345|ref|NP_110295.1| phosphopyruvate hydratase [Mycoplasma pneumoniae M129]			x	
1673903	>gi|1673903|gb|AAB95884.1| enolase (eno) [Mycoplasma pneumoniae M129]			x	
2494352	>gi|2494352|sp|P75189|ENO_MYCPN Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
33633710	>gi|33633710|emb|CAE18667.1| Enolase [Prochlorococcus marinus subsp. pastoris str. CCMP1986]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
33860768	>gi|33860768|ref|NP_892329.1| Enolase [Prochlorococcus marinus subsp. pastoris str. CCMP1986]			x	
59797616	>gi|59797616|sp|Q7V377|ENO_PROMP Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
2655163	>gi|2655163|gb|AAB87891.1| enolase [Drosophila subobscura]			x	
82702357	>gi|82702357|ref|YP_411923.1| enolase [Nitrosospira multiformis ATCC 25196]			x	
82410422	>gi|82410422|gb|ABB74531.1| enolase [Nitrosospira multiformis ATCC 25196]			x	
40063711	>gi|40063711|gb|AAR38492.1| enolase [uncultured bacterium 583]			x	
28271404	>gi|28271404|emb|CAD64309.1| phosphopyruvate hydratase [Lactobacillus plantarum WCFS1]			x	
28378568	>gi|28378568|ref|NP_785460.1| phosphopyruvate hydratase [Lactobacillus plantarum WCFS1]			x	
38257511	>gi|38257511|sp|Q88VW2|ENO2_LACPL Enolase 2 (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x	
86169224	>gi|86169224|gb|EAQ70480.1| Enolase [Synechococcus sp. RS9917]			x	
32440997	>gi|32440997|gb|AAP81756.1| enolase [Onchocerca volvulus]			x	
78170022	>gi|78170022|gb|ABB27119.1| Enolase [Synechococcus sp. CC9902]			x	
78185728	>gi|78185728|ref|YP_378162.1| Enolase [Synechococcus sp. CC9902]			x	
33641127	>gi|33641127|emb|CAE22257.1| Enolase [Prochlorococcus marinus str. MIT 9313]			x	
33864347	>gi|33864347|ref|NP_895907.1| Enolase [Prochlorococcus marinus str. MIT 9313]			x	
59797617	>gi|59797617|sp|Q7V483|ENO_PROMM Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
78712095	>gi|78712095|gb|ABB49272.1| enolase [Prochlorococcus marinus str. MIT 9312]			x	
78778596	>gi|78778596|ref|YP_396708.1| enolase [Prochlorococcus marinus str. MIT 9312]			x	
53754768	>gi|53754768|emb|CAH16255.1| enolase [Legionella pneumophila str. Lens]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
68053537	>gi|68053537|sp|Q5WV02|ENO_LEGPL Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
54294936	>gi|54294936|ref|YP_127351.1| enolase [Legionella pneumophila str. Lens]			x	
60099812	>gi|60099812|gb|AAX13040.1| enolase [Drosophila pseudoobscura]			x	
85716527	>gi|85716527|ref|ZP_01047498.1| enolase [Nitrobacter sp. Nb-311A]			x	
85696716	>gi|85696716|gb|EAQ34603.1| enolase [Nitrobacter sp. Nb-311A]			x	
34483549	>gi|34483549|emb|CAE10546.1| PUTATIVE ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) [Wolinella succinogenes]			x	
34557831	>gi|34557831|ref|NP_907646.1| phosphopyruvate hydratase [Wolinella succinogenes DSM 1740]			x	
59797607	>gi|59797607|sp|Q7M8Q0|ENO_WOLSU Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
74420888	>gi|74420888|gb|ABA05087.1| enolase [Nitrobacter winogradskyi Nb-255]			x	
75676018	>gi|75676018|ref|YP_318439.1| enolase [Nitrobacter winogradskyi Nb-255]			x	
86607174	>gi|86607174|ref|YP_475937.1| phosphopyruvate hydratase [Cyanobacteria bacterium Yellowstone A-Prime]			x	
86555716	>gi|86555716|gb|ABD00674.1| phosphopyruvate hydratase [Cyanobacteria bacterium Yellowstone A-Prime]			x	
33639479	>gi|33639479|emb|CAE08863.1| Enolase [Synechococcus sp. WH 8102]			x	
33866878	>gi|33866878|ref|NP_898437.1| Enolase [Synechococcus sp. WH 8102]			x	
59797614	>gi|59797614|sp|Q7U3T1|ENO_SYNPX Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
77176833	>gi|77176833|gb|ABA64522.1| enolase [Leishmania mexicana]			x	
29542233	>gi|29542233|gb|AAO91170.1| enolase [Coxiella burnetii RSA 493]			x	
29654964	>gi|29654964|ref|NP_820656.1| enolase [Coxiella burnetii RSA 493]			x	
59797628	>gi|59797628|sp|Q83B44|ENO_COXBU Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
58698888	>gi|58698888|ref|ZP_00373755.1| enolase [Wolbachia endosymbiont of Drosophila ananassae]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>58534597</td><td>>gi|58534597|gb|EAL58729.1| enolase [Wolbachia endosymbiont of Drosophila ananassae]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>33237212</td><td>>gi|33237212|gb|AAP99281.1| Enolase [Prochlorococcus marinus subsp. marinus str. CCMP1375]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>59797618</td><td>>gi|59797618|sp|Q7VDY0|ENO_PROMA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>33239687</td><td>>gi|33239687|ref|NP_874629.1| Enolase [Prochlorococcus marinus subsp. marinus str. CCMP1375]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>535442</td><td>>gi|535442|gb|AAA70080.1| enolase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78707886</td><td>>gi|78707886|gb|ABB46861.1| enolase [Oryza sativa (japonica cultivar-group)]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78778195</td><td>>gi|78778195|ref|YP_394510.1| Phosphopyruvate hydratase [Thiomicrospira denitrificans ATCC 33889]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78498735</td><td>>gi|78498735|gb|ABB45275.1| Phosphopyruvate hydratase [Thiomicrospira denitrificans ATCC 33889]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>52629365</td><td>>gi|52629365|gb|AAU28106.1| enolase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>52842254</td><td>>gi|52842254|ref|YP_096053.1| enolase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68053539</td><td>>gi|68053539|sp|Q5ZTX1|ENO_LEGPH Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>39574904</td><td>>gi|39574904|emb|CAE78745.1| phosphopyruvate hydratase [Bdellovibrio bacteriovorus HD100]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>59797569</td><td>>gi|59797569|sp|Q6MPQ2|ENO_BDEBA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>42522372</td><td>>gi|42522372|ref|NP_967752.1| phosphopyruvate hydratase [Bdellovibrio bacteriovorus HD100]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>2655161</td><td>>gi|2655161|gb|AAB87890.1| enolase [Drosophila pseudoobscura]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>60099832</td><td>>gi|60099832|gb|AAX13050.1| enolase [Drosophila miranda]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84501065</td><td>>gi|84501065|ref|ZP_00999300.1| Enolase [Oceanicola batsensis HTCC2597]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84391132</td><td>>gi|84391132|gb|EAQ03550.1| Enolase [Oceanicola batsensis HTCC2597]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>68125330</td><td>>gi|68125330|emb|CAJ03181.1| enolase [Leishmania major]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78198443</td><td>>gi|78198443|gb|ABB36208.1| enolase [Synechococcus sp. CC9605]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78213984</td><td>>gi|78213984|ref|YP_382763.1| enolase [Synechococcus sp. CC9605]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>72003261</td><td>>gi|72003261|gb|AAZ59063.1| enolase [Prochlorococcus marinus str. NATL2A]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>72383411</td><td>>gi|72383411|ref|YP_292766.1| enolase [Prochlorococcus marinus str. NATL2A]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>33517294</td><td>>gi|33517294|emb|CAD83678.1| enolase [Candidatus Blochmannia floridanus]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>59797621</td><td>>gi|59797621|sp|Q7VQH3|ENO_BLOFL Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>33519631</td><td>>gi|33519631|ref|NP_878463.1| enolase [Candidatus Blochmannia floridanus]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>53751750</td><td>>gi|53751750|emb|CAH13172.1| enolase [Legionella pneumophila str. Paris]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68053538</td><td>>gi|68053538|sp|Q5X3L4|ENO_LEGPA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>54297965</td><td>>gi|54297965|ref|YP_124334.1| enolase [Legionella pneumophila str. Paris]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>32262179</td><td>>gi|32262179|gb|AAP77228.1| enolase [Helicobacter hepaticus ATCC 51449]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>59797619</td><td>>gi|59797619|sp|Q7VIH4|ENO_HELHP Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>32266130</td><td>>gi|32266130|ref|NP_860162.1| phosphopyruvate hydratase [Helicobacter hepaticus ATCC 51449]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>71548704</td><td>>gi|71548704|ref|ZP_00668928.1| Enolase [Nitrosomonas eutropha C71]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>71485885</td><td>>gi|71485885|gb|EAO18434.1| Enolase [Nitrosomonas eutropha C71]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>66828593</td><td>>gi|66828593|ref|XP_647650.1| 2-phospho-D-glycerate hydrolase [Dictyostelium discoideum]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>60475625</td><td>>gi|60475625|gb|EAL73560.1| phosphopyruvate hydratase [Dictyostelium discoideum]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>66044729</td><td>>gi|66044729|ref|YP_234570.1| Enolase [Pseudomonas syringae pv. syringae B728a]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>63255436</td><td>>gi|63255436|gb|AAY36532.1| Enolase [Pseudomonas syringae pv. syringae B728a]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>76882684</td><td>>gi|76882684|gb|ABA57365.1| Phosphopyruvate hydratase [Nitrosococcus oceani ATCC 19707]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77164370</td><td>>gi|77164370|ref|YP_342895.1| Phosphopyruvate hydratase [Nitrosococcus oceani ATCC 19707]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78707887</td><td>>gi|78707887|gb|ABB46862.1| enolase [Oryza sativa (japonica cultivar-group)]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>28871748</td><td>>gi|28871748|ref|NP_794367.1| enolase [Pseudomonas syringae pv. tomato str. DC3000]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>38372191</td><td>>gi|38372191|sp|Q87WD5|ENO2_PSESM Enolase 2 (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>28855000</td><td>>gi|28855000|gb|AAO58062.1| enolase [Pseudomonas syringae pv. tomato str. DC3000]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>22652630</td><td>>gi|22652630|gb|AAN03783.1| enolase [Clonorchis sinensis]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>37531422</td><td>>gi|37531422|ref|NP_920013.1| putative enolase (2-phospho-D-glycerate hydroylase) [Oryza sativa (japonica cultivar-group)]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>22655764</td><td>>gi|22655764|gb|AAN04181.1| Putative enolase (2-phospho-D-glycerate hydroylase) [Oryza sativa (japonica cultivar-group)]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>86609966</td><td>>gi|86609966|ref|YP_478728.1| phosphopyruvate hydratase [Cyanobacteria bacterium Yellowstone B-Prime]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>86558508</td><td>>gi|86558508|gb|ABD03465.1| phosphopyruvate hydratase [Cyanobacteria bacterium Yellowstone B-Prime]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78704928</td><td>>gi|78704928|ref|ZP_00869322.1| Enolase [Methanospirillum hungatei JF-1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78501730</td><td>>gi|78501730|gb|EAP15371.1| Enolase [Methanospirillum hungatei JF-1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84518726</td><td>>gi|84518726|ref|ZP_01006075.1| Enolase [Prochlorococcus marinus str. MIT 9211]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84513475</td><td>>gi|84513475|gb|EAQ09813.1| Enolase [Prochlorococcus marinus str. MIT 9211]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>30138660</td><td>>gi|30138660|emb|CAD84955.1| Enolase [Nitrosomonas europaea ATCC 19718]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
30249043	>gi|30249043|ref|NP_841113.1| phosphopyruvate hydratase [Nitrosomonas europaea ATCC 19718]			x	
6015097	>gi|6015097|sp|O85348|ENO_NITEU Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
3493583	>gi|3493583|gb|AAC33442.1| enolase; 2-phospho-D-glycerate hydrolase [Nitrosomonas europaea]			x	
86154615	>gi|86154615|ref|ZP_01072782.1| phosphopyruvate hydratase [Campylobacter fetus subsp. fetus 82-40]			x	
85845109	>gi|85845109|gb|EAQ62311.1| phosphopyruvate hydratase [Campylobacter fetus subsp. fetus 82-40]			x	
51980244	>gi|51980244|gb|AAU20794.1| enolase 2 [Heterocapsa triquetra]			x	
18481669	>gi|18481669|gb|AAL73509.1| enolase [Giardia intestinalis]			x	
71077261	>gi|71077261|ref|XP_771145.1| enolase [Giardia lamblia ATCC 50803]			x	
29249462	>gi|29249462|gb|EAA40973.1| GLP_25_44587_43250 [Giardia lamblia ATCC 50803]			x	
28476792	>gi|28476792|gb|AAO44880.1| enolase [Tropheryma whipplei str. Twist]			x	
28493750	>gi|28493750|ref|NP_787911.1| enolase [Tropheryma whipplei str. Twist]			x	
6969088	>gi|6969088|emb|CAB73659.1| enolase [Campylobacter jejuni subsp. jejuni NCTC 11168]			x	
86149479	>gi|86149479|ref|ZP_01067710.1| enolase [Campylobacter jejuni subsp. jejuni CF93-6]			x	
85840261	>gi|85840261|gb|EAQ57519.1| enolase [Campylobacter jejuni subsp. jejuni CF93-6]			x	
15792976	>gi|15792976|ref|NP_282799.1| phosphopyruvate hydratase [Campylobacter jejuni subsp. jejuni NCTC 11168]			x	
9297093	>gi|9297093|sp|P42448|ENO_CAMJE Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
86153067	>gi|86153067|ref|ZP_01071272.1| phosphopyruvate hydratase [Campylobacter jejuni subsp. jejuni HB93-13]			x	
85843952	>gi|85843952|gb|EAQ61162.1| phosphopyruvate hydratase [Campylobacter jejuni subsp. jejuni HB93-13]			x	
42410100	>gi|42410100|gb|AAS14211.1| enolase [Wolbachia endosymbiont of Drosophila melanogaster]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
59797595	>gi|59797595|sp|Q73HQ2|ENO_WOLPM Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
42520362	>gi|42520362|ref|NP_966277.1| enolase [Wolbachia endosymbiont of Drosophila melanogaster]			x	
57227282	>gi|57227282|gb|AAW43741.1| enolase 1, putative [Cryptococcus neoformans var. neoformans JEC21]			x	
57226926	>gi|57226926|gb|AAW43385.1| enolase 1, putative [Cryptococcus neoformans var. neoformans JEC21]			x	
58267784	>gi|58267784|ref|XP_571048.1| enolase 1 [Cryptococcus neoformans var. neoformans JEC21]			x	
58267072	>gi|58267072|ref|XP_570692.1| enolase 1 [Cryptococcus neoformans var. neoformans JEC21]			x	
57167487	>gi|57167487|gb|AAW36266.1| enolase [Campylobacter jejuni RM1221]			x	
68053525	>gi|68053525|sp|Q5HSC1|ENO_CAMJR Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
57238683	>gi|57238683|ref|YP_179814.1| phosphopyruvate hydratase [Campylobacter jejuni RM1221]			x	
28411067	>gi|28411067|emb|CAD67452.1| enolase [Tropheryma whipplei TW08/27]			x	
28572934	>gi|28572934|ref|NP_789714.1| enolase [Tropheryma whipplei TW08/27]			x	
59797629	>gi|59797629|sp|Q83FF7|ENO_TROWT Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
59797630	>gi|59797630|sp|Q83H73|ENO_TROW8 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
12723138	>gi|12723138|gb|AAK04374.1| 2-phosphoglycerate dehydratase (EC 4.2.1.11) [Lactococcus lactis subsp. lactis Il1403]			x	
15672258	>gi|15672258|ref|NP_266432.1| phosphopyruvate hydratase [Lactococcus lactis subsp. lactis Il1403]			x	
21263620	>gi|21263620|sp|Q9CIT0|ENO2_LACLA Enolase 2 (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x	
10039081	>gi|10039081|dbj|BAB13115.1| enolase [Buchnera aphidicola str. APS (Acyrthosiphon pisum)]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>15617016</td><td>>gi|15617016|ref|NP_240229.1| enolase [Buchnera aphidicola str. APS (Acyrthosiphon pisum)]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>11131988</td><td>>gi|11131988|sp|P57492|ENO_BUCAI Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>25291620</td><td>>gi|25291620|pir||C84978 phosphopyruvate hydratase (EC 4.2.1.11) [imported] - Buchnera sp. (strain APS)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>27904258</td><td>>gi|27904258|gb|AAO27091.1| enolase [Buchnera aphidicola str. Bp (Baizongia pistaciae)]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>29839230</td><td>>gi|29839230|sp|P59566|ENO_BUCBP Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>27904860</td><td>>gi|27904860|ref|NP_777986.1| enolase [Buchnera aphidicola str. Bp (Baizongia pistaciae)]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>29835068</td><td>>gi|29835068|gb|AAP05702.1| enolase [Chlamydophila caviae GPIC]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>33301045</td><td>>gi|33301045|sp|Q821H7|ENO_CHLCV Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>29840718</td><td>>gi|29840718|ref|NP_829824.1| phosphopyruvate hydratase [Chlamydophila caviae GPIC]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>86152289</td><td>>gi|86152289|ref|ZP_01070500.1| enolase [Campylobacter jejuni subsp. jejuni 260.94]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>85840778</td><td>>gi|85840778|gb|EAQ58029.1| enolase [Campylobacter jejuni subsp. jejuni 260.94]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>57504666</td><td>>gi|57504666|ref|ZP_00370744.1| enolase [Campylobacter coli RM2228]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>57019435</td><td>>gi|57019435|gb|EAL56130.1| enolase [Campylobacter coli RM2228]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>62148599</td><td>>gi|62148599|emb|CAH64371.1| enolase [Chlamydophila abortus S26/3]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>62185532</td><td>>gi|62185532|ref|YP_220317.1| phosphopyruvate hydratase [Chlamydophila abortus S26/3]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78706225</td><td>>gi|78706225|ref|ZP_00870566.1| Enolase [Methanospirillum hungatei JF-1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78500448</td><td>>gi|78500448|gb|EAP14142.1| Enolase [Methanospirillum hungatei JF-1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>54020356</td><td>>gi|54020356|ref|YP_115643.1| phosphopyruvate hydratase [Mycoplasma hyopneumoniae 232]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
53987529	>gi|53987529|gb|AAV27730.1| enolase [Mycoplasma hyopneumoniae 232]			x	
59797500	>gi|59797500|sp|Q601S2|ENO_MYCH2 Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
71851725	>gi|71851725|gb|AAZ44333.1| enolase [Mycoplasma hyopneumoniae J]			x	
71893598	>gi|71893598|ref|YP_279044.1| phosphopyruvate hydratase [Mycoplasma hyopneumoniae J]			x	
53757787	>gi|53757787|gb|AAU92078.1| enolase [Methylococcus capsulatus str. Bath]			x	
53804026	>gi|53804026|ref|YP_114366.1| enolase [Methylococcus capsulatus str. Bath]			x	
59797674	>gi|59797674|sp|Q606T2|ENO1_METCA Enolase 1 (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x	
62463961	>gi|62463961|ref|ZP_00383267.1| COG0148: Enolase [Lactococcus lactis subsp. cremoris SK11]			x	
71913713	>gi|71913713|gb|AAZ53624.1| enolase [Mycoplasma hyopneumoniae 7448]			x	
72080589	>gi|72080589|ref|YP_287647.1| phosphopyruvate hydratase [Mycoplasma hyopneumoniae 7448]			x	
6899148	>gi|6899148|gb|AAF30591.1| enolase [Ureaplasma parvum serovar 3 str. ATCC 700970]			x	
13124152	>gi|13124152|sp|Q9PQV9|ENO_UREPA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
13357742	>gi|13357742|ref|NP_078016.1| enolase [Ureaplasma parvum serovar 3 str. ATCC 700970]			x	
11268951	>gi|11268951|pir||H82922 enolase UU184 [imported] - Ureaplasma urealyticum			x	
5106162	>gi|5106162|dbj|BAA81473.1| 432aa long hypothetical enolase [Aeropyrum pernix K1]			x	
13124162	>gi|13124162|sp|Q9Y927|ENO_AERPE Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
14602076	>gi|14602076|ref|NP_148623.1| enolase [Aeropyrum pernix K1]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
21623311	>gi|21623311|gb|AAM67951.1| enolase [Buchnera aphidicola str. Sg (Schizaphis graminum)]			x	
25008418	>gi|25008418|sp|Q8K9E0|ENO_BUCAP Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
21672673	>gi|21672673|ref|NP_660740.1| enolase [Buchnera aphidicola str. Sg (Schizaphis graminum)]			x	
72397477	>gi|72397477|gb|AAZ71750.1| phosphopyruvate hydratase [Methanosarcina barkeri str. fusaro]			x	
73670315	>gi|73670315|ref|YP_306330.1| phosphopyruvate hydratase [Methanosarcina barkeri str. fusaro]			x	
4106354	>gi|4106354|gb|AAD02812.1| enolase [Pneumocystis carinii f. sp. ratti]			x	
14585753	>gi|14585753|gb|AAK67491.1| enolase [Curvularia lunata]			x	
74664725	>gi|74664725|sp|Q96VP4|ENO_CURLU Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
6624237	>gi|6624237|dbj|BAA88483.1| enolase-2 [Lethenteron reissneri]			x	
57505300	>gi|57505300|ref|ZP_00371229.1| enolase [Campylobacter upsaliensis RM3195]			x	
57016436	>gi|57016436|gb|EAL53221.1| enolase [Campylobacter upsaliensis RM3195]			x	
58418695	>gi|58418695|gb|AAW70710.1| Enolase [Wolbachia endosymbiont strain TRS of Brugia malayi]			x	
58584379	>gi|58584379|ref|YP_197952.1| Enolase [Wolbachia endosymbiont strain TRS of Brugia malayi]			x	
57240685	>gi|57240685|ref|ZP_00368633.1| enolase [Campylobacter lari RM2100]			x	
57018304	>gi|57018304|gb|EAL55078.1| enolase [Campylobacter lari RM2100]			x	
58254511	>gi|58254511|gb|AAV42748.1| 2-phosphoglycerate dehydratase [Lactobacillus acidophilus NCFM]			x	
68053520	>gi|68053520|sp|Q5FKM6|ENO_LACAC Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
58337194	>gi|58337194|ref|YP_193779.1| phosphopyruvate hydratase [Lactobacillus acidophilus NCFM]			x	
12045269	>gi|12045269|ref|NP_073080.1| phosphopyruvate hydratase [Mycoplasma genitalium G37]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
3845000	>gi|3845000|gb|AAC71635.1| enolase [Mycoplasma genitalium G37]			x	
1352367	>gi|1352367|sp|P47647|ENO_MYCGE Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
68207426	>gi|68207426|ref|ZP_00559588.1| Enolase [Desulfitobacterium hafniense DCB-2]			x	
68168666	>gi|68168666|gb|EAM96590.1| Enolase [Desulfitobacterium hafniense DCB-2]			x	
85712138	>gi|85712138|ref|ZP_01043191.1| Enolase [Idiomarina baltica OS145]			x	
85694128	>gi|85694128|gb|EAQ32073.1| Enolase [Idiomarina baltica OS145]			x	
58429954	>gi|58429954|gb|AAW78351.1| enolase [Trichomonas vaginalis]			x	
81096520	>gi|81096520|ref|ZP_00874861.1| Enolase [Streptococcus suis 89/1591]			x	
80977400	>gi|80977400|gb|EAP40942.1| Enolase [Streptococcus suis 89/1591]			x	
68210333	>gi|68210333|ref|ZP_00562199.1| Enolase [Methanococcoides burtonii DSM 6242]			x	
68186445	>gi|68186445|gb|EAN01162.1| Enolase [Methanococcoides burtonii DSM 6242]			x	
6624229	>gi|6624229|dbj|BAA88479.1| enolase [Eptatretus burgeri]			x	
62515717	>gi|62515717|ref|ZP_00387107.1| COG0148: Enolase [Lactobacillus delbrueckii subsp. bulgaricus ATCC BAA-365]			x	
82623425	>gi|82623425|gb|ABB87127.1| enolase-like [Solanum tuberosum]			x	
57336904	>gi|57336904|emb|CAH60998.1| alpha-enolase [Lactobacillus crispatus]			x	
52550388	>gi|52550388|gb|AAU84237.1| phosphopyruvate hydratase enolase [uncultured archaeon GZfos3D4]			x	
15835490	>gi|15835490|ref|NP_297249.1| phosphopyruvate hydratase [Chlamydia muridarum Nigg]			x	
7190904	>gi|7190904|gb|AAF39672.1| enolase [Chlamydia muridarum Nigg]			x	
13124148	>gi|13124148|sp|Q9PJF3|ENO_CHLMU Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
19915551	>gi|19915551|gb|AAM05080.1| phosphopyruvate hydratase [Methanosarcina acetivorans C2A]			x	
20090525	>gi|20090525|ref|NP_616600.1| phosphopyruvate hydratase [Methanosarcina acetivorans C2A]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>23814073</td><td>>gi|23814073|sp|Q8TQ79|ENO_METAC Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>37572552</td><td>>gi|37572552|dbj|BAC98826.1| enolase [Trichonympha agilis]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>42519286</td><td>>gi|42519286|ref|NP_965216.1| phosphopyruvate hydratase [Lactobacillus johnsonii NCC 533]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>41583574</td><td>>gi|41583574|gb|AAS09182.1| enolase [Lactobacillus johnsonii NCC 533]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>59797823</td><td>>gi|59797823|sp|Q74IV0|ENO3_LACJO Enolase 3 (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 3)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>6624235</td><td>>gi|6624235|dbj|BAA88482.1| enolase-1 [Lethenteron reissneri]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>23002885</td><td>>gi|23002885|ref|ZP_00046557.1| COG0148: Enolase [Lactobacillus gasseri]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>21228938</td><td>>gi|21228938|ref|NP_634860.1| Enolase [Methanosarcina mazei Go1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>20907473</td><td>>gi|20907473|gb|AAM32532.1| Enolase [Methanosarcina mazei Go1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>23814067</td><td>>gi|23814067|sp|Q8PT81|ENO_METMA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>76167854</td><td>>gi|76167854|gb|AAX50862.1| enolase [Chlamydia trachomatis A/HAR-13]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>3329030</td><td>>gi|3329030|gb|AAC68189.1| Enolase [Chlamydia trachomatis D/UW-3/CX]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15605316</td><td>>gi|15605316|ref|NP_220102.1| phosphopyruvate hydratase [Chlamydia trachomatis D/UW-3/CX]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>6225296</td><td>>gi|6225296|sp|O84591|ENO_CHLTR Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>76789324</td><td>>gi|76789324|ref|YP_328410.1| phosphopyruvate hydratase [Chlamydia trachomatis A/HAR-13]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>17739845</td><td>>gi|17739845|gb|AAL42432.1| enolase [Agrobacterium tumefaciens str. C58]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>17935326</td><td>>gi|17935326|ref|NP_532116.1| enolase [Agrobacterium tumefaciens str. C58]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>25291636</td><td>>gi|25291636|pir||AB2752 enolase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
67762048	>gi|67762048|ref|ZP_00500752.1| COG0148: Enolase [Burkholderia pseudomallei S13]			x	
67754306	>gi|67754306|ref|ZP_00493217.1| COG0148: Enolase [Burkholderia pseudomallei Pasteur]			x	
67737197	>gi|67737197|ref|ZP_00487995.1| COG0148: Enolase [Burkholderia pseudomallei 668]			x	
67681454	>gi|67681454|ref|ZP_00475810.1| COG0148: Enolase [Burkholderia pseudomallei 1710a]			x	
67670807	>gi|67670807|ref|ZP_00467605.1| COG0148: Enolase [Burkholderia pseudomallei 1655]			x	
67646759	>gi|67646759|ref|ZP_00445012.1| COG0148: Enolase [Burkholderia mallei NCTC 10247]			x	
85067256	>gi|85067256|ref|ZP_01028109.1| COG0148: Enolase [Burkholderia mallei 10229]			x	
84522300	>gi|84522300|ref|ZP_01009436.1| COG0148: Enolase [Burkholderia mallei SAVP1]			x	
83679486	>gi|83679486|ref|ZP_00941199.1| COG0148: Enolase [Burkholderia pseudomallei 406e]			x	
82536728	>gi|82536728|ref|ZP_00895731.1| COG0148: Enolase [Burkholderia pseudomallei 1106b]			x	
82531609	>gi|82531609|ref|ZP_00890826.1| COG0148: Enolase [Burkholderia pseudomallei 1106a]			x	
71796051	>gi|71796051|gb|AAZ40802.1| enolase [Candidatus Blochmannia pennsylvanicus str. BPEN]			x	
71891945	>gi|71891945|ref|YP_277675.1| enolase [Candidatus Blochmannia pennsylvanicus str. BPEN]			x	
68555849	>gi|68555849|ref|ZP_00595193.1| Enolase [Ralstonia metallidurans CH34]			x	
68530319	>gi|68530319|gb|EAN53281.1| Enolase [Ralstonia metallidurans CH34]			x	
56416785	>gi|56416785|ref|YP_153859.1| Enolase 1 (2-phosphoglycerate dehydratase 1) [Anaplasma marginale str. St. Maries]			x	
56388017	>gi|56388017|gb|AAV86604.1| Enolase 1 (2-phosphoglycerate dehydratase 1) [Anaplasma marginale str. St. Maries]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
24374950	>gi|24374950|ref|NP_718993.1| enolase [Shewanella oneidensis MR-1]			x	
24349668	>gi|24349668|gb|AAN56437.1| enolase [Shewanella oneidensis MR-1]			x	
42519171	>gi|42519171|ref|NP_965101.1| phosphopyruvate hydratase [Lactobacillus johnsonii NCC 533]			x	
41583458	>gi|41583458|gb|AAS09067.1| enolase [Lactobacillus johnsonii NCC 533]			x	
59797824	>gi|59797824|sp|Q74J64|ENO2_LACJO Enolase 2 (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x	
2921237	>gi|2921237|gb|AAC64907.1| enolase [Streptococcus thermophilus]			x	
6015100	>gi|6015100|sp|O52191|ENO_STRTR Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
31179	>gi|31179|emb|CAA47179.1| enolase [Homo sapiens]			x	
729422	>gi|729422|sp|Q05524|ENO1B_HUMAN Alpha-enolase, lung specific (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (HLE1)			x	
8101742	>gi|8101742|gb|AAF72640.1| enolase [Scolopendra polymorpha]			x	
72394249	>gi|72394249|gb|AAZ68526.1| Enolase [Ehrlichia canis str. Jake]			x	
73667108	>gi|73667108|ref|YP_303124.1| Enolase [Ehrlichia canis str. Jake]			x	
58417796	>gi|58417796|emb|CAI27000.1| Enolase (2-phosphoglycerate dehydratase) [Ehrlichia ruminantium str. Welgevonden]			x	
57161291	>gi|57161291|emb|CAH58212.1| enolase [Ehrlichia ruminantium str. Welgevonden]			x	
58579170	>gi|58579170|ref|YP_197382.1| Enolase (2-phosphoglycerate dehydratase) [Ehrlichia ruminantium str. Welgevonden]			x	
57239212	>gi|57239212|ref|YP_180348.1| enolase [Ehrlichia ruminantium str. Welgevonden]			x	
71000241	>gi|71000241|dbj|BAE07171.1| enolase 3 [Karenia mikimotoi]			x	
4416385	>gi|4416385|gb|AAD20345.1| alpha enolase [Trachemys scripta]			x	
31340055	>gi|31340055|sp|Q8D2K1|ENO_WIGBR Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
4416387	>gi|4416387|gb|AAD20346.1| alpha enolase [Pelusios subniger]			x	
8101744	>gi|8101744|gb|AAF72641.1| enolase [Tomocerus sp. 'Tom']			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
58416835	>gi|58416835|emb|CAI27948.1| Enolase (2-phosphoglycerate dehydratase) [Ehrlichia ruminantium str. Gardel]			x	
58617223	>gi|58617223|ref|YP_196422.1| Enolase (2-phosphoglycerate dehydratase) [Ehrlichia ruminantium str. Gardel]			x	
4416383	>gi|4416383|gb|AAD20344.1| alpha enolase [Eumeces inexpectatus]			x	
68171488	>gi|68171488|ref|ZP_00544872.1| Enolase [Ehrlichia chaffeensis str. Sapulpa]			x	
67999094	>gi|67999094|gb|EAM85761.1| Enolase [Ehrlichia chaffeensis str. Sapulpa]			x	
71000219	>gi|71000219|dbj|BAE07165.1| enolase 3 [Karenia brevis]			x	
40949686	>gi|40949686|gb|AAR97554.1| enolase [Thraustotheca clavata]			x	
4416379	>gi|4416379|gb|AAD20342.1| alpha enolase [Caiman crocodilus]			x	
60099838	>gi|60099838|gb|AAX13053.1| enolase [Drosophila miranda]			x	
60099836	>gi|60099836|gb|AAX13052.1| enolase [Drosophila miranda]			x	
60099834	>gi|60099834|gb|AAX13051.1| enolase [Drosophila miranda]			x	
60099830	>gi|60099830|gb|AAX13049.1| enolase [Drosophila miranda]			x	
60099828	>gi|60099828|gb|AAX13048.1| enolase [Drosophila miranda]			x	
60099826	>gi|60099826|gb|AAX13047.1| enolase [Drosophila miranda]			x	
60099824	>gi|60099824|gb|AAX13046.1| enolase [Drosophila miranda]			x	
60099822	>gi|60099822|gb|AAX13045.1| enolase [Drosophila miranda]			x	
60099820	>gi|60099820|gb|AAX13044.1| enolase [Drosophila miranda]			x	
60099818	>gi|60099818|gb|AAX13043.1| enolase [Drosophila miranda]			x	
60099816	>gi|60099816|gb|AAX13042.1| enolase [Drosophila miranda]			x	
40949674	>gi|40949674|gb|AAR97548.1| enolase [Heterosigma akashiwo]			x	
40949684	>gi|40949684|gb|AAR97553.1| enolase [Prymnesium parvum]			x	
40949672	>gi|40949672|gb|AAR97547.1| enolase 2 [Apodachlya brachynema]			x	
40949670	>gi|40949670|gb|AAR97546.1| enolase 1 [Apodachlya brachynema]			x	
15667719	>gi|15667719|gb|AAL05466.1| enolase [Colpidium aqueous]			x	
4416381	>gi|4416381|gb|AAD20343.1| alpha enolase [Sphenodon punctatus]			x	
11999265	>gi|11999265|gb|AAG16310.1| alpha-1 enolase-1 [Salmo trutta]			x	
8101740	>gi|8101740|gb|AAF72639.1| enolase [Polyxenus fasciculatus]			x	
40949682	>gi|40949682|gb|AAR97552.1| enolase [Phytophthora palmivora]			x	
14161523	>gi|14161523|gb|AAK54778.1| enolase [Hypocryphalus mangiferae]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
71000247	>gi|71000247|dbj|BAE07173.1| enolase 3 [Karenia mikimotoi]			x	
15667721	>gi|15667721|gb|AAL05467.1| enolase [Tetrahymena thermophila]			x	
11999259	>gi|11999259|gb|AAG16307.1| beta enolase-1 [Neoceratodus forsteri]			x	
15667723	>gi|15667723|gb|AAL05468.1| enolase [Tetrahymena bergeri]			x	
15667717	>gi|15667717|gb|AAL05465.1| enolase [Paramecium tetraurelia]			x	
40949676	>gi|40949676|gb|AAR97549.1| enolase [Isochrysis galbana]			x	
2621078	>gi|2621078|gb|AAB84550.1| enolase [Methanothermobacter thermautotrophicus str. Delta H]			x	
6015096	>gi|6015096|sp|O26149|ENO_METTH Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
15678072	>gi|15678072|ref|NP_275186.1| phosphopyruvate hydratase [Methanothermobacter thermautotrophicus str. Delta H]			x	
11999257	>gi|11999257|gb|AAG16306.1| beta enolase-1 [Lepidosiren paradoxa]			x	
11999249	>gi|11999249|gb|AAG16302.1| beta enolase-1 [Amia calva]			x	
41394391	>gi|41394391|gb|AAS02299.1| 2-phospho-D-glycerate hydrolase [Phormictopus sp. SBH266263]			x	
41394405	>gi|41394405|gb|AAS02306.1| 2-phospho-D-glycerate hydrolase [Centruroides sp. SBH266264]			x	
11999247	>gi|11999247|gb|AAG16301.1| alpha enolase-1 [Amia calva]			x	
15667709	>gi|15667709|gb|AAL05461.1| enolase 1 [Prionitis lanceolata]			x	
13814095	>gi|13814095|gb|AAK41195.1| Enolase [Sulfolobus solfataricus P2]			x	
21263600	>gi|21263600|sp|Q97ZJ3|ENO_SULSO Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
15897800	>gi|15897800|ref|NP_342405.1| Enolase [Sulfolobus solfataricus P2]			x	
3089611	>gi|3089611|gb|AAC70360.1| enolase [Zymomonas mobilis]			x	
7465695	>gi|7465695|pir||T33721 phosphopyruvate hydratase (EC 4.2.1.11) eno - Zymomonas mobilis			x	
11999263	>gi|11999263|gb|AAG16309.1| beta enolase-1 [Chiloscyllium punctatum]			x	
11999251	>gi|11999251|gb|AAG16303.1| alpha enolase-1 [Latimeria chalumnae]			x	
19074779	>gi|19074779|ref|NP_586285.1| ENOLASE [Encephalitozoon cuniculi GB-M1]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>19069421</td><td>>gi|19069421|emb|CAD25889.1| ENOLASE [Encephalitozoon cuniculi GB-M1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>40949680</td><td>>gi|40949680|gb|AAR97551.1| enolase [Phaeodactylum tricornutum]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>11999267</td><td>>gi|11999267|gb|AAG16311.1| alpha-2 enolase-1 [Salmo trutta]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>41394395</td><td>>gi|41394395|gb|AAS02301.1| 2-phospho-D-glycerate hydrolase [Artemia sp. SBH266677]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>71062748</td><td>>gi|71062748|gb|AAZ21751.1| Enolase [Candidatus Pelagibacter ubique HTCC1062]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>71083635</td><td>>gi|71083635|ref|YP_266355.1| Enolase [Candidatus Pelagibacter ubique HTCC1062]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>13124708</td><td>>gi|13124708|sp|O29133|ENO_ARCFU Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15667704</td><td>>gi|15667704|gb|AAL05459.1| enolase 1 [Mastocarpus papillatus]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>41394399</td><td>>gi|41394399|gb|AAS02303.1| 2-phospho-D-glycerate hydrolase [Callinectes sapidus]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>39598768</td><td>>gi|39598768|gb|AAR28941.1| enolase [Zootermopsis parabasalian symbiont 29]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>76556213</td><td>>gi|76556213|emb|CAD48739.1| enolase 2 [Propionibacterium freudenreichii subsp. shermanii]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>41394387</td><td>>gi|41394387|gb|AAS02297.1| 2-phospho-D-glycerate hydrolase [Lithobius sp. SBH266126]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>41394397</td><td>>gi|41394397|gb|AAS02302.1| 2-phospho-D-glycerate hydrolase [Daphnia magna]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>11999261</td><td>>gi|11999261|gb|AAG16308.1| alpha enolase-1 [Chiloscyllium punctatum]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>39598762</td><td>>gi|39598762|gb|AAR28938.1| enolase [Zootermopsis parabasalian symbiont 17]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>41394389</td><td>>gi|41394389|gb|AAS02298.1| 2-phospho-D-glycerate hydrolase [Diplopoda sp. SBH266145]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15667711</td><td>>gi|15667711|gb|AAL05462.1| enolase 2 [Prionitis lanceolata]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>39598770</td><td>>gi|39598770|gb|AAR28942.1| enolase [Zootermopsis parabasalian symbiont 30]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
39598764	>gi|39598764|gb|AAR28939.1| enolase [Zootermopsis parabasalian symbiont 19]			x	
5566208	>gi|5566208|gb|AAD45339.1| enolase [Trypanosoma brucei]			x	
15622261	>gi|15622261|dbj|BAB66253.1| 416aa long hypothetical enolase [Sulfolobus tokodaii str. 7]			x	
21263595	>gi|21263595|sp|Q972B6|ENO_SULTO Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
15921475	>gi|15921475|ref|NP_377144.1| hypothetical enolase [Sulfolobus tokodaii str. 7]			x	
39598760	>gi|39598760|gb|AAR28937.1| enolase [Zootermopsis parabasalian symbiont 13]			x	
71000227	>gi|71000227|dbj|BAE07167.1| enolase 3 [Karenia brevis]			x	
84489662	>gi|84489662|ref|YP_447894.1| enolase [Methanosphaera stadtmanae DSM 3091]			x	
84372981	>gi|84372981|gb|ABC57251.1| enolase [Methanosphaera stadtmanae DSM 3091]			x	
41394401	>gi|41394401|gb|AAS02304.1| 2-phospho-D-glycerate hydrolase [Nereis macrydi]			x	
55377005	>gi|55377005|ref|YP_134855.1| phosphopyruvate hydratase [Haloarcula marismortui ATCC 43049]			x	
55229730	>gi|55229730|gb|AAV45149.1| enolase [Haloarcula marismortui ATCC 43049]			x	
57015274	>gi|57015274|sp|P29201|ENO_HALMA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
41394393	>gi|41394393|gb|AAS02300.1| 2-phospho-D-glycerate hydrolase [Limulus polyphemus]			x	
41394403	>gi|41394403|gb|AAS02305.1| 2-phospho-D-glycerate hydrolase [Ostracoda sp. SBH266127]			x	
148781	>gi|148781|gb|AAA73101.1| 2-phosphoglycerate dehydratase			x	
76557930	>gi|76557930|emb|CAI49514.1| phosphopyruvate hydratase (EC 4.2.1.11) (enolase) [Natronomonas pharaonis DSM 2160]			x	
76802065	>gi|76802065|ref|YP_327073.1| phosphopyruvate hydratase [Natronomonas pharaonis DSM 2160]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
39598774	>gi|39598774|gb|AAR28944.1| enolase [Zootermopsis parabasalian symbiont 33]			x	
39598758	>gi|39598758|gb|AAR28936.1| enolase [Zootermopsis parabasalian symbiont 11]			x	
39598772	>gi|39598772|gb|AAR28943.1| enolase [Zootermopsis parabasalian symbiont 31]			x	
15667706	>gi|15667706|gb|AAL05460.1| enolase 2 [Mastocarpus papillatus]			x	
71000239	>gi|71000239|dbj|BAE07170.1| enolase 2 [Karenia mikimotoi]			x	
39598766	>gi|39598766|gb|AAR28940.1| enolase [Zootermopsis parabasalian symbiont 22]			x	
71000213	>gi|71000213|dbj|BAE07164.1| enolase 2 [Karenia brevis]			x	
68567781	>gi|68567781|gb|AAY80710.1| enolase [Sulfolobus acidocaldarius DSM 639]			x	
76364182	>gi|76364182|sp|Q4J920|ENO_SULAC Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
70607133	>gi|70607133|ref|YP_256003.1| enolase [Sulfolobus acidocaldarius DSM 639]			x	
18159635	>gi|18159635|gb|AAL63046.1| enolase [Pyrobaculum aerophilum str. IM2]			x	
21263589	>gi|21263589|sp|Q8ZYE7|ENO_PYRAE Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
18312197	>gi|18312197|ref|NP_558864.1| enolase [Pyrobaculum aerophilum str. IM2]			x	
68140076	>gi|68140076|gb|EAM93386.1| Phosphopyruvate hydratase [Ferroplasma acidarmanus Fer1]			x	
69269805	>gi|69269805|ref|ZP_00610109.1| Phosphopyruvate hydratase [Ferroplasma acidarmanus Fer1]			x	
78705604	>gi|78705604|ref|ZP_00869981.1| Enolase [Methanospirillum hungatei JF-1]			x	
78501103	>gi|78501103|gb|EAP14761.1| Enolase [Methanospirillum hungatei JF-1]			x	
11498732	>gi|11498732|ref|NP_069961.1| phosphopyruvate hydratase [Archaeoglobus fulgidus DSM 4304]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
2649457	>gi|2649457|gb|AAB90112.1| enolase (eno) [Archaeoglobus fulgidus DSM 4304]			x	
10580680	>gi|10580680|gb|AAG19526.1| phosphopyruvate hydratase; Eno [Halobacterium sp. NRC-1]			x	
21263609	>gi|21263609|sp|Q9HQI9|ENO_HALSA Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
15790222	>gi|15790222|ref|NP_280046.1| phosphopyruvate hydratase [Halobacterium sp. NRC-1]			x	
71000211	>gi|71000211|dbj|BAE07163.1| enolase 2 [Karenia brevis]			x	
41033679	>gi|41033679|emb|CAF18506.1| enolase [Thermoproteus tenax]			x	
13124124	>gi|13124124|sp|Q9HJT1|ENO_THEAC Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
16081933	>gi|16081933|ref|NP_394341.1| phosphopyruvate hydratase [Thermoplasma acidophilum DSM 1728]			x	
14325249	>gi|14325249|dbj|BAB60153.1| enolase [Thermoplasma volcanium GSS1]			x	
21263596	>gi|21263596|sp|Q979Z9|ENO_THEVO Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
13541812	>gi|13541812|ref|NP_111500.1| phosphopyruvate hydratase [Thermoplasma volcanium GSS1]			x	
48430954	>gi|48430954|gb|AAT43819.1| enolase [Picrophilus torridus DSM 9790]			x	
48478306	>gi|48478306|ref|YP_024012.1| phosphopyruvate hydratase [Picrophilus torridus DSM 9790]			x	
5566207	>gi|5566207|gb|AAD45338.1| enolase 5 [Trichomonas vaginalis]			x	
5566204	>gi|5566204|gb|AAD45335.1| enolase 2 [Trichomonas vaginalis]			x	
5566203	>gi|5566203|gb|AAD45334.1| enolase 1 [Trichomonas vaginalis]			x	
5566205	>gi|5566205|gb|AAD45336.1| enolase 3 [Trichomonas vaginalis]			x	
5566206	>gi|5566206|gb|AAD45337.1| enolase 4 [Trichomonas vaginalis]			x	
33465419	>gi|33465419|gb|AAQ19195.1| enolase [Tetratrichomonas gallinarum]			x	
5566201	>gi|5566201|gb|AAD45332.1| enolase 2 [Monocercomonas ATCC50210]			x	
33465417	>gi|33465417|gb|AAQ19194.1| enolase [Tritrichomonas foetus]			x	
15140365	>gi|15140365|emb|CAC48892.1| probable galactonate dehydratase protein [Sinorhizobium meliloti 1021]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
16264240	>gi|16264240|ref|NP_437032.1| probable galactonate dehydratase protein [Sinorhizobium meliloti 1021]			x	
86359287	>gi|86359287|ref|YP_471179.1| galactonate dehydratase protein [Rhizobium etli CFN 42]			x	
86283389	>gi|86283389|gb|ABC92452.1| galactonate dehydratase protein [Rhizobium etli CFN 42]			x	
71554501	>gi|71554501|gb|AAZ33712.1| galactonate dehydratase [Pseudomonas syringae pv. phaseolicola 1448A]			x	
71733948	>gi|71733948|ref|YP_274182.1| galactonate dehydratase [Pseudomonas syringae pv. phaseolicola 1448A]			x	
52208756	>gi|52208756|emb|CAH34692.1| putative galactonate dehydratase protein [Burkholderia pseudomallei K96243]			x	
53718342	>gi|53718342|ref|YP_107328.1| putative galactonate dehydratase protein [Burkholderia pseudomallei K96243]			x	
37201785	>gi|37201785|dbj|BAC97606.1| probable galactonate dehydratase protein [Vibrio vulnificus YJ016]			x	
37677240	>gi|37677240|ref|NP_937636.1| probable galactonate dehydratase protein [Vibrio vulnificus YJ016]			x	
56380332	>gi|56380332|dbj|BAD76240.1| galactonate dehydratase [Geobacillus kaustophilus HTA426]			x	
56420490	>gi|56420490|ref|YP_147808.1| galactonate dehydratase [Geobacillus kaustophilus HTA426]			x	
48994953	>gi|48994953|gb|AAT48197.1| galactonate dehydratase [Escherichia coli K12]			x	
85676352	>gi|85676352|dbj|BAE77602.1| galactonate dehydratase [Escherichia coli W3110]			x	
49176390	>gi|49176390|ref|YP_026237.1| galactonate dehydratase [Escherichia coli K12]			x	
55977863	>gi|55977863|sp|Q6BF17|DGOD_ECOLI Galactonate dehydratase			x	
17429773	>gi|17429773|emb|CAD16458.1| PUTATIVE GALACTONATE DEHYDRATASE PROTEIN [Ralstonia solanacearum]			x	
17547470	>gi|17547470|ref|NP_520872.1| PUTATIVE GALACTONATE DEHYDRATASE PROTEIN [Ralstonia solanacearum GMI1000]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>56908537</td><td>>gi|56908537|dbj|BAD63064.1| galactonate dehydratase [Bacillus clausii KSM-K16]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>56962300</td><td>>gi|56962300|ref|YP_174025.1| galactonate dehydratase [Bacillus clausii KSM-K16]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>62182315</td><td>>gi|62182315|ref|YP_218732.1| galactonate dehydratase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>62129948</td><td>>gi|62129948|gb|AAX67651.1| galactonate dehydratase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>83375076</td><td>>gi|83375076|ref|ZP_00919840.1| probable galactonate dehydratase protein [Rhodobacter sphaeroides ATCC 17029]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>83363605</td><td>>gi|83363605|gb|EAP67101.1| probable galactonate dehydratase protein [Rhodobacter sphaeroides ATCC 17029]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78035782</td><td>>gi|78035782|emb|CAJ23473.1| Galactonate dehydratase [Xanthomonas campestris pv. vesicatoria str. 85-10]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78047352</td><td>>gi|78047352|ref|YP_363527.1| Galactonate dehydratase [Xanthomonas campestris pv. vesicatoria str. 85-10]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>151356</td><td>>gi|151356|gb|AAC15504.1| mandelate racemase [Pseudomonas putida]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>126731</td><td>>gi|126731|sp|P11444|MANR_PSEPU Mandelate racemase (MR)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>151352</td><td>>gi|151352|gb|AAA25887.1| mandelate racemase (EC 5.1.2.2)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>640264</td><td>>gi|640264|pdb|1MDR| Mandelate Racemase (E.C.5.1.2.2)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>494811</td><td>>gi|494811|pdb|2MNR| Mandelate Racemase (E.C.5.1.2.2)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>443131</td><td>>gi|443131|pdb|1MNS| Mandelate Racemase (E.C.5.1.2.2)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>82740091</td><td>>gi|82740091|ref|ZP_00902855.1| glucarate dehydratase [Pseudomonas putida F1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>82712829</td><td>>gi|82712829|gb|EAP47979.1| glucarate dehydratase [Pseudomonas putida F1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>66046349</td><td>>gi|66046349|ref|YP_236190.1| Glucarate dehydratase [Pseudomonas syringae pv. syringae B728a]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>63257056</td><td>>gi|63257056|gb|AAY38152.1| Glucarate dehydratase [Pseudomonas syringae pv. syringae B728a]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>26991438</td><td>>gi|26991438|ref|NP_746863.1| glucarate dehydratase [Pseudomonas putida KT2440]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
24986512	>gi|24986512|gb|AAN70327.1| glucarate dehydratase [Pseudomonas putida KT2440]			x	
28870449	>gi|28870449|ref|NP_793068.1| glucarate dehydratase [Pseudomonas syringae pv. tomato str. DC3000]			x	
28853696	>gi|28853696|gb|AAO56763.1| glucarate dehydratase [Pseudomonas syringae pv. tomato str. DC3000]			x	
1170130	>gi|1170130|sp|P42238|GUDH_BACSU Probable glucarate dehydratase (GDH) (GlucD)			x	
710000	>gi|710000|dbj|BAA06470.1| glucarate dehydratase [Bacillus subtilis]			x	
1170131	>gi|1170131|sp|P42206|GUDH_PSEPU Glucarate dehydratase (GDH) (GlucD)			x	
5107516	>gi|5107516|pdb|1BQG| The Structure Of The D-Glucarate Dehydratase Protein From Pseudomonas Putida			x	
151315	>gi|151315|gb|AAA25868.1| glucarate dehydratase			x	
83749284	>gi|83749284|ref|ZP_00946283.1| Glucarate dehydratase [Ralstonia solanacearum UW551]			x	
83724065	>gi|83724065|gb|EAP71244.1| Glucarate dehydratase [Ralstonia solanacearum UW551]			x	
49613022	>gi|49613022|emb|CAG76473.1| glucarate dehydratase [Erwinia carotovora subsp. atroseptica SCRI1043]			x	
50122496	>gi|50122496|ref|YP_051663.1| glucarate dehydratase [Erwinia carotovora subsp. atroseptica SCRI1043]			x	
68555520	>gi|68555520|ref|ZP_00594864.1| Glucarate dehydratase [Ralstonia metallidurans CH34]			x	
68529990	>gi|68529990|gb|EAN52952.1| Glucarate dehydratase [Ralstonia metallidurans CH34]			x	
72120887	>gi|72120887|gb|AAZ63073.1| Glucarate dehydratase [Ralstonia eutropha JMP134]			x	
73537550	>gi|73537550|ref|YP_297917.1| Glucarate dehydratase [Ralstonia eutropha JMP134]			x	
16421511	>gi|16421511|gb|AAL21840.1| d-glucarate dehydratase [Salmonella typhimurium LT2]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
62181470	>gi|62181470|ref|YP_217887.1| d-glucarate dehydratase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]			x	
62129103	>gi|62129103|gb|AAX66806.1| d-glucarate dehydratase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]			x	
16766266	>gi|16766266|ref|NP_461881.1| d-glucarate dehydratase [Salmonella typhimurium LT2]			x	
22778523	>gi|22778523|dbj|BAC14792.1| glucarate dehydratase [Oceanobacillus iheyensis HTE831]			x	
23100291	>gi|23100291|ref|NP_693758.1| glucarate dehydratase [Oceanobacillus iheyensis HTE831]			x	
16504040	>gi|16504040|emb|CAD06074.1| probable glucarate dehydratase 1 [Salmonella enterica subsp. enterica serovar Typhi]			x	
29138856	>gi|29138856|gb|AAO70425.1| probable glucarate dehydratase 1 [Salmonella enterica subsp. enterica serovar Typhi Ty2]			x	
16761739	>gi|16761739|ref|NP_457356.1| probable glucarate dehydratase 1 [Salmonella enterica subsp. enterica serovar Typhi str. CT18]			x	
29143223	>gi|29143223|ref|NP_806565.1| probable glucarate dehydratase 1 [Salmonella enterica subsp. enterica serovar Typhi Ty2]			x	
25291986	>gi|25291986|pir||AC0861 glucarate dehydratase (EC 4.2.1.40) - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)			x	
17428092	>gi|17428092|emb|CAD14781.1| PROBABLE GLUCARATE DEHYDRATASE PROTEIN [Ralstonia solanacearum]			x	
17545798	>gi|17545798|ref|NP_519200.1| PROBABLE GLUCARATE DEHYDRATASE PROTEIN [Ralstonia solanacearum GMI1000]			x	
75428530	>gi|75428530|ref|ZP_00731732.1| Glucarate dehydratase [Actinobacillus succinogenes 130Z]			x	
74277622	>gi|74277622|gb|EAO51194.1| Glucarate dehydratase [Actinobacillus succinogenes 130Z]			x	
1789150	>gi|1789150|gb|AAC75829.1| (D)-glucarate dehydratase 1 [Escherichia coli K12]			x	
85675606	>gi|85675606|dbj|BAA16572.2| (D)-glucarate dehydratase 1 [Escherichia coli W3110]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>13363118</td><td>>gi|13363118|dbj|BAB37070.1| putative glucarate dehydratase [Escherichia coli O157:H7]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>16130694</td><td>>gi|16130694|ref|NP_417267.1| (D)-glucarate dehydratase 1 [Escherichia coli K12]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15832901</td><td>>gi|15832901|ref|NP_311674.1| putative glucarate dehydratase [Escherichia coli O157:H7]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84028816</td><td>>gi|84028816|sp|P0AES2|GUDH_ECOLI Glucarate dehydratase (GDH) (GlucD)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84028815</td><td>>gi|84028815|sp|P0AES3|GUDH_ECO57 Glucarate dehydratase (GDH) (GlucD)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>8569464</td><td>>gi|8569464|pdb|1EC7|D Chain D, E. Coli Glucarate Dehydratase Native Enzyme</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>8569463</td><td>>gi|8569463|pdb|1EC7|C Chain C, E. Coli Glucarate Dehydratase Native Enzyme</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>8569462</td><td>>gi|8569462|pdb|1EC7|B Chain B, E. Coli Glucarate Dehydratase Native Enzyme</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>8569461</td><td>>gi|8569461|pdb|1EC7|A Chain A, E. Coli Glucarate Dehydratase Native Enzyme</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>8569476</td><td>>gi|8569476|pdb|1ECQ|D Chain D, E. Coli Glucarate Dehydratase Bound To 4-Deoxyglucarate</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>8569475</td><td>>gi|8569475|pdb|1ECQ|C Chain C, E. Coli Glucarate Dehydratase Bound To 4-Deoxyglucarate</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>8569474</td><td>>gi|8569474|pdb|1ECQ|B Chain B, E. Coli Glucarate Dehydratase Bound To 4-Deoxyglucarate</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>8569473</td><td>>gi|8569473|pdb|1ECQ|A Chain A, E. Coli Glucarate Dehydratase Bound To 4-Deoxyglucarate</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>8569472</td><td>>gi|8569472|pdb|1EC9|D Chain D, E. Coli Glucarate Dehydratase Bound To Xylarohydroxamate</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>8569471</td><td>>gi|8569471|pdb|1EC9|C Chain C, E. Coli Glucarate Dehydratase Bound To Xylarohydroxamate</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>8569470</td><td>>gi|8569470|pdb|1EC9|B Chain B, E. Coli Glucarate Dehydratase Bound To Xylarohydroxamate</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
8569469	>gi|8569469|pdb|1EC9|A Chain A, E. Coli Glucarate Dehydratase Bound To Xylarohydroxamate			x	
8569468	>gi|8569468|pdb|1EC8|D Chain D, E. Coli Glucarate Dehydratase Bound To Product 2,3- Dihydroxy-5-Oxo-Hexanedioate			x	
8569467	>gi|8569467|pdb|1EC8|C Chain C, E. Coli Glucarate Dehydratase Bound To Product 2,3- Dihydroxy-5-Oxo-Hexanedioate			x	
8569466	>gi|8569466|pdb|1EC8|B Chain B, E. Coli Glucarate Dehydratase Bound To Product 2,3- Dihydroxy-5-Oxo-Hexanedioate			x	
8569465	>gi|8569465|pdb|1EC8|A Chain A, E. Coli Glucarate Dehydratase Bound To Product 2,3- Dihydroxy-5-Oxo-Hexanedioate			x	
24053199	>gi|24053199|gb|AAN44288.1| putative glucarate dehydratase [Shigella flexneri 2a str. 301]			x	
30042388	>gi|30042388|gb|AAP18113.1| putative glucarate dehydratase [Shigella flexneri 2a str. 2457T]			x	
30064132	>gi|30064132|ref|NP_838303.1| putative glucarate dehydratase [Shigella flexneri 2a str. 2457T]			x	
24114071	>gi|24114071|ref|NP_708581.1| putative glucarate dehydratase [Shigella flexneri 2a str. 301]			x	
12517262	>gi|12517262|gb|AAG57900.1| putative glucarate dehydratase [Escherichia coli O157:H7 EDL933]			x	
15803308	>gi|15803308|ref|NP_289341.1| putative glucarate dehydratase [Escherichia coli O157:H7 EDL933]			x	
25291985	>gi|25291985|pir||H85929 probable glucarate dehydratase ygcX [imported] - Escherichia coli (strain O157:H7, substrain EDL933)			x	
82545086	>gi|82545086|ref|YP_409033.1| putative glucarate dehydratase [Shigella boydii Sb227]			x	
81246497	>gi|81246497|gb|ABB67205.1| putative glucarate dehydratase [Shigella boydii Sb227]			x	
83719461	>gi|83719461|ref|YP_440747.1| glucarate dehydratase [Burkholderia thailandensis E264]			x	
83653286	>gi|83653286|gb|ABC37349.1| glucarate dehydratase [Burkholderia thailandensis E264]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
56129169	>gi|56129169|gb|AAV78675.1| probable glucarate dehydratase 1 [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]			x	
56414912	>gi|56414912|ref|YP_151987.1| probable glucarate dehydratase 1 [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]			x	
67778298	>gi|67778298|gb|EAM37921.1| Glucarate dehydratase [Polaromonas sp. JS666]			x	
67909708	>gi|67909708|ref|ZP_00508103.1| Glucarate dehydratase [Polaromonas sp. JS666]			x	
74313359	>gi|74313359|ref|YP_311778.1| putative glucarate dehydratase [Shigella sonnei Ss046]			x	
73856836	>gi|73856836|gb|AAZ89543.1| putative glucarate dehydratase [Shigella sonnei Ss046]			x	
27354149	>gi|27354149|dbj|BAC51137.1| glucarate dehydratase [Bradyrhizobium japonicum USDA 110]			x	
27380983	>gi|27380983|ref|NP_772512.1| glucarate dehydratase [Bradyrhizobium japonicum USDA 110]			x	
21114479	>gi|21114479|gb|AAM42512.1| glucarate hydratase [Xanthomonas campestris pv. campestris str. ATCC 33913]			x	
66572615	>gi|66572615|gb|AAY48025.1| glucarate hydratase [Xanthomonas campestris pv. campestris str. 8004]			x	
66767283	>gi|66767283|ref|YP_242045.1| glucarate hydratase [Xanthomonas campestris pv. campestris str. 8004]			x	
21232671	>gi|21232671|ref|NP_638588.1| glucarate hydratase [Xanthomonas campestris pv. campestris str. ATCC 33913]			x	
78694788	>gi|78694788|ref|ZP_00859301.1| Glucarate dehydratase [Bradyrhizobium sp. BTAi1]			x	
78517904	>gi|78517904|gb|EAP31202.1| Glucarate dehydratase [Bradyrhizobium sp. BTAi1]			x	
84715424	>gi|84715424|ref|ZP_01022525.1| glucarate dehydratase [Polaromonas naphthalenivorans CJ2]			x	
84693248	>gi|84693248|gb|EAQ19050.1| glucarate dehydratase [Polaromonas naphthalenivorans CJ2]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
49529393	>gi|49529393|emb|CAG67105.1| D-glucarate dehydratase [Acinetobacter sp. ADP1]			x	
50083417	>gi|50083417|ref|YP_044927.1| D-glucarate dehydratase [Acinetobacter sp. ADP1]			x	
77965618	>gi|77965618|gb|ABB06998.1| Glucarate dehydratase [Burkholderia sp. 383]			x	
78064873	>gi|78064873|ref|YP_367642.1| Glucarate dehydratase [Burkholderia sp. 383]			x	
67666682	>gi|67666682|ref|ZP_00463925.1| Glucarate dehydratase [Burkholderia cenocepacia HI2424]			x	
67661211	>gi|67661211|ref|ZP_00458533.1| Glucarate dehydratase [Burkholderia cenocepacia AU 1054]			x	
67099777	>gi|67099777|gb|EAM16944.1| Glucarate dehydratase [Burkholderia cenocepacia HI2424]			x	
67091199	>gi|67091199|gb|EAM08786.1| Glucarate dehydratase [Burkholderia cenocepacia AU 1054]			x	
74019874	>gi|74019874|ref|ZP_00690485.1| Glucarate dehydratase [Burkholderia ambifaria AMMD]			x	
72607384	>gi|72607384|gb|EAO43345.1| Glucarate dehydratase [Burkholderia ambifaria AMMD]			x	
83748918	>gi|83748918|ref|ZP_00945928.1| Glucarate dehydratase [Ralstonia solanacearum UW551]			x	
83724417	>gi|83724417|gb|EAP71585.1| Glucarate dehydratase [Ralstonia solanacearum UW551]			x	
67549363	>gi|67549363|ref|ZP_00427228.1| Glucarate dehydratase [Burkholderia vietnamiensis G4]			x	
67529304	>gi|67529304|gb|EAM26174.1| Glucarate dehydratase [Burkholderia vietnamiensis G4]			x	
17431301	>gi|17431301|emb|CAD17980.1| PROBABLE GLUCARATE DEHYDRATASE PROTEIN [Ralstonia solanacearum]			x	
17549050	>gi|17549050|ref|NP_522390.1| PROBABLE GLUCARATE DEHYDRATASE PROTEIN [Ralstonia solanacearum GMI1000]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
68206184	>gi|68206184|ref|ZP_00558376.1| Methylaspartate ammonia-lyase [Desulfitobacterium hafniense DCB-2]			x	
68169895	>gi|68169895|gb|EAM97789.1| Methylaspartate ammonia-lyase [Desulfitobacterium hafniense DCB-2]			x	
3184397	>gi|3184397|dbj|BAA28709.1| 3-methylaspartate ammonia-lyase [Citrobacter amalonaticus]			x	
259429	>gi|259429|gb|AAB24070.1| beta-methylaspartase; 3-methylaspartate ammonia-lyase [Clostridium tetanomorphum]			x	
729971	>gi|729971|sp|Q05514|MAAL_CLOTT Methylaspartate ammonia-lyase (Beta-methylaspartase)			x	
13360220	>gi|13360220|dbj|BAB34184.1| 3-methylaspartate ammonia-lyase [Escherichia coli O157:H7]			x	
15830015	>gi|15830015|ref|NP_308788.1| 3-methylaspartate ammonia-lyase [Escherichia coli O157:H7]			x	
12513655	>gi|12513655|gb|AAG55061.1| putative methylaspartate ammonia-lyase [Escherichia coli O157:H7 EDL933]			x	
15800441	>gi|15800441|ref|NP_286453.1| putative methylaspartate ammonia-lyase [Escherichia coli O157:H7 EDL933]			x	
18159000	>gi|18159000|pdb|1KCZ|B Chain B, Crystal Structure Of Beta-Methylaspartase From Clostridium Tetanomorphum. Mg-Complex.			x	
18158999	>gi|18158999|pdb|1KCZ|A Chain A, Crystal Structure Of Beta-Methylaspartase From Clostridium Tetanomorphum. Mg-Complex			x	
82776003	>gi|82776003|ref|YP_402350.1| putative methylaspartate ammonia-lyase [Shigella dysenteriae Sd197]			x	
81240151	>gi|81240151|gb|ABB60861.1| putative methylaspartate ammonia-lyase [Shigella dysenteriae Sd197]			x	
18655552	>gi|18655552|pdb|1KKR|B Chain B, Crystal Structure Of Citrobacter Amalonaticus Methylaspartate Ammonia Lyase Containing (2s,3s)-3-Methylaspartic Acid			x	
18655551	>gi|18655551|pdb|1KKR|A Chain A, Crystal Structure Of Citrobacter Amalonaticus Methylaspartate Ammonia Lyase Containing (2s,3s)-3-Methylaspartic Acid			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
18655550	>gi|18655550|pdb|1KKO|B Chain B, Crystal Structure Of Citrobacter Amalonaticus Methylaspartate Ammonia Lyase			x	
18655549	>gi|18655549|pdb|1KKO|A Chain A, Crystal Structure Of Citrobacter Amalonaticus Methylaspartate Ammonia Lyase			x	
14025840	>gi|14025840|dbj|BAB52439.1| 3-methylaspartate ammonia-lyase [Mesorhizobium loti MAFF303099]			x	
13475089	>gi|13475089|ref|NP_106653.1| 3-methylaspartate ammonia-lyase [Mesorhizobium loti MAFF303099]			x	
28204585	>gi|28204585|gb|AAO37022.1| methylaspartate ammonia-lyase [Clostridium tetani E88]			x	
28212141	>gi|28212141|ref|NP_783085.1| methylaspartate ammonia-lyase [Clostridium tetani E88]			x	
18159002	>gi|18159002|pdb|1KD0|B Chain B, Crystal Structure Of Beta-Methylaspartase From Clostridium Tetanomorphum. Apo-Structure.			x	
18159001	>gi|18159001|pdb|1KD0|A Chain A, Crystal Structure Of Beta-Methylaspartase From Clostridium Tetanomorphum. Apo-Structure			x	
10581701	>gi|10581701|gb|AAG20402.1| methylaspartate ammonia-lyase; Mal [Halobacterium sp. NRC-1]			x	
17368773	>gi|17368773|sp|Q9CLV7|MENC_PASMU O-succinylbenzoate synthase (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x	
15602959	>gi|15602959|ref|NP_246031.1| O-succinylbenzoate synthase [Pasteurella multocida subsp. multocida str. Pm70]			x	
54309783	>gi|54309783|ref|YP_130803.1| O-succinylbenzoate synthase [Photobacterium profundum SS9]			x	
1073792	>gi|1073792|pir||C64105 o-succinylbenzoate synthase - Haemophilus influenzae (strain Rd KW20)			x	
25027033	>gi|25027033|ref|NP_737087.1| O-succinylbenzoate synthase [Corynebacterium efficiens YS-314]			x	
32029563	>gi|32029563|ref|ZP_00132566.1| COG1441: O-succinylbenzoate synthase [Haemophilus somnus 2336]			x	
30995414	>gi|30995414|ref|NP_439130.2| O-succinylbenzoate synthase [Haemophilus influenzae Rd KW20]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
23467878	>gi|23467878|ref|ZP_00123455.1| COG1441: O-succinylbenzoate synthase [Haemophilus somnus 129PT]			x	
77975452	>gi|77975452|ref|ZP_00830987.1| COG1441: O-succinylbenzoate synthase [Yersinia frederiksenii ATCC 33641]			x	
77976638	>gi|77976638|ref|ZP_00832116.1| COG1441: O-succinylbenzoate synthase [Yersinia intermedia ATCC 29909]			x	
77961210	>gi|77961210|ref|ZP_00825054.1| COG1441: O-succinylbenzoate synthase [Yersinia mollaretii ATCC 43969]			x	
77629610	>gi|77629610|ref|ZP_00792196.1| COG1441: O-succinylbenzoate synthase [Yersinia pseudotuberculosis IP 31758]			x	
77636599	>gi|77636599|ref|ZP_00798672.1| COG1441: O-succinylbenzoate synthase [Yersinia pestis Angola]			x	
22125558	>gi|22125558|ref|NP_668981.1| O-succinylbenzoate synthase [Yersinia pestis KIM]			x	
45442125	>gi|45442125|ref|NP_993664.1| O-succinylbenzoate synthase [Yersinia pestis biovar Medievalis str. 91001]			x	
16122743	>gi|16122743|ref|NP_406056.1| O-succinylbenzoate synthase [Yersinia pestis CO92]			x	
20138547	>gi|20138547|sp|P58487|MENC_YERPE O-succinylbenzoate synthase (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x	
50120153	>gi|50120153|ref|YP_049320.1| O-succinylbenzoate synthase [Erwinia carotovora subsp. atroseptica SCRI1043]			x	
77957630	>gi|77957630|ref|ZP_00821681.1| COG1441: O-succinylbenzoate synthase [Yersinia bercovieri ATCC 43970]			x	
51596876	>gi|51596876|ref|YP_071067.1| O-succinylbenzoate synthase [Yersinia pseudotuberculosis IP 32953]			x	
28897706	>gi|28897706|ref|NP_797311.1| O-succinylbenzoate synthase [Vibrio parahaemolyticus RIMD 2210633]			x	
24376048	>gi|24376048|ref|NP_720091.1| O-succinylbenzoate synthase [Shewanella oneidensis MR-1]			x	
52425846	>gi|52425846|ref|YP_088983.1| O-succinylbenzoate synthase [Mannheimia succiniciproducens MBEL55E]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
29336578	>gi|29336578|sp|O34514|MENC_BACSU O-succinylbenzoate synthase (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x	
37526958	>gi|37526958|ref|NP_930302.1| O-succinylbenzoate synthase [Photorhabdus luminescens subsp. laumondii TTO1]			x	
75830779	>gi|75830779|ref|ZP_00760051.1| COG1441: O-succinylbenzoate synthase [Vibrio cholerae MO10]			x	
75815076	>gi|75815076|ref|ZP_00745604.1| COG1441: O-succinylbenzoate synthase [Vibrio cholerae V52]			x	
15641974	>gi|15641974|ref|NP_231606.1| O-succinylbenzoate synthase [Vibrio cholerae O1 biovar eltor str. N16961]			x	
17369119	>gi|17369119|sp|Q9KQM6|MENC_VIBCH O-succinylbenzoate synthase (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x	
37198046	>gi|37198046|dbj|BAC93883.1| O-succinylbenzoate synthase [Vibrio vulnificus YJ016]			x	
37679303	>gi|37679303|ref|NP_933912.1| O-succinylbenzoate synthase [Vibrio vulnificus YJ016]			x	
27362631	>gi|27362631|gb|AAO11485.1| O-succinylbenzoate synthase [Vibrio vulnificus CMCP6]			x	
27366430	>gi|27366430|ref|NP_761958.1| O-succinylbenzoate synthase [Vibrio vulnificus CMCP6]			x	
75827285	>gi|75827285|ref|ZP_00756720.1| COG1441: O-succinylbenzoate synthase [Vibrio cholerae O395]			x	
17380438	>gi|17380438|sp|P44961|MENC_HAEIN O-succinylbenzoate synthase (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x	
75823556	>gi|75823556|ref|ZP_00753049.1| COG1441: O-succinylbenzoate synthase [Vibrio cholerae RC385]			x	
75243077	>gi|75243077|ref|ZP_00726783.1| COG1441: O-succinylbenzoate synthase [Escherichia coli F11]			x	
10120813	>gi|10120813|pdb|1FHV|A Chain A, Crystal Structure Analysis Of O-Succinylbenzoate Synthase From E. Coli Complexed With Mg And Osb			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
16130196	>gi|16130196|ref|NP_416764.1| O-succinylbenzoate synthase [Escherichia coli K12]			x	
83588248	>gi|83588248|ref|ZP_00926873.1| COG1441: O-succinylbenzoate synthase [Escherichia coli 101-1]			x	
2507062	>gi|2507062|sp|P29208|MENC_ECOLI O-succinylbenzoate synthase (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x	
10120812	>gi|10120812|pdb|1FHU|A Chain A, Crystal Structure Analysis Of O-Succinylbenzoate Synthase From E. Coli			x	
75259725	>gi|75259725|ref|ZP_00731027.1| COG1441: O-succinylbenzoate synthase [Escherichia coli E22]			x	
75211670	>gi|75211670|ref|ZP_00711749.1| COG1441: O-succinylbenzoate synthase [Escherichia coli B171]			x	
75187048	>gi|75187048|ref|ZP_00700315.1| COG1441: O-succinylbenzoate synthase [Escherichia coli E24377A]			x	
74312783	>gi|74312783|ref|YP_311202.1| O-succinylbenzoate synthase [Shigella sonnei Ss046]			x	
15832403	>gi|15832403|ref|NP_311176.1| O-succinylbenzoate synthase [Escherichia coli O157:H7]			x	
20138544	>gi|20138544|sp|P58484|MENC_ECO57 O-succinylbenzoate synthase (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x	
15802812	>gi|15802812|ref|NP_288839.1| O-succinylbenzoate synthase [Escherichia coli O157:H7 EDL933]			x	
26248650	>gi|26248650|ref|NP_754690.1| O-succinylbenzoate synthase [Escherichia coli CFT073]			x	
75238050	>gi|75238050|ref|ZP_00722055.1| COG1441: O-succinylbenzoate synthase [Escherichia coli E110019]			x	
62180876	>gi|62180876|ref|YP_217293.1| O-succinylbenzoate synthase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]			x	
16765633	>gi|16765633|ref|NP_461248.1| O-succinylbenzoate synthase [Salmonella typhimurium LT2]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>20138546</td><td>>gi|20138546|sp|P58486|MENC_SALTY O-succinylbenzoate synthase (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>30063692</td><td>>gi|30063692|ref|NP_837863.1| O-succinylbenzoate synthase [Shigella flexneri 2a str. 2457T]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>24113637</td><td>>gi|24113637|ref|NP_708147.1| O-succinylbenzoate synthase [Shigella flexneri 2a str. 301]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>75818947</td><td>>gi|75818947|ref|ZP_00749056.1| COG1441: O-succinylbenzoate synthase [Vibrio cholerae V51]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>75177946</td><td>>gi|75177946|ref|ZP_00698008.1| COG1441: O-succinylbenzoate synthase [Shigella boydii BS512]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>75230352</td><td>>gi|75230352|ref|ZP_00716842.1| COG1441: O-succinylbenzoate synthase [Escherichia coli B7A]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>75196304</td><td>>gi|75196304|ref|ZP_00706374.1| COG1441: O-succinylbenzoate synthase [Escherichia coli HS]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>46129092</td><td>>gi|46129092|ref|ZP_00155737.2| COG1441: O-succinylbenzoate synthase [Haemophilus influenzae R2846]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68057755</td><td>>gi|68057755|gb|AAX88008.1| O-succinylbenzoate synthase [Haemophilus influenzae 86-028NP]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68249556</td><td>>gi|68249556|ref|YP_248668.1| O-succinylbenzoate synthase [Haemophilus influenzae 86-028NP]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>56412796</td><td>>gi|56412796|ref|YP_149871.1| O-succinylbenzoate synthase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>42631291</td><td>>gi|42631291|ref|ZP_00156829.1| COG1441: O-succinylbenzoate synthase [Haemophilus influenzae R2866]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>20138545</td><td>>gi|20138545|sp|P58485|MENC_SALTI O-succinylbenzoate synthase (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>16761232</td><td>>gi|16761232|ref|NP_456849.1| O-succinylbenzoate synthase [Salmonella enterica subsp. enterica serovar Typhi str. CT18]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>29141072</td><td>>gi|29141072|ref|NP_804414.1| O-succinylbenzoate synthase [Salmonella enterica subsp. enterica serovar Typhi Ty2]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
33152187	>gi|33152187|ref|NP_873540.1| O-succinylbenzoate synthase [Haemophilus ducreyi 35000HP]			x	
75854299	>gi|75854299|ref|ZP_00762001.1| COG1441: O-succinylbenzoate synthase [Vibrio sp. Ex25]			x	
75512739	>gi|75512739|ref|ZP_00735241.1| COG1441: O-succinylbenzoate synthase [Escherichia coli 53638]			x	
51974118	>gi|51974118|gb|AAU15668.1| possible N-acylamino acid racemase; possible O-succinylbenzoate synthase [Bacillus cereus E33L]			x	
52140649	>gi|52140649|ref|YP_086181.1| possible N-acylamino acid racemase; possible O-succinylbenzoate synthase [Bacillus cereus E33L]			x	
146811	>gi|146811|gb|AAA71917.1| 4-(2'-carboxyphenyl)-4-oxybutyric acid synthase			x	
84387750	>gi|84387750|ref|ZP_00990766.1| O-succinylbenzoate synthase [Vibrio splendidus 12B01]			x	
84377433	>gi|84377433|gb|EAP94300.1| O-succinylbenzoate synthase [Vibrio splendidus 12B01]			x	
17368727	>gi|17368727|sp|Q9CBB2|MENC_MYCLE Probable O-succinylbenzoate synthase (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x	
15828213	>gi|15828213|ref|NP_302476.1| O-succinylbenzoate synthase [Mycobacterium leprae TN]			x	
59712274	>gi|59712274|ref|YP_205050.1| O-succinylbenzoate synthase [Vibrio fischeri ES114]			x	
59480375	>gi|59480375|gb|AAW86162.1| O-succinylbenzoate synthase [Vibrio fischeri ES114]			x	
62389364	>gi|62389364|ref|YP_224766.1| O-succinylbenzoate synthase [Corynebacterium glutamicum ATCC 13032]			x	
19551709	>gi|19551709|ref|NP_599711.1| O-succinylbenzoate synthase [Corynebacterium glutamicum ATCC 13032]			x	
86148507	>gi|86148507|ref|ZP_01066795.1| O-succinylbenzoate synthase [Vibrio sp. MED222]			x	
85833698	>gi|85833698|gb|EAQ51868.1| O-succinylbenzoate synthase [Vibrio sp. MED222]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
47568030	>gi|47568030|ref|ZP_00238736.1| O-succinylbenzoic acid (OSB) synthetase [Bacillus cereus G9241]			x	
47555333	>gi|47555333|gb|EAL13678.1| O-succinylbenzoic acid (OSB) synthetase [Bacillus cereus G9241]			x	
50954034	>gi|50954034|ref|YP_061322.1| O-succinylbenzoate synthase [Leifsonia xyli subsp. xyli str. CTCB07]			x	
31791735	>gi|31791735|ref|NP_854228.1| O-succinylbenzoate synthase [Mycobacterium bovis AF2122/97]			x	
15607693	>gi|15607693|ref|NP_215067.1| O-succinylbenzoate synthase [Mycobacterium tuberculosis H37Rv]			x	
15839951	>gi|15839951|ref|NP_334988.1| O-succinylbenzoate synthase [Mycobacterium tuberculosis CDC1551]			x	
54041485	>gi|54041485|sp|P65425|MENC_MYCTU Probable O-succinylbenzoate synthase (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x	
54037781	>gi|54037781|sp|P65426|MENC_MYCBO Probable O-succinylbenzoate synthase (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x	
50842386	>gi|50842386|ref|YP_055613.1| O-succinylbenzoate synthase [Propionibacterium acnes KPA171202]			x	
41410148	>gi|41410148|ref|NP_962984.1| O-succinylbenzoate synthase [Mycobacterium avium subsp. paratuberculosis K-10]			x	
72161814	>gi|72161814|ref|YP_289471.1| O-succinylbenzoate synthase [Thermobifida fusca YX]			x	
38233036	>gi|38233036|ref|NP_938803.1| O-succinylbenzoate synthase [Corynebacterium diphtheriae NCTC 13129]			x	
75702573	>gi|75702573|gb|ABA22249.1| O-succinylbenzoic acid synthase [Anabaena variabilis ATCC 29413]			x	
75908848	>gi|75908848|ref|YP_323144.1| O-succinylbenzoate synthase [Anabaena variabilis ATCC 29413]			x	
17135012	>gi|17135012|dbj|BAB77558.1| O-succinylbenzoic acid synthase [Nostoc sp. PCC 7120]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
17227530	>gi|17227530|ref|NP_484078.1| O-succinylbenzoate synthase [Nostoc sp. PCC 7120]			x	
33639437	>gi|33639437|emb|CAE08821.1| putative O-succinylbenzoate synthase [Synechococcus sp. WH 8102]			x	
33866836	>gi|33866836|ref|NP_898395.1| putative O-succinylbenzoate synthase [Synechococcus sp. WH 8102]			x	
46143800	>gi|46143800|ref|ZP_00133907.2| COG1441: O-succinylbenzoate synthase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]			x	
14247568	>gi|14247568|dbj|BAB57958.1| o-succinylbenzoic acid synthetase [Staphylococcus aureus subsp. aureus Mu50]			x	
13701589	>gi|13701589|dbj|BAB42882.1| o-succinylbenzoic acid synthetase [Staphylococcus aureus subsp. aureus N315]			x	
15927370	>gi|15927370|ref|NP_374903.1| o-succinylbenzoic acid synthetase [Staphylococcus aureus subsp. aureus N315]			x	
15924786	>gi|15924786|ref|NP_372320.1| o-succinylbenzoic acid synthetase [Staphylococcus aureus subsp. aureus Mu50]			x	
57284767	>gi|57284767|gb|AAW36861.1| o-succinylbenzoic acid (OSB) synthetase, putative [Staphylococcus aureus subsp. aureus COL]			x	
57650581	>gi|57650581|ref|YP_186674.1| o-succinylbenzoic acid (OSB) synthetase, putative [Staphylococcus aureus subsp. aureus COL]			x	
1255260	>gi|1255260|gb|AAA96059.1| o-succinylbenzoic acid (OSB) synthetase			x	
16331451	>gi|16331451|ref|NP_442179.1| O-succinylbenzoate synthase [Synechocystis sp. PCC 6803]			x	
20138596	>gi|20138596|sp|Q55117|MENC_SYNY3 Probable O-succinylbenzoate synthase (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x	
21204904	>gi|21204904|dbj|BAB95599.1| o-succinylbenzoic acid synthetase [Staphylococcus aureus subsp. aureus MW2]			x	
21283463	>gi|21283463|ref|NP_646551.1| o-succinylbenzoic acid synthetase [Staphylococcus aureus subsp. aureus MW2]			x	
33641103	>gi|33641103|emb|CAE22232.1| putative O-succinylbenzoate synthase [Prochlorococcus marinus str. MIT 9313]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>33864323</td><td>>gi|33864323|ref|NP_895883.1| putative O-succinylbenzoate synthase [Prochlorococcus marinus str. MIT 9313]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>82751377</td><td>>gi|82751377|ref|YP_417118.1| o-succinylbenzoic acid synthetase [Staphylococcus aureus RF122]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>6466408</td><td>>gi|6466408|gb|AAF12990.1| unknown; 4-(2'-carboxyphenyl)-4-oxybutyric acid synthase [Cyanidium caldarium]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>11465504</td><td>>gi|11465504|ref|NP_045105.1| 4-(2'-carboxyphenyl)-4-oxybutyric acid synthase [Cyanidium caldarium]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>27315928</td><td>>gi|27315928|gb|AAO05062.1| o-succinylbenzoic acid (OSB) synthetase [Staphylococcus epidermidis ATCC 12228]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>27468381</td><td>>gi|27468381|ref|NP_765018.1| o-succinylbenzoic acid (OSB) synthetase [Staphylococcus epidermidis ATCC 12228]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>57867276</td><td>>gi|57867276|ref|YP_188928.1| O-succinylbenzoic acid synthetase, putative [Staphylococcus epidermidis RP62A]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>57637934</td><td>>gi|57637934|gb|AAW54722.1| O-succinylbenzoic acid synthetase, putative [Staphylococcus epidermidis RP62A]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>49176099</td><td>>gi|49176099|ref|NP_415841.3| L-Ala-D/L-Glu epimerase, a muconate lactonizing enzyme [Escherichia coli K12]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>18158849</td><td>>gi|18158849|pdb|1JPD|X Chain X, L-Ala-DL-Glu Epimerase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1742170</td><td>>gi|1742170|dbj|BAA14907.1| L-Ala-D/L-Glu epimerase [Escherichia coli W3110]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>52695821</td><td>>gi|52695821|pdb|1TKK|H Chain H, The Structure Of A Substrate-Liganded Complex Of The L-Ala- DL-Glu Epimerase From Bacillus Subtilis</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>52695820</td><td>>gi|52695820|pdb|1TKK|G Chain G, The Structure Of A Substrate-Liganded Complex Of The L-Ala- DL-Glu Epimerase From Bacillus Subtilis</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>52695819</td><td>>gi|52695819|pdb|1TKK|F Chain F, The Structure Of A Substrate-Liganded Complex Of The L-Ala- DL-Glu Epimerase From Bacillus Subtilis</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>52695818</td><td>>gi|52695818|pdb|1TKK|E Chain E, The Structure Of A Substrate-Liganded Complex Of The L-Ala- DL-Glu Epimerase From Bacillus Subtilis</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
52695817	>gi|52695817|pdb|1TKK|D Chain D, The Structure Of A Substrate-Liganded Complex Of The L-Ala- DL-Glu Epimerase From Bacillus Subtilis			x	
52695816	>gi|52695816|pdb|1TKK|C Chain C, The Structure Of A Substrate-Liganded Complex Of The L-Ala- DL-Glu Epimerase From Bacillus Subtilis			x	
52695815	>gi|52695815|pdb|1TKK|B Chain B, The Structure Of A Substrate-Liganded Complex Of The L-Ala- DL-Glu Epimerase From Bacillus Subtilis			x	
52695814	>gi|52695814|pdb|1TKK|A Chain A, The Structure Of A Substrate-Liganded Complex Of The L-Ala- DL-Glu Epimerase From Bacillus Subtilis			x	
18158853	>gi|18158853|pdb|1JPM|D Chain D, L-Ala-DL-Glu Epimerase			x	
18158852	>gi|18158852|pdb|1JPM|C Chain C, L-Ala-DL-Glu Epimerase			x	
18158851	>gi|18158851|pdb|1JPM|B Chain B, L-Ala-DL-Glu Epimerase			x	
18158850	>gi|18158850|pdb|1JPM|A Chain A, L-Ala-DL-Glu Epimerase			x	
75761536	>gi|75761536|ref|ZP_00741495.1| L-Ala-D/L-Glu racemase [Bacillus thuringiensis serovar israelensis ATCC 35646]			x	
74490966	>gi|74490966|gb|EAO54223.1| L-Ala-D/L-Glu racemase [Bacillus thuringiensis serovar israelensis ATCC 35646]			x	
135517	>gi|135517|sp|P27099|TCBD_PSESQ Chloromuconate cycloisomerase (Muconate cycloisomerase II)			x	
151578	>gi|151578|gb|AAD13626.1| cycloisomerase II [Pseudomonas sp.]			x	
40889146	>gi|40889146|pdb|1NU5|A Chain A, Crystal Structure Of Pseudomonas Sp. P51 Chloromuconate Lactonizing Enzyme			x	
26185980	>gi|26185980|emb|CAD56207.1| chloromuconate cycloisomerase [Achromobacter xylosoxidans]			x	
19386505	>gi|19386505|gb|AAK57008.2| chloromuconate cycloisomerase [Delftia acidovorans]			x	
44888544	>gi|44888544|sp|Q9RNZ9|TFDD_COMAC Chloromuconate cycloisomerase			x	
58616645	>gi|58616645|ref|YP_195854.1| chloromuconate cycloisomerase [Achromobacter xylosoxidans]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
54035685	>gi|54035685|sp|P83763|CBNB_RALEU Chloromuconate cycloisomerase cbnB (Muconate cycloisomerase II cbnB)			x	
4210466	>gi|4210466|dbj|BAA74531.1| chloromuconate cycloisomerase [Ralstonia eutropha]			x	
15026865	>gi|15026865|gb|AAK81674.1| chloromuconate cycloisomerase [Burkholderia cepacia]			x	
6521701	>gi|6521701|dbj|BAA88065.1| chloromuconate cycloisomerase [Variovorax paradoxus]			x	
14209510	>gi|14209510|dbj|BAB56010.1| chloromuconate cycloisomerase [Burkholderia sp. NK8]			x	
40019136	>gi|40019136|emb|CAE92860.1| chloromuconate cycloisomerase [Pseudomonas putida]			x	
6002924	>gi|6002924|gb|AAF00202.1| chloromuconate cycloisomerase [Pseudomonas aeruginosa]			x	
49176883	>gi|49176883|ref|YP_025386.1| chloromuconate cycloisomerase [Ralstonia eutropha JMP134]			x	
39777463	>gi|39777463|gb|AAR31038.1| chloromuconate cycloisomerase [Ralstonia eutropha JMP134]			x	
150768	>gi|150768|gb|AAA98263.1| chloromuconate cycloisomerase [Ralstonia eutropha]			x	
135651	>gi|135651|sp|P05404|TFDD1_RALEJ Chloromuconate cycloisomerase (Muconate cycloisomerase II)			x	
1127206	>gi|1127206|pdb|2CHR| Chloromuconate Cycloisomerase (Cmci) (E.C.5.5.1.7)			x	
442737	>gi|442737|pdb|1CHR|B Chain B, Chloromuconate Cycloisomerase (E.C.5.5.1.7)			x	
442736	>gi|442736|pdb|1CHR|A Chain A, Chloromuconate Cycloisomerase (E.C.5.5.1.7)			x	
6002915	>gi|6002915|gb|AAF00196.1| chloromuconate cycloisomerase [Pseudomonas aeruginosa]			x	
3643989	>gi|3643989|gb|AAC69475.1| chloromuconate cycloisomerase [Pseudomonas aeruginosa]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>116506</td><td>>gi|116506|sp|P11452|CLCB_PSEPU Chloromuconate cycloisomerase (Muconate cycloisomerase II)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>150763</td><td>>gi|150763|gb|AAA98260.1| cycloisomerase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>141917</td><td>>gi|141917|gb|AAA98282.1| muconate cycloisomerase II</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>23094408</td><td>>gi|23094408|emb|CAD28144.1| chloromuconate cycloisomerase [Rhodococcus opacus]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>2935031</td><td>>gi|2935031|gb|AAC38249.1| chloromuconate cycloisomerase [Rhodococcus opacus]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>23491535</td><td>>gi|23491535|dbj|BAC16768.1| cis,cis-muconate lactonizing enzyme [Burkholderia sp. TH2]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>12862418</td><td>>gi|12862418|dbj|BAB32456.1| cis,cis-muconate cycloisomerase CatB [Pseudomonas sp. CA10]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>11967279</td><td>>gi|11967279|gb|AAG42035.1| putative muconate cycloisomerase [Ralstonia eutropha]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>13660733</td><td>>gi|13660733|gb|AAK33064.1| cis,cis-muconate lactonizing enzyme [Pseudomonas putida]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>26990423</td><td>>gi|26990423|ref|NP_745848.1| muconate cycloisomerase [Pseudomonas putida KT2440]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>24985391</td><td>>gi|24985391|gb|AAN69312.1| muconate cycloisomerase [Pseudomonas putida KT2440]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>82735481</td><td>>gi|82735481|ref|ZP_00898343.1| muconate cycloisomerase [Pseudomonas putida F1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>82717114</td><td>>gi|82717114|gb|EAP52166.1| muconate cycloisomerase [Pseudomonas putida F1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1633162</td><td>>gi|1633162|pdb|1MUC|B Chain B, Structure Of Muconate Lactonizing Enzyme At 1.85 Angstroms Resolution</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1633161</td><td>>gi|1633161|pdb|1MUC|A Chain A, Structure Of Muconate Lactonizing Enzyme At 1.85 Angstroms Resolution</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>12539415</td><td>>gi|12539415|dbj|BAB21460.1| muconate cycloisomerase [Burkholderia sp. NK8]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>115713</td><td>>gi|115713|sp|P08310|CATB_PSEPU Muconate cycloisomerase I (Cis,cis-muconate lactonizing enzyme I) (MLE)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>225599</td><td>>gi|225599|prf||1307186A muconate lactonizing enzyme I</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>6730024</td><td>>gi|6730024|pdb|2MUC|B Chain B, Muconate Cycloisomerase Variant F329i</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>6730023</td><td>>gi|6730023|pdb|2MUC|A Chain A, Muconate Cycloisomerase Variant F329i</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>34392416</td><td>>gi|34392416|dbj|BAC82532.1| muconate cycloisomerase [Frateuria sp. ANA-18]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>4579699</td><td>>gi|4579699|dbj|BAA75205.1| muconate cycloisomerase [Frateuria sp. ANA-18]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>2589174</td><td>>gi|2589174|gb|AAC46226.1| cic,cis-muconate lactonizing enzyme I [Acinetobacter lwoffii K24]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>6014740</td><td>>gi|6014740|sp|O33946|CATB1_ACILW Muconate cycloisomerase I 1 (Cis,cis-muconate lactonizing enzyme I 1) (MLE 1)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>3419684</td><td>>gi|3419684|gb|AAC31766.1| cic,cis-muconate lactonizing enzyme I [Acinetobacter lwoffii K24]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>151125</td><td>>gi|151125|gb|AAA25766.1| cis,cis-muconate lactonizing enzyme I (EC 5.5.1.1)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>38638066</td><td>>gi|38638066|ref|NP_943040.1| putative muconate cycloisomerase [Cupriavidus necator]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>32527404</td><td>>gi|32527404|gb|AAP86154.1| putative muconate cycloisomerase [Ralstonia eutropha]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>151123</td><td>>gi|151123|gb|AAA25765.1| cis,cis-muconate lactonizing enzyme I (E.C. 5.5.1.1)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>6730036</td><td>>gi|6730036|pdb|3MUC|B Chain B, Muconate Cycloisomerase Variant I54v</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>6730035</td><td>>gi|6730035|pdb|3MUC|A Chain A, Muconate Cycloisomerase Variant I54v</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>13399453</td><td>>gi|13399453|pdb|1F9C|B Chain B, Crystal Structure Of Mle D178n Variant</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>13399452</td><td>>gi|13399452|pdb|1F9C|A Chain A, Crystal Structure Of Mle D178n Variant</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>23491545</td><td>>gi|23491545|dbj|BAC16777.1| cis,cis-muconate lactonizing enzyme [Burkholderia sp. TH2]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>4579705</td><td>>gi|4579705|dbj|BAA75210.1| muconate cycloisomerase [Frateuria sp. ANA-18]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>14132758</td><td>>gi|14132758|gb|AAK52296.1| putative muconate cycloisomerase I CatB [Pseudomonas putida]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68345520</td><td>>gi|68345520|gb|AAY93126.1| muconate cycloisomerase [Pseudomonas fluorescens Pf-5]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>70731221</td><td>>gi|70731221|ref|YP_260962.1| muconate cycloisomerase [Pseudomonas fluorescens Pf-5]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>9948563</td><td>>gi|9948563|gb|AAG05897.1| muconate cycloisomerase I [Pseudomonas aeruginosa PAO1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15597705</td><td>>gi|15597705|ref|NP_251199.1| muconate cycloisomerase I [Pseudomonas aeruginosa PAO1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>2996615</td><td>>gi|2996615|gb|AAC46430.1| muconate cycloisomerase [Acinetobacter sp. ADP1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>740997</td><td>>gi|740997|prf||2006268E muconate cycloisomerase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>49530597</td><td>>gi|49530597|emb|CAG68309.1| muconate cycloisomerase I (Cis,cis-muconate lactonizing enzyme I) (MLE) [Acinetobacter sp. ADP1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>50084621</td><td>>gi|50084621|ref|YP_046131.1| muconate cycloisomerase I (Cis,cis-muconate lactonizing enzyme I) (MLE) [Acinetobacter sp. ADP1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>51704317</td><td>>gi|51704317|sp|Q43931|CATB_ACIAD Muconate cycloisomerase I (Cis,cis-muconate lactonizing enzyme I) (MLE)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>38638055</td><td>>gi|38638055|ref|NP_943029.1| putative muconate cycloisomerase [Cupriavidus necator]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>32527393</td><td>>gi|32527393|gb|AAP86143.1| putative muconate cycloisomerase [Ralstonia eutropha]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>69936817</td><td>>gi|69936817|ref|ZP_00631572.1| Muconate cycloisomerase [Paracoccus denitrificans PD1222]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>69151840</td><td>>gi|69151840|gb|EAN65022.1| Muconate cycloisomerase [Paracoccus denitrificans PD1222]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77971060</td><td>>gi|77971060|gb|ABB12439.1| Muconate cycloisomerase [Burkholderia sp. 383]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78063175</td><td>>gi|78063175|ref|YP_373083.1| Muconate cycloisomerase [Burkholderia sp. 383]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
67665468	>gi|67665468|ref|ZP_00462731.1| Muconate cycloisomerase [Burkholderia cenocepacia HI2424]			x	
67656859	>gi|67656859|ref|ZP_00454240.1| Muconate cycloisomerase [Burkholderia cenocepacia AU 1054]			x	
67101001	>gi|67101001|gb|EAM18148.1| Muconate cycloisomerase [Burkholderia cenocepacia HI2424]			x	
67095576	>gi|67095576|gb|EAM13104.1| Muconate cycloisomerase [Burkholderia cenocepacia AU 1054]			x	
83716982	>gi|83716982|ref|YP_438685.1| muconate cycloisomerase [Burkholderia thailandensis E264]			x	
83650807	>gi|83650807|gb|ABC34871.1| muconate cycloisomerase [Burkholderia thailandensis E264]			x	
3891691	>gi|3891691|pdb|1BKH|B Chain B, Muconate Lactonizing Enzyme From Pseudomonas Putida			x	
56710236	>gi|56710236|dbj|BAD80960.1| muconate lactonizing enzyme I [uncultured bacterium]			x	
52213326	>gi|52213326|emb|CAH39369.1| muconate cycloisomerase I [Burkholderia pseudomallei K96243]			x	
53722912	>gi|53722912|ref|YP_111897.1| muconate cycloisomerase I [Burkholderia pseudomallei K96243]			x	
52422485	>gi|52422485|gb|AAU46055.1| muconate cycloisomerase [Burkholderia mallei ATCC 23344]			x	
53716515	>gi|53716515|ref|YP_105027.1| muconate cycloisomerase [Burkholderia mallei ATCC 23344]			x	
3891692	>gi|3891692|pdb|1BKH|C Chain C, Muconate Lactonizing Enzyme From Pseudomonas Putida			x	
76583804	>gi|76583804|gb|ABA53278.1| muconate cycloisomerase [Burkholderia pseudomallei 1710b]			x	
76819331	>gi|76819331|ref|YP_336144.1| muconate cycloisomerase [Burkholderia pseudomallei 1710b]			x	
3891690	>gi|3891690|pdb|1BKH|A Chain A, Muconate Lactonizing Enzyme From Pseudomonas Putida			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
23494145	>gi|23494145|dbj|BAC19113.1| putative muconate cycloisomerase [Corynebacterium efficiens YS-314]			x	
25028859	>gi|25028859|ref|NP_738913.1| putative muconate cycloisomerase [Corynebacterium efficiens YS-314]			x	
83749259	>gi|83749259|ref|ZP_00946259.1| Muconate cycloisomerase [Ralstonia solanacearum UW551]			x	
83724099	>gi|83724099|gb|EAP71277.1| Muconate cycloisomerase [Ralstonia solanacearum UW551]			x	
1771524	>gi|1771524|emb|CAA67934.1| muconate cycloisomerase [Rhodococcus opacus]			x	
5915882	>gi|5915882|sp|P95608|CATB_RHOOP Muconate cycloisomerase I (Cis,cis-muconate lactonizing enzyme I) (MLE)			x	
60594324	>gi|60594324|pdb|1YEY|D Chain D, Crystal Structure Of L-Fuconate Dehydratase From Xanthomonas Campestris Pv. Campestris Str. Atcc 33913			x	
60594323	>gi|60594323|pdb|1YEY|C Chain C, Crystal Structure Of L-Fuconate Dehydratase From Xanthomonas Campestris Pv. Campestris Str. Atcc 33913			x	
60594322	>gi|60594322|pdb|1YEY|B Chain B, Crystal Structure Of L-Fuconate Dehydratase From Xanthomonas Campestris Pv. Campestris Str. Atcc 33913			x	
60594321	>gi|60594321|pdb|1YEY|A Chain A, Crystal Structure Of L-Fuconate Dehydratase From Xanthomonas Campestris Pv. Campestris Str. Atcc 33913			x	
1176845	>gi|1176845|sp|P45314|KDOP_HAEIN 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (KDO 8-P phosphatase)			x	
20150637	>gi|20150637|pdb|1K1E|L Chain L, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x	
20150636	>gi|20150636|pdb|1K1E|K Chain K, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
20150635	>gi|20150635|pdb|1K1E|J Chain J, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x	
20150634	>gi|20150634|pdb|1K1E|I Chain I, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x	
20150633	>gi|20150633|pdb|1K1E|H Chain H, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x	
20150632	>gi|20150632|pdb|1K1E|G Chain G, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x	
20150631	>gi|20150631|pdb|1K1E|F Chain F, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x	
20150630	>gi|20150630|pdb|1K1E|E Chain E, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x	
20150629	>gi|20150629|pdb|1K1E|D Chain D, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x	
20150628	>gi|20150628|pdb|1K1E|C Chain C, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x	
20150627	>gi|20150627|pdb|1K1E|B Chain B, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x	
20150626	>gi|20150626|pdb|1K1E|A Chain A, Structure Of The Cobalt-Bound Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x	
68058479	>gi|68058479|gb|AAX88732.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Haemophilus influenzae 86-028NP]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
68250280	>gi|68250280|ref|YP_249392.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Haemophilus influenzae 86-028NP]			x	
68342600	>gi|68342600|gb|AAY90206.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Pseudomonas fluorescens Pf-5]			x	
70728301	>gi|70728301|ref|YP_258050.1| 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Pseudomonas fluorescens Pf-5]			x	
20150364	>gi|20150364|pdb|1J8D|D Chain D, Structure Of The Metal-Free Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x	
20150363	>gi|20150363|pdb|1J8D|C Chain C, Structure Of The Metal-Free Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x	
20150362	>gi|20150362|pdb|1J8D|B Chain B, Structure Of The Metal-Free Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x	
20150361	>gi|20150361|pdb|1J8D|A Chain A, Structure Of The Metal-Free Form Of The Deoxy-D-Mannose- Octulosonate 8-Phosphate Phosphatase (Yrbi) From Haemophilus Influenzae (Hi1679)			x	
75431114	>gi|75431114|ref|ZP_00732941.1| 3-deoxy-manno-octulosonate-8-phosphatase [Actinobacillus succinogenes 130Z]			x	
74276377	>gi|74276377|gb|EAO49988.1| 3-deoxy-manno-octulosonate-8-phosphatase [Actinobacillus succinogenes 130Z]			x	
37200675	>gi|37200675|dbj|BAC96500.1| phosphonoacetaldehyde phosphonohydrolase [Vibrio vulnificus YJ016]			x	
37676134	>gi|37676134|ref|NP_936530.1| phosphonoacetaldehyde phosphonohydrolase [Vibrio vulnificus YJ016]			x	
77383909	>gi|77383909|gb|ABA75422.1| Phosphonoacetaldehyde hydrolase [Pseudomonas fluorescens PfO-1]			x	
77459906	>gi|77459906|ref|YP_349413.1| Phosphonoacetaldehyde hydrolase [Pseudomonas fluorescens PfO-1]			x	
18996325	>gi|18996325|emb|CAD24489.1| 2-phosphonoacetaldehyde hydrolase [Pseudomonas putida]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
68345624	>gi|68345624|gb|AAY93230.1| 2-phosphonoacetaldehyde hydrolase [Pseudomonas fluorescens Pf-5]			x	
70731325	>gi|70731325|ref|YP_261066.1| 2-phosphonoacetaldehyde hydrolase [Pseudomonas fluorescens Pf-5]			x	
9947248	>gi|9947248|gb|AAG04700.1| 2-phosphonoacetaldehyde hydrolase [Pseudomonas aeruginosa PAO1]			x	
15596508	>gi|15596508|ref|NP_250002.1| 2-phosphonoacetaldehyde hydrolase [Pseudomonas aeruginosa PAO1]			x	
1177876	>gi|1177876|gb|AAC45742.1| 2-phosphonoacetaldehyde hydrolase [Pseudomonas aeruginosa]			x	
26988932	>gi|26988932|ref|NP_744357.1| 2-phosphonoacetaldehyde hydrolase [Pseudomonas putida KT2440]			x	
24983745	>gi|24983745|gb|AAN67821.1| 2-phosphonoacetaldehyde hydrolase [Pseudomonas putida KT2440]			x	
82737769	>gi|82737769|ref|ZP_00900614.1| Phosphonoacetaldehyde hydrolase:HAD-superfamily hydrolase subfamily IA, variant 3 [Pseudomonas putida F1]			x	
82715142	>gi|82715142|gb|EAP50211.1| Phosphonoacetaldehyde hydrolase:HAD-superfamily hydrolase subfamily IA, variant 3 [Pseudomonas putida F1]			x	
9658018	>gi|9658018|gb|AAF96507.1| phosphonoacetaldehyde phosphonohydrolase [Vibrio cholerae O1 biovar eltor str. N16961]			x	
15601364	>gi|15601364|ref|NP_232995.1| phosphonoacetaldehyde phosphonohydrolase [Vibrio cholerae O1 biovar eltor str. N16961]			x	
28808371	>gi|28808371|dbj|BAC61576.1| phosphonoacetaldehyde phosphonohydrolase [Vibrio parahaemolyticus RIMD 2210633]			x	
28900088	>gi|28900088|ref|NP_799743.1| phosphonoacetaldehyde phosphonohydrolase [Vibrio parahaemolyticus RIMD 2210633]			x	
16501700	>gi|16501700|emb|CAD08888.1| phosphonoacetaldehyde phosphonohydrolase [Salmonella enterica subsp. enterica serovar Typhi]			x	
29138451	>gi|29138451|gb|AAO70021.1| phosphonoacetaldehyde phosphonohydrolase [Salmonella enterica subsp. enterica serovar Typhi Ty2]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>16759409</td><td>>gi|16759409|ref|NP_455026.1| phosphonoacetaldehyde phosphonohydrolase [Salmonella enterica subsp. enterica serovar Typhi str. CT18]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>29142819</td><td>>gi|29142819|ref|NP_806161.1| phosphonoacetaldehyde phosphonohydrolase [Salmonella enterica subsp. enterica serovar Typhi Ty2]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>25513095</td><td>>gi|25513095|pir||AH0555 phosphonoacetaldehyde phosphonohydrolase [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>56128670</td><td>>gi|56128670|gb|AAV78176.1| phosphonoacetaldehyde phosphonohydrolase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>56414413</td><td>>gi|56414413|ref|YP_151488.1| phosphonoacetaldehyde phosphonohydrolase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>18254515</td><td>>gi|18254515|gb|AAB86434.2| phosphonoacetaldehyde hydrolase [Bacillus cereus]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>48425373</td><td>>gi|48425373|pdb|1RQN|B Chain B, Phosphonoacetaldehyde Hydrolase Complexed With Magnesium</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>48425372</td><td>>gi|48425372|pdb|1RQN|A Chain A, Phosphonoacetaldehyde Hydrolase Complexed With Magnesium</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>48425371</td><td>>gi|48425371|pdb|1RQL|B Chain B, Crystal Structure Of Phosponoacetaldehyde Hydrolase Complexed With Magnesium And The Inhibitor Vinyl Sulfonate</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>48425370</td><td>>gi|48425370|pdb|1RQL|A Chain A, Crystal Structure Of Phosponoacetaldehyde Hydrolase Complexed With Magnesium And The Inhibitor Vinyl Sulfonate</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>52695385</td><td>>gi|52695385|pdb|1RDF|F Chain F, G50p Mutant Of Phosphonoacetaldehyde Hydrolase In Complex With Substrate Analogue Vinyl Sulfonate</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>52695384</td><td>>gi|52695384|pdb|1RDF|E Chain E, G50p Mutant Of Phosphonoacetaldehyde Hydrolase In Complex With Substrate Analogue Vinyl Sulfonate</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
52695383	>gi|52695383|pdb|1RDF|D Chain D, G50p Mutant Of Phosphonoacetaldehyde Hydrolase In Complex With Substrate Analogue Vinyl Sulfonate			x	
52695382	>gi|52695382|pdb|1RDF|C Chain C, G50p Mutant Of Phosphonoacetaldehyde Hydrolase In Complex With Substrate Analogue Vinyl Sulfonate			x	
52695381	>gi|52695381|pdb|1RDF|B Chain B, G50p Mutant Of Phosphonoacetaldehyde Hydrolase In Complex With Substrate Analogue Vinyl Sulfonate			x	
52695380	>gi|52695380|pdb|1RDF|A Chain A, G50p Mutant Of Phosphonoacetaldehyde Hydrolase In Complex With Substrate Analogue Vinyl Sulfonate			x	
42780513	>gi|42780513|ref|NP_977760.1| phosphonoacetaldehyde phosphonohydrolase [Bacillus cereus ATCC 10987]			x	
42736433	>gi|42736433|gb|AAS40368.1| phosphonoacetaldehyde phosphonohydrolase [Bacillus cereus ATCC 10987]			x	
49331329	>gi|49331329|gb|AAT61975.1| possible phosphonoacetaldehyde hydrolase [Bacillus thuringiensis serovar konkukian str. 97-27]			x	
47501757	>gi|47501757|gb|AAT30433.1| phosphonoacetaldehyde phosphonohydrolase [Bacillus anthracis str. 'Ames Ancestor']			x	
49178183	>gi|49178183|gb|AAT53559.1| phosphonoacetaldehyde phosphonohydrolase [Bacillus anthracis str. Sterne]			x	
49184256	>gi|49184256|ref|YP_027508.1| phosphonoacetaldehyde phosphonohydrolase [Bacillus anthracis str. Sterne]			x	
49479773	>gi|49479773|ref|YP_035550.1| possible phosphonoacetaldehyde hydrolase [Bacillus thuringiensis serovar konkukian str. 97-27]			x	
30255280	>gi|30255280|gb|AAP25289.1| phosphonoacetaldehyde phosphonohydrolase [Bacillus anthracis str. Ames]			x	
47526609	>gi|47526609|ref|YP_017958.1| phosphonoacetaldehyde phosphonohydrolase [Bacillus anthracis str. 'Ames Ancestor']			x	
30261426	>gi|30261426|ref|NP_843803.1| phosphonoacetaldehyde phosphonohydrolase [Bacillus anthracis str. Ames]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>51977481</td><td>>gi|51977481|gb|AAU19031.1| possible phosphonoacetaldehyde hydrolase [Bacillus cereus E33L]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>52144012</td><td>>gi|52144012|ref|YP_082816.1| possible phosphonoacetaldehyde hydrolase [Bacillus cereus E33L]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>10835408</td><td>>gi|10835408|pdb|1FEZ|D Chain D, The Crystal Structure Of Bacillus Cereus Phosphonoacetaldehyde Hydrolase Complexed With Tungstate, A Product Analog</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>10835407</td><td>>gi|10835407|pdb|1FEZ|C Chain C, The Crystal Structure Of Bacillus Cereus Phosphonoacetaldehyde Hydrolase Complexed With Tungstate, A Product Analog</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>10835406</td><td>>gi|10835406|pdb|1FEZ|B Chain B, The Crystal Structure Of Bacillus Cereus Phosphonoacetaldehyde Hydrolase Complexed With Tungstate, A Product Analog</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>10835405</td><td>>gi|10835405|pdb|1FEZ|A Chain A, The Crystal Structure Of Bacillus Cereus Phosphonoacetaldehyde Hydrolase Complexed With Tungstate, A Product Analog</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>47566213</td><td>>gi|47566213|ref|ZP_00237241.1| phosphonoacetaldehyde phosphonohydrolase VCA0606 [Bacillus cereus G9241]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>47556766</td><td>>gi|47556766|gb|EAL15097.1| phosphonoacetaldehyde phosphonohydrolase VCA0606 [Bacillus cereus G9241]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>28270410</td><td>>gi|28270410|emb|CAD63313.1| phosphonoacetaldehyde hydrolase [Lactobacillus plantarum WCFS1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>28377578</td><td>>gi|28377578|ref|NP_784470.1| phosphonoacetaldehyde hydrolase [Lactobacillus plantarum WCFS1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>6435583</td><td>>gi|6435583|pdb|1QQ5|B Chain B, Structure Of L-2-Haloacid Dehalogenase From Xanthobacter Autotrophicus</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>6435582</td><td>>gi|6435582|pdb|1QQ5|A Chain A, Structure Of L-2-Haloacid Dehalogenase From Xanthobacter Autotrophicus</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>3122178</td><td>>gi|3122178|sp|Q60099|HAD_XANAU (S)-2-haloacid dehalogenase (2-haloalkanoic acid dehalogenase) (L-2-haloacid dehalogenase) (Halocarboxylic acid halidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>2914421</td><td>>gi|2914421|pdb|1AQ6|B Chain B, Structure Of L-2-Haloacid Dehalogenase From Xanthobacter Autotrophicus</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
2914420	>gi|2914420|pdb|1AQ6|A Chain A, Structure Of L-2-Haloacid Dehalogenase From Xanthobacter Autotrophicus			x	
155350	>gi|155350|gb|AAA27590.1| halocarboxylic acid halidohydrolase			x	
691747	>gi|691747|gb|AAB32245.1| L-2-halo acid dehalogenase; L-DEX [Pseudomonas sp.]			x	
3122176	>gi|3122176|sp|Q53464|HAD_PSEUY (S)-2-haloacid dehalogenase (2-haloalkanoic acid dehalogenase) (L-2-haloacid dehalogenase) (Halocarboxylic acid halidohydrolase) (L-DEX)			x	
3212552	>gi|3212552|pdb|1JUD| L-2-Haloacid Dehalogenase			x	
8569435	>gi|8569435|pdb|1QH9|A Chain A, Enzyme-Product Complex Of L-2-Haloacid Dehalogenase			x	
4699780	>gi|4699780|pdb|1ZRN| Intermediate Structure Of L-2-Haloacid Dehalogenase With Monochloroacetate			x	
4699779	>gi|4699779|pdb|1ZRM| Crystal Structure Of The Reaction Intermediate Of L-2-Haloacid Dehalogenase With 2-Chloro-N-Butyrate			x	
39651117	>gi|39651117|emb|CAE29640.1| putative 2-haloacid halidohydrolase Iva [Rhodopseudomonas palustris CGA009]			x	
39937259	>gi|39937259|ref|NP_949535.1| putative 2-haloacid halidohydrolase Iva [Rhodopseudomonas palustris CGA009]			x	
27355843	>gi|27355843|dbj|BAC52825.1| 2-haloalkanoic acid dehalogenase [Bradyrhizobium japonicum USDA 110]			x	
27382671	>gi|27382671|ref|NP_774200.1| 2-haloalkanoic acid dehalogenase [Bradyrhizobium japonicum USDA 110]			x	
17428377	>gi|17428377|emb|CAD15064.1| PUTATIVE 2-HALOALKANOIC ACID DEHALOGENASE PROTEIN [Ralstonia solanacearum]			x	
17546081	>gi|17546081|ref|NP_519483.1| PUTATIVE 2-HALOALKANOIC ACID DEHALOGENASE PROTEIN [Ralstonia solanacearum GMI1000]			x	
3122191	>gi|3122191|sp|Q52087|HADL_PSEPU (S)-2-haloacid dehalogenase (2-haloalkanoic acid dehalogenase) (L-2-haloacid dehalogenase) (Halocarboxylic acid halidohydrolase)			x	
151246	>gi|151246|gb|AAA25832.1| L-2-haloalkanoate dehalogenase			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
3122193	>gi|3122193|sp|Q59728|HAD9_PSEPU (S)-2-haloacid dehalogenase H-109 (2-haloalkanoic acid dehalogenase H-109) (L-2-haloacid dehalogenase H-109) (Halocarboxylic acid halidohydrolase H-109)			x	
440136	>gi|440136|dbj|BAA04474.1| 2-haloacid dehalogenase H-109 [Pseudomonas putida]			x	
740928	>gi|740928|prf||2006222A 2-haloacid dehalogenase			x	
396771	>gi|396771|emb|CAA46976.1| 2-haloacid halidohydrolase IVa [Burkholderia cepacia]			x	
3122190	>gi|3122190|sp|Q51645|HAD4_BURCE (S)-2-haloacid dehalogenase IVA (2-haloalkanoic acid dehalogenase IVA) (L-2-haloacid dehalogenase IVA) (Halocarboxylic acid halidohydrolase IVA)			x	
321693	>gi|321693|pir||S29096 2-haloacid halidohydrolase IVa - Pseudomonas cepacia			x	
83748574	>gi|83748574|ref|ZP_00945594.1| 2-haloalkanoic acid dehalogenase [Ralstonia solanacearum UW551]			x	
83724782	>gi|83724782|gb|EAP71940.1| 2-haloalkanoic acid dehalogenase [Ralstonia solanacearum UW551]			x	
122212	>gi|122212|sp|P24070|HAD2_PSEUC (S)-2-haloacid dehalogenase II (2-haloalkanoic acid dehalogenase II) (L-2-haloacid dehalogenase II) (Halocarboxylic acid halidohydrolase II) (DEHCII)			x	
151250	>gi|151250|gb|AAA25833.1| 2-haloalkanoic acid dehalogenase II			x	
4468652	>gi|4468652|emb|CAB38090.1| haloalkanoic acid dehalogenase [Pseudomonas putida]			x	
6580616	>gi|6580616|emb|CAA63861.2| 2-haloacid dehalogenase; L-2-halidohydrolase [Pseudomonas fluorescens]			x	
18280629	>gi|18280629|sp|Q59666|HAD_PSEFL (S)-2-haloacid dehalogenase (2-haloalkanoic acid dehalogenase) (L-2-haloacid dehalogenase) (Halocarboxylic acid halidohydrolase)			x	
417106	>gi|417106|sp|P24069|HAD1_PSEUC (S)-2-haloacid dehalogenase I (2-haloalkanoic acid dehalogenase I) (L-2-haloacid dehalogenase I) (Halocarboxylic acid halidohydrolase I) (DEHCI)			x	
151248	>gi|151248|gb|AAA63640.1| 2-haloalkanoic acid dehalogenase I			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
78693202	>gi|78693202|ref|ZP_00857716.1| Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2:HAD-superfamily hydrolase, subfamily IA, variant 1 [Bradyrhizobium sp. BTAi1]			x	
78518757	>gi|78518757|gb|EAP32054.1| Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2:HAD-superfamily hydrolase, subfamily IA, variant 1 [Bradyrhizobium sp. BTAi1]			x	
76578370	>gi|76578370|gb|ABA47845.1| haloacid dehalogenase, type II [Burkholderia pseudomallei 1710b]			x	
76808917	>gi|76808917|ref|YP_334008.1| haloacid dehalogenase, type II [Burkholderia pseudomallei 1710b]			x	
52427537	>gi|52427537|gb|AAU48130.1| haloacid dehalogenase, type II [Burkholderia mallei ATCC 23344]			x	
67669257	>gi|67669257|ref|ZP_00466102.1| COG1011: Predicted hydrolase (HAD superfamily) [Burkholderia pseudomallei 1655]			x	
67639054	>gi|67639054|ref|ZP_00437975.1| COG1011: Predicted hydrolase (HAD superfamily) [Burkholderia mallei GB8 horse 4]			x	
67638982	>gi|67638982|ref|ZP_00437917.1| COG1011: Predicted hydrolase (HAD superfamily) [Burkholderia mallei 10399]			x	
67763205	>gi|67763205|ref|ZP_00501902.1| COG1011: Predicted hydrolase (HAD superfamily) [Burkholderia pseudomallei S13]			x	
67648291	>gi|67648291|ref|ZP_00446523.1| COG1011: Predicted hydrolase (HAD superfamily) [Burkholderia mallei NCTC 10247]			x	
85067337	>gi|85067337|ref|ZP_01028190.1| COG1011: Predicted hydrolase (HAD superfamily) [Burkholderia mallei 10229]			x	
84522381	>gi|84522381|ref|ZP_01009517.1| COG1011: Predicted hydrolase (HAD superfamily) [Burkholderia mallei SAVP1]			x	
83676123	>gi|83676123|ref|ZP_00937921.1| COG1011: Predicted hydrolase (HAD superfamily) [Burkholderia pseudomallei 406e]			x	
83622394	>gi|83622394|ref|ZP_00932714.1| COG1011: Predicted hydrolase (HAD superfamily) [Burkholderia mallei JHU]			x	
83617285	>gi|83617285|ref|ZP_00927802.1| COG1011: Predicted hydrolase (HAD superfamily) [Burkholderia mallei FMH]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
82533898	>gi|82533898|ref|ZP_00892949.1| COG1011: Predicted hydrolase (HAD superfamily) [Burkholderia pseudomallei 1106b]			x	
82530895	>gi|82530895|ref|ZP_00890120.1| COG1011: Predicted hydrolase (HAD superfamily) [Burkholderia pseudomallei 1106a]			x	
67753741	>gi|67753741|ref|ZP_00492667.1| COG1011: Predicted hydrolase (HAD superfamily) [Burkholderia pseudomallei Pasteur]			x	
67734827	>gi|67734827|ref|ZP_00485901.1| COG1011: Predicted hydrolase (HAD superfamily) [Burkholderia pseudomallei 668]			x	
44887977	>gi|44887977|sp|P60527|HAD_AGRTR 2-haloalkanoic acid dehalogenase (L-2-haloacid dehalogenase) (Halocarboxylic acid halidohydrolase) (L-DEX) (Cryptic L-isomer-specific dehalogenase) (DhlS5I)			x	
72119053	>gi|72119053|gb|AAZ61316.1| Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2 [Ralstonia eutropha JMP134]			x	
73541640	>gi|73541640|ref|YP_296160.1| Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2 [Ralstonia eutropha JMP134]			x	
84362170	>gi|84362170|ref|ZP_00986804.1| COG1011: Predicted hydrolase (HAD superfamily) [Burkholderia dolosa AUO158]			x	
83719028	>gi|83719028|ref|YP_442519.1| haloacid dehalogenase, type II [Burkholderia thailandensis E264]			x	
83652853	>gi|83652853|gb|ABC36916.1| haloacid dehalogenase, type II [Burkholderia thailandensis E264]			x	
74017830	>gi|74017830|ref|ZP_00688453.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Burkholderia ambifaria AMMD]			x	
72609715	>gi|72609715|gb|EAO45664.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Burkholderia ambifaria AMMD]			x	
14027103	>gi|14027103|dbj|BAB54057.1| 2-haloacid halidohydrolase Iva [Mesorhizobium loti MAFF303099]			x	
13476342	>gi|13476342|ref|NP_107912.1| 2-haloacid halidohydrolase Iva [Mesorhizobium loti MAFF303099]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>67666092</td><td>>gi|67666092|ref|ZP_00463346.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Burkholderia cenocepacia HI2424]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67658833</td><td>>gi|67658833|ref|ZP_00456202.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Burkholderia cenocepacia AU 1054]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67100388</td><td>>gi|67100388|gb|EAM17544.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Burkholderia cenocepacia HI2424]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67093680</td><td>>gi|67093680|gb|EAM11220.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Burkholderia cenocepacia AU 1054]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67549078</td><td>>gi|67549078|ref|ZP_00426952.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Burkholderia vietnamiensis G4]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67529584</td><td>>gi|67529584|gb|EAM26445.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Burkholderia vietnamiensis G4]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77967574</td><td>>gi|77967574|gb|ABB08954.1| Haloacid dehalogenase, type II [Burkholderia sp. 383]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78066829</td><td>>gi|78066829|ref|YP_369598.1| Haloacid dehalogenase, type II [Burkholderia sp. 383]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>62086241</td><td>>gi|62086241|dbj|BAD91552.1| L-2-haloacid dehalogenase [Burkholderia sp. WS]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15073899</td><td>>gi|15073899|emb|CAC45540.1| PUTATIVE ALPHA-HALOCARBOXYLIC ACID DEHALOGENASE PROTEIN [Sinorhizobium meliloti]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15964721</td><td>>gi|15964721|ref|NP_385074.1| PUTATIVE ALPHA-HALOCARBOXYLIC ACID DEHALOGENASE PROTEIN [Sinorhizobium meliloti 1021]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>62289533</td><td>>gi|62289533|ref|YP_221326.1| haloacid dehalogenase [Brucella abortus biovar 1 str. 9-941]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>62195665</td><td>>gi|62195665|gb|AAX73965.1| haloacid dehalogenase [Brucella abortus biovar 1 str. 9-941]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>23347357</td><td>>gi|23347357|gb|AAN29496.1| haloacid dehalogenase, type II [Brucella suis 1330]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>23501454</td><td>>gi|23501454|ref|NP_697581.1| haloacid dehalogenase, type II [Brucella suis 1330]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>23014332</td><td>>gi|23014332|ref|ZP_00054154.1| COG1011: Predicted hydrolase (HAD superfamily) [Magnetospirillum magnetotacticum MS-1]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>67777344</td><td>>gi|67777344|gb|EAM36972.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Polaromonas sp. JS666]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67910416</td><td>>gi|67910416|ref|ZP_00508806.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Polaromonas sp. JS666]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67907457</td><td>>gi|67907457|ref|ZP_00505859.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Polaromonas sp. JS666]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67780274</td><td>>gi|67780274|gb|EAM39890.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Polaromonas sp. JS666]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>56311903</td><td>>gi|56311903|emb|CAI06548.1| putative 2-haloalkanoic acid dehalogenase [Azoarcus sp. EbN1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>56475860</td><td>>gi|56475860|ref|YP_157449.1| putative 2-haloalkanoic acid dehalogenase [Azoarcus sp. EbN1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68189622</td><td>>gi|68189622|gb|EAN04287.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Mesorhizobium sp. BNC1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>69280198</td><td>>gi|69280198|ref|ZP_00614870.1| HAD-superfamily hydrolase, subfamily IA, variant 2 [Mesorhizobium sp. BNC1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>82946478</td><td>>gi|82946478|dbj|BAE51342.1| 2-haloalkanoic acid dehalogenase I [Magnetospirillum magneticum AMB-1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>83311637</td><td>>gi|83311637|ref|YP_421901.1| 2-haloalkanoic acid dehalogenase I [Magnetospirillum magneticum AMB-1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>76259263</td><td>>gi|76259263|ref|ZP_00766913.1| Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2 [Chloroflexus aurantiacus J-10-fl]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>76165790</td><td>>gi|76165790|gb|EAO59920.1| Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2 [Chloroflexus aurantiacus J-10-fl]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>86160229</td><td>>gi|86160229|ref|YP_467014.1| haloacid dehalogenase, type II [Anaeromyxobacter dehalogenans 2CP-C]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>85776740</td><td>>gi|85776740|gb|ABC83577.1| haloacid dehalogenase, type II [Anaeromyxobacter dehalogenans 2CP-C]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>47574019</td><td>>gi|47574019|ref|ZP_00244056.1| COG1011: Predicted hydrolase (HAD superfamily) [Rubrivivax gelatinosus PM1]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>4127501</td><td>>gi|4127501|emb|CAA06738.1| cryptic haloacid dehalogenase 1 [Burkholderia cepacia]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>2635968</td><td>>gi|2635968|emb|CAB15460.1| beta-phosphoglucomutase; glucose-1-phosphate phosphodismutase [Bacillus subtilis subsp. subtilis str. 168]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>3024396</td><td>>gi|3024396|sp|O06995|PGMB_BACSU Putative beta-phosphoglucomutase (Beta-PGM)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>16080508</td><td>>gi|16080508|ref|NP_391335.1| beta-phosphoglucomutase [Bacillus subtilis subsp. subtilis str. 168]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>28269830</td><td>>gi|28269830|emb|CAD62727.1| beta-phosphoglucomutase [Lactobacillus plantarum WCFS1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>28376999</td><td>>gi|28376999|ref|NP_783891.1| beta-phosphoglucomutase [Lactobacillus plantarum WCFS1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>3724126</td><td>>gi|3724126|emb|CAA11906.1| beta-phosphoglucomutase [Lactobacillus sanfranciscensis]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>7225613</td><td>>gi|7225613|gb|AAF40831.1| beta-phosphoglucomutase [Neisseria meningitidis MC58]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15676305</td><td>>gi|15676305|ref|NP_273440.1| beta-phosphoglucomutase [Neisseria meningitidis MC58]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1495997</td><td>>gi|1495997|emb|CAA94734.1| beta-phosphoglucomutase [Lactococcus lactis]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>75765829</td><td>>gi|75765829|pdb|1ZOL|A Chain A, Native Beta-Pgm</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>66361316</td><td>>gi|66361316|pdb|1Z4O|B Chain B, Structure Of Beta-Phosphoglucomutase With Inhibitor Bound Alpha-Galactose 1-Phosphate</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>66361315</td><td>>gi|66361315|pdb|1Z4O|A Chain A, Structure Of Beta-Phosphoglucomutase With Inhibitor Bound Alpha-Galactose 1-Phosphate</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>66361314</td><td>>gi|66361314|pdb|1Z4N|B Chain B, Structure Of Beta-Phosphoglucomutase With Inhibitor Bound Alpha-Galactose 1-Phosphate Cocrystallized With Fluoride</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>66361313</td><td>>gi|66361313|pdb|1Z4N|A Chain A, Structure Of Beta-Phosphoglucomutase With Inhibitor Bound Alpha-Galactose 1-Phosphate Cocrystallized With Fluoride</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
29726863	>gi|29726863|pdb|1O08|A Chain A, Structure Of Pentavalent Phosphorous Intermediate Of An Enzyme Catalyzed Phosphoryl Transfer Reaction Observed On Cocrystallization With Glucose 1-Phosphate			x	
29726862	>gi|29726862|pdb|1O03|A Chain A, Structure Of Pentavalent Phosphorous Intermediate Of An Enzyme Catalyzed Phosphoryl Transfer Reaction Observed On Cocrystallization With Glucose 6-Phosphate			x	
12723306	>gi|12723306|gb|AAK04527.1| beta-phosphoglucomutase (EC 5.4.2.6) [Lactococcus lactis subsp. lactis Il1403]			x	
15672411	>gi|15672411|ref|NP_266585.1| beta-phosphoglucomutase [Lactococcus lactis subsp. lactis Il1403]			x	
13432244	>gi|13432244|sp|P71447|PGMB_LACLA Beta-phosphoglucomutase (Beta-PGM)			x	
28269859	>gi|28269859|emb|CAD62756.1| beta-phosphoglucomutase [Lactobacillus plantarum WCFS1]			x	
28377028	>gi|28377028|ref|NP_783920.1| beta-phosphoglucomutase [Lactobacillus plantarum WCFS1]			x	
7380718	>gi|7380718|emb|CAB85309.1| beta-phosphoglucomutase [Neisseria meningitidis Z2491]			x	
15794968	>gi|15794968|ref|NP_284790.1| beta-phosphoglucomutase [Neisseria meningitidis Z2491]			x	
13361361	>gi|13361361|dbj|BAB35319.1| putative beta-phosphoglucomutase [Escherichia coli O157:H7]			x	
15831150	>gi|15831150|ref|NP_309923.1| putative beta-phosphoglucomutase [Escherichia coli O157:H7]			x	
12515452	>gi|12515452|gb|AAG56485.1| putative beta-phosphoglucomutase [Escherichia coli O157:H7 EDL933]			x	
15801853	>gi|15801853|ref|NP_287871.1| putative beta-phosphoglucomutase [Escherichia coli O157:H7 EDL933]			x	
24051633	>gi|24051633|gb|AAN42930.1| putative beta-phosphoglucomutase [Shigella flexneri 2a str. 301]			x	
30041084	>gi|30041084|gb|AAP16814.1| putative beta-phosphoglucomutase [Shigella flexneri 2a str. 2457T]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>30062836</td><td>>gi|30062836|ref|NP_837007.1| putative beta-phosphoglucomutase [Shigella flexneri 2a str. 2457T]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>24112713</td><td>>gi|24112713|ref|NP_707223.1| putative beta-phosphoglucomutase [Shigella flexneri 2a str. 301]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>47097361</td><td>>gi|47097361|ref|ZP_00234914.1| beta-phosphoglucomutase [Listeria monocytogenes str. 1/2a F6854]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>47014256</td><td>>gi|47014256|gb|EAL05236.1| beta-phosphoglucomutase [Listeria monocytogenes str. 1/2a F6854]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>46909020</td><td>>gi|46909020|ref|YP_015409.1| beta-phosphoglucomutase [Listeria monocytogenes str. 4b F2365]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>46882293</td><td>>gi|46882293|gb|AAT05586.1| beta-phosphoglucomutase [Listeria monocytogenes str. 4b F2365]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>47093202</td><td>>gi|47093202|ref|ZP_00230975.1| beta-phosphoglucomutase [Listeria monocytogenes str. 4b H7858]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>47018396</td><td>>gi|47018396|gb|EAL09156.1| beta-phosphoglucomutase [Listeria monocytogenes str. 4b H7858]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>7380722</td><td>>gi|7380722|emb|CAB85313.1| beta-phosphoglucomutase [Neisseria meningitidis Z2491]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15794972</td><td>>gi|15794972|ref|NP_284794.1| beta-phosphoglucomutase [Neisseria meningitidis Z2491]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>26108055</td><td>>gi|26108055|gb|AAN80255.1| Putative beta-phosphoglucomutase [Escherichia coli CFT073]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>26247653</td><td>>gi|26247653|ref|NP_753693.1| Putative beta-phosphoglucomutase [Escherichia coli CFT073]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1787576</td><td>>gi|1787576|gb|AAC74399.1| putative beta-phosphoglucomutase [Escherichia coli K12]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1742154</td><td>>gi|1742154|dbj|BAA14892.1| predicted beta-phosphoglucomutase [Escherichia coli W3110]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>16129278</td><td>>gi|16129278|ref|NP_415833.1| putative beta phosphoglucomutase, contains a phophatase-like domain [Escherichia coli K12]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>3024403</td><td>>gi|3024403|sp|P77366|PGMB_ECOLI Putative beta-phosphoglucomutase (Beta-PGM)</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
74312316	>gi|74312316|ref|YP_310735.1| putative beta-phosphoglucomutase [Shigella sonnei Ss046]			x	
73855793	>gi|73855793|gb|AAZ88500.1| putative beta-phosphoglucomutase [Shigella sonnei Ss046]			x	
29342999	>gi|29342999|gb|AAO80763.1| beta-phosphoglucomutase [Enterococcus faecalis V583]			x	
29375539	>gi|29375539|ref|NP_814693.1| beta-phosphoglucomutase [Enterococcus faecalis V583]			x	
52002312	>gi|52002312|gb|AAU22254.1| beta-phosphoglucomutase and glucose-1-phosphate phosphodismutase [Bacillus licheniformis ATCC 14580]			x	
52079101	>gi|52079101|ref|YP_077892.1| beta-phosphoglucomutase and glucose-1-phosphate phosphodismutase [Bacillus licheniformis ATCC 14580]			x	
14090050	>gi|14090050|emb|CAC13808.1| BETA-PHOSPHOGLUCOMUTASE (BETA-PGM) [Mycoplasma pulmonis]			x	
15829106	>gi|15829106|ref|NP_326466.1| BETA-PHOSPHOGLUCOMUTASE (BETA-PGM) [Mycoplasma pulmonis UAB CTIP]			x	
505588	>gi|505588|gb|AAA19216.1| 5-epi-aristolochene synthase			x	
2624696	>gi|2624696|pdb|5EAS| 5-Epi-Aristolochene Synthase From Nicotiana Tabacum			x	
2624425	>gi|2624425|pdb|5EAT| 5-Epi-Aristolochene Synthase From Nicotiana Tabacum With Substrate Analog Farnesyl Hydroxyphosphonate			x	
3121724	>gi|3121724|sp|Q40577|5EAS_TOBAC Aristolchene synthase (5-epi-aristolochene synthase) (EAS)			x	
3114378	>gi|3114378|pdb|5EAU| 5-Epi-Aristolochene Synthase From Nicotiana Tabacum			x	
29837353	>gi|29837353|gb|AAP05761.1| 5-epi-aristolochene synthase 34 [Nicotiana attenuata]			x	
29837355	>gi|29837355|gb|AAP05762.1| 5-epi-aristolochene synthase 37 [Nicotiana attenuata]			x	
29468500	>gi|29468500|gb|AAO85555.1| 5-epi-aristolochene synthase [Nicotiana attenuata]			x	
29837351	>gi|29837351|gb|AAP05760.1| 5-epi-aristolochene synthase 12 [Nicotiana attenuata]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
62899675	>gi|62899675|sp|O81192|BPPS_SALOF (+)-bornyl diphosphate synthase, chloroplast precursor (SBS) (BPPS)			x	
3309119	>gi|3309119|gb|AAC26017.1| (+)-bornyl diphosphate synthase [Salvia officinalis]			x	
27065865	>gi|27065865|pdb|1N24|B Chain B, (+)-Bornyl Diphosphate Synthase: Complex With Mg And Product			x	
27065864	>gi|27065864|pdb|1N24|A Chain A, (+)-Bornyl Diphosphate Synthase: Complex With Mg And Product			x	
27065862	>gi|27065862|pdb|1N23|B Chain B, (+)-Bornyl Diphosphate Synthase: Complex With Mg, Pyrophosphate, And (1r,4s)-2-Azabornane			x	
27065861	>gi|27065861|pdb|1N23|A Chain A, (+)-Bornyl Diphosphate Synthase: Complex With Mg, Pyrophosphate, And (1r,4s)-2-Azabornane			x	
27065855	>gi|27065855|pdb|1N22|B Chain B, (+)-Bornyl Diphosphate Synthase: Complex With Mg, Pyrophosphate, And (4r)-7-Aza-7,8-Dihydrolimonene			x	
27065854	>gi|27065854|pdb|1N22|A Chain A, (+)-Bornyl Diphosphate Synthase: Complex With Mg, Pyrophosphate, And (4r)-7-Aza-7,8-Dihydrolimonene			x	
27065853	>gi|27065853|pdb|1N21|A Chain A, (+)-Bornyl Diphosphate Synthase: Cocrystal With Mg And 3- Aza-2,3-Dihydrogeranyl Diphosphate			x	
27065851	>gi|27065851|pdb|1N20|B Chain B, (+)-Bornyl Diphosphate Synthase: Complex With Mg And 3-Aza- 2,3-Dihydrogeranyl Diphosphate			x	
27065850	>gi|27065850|pdb|1N20|A Chain A, (+)-Bornyl Diphosphate Synthase: Complex With Mg And 3-Aza- 2,3-Dihydrogeranyl Diphosphate			x	
27065849	>gi|27065849|pdb|1N1Z|B Chain B, (+)-Bornyl Diphosphate Synthase: Complex With Mg And Pyrophosphate			x	
27065848	>gi|27065848|pdb|1N1Z|A Chain A, (+)-Bornyl Diphosphate Synthase: Complex With Mg And Pyrophosphate			x	
27065842	>gi|27065842|pdb|1N1B|B Chain B, Crystal Structure Of (+)-Bornyl Diphosphate Synthase From Sage			x	
27065841	>gi|27065841|pdb|1N1B|A Chain A, Crystal Structure Of (+)-Bornyl Diphosphate Synthase From Sage			x	
2833457	>gi|2833457|sp|Q55012|PTLS_STRS3 Pentalenene synthase			x	
2127584	>gi|2127584|pir||A54214 C 4.2.3.7 pentalenene synthase () - Streptomyces sp. (strain UC5319)			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
3114507	>gi|3114507|pdb|1PS1|B Chain B, Pentalenene Synthase			x	
3114506	>gi|3114506|pdb|1PS1|A Chain A, Pentalenene Synthase			x	
451846	>gi|451846|gb|AAA19131.1| pentalenene synthase			x	
29606648	>gi|29606648|dbj|BAC70709.1| pentalenene synthase [Streptomyces avermitilis MA-4680]			x	
29829540	>gi|29829540|ref|NP_824174.1| pentalenene synthase [Streptomyces avermitilis MA-4680]			x	
39985098	>gi|39985098|gb|AAR36453.1| squalene-hopene cyclase [Geobacter sulfurreducens PCA]			x	
39998152	>gi|39998152|ref|NP_954103.1| squalene-hopene cyclase [Geobacter sulfurreducens PCA]			x	
39982558	>gi|39982558|gb|AAR34018.1| squalene-hopene cyclase [Geobacter sulfurreducens PCA]			x	
39995794	>gi|39995794|ref|NP_951745.1| squalene-hopene cyclase [Geobacter sulfurreducens PCA]			x	
78192895	>gi|78192895|gb|ABB30662.1| Terpene synthase:Squalene cyclase [Geobacter metallireducens GS-15]			x	
78221640	>gi|78221640|ref|YP_383387.1| Terpene synthase:Squalene cyclase [Geobacter metallireducens GS-15]			x	
4539168	>gi|4539168|emb|CAB39697.1| putative squalene-hopene cyclase [Streptomyces coelicolor A3(2)]			x	
21225057	>gi|21225057|ref|NP_630836.1| squalene-hopene cyclase [Streptomyces coelicolor A3(2)]			x	
78195271	>gi|78195271|gb|ABB33038.1| Terpene synthase:Squalene cyclase [Geobacter metallireducens GS-15]			x	
78224016	>gi|78224016|ref|YP_385763.1| Terpene synthase:Squalene cyclase [Geobacter metallireducens GS-15]			x	
77690249	>gi|77690249|ref|ZP_00805427.1| Terpene synthase:Squalene cyclase [Rhodopseudomonas palustris BisB5]			x	
77653065	>gi|77653065|gb|EAO84921.1| Terpene synthase:Squalene cyclase [Rhodopseudomonas palustris BisB5]			x	
3164106	>gi|3164106|emb|CAA71101.1| squalene-hopene cyclase [Rhodopseudomonas palustris]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
39650658	>gi|39650658|emb|CAE29181.1| squalene-hopene-cyclase [Rhodopseudomonas palustris CGA009]			x	
39936801	>gi|39936801|ref|NP_949077.1| squalene-hopene-cyclase [Rhodopseudomonas palustris CGA009]			x	
29605294	>gi|29605294|dbj|BAC69361.1| squalene-hopene cyclase [Streptomyces avermitilis MA-4680]			x	
29828192	>gi|29828192|ref|NP_822826.1| squalene-hopene cyclase [Streptomyces avermitilis MA-4680]			x	
22296036	>gi|22296036|dbj|BAC09861.1| squalene-hopene-cyclase [Thermosynechococcus elongatus BP-1]			x	
22299852	>gi|22299852|ref|NP_683099.1| squalene-hopene-cyclase [Thermosynechococcus elongatus BP-1]			x	
27351262	>gi|27351262|dbj|BAC48269.1| squalene-hopene cyclase [Bradyrhizobium japonicum USDA 110]			x	
30179753	>gi|30179753|sp|P54924|SQHC_BRAJA Squalene--hopene cyclase			x	
27378115	>gi|27378115|ref|NP_769644.1| squalene-hopene cyclase [Bradyrhizobium japonicum USDA 110]			x	
2113823	>gi|2113823|emb|CAA60250.1| squalene-hopene cyclase [Bradyrhizobium japonicum]			x	
17130120	>gi|17130120|dbj|BAB72732.1| squalene-hopene-cyclase [Nostoc sp. PCC 7120]			x	
17228270	>gi|17228270|ref|NP_484818.1| squalene-hopene-cyclase [Nostoc sp. PCC 7120]			x	
677871	>gi|677871|emb|CAA56749.1| squalene-hopene cyclase [Zymomonas mobilis]			x	
405608	>gi|405608|emb|CAA51958.1| Squalene Hopene Cyclase [Zymomonas mobilis]			x	
2598077	>gi|2598077|emb|CAA04735.1| squalene-hopene cyclase [Zymomonas mobilis]			x	
6466213	>gi|6466213|gb|AAF12829.1| squalene hopene cyclase [Zymomonas mobilis]			x	
2851526	>gi|2851526|sp|P33247|SQHC_ALIAC Squalene--hopene cyclase			x	
37927116	>gi|37927116|pdb|1O6H|C Chain C, Squalene-Hopene Cyclase			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
37927115	>gi|37927115|pdb|1O6H|B Chain B, Squalene-Hopene Cyclase			x	
37927114	>gi|37927114|pdb|1O6H|A Chain A, Squalene-Hopene Cyclase			x	
38492598	>gi|38492598|pdb|1O79|C Chain C, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
38492597	>gi|38492597|pdb|1O79|B Chain B, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
38492596	>gi|38492596|pdb|1O79|A Chain A, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
38492592	>gi|38492592|pdb|1O6R|C Chain C, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
38492591	>gi|38492591|pdb|1O6R|B Chain B, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
38492590	>gi|38492590|pdb|1O6R|A Chain A, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
38492589	>gi|38492589|pdb|1O6Q|C Chain C, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
38492588	>gi|38492588|pdb|1O6Q|B Chain B, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
38492587	>gi|38492587|pdb|1O6Q|A Chain A, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
28373287	>gi|28373287|pdb|1GSZ|C Chain C, Crystal Structure Of A Squalene Cyclase In Complex With The Potential Anticholesteremic Drug Ro48-8071			x	
28373286	>gi|28373286|pdb|1GSZ|B Chain B, Crystal Structure Of A Squalene Cyclase In Complex With The Potential Anticholesteremic Drug Ro48-8071			x	
28373285	>gi|28373285|pdb|1GSZ|A Chain A, Crystal Structure Of A Squalene Cyclase In Complex With The Potential Anticholesteremic Drug Ro48-8071			x	
34810416	>gi|34810416|pdb|1H3C|C Chain C, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
34810415	>gi|34810415|pdb|1H3C|B Chain B, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
34810414	>gi|34810414|pdb|1H3C|A Chain A, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
34810413	>gi|34810413|pdb|1H3B|C Chain C, Squalene-Hopene Cyclase			x	
34810412	>gi|34810412|pdb|1H3B|B Chain B, Squalene-Hopene Cyclase			x	
34810411	>gi|34810411|pdb|1H3B|A Chain A, Squalene-Hopene Cyclase			x	
34810410	>gi|34810410|pdb|1H3A|C Chain C, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
34810409	>gi|34810409|pdb|1H3A|B Chain B, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
34810408	>gi|34810408|pdb|1H3A|A Chain A, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
34810407	>gi|34810407|pdb|1H39|C Chain C, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
34810406	>gi|34810406|pdb|1H39|B Chain B, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
34810405	>gi|34810405|pdb|1H39|A Chain A, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
34810404	>gi|34810404|pdb|1H37|C Chain C, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
34810403	>gi|34810403|pdb|1H37|B Chain B, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
34810402	>gi|34810402|pdb|1H37|A Chain A, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
34810401	>gi|34810401|pdb|1H36|C Chain C, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
34810400	>gi|34810400|pdb|1H36|B Chain B, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
34810399	>gi|34810399|pdb|1H36|A Chain A, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
34810398	>gi|34810398|pdb|1H35|C Chain C, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	
34810397	>gi|34810397|pdb|1H35|B Chain B, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>34810396</td><td>>gi|34810396|pdb|1H35|A Chain A, Structures Of Human Oxidosqualene Cyclase Inhibitors Bound To A Homolgous Enzyme</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>2781075</td><td>>gi|2781075|pdb|1SQC| Squalene-Hopene-Cyclase From Alicyclobacillus Acidocaldarius</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>2970047</td><td>>gi|2970047|dbj|BAA25185.1| Squalene-hopene cyclase [Alicyclobacillus acidocaldarius]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>59803022</td><td>>gi|59803022|sp|P33990|SQHC_ZYMMO Squalene--hopene cyclase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>56551768</td><td>>gi|56551768|ref|YP_162607.1| squalene--hopene cyclase [Zymomonas mobilis subsp. mobilis ZM4]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>56543342</td><td>>gi|56543342|gb|AAV89496.1| squalene--hopene cyclase [Zymomonas mobilis subsp. mobilis ZM4]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>987617</td><td>>gi|987617|gb|AAA75452.1| squalene-hopene-cyclase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>86571877</td><td>>gi|86571877|gb|ABD06434.1| Squalene cyclase [Rhodopseudomonas palustris HaA2]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>1653061</td><td>>gi|1653061|dbj|BAA17978.1| squalene-hopene-cyclase [Synechocystis sp. PCC 6803]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>16330570</td><td>>gi|16330570|ref|NP_441298.1| squalene-hopene-cyclase [Synechocystis sp. PCC 6803]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78492501</td><td>>gi|78492501|ref|ZP_00844737.1| Terpene synthase:Squalene cyclase [Rhodopseudomonas palustris BisB18]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>78390244</td><td>>gi|78390244|gb|EAP13028.1| Terpene synthase:Squalene cyclase [Rhodopseudomonas palustris BisB18]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>35214631</td><td>>gi|35214631|dbj|BAC91998.1| squalene-hopene cyclase [Gloeobacter violaceus PCC 7421]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>37523626</td><td>>gi|37523626|ref|NP_927003.1| squalene-hopene cyclase [Gloeobacter violaceus PCC 7421]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>53758581</td><td>>gi|53758581|gb|AAU92872.1| squalene-hopene cyclase [Methylococcus capsulatus str. Bath]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>53804820</td><td>>gi|53804820|ref|YP_113312.1| squalene-hopene cyclase [Methylococcus capsulatus str. Bath]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>71836951</td><td>>gi|71836951|ref|ZP_00676718.1| Terpene synthase [Pelobacter propionicus DSM 2379]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
71742617	>gi|71742617|gb|EAO37768.1| Terpene synthase [Pelobacter propionicus DSM 2379]			x	
23126680	>gi|23126680|ref|ZP_00108569.1| COG1657: Squalene cyclase [Nostoc punctiforme PCC 73102]			x	
3164082	>gi|3164082|emb|CAA71098.1| squalene-hopene cyclase [Methylococcus capsulatus str. Bath]			x	
74421324	>gi|74421324|gb|ABA05523.1| terpene synthase/Squalene cyclase [Nitrobacter winogradskyi Nb-255]			x	
75676454	>gi|75676454|ref|YP_318875.1| terpene synthase/Squalene cyclase [Nitrobacter winogradskyi Nb-255]			x	
927384	>gi|927384|emb|CAA61950.1| squalene-hopene cyclase [Alicyclobacillus acidoterrestris]			x	
85716675	>gi|85716675|ref|ZP_01047644.1| terpene synthase/Squalene cyclase [Nitrobacter sp. Nb-311A]			x	
85696515	>gi|85696515|gb|EAQ34404.1| terpene synthase/Squalene cyclase [Nitrobacter sp. Nb-311A]			x	
2500864	>gi|2500864|sp|P55348|SQHC_RHISN Probable squalene--hopene cyclase			x	
67857855	>gi|67857855|gb|EAM53094.1| Terpene synthase [Crocosphaera watsonii WH 8501]			x	
48782682	>gi|48782682|ref|ZP_00279188.1| COG1657: Squalene cyclase [Burkholderia fungorum LB400]			x	
67680231	>gi|67680231|ref|ZP_00474818.1| COG1657: Squalene cyclase [Burkholderia pseudomallei 1710a]			x	
67735178	>gi|67735178|ref|ZP_00486202.1| COG1657: Squalene cyclase [Burkholderia pseudomallei 668]			x	
67670042	>gi|67670042|ref|ZP_00466857.1| COG1657: Squalene cyclase [Burkholderia pseudomallei 1655]			x	
52213770	>gi|52213770|emb|CAH39825.1| squalene--hopene cyclase [Burkholderia pseudomallei K96243]			x	
53723356	>gi|53723356|ref|YP_112341.1| squalene--hopene cyclase [Burkholderia pseudomallei K96243]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
83675784	>gi|83675784|ref|ZP_00937602.1| COG1657: Squalene cyclase [Burkholderia pseudomallei 406e]			x	
82534427	>gi|82534427|ref|ZP_00893462.1| COG1657: Squalene cyclase [Burkholderia pseudomallei 1106b]			x	
82529133	>gi|82529133|ref|ZP_00888387.1| COG1657: Squalene cyclase [Burkholderia pseudomallei 1106a]			x	
67645915	>gi|67645915|ref|ZP_00444187.1| COG1657: Squalene cyclase [Burkholderia mallei NCTC 10247]			x	
67639611	>gi|67639611|ref|ZP_00438455.1| COG1657: Squalene cyclase [Burkholderia mallei GB8 horse 4]			x	
67636915	>gi|67636915|ref|ZP_00435857.1| COG1657: Squalene cyclase [Burkholderia mallei 10399]			x	
85063930	>gi|85063930|ref|ZP_01024784.1| COG1657: Squalene cyclase [Burkholderia mallei 10229]			x	
84520988	>gi|84520988|ref|ZP_01008125.1| COG1657: Squalene cyclase [Burkholderia mallei SAVP1]			x	
77544139	>gi|77544139|gb|ABA87701.1| squalene-hopene cyclase [Pelobacter carbinolicus DSM 2380]			x	
77918056	>gi|77918056|ref|YP_355871.1| squalene-hopene cyclase [Pelobacter carbinolicus DSM 2380]			x	
67759490	>gi|67759490|ref|ZP_00498226.1| COG1657: Squalene cyclase [Burkholderia pseudomallei S13]			x	
67752591	>gi|67752591|ref|ZP_00491563.1| COG1657: Squalene cyclase [Burkholderia pseudomallei Pasteur]			x	
83716953	>gi|83716953|ref|YP_440546.1| squalene-hopene cyclase [Burkholderia thailandensis E264]			x	
83650778	>gi|83650778|gb|ABC34842.1| squalene-hopene cyclase [Burkholderia thailandensis E264]			x	
84358827	>gi|84358827|ref|ZP_00983594.1| COG1657: Squalene cyclase [Burkholderia dolosa AUO158]			x	
76583469	>gi|76583469|gb|ABA52943.1| squalene-hopene cyclase [Burkholderia pseudomallei 1710b]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
76818996	>gi|76818996|ref|YP_336647.1| squalene-hopene cyclase [Burkholderia pseudomallei 1710b]			x	
52421851	>gi|52421851|gb|AAU45421.1| squalene-hopene cyclase [Burkholderia mallei ATCC 23344]			x	
53715881	>gi|53715881|ref|YP_106607.1| squalene-hopene cyclase [Burkholderia mallei ATCC 23344]			x	
84353268	>gi|84353268|ref|ZP_00978203.1| COG1657: Squalene cyclase [Burkholderia cenocepacia PC184]			x	
77968757	>gi|77968757|gb|ABB10136.1| Terpene synthase/Squalene cyclase [Burkholderia sp. 383]			x	
78060872	>gi|78060872|ref|YP_370780.1| Terpene synthase/Squalene cyclase [Burkholderia sp. 383]			x	
72122116	>gi|72122116|gb|AAZ64302.1| Terpene synthase:Squalene cyclase [Ralstonia eutropha JMP134]			x	
73538779	>gi|73538779|ref|YP_299146.1| Terpene synthase:Squalene cyclase [Ralstonia eutropha JMP134]			x	
46203107	>gi|46203107|ref|ZP_00052068.2| COG1657: Squalene cyclase [Magnetospirillum magnetotacticum MS-1]			x	
58003100	>gi|58003100|gb|AAW61994.1| Squalene-hopene cyclase [Gluconobacter oxydans 621H]			x	
58040686	>gi|58040686|ref|YP_192650.1| Squalene-hopene cyclase [Gluconobacter oxydans 621H]			x	
76883137	>gi|76883137|gb|ABA57818.1| Terpene synthase/Squalene cyclase [Nitrosococcus oceani ATCC 19707]			x	
77164823	>gi|77164823|ref|YP_343348.1| Terpene synthase/Squalene cyclase [Nitrosococcus oceani ATCC 19707]			x	
42782622	>gi|42782622|ref|NP_979869.1| squalene-hopene cyclase [Bacillus cereus ATCC 10987]			x	
42738548	>gi|42738548|gb|AAS42477.1| squalene-hopene cyclase [Bacillus cereus ATCC 10987]			x	
29897214	>gi|29897214|gb|AAP10491.1| Squalene--hopene cyclase [Bacillus cereus ATCC 14579]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
30021659	>gi|30021659|ref|NP_833290.1| Squalene--hopene cyclase [Bacillus cereus ATCC 14579]			x	
32468770	>gi|32468770|emb|CAB13824.2| squalene-hopene cyclase [Bacillus subtilis subsp. subtilis str. 168]			x	
50812246	>gi|50812246|ref|NP_389814.2| squalene-hopene cyclase [Bacillus subtilis subsp. subtilis str. 168]			x	
47568915	>gi|47568915|ref|ZP_00239607.1| squalene--hopene cyclase [Bacillus cereus G9241]			x	
47554399	>gi|47554399|gb|EAL12758.1| squalene--hopene cyclase [Bacillus cereus G9241]			x	
83591402	>gi|83591402|ref|YP_425154.1| terpene synthase, squalene cyclase [Rhodospirillum rubrum ATCC 11170]			x	
83574316	>gi|83574316|gb|ABC20867.1| terpene synthase, squalene cyclase [Rhodospirillum rubrum ATCC 11170]			x	
49329830	>gi|49329830|gb|AAT60476.1| squalene-hopene cyclase [Bacillus thuringiensis serovar konkukian str. 97-27]			x	
49478274	>gi|49478274|ref|YP_037637.1| squalene-hopene cyclase [Bacillus thuringiensis serovar konkukian str. 97-27]			x	
65320833	>gi|65320833|ref|ZP_00393792.1| COG1657: Squalene cyclase [Bacillus anthracis str. A2012]			x	
47551890	>gi|47551890|gb|AAT32722.2| squalene-hopene cyclase [Bacillus anthracis str. 'Ames Ancestor']			x	
49180283	>gi|49180283|gb|AAT55659.1| squalene-hopene cyclase [Bacillus anthracis str. Sterne]			x	
49186356	>gi|49186356|ref|YP_029608.1| squalene-hopene cyclase [Bacillus anthracis str. Sterne]			x	
30258140	>gi|30258140|gb|AAP27368.1| squalene-hopene cyclase [Bacillus anthracis str. Ames]			x	
47778185	>gi|47778185|ref|YP_020247.2| squalene-hopene cyclase [Bacillus anthracis str. 'Ames Ancestor']			x	
30263505	>gi|30263505|ref|NP_845882.1| squalene-hopene cyclase [Bacillus anthracis str. Ames]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
51975448	>gi|51975448|gb|AAU16998.1| squalene-hopene cyclase [Bacillus cereus E33L]			x	
52141979	>gi|52141979|ref|YP_084851.1| squalene-hopene cyclase [Bacillus cereus E33L]			x	
82703671	>gi|82703671|ref|YP_413237.1| Squalene cyclase [Nitrosospira multiformis ATCC 25196]			x	
82411736	>gi|82411736|gb|ABB75845.1| Squalene cyclase [Nitrosospira multiformis ATCC 25196]			x	
86739536	>gi|86739536|ref|YP_479936.1| Squalene cyclase [Frankia sp. CcI3]			x	
86566398	>gi|86566398|gb|ABD10207.1| Squalene cyclase [Frankia sp. CcI3]			x	
77965182	>gi|77965182|gb|ABB06563.1| Terpene synthase/Squalene cyclase [Burkholderia sp. 383]			x	
78060632	>gi|78060632|ref|YP_367207.1| Terpene synthase/Squalene cyclase [Burkholderia sp. 383]			x	
56552444	>gi|56552444|ref|YP_163283.1| squalene--hopene cyclase [Zymomonas mobilis subsp. mobilis ZM4]			x	
56544018	>gi|56544018|gb|AAV90172.1| squalene--hopene cyclase [Zymomonas mobilis subsp. mobilis ZM4]			x	
77544053	>gi|77544053|gb|ABA87615.1| squalene--hopene cyclase [Pelobacter carbinolicus DSM 2380]			x	
77917970	>gi|77917970|ref|YP_355785.1| squalene--hopene cyclase [Pelobacter carbinolicus DSM 2380]			x	
84352143	>gi|84352143|ref|ZP_00977114.1| COG1657: Squalene cyclase [Burkholderia cenocepacia PC184]			x	
168190	>gi|168190|gb|AAB02038.1| trichodiene synthase			x	
136011	>gi|136011|sp|P27679|TRI5_GIBPU Trichodiene synthase (Sesquiterpene cyclase) (TS)			x	
42549660	>gi|42549660|gb|EAA72503.1| TRI5_GIBZE Trichodiene synthase (Sesquiterpene cyclase) (TS) [Gibberella zeae PH-1]			x	
46115390	>gi|46115390|ref|XP_383713.1| TRI5_GIBZE Trichodiene synthase (Sesquiterpene cyclase) (TS) [Gibberella zeae PH-1]			x	
13621080	>gi|13621080|gb|AAK33084.1| trichodiene synthase [Gibberella zeae]			x	
14091070	>gi|14091070|gb|AAK53586.1| trichodiene synthase [Gibberella zeae]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
4033479	>gi|4033479|sp|Q00909|TRI5_GIBZE Trichodiene synthase (Sesquiterpene cyclase) (TS)			x	
21429596	>gi|21429596|gb|AAM49054.1| trichodiene synthase [Gibberella zeae]			x	
21429578	>gi|21429578|gb|AAM49038.1| trichodiene synthase [Gibberella zeae]			x	
21429380	>gi|21429380|gb|AAM48862.1| trichodiene synthase [Gibberella zeae]			x	
2218058	>gi|2218058|gb|AAB72033.1| trichodiene synthase [Gibberella zeae]			x	
21429542	>gi|21429542|gb|AAM49006.1| trichodiene synthase [Gibberella zeae]			x	
21429434	>gi|21429434|gb|AAM48910.1| trichodiene synthase [Gibberella zeae]			x	
21429353	>gi|21429353|gb|AAM48838.1| trichodiene synthase [Fusarium acaciae-mearnsii]			x	
21429344	>gi|21429344|gb|AAM48830.1| trichodiene synthase [Fusarium acaciae-mearnsii]			x	
21429335	>gi|21429335|gb|AAM48822.1| trichodiene synthase [Fusarium acaciae-mearnsii]			x	
21429308	>gi|21429308|gb|AAM48798.1| trichodiene synthase [Fusarium mesoamericanum]			x	
21429254	>gi|21429254|gb|AAM48750.1| trichodiene synthase [Gibberella zeae]			x	
33413587	>gi|33413587|gb|AAN05032.1| trichodiene synthase [Gibberella zeae]			x	
21429569	>gi|21429569|gb|AAM49030.1| trichodiene synthase [Fusarium culmorum]			x	
21429407	>gi|21429407|gb|AAM48886.1| trichodiene synthase [Gibberella zeae]			x	
21429290	>gi|21429290|gb|AAM48782.1| trichodiene synthase [Fusarium culmorum]			x	
21429524	>gi|21429524|gb|AAM48990.1| trichodiene synthase [Fusarium boothii]			x	
21429506	>gi|21429506|gb|AAM48974.1| trichodiene synthase [Fusarium boothii]			x	
21429497	>gi|21429497|gb|AAM48966.1| trichodiene synthase [Fusarium boothii]			x	
21429362	>gi|21429362|gb|AAM48846.1| trichodiene synthase [Fusarium boothii]			x	
21429587	>gi|21429587|gb|AAM49046.1| trichodiene synthase [Fusarium asiaticum]			x	
21429461	>gi|21429461|gb|AAM48934.1| trichodiene synthase [Fusarium asiaticum]			x	
21429389	>gi|21429389|gb|AAM48870.1| trichodiene synthase [Fusarium pseudograminearum]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
21429515	>gi|21429515|gb|AAM48982.1| trichodiene synthase [Fusarium austroamericanum]			x	
21429452	>gi|21429452|gb|AAM48926.1| trichodiene synthase [Fusarium austroamericanum]			x	
21429533	>gi|21429533|gb|AAM48998.1| trichodiene synthase [Fusarium mesoamericanum]			x	
21429317	>gi|21429317|gb|AAM48806.1| trichodiene synthase [Fusarium cerealis]			x	
21429299	>gi|21429299|gb|AAM48790.1| trichodiene synthase [Fusarium cerealis]			x	
21429281	>gi|21429281|gb|AAM48774.1| trichodiene synthase [Fusarium asiaticum]			x	
21429272	>gi|21429272|gb|AAM48766.1| trichodiene synthase [Fusarium cerealis]			x	
21429416	>gi|21429416|gb|AAM48894.1| trichodiene synthase [Fusarium pseudograminearum]			x	
21429398	>gi|21429398|gb|AAM48878.1| trichodiene synthase [Fusarium pseudograminearum]			x	
21429371	>gi|21429371|gb|AAM48854.1| trichodiene synthase [Fusarium pseudograminearum]			x	
14091062	>gi|14091062|gb|AAK53579.1| trichodiene synthase [Gibberella zeae]			x	
24371019	>gi|24371019|dbj|BAC22117.1| trichodiene synthase [Gibberella zeae]			x	
21429326	>gi|21429326|gb|AAM48814.1| trichodiene synthase [Fusarium asiaticum]			x	
33413589	>gi|33413589|gb|AAN05033.1| trichodiene synthase [Fusarium culmorum]			x	
558954	>gi|558954|gb|AAA50765.1| trichodiene synthase [Fusarium poae]			x	
4033478	>gi|4033478|sp|Q00835|TRI5_FUSPO Trichodiene synthase (Sesquiterpene cyclase) (TS)			x	
21429560	>gi|21429560|gb|AAM49022.1| trichodiene synthase [Fusarium cortaderiae]			x	
21429551	>gi|21429551|gb|AAM49014.1| trichodiene synthase [Fusarium cortaderiae]			x	
21429488	>gi|21429488|gb|AAM48958.1| trichodiene synthase [Fusarium meridionale]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>21429479</td><td>>gi|21429479|gb|AAM48950.1| trichodiene synthase [Fusarium meridionale]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>21429470</td><td>>gi|21429470|gb|AAM48942.1| trichodiene synthase [Gibberella zeae]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>21429443</td><td>>gi|21429443|gb|AAM48918.1| trichodiene synthase [Fusarium austroamericanum]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>21429425</td><td>>gi|21429425|gb|AAM48902.1| trichodiene synthase [Fusarium meridionale]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>21429263</td><td>>gi|21429263|gb|AAM48758.1| trichodiene synthase [Fusarium lunulosporum]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>22087480</td><td>>gi|22087480|gb|AAM90954.1| trichodiene synthetase [Gibberella zeae]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>13621069</td><td>>gi|13621069|gb|AAK33074.1| trichodiene synthase [Fusarium sporotrichioides]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>168160</td><td>>gi|168160|gb|AAD13657.1| trichodiene synthase TRI5 [Fusarium sporotrichioides]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15054400</td><td>>gi|15054400|gb|AAK77935.1| trichodiene synthase [Fusarium sporotrichioides]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68280</td><td>>gi|68280|pir||SYFUTP trichodiene synthase (EC 4.2.3.6) - fungus (Fusarium sporotrichioides)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>136010</td><td>>gi|136010|sp|P13513|TRI5_FUSSP Trichodiene synthase (Sesquiterpene cyclase) (TS)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>17942972</td><td>>gi|17942972|pdb|1JFA|B Chain B, Trichodiene Synthase From Fusarium Sporotrichioides</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>17942971</td><td>>gi|17942971|pdb|1JFA|A Chain A, Trichodiene Synthase From Fusarium Sporotrichioides</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>17942970</td><td>>gi|17942970|pdb|1JFG|B Chain B, Trichodiene Synthase From Fusarium Sporotrichioides Complexed With Diphosphate</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>17942969</td><td>>gi|17942969|pdb|1JFG|A Chain A, Trichodiene Synthase From Fusarium Sporotrichioides Complexed With Diphosphate</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>33413595</td><td>>gi|33413595|gb|AAN05036.1| trichodiene synthase [Fusarium poae]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>22087477</td><td>>gi|22087477|gb|AAM90953.1| trichodiene synthetase [Gibberella zeae]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>33413593</td><td>>gi|33413593|gb|AAN05035.1| trichodiene synthase [Fusarium sporotrichioides]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
12584945	>gi|12584945|gb|AAG59895.1| trichodiene synthase [Stachybotrys chartarum]			x	
3023077	>gi|3023077|gb|AAC12640.1| trichodiene synthase [Stachybotrys chartarum]			x	
4033477	>gi|4033477|sp|O59947|TRI5_STACH Trichodiene synthase (Sesquiterpene cyclase) (TS)			x	
2267599	>gi|2267599|gb|AAC49957.1| trichodiene synthase [Myrothecium roridum]			x	
4033476	>gi|4033476|sp|O13489|TRI5_MYRRO Trichodiene synthase (Sesquiterpene cyclase) (TS)			x	
416643	>gi|416643|sp|Q03471|ARIS_PENRO Aristolochene synthase (Sesquiterpene cyclase) (AS)			x	
169178	>gi|169178|gb|AAA33694.1| aristolochene synthase			x	
6467980	>gi|6467980|gb|AAF13264.1| aristolochene synthase [Aspergillus terreus]			x	
6467978	>gi|6467978|gb|AAF13263.1| aristolochene synthase [Aspergillus terreus]			x	
13096103	>gi|13096103|pdb|1DGP|B Chain B, Aristolochene Synthase Farnesol Complex			x	
13096102	>gi|13096102|pdb|1DGP|A Chain A, Aristolochene Synthase Farnesol Complex			x	
10120634	>gi|10120634|pdb|1DI1|B Chain B, Crystal Structure Of Aristolochene Synthase From Penicillium Roqueforti			x	
10120633	>gi|10120633|pdb|1DI1|A Chain A, Crystal Structure Of Aristolochene Synthase From Penicillium Roqueforti			x	
21314762	>gi|21314762|ref|NP_115990.2| methylmalonyl-CoA epimerase [Homo sapiens]			x	
18089166	>gi|18089166|gb|AAH20825.1| Methylmalonyl-CoA epimerase [Homo sapiens]			x	
14010614	>gi|14010614|gb|AAK52052.1| methylmalonyl-CoA epimerase [Homo sapiens]			x	
50401130	>gi|50401130|sp|Q96PE7|MCEE_HUMAN Methylmalonyl-CoA epimerase, mitochondrial precursor (DL-methylmalonyl-CoA racemase)			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
55596688	>gi|55596688|ref|XP_515538.1| PREDICTED: similar to Methylmalonyl-CoA epimerase, mitochondrial precursor (DL-methylmalonyl-CoA racemase) [Pan troglodytes]			x	
22022367	>gi|22022367|gb|AAL02261.1| methylmalonyl-CoA epimerase [Propionibacterium freudenreichii subsp. shermanii]			x	
18042135	>gi|18042135|gb|AAL57846.1| methylmalonyl CoA epimerase [Propionibacterium freudenreichii subsp. shermanii]			x	
15826393	>gi|15826393|pdb|1JC5|F Chain F, Crystal Structure Of Native Methylmalonyl-Coa Epimerase			x	
15826392	>gi|15826392|pdb|1JC5|E Chain E, Crystal Structure Of Native Methylmalonyl-Coa Epimerase			x	
15826391	>gi|15826391|pdb|1JC5|D Chain D, Crystal Structure Of Native Methylmalonyl-Coa Epimerase			x	
15826390	>gi|15826390|pdb|1JC5|C Chain C, Crystal Structure Of Native Methylmalonyl-Coa Epimerase			x	
15826389	>gi|15826389|pdb|1JC5|B Chain B, Crystal Structure Of Native Methylmalonyl-Coa Epimerase			x	
15826388	>gi|15826388|pdb|1JC5|A Chain A, Crystal Structure Of Native Methylmalonyl-Coa Epimerase			x	
73951163	>gi|73951163|ref|XP_536170.2| PREDICTED: similar to Methylmalonyl-CoA epimerase, mitochondrial precursor (DL-methylmalonyl-CoA racemase) [Canis familiaris]			x	
15826387	>gi|15826387|pdb|1JC4|D Chain D, Crystal Structure Of Se-Met Methylmalonyl-Coa Epimerase			x	
15826386	>gi|15826386|pdb|1JC4|C Chain C, Crystal Structure Of Se-Met Methylmalonyl-Coa Epimerase			x	
15826385	>gi|15826385|pdb|1JC4|B Chain B, Crystal Structure Of Se-Met Methylmalonyl-Coa Epimerase			x	
15826384	>gi|15826384|pdb|1JC4|A Chain A, Crystal Structure Of Se-Met Methylmalonyl-Coa Epimerase			x	
58037329	>gi|58037329|ref|NP_082902.1| methylmalonyl CoA epimerase [Mus musculus]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
50401156	>gi|50401156|sp|Q9D1I5|MCEE_MOUSE Methylmalonyl-CoA epimerase, mitochondrial precursor (DL-methylmalonyl-CoA racemase)			x	
23959190	>gi|23959190|gb|AAH38157.1| Methylmalonyl CoA epimerase [Mus musculus]			x	
14010616	>gi|14010616|gb|AAK52053.1| methylmalonyl-CoA epimerase [Pyrococcus horikoshii]			x	
48782365	>gi|48782365|ref|ZP_00278894.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia fungorum LB400]			x	
34496424	>gi|34496424|ref|NP_900639.1| 4-hydroxyphenylpyruvate dioxygenase [Chromobacterium violaceum ATCC 12472]			x	
34102277	>gi|34102277|gb|AAQ58643.1| 4-hydroxyphenylpyruvate dioxygenase [Chromobacterium violaceum ATCC 12472]			x	
67680488	>gi|67680488|ref|ZP_00475018.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia pseudomallei 1710a]			x	
67669126	>gi|67669126|ref|ZP_00465985.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia pseudomallei 1655]			x	
67634516	>gi|67634516|ref|ZP_00433487.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia mallei 10399]			x	
67758155	>gi|67758155|ref|ZP_00496935.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia pseudomallei S13]			x	
67752534	>gi|67752534|ref|ZP_00491509.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia pseudomallei Pasteur]			x	
67734540	>gi|67734540|ref|ZP_00485666.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia pseudomallei 668]			x	
67644912	>gi|67644912|ref|ZP_00443244.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia mallei NCTC 10247]			x	
67640825	>gi|67640825|ref|ZP_00439618.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia mallei GB8 horse 4]			x	
52427645	>gi|52427645|gb|AAU48238.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei ATCC 23344]			x	
76581302	>gi|76581302|gb|ABA50777.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 1710b]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
52211261	>gi|52211261|emb|CAH37250.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei K96243]			x	
85066267	>gi|85066267|ref|ZP_01027120.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia mallei 10229]			x	
76811849	>gi|76811849|ref|YP_331434.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 1710b]			x	
84521528	>gi|84521528|ref|ZP_01008664.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia mallei SAVP1]			x	
83675951	>gi|83675951|ref|ZP_00937758.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia pseudomallei 406e]			x	
83623746	>gi|83623746|ref|ZP_00934008.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia mallei JHU]			x	
83618910	>gi|83618910|ref|ZP_00929357.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia mallei FMH]			x	
82533333	>gi|82533333|ref|ZP_00892412.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia pseudomallei 1106b]			x	
82527657	>gi|82527657|ref|ZP_00886979.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia pseudomallei 1106a]			x	
53720847	>gi|53720847|ref|YP_109833.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei K96243]			x	
83720009	>gi|83720009|ref|YP_443601.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia thailandensis E264]			x	
83653834	>gi|83653834|gb|ABC37897.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia thailandensis E264]			x	
84363553	>gi|84363553|ref|ZP_00988128.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia dolosa AUO158]			x	
67549551	>gi|67549551|ref|ZP_00427409.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia vietnamiensis G4]			x	
67529133	>gi|67529133|gb|EAM26010.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia vietnamiensis G4]			x	
17430127	>gi|17430127|emb|CAD16812.1| PROBABLE 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE OXIDOREDUCTASE PROTEIN [Ralstonia solanacearum]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
17547822	>gi|17547822|ref|NP_521224.1| PROBABLE 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE OXIDOREDUCTASE PROTEIN [Ralstonia solanacearum GMI1000]			x	
67667845	>gi|67667845|ref|ZP_00465053.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia HI2424]			x	
67661102	>gi|67661102|ref|ZP_00458430.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia AU 1054]			x	
67098592	>gi|67098592|gb|EAM15794.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia HI2424]			x	
67091310	>gi|67091310|gb|EAM08891.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia AU 1054]			x	
84356200	>gi|84356200|ref|ZP_00981057.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia cenocepacia PC184]			x	
74020299	>gi|74020299|ref|ZP_00690899.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria AMMD]			x	
72606991	>gi|72606991|gb|EAO42963.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria AMMD]			x	
83746408	>gi|83746408|ref|ZP_00943460.1| 4-hydroxyphenylpyruvate dioxygenase [Ralstonia solanacearum UW551]			x	
83726949	>gi|83726949|gb|EAP74075.1| 4-hydroxyphenylpyruvate dioxygenase [Ralstonia solanacearum UW551]			x	
77965642	>gi|77965642|gb|ABB07022.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. 383]			x	
78064897	>gi|78064897|ref|YP_367666.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. 383]			x	
27362256	>gi|27362256|gb|AAO11111.1| 4-hydroxyphenylpyruvate dioxygenase [Vibrio vulnificus CMCP6]			x	
27366056	>gi|27366056|ref|NP_761584.1| 4-hydroxyphenylpyruvate dioxygenase [Vibrio vulnificus CMCP6]			x	
75826731	>gi|75826731|ref|ZP_00756166.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Vibrio cholerae O395]			x	
75824206	>gi|75824206|ref|ZP_00753668.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Vibrio cholerae RC385]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
75820486	>gi|75820486|ref|ZP_00750532.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Vibrio cholerae V51]			x	
75816957	>gi|75816957|ref|ZP_00747414.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Vibrio cholerae V52]			x	
9655836	>gi|9655836|gb|AAF94502.1| 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae O1 biovar eltor str. N16961]			x	
15641356	>gi|15641356|ref|NP_230988.1| 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae O1 biovar eltor str. N16961]			x	
6648538	>gi|6648538|gb|AAF21216.1| p-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae]			x	
75829730	>gi|75829730|ref|ZP_00759024.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Vibrio cholerae MO10]			x	
18104608	>gi|18104608|gb|AAL59614.1| 4-hydroxyphenylpyruvate dioxygenase [Listonella anguillarum]			x	
75856539	>gi|75856539|ref|ZP_00764165.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Vibrio sp. Ex25]			x	
32040878	>gi|32040878|ref|ZP_00138461.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Pseudomonas aeruginosa UCBPP-PA14]			x	
9946763	>gi|9946763|gb|AAG04254.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas aeruginosa PAO1]			x	
15596062	>gi|15596062|ref|NP_249556.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas aeruginosa PAO1]			x	
84322674	>gi|84322674|ref|ZP_00970758.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Pseudomonas aeruginosa 2192]			x	
84316635	>gi|84316635|ref|ZP_00965107.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Pseudomonas aeruginosa C3719]			x	
28806337	>gi|28806337|dbj|BAC59612.1| 4-hydroxyphenylpyruvate dioxygenase [Vibrio parahaemolyticus RIMD 2210633]			x	
28898123	>gi|28898123|ref|NP_797728.1| 4-hydroxyphenylpyruvate dioxygenase [Vibrio parahaemolyticus RIMD 2210633]			x	
14027622	>gi|14027622|dbj|BAB53891.1| 4-hydroxyphenylpyruvate dioxygenase [Mesorhizobium loti MAFF303099]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>13476861</td><td>>gi|13476861|ref|NP_108430.1| 4-hydroxyphenylpyruvate dioxygenase [Mesorhizobium loti MAFF303099]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77383145</td><td>>gi|77383145|gb|ABA74658.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas fluorescens PfO-1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77459142</td><td>>gi|77459142|ref|YP_348648.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas fluorescens PfO-1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>66046559</td><td>>gi|66046559|ref|YP_236400.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. syringae B728a]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>63257266</td><td>>gi|63257266|gb|AAY38362.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. syringae B728a]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>27348587</td><td>>gi|27348587|dbj|BAC45604.1| 4-hydroxyphenylpyruvate dioxygenase [Bradyrhizobium japonicum USDA 110]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>27375450</td><td>>gi|27375450|ref|NP_766979.1| 4-hydroxyphenylpyruvate dioxygenase [Bradyrhizobium japonicum USDA 110]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68345050</td><td>>gi|68345050|gb|AAY92656.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas fluorescens Pf-5]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>70730751</td><td>>gi|70730751|ref|YP_260492.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas fluorescens Pf-5]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>26990146</td><td>>gi|26990146|ref|NP_745571.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida KT2440]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>24985082</td><td>>gi|24985082|gb|AAN69035.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida KT2440]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67780042</td><td>>gi|67780042|gb|EAM39659.1| 4-hydroxyphenylpyruvate dioxygenase [Polaromonas sp. JS666]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67907968</td><td>>gi|67907968|ref|ZP_00506369.1| 4-hydroxyphenylpyruvate dioxygenase [Polaromonas sp. JS666]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84386189</td><td>>gi|84386189|ref|ZP_00989218.1| 4-hydroxyphenylpyruvate dioxygenase [Vibrio splendidus 12B01]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84378959</td><td>>gi|84378959|gb|EAP95813.1| 4-hydroxyphenylpyruvate dioxygenase [Vibrio splendidus 12B01]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>28870714</td><td>>gi|28870714|ref|NP_793333.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. tomato str. DC3000]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
28853962	>gi|28853962|gb|AAO57028.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. tomato str. DC3000]			x	
71557567	>gi|71557567|gb|AAZ36778.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. phaseolicola 1448A]			x	
71737014	>gi|71737014|ref|YP_275410.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. phaseolicola 1448A]			x	
86144791	>gi|86144791|ref|ZP_01063123.1| 4-hydroxyphenylpyruvate dioxygenase [Vibrio sp. MED222]			x	
85837690	>gi|85837690|gb|EAQ55802.1| 4-hydroxyphenylpyruvate dioxygenase [Vibrio sp. MED222]			x	
82735751	>gi|82735751|ref|ZP_00898613.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida F1]			x	
82717384	>gi|82717384|gb|EAP52436.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida F1]			x	
37727200	>gi|37727200|gb|AAO12525.1| p-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida]			x	
86166180	>gi|86166180|gb|EAQ67446.1| 4-hydroxyphenylpyruvate dioxygenase [Marinomonas sp. MED121]			x	
248959	>gi|248959|gb|AAB22111.1| 4-hydroxyphenylpyruvate dioxygenase {EC 1.13.11.27} [Pseudomonas, P.J. 874, Peptide, 357 aa]			x	
123491	>gi|123491|sp|P80064|HPPD_PSEUJ 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase)			x	
78694655	>gi|78694655|ref|ZP_00859168.1| 4-hydroxyphenylpyruvate dioxygenase [Bradyrhizobium sp. BTAi1]			x	
78517771	>gi|78517771|gb|EAP31069.1| 4-hydroxyphenylpyruvate dioxygenase [Bradyrhizobium sp. BTAi1]			x	
68556085	>gi|68556085|ref|ZP_00595428.1| 4-hydroxyphenylpyruvate dioxygenase [Ralstonia metallidurans CH34]			x	
68529258	>gi|68529258|gb|EAN52221.1| 4-hydroxyphenylpyruvate dioxygenase [Ralstonia metallidurans CH34]			x	
79039649	>gi|79039649|ref|ZP_00871355.1| 4-hydroxyphenylpyruvate dioxygenase [Novosphingobium aromaticivorans DSM 12444]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>78775290</td><td>>gi|78775290|gb|EAP38945.1| 4-hydroxyphenylpyruvate dioxygenase [Novosphingobium aromaticivorans DSM 12444]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15075967</td><td>>gi|15075967|emb|CAC47521.1| PUTATIVE 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE PROTEIN [Sinorhizobium meliloti]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>15966695</td><td>>gi|15966695|ref|NP_387048.1| PUTATIVE 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE PROTEIN [Sinorhizobium meliloti 1021]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>47573686</td><td>>gi|47573686|ref|ZP_00243724.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Rubrivivax gelatinosus PM1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>7766901</td><td>>gi|7766901|pdb|1CJX|D Chain D, Crystal Structure Of Pseudomonas Fluorescens Hppd</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>7766900</td><td>>gi|7766900|pdb|1CJX|C Chain C, Crystal Structure Of Pseudomonas Fluorescens Hppd</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>7766899</td><td>>gi|7766899|pdb|1CJX|B Chain B, Crystal Structure Of Pseudomonas Fluorescens Hppd</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>7766898</td><td>>gi|7766898|pdb|1CJX|A Chain A, Crystal Structure Of Pseudomonas Fluorescens Hppd</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>72121665</td><td>>gi|72121665|gb|AAZ63851.1| 4-hydroxyphenylpyruvate dioxygenase [Ralstonia eutropha JMP134]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>73538328</td><td>>gi|73538328|ref|YP_298695.1| 4-hydroxyphenylpyruvate dioxygenase [Ralstonia eutropha JMP134]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84715414</td><td>>gi|84715414|ref|ZP_01022515.1| 4-hydroxyphenylpyruvate dioxygenase [Polaromonas naphthalenivorans CJ2]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84693238</td><td>>gi|84693238|gb|EAQ19040.1| 4-hydroxyphenylpyruvate dioxygenase [Polaromonas naphthalenivorans CJ2]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67155173</td><td>>gi|67155173|ref|ZP_00416801.1| 4-hydroxyphenylpyruvate dioxygenase [Azotobacter vinelandii AvOP]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67086974</td><td>>gi|67086974|gb|EAM06441.1| 4-hydroxyphenylpyruvate dioxygenase [Azotobacter vinelandii AvOP]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>86277802</td><td>>gi|86277802|gb|ABC88387.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas fluorescens]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
39652710	>gi|39652710|emb|CAE25449.1| 4-hydroxyphenylpyruvate dioxygenase [Rhodopseudomonas palustris CGA009]			x	
39933085	>gi|39933085|ref|NP_945361.1| 4-hydroxyphenylpyruvate dioxygenase [Rhodopseudomonas palustris CGA009]			x	
86357375	>gi|86357375|ref|YP_469267.1| probable 4-hydroxyphenylpyruvate dioxygenase protein [Rhizobium etli CFN 42]			x	
86281477	>gi|86281477|gb|ABC90540.1| probable 4-hydroxyphenylpyruvate dioxygenase protein [Rhizobium etli CFN 42]			x	
76883245	>gi|76883245|gb|ABA57926.1| 4-hydroxyphenylpyruvate dioxygenase [Nitrosococcus oceani ATCC 19707]			x	
77164931	>gi|77164931|ref|YP_343456.1| 4-hydroxyphenylpyruvate dioxygenase [Nitrosococcus oceani ATCC 19707]			x	
68192496	>gi|68192496|gb|EAN07150.1| 4-hydroxyphenylpyruvate dioxygenase [Mesorhizobium sp. BNC1]			x	
69276590	>gi|69276590|ref|ZP_00612184.1| 4-hydroxyphenylpyruvate dioxygenase [Mesorhizobium sp. BNC1]			x	
83643833	>gi|83643833|ref|YP_432268.1| 4-hydroxyphenylpyruvate dioxygenase [Hahella chejuensis KCTC 2396]			x	
83631876	>gi|83631876|gb|ABC27843.1| 4-hydroxyphenylpyruvate dioxygenase [Hahella chejuensis KCTC 2396]			x	
21106538	>gi|21106538|gb|AAM35343.1| 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas axonopodis pv. citri str. 306]			x	
21241225	>gi|21241225|ref|NP_640807.1| 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas axonopodis pv. citri str. 306]			x	
46916283	>gi|46916283|emb|CAG23052.1| putative 4-hydroxyphenylpyruvate dioxygenase [Photobacterium profundum SS9]			x	
54302859	>gi|54302859|ref|YP_132852.1| putative 4-hydroxyphenylpyruvate dioxygenase [Photobacterium profundum SS9]			x	
78034468	>gi|78034468|emb|CAJ22113.1| 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas campestris pv. vesicatoria str. 85-10]			x	
78046038	>gi|78046038|ref|YP_362213.1| 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas campestris pv. vesicatoria str. 85-10]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
68540317	>gi|68540317|ref|ZP_00580078.1| 4-hydroxyphenylpyruvate dioxygenase [Sphingopyxis alaskensis RB2256]			x	
68522336	>gi|68522336|gb|EAN45492.1| 4-hydroxyphenylpyruvate dioxygenase [Sphingopyxis alaskensis RB2256]			x	
21111421	>gi|21111421|gb|AAM39754.1| 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas campestris pv. campestris str. ATCC 33913]			x	
66572122	>gi|66572122|gb|AAY47532.1| 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas campestris pv. campestris str. 8004]			x	
66766790	>gi|66766790|ref|YP_241552.1| 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas campestris pv. campestris str. 8004]			x	
21229913	>gi|21229913|ref|NP_635830.1| 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas campestris pv. campestris str. ATCC 33913]			x	
84787193	>gi|84787193|gb|ABC63375.1| 4-hydroxyphenylpyruvate dioxygenase [Erythrobacter litoralis HTCC2594]			x	
85374110	>gi|85374110|ref|YP_458172.1| 4-hydroxyphenylpyruvate dioxygenase [Erythrobacter litoralis HTCC2594]			x	
52629602	>gi|52629602|gb|AAU28343.1| 4-hydroxyphenylpyruvate dioxygenase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]			x	
52842491	>gi|52842491|ref|YP_096290.1| 4-hydroxyphenylpyruvate dioxygenase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]			x	
69934333	>gi|69934333|ref|ZP_00629411.1| 4-hydroxyphenylpyruvate dioxygenase [Paracoccus denitrificans PD1222]			x	
69153857	>gi|69153857|gb|EAN66974.1| 4-hydroxyphenylpyruvate dioxygenase [Paracoccus denitrificans PD1222]			x	
58583694	>gi|58583694|ref|YP_202710.1| 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas oryzae pv. oryzae KACC10331]			x	
58428288	>gi|58428288|gb|AAW77325.1| 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas oryzae pv. oryzae KACC10331]			x	
53754956	>gi|53754956|emb|CAH16444.1| 4-hydroxyphenylpyruvate dioxygenase (legiolysin) [Legionella pneumophila str. Lens]			x	
60392610	>gi|60392610|sp|Q5ZT84|LLY_LEGPH 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (Legiolysin)			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
54295124	>gi|54295124|ref|YP_127539.1| 4-hydroxyphenylpyruvate dioxygenase (legiolysin) [Legionella pneumophila str. Lens]			x	
84369443	>gi|84369443|dbj|BAE70601.1| 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas oryzae pv. oryzae MAFF 311018]			x	
84625503	>gi|84625503|ref|YP_452875.1| 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas oryzae pv. oryzae MAFF 311018]			x	
60392609	>gi|60392609|sp|P69053|LLY_LEGPN 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (Legiolysin)			x	
85710284	>gi|85710284|ref|ZP_01041349.1| 4-hydroxyphenylpyruvate dioxygenase [Erythrobacter sp. NAP1]			x	
85688994	>gi|85688994|gb|EAQ28998.1| 4-hydroxyphenylpyruvate dioxygenase [Erythrobacter sp. NAP1]			x	
85712096	>gi|85712096|ref|ZP_01043149.1| 4-hydroxyphenylpyruvate dioxygenase [Idiomarina baltica OS145]			x	
85694086	>gi|85694086|gb|EAQ32031.1| 4-hydroxyphenylpyruvate dioxygenase [Idiomarina baltica OS145]			x	
76791393	>gi|76791393|ref|ZP_00773900.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudoalteromonas atlantica T6c]			x	
76593504	>gi|76593504|gb|EAO69687.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudoalteromonas atlantica T6c]			x	
53751960	>gi|53751960|emb|CAH13384.1| 4-hydroxyphenylpyruvate dioxygenase (legiolysin) [Legionella pneumophila str. Paris]			x	
54298175	>gi|54298175|ref|YP_124544.1| 4-hydroxyphenylpyruvate dioxygenase (legiolysin) [Legionella pneumophila str. Paris]			x	
76791947	>gi|76791947|ref|ZP_00774450.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudoalteromonas atlantica T6c]			x	
76592636	>gi|76592636|gb|EAO68823.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudoalteromonas atlantica T6c]			x	
13424094	>gi|13424094|gb|AAK24504.1| 4-hydroxyphenylpyruvate dioxygenase [Caulobacter crescentus CB15]			x	
16126772	>gi|16126772|ref|NP_421336.1| 4-hydroxyphenylpyruvate dioxygenase [Caulobacter crescentus CB15]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
83858849	>gi|83858849|ref|ZP_00952371.1| 4-hydroxyphenylpyruvate dioxygenase [Oceanicaulis alexandrii HTCC2633]			x	
83853672	>gi|83853672|gb|EAP91524.1| 4-hydroxyphenylpyruvate dioxygenase [Oceanicaulis alexandrii HTCC2633]			x	
56178841	>gi|56178841|gb|AAV81563.1| 4-hydroxyphenylpyruvate dioxygenase [Idiomarina loihiensis L2TR]			x	
56459831	>gi|56459831|ref|YP_155112.1| 4-hydroxyphenylpyruvate dioxygenase [Idiomarina loihiensis L2TR]			x	
71364775	>gi|71364775|ref|ZP_00655353.1| 4-hydroxyphenylpyruvate dioxygenase [Psychrobacter cryohalolentis K5]			x	
71160011	>gi|71160011|gb|EAO09834.1| 4-hydroxyphenylpyruvate dioxygenase [Psychrobacter cryohalolentis K5]			x	
67156324	>gi|67156324|ref|ZP_00417917.1| 4-hydroxyphenylpyruvate dioxygenase [Azotobacter vinelandii AvOP]			x	
67086083	>gi|67086083|gb|EAM05553.1| 4-hydroxyphenylpyruvate dioxygenase [Azotobacter vinelandii AvOP]			x	
77385129	>gi|77385129|gb|ABA76642.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas fluorescens PfO-1]			x	
77461126	>gi|77461126|ref|YP_350633.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas fluorescens PfO-1]			x	
84324619	>gi|84324619|ref|ZP_00972676.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Pseudomonas aeruginosa 2192]			x	
32043410	>gi|32043410|ref|ZP_00140672.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Pseudomonas aeruginosa UCBPP-PA14]			x	
84318579	>gi|84318579|ref|ZP_00967002.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Pseudomonas aeruginosa C3719]			x	
13898392	>gi|13898392|gb|AAK48714.1| 4-hydroxyphenylpyruvate dioxygenase [Magnaporthe grisea]			x	
74630846	>gi|74630846|sp|Q96X22|HPPD_MAGGR 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase)			x	
28881241	>gi|28881241|emb|CAD70479.1| probable 4-hydroxyphenylpyruvate dioxygenase [Neurospora crassa]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>74629496</td><td>>gi|74629496|sp|Q872T7|HPPD_NEUCR 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>26989274</td><td>>gi|26989274|ref|NP_744699.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas putida KT2440]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>24984122</td><td>>gi|24984122|gb|AAN68163.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas putida KT2440]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>82735075</td><td>>gi|82735075|ref|ZP_00897938.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas putida F1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>82717750</td><td>>gi|82717750|gb|EAP52801.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas putida F1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>28869544</td><td>>gi|28869544|ref|NP_792163.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas syringae pv. tomato str. DC3000]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>28852786</td><td>>gi|28852786|gb|AAO55858.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas syringae pv. tomato str. DC3000]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>66045370</td><td>>gi|66045370|ref|YP_235211.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. syringae B728a]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>63256077</td><td>>gi|63256077|gb|AAY37173.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. syringae B728a]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>83744141</td><td>>gi|83744141|gb|ABC42332.1| 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas chlororaphis]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>71557637</td><td>>gi|71557637|gb|AAZ36848.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas syringae pv. phaseolicola 1448A]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>71737084</td><td>>gi|71737084|ref|YP_274324.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas syringae pv. phaseolicola 1448A]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68182021</td><td>>gi|68182021|ref|ZP_00555002.1| 4-hydroxyphenylpyruvate dioxygenase [Jannaschia sp. CCS1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67977675</td><td>>gi|67977675|gb|EAM67294.1| 4-hydroxyphenylpyruvate dioxygenase [Jannaschia sp. CCS1]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>3860238</td><td>>gi|3860238|gb|AAC73008.1| 4-hydroxyphenylpyruvate-dioxygenase [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>55666795</td><td>>gi|55666795|ref|XP_528667.1| PREDICTED: 4-hydroxyphenylpyruvate dioxygenase [Pan troglodytes]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
68346989	>gi|68346989|gb|AAY94595.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas fluorescens Pf-5]			x	
70732690	>gi|70732690|ref|YP_262453.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas fluorescens Pf-5]			x	
4504477	>gi|4504477|ref|NP_002141.1| 4-hydroxyphenylpyruvate dioxygenase [Homo sapiens]			x	
288105	>gi|288105|emb|CAA51082.1| 4-hydroxyphenylpyruvate dioxygenase [Homo sapiens]			x	
18999511	>gi|18999511|gb|AAH24287.1| 4-hydroxyphenylpyruvate dioxygenase [Homo sapiens]			x	
417144	>gi|417144|sp|P32754|HPPD_HUMAN 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase)			x	
1100256	>gi|1100256|dbj|BAA06498.1| 4-hydroxyphenylpyruvic acid dioxgenase (HPD) [Homo sapiens]			x	
15426479	>gi|15426479|gb|AAH13343.1| 4-hydroxyphenylpyruvic acid dioxygenase [Mus musculus]			x	
33859486	>gi|33859486|ref|NP_032303.1| 4-hydroxyphenylpyruvic acid dioxygenase [Mus musculus]			x	
83303597	>gi|83303597|sp|P49429|HPPD_MOUSE 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) (F protein) (F Alloantigen)			x	
62751490	>gi|62751490|ref|NP_001015611.1| 4-hydroxyphenylpyruvate dioxygenase [Bos taurus]			x	
75948304	>gi|75948304|gb|AAI05226.1| 4-hydroxyphenylpyruvate dioxygenase [Bos taurus]			x	
59857863	>gi|59857863|gb|AAX08766.1| 4-hydroxyphenylpyruvate dioxygenase [Bos taurus]			x	
75057880	>gi|75057880|sp|Q5EA20|HPPD_BOVIN 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase)			x	
51980500	>gi|51980500|gb|AAH81819.1| 4-hydroxyphenylpyruvic acid dioxygenase [Rattus norvegicus]			x	
3435296	>gi|3435296|gb|AAC32387.1| 4-hydroxyphenylpyruvate dioxygenase [Rattus norvegicus]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
8393557	>gi|8393557|ref|NP_058929.1| 4-hydroxyphenylpyruvic acid dioxygenase [Rattus norvegicus]			x	
83303639	>gi|83303639|sp|P32755|HPPD_RAT 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) (F protein) (F alloantigen)			x	
52695554	>gi|52695554|pdb|1SQI|B Chain B, Structural Basis For Inhibitor Selectivity Revealed By Crystal Structures Of Plant And Mammalian 4-Hydroxyphenylpyruvate Dioxygenases			x	
52695553	>gi|52695553|pdb|1SQI|A Chain A, Structural Basis For Inhibitor Selectivity Revealed By Crystal Structures Of Plant And Mammalian 4-Hydroxyphenylpyruvate Dioxygenases			x	
849053	>gi|849053|dbj|BAA06267.1| 4-hydroxyphenylpyruvate dioxygenase [Mus musculus]			x	
31324014	>gi|31324014|gb|AAP47152.1| 4-hydroxyphenylpyruvate dioxygenase [uncultured soil bacterium]			x	
69298020	>gi|69298020|ref|ZP_00620300.1| 4-hydroxyphenylpyruvate dioxygenase [Silicibacter sp. TM1040]			x	
69134367	>gi|69134367|gb|EAN57582.1| 4-hydroxyphenylpyruvate dioxygenase [Silicibacter sp. TM1040]			x	
83942846	>gi|83942846|ref|ZP_00955307.1| 4-hydroxyphenylpyruvate dioxygenase [Sulfitobacter sp. EE-36]			x	
83846939	>gi|83846939|gb|EAP84815.1| 4-hydroxyphenylpyruvate dioxygenase [Sulfitobacter sp. EE-36]			x	
83955679	>gi|83955679|ref|ZP_00964259.1| 4-hydroxyphenylpyruvate dioxygenase [Sulfitobacter sp. NAS-14.1]			x	
83839973	>gi|83839973|gb|EAP79149.1| 4-hydroxyphenylpyruvate dioxygenase [Sulfitobacter sp. NAS-14.1]			x	
73995174	>gi|73995174|ref|XP_853422.1| PREDICTED: similar to 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) [Canis familiaris]			x	
84500900	>gi|84500900|ref|ZP_00999135.1| 4-hydroxyphenylpyruvate dioxygenase [Oceanicola batsensis HTCC2597]			x	
84390967	>gi|84390967|gb|EAQ03385.1| 4-hydroxyphenylpyruvate dioxygenase [Oceanicola batsensis HTCC2597]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
86137851	>gi|86137851|ref|ZP_01056427.1| 4-hydroxyphenylpyruvate dioxygenase [Roseobacter sp. MED193]			x	
85825443	>gi|85825443|gb|EAQ45642.1| 4-hydroxyphenylpyruvate dioxygenase [Roseobacter sp. MED193]			x	
78368776	>gi|78368776|ref|ZP_00838982.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. PV-4]			x	
78359179	>gi|78359179|gb|EAP01056.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. PV-4]			x	
77816006	>gi|77816006|ref|ZP_00815218.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella putrefaciens CN-32]			x	
77809038	>gi|77809038|gb|EAO93448.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella putrefaciens CN-32]			x	
22530912	>gi|22530912|gb|AAM96960.1| 4-hydroxyphenylpyruvate dioxygenase HPD [Arabidopsis thaliana]			x	
56678047	>gi|56678047|gb|AAV94713.1| 4-hydroxyphenylpyruvate dioxygenase [Silicibacter pomeroyi DSS-3]			x	
56696310	>gi|56696310|ref|YP_166667.1| 4-hydroxyphenylpyruvate dioxygenase [Silicibacter pomeroyi DSS-3]			x	
82740811	>gi|82740811|ref|ZP_00903545.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. W3-18-1]			x	
82721797	>gi|82721797|gb|EAP56629.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. W3-18-1]			x	
22136134	>gi|22136134|gb|AAM91145.1| 4-hydroxyphenylpyruvate dioxygenase (HPD) [Arabidopsis thaliana]			x	
18252207	>gi|18252207|gb|AAL61936.1| 4-hydroxyphenylpyruvate dioxygenase (HPD) [Arabidopsis thaliana]			x	
3098559	>gi|3098559|gb|AAC15697.1| 4-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana]			x	
3334223	>gi|3334223|sp|P93836|HPPD_ARATH 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase)			x	
2392518	>gi|2392518|gb|AAB70025.1| p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
2145039	>gi|2145039|gb|AAB58404.1| p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana]			x	
55669758	>gi|55669758|pdb|1SP9|B Chain B, 4-Hydroxyphenylpyruvate Dioxygenase			x	
55669757	>gi|55669757|pdb|1SP9|A Chain A, 4-Hydroxyphenylpyruvate Dioxygenase			x	
52695751	>gi|52695751|pdb|1TG5|A Chain A, Crystal Structures Of Plant 4-Hydroxyphenylpyruvate Dioxygenases Complexed With Das645			x	
52695750	>gi|52695750|pdb|1TFZ|A Chain A, Structural Basis For Herbicidal Inhibitor Selectivity Revealed By Comparison Of Crystal Structures Of Plant And Mammalian 4-Hydroxyphenylpyruvate Dioxygenases			x	
52695552	>gi|52695552|pdb|1SQD|A Chain A, Structural Basis For Inhibitor Selectivity Revealed By Crystal Structures Of Plant And Mammalian 4-Hydroxyphenylpyruvate Dioxygenases			x	
68542976	>gi|68542976|ref|ZP_00582695.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella baltica OS155]			x	
68519345	>gi|68519345|gb|EAN42883.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella baltica OS155]			x	
2231615	>gi|2231615|gb|AAC49815.1| 4-hydroxyphenylpyruvate dioxygenase [Daucus carota]			x	
3334219	>gi|3334219|sp|O23920|HPPD_DAUCA 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase)			x	
24373526	>gi|24373526|ref|NP_717569.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella oneidensis MR-1]			x	
24347835	>gi|24347835|gb|AAN55013.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella oneidensis MR-1]			x	
78691757	>gi|78691757|ref|ZP_00856354.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. MR-7]			x	
78686389	>gi|78686389|ref|ZP_00851157.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. ANA-3]			x	
78508840	>gi|78508840|gb|EAP22265.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. MR-7]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
78505858	>gi|78505858|gb|EAP19383.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. ANA-3]			x	
82496693	>gi|82496693|ref|ZP_00882258.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. MR-4]			x	
82405268	>gi|82405268|gb|EAP45943.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. MR-4]			x	
67157862	>gi|67157862|ref|ZP_00419007.1| 4-hydroxyphenylpyruvate dioxygenase [Azotobacter vinelandii AvOP]			x	
67085131	>gi|67085131|gb|EAM04607.1| 4-hydroxyphenylpyruvate dioxygenase [Azotobacter vinelandii AvOP]			x	
5531376	>gi|5531376|emb|CAB51008.1| putative 4-hydroxyphenylpyruvate dioxygenase [Streptomyces coelicolor A3(2)]			x	
21221374	>gi|21221374|ref|NP_627153.1| 4-hydroxyphenylpyruvate dioxygenase [Streptomyces coelicolor A3(2)]			x	
81625146	>gi|81625146|sp|Q9S2F4|HPPD_STRCO 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase)			x	
68547720	>gi|68547720|ref|ZP_00587251.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella amazonensis SB2B]			x	
68514611	>gi|68514611|gb|EAN38341.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella amazonensis SB2B]			x	
69951167	>gi|69951167|ref|ZP_00638934.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella frigidimarina NCIMB 400]			x	
69165261	>gi|69165261|gb|EAN74284.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella frigidimarina NCIMB 400]			x	
69157650	>gi|69157650|gb|EAN69869.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella denitrificans OS217]			x	
69944221	>gi|69944221|ref|ZP_00635642.1| 4-hydroxyphenylpyruvate dioxygenase [Shewanella denitrificans OS-217]			x	
48784496	>gi|48784496|ref|ZP_00280862.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia fungorum LB400]			x	
47523532	>gi|47523532|ref|NP_999389.1| 4-hydroxyphenylpyruvic acid dioxygenase [Sus scrofa]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
217692	>gi|217692|dbj|BAA02660.1| 4-hydroxyphenylpyruvic acid dioxygenase [Sus scrofa]			x	
1346310	>gi|1346310|sp|Q02110|HPPD_PIG 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase)			x	
27376164	>gi|27376164|ref|NP_767693.1| putative 4-hydroxyphenylpyruvate dioxygenase protein [Bradyrhizobium japonicum USDA 110]			x	
29608808	>gi|29608808|dbj|BAC72861.1| 4-hydroxyphenylpyruvate dioxygenase [Streptomyces avermitilis MA-4680]			x	
29831692	>gi|29831692|ref|NP_826326.1| 4-hydroxyphenylpyruvate dioxygenase [Streptomyces avermitilis MA-4680]			x	
30581067	>gi|30581067|sp|Q53586|HPPD_STRAW 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase)			x	
50513703	>gi|50513703|pdb|1T47|B Chain B, Structure Of Fe2-Hppd Bound To Ntbc			x	
50513702	>gi|50513702|pdb|1T47|A Chain A, Structure Of Fe2-Hppd Bound To Ntbc			x	
15823928	>gi|15823928|dbj|BAB69150.1| 4-hydroxyphenylpyruvate dioxygenase [Streptomyces avermitilis]			x	
555806	>gi|555806|gb|AAA50231.1| 4-hydroxyphenylpyruvate acid dioxygenase			x	
17431820	>gi|17431820|emb|CAD18498.1| PROBABLE 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE OXIDOREDUCTASE PROTEIN [Ralstonia solanacearum]			x	
17431789	>gi|17431789|emb|CAD18467.1| PROBABLE 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE OXIDOREDUCTASE PROTEIN [Ralstonia solanacearum]			x	
17549566	>gi|17549566|ref|NP_522906.1| PROBABLE 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE OXIDOREDUCTASE PROTEIN [Ralstonia solanacearum GMI1000]			x	
17549535	>gi|17549535|ref|NP_522875.1| PROBABLE 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE OXIDOREDUCTASE PROTEIN [Ralstonia solanacearum GMI1000]			x	
48783552	>gi|48783552|ref|ZP_00280004.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia fungorum LB400]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
76876002	>gi|76876002|emb|CAI87224.1| 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) [Pseudoalteromonas haloplanktis TAC125]			x	
77361091	>gi|77361091|ref|YP_340666.1| 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) [Pseudoalteromonas haloplanktis TAC125]			x	
13810184	>gi|13810184|emb|CAC37394.1| 4-hydroxyphenylpyruvate dioxygenase [Solenostemon scutellarioides]			x	
17366672	>gi|17366672|sp|Q9ARF9|HPPD_SOLSC 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase)			x	
83816571	>gi|83816571|ref|YP_445494.1| 4-hydroxyphenylpyruvate dioxygenase [Salinibacter ruber DSM 13855]			x	
83757965	>gi|83757965|gb|ABC46078.1| 4-hydroxyphenylpyruvate dioxygenase [Salinibacter ruber DSM 13855]			x	
3694811	>gi|3694811|gb|AAC62457.1| p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana]			x	
84359805	>gi|84359805|ref|ZP_00984535.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia dolosa AUO158]			x	
67664502	>gi|67664502|ref|ZP_00461775.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia HI2424]			x	
67656086	>gi|67656086|ref|ZP_00453470.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia AU 1054]			x	
67101837	>gi|67101837|gb|EAM18974.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia HI2424]			x	
67096246	>gi|67096246|gb|EAM13771.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia AU 1054]			x	
84354433	>gi|84354433|ref|ZP_00979339.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia cenocepacia PC184]			x	
3334221	>gi|3334221|sp|O42764|HPPD_MYCGR 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase)			x	
2708690	>gi|2708690|gb|AAC15884.1| 4-hydroxyphenylpyruvate dioxygenase [Mycosphaerella graminicola]			x	
77970360	>gi|77970360|gb|ABB11739.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. 383]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
78062475	>gi|78062475|ref|YP_372383.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. 383]			x	
39577105	>gi|39577105|emb|CAE78334.1| 4-hydroxyphenylpyruvate dioxygenase [Bdellovibrio bacteriovorus HD100]			x	
42524895	>gi|42524895|ref|NP_970275.1| 4-hydroxyphenylpyruvate dioxygenase [Bdellovibrio bacteriovorus HD100]			x	
79040915	>gi|79040915|ref|ZP_00872288.1| 4-hydroxyphenylpyruvate dioxygenase [Novosphingobium aromaticivorans DSM 12444]			x	
78774230	>gi|78774230|gb|EAP37886.1| 4-hydroxyphenylpyruvate dioxygenase [Novosphingobium aromaticivorans DSM 12444]			x	
62003087	>gi|62003087|gb|AAX59006.1| 4-hydroxyphenylpyruvate dioxygenase [Medicago truncatula]			x	
74016264	>gi|74016264|ref|ZP_00686890.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria AMMD]			x	
72610635	>gi|72610635|gb|EAO46581.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria AMMD]			x	
67542525	>gi|67542525|ref|ZP_00420461.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia vietnamiensis G4]			x	
67536239	>gi|67536239|gb|EAM32958.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia vietnamiensis G4]			x	
78696078	>gi|78696078|ref|ZP_00860588.1| 4-hydroxyphenylpyruvate dioxygenase [Bradyrhizobium sp. BTAi1]			x	
78515656	>gi|78515656|gb|EAP28957.1| 4-hydroxyphenylpyruvate dioxygenase [Bradyrhizobium sp. BTAi1]			x	
86130810	>gi|86130810|ref|ZP_01049409.1| 4-hydroxyphenylpyruvate dioxygenase [Cellulophaga sp. MED134]			x	
85818221	>gi|85818221|gb|EAQ39381.1| 4-hydroxyphenylpyruvate dioxygenase [Cellulophaga sp. MED134]			x	
47567476	>gi|47567476|ref|ZP_00238188.1| 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus G9241]			x	
47555878	>gi|47555878|gb|EAL14217.1| 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus G9241]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
66847183	>gi|66847183|gb|EAL87514.1| 4-hydroxyphenylpyruvate dioxygenase [Aspergillus fumigatus Af293]			x	
70989405	>gi|70989405|ref|XP_749552.1| 4-hydroxyphenylpyruvate dioxygenase [Aspergillus fumigatus Af293]			x	
74669096	>gi|74669096|sp|Q4WHU1|HPPD1_ASPFU Probable 4-hydroxyphenylpyruvate dioxygenase 1 (4HPPD 1) (HPD 1) (HPPDase 1)			x	
75760149	>gi|75760149|ref|ZP_00740208.1| 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar israelensis ATCC 35646]			x	
74492352	>gi|74492352|gb|EAO55509.1| 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar israelensis ATCC 35646]			x	
29894029	>gi|29894029|gb|AAP07321.1| 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus ATCC 14579]			x	
30018489	>gi|30018489|ref|NP_830120.1| 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus ATCC 14579]			x	
65317666	>gi|65317666|ref|ZP_00390625.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Bacillus anthracis str. A2012]			x	
49330698	>gi|49330698|gb|AAT61344.1| 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar konkukian str. 97-27]			x	
47500645	>gi|47500645|gb|AAT29321.1| 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. 'Ames Ancestor']			x	
49177186	>gi|49177186|gb|AAT52562.1| 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. Sterne]			x	
51978468	>gi|51978468|gb|AAU20018.1| 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus E33L]			x	
49183259	>gi|49183259|ref|YP_026511.1| 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. Sterne]			x	
49479142	>gi|49479142|ref|YP_034568.1| 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar konkukian str. 97-27]			x	
42779341	>gi|42779341|ref|NP_976588.1| 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus ATCC 10987]			x	
30253738	>gi|30253738|gb|AAP24280.1| 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. Ames]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
42735256	>gi|42735256|gb|AAS39196.1| 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus ATCC 10987]			x	
52144999	>gi|52144999|ref|YP_081830.1| 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus E33L]			x	
47525497	>gi|47525497|ref|YP_016846.1| 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. 'Ames Ancestor']			x	
30260417	>gi|30260417|ref|NP_842794.1| 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. Ames]			x	
71147316	>gi|71147316|gb|AAZ27789.1| 4-hydroxyphenylpyruvate dioxygenase [Colwellia psychrerythraea 34H]			x	
71281576	>gi|71281576|ref|YP_270158.1| 4-hydroxyphenylpyruvate dioxygenase [Colwellia psychrerythraea 34H]			x	
37681833	>gi|37681833|gb|AAQ97794.1| 4-hydroxyphenylpyruvate dioxygenase [Danio rerio]			x	
82187435	>gi|82187435|sp|Q6TGZ5|HPPD_BRARE 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase)			x	
83716682	>gi|83716682|ref|YP_439418.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia thailandensis E264]			x	
83650507	>gi|83650507|gb|ABC34571.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia thailandensis E264]			x	
82178627	>gi|82178627|sp|Q5BKL0|HPPD_XENTR 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase)			x	
67928870	>gi|67928870|ref|ZP_00522055.1| 4-hydroxyphenylpyruvate dioxygenase [Solibacter usitatus Ellin6076]			x	
67863773	>gi|67863773|gb|EAM58782.1| 4-hydroxyphenylpyruvate dioxygenase [Solibacter usitatus Ellin6076]			x	
86143740	>gi|86143740|ref|ZP_01062116.1| 4-hydroxyphenylpyruvate dioxygenase [Flavobacterium sp. MED217]			x	
85829783	>gi|85829783|gb|EAQ48245.1| 4-hydroxyphenylpyruvate dioxygenase [Flavobacterium sp. MED217]			x	
3334224	>gi|3334224|sp|Q00415|HPPD_COCIM 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) (T-cell reactive protein)			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
74018538	>gi|74018538|ref|ZP_00689158.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria AMMD]			x	
72608471	>gi|72608471|gb|EAO44423.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria AMMD]			x	
84359134	>gi|84359134|ref|ZP_00983890.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia dolosa AUO158]			x	
74635204	>gi|74635204|sp|Q6CDR5|HPPD_YARLI 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase)			x	
67667262	>gi|67667262|ref|ZP_00464490.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia HI2424]			x	
67655532	>gi|67655532|ref|ZP_00452918.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia AU 1054]			x	
67099157	>gi|67099157|gb|EAM16339.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia HI2424]			x	
67096811	>gi|67096811|gb|EAM14334.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia AU 1054]			x	
83855941	>gi|83855941|ref|ZP_00949470.1| 4-hydroxyphenylpyruvate dioxygenase [Croceibacter atlanticus HTCC2559]			x	
83849741	>gi|83849741|gb|EAP87609.1| 4-hydroxyphenylpyruvate dioxygenase [Croceibacter atlanticus HTCC2559]			x	
76261015	>gi|76261015|ref|ZP_00768638.1| 4-hydroxyphenylpyruvate dioxygenase [Chloroflexus aurantiacus J-10-fl]			x	
76164065	>gi|76164065|gb|EAO58222.1| 4-hydroxyphenylpyruvate dioxygenase [Chloroflexus aurantiacus J-10-fl]			x	
86134911	>gi|86134911|ref|ZP_01053493.1| 4-hydroxyphenylpyruvate dioxygenase [Tenacibaculum sp. MED152]			x	
85821774	>gi|85821774|gb|EAQ42921.1| 4-hydroxyphenylpyruvate dioxygenase [Tenacibaculum sp. MED152]			x	
50057356	>gi|50057356|emb|CAH03340.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Paramecium tetraurelia]			x	
50404979	>gi|50404979|ref|YP_054071.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Paramecium tetraurelia]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
67648133	>gi|67648133|ref|ZP_00446366.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia mallei NCTC 10247]			x	
67639699	>gi|67639699|ref|ZP_00438538.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia mallei GB8 horse 4]			x	
85064543	>gi|85064543|ref|ZP_01025397.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia mallei 10229]			x	
52423541	>gi|52423541|gb|AAU47111.1| putative 4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei ATCC 23344]			x	
53717571	>gi|53717571|ref|YP_105549.1| putative 4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei ATCC 23344]			x	
84521446	>gi|84521446|ref|ZP_01008583.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia mallei SAVP1]			x	
83623085	>gi|83623085|ref|ZP_00933368.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia mallei JHU]			x	
83618110	>gi|83618110|ref|ZP_00928582.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia mallei FMH]			x	
67635375	>gi|67635375|ref|ZP_00434332.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia mallei 10399]			x	
77969080	>gi|77969080|gb|ABB10459.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. 383]			x	
78061195	>gi|78061195|ref|YP_371103.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. 383]			x	
3334226	>gi|3334226|sp|Q27203|HPPD_TETTH 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) (F-antigen homolog) (TF-AG)			x	
83675448	>gi|83675448|ref|ZP_00937296.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia pseudomallei 406e]			x	
67669109	>gi|67669109|ref|ZP_00465970.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia pseudomallei 1655]			x	
67737541	>gi|67737541|ref|ZP_00488301.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia pseudomallei 668]			x	
67758027	>gi|67758027|ref|ZP_00496816.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia pseudomallei S13]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
82535273	>gi|82535273|ref|ZP_00894292.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia pseudomallei 1106b]			x	
82527796	>gi|82527796|ref|ZP_00887103.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia pseudomallei 1106a]			x	
67752295	>gi|67752295|ref|ZP_00491289.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia pseudomallei Pasteur]			x	
67680688	>gi|67680688|ref|ZP_00475173.1| COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Burkholderia pseudomallei 1710a]			x	
67542103	>gi|67542103|ref|ZP_00420040.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia vietnamiensis G4]			x	
67536382	>gi|67536382|gb|EAM33096.1| 4-hydroxyphenylpyruvate dioxygenase [Burkholderia vietnamiensis G4]			x	
86360259	>gi|86360259|ref|YP_472148.1| putative 4-hydroxyphenylpyruvate dioxygenase protein [Rhizobium etli CFN 42]			x	
86284361	>gi|86284361|gb|ABC93421.1| putative 4-hydroxyphenylpyruvate dioxygenase protein [Rhizobium etli CFN 42]			x	
66849398	>gi|66849398|gb|EAL89726.1| 4-hydroxyphenylpyruvate dioxygenase [Aspergillus fumigatus Af293]			x	
70993834	>gi|70993834|ref|XP_751764.1| 4-hydroxyphenylpyruvate dioxygenase [Aspergillus fumigatus Af293]			x	
74671554	>gi|74671554|sp|Q4WPV8|HPPD2_ASPFU Probable 4-hydroxyphenylpyruvate dioxygenase 2 (4HPPD 2) (HPD 2) (HPPDase 2)			x	
68232050	>gi|68232050|ref|ZP_00571206.1| 4-hydroxyphenylpyruvate dioxygenase [Frankia sp. EAN1pec]			x	
68200309	>gi|68200309|gb|EAN14525.1| 4-hydroxyphenylpyruvate dioxygenase [Frankia sp. EAN1pec]			x	
71366476	>gi|71366476|ref|ZP_00657018.1| 4-hydroxyphenylpyruvate dioxygenase [Nocardioides sp. JS614]			x	
71157845	>gi|71157845|gb|EAO08230.1| 4-hydroxyphenylpyruvate dioxygenase [Nocardioides sp. JS614]			x	
74846152	>gi|74846152|sp|Q60Y65|HPPD_CAEBR 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase)			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
17555220	>gi|17555220|ref|NP_499324.1| 4-HydroxyPhenylpyruvate Dioxygenase (HPD) family member (hpd-1) [Caenorhabditis elegans]			x	
3334225	>gi|3334225|sp|Q22633|HPPD_CAEEL 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase)			x	
50905533	>gi|50905533|ref|XP_464255.1| putative 4-hydroxyphenylpyruvate dioxygenase [Oryza sativa (japonica cultivar-group)]			x	
49388595	>gi|49388595|dbj|BAD25710.1| putative 4-hydroxyphenylpyruvate dioxygenase [Oryza sativa (japonica cultivar-group)]			x	
49387760	>gi|49387760|dbj|BAD26248.1| putative 4-hydroxyphenylpyruvate dioxygenase [Oryza sativa (japonica cultivar-group)]			x	
83718326	>gi|83718326|ref|YP_440247.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Burkholderia thailandensis E264]			x	
83652151	>gi|83652151|gb|ABC36215.1| 4-hydroxyphenylpyruvate dioxygenase, putative [Burkholderia thailandensis E264]			x	
72122190	>gi|72122190|gb|AAZ64376.1| 4-hydroxyphenylpyruvate dioxygenase [Ralstonia eutropha JMP134]			x	
73538853	>gi|73538853|ref|YP_299220.1| 4-hydroxyphenylpyruvate dioxygenase [Ralstonia eutropha JMP134]			x	
84494414	>gi|84494414|ref|ZP_00993533.1| putative 4-hydroxyphenylpyruvate dioxygenase [Janibacter sp. HTCC2649]			x	
84383907	>gi|84383907|gb|EAP99787.1| putative 4-hydroxyphenylpyruvate dioxygenase [Janibacter sp. HTCC2649]			x	
72122197	>gi|72122197|gb|AAZ64383.1| 4-hydroxyphenylpyruvate dioxygenase [Ralstonia eutropha JMP134]			x	
73538860	>gi|73538860|ref|YP_299227.1| 4-hydroxyphenylpyruvate dioxygenase [Ralstonia eutropha JMP134]			x	
54018563	>gi|54018563|dbj|BAD59933.1| putative 4-hydroxyphenylpyruvate dioxygenase [Nocardia farcinica IFM 10152]			x	
54027055	>gi|54027055|ref|YP_121297.1| putative 4-hydroxyphenylpyruvate dioxygenase [Nocardia farcinica IFM 10152]			x	
68189545	>gi|68189545|gb|EAN04210.1| 4-hydroxyphenylpyruvate dioxygenase [Mesorhizobium sp. BNC1]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
69280121	>gi|69280121|ref|ZP_00614793.1| 4-hydroxyphenylpyruvate dioxygenase [Mesorhizobium sp. BNC1]			x	
55669756	>gi|55669756|pdb|1SP8|D Chain D, 4-Hydroxyphenylpyruvate Dioxygenase			x	
55669755	>gi|55669755|pdb|1SP8|C Chain C, 4-Hydroxyphenylpyruvate Dioxygenase			x	
55669754	>gi|55669754|pdb|1SP8|B Chain B, 4-Hydroxyphenylpyruvate Dioxygenase			x	
55669753	>gi|55669753|pdb|1SP8|A Chain A, 4-Hydroxyphenylpyruvate Dioxygenase			x	
46395699	>gi|46395699|sp|Q56415|FOSA_SERMA Glutathione transferase fosA (Fosfomycin resistance protein)			x	
46395995	>gi|46395995|sp|Q9I4K6|FOSA_PSEAE Glutathione transferase fosA (Fosfomycin resistance protein)			x	
42543067	>gi|42543067|pdb|1NKI|B Chain B, Crystal Strucure Of The Fosfomycin Resistance Protein A (Fosa) Containing Bound Phosphonoformate			x	
42543066	>gi|42543066|pdb|1NKI|A Chain A, Crystal Strucure Of The Fosfomycin Resistance Protein A (Fosa) Containing Bound Phosphonoformate			x	
24158887	>gi|24158887|pdb|1LQO|B Chain B, Crystal Strutcure Of The Fosfomycin Resistance Protein A (Fosa) Containing Bound Thallium Cations			x	
24158886	>gi|24158886|pdb|1LQO|A Chain A, Crystal Strutcure Of The Fosfomycin Resistance Protein A (Fosa) Containing Bound Thallium Cations			x	
24158889	>gi|24158889|pdb|1LQP|B Chain B, Crystal Structure Of The Fosfomycin Resistance Protein (Fosa) Containing Bound Substrate			x	
24158888	>gi|24158888|pdb|1LQP|A Chain A, Crystal Structure Of The Fosfomycin Resistance Protein (Fosa) Containing Bound Substrate			x	
24158885	>gi|24158885|pdb|1LQK|B Chain B, High Resolution Structure Of Fosfomycin Resistance Protein A (Fosa)			x	
24158884	>gi|24158884|pdb|1LQK|A Chain A, High Resolution Structure Of Fosfomycin Resistance Protein A (Fosa)			x	
11182130	>gi|11182130|emb|CAC16163.1| glyoxalase I [Saccharomyces cerevisiae]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
66848318	>gi|66848318|gb|EAL88647.1| lactoylglutathione lyase [Aspergillus fumigatus Af293]			x	
70991673	>gi|70991673|ref|XP_750685.1| lactoylglutathione lyase [Aspergillus fumigatus Af293]			x	
1430957	>gi|1430957|emb|CAA67622.1| glyoxalase I [Saccharomyces cerevisiae]			x	
6323639	>gi|6323639|ref|NP_013710.1| Monomeric glyoxalase I, catalyzes the detoxification of methylglyoxal (a by-product of glycolysis) via condensation with glutathione to produce S-D-lactoylglutathione; expression regulated by methylglyoxal levels and osmotic stress; Glo1p [Saccharomyces cerevisiae]			x	
1708808	>gi|1708808|sp|P50107|LGUL_YEAST Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
50295647	>gi|50295647|gb|AAT73077.1| glyoxylase I [Phaeosphaeria nodorum]			x	
1175430	>gi|1175430|sp|Q09751|LGUL_SCHPO Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
30016920	>gi|30016920|gb|AAP03992.1| glyoxalase I [Paracoccidioides brasiliensis]			x	
56495052	>gi|56495052|emb|CAH99110.1| glyoxalase I, putative [Plasmodium berghei]			x	
68067501	>gi|68067501|ref|XP_675710.1| glyoxalase I [Plasmodium berghei strain ANKA]			x	
82597002	>gi|82597002|ref|XP_726497.1| lactoylglutathione lyase [Plasmodium yoelii yoelii str. 17XNL]			x	
23481927	>gi|23481927|gb|EAA18062.1| lactoylglutathione lyase, putative [Plasmodium yoelii yoelii]			x	
23508336	>gi|23508336|ref|NP_701005.1| glyoxalase I, putative [Plasmodium falciparum 3D7]			x	
33320674	>gi|33320674|gb|AAQ05975.1| glyoxalase I [Plasmodium falciparum]			x	
33149273	>gi|33149273|gb|AAP96758.1| glyoxalase I [Plasmodium falciparum]			x	
23496068	>gi|23496068|gb|AAN35729.1| glyoxalase I, putative [Plasmodium falciparum 3D7]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
68473834	>gi|68473834|ref|XP_719020.1| glyoxalase I [Candida albicans SC5314]			x	
68474043	>gi|68474043|ref|XP_718918.1| glyoxalase I [Candida albicans SC5314]			x	
70950284	>gi|70950284|ref|XP_744478.1| glyoxalase I [Plasmodium chabaudi chabaudi]			x	
56524449	>gi|56524449|emb|CAH88211.1| glyoxalase I, putative [Plasmodium chabaudi]			x	
7619802	>gi|7619802|emb|CAB50787.2| putative glyoxalase I [Triticum aestivum]			x	
50252391	>gi|50252391|dbj|BAD28547.1| putative glyoxalase I [Oryza sativa (japonica cultivar-group)]			x	
15220397	>gi|15220397|ref|NP_176896.1| lactoylglutathione lyase [Arabidopsis thaliana]			x	
50941905	>gi|50941905|ref|XP_480480.1| glyoxalase I [Oryza sativa (japonica cultivar-group)]			x	
40253650	>gi|40253650|dbj|BAD05593.1| glyoxalase I [Oryza sativa (japonica cultivar-group)]			x	
84029333	>gi|84029333|sp|Q948T6|LGUL_ORYSA Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase) (Allergen Ory s ?) (Allergen Glb33) (PP33)			x	
4126809	>gi|4126809|dbj|BAA36759.1| glyoxalase I [Oryza sativa (japonica cultivar-group)]			x	
21537360	>gi|21537360|gb|AAM61701.1| glyoxalase I, putative [Arabidopsis thaliana]			x	
16580747	>gi|16580747|dbj|BAB71741.1| glyoxalase I [Oryza sativa (japonica cultivar-group)]			x	
50933389	>gi|50933389|ref|XP_476222.1| putative glyoxalase [Oryza sativa (japonica cultivar-group)]			x	
46485858	>gi|46485858|gb|AAS98483.1| putative glyoxalase [Oryza sativa (japonica cultivar-group)]			x	
37932483	>gi|37932483|gb|AAP76396.1| glyoxalase I [Zea mays]			x	
1177314	>gi|1177314|emb|CAA88233.1| glyoxalase-I [Lycopersicon esculentum]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
2494844	>gi|2494844|sp|Q42891|LGUL_LYCES Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
2113825	>gi|2113825|emb|CAA73691.1| Glyoxalase I [Brassica juncea]			x	
3334244	>gi|3334244|sp|O04885|LGUL_BRAJU Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
2909424	>gi|2909424|emb|CAA12028.1| Glyoxalase I [Cicer arietinum]			x	
3334245	>gi|3334245|sp|O49818|LGUL_CICAR Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
79317307	>gi|79317307|ref|NP_001030996.1| calmodulin binding / lactoylglutathione lyase [Arabidopsis thaliana]			x	
30680509	>gi|30680509|ref|NP_849609.1| calmodulin binding / lactoylglutathione lyase [Arabidopsis thaliana]			x	
15223126	>gi|15223126|ref|NP_172291.1| calmodulin binding / lactoylglutathione lyase [Arabidopsis thaliana]			x	
79317300	>gi|79317300|ref|NP_001030995.1| calmodulin binding / lactoylglutathione lyase [Arabidopsis thaliana]			x	
25083005	>gi|25083005|gb|AAN72031.1| glyoxalase I, putative [Arabidopsis thaliana]			x	
75244584	>gi|75244584|sp|Q8H0V3|LGUL_ARATH Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
4127862	>gi|4127862|emb|CAA09177.1| glyoxalase I [Glycine max]			x	
77383151	>gi|77383151|gb|ABA74664.1| Glyoxalase I [Pseudomonas fluorescens PfO-1]			x	
77459148	>gi|77459148|ref|YP_348654.1| Glyoxalase I [Pseudomonas fluorescens PfO-1]			x	
38181954	>gi|38181954|gb|AAH61570.1| Glyoxylase 1 [Rattus norvegicus]			x	
46485429	>gi|46485429|ref|NP_997477.1| glyoxylase 1 [Rattus norvegicus]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
81885359	>gi|81885359|sp|Q6P7Q4|LGUL_RAT Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
12744892	>gi|12744892|gb|AAK06838.1| glyoxalase I [Avicennia marina]			x	
15810219	>gi|15810219|gb|AAL07227.1| putative lactoylglutathione lyase [Arabidopsis thaliana]			x	
15030212	>gi|15030212|gb|AAH11365.1| Glyoxalase I [Homo sapiens]			x	
19354350	>gi|19354350|gb|AAH24663.1| Glyoxalase 1 [Mus musculus]			x	
31981282	>gi|31981282|ref|NP_079650.2| glyoxalase 1 [Mus musculus]			x	
54696834	>gi|54696834|gb|AAV38789.1| glyoxalase I [synthetic construct]			x	
61367890	>gi|61367890|gb|AAX43062.1| glyoxalase I [synthetic construct]			x	
61367882	>gi|61367882|gb|AAX43061.1| glyoxalase I [synthetic construct]			x	
54696838	>gi|54696838|gb|AAV38791.1| glyoxalase I [Homo sapiens]			x	
54696836	>gi|54696836|gb|AAV38790.1| glyoxalase I [Homo sapiens]			x	
12804633	>gi|12804633|gb|AAH01741.1| Glyoxalase I [Homo sapiens]			x	
56205611	>gi|56205611|emb|CAI21586.1| glyoxalase I [Homo sapiens]			x	
1881782	>gi|1881782|gb|AAB49495.1| glyoxalase I [Homo sapiens]			x	
61357692	>gi|61357692|gb|AAX41429.1| glyoxalase I [synthetic construct]			x	
61357687	>gi|61357687|gb|AAX41428.1| glyoxalase I [synthetic construct]			x	
62089188	>gi|62089188|dbj|BAD93038.1| glyoxalase I variant [Homo sapiens]			x	
6573422	>gi|6573422|pdb|1QIP|D Chain D, Human Glyoxalase I Complexed With S-P-Nitrobenzyloxycarbonylglutathione			x	
6573421	>gi|6573421|pdb|1QIP|C Chain C, Human Glyoxalase I Complexed With S-P-Nitrobenzyloxycarbonylglutathione			x	
6573420	>gi|6573420|pdb|1QIP|B Chain B, Human Glyoxalase I Complexed With S-P-Nitrobenzyloxycarbonylglutathione			x	
6573419	>gi|6573419|pdb|1QIP|A Chain A, Human Glyoxalase I Complexed With S-P-Nitrobenzyloxycarbonylglutathione			x	
6573418	>gi|6573418|pdb|1QIN|B Chain B, Human Glyoxalase I Complexed With S-(N-Hydroxy-N-P- Iodophenylcarbamoyl) Glutathione			x	
6573417	>gi|6573417|pdb|1QIN|A Chain A, Human Glyoxalase I Complexed With S-(N-Hydroxy-N-P- Iodophenylcarbamoyl) Glutathione			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>2392341</td><td>>gi|2392341|pdb|1FRO|D Chain D, Human Glyoxalase I With Benzyl-Glutathione Inhibitor</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>2392340</td><td>>gi|2392340|pdb|1FRO|C Chain C, Human Glyoxalase I With Benzyl-Glutathione Inhibitor</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>2392339</td><td>>gi|2392339|pdb|1FRO|B Chain B, Human Glyoxalase I With Benzyl-Glutathione Inhibitor</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>2392338</td><td>>gi|2392338|pdb|1FRO|A Chain A, Human Glyoxalase I With Benzyl-Glutathione Inhibitor</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>26990471</td><td>>gi|26990471|ref|NP_745896.1| lactoylglutathione lyase [Pseudomonas putida KT2440]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>24985444</td><td>>gi|24985444|gb|AAN69360.1| lactoylglutathione lyase [Pseudomonas putida KT2440]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>16198506</td><td>>gi|16198506|gb|AAH15934.1| Glyoxalase I [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>5729842</td><td>>gi|5729842|ref|NP_006699.1| glyoxalase I [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>5020074</td><td>>gi|5020074|gb|AAD38008.1| glyoxalase-I [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>417246</td><td>>gi|417246|sp|Q04760|LGUL_HUMAN Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>183258</td><td>>gi|183258|gb|AAA52565.1| glyoxaslase I</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>219664</td><td>>gi|219664|dbj|BAA02572.1| lactoyl glutathione lyase [Homo sapiens]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>75076014</td><td>>gi|75076014|sp|Q4R5F2|LGUL_MACFA Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>51859026</td><td>>gi|51859026|gb|AAH81432.1| Glyoxalase 1 [Mus musculus]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>21362640</td><td>>gi|21362640|sp|Q9CPU0|LGUL_MOUSE Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>68345056</td><td>>gi|68345056|gb|AAY92662.1| lactoylglutathione lyase [Pseudomonas fluorescens Pf-5]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>70730757</td><td>>gi|70730757|ref|YP_260498.1| lactoylglutathione lyase [Pseudomonas fluorescens Pf-5]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>71554395</td><td>>gi|71554395|gb|AAZ33606.1| lactoylglutathione lyase [Pseudomonas syringae pv. phaseolicola 1448A]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
71733842	>gi|71733842|ref|YP_274476.1| lactoylglutathione lyase [Pseudomonas syringae pv. phaseolicola 1448A]			x	
2506469	>gi|2506469|sp|P16635|LGUL_PSEPU Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
499661	>gi|499661|gb|AAA61758.1| glyoxalase I			x	
66046204	>gi|66046204|ref|YP_236045.1| Glyoxalase I [Pseudomonas syringae pv. syringae B728a]			x	
63256911	>gi|63256911|gb|AAY38007.1| Glyoxalase I [Pseudomonas syringae pv. syringae B728a]			x	
82735426	>gi|82735426|ref|ZP_00898288.1| Glyoxalase I [Pseudomonas putida F1]			x	
82717059	>gi|82717059|gb|EAP52111.1| Glyoxalase I [Pseudomonas putida F1]			x	
28870279	>gi|28870279|ref|NP_792898.1| lactoylglutathione lyase [Pseudomonas syringae pv. tomato str. DC3000]			x	
28853526	>gi|28853526|gb|AAO56593.1| lactoylglutathione lyase [Pseudomonas syringae pv. tomato str. DC3000]			x	
47085917	>gi|47085917|ref|NP_998316.1| glyoxalase 1 [Danio rerio]			x	
38382733	>gi|38382733|gb|AAH62383.1| Glyoxalase 1 [Danio rerio]			x	
21111572	>gi|21111572|gb|AAM39891.1| lactoylglutathione lyase [Xanthomonas campestris pv. campestris str. ATCC 33913]			x	
66575289	>gi|66575289|gb|AAY50699.1| lactoylglutathione lyase [Xanthomonas campestris pv. campestris str. 8004]			x	
66769957	>gi|66769957|ref|YP_244719.1| lactoylglutathione lyase [Xanthomonas campestris pv. campestris str. 8004]			x	
21230050	>gi|21230050|ref|NP_635967.1| lactoylglutathione lyase [Xanthomonas campestris pv. campestris str. ATCC 33913]			x	
28198538	>gi|28198538|ref|NP_778852.1| lactoylglutathione lyase [Xylella fastidiosa Temecula1]			x	
28056622	>gi|28056622|gb|AAO28501.1| lactoylglutathione lyase [Xylella fastidiosa Temecula1]			x	
39576464	>gi|39576464|emb|CAE80629.1| lactoylglutathione lyase [Bdellovibrio bacteriovorus HD100]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
42524256	>gi|42524256|ref|NP_969636.1| lactoylglutathione lyase [Bdellovibrio bacteriovorus HD100]			x	
9106409	>gi|9106409|gb|AAF84208.1| lactoylglutathione lyase [Xylella fastidiosa 9a5c]			x	
15838000	>gi|15838000|ref|NP_298688.1| lactoylglutathione lyase [Xylella fastidiosa 9a5c]			x	
71897576	>gi|71897576|ref|ZP_00679821.1| Glyoxalase I [Xylella fastidiosa Ann-1]			x	
71732479	>gi|71732479|gb|EAO34532.1| Glyoxalase I [Xylella fastidiosa Ann-1]			x	
71900928	>gi|71900928|ref|ZP_00683042.1| Glyoxalase I [Xylella fastidiosa Ann-1]			x	
71729287	>gi|71729287|gb|EAO31404.1| Glyoxalase I [Xylella fastidiosa Ann-1]			x	
71274818	>gi|71274818|ref|ZP_00651106.1| Glyoxalase I [Xylella fastidiosa Dixon]			x	
71164550	>gi|71164550|gb|EAO14264.1| Glyoxalase I [Xylella fastidiosa Dixon]			x	
9951408	>gi|9951408|gb|AAG08496.1| lactoylglutathione lyase [Pseudomonas aeruginosa PAO1]			x	
15600304	>gi|15600304|ref|NP_253798.1| lactoylglutathione lyase [Pseudomonas aeruginosa PAO1]			x	
78037735	>gi|78037735|emb|CAJ25480.1| Lactoylglutathione lyase [Xanthomonas campestris pv. vesicatoria str. 85-10]			x	
78049305	>gi|78049305|ref|YP_365480.1| Lactoylglutathione lyase [Xanthomonas campestris pv. vesicatoria str. 85-10]			x	
77953933	>gi|77953933|ref|ZP_00818336.1| Glyoxalase I [Marinobacter aquaeolei VT8]			x	
77867230	>gi|77867230|gb|EAO98510.1| Glyoxalase I [Marinobacter aquaeolei VT8]			x	
21110013	>gi|21110013|gb|AAM38475.1| lactoylglutathione lyase [Xanthomonas axonopodis pv. citri str. 306]			x	
21244357	>gi|21244357|ref|NP_643939.1| lactoylglutathione lyase [Xanthomonas axonopodis pv. citri str. 306]			x	
58580377	>gi|58580377|ref|YP_199393.1| lactoylglutathione lyase [Xanthomonas oryzae pv. oryzae KACC10331]			x	
58424971	>gi|58424971|gb|AAW74008.1| lactoylglutathione lyase [Xanthomonas oryzae pv. oryzae KACC10331]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>84366281</td><td>>gi|84366281|dbj|BAE67439.1| lactoylglutathione lyase [Xanthomonas oryzae pv. oryzae MAFF 311018]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>84622341</td><td>>gi|84622341|ref|YP_449713.1| lactoylglutathione lyase [Xanthomonas oryzae pv. oryzae MAFF 311018]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>2494843</td><td>>gi|2494843|sp|Q39366|LGUL_BRAOG Putative lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>76875453</td><td>>gi|76875453|emb|CAI86674.1| Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase) [Pseudoalteromonas haloplanktis TAC125]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>77360542</td><td>>gi|77360542|ref|YP_340117.1| Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase) [Pseudoalteromonas haloplanktis TAC125]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>85712601</td><td>>gi|85712601|ref|ZP_01043648.1| Lactoylglutathione lyase [Idiomarina baltica OS145]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>85693592</td><td>>gi|85693592|gb|EAQ31543.1| Lactoylglutathione lyase [Idiomarina baltica OS145]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67674810</td><td>>gi|67674810|ref|ZP_00471570.1| Glyoxalase I [Chromohalobacter salexigens DSM 3043]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67521475</td><td>>gi|67521475|gb|EAM25415.1| Glyoxalase I [Chromohalobacter salexigens DSM 3043]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>2494847</td><td>>gi|2494847|sp|Q55595|LGUL_SYNY3 Probable lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67663996</td><td>>gi|67663996|ref|ZP_00461274.1| Glyoxalase I [Burkholderia cenocepacia HI2424]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67658610</td><td>>gi|67658610|ref|ZP_00455980.1| Glyoxalase I [Burkholderia cenocepacia AU 1054]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>67102512</td><td>>gi|67102512|gb|EAM19644.1| Glyoxalase I [Burkholderia cenocepacia HI2424]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
67093698	>gi|67093698|gb|EAM11237.1| Glyoxalase I [Burkholderia cenocepacia AU 1054]			x	
74014235	>gi|74014235|ref|ZP_00684864.1| Glyoxalase I [Burkholderia ambifaria AMMD]			x	
72612837	>gi|72612837|gb|EAO48780.1| Glyoxalase I [Burkholderia ambifaria AMMD]			x	
9655474	>gi|9655474|gb|AAF94171.1| lactoylglutathione lyase [Vibrio cholerae O1 biovar eltor str. N16961]			x	
15641025	>gi|15641025|ref|NP_230656.1| lactoylglutathione lyase [Vibrio cholerae O1 biovar eltor str. N16961]			x	
14548103	>gi|14548103|sp|Q9KT93|LGUL_VIBCH Probable lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
67547158	>gi|67547158|ref|ZP_00425064.1| Glyoxalase I [Burkholderia vietnamiensis G4]			x	
67531477	>gi|67531477|gb|EAM28288.1| Glyoxalase I [Burkholderia vietnamiensis G4]			x	
76791872	>gi|76791872|ref|ZP_00774376.1| Glyoxalase I [Pseudoalteromonas atlantica T6c]			x	
76592844	>gi|76592844|gb|EAO69030.1| Glyoxalase I [Pseudoalteromonas atlantica T6c]			x	
77968247	>gi|77968247|gb|ABB09627.1| Glyoxalase I [Burkholderia sp. 383]			x	
78067502	>gi|78067502|ref|YP_370271.1| Glyoxalase I [Burkholderia sp. 383]			x	
17131413	>gi|17131413|dbj|BAB74020.1| lactoylglutathione lyase [Nostoc sp. PCC 7120]			x	
17229813	>gi|17229813|ref|NP_486361.1| lactoylglutathione lyase [Nostoc sp. PCC 7120]			x	
83720549	>gi|83720549|ref|YP_441137.1| lactoylglutathione lyase [Burkholderia thailandensis E264]			x	
83654374	>gi|83654374|gb|ABC38437.1| lactoylglutathione lyase [Burkholderia thailandensis E264]			x	
75700089	>gi|75700089|gb|ABA19765.1| Glyoxalase I [Anabaena variabilis ATCC 29413]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
75906364	>gi|75906364|ref|YP_320660.1| Glyoxalase I [Anabaena variabilis ATCC 29413]			x	
71677562	>gi|71677562|ref|ZP_00675298.1| Glyoxalase I [Trichodesmium erythraeum IMS101]			x	
71669193	>gi|71669193|gb|EAO25867.1| Glyoxalase I [Trichodesmium erythraeum IMS101]			x	
2281946	>gi|2281946|emb|CAA74673.1| lactoylglutathione lyase [Neisseria meningitidis]			x	
7380768	>gi|7380768|emb|CAB85359.1| lactoylglutathione lyase [Neisseria meningitidis Z2491]			x	
7225560	>gi|7225560|gb|AAF40783.1| lactoylglutathione lyase [Neisseria meningitidis MC58]			x	
15795018	>gi|15795018|ref|NP_284840.1| lactoylglutathione lyase [Neisseria meningitidis Z2491]			x	
15676255	>gi|15676255|ref|NP_273389.1| lactoylglutathione lyase [Neisseria meningitidis MC58]			x	
60392612	>gi|60392612|sp|P0A0T3|LGUL_NEIMB Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
60392611	>gi|60392611|sp|P0A0T2|LGUL_NEIMA Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
52428442	>gi|52428442|gb|AAU49035.1| lactoylglutathione lyase [Burkholderia mallei ATCC 23344]			x	
52208720	>gi|52208720|emb|CAH34656.1| lactoylglutathione lyase [Burkholderia pseudomallei K96243]			x	
53718306	>gi|53718306|ref|YP_107292.1| lactoylglutathione lyase [Burkholderia pseudomallei K96243]			x	
76578699	>gi|76578699|gb|ABA48174.1| lactoylglutathione lyase [Burkholderia pseudomallei 1710b]			x	
76809246	>gi|76809246|ref|YP_332289.1| lactoylglutathione lyase [Burkholderia pseudomallei 1710b]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
56180743	>gi|56180743|gb|AAV83465.1| Lactoylglutathione lyase [Idiomarina loihiensis L2TR]			x	
56461733	>gi|56461733|ref|YP_157014.1| Lactoylglutathione lyase [Idiomarina loihiensis L2TR]			x	
24052010	>gi|24052010|gb|AAN43259.1| lactoylglutathione lyase [Shigella flexneri 2a str. 301]			x	
1787940	>gi|1787940|gb|AAC74723.1| lactoylglutathione lyase [Escherichia coli K12]			x	
85675062	>gi|85675062|dbj|BAE76494.1| glyoxalase I, Ni-dependent [Escherichia coli W3110]			x	
30041419	>gi|30041419|gb|AAP17147.1| lactoylglutathione lyase [Shigella flexneri 2a str. 2457T]			x	
13361827	>gi|13361827|dbj|BAB35783.1| lactoylglutathione lyase [Escherichia coli O157:H7]			x	
82777128	>gi|82777128|ref|YP_403477.1| lactoylglutathione lyase [Shigella dysenteriae Sd197]			x	
30063167	>gi|30063167|ref|NP_837338.1| lactoylglutathione lyase [Shigella flexneri 2a str. 2457T]			x	
24113042	>gi|24113042|ref|NP_707552.1| lactoylglutathione lyase [Shigella flexneri 2a str. 301]			x	
16129609	>gi|16129609|ref|NP_416168.1| glyoxalase I, nickel isomerase [Escherichia coli K12]			x	
81170962	>gi|81170962|sp|P0AC83|LGUL_SHIFL Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
81170961	>gi|81170961|sp|P0AC81|LGUL_ECOLI Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
81170960	>gi|81170960|sp|P0AC82|LGUL_ECO57 Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
15831614	>gi|15831614|ref|NP_310387.1| lactoylglutathione lyase [Escherichia coli O157:H7]			x	

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>1354845</td><td>>gi|1354845|gb|AAC27133.1| S-D-lactoylglutathione methylglyoxal lyase [Escherichia coli]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>74312021</td><td>>gi|74312021|ref|YP_310440.1| lactoylglutathione lyase [Shigella sonnei Ss046]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>81241276</td><td>>gi|81241276|gb|ABB61986.1| lactoylglutathione lyase [Shigella dysenteriae Sd197]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>10835721</td><td>>gi|10835721|pdb|1FA8|B Chain B, Crystal Structure Of The Apo Form Glyoxalase I Of Escherichia Coli</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>10835720</td><td>>gi|10835720|pdb|1FA8|A Chain A, Crystal Structure Of The Apo Form Glyoxalase I Of Escherichia Coli</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>10835719</td><td>>gi|10835719|pdb|1FA7|B Chain B, Crystal Structure Of Cd(Ii)-Bound Glyoxalase I Of Escherichia Coli</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>10835718</td><td>>gi|10835718|pdb|1FA7|A Chain A, Crystal Structure Of Cd(Ii)-Bound Glyoxalase I Of Escherichia Coli</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>10835717</td><td>>gi|10835717|pdb|1FA6|B Chain B, Crystal Structure Of The Co(Ii)-Bound Glyoxalase I Of Escherichia Coli</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>10835716</td><td>>gi|10835716|pdb|1FA6|A Chain A, Crystal Structure Of The Co(Ii)-Bound Glyoxalase I Of Escherichia Coli</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>10835715</td><td>>gi|10835715|pdb|1FA5|B Chain B, Crystal Structure Of The Zn(Ii)-Bound Glyoxalase I Of Escherichia Coli</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>10835714</td><td>>gi|10835714|pdb|1FA5|A Chain A, Crystal Structure Of The Zn(Ii)-Bound Glyoxalase I Of Escherichia Coli</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>10835713</td><td>>gi|10835713|pdb|1F9Z|B Chain B, Crystal Structure Of The Ni(Ii)-Bound Glyoxalase I From Escherichia Coli</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>10835712</td><td>>gi|10835712|pdb|1F9Z|A Chain A, Crystal Structure Of The Ni(Ii)-Bound Glyoxalase I From Escherichia Coli</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>73855498</td><td>>gi|73855498|gb|AAZ88205.1| lactoylglutathione lyase [Shigella sonnei Ss046]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>59711535</td><td>>gi|59711535|ref|YP_204311.1| lactoylglutathione lyase [Vibrio fischeri ES114]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>59479636</td><td>>gi|59479636|gb|AAW85423.1| lactoylglutathione lyase [Vibrio fischeri ES114]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
26108302	>gi|26108302|gb|AAN80504.1| Lactoylglutathione lyase [Escherichia coli CFT073]			x	
26247899	>gi|26247899|ref|NP_753939.1| Lactoylglutathione lyase [Escherichia coli CFT073]			x	
56313950	>gi|56313950|emb|CAI08595.1| Lactoylglutathione lyase [Azoarcus sp. EbN1]			x	
56477907	>gi|56477907|ref|YP_159496.1| Lactoylglutathione lyase [Azoarcus sp. EbN1]			x	
49531298	>gi|49531298|emb|CAG69010.1| lactoylglutathione lyase [Acinetobacter sp. ADP1]			x	
50085322	>gi|50085322|ref|YP_046832.1| lactoylglutathione lyase [Acinetobacter sp. ADP1]			x	
28807102	>gi|28807102|dbj|BAC60372.1| lactoylglutathione lyase [Vibrio parahaemolyticus RIMD 2210633]			x	
29611956	>gi|29611956|sp|P46235|LGUL_VIBPA Probable lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
28898883	>gi|28898883|ref|NP_798488.1| lactoylglutathione lyase [Vibrio parahaemolyticus RIMD 2210633]			x	
34497115	>gi|34497115|ref|NP_901330.1| lactoylglutathione lyase [Chromobacterium violaceum ATCC 12472]			x	
34102972	>gi|34102972|gb|AAQ59336.1| lactoylglutathione lyase [Chromobacterium violaceum ATCC 12472]			x	
9949673	>gi|9949673|gb|AAG06912.1| lactoylglutathione lyase [Pseudomonas aeruginosa PAO1]			x	
15598720	>gi|15598720|ref|NP_252214.1| lactoylglutathione lyase [Pseudomonas aeruginosa PAO1]			x	
16502774	>gi|16502774|emb|CAD01932.1| lactoylglutathione lyase [Salmonella enterica subsp. enterica serovar Typhi]			x	
16419955	>gi|16419955|gb|AAL20357.1| glyoxalase I; nickel isomerase [Salmonella typhimurium LT2]			x	
62180024	>gi|62180024|ref|YP_216441.1| glyoxalase I, nickel isomerase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
56127853	>gi|56127853|gb|AAV77359.1| lactoylglutathione lyase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]			x	
29137390	>gi|29137390|gb|AAO68953.1| lactoylglutathione lyase [Salmonella enterica subsp. enterica serovar Typhi Ty2]			x	
62127657	>gi|62127657|gb|AAX65360.1| glyoxalase I, nickel isomerase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]			x	
61227640	>gi|61227640|sp|P0A1Q2|LGUL_SALTY Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
16764783	>gi|16764783|ref|NP_460398.1| glyoxalase I [Salmonella typhimurium LT2]			x	
56413596	>gi|56413596|ref|YP_150671.1| lactoylglutathione lyase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]			x	
61227642	>gi|61227642|sp|P0A1Q3|LGUL_SALTI Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
16760478	>gi|16760478|ref|NP_456095.1| lactoylglutathione lyase [Salmonella enterica subsp. enterica serovar Typhi str. CT18]			x	
29141762	>gi|29141762|ref|NP_805104.1| lactoylglutathione lyase [Salmonella enterica subsp. enterica serovar Typhi Ty2]			x	
25518334	>gi|25518334|pir||AC0695 lactoylglutathione lyase (EC 4.4.1.5) [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)			x	
82543983	>gi|82543983|ref|YP_407930.1| lactoylglutathione lyase [Shigella boydii Sb227]			x	
81245394	>gi|81245394|gb|ABB66102.1| lactoylglutathione lyase [Shigella boydii Sb227]			x	
49611385	>gi|49611385|emb|CAG74832.1| lactoylglutathione lyase [Erwinia carotovora subsp. atroseptica SCRI1043]			x	
50120859	>gi|50120859|ref|YP_050026.1| lactoylglutathione lyase [Erwinia carotovora subsp. atroseptica SCRI1043]			x	
1354847	>gi|1354847|gb|AAC44877.1| S-D-lactolylglutathione methylglyoxal lyase			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
86605927	>gi|86605927|ref|YP_474690.1| lactoylglutathione lyase [Cyanobacteria bacterium Yellowstone A-Prime]			x	
75431428	>gi|75431428|ref|ZP_00733000.1| Lactoylglutathione lyase [Actinobacillus succinogenes 130Z]			x	
74276309	>gi|74276309|gb|EAO49924.1| Lactoylglutathione lyase [Actinobacillus succinogenes 130Z]			x	
33568699	>gi|33568699|emb|CAE34457.1| lactoylglutathione lyase [Bordetella bronchiseptica RB50]			x	
33566732	>gi|33566732|emb|CAE38943.1| lactoylglutathione lyase [Bordetella parapertussis]			x	
33570950	>gi|33570950|emb|CAE40417.1| lactoylglutathione lyase [Bordetella pertussis Tohama I]			x	
33591308	>gi|33591308|ref|NP_878952.1| lactoylglutathione lyase [Bordetella pertussis Tohama I]			x	
33598174	>gi|33598174|ref|NP_885817.1| lactoylglutathione lyase [Bordetella parapertussis 12822]			x	
33603068	>gi|33603068|ref|NP_890628.1| lactoylglutathione lyase [Bordetella bronchiseptica RB50]			x	
76884453	>gi|76884453|gb|ABA59134.1| Glyoxalase I [Nitrosococcus oceani ATCC 19707]			x	
77166139	>gi|77166139|ref|YP_344664.1| Glyoxalase I [Nitrosococcus oceani ATCC 19707]			x	
84715589	>gi|84715589|ref|ZP_01022618.1| Glyoxalase I [Polaromonas naphthalenivorans CJ2]			x	
84693129	>gi|84693129|gb|EAQ18932.1| Glyoxalase I [Polaromonas naphthalenivorans CJ2]			x	
45436822	>gi|45436822|gb|AAS62375.1| lactoylglutathione lyase [Yersinia pestis biovar Medievalis str. 91001]			x	
21958780	>gi|21958780|gb|AAM85523.1| lactoylglutathione lyase [Yersinia pestis KIM]			x	
22125849	>gi|22125849|ref|NP_669272.1| lactoylglutathione lyase [Yersinia pestis KIM]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
45441959	>gi|45441959|ref|NP_993498.1| lactoylglutathione lyase [Yersinia pestis biovar Medievalis str. 91001]			x	
56685855	>gi|56685855|dbj|BAD79077.1| lactoylglutathione lyase [Synechococcus elongatus PCC 6301]			x	
56750896	>gi|56750896|ref|YP_171597.1| lactoylglutathione lyase [Synechococcus elongatus PCC 6301]			x	
81299449	>gi|81299449|ref|YP_399657.1| Glyoxalase I [Synechococcus elongatus PCC 7942]			x	
81168330	>gi|81168330|gb|ABB56670.1| Glyoxalase I [Synechococcus elongatus PCC 7942]			x	
67157387	>gi|67157387|ref|ZP_00418689.1| Glyoxalase I [Azotobacter vinelandii AvOP]			x	
67085654	>gi|67085654|gb|EAM05127.1| Glyoxalase I [Azotobacter vinelandii AvOP]			x	
37198112	>gi|37198112|dbj|BAC93949.1| lactoylglutathione lyase [Vibrio vulnificus YJ016]			x	
37679369	>gi|37679369|ref|NP_933978.1| lactoylglutathione lyase [Vibrio vulnificus YJ016]			x	
67920488	>gi|67920488|ref|ZP_00514008.1| Glyoxalase I [Crocosphaera watsonii WH 8501]			x	
67857972	>gi|67857972|gb|EAM53211.1| Glyoxalase I [Crocosphaera watsonii WH 8501]			x	
67777486	>gi|67777486|gb|EAM37113.1| Glyoxalase I [Polaromonas sp. JS666]			x	
67910319	>gi|67910319|ref|ZP_00508710.1| Glyoxalase I [Polaromonas sp. JS666]			x	
86147966	>gi|86147966|ref|ZP_01066270.1| lactoylglutathione lyase [Vibrio sp. MED222]			x	
85834291	>gi|85834291|gb|EAQ52445.1| lactoylglutathione lyase [Vibrio sp. MED222]			x	
84393401	>gi|84393401|ref|ZP_00992160.1| lactoylglutathione lyase [Vibrio splendidus 12B01]			x	
84376010	>gi|84376010|gb|EAP92899.1| lactoylglutathione lyase [Vibrio splendidus 12B01]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
30138761	>gi|30138761|emb|CAD85338.1| possible gloA; lactoylglutathione lyase [Nitrosomonas europaea ATCC 19718]			x	
30249398	>gi|30249398|ref|NP_841468.1| possible gloA; lactoylglutathione lyase [Nitrosomonas europaea ATCC 19718]			x	
36785924	>gi|36785924|emb|CAE14976.1| lactoylglutathione lyase (methylglyoxalase) (S-D-lactolyglutathione methylglyoxal lyase) [Photorhabdus luminescens subsp. laumondii TTO1]			x	
37526493	>gi|37526493|ref|NP_929837.1| lactoylglutathione lyase (methylglyoxalase) (S-D-lactolyglutathione methylglyoxal lyase) [Photorhabdus luminescens subsp. laumondii TTO1]			x	
51589901	>gi|51589901|emb|CAH21533.1| lactoylglutathione lyase [Yersinia pseudotuberculosis IP 32953]			x	
51596619	>gi|51596619|ref|YP_070810.1| lactoylglutathione lyase [Yersinia pseudotuberculosis IP 32953]			x	
15980377	>gi|15980377|emb|CAC91186.1| lactoylglutathione lyase [Yersinia pestis CO92]			x	
16122604	>gi|16122604|ref|NP_405917.1| lactoylglutathione lyase [Yersinia pestis CO92]			x	
71550295	>gi|71550295|ref|ZP_00670425.1| Glyoxalase I [Nitrosomonas eutropha C71]			x	
71484520	>gi|71484520|gb|EAO17079.1| Glyoxalase I [Nitrosomonas eutropha C71]			x	
68188408	>gi|68188408|gb|EAN03088.1| Glyoxalase I [Methylobacillus flagellatus KT]			x	
68213116	>gi|68213116|ref|ZP_00564950.1| Glyoxalase I [Methylobacillus flagellatus KT]			x	
72117622	>gi|72117622|gb|AAZ59885.1| Glyoxalase I [Ralstonia eutropha JMP134]			x	
73540209	>gi|73540209|ref|YP_294729.1| Glyoxalase I [Ralstonia eutropha JMP134]			x	
82703738	>gi|82703738|ref|YP_413304.1| Glyoxalase I [Nitrosospira multiformis ATCC 25196]			x	
82411803	>gi|82411803|gb|ABB75912.1| Glyoxalase I [Nitrosospira multiformis ATCC 25196]			x	

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
71848772	>gi|71848772|gb|AAZ48268.1| Glyoxalase I [Dechloromonas aromatica RCB]			x	
71909151	>gi|71909151|ref|YP_286738.1| Glyoxalase I [Dechloromonas aromatica RCB]			x	
33639478	>gi|33639478|emb|CAE08862.1| lactoylglutathione lyase [Synechococcus sp. WH 8102]			x	
33866877	>gi|33866877|ref|NP_898436.1| lactoylglutathione lyase [Synechococcus sp. WH 8102]			x	
1175222	>gi|1175222|sp|P44638|LGUL_HAEIN Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
28809009	>gi|28809009|dbj|BAC62117.1| lactoylglutathione lyase [Vibrio parahaemolyticus RIMD 2210633]			x	
28900629	>gi|28900629|ref|NP_800284.1| lactoylglutathione lyase [Vibrio parahaemolyticus RIMD 2210633]			x	
83594120	>gi|83594120|ref|YP_427872.1| N-isopropylammelide isopropylaminohydrolase [Rhodospirillum rubrum ATCC 11170]		x		
83577034	>gi|83577034|gb|ABC23585.1| N-isopropylammelide isopropylaminohydrolase [Rhodospirillum rubrum ATCC 11170]		x		
72121163	>gi|72121163|gb|AAZ63349.1| TatD-related deoxyribonuclease [Ralstonia eutropha JMP134]		x		
83373235	>gi|83373235|ref|ZP_00918014.1| N-isopropylammelide isopropylaminohydrolase [Rhodobacter sphaeroides ATCC 17029]		x		
83365707	>gi|83365707|gb|EAP69194.1| N-isopropylammelide isopropylaminohydrolase [Rhodobacter sphaeroides ATCC 17029]		x		
77384004	>gi|77384004|gb|ABA75517.1| N-isopropylammelide isopropylaminohydrolase [Pseudomonas fluorescens PfO-1]		x		
77460001	>gi|77460001|ref|YP_349508.1| N-isopropylammelide isopropylaminohydrolase [Pseudomonas fluorescens PfO-1]		x		
83368279	>gi|83368279|ref|ZP_00913143.1| N-isopropylammelide isopropylaminohydrolase [Rhodobacter sphaeroides ATCC 17025]		x		
83361992	>gi|83361992|gb|EAP65504.1| N-isopropylammelide isopropylaminohydrolase [Rhodobacter sphaeroides ATCC 17025]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
77969535	>gi|77969535|gb|ABB10914.1| N-isopropylammelide isopropylaminohydrolase [Burkholderia sp. 383]		x		
78061650	>gi|78061650|ref|YP_371558.1| N-isopropylammelide isopropylaminohydrolase [Burkholderia sp. 383]		x		
74016317	>gi|74016317|ref|ZP_00686943.1| N-isopropylammelide isopropylaminohydrolase [Burkholderia ambifaria AMMD]		x		
72610688	>gi|72610688|gb|EAO46634.1| N-isopropylammelide isopropylaminohydrolase [Burkholderia ambifaria AMMD]		x		
67542566	>gi|67542566|ref|ZP_00420502.1| N-isopropylammelide isopropylaminohydrolase [Burkholderia vietnamiensis G4]		x		
67536280	>gi|67536280|gb|EAM32999.1| N-isopropylammelide isopropylaminohydrolase [Burkholderia vietnamiensis G4]		x		
67656146	>gi|67656146|ref|ZP_00453530.1| N-isopropylammelide isopropylaminohydrolase [Burkholderia cenocepacia AU 1054]		x		
67096306	>gi|67096306|gb|EAM13831.1| N-isopropylammelide isopropylaminohydrolase [Burkholderia cenocepacia AU 1054]		x		
68183854	>gi|68183854|ref|ZP_00556825.1| N-isopropylammelide isopropylaminohydrolase [Jannaschia sp. CCS1]		x		
67975993	>gi|67975993|gb|EAM65626.1| N-isopropylammelide isopropylaminohydrolase [Jannaschia sp. CCS1]		x		
75258409	>gi|75258409|ref|ZP_00729840.1| COG1820: N-acetylglucosamine-6-phosphate deacetylase [Escherichia coli E22]		x		
75515511	>gi|75515511|ref|ZP_00737668.1| COG1820: N-acetylglucosamine-6-phosphate deacetylase [Escherichia coli 53638]		x		
75198143	>gi|75198143|ref|ZP_00708213.1| COG1820: N-acetylglucosamine-6-phosphate deacetylase [Escherichia coli HS]		x		
75229725	>gi|75229725|ref|ZP_00716258.1| COG1820: N-acetylglucosamine-6-phosphate deacetylase [Escherichia coli B7A]		x		
75189047	>gi|75189047|ref|ZP_00702314.1| COG1820: N-acetylglucosamine-6-phosphate deacetylase [Escherichia coli E24377A]		x		
83586647	>gi|83586647|ref|ZP_00925279.1| COG1820: N-acetylglucosamine-6-phosphate deacetylase [Escherichia coli 101-1]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
75242238	>gi|75242238|ref|ZP_00726000.1| COG1820: N-acetylglucosamine-6-phosphate deacetylase [Escherichia coli F11]		x		
75179389	>gi|75179389|ref|ZP_00699393.1| COG1820: N-acetylglucosamine-6-phosphate deacetylase [Shigella boydii BS512]		x		
75212111	>gi|75212111|ref|ZP_00712151.1| COG1820: N-acetylglucosamine-6-phosphate deacetylase [Escherichia coli B171]		x		
75235099	>gi|75235099|ref|ZP_00719355.1| COG1820: N-acetylglucosamine-6-phosphate deacetylase [Escherichia coli E110019]		x		
737714	>gi|737714|prf||1923271A enoyl-CoA isomerase		x		
15080016	>gi|15080016|gb|AAH11792.1| Peroxisomal enoyl-coenzyme A hydratase-like protein [Homo sapiens]		x		
70995211	>gi|70995211|ref|NP_001389.2| peroxisomal enoyl-coenzyme A hydratase-like protein [Homo sapiens]		x		
16924265	>gi|16924265|gb|AAH17408.1| Peroxisomal enoyl-coenzyme A hydratase-like protein [Homo sapiens]		x		
38566122	>gi|38566122|gb|AAH62226.1| Enoyl coenzyme A hydratase 1, peroxisomal [Rattus norvegicus]		x		
12018256	>gi|12018256|ref|NP_072116.1| enoyl coenzyme A hydratase 1, peroxisomal [Rattus norvegicus]		x		
478984	>gi|478984|gb|AAA82008.1| peroxisomal enoyl hydratase-like protein		x		
7949037	>gi|7949037|ref|NP_058052.1| enoyl coenzyme A hydratase 1, peroxisomal [Mus musculus]		x		
45829801	>gi|45829801|gb|AAH68112.1| Enoyl coenzyme A hydratase 1, peroxisomal [Mus musculus]		x		
56789390	>gi|56789390|gb|AAH87924.1| Enoyl coenzyme A hydratase 1, peroxisomal [Mus musculus]		x		
564065	>gi|564065|gb|AAC50222.1| peroxisomal enoyl-CoA hydratase-like protein [Homo sapiens]		x		
57036579	>gi|57036579|ref|XP_533678.1| PREDICTED: similar to peroxisomal enoyl-coenzyme A hydratase-like protein isoform 1 [Canis familiaris]		x		
26990733	>gi|26990733|ref|NP_746158.1| enoyl-CoA hydratase [Pseudomonas putida KT2440]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
76641602	>gi|76641602|ref|XP_871981.1| PREDICTED: similar to peroxisomal enoyl-coenzyme A hydratase-like protein isoform 2 [Bos taurus]		x		
77383110	>gi|77383110|gb|ABA74623.1| Enoyl-CoA hydratase/isomerase [Pseudomonas fluorescens PfO-1]		x		
77459107	>gi|77459107|ref|YP_348613.1| enoyl-CoA hydratase [Pseudomonas fluorescens PfO-1]		x		
28869906	>gi|28869906|ref|NP_792525.1| enoyl-CoA hydratase [Pseudomonas syringae pv. tomato str. DC3000]		x		
66045688	>gi|66045688|ref|YP_235529.1| enoyl-CoA hydratase [Pseudomonas syringae pv. syringae B728a]		x		
63256395	>gi|63256395|gb|AAY37491.1| Enoyl-CoA hydratase/isomerase [Pseudomonas syringae pv. syringae B728a]		x		
70730631	>gi|70730631|ref|YP_260372.1| enoyl-CoA hydratase [Pseudomonas fluorescens Pf-5]		x		
32041895	>gi|32041895|ref|ZP_00139478.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Pseudomonas aeruginosa UCBPP-PA14]		x		
9947806	>gi|9947806|gb|AAG05210.1| probable enoyl-CoA hydratase/isomerase [Pseudomonas aeruginosa PAO1]		x		
15597018	>gi|15597018|ref|NP_250512.1| enoyl-CoA hydratase [Pseudomonas aeruginosa PAO1]		x		
84327857	>gi|84327857|ref|ZP_00975871.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Pseudomonas aeruginosa 2192]		x		
84321283	>gi|84321283|ref|ZP_00969641.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Pseudomonas aeruginosa C3719]		x		
54020920	>gi|54020920|ref|NP_001005704.1| enoyl Coenzyme A hydratase 1, peroxisomal [Xenopus tropicalis]		x		
49522300	>gi|49522300|gb|AAH75277.1| Enoyl Coenzyme A hydratase 1, peroxisomal [Xenopus tropicalis]		x		
15239823	>gi|15239823|ref|NP_199142.1| catalytic/ enoyl-CoA hydratase [Arabidopsis thaliana]		x		
18252833	>gi|18252833|gb|AAL62343.1| enoyl CoA hydratase-like protein [Arabidopsis thaliana]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
10177390	>gi|10177390|dbj|BAB10591.1| enoyl CoA hydratase-like protein [Arabidopsis thaliana]		x		
25084271	>gi|25084271|gb|AAN72209.1| enoyl CoA hydratase-like protein [Arabidopsis thaliana]		x		
73746067	>gi|73746067|gb|AAZ82038.1| peroxisomal enoyl coenzyme A hydratase 1 [Sus scrofa]		x		
50904363	>gi|50904363|ref|XP_463670.1| enoyl CoA hydratase-like protein [Oryza sativa (japonica cultivar-group)]		x		
20161749	>gi|20161749|dbj|BAB90665.1| putative enoyl coenzyme A hydratase 1, peroxisomal [Oryza sativa (japonica cultivar-group)]		x		
20160715	>gi|20160715|dbj|BAB89657.1| enoyl CoA hydratase-like protein [Oryza sativa (japonica cultivar-group)]		x		
76782375	>gi|76782375|ref|ZP_00769580.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Mycobacterium tuberculosis F11]		x		
1552857	>gi|1552857|emb|CAB02481.1| POSSIBLE ENOYL-CoA HYDRATASE ECHA21 (ENOYL HYDRASE) (UNSATURATED ACYL-CoA HYDRATASE) (CROTONASE) [Mycobacterium tuberculosis H37Rv]		x		
31620545	>gi|31620545|emb|CAD95989.1| PUTATIVE ENOYL-COA HYDRATASE ECHA21 (ENOYL HYDRASE) (UNSATURATED ACYL-COA HYDRATASE) (CROTONASE) [Mycobacterium bovis AF2122/97]		x		
31794947	>gi|31794947|ref|NP_857440.1| enoyl-CoA hydratase [Mycobacterium bovis AF2122/97]		x		
15610910	>gi|15610910|ref|NP_218291.1| enoyl-CoA hydratase [Mycobacterium tuberculosis H37Rv]		x		
15843397	>gi|15843397|ref|NP_338434.1| enoyl-CoA hydratase [Mycobacterium tuberculosis CDC1551]		x		
81252859	>gi|81252859|ref|ZP_00877435.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Mycobacterium tuberculosis C]		x		
1502424	>gi|1502424|gb|AAB06504.1| enoyl-CoA hydratase [Mycobacterium tuberculosis]		x		
13092500	>gi|13092500|emb|CAC29628.1| putative enoyl-CoA hydratase [Mycobacterium leprae]		x		

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>15826953</td><td>>gi|15826953|ref|NP_301216.1| enoyl-CoA hydratase [Mycobacterium leprae TN]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>73947714</td><td>>gi|73947714|ref|XP_867316.1| PREDICTED: similar to peroxisomal enoyl-coenzyme A hydratase-like protein isoform 2 [Canis familiaris]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>24194552</td><td>>gi|24194552|gb|AAN48231.1| enoyl-CoA hydratase [Leptospira interrogans serovar Lai str. 56601]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>24213732</td><td>>gi|24213732|ref|NP_711213.1| enoyl-CoA hydratase [Leptospira interrogans serovar Lai str. 56601]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>54022347</td><td>>gi|54022347|ref|YP_116589.1| enoyl-CoA hydratase [Nocardia farcinica IFM 10152]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>76641609</td><td>>gi|76641609|ref|XP_884451.1| PREDICTED: similar to peroxisomal enoyl-coenzyme A hydratase-like protein isoform 6 [Bos taurus]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>41406347</td><td>>gi|41406347|ref|NP_959183.1| enoyl-CoA hydratase [Mycobacterium avium subsp. paratuberculosis K-10]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>76792596</td><td>>gi|76792596|ref|ZP_00775094.1| Enoyl-CoA hydratase/isomerase [Pseudoalteromonas atlantica T6c]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>76592171</td><td>>gi|76592171|gb|EAO68363.1| Enoyl-CoA hydratase/isomerase [Pseudoalteromonas atlantica T6c]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>69952303</td><td>>gi|69952303|ref|ZP_00639816.1| Enoyl-CoA hydratase/isomerase [Shewanella frigidimarina NCIMB 400]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>69164309</td><td>>gi|69164309|gb|EAN73387.1| Enoyl-CoA hydratase/isomerase [Shewanella frigidimarina NCIMB 400]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>45658466</td><td>>gi|45658466|ref|YP_002552.1| enoyl-CoA hydratase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>45601709</td><td>>gi|45601709|gb|AAS71189.1| enoyl-CoA hydratase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>34497940</td><td>>gi|34497940|ref|NP_902155.1| enoyl-CoA hydratase [Chromobacterium violaceum ATCC 12472]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>34103795</td><td>>gi|34103795|gb|AAQ60156.1| probable enoyl-CoA hydratase [Chromobacterium violaceum ATCC 12472]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>68233383</td><td>>gi|68233383|ref|ZP_00572505.1| Enoyl-CoA hydratase/isomerase [Frankia sp. EAN1pec]</td><td></td><td>x</td><td></td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>68199001</td><td>>gi|68199001|gb|EAN13251.1| Enoyl-CoA hydratase/isomerase [Frankia sp. EAN1pec]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>3355325</td><td>>gi|3355325|emb|CAA76876.1| putative peroxisomal enoyl-CoA hydratase [Agaricus bisporus]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>75258517</td><td>>gi|75258517|ref|ZP_00729939.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Escherichia coli E22]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>75212468</td><td>>gi|75212468|ref|ZP_00712492.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Escherichia coli B171]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>75178812</td><td>>gi|75178812|ref|ZP_00698848.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Shigella boydii BS512]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>75515297</td><td>>gi|75515297|ref|ZP_00737481.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Escherichia coli 53638]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>75239514</td><td>>gi|75239514|ref|ZP_00723485.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Escherichia coli E110019]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>75196870</td><td>>gi|75196870|ref|ZP_00706940.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Escherichia coli HS]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>75187633</td><td>>gi|75187633|ref|ZP_00700900.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Escherichia coli E24377A]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>83587686</td><td>>gi|83587686|ref|ZP_00926313.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Escherichia coli 101-1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>75228586</td><td>>gi|75228586|ref|ZP_00715215.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Escherichia coli B7A]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>46202591</td><td>>gi|46202591|ref|ZP_00208575.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Magnetospirillum magnetotacticum MS-1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>48782635</td><td>>gi|48782635|ref|ZP_00279141.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia fungorum LB400]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>7287999</td><td>>gi|7287999|emb|CAB81837.1| enoyl-CoA-hydratase-like protein [Arabidopsis thaliana]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>77383092</td><td>>gi|77383092|gb|ABA74605.1| Enoyl-CoA hydratase/isomerase [Pseudomonas fluorescens PfO-1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>77459089</td><td>>gi|77459089|ref|YP_348595.1| Enoyl-CoA hydratase/isomerase [Pseudomonas fluorescens PfO-1]</td><td></td><td>x</td><td></td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
68344726	>gi|68344726|gb|AAY92332.1| enoly-coenzyme A hydratase/isomerase family protein [Pseudomonas fluorescens Pf-5]		x		
70730427	>gi|70730427|ref|YP_260168.1| enoly-coenzyme A hydratase/isomerase family protein [Pseudomonas fluorescens Pf-5]		x		
15891433	>gi|15891433|ref|NP_357105.1| enoyl-CoA hydratase [Agrobacterium tumefaciens str. C58]		x		
26990203	>gi|26990203|ref|NP_745628.1| enoly-coenzyme A hydratase/isomerase family protein [Pseudomonas putida KT2440]		x		
24985146	>gi|24985146|gb|AAN69092.1| enoly-coenzyme A hydratase/isomerase family protein [Pseudomonas putida KT2440]		x		
68557951	>gi|68557951|ref|ZP_00597290.1| Enoyl-CoA hydratase/isomerase [Ralstonia metallidurans CH34]		x		
68527505	>gi|68527505|gb|EAN50472.1| Enoyl-CoA hydratase/isomerase [Ralstonia metallidurans CH34]		x		
67156734	>gi|67156734|ref|ZP_00418231.1| Enoyl-CoA hydratase/isomerase [Azotobacter vinelandii AvOP]		x		
67085923	>gi|67085923|gb|EAM05394.1| Enoyl-CoA hydratase/isomerase [Azotobacter vinelandii AvOP]		x		
66045015	>gi|66045015|ref|YP_234856.1| Enoyl-CoA hydratase/isomerase [Pseudomonas syringae pv. syringae B728a]		x		
63255722	>gi|63255722|gb|AAY36818.1| Enoyl-CoA hydratase/isomerase [Pseudomonas syringae pv. syringae B728a]		x		
28870860	>gi|28870860|ref|NP_793479.1| enoly-CoA hydratase/isomerase family protein [Pseudomonas syringae pv. tomato str. DC3000]		x		
28854109	>gi|28854109|gb|AAO57174.1| enoly-CoA hydratase/isomerase family protein [Pseudomonas syringae pv. tomato str. DC3000]		x		
17741908	>gi|17741908|gb|AAL44318.1| enoyl-CoA hydratase [Agrobacterium tumefaciens str. C58]		x		
17937213	>gi|17937213|ref|NP_534002.1| enoyl-CoA hydratase [Agrobacterium tumefaciens str. C58]		x		
71555597	>gi|71555597|gb|AAZ34808.1| enoly-CoA hydratase/isomerase family protein [Pseudomonas syringae pv. phaseolicola 1448A]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
71735044	>gi|71735044|ref|YP_273958.1| enoly-CoA hydratase/isomerase family protein [Pseudomonas syringae pv. phaseolicola 1448A]		x		
82735704	>gi|82735704|ref|ZP_00898566.1| enoly-coenzyme A hydratase/isomerase family protein [Pseudomonas putida F1]		x		
82717337	>gi|82717337|gb|EAP52389.1| enoly-coenzyme A hydratase/isomerase family protein [Pseudomonas putida F1]		x		
17546017	>gi|17546017|ref|NP_519419.1| enoyl-CoA hydratase [Ralstonia solanacearum GMI1000]		x		
29542410	>gi|29542410|gb|AAO91347.1| enoyl-CoA hydratase/isomerase family protein [Coxiella burnetii RSA 493]		x		
29655141	>gi|29655141|ref|NP_820833.1| enoyl-CoA hydratase/isomerase family protein [Coxiella burnetii RSA 493]		x		
39650366	>gi|39650366|emb|CAE28888.1| putative enoyl-CoA hydratase/isomerase [Rhodopseudomonas palustris CGA009]		x		
39936510	>gi|39936510|ref|NP_948786.1| enoyl-CoA hydratase [Rhodopseudomonas palustris CGA009]		x		
46201010	>gi|46201010|ref|ZP_00207929.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Magnetospirillum magnetotacticum MS-1]		x		
83593169	>gi|83593169|ref|YP_426921.1| Enoyl-CoA hydratase/isomerase [Rhodospirillum rubrum ATCC 11170]		x		
83576083	>gi|83576083|gb|ABC22634.1| Enoyl-CoA hydratase/isomerase [Rhodospirillum rubrum ATCC 11170]		x		
46202084	>gi|46202084|ref|ZP_00208375.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Magnetospirillum magnetotacticum MS-1]		x		
17431118	>gi|17431118|emb|CAD17798.1| PUTATIVE ENOYL-COENZYME A HYDRATASE PROTEIN [Ralstonia solanacearum]		x		
17548868	>gi|17548868|ref|NP_522208.1| PUTATIVE ENOYL-COENZYME A HYDRATASE PROTEIN [Ralstonia solanacearum GMI1000]		x		
24373249	>gi|24373249|ref|NP_717292.1| enoyl-CoA hydratase/isomerase family protein [Shewanella oneidensis MR-1]		x		

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>24347483</td><td>>gi|24347483|gb|AAN54736.1| enoyl-CoA hydratase/isomerase family protein [Shewanella oneidensis MR-1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>82947523</td><td>>gi|82947523|dbj|BAE52387.1| Enoyl-CoA hydratase/carnithine racemase [Magnetospirillum magneticum AMB-1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>83312682</td><td>>gi|83312682|ref|YP_422946.1| Enoyl-CoA hydratase/carnithine racemase [Magnetospirillum magneticum AMB-1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>16944696</td><td>>gi|16944696|emb|CAC28821.2| related to enoyl-CoA-hydratase [Neurospora crassa]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>85101280</td><td>>gi|85101280|ref|XP_961123.1| related to enoyl-CoA-hydratase [MIPS] [Neurospora crassa N150]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>32404930</td><td>>gi|32404930|ref|XP_323078.1| related to enoyl-CoA-hydratase [MIPS] [Neurospora crassa]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>28922662</td><td>>gi|28922662|gb|EAA31887.1| related to enoyl-CoA-hydratase [MIPS] [Neurospora crassa]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>82496410</td><td>>gi|82496410|ref|ZP_00881978.1| enoyl-CoA hydratase/isomerase family protein [Shewanella sp. MR-4]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>82405559</td><td>>gi|82405559|gb|EAP46231.1| enoyl-CoA hydratase/isomerase family protein [Shewanella sp. MR-4]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>78685608</td><td>>gi|78685608|ref|ZP_00850385.1| enoyl-CoA hydratase/isomerase family protein [Shewanella sp. ANA-3]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>78506726</td><td>>gi|78506726|gb|EAP20242.1| enoyl-CoA hydratase/isomerase family protein [Shewanella sp. ANA-3]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>67153773</td><td>>gi|67153773|ref|ZP_00415518.1| Enoyl-CoA hydratase/isomerase [Azotobacter vinelandii AvOP]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>67087906</td><td>>gi|67087906|gb|EAM07372.1| Enoyl-CoA hydratase/isomerase [Azotobacter vinelandii AvOP]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>48788634</td><td>>gi|48788634|ref|ZP_00284613.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia fungorum LB400]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>78691657</td><td>>gi|78691657|ref|ZP_00856261.1| enoyl-CoA hydratase/isomerase family protein [Shewanella sp. MR-7]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>78508940</td><td>>gi|78508940|gb|EAP22358.1| enoyl-CoA hydratase/isomerase family protein [Shewanella sp. MR-7]</td><td></td><td>x</td><td></td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
77738926	>gi|77738926|ref|ZP_00807419.1| Enoyl-CoA hydratase/isomerase [Rhodopseudomonas palustris BisA53]		x		
77701394	>gi|77701394|gb|EAO92531.1| Enoyl-CoA hydratase/isomerase [Rhodopseudomonas palustris BisA53]		x		
74484320	>gi|74484320|gb|ABA10805.1| enoyl CoA hydratase [Pseudomonas putida]		x		
82735325	>gi|82735325|ref|ZP_00898188.1| enoly-coenzyme A hydratase/isomerase family protein [Pseudomonas putida F1]		x		
82718000	>gi|82718000|gb|EAP53051.1| enoly-coenzyme A hydratase/isomerase family protein [Pseudomonas putida F1]		x		
2228238	>gi|2228238|gb|AAB62303.1| enoly-coenzyme A hydratase [Pseudomonas putida]		x		
11138233	>gi|11138233|dbj|BAB17782.1| enoyl-CoA hydratase [Pseudomonas putida]		x		
15141332	>gi|15141332|emb|CAC49844.1| putative enoyl-CoA hydratase protein [Sinorhizobium meliloti 1021]		x		
16265192	>gi|16265192|ref|NP_437984.1| enoyl-CoA hydratase [Sinorhizobium meliloti 1021]		x		
77688208	>gi|77688208|ref|ZP_00803393.1| Enoyl-CoA hydratase/isomerase [Rhodopseudomonas palustris BisB5]		x		
77655483	>gi|77655483|gb|EAO87124.1| Enoyl-CoA hydratase/isomerase [Rhodopseudomonas palustris BisB5]		x		
17983175	>gi|17983175|gb|AAL52377.1| ENOYL-COA HYDRATASE [Brucella melitensis 16M]		x		
17987479	>gi|17987479|ref|NP_540113.1| enoyl-CoA hydratase [Brucella melitensis 16M]		x		
23347564	>gi|23347564|gb|AAN29687.1| enoyl-CoA hydratase/isomerase family protein [Brucella suis 1330]		x		
23501645	>gi|23501645|ref|NP_697772.1| enoyl-CoA hydratase [Brucella suis 1330]		x		
23098272	>gi|23098272|ref|NP_691738.1| enoyl-CoA hydratase [Oceanobacillus iheyensis HTE831]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
69926900	>gi|69926900|ref|ZP_00624371.1| Enoyl-CoA hydratase/isomerase [Nitrobacter hamburgensis X14]		x		
69144563	>gi|69144563|gb|EAN63050.1| Enoyl-CoA hydratase/isomerase [Nitrobacter hamburgensis X14]		x		
68542471	>gi|68542471|ref|ZP_00582201.1| Enoyl-CoA hydratase/isomerase [Shewanella baltica OS155]		x		
68519854	>gi|68519854|gb|EAN43377.1| Enoyl-CoA hydratase/isomerase [Shewanella baltica OS155]		x		
27352217	>gi|27352217|dbj|BAC49221.1| enoyl-CoA hydratase [Bradyrhizobium japonicum USDA 110]		x		
27379067	>gi|27379067|ref|NP_770596.1| enoyl-CoA hydratase [Bradyrhizobium japonicum USDA 110]		x		
82699640	>gi|82699640|ref|YP_414214.1| Enoyl-CoA hydratase/isomerase [Brucella melitensis biovar Abortus 2308]		x		
62289711	>gi|62289711|ref|YP_221504.1| enoyl-CoA hydratase [Brucella abortus biovar 1 str. 9-941]		x		
62195843	>gi|62195843|gb|AAX74143.1| enoyl-CoA hydratase/isomerase family protein [Brucella abortus biovar 1 str. 9-941]		x		
82615741	>gi|82615741|emb|CAJ10737.1| Enoyl-CoA hydratase/isomerase [Brucella melitensis biovar Abortus]		x		
78035352	>gi|78035352|emb|CAJ22997.1| Enoyl-CoA hydratase/isomerase family protein [Xanthomonas campestris pv. vesicatoria str. 85-10]		x		
78046922	>gi|78046922|ref|YP_363097.1| Enoyl-CoA hydratase/isomerase family protein [Xanthomonas campestris pv. vesicatoria str. 85-10]		x		
86572270	>gi|86572270|gb|ABD06827.1| Enoyl-CoA hydratase/isomerase [Rhodopseudomonas palustris HaA2]		x		
30020424	>gi|30020424|ref|NP_832055.1| enoyl-CoA hydratase [Bacillus cereus ATCC 14579]		x		
77812935	>gi|77812935|ref|ZP_00812218.1| Enoyl-CoA hydratase/isomerase [Shewanella putrefaciens CN-32]		x		
77812168	>gi|77812168|gb|EAO96536.1| Enoyl-CoA hydratase/isomerase [Shewanella putrefaciens CN-32]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
21107473	>gi|21107473|gb|AAM36186.1| enoyl-CoA hydratase [Xanthomonas axonopodis pv. citri str. 306]		x		
21242068	>gi|21242068|ref|NP_641650.1| enoyl-CoA hydratase [Xanthomonas axonopodis pv. citri str. 306]		x		
48785709	>gi|48785709|ref|ZP_00281918.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia fungorum LB400]		x		
42781447	>gi|42781447|ref|NP_978694.1| enoyl-CoA hydratase [Bacillus cereus ATCC 10987]		x		
42737369	>gi|42737369|gb|AAS41302.1| enoyl-CoA hydratase/isomerase family protein [Bacillus cereus ATCC 10987]		x		
52143120	>gi|52143120|ref|YP_083709.1| enoyl-CoA hydratase [Bacillus cereus E33L]		x		
78708994	>gi|78708994|gb|ABB47969.1| enoyl-CoA-hydratase, putative [Oryza sativa (japonica cultivar-group)]		x		
37536724	>gi|37536724|ref|NP_922664.1| putative enoyl-CoA-hydratase [Oryza sativa (japonica cultivar-group)]		x		
10140648	>gi|10140648|gb|AAG13484.1| putative enoyl-CoA-hydratase [Oryza sativa (japonica cultivar-group)]		x		
49477633	>gi|49477633|ref|YP_036459.1| enoyl-CoA hydratase [Bacillus thuringiensis serovar konkukian str. 97-27]		x		
13422701	>gi|13422701|gb|AAK23333.1| enoyl-CoA hydratase/isomerase family protein [Caulobacter crescentus CB15]		x		
16125601	>gi|16125601|ref|NP_420165.1| enoyl-CoA hydratase/isomerase family protein [Caulobacter crescentus CB15]		x		
48784091	>gi|48784091|ref|ZP_00280472.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia fungorum LB400]		x		
47502799	>gi|47502799|gb|AAT31475.1| enoyl-CoA hydratase/isomerase family protein [Bacillus anthracis str. 'Ames Ancestor']		x		
49179131	>gi|49179131|gb|AAT54507.1| enoyl-CoA hydratase/isomerase family protein [Bacillus anthracis str. Sterne]		x		
49185204	>gi|49185204|ref|YP_028456.1| enoyl-CoA hydratase [Bacillus anthracis str. Sterne]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
30256992	>gi|30256992|gb|AAP26224.1| enoyl-CoA hydratase/isomerase family protein [Bacillus anthracis str. Ames]		x		
47527651	>gi|47527651|ref|YP_019000.1| enoyl-CoA hydratase [Bacillus anthracis str. 'Ames Ancestor']		x		
30262361	>gi|30262361|ref|NP_844738.1| enoyl-CoA hydratase [Bacillus anthracis str. Ames]		x		
76785131	>gi|76785131|ref|ZP_00772304.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Mycobacterium tuberculosis F11]		x		
13880681	>gi|13880681|gb|AAK45357.1| enoyl-CoA hydratase/isomerase family protein [Mycobacterium tuberculosis CDC1551]		x		
2896708	>gi|2896708|emb|CAA17187.1| POSSIBLE ENOYL-CoA HYDRATASE ECHA9 (ENOYL HYDRASE) (UNSATURATED ACYL-CoA HYDRATASE) (CROTONASE) [Mycobacterium tuberculosis H37Rv]		x		
31617850	>gi|31617850|emb|CAD93960.1| POSSIBLE ENOYL-COA HYDRATASE ECHA9 (ENOYL HYDRASE) (UNSATURATED ACYL-COA HYDRATASE) (CROTONASE) [Mycobacterium bovis AF2122/97]		x		
31792262	>gi|31792262|ref|NP_854755.1| enoyl-CoA hydratase [Mycobacterium bovis AF2122/97]		x		
15608211	>gi|15608211|ref|NP_215587.1| enoyl-CoA hydratase [Mycobacterium tuberculosis H37Rv]		x		
15840506	>gi|15840506|ref|NP_335543.1| enoyl-CoA hydratase [Mycobacterium tuberculosis CDC1551]		x		
81255001	>gi|81255001|ref|ZP_00879494.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Mycobacterium tuberculosis C]		x		
82742573	>gi|82742573|ref|ZP_00905261.1| enoyl-CoA hydratase/isomerase family protein [Shewanella sp. W3-18-1]		x		
82720083	>gi|82720083|gb|EAP54961.1| enoyl-CoA hydratase/isomerase family protein [Shewanella sp. W3-18-1]		x		
66574616	>gi|66574616|gb|AAY50026.1| enoyl-CoA hydratase [Xanthomonas campestris pv. campestris str. 8004]		x		
66769284	>gi|66769284|ref|YP_244046.1| enoyl-CoA hydratase [Xanthomonas campestris pv. campestris str. 8004]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
13476928	>gi|13476928|ref|NP_108497.1| enoyl-CoA hydratase [Mesorhizobium loti MAFF303099]		x		
47565713	>gi|47565713|ref|ZP_00236753.1| enoly-CoA hydratase/isomerase family protein [Bacillus cereus G9241]		x		
47557349	>gi|47557349|gb|EAL15677.1| enoly-CoA hydratase/isomerase family protein [Bacillus cereus G9241]		x		
21281145	>gi|21281145|gb|AAM45067.1| putative enoyl-CoA hydratase [Arabidopsis thaliana]		x		
19424019	>gi|19424019|gb|AAL87270.1| putative enoyl-CoA hydratase [Arabidopsis thaliana]		x		
65319652	>gi|65319652|ref|ZP_00392611.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Bacillus anthracis str. A2012]		x		
58581468	>gi|58581468|ref|YP_200484.1| enoyl-CoA hydratase [Xanthomonas oryzae pv. oryzae KACC10331]		x		
58426062	>gi|58426062|gb|AAW75099.1| enoyl-CoA hydratase [Xanthomonas oryzae pv. oryzae KACC10331]		x		
84367338	>gi|84367338|dbj|BAE68496.1| enoyl-CoA hydratase [Xanthomonas oryzae pv. oryzae MAFF 311018]		x		
84623398	>gi|84623398|ref|YP_450770.1| enoyl-CoA hydratase [Xanthomonas oryzae pv. oryzae MAFF 311018]		x		
78492767	>gi|78492767|ref|ZP_00845003.1| Enoyl-CoA hydratase/isomerase [Rhodopseudomonas palustris BisB18]		x		
78390510	>gi|78390510|gb|EAP13294.1| Enoyl-CoA hydratase/isomerase [Rhodopseudomonas palustris BisB18]		x		
79039897	>gi|79039897|ref|ZP_00871603.1| enoyl-CoA hydratase/isomerase family protein [Novosphingobium aromaticivorans DSM 12444]		x		
78775538	>gi|78775538|gb|EAP39193.1| enoyl-CoA hydratase/isomerase family protein [Novosphingobium aromaticivorans DSM 12444]		x		
74018482	>gi|74018482|ref|ZP_00689103.1| Enoyl-CoA hydratase/isomerase [Burkholderia ambifaria AMMD]		x		
72609014	>gi|72609014|gb|EAO44965.1| Enoyl-CoA hydratase/isomerase [Burkholderia ambifaria AMMD]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
74421212	>gi|74421212|gb|ABA05411.1| enoyl-CoA hydratase/isomerase [Nitrobacter winogradskyi Nb-255]		x		
75676342	>gi|75676342|ref|YP_318763.1| enoyl-CoA hydratase [Nitrobacter winogradskyi Nb-255]		x		
83858218	>gi|83858218|ref|ZP_00951740.1| enoyl-CoA hydratase/isomerase family protein [Oceanicaulis alexandrii HTCC2633]		x		
83853041	>gi|83853041|gb|EAP90893.1| enoyl-CoA hydratase/isomerase family protein [Oceanicaulis alexandrii HTCC2633]		x		
21112312	>gi|21112312|gb|AAM40561.1| enoyl-CoA hydratase [Xanthomonas campestris pv. campestris str. ATCC 33913]		x		
21230720	>gi|21230720|ref|NP_636637.1| enoyl-CoA hydratase [Xanthomonas campestris pv. campestris str. ATCC 33913]		x		
41407116	>gi|41407116|ref|NP_959952.1| enoyl-CoA hydratase [Mycobacterium avium subsp. paratuberculosis K-10]		x		
85715651	>gi|85715651|ref|ZP_01046631.1| enoyl-CoA hydratase [Nitrobacter sp. Nb-311A]		x		
85697590	>gi|85697590|gb|EAQ35467.1| enoyl-CoA hydratase [Nitrobacter sp. Nb-311A]		x		
84787916	>gi|84787916|gb|ABC64098.1| enoyl-CoA hydratase/isomerase family protein [Erythrobacter litoralis HTCC2594]		x		
85374833	>gi|85374833|ref|YP_458895.1| enoyl-CoA hydratase/isomerase family protein [Erythrobacter litoralis HTCC2594]		x		
82946501	>gi|82946501|dbj|BAE51365.1| Enoyl-CoA hydratase/carnithine racemase [Magnetospirillum magneticum AMB-1]		x		
83311660	>gi|83311660|ref|YP_421924.1| Enoyl-CoA hydratase/carnithine racemase [Magnetospirillum magneticum AMB-1]		x		
13093984	>gi|13093984|emb|CAC31917.1| putative enoyl-CoA hydratase/isomerase [Mycobacterium leprae]		x		
15828291	>gi|15828291|ref|NP_302554.1| enoyl-CoA hydratase [Mycobacterium leprae TN]		x		
77969454	>gi|77969454|gb|ABB10833.1| Enoyl-CoA hydratase/isomerase [Burkholderia sp. 383]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
78061569	>gi|78061569|ref|YP_371477.1| Enoyl-CoA hydratase/isomerase [Burkholderia sp. 383]		x		
72119120	>gi|72119120|gb|AAZ61383.1| Enoyl-CoA hydratase/isomerase [Ralstonia eutropha JMP134]		x		
73541707	>gi|73541707|ref|YP_296227.1| enoyl-CoA hydratase [Ralstonia eutropha JMP134]		x		
78695778	>gi|78695778|ref|ZP_00860289.1| enoyl-CoA hydratase [Bradyrhizobium sp. BTAi1]		x		
78516341	>gi|78516341|gb|EAP29641.1| enoyl-CoA hydratase [Bradyrhizobium sp. BTAi1]		x		
84352615	>gi|84352615|ref|ZP_00977568.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia cenocepacia PC184]		x		
67543192	>gi|67543192|ref|ZP_00421125.1| Enoyl-CoA hydratase/isomerase [Burkholderia vietnamiensis G4]		x		
67535371	>gi|67535371|gb|EAM32103.1| Enoyl-CoA hydratase/isomerase [Burkholderia vietnamiensis G4]		x		
67760200	>gi|67760200|ref|ZP_00498924.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia pseudomallei S13]		x		
67755620	>gi|67755620|ref|ZP_00494513.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia pseudomallei Pasteur]		x		
67736263	>gi|67736263|ref|ZP_00487157.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia pseudomallei 668]		x		
67672806	>gi|67672806|ref|ZP_00469579.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia pseudomallei 1655]		x		
67684559	>gi|67684559|ref|ZP_00478505.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia pseudomallei 1710a]		x		
76582384	>gi|76582384|gb|ABA51858.1| enoyl-CoA hydratase/isomerase family [Burkholderia pseudomallei 1710b]		x		
52212072	>gi|52212072|emb|CAH38079.1| enoyl-CoA hydratase/isomerase family [Burkholderia pseudomallei K96243]		x		
76817911	>gi|76817911|ref|YP_337334.1| enoyl-CoA hydratase/isomerase family [Burkholderia pseudomallei 1710b]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
53721658	>gi|53721658|ref|YP_110643.1| enoyl-CoA hydratase/isomerase family [Burkholderia pseudomallei K96243]		x		
83678446	>gi|83678446|ref|ZP_00940173.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia pseudomallei 406e]		x		
82535504	>gi|82535504|ref|ZP_00894520.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia pseudomallei 1106b]		x		
82530725	>gi|82530725|ref|ZP_00889952.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia pseudomallei 1106a]		x		
82739983	>gi|82739983|ref|ZP_00902757.1| enoyl-CoA hydratase/isomerase family protein [Pseudomonas putida F1]		x		
82712945	>gi|82712945|gb|EAP48085.1| enoyl-CoA hydratase/isomerase family protein [Pseudomonas putida F1]		x		
86356224	>gi|86356224|ref|YP_468116.1| probable enoyl-CoA hydratase protein [Rhizobium etli CFN 42]		x		
86280326	>gi|86280326|gb|ABC89389.1| probable enoyl-CoA hydratase protein [Rhizobium etli CFN 42]		x		
68523260	>gi|68523260|gb|EAN46393.1| Enoyl-CoA hydratase/isomerase [Sphingopyxis alaskensis RB2256]		x		
68539419	>gi|68539419|ref|ZP_00579191.1| Enoyl-CoA hydratase/isomerase [Sphingopyxis alaskensis RB2256]		x		
84322815	>gi|84322815|ref|ZP_00970896.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Pseudomonas aeruginosa 2192]		x		
53727306	>gi|53727306|ref|ZP_00138342.2| COG1024: Enoyl-CoA hydratase/carnithine racemase [Pseudomonas aeruginosa UCBPP-PA14]		x		
9946630	>gi|9946630|gb|AAG04133.1| probable enoyl-CoA hydratase/isomerase [Pseudomonas aeruginosa PAO1]		x		
15595941	>gi|15595941|ref|NP_249435.1| probable enoyl-CoA hydratase/isomerase [Pseudomonas aeruginosa PAO1]		x		
84316787	>gi|84316787|ref|ZP_00965252.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Pseudomonas aeruginosa C3719]		x		
26988145	>gi|26988145|ref|NP_743570.1| enoyl-CoA hydratase/isomerase family protein [Pseudomonas putida KT2440]		x		

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>24982877</td><td>>gi|24982877|gb|AAN67034.1| enoyl-CoA hydratase/isomerase family protein [Pseudomonas putida KT2440]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>27358491</td><td>>gi|27358491|gb|AAO07441.1| Enoyl-CoA hydratase/carnithine racemase [Vibrio vulnificus CMCP6]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>27366924</td><td>>gi|27366924|ref|NP_762451.1| Enoyl-CoA hydratase/carnithine racemase [Vibrio vulnificus CMCP6]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>67668205</td><td>>gi|67668205|ref|ZP_00465390.1| Enoyl-CoA hydratase/isomerase [Burkholderia cenocepacia HI2424]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>67660620</td><td>>gi|67660620|ref|ZP_00457962.1| Enoyl-CoA hydratase/isomerase [Burkholderia cenocepacia AU 1054]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>67098230</td><td>>gi|67098230|gb|EAM15455.1| Enoyl-CoA hydratase/isomerase [Burkholderia cenocepacia HI2424]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>67091760</td><td>>gi|67091760|gb|EAM09327.1| Enoyl-CoA hydratase/isomerase [Burkholderia cenocepacia AU 1054]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>83721249</td><td>>gi|83721249|ref|YP_443024.1| enoyl-CoA hydratase/isomerase family protein [Burkholderia thailandensis E264]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>83655074</td><td>>gi|83655074|gb|ABC39137.1| enoyl-CoA hydratase/isomerase family protein [Burkholderia thailandensis E264]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>83717427</td><td>>gi|83717427|ref|YP_439992.1| enoyl-CoA hydratase/isomerase family [Burkholderia thailandensis E264]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>83651252</td><td>>gi|83651252|gb|ABC35316.1| enoyl-CoA hydratase/isomerase family [Burkholderia thailandensis E264]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>84359397</td><td>>gi|84359397|ref|ZP_00984144.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia dolosa AUO158]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>37201242</td><td>>gi|37201242|dbj|BAC97065.1| putative enoyl-CoA hydratase/isomerase [Vibrio vulnificus YJ016]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>37676699</td><td>>gi|37676699|ref|NP_937095.1| putative enoyl-CoA hydratase/isomerase [Vibrio vulnificus YJ016]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>85709281</td><td>>gi|85709281|ref|ZP_01040346.1| enoyl-CoA hydratase/isomerase family protein [Erythrobacter sp. NAP1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>85687991</td><td>>gi|85687991|gb|EAQ27995.1| enoyl-CoA hydratase/isomerase family protein [Erythrobacter sp. NAP1]</td><td></td><td>x</td><td></td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
28809420	>gi|28809420|dbj|BAC62462.1| putative enoyl-CoA hydratase/isomerase [Vibrio parahaemolyticus RIMD 2210633]		x		
28900974	>gi|28900974|ref|NP_800629.1| putative enoyl-CoA hydratase/isomerase [Vibrio parahaemolyticus RIMD 2210633]		x		
67669989	>gi|67669989|ref|ZP_00466805.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia pseudomallei 1655]		x		
83677743	>gi|83677743|ref|ZP_00939484.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia pseudomallei 406e]		x		
82534320	>gi|82534320|ref|ZP_00893360.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia pseudomallei 1106b]		x		
82529056	>gi|82529056|ref|ZP_00888312.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia pseudomallei 1106a]		x		
67753853	>gi|67753853|ref|ZP_00492775.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia pseudomallei Pasteur]		x		
67681882	>gi|67681882|ref|ZP_00476183.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia pseudomallei 1710a]		x		
67647999	>gi|67647999|ref|ZP_00446234.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia mallei NCTC 10247]		x		
67636586	>gi|67636586|ref|ZP_00435531.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia mallei 10399]		x		
52426873	>gi|52426873|gb|AAU47466.1| enoyl-CoA hydratase/isomerase family protein [Burkholderia mallei ATCC 23344]		x		
76579559	>gi|76579559|gb|ABA49034.1| enoyl-CoA hydratase/isomerase family protein [Burkholderia pseudomallei 1710b]		x		
85064890	>gi|85064890|ref|ZP_01025743.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia mallei 10229]		x		
76810106	>gi|76810106|ref|YP_333381.1| enoyl-CoA hydratase [Burkholderia pseudomallei 1710b]		x		
84522689	>gi|84522689|ref|ZP_01009825.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia mallei SAVP1]		x		
83625971	>gi|83625971|ref|ZP_00936198.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia mallei JHU]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
83618593	>gi|83618593|ref|ZP_00929049.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia mallei FMH]		x		
28808859	>gi|28808859|dbj|BAC61967.1| putative enoyl-CoA hydratase/isomerase [Vibrio parahaemolyticus RIMD 2210633]		x		
28900479	>gi|28900479|ref|NP_800134.1| putative enoyl-CoA hydratase/isomerase [Vibrio parahaemolyticus RIMD 2210633]		x		
54014514	>gi|54014514|dbj|BAD55884.1| putative enoyl-CoA hydratase/isomerase family protein [Nocardia farcinica IFM 10152]		x		
54023006	>gi|54023006|ref|YP_117248.1| enoyl-CoA hydratase [Nocardia farcinica IFM 10152]		x		
72121428	>gi|72121428|gb|AAZ63614.1| Enoyl-CoA hydratase/isomerase [Ralstonia eutropha JMP134]		x		
73538091	>gi|73538091|ref|YP_298458.1| Enoyl-CoA hydratase/isomerase [Ralstonia eutropha JMP134]		x		
48785252	>gi|48785252|ref|ZP_00281502.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia fungorum LB400]		x		
67737730	>gi|67737730|ref|ZP_00488462.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia pseudomallei 668]		x		
53719473	>gi|53719473|ref|YP_108459.1| enoyl-CoA hydratase [Burkholderia pseudomallei K96243]		x		
67759433	>gi|67759433|ref|ZP_00498170.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia pseudomallei S13]		x		
77953636	>gi|77953636|ref|ZP_00818042.1| enoyl-CoA hydratase/isomerase family protein [Marinobacter aquaeolei VT8]		x		
77867406	>gi|77867406|gb|EAO98683.1| enoyl-CoA hydratase/isomerase family protein [Marinobacter aquaeolei VT8]		x		
75857232	>gi|75857232|ref|ZP_00764849.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Vibrio sp. Ex25]		x		
84361651	>gi|84361651|ref|ZP_00986306.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia dolosa AUO158]		x		
68233952	>gi|68233952|ref|ZP_00573055.1| Enoyl-CoA hydratase/isomerase [Frankia sp. EAN1pec]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
68198429	>gi|68198429|gb|EAN12698.1| Enoyl-CoA hydratase/isomerase [Frankia sp. EAN1pec]		x		
67906902	>gi|67906902|ref|ZP_00505307.1| Enoyl-CoA hydratase/isomerase [Polaromonas sp. JS666]		x		
67780552	>gi|67780552|gb|EAM40167.1| Enoyl-CoA hydratase/isomerase [Polaromonas sp. JS666]		x		
52003684	>gi|52003684|gb|AAU23626.1| Enoyl-CoA hydratase/isomerase [Bacillus licheniformis ATCC 14580]		x		
52080473	>gi|52080473|ref|YP_079264.1| enoyl-CoA hydratase [Bacillus licheniformis ATCC 14580]		x		
52785855	>gi|52785855|ref|YP_091684.1| enoyl-CoA hydratase [Bacillus licheniformis ATCC 14580]		x		
77966917	>gi|77966917|gb|ABB08297.1| Enoyl-CoA hydratase/isomerase [Burkholderia sp. 383]		x		
78066172	>gi|78066172|ref|YP_368941.1| enoyl-CoA hydratase [Burkholderia sp. 383]		x		
66963447	>gi|66963447|ref|ZP_00411019.1| Enoyl-CoA hydratase/isomerase [Arthrobacter sp. FB24]		x		
66871107	>gi|66871107|gb|EAL98471.1| Enoyl-CoA hydratase/isomerase [Arthrobacter sp. FB24]		x		
67530724	>gi|67530724|gb|EAM27559.1| Enoyl-CoA hydratase/isomerase [Burkholderia vietnamiensis G4]		x		
67548005	>gi|67548005|ref|ZP_00425901.1| Enoyl-CoA hydratase/isomerase [Burkholderia vietnamiensis G4]		x		
85712006	>gi|85712006|ref|ZP_01043060.1| Enoyl-CoA hydratase/isomerase family protein [Idiomarina baltica OS145]		x		
85694192	>gi|85694192|gb|EAQ32136.1| Enoyl-CoA hydratase/isomerase family protein [Idiomarina baltica OS145]		x		
68191586	>gi|68191586|gb|EAN06242.1| Enoyl-CoA hydratase/isomerase [Mesorhizobium sp. BNC1]		x		
69277709	>gi|69277709|ref|ZP_00613044.1| Enoyl-CoA hydratase/isomerase [Mesorhizobium sp. BNC1]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
68343112	>gi|68343112|gb|AAY90718.1| enoyl-CoA hydratase/isomerase family protein [Pseudomonas fluorescens Pf-5]		x		
70728813	>gi|70728813|ref|YP_258562.1| enoyl-CoA hydratase/isomerase family protein [Pseudomonas fluorescens Pf-5]		x		
84357656	>gi|84357656|ref|ZP_00982469.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Burkholderia cenocepacia PC184]		x		
75856921	>gi|75856921|ref|ZP_00764542.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Vibrio sp. Ex25]		x		
77381578	>gi|77381578|gb|ABA73091.1| Enoyl-CoA hydratase/isomerase [Pseudomonas fluorescens PfO-1]		x		
77457575	>gi|77457575|ref|YP_347080.1| Enoyl-CoA hydratase/isomerase [Pseudomonas fluorescens PfO-1]		x		
67664923	>gi|67664923|ref|ZP_00462192.1| Enoyl-CoA hydratase/isomerase [Burkholderia cenocepacia HI2424]		x		
67658424	>gi|67658424|ref|ZP_00455796.1| Enoyl-CoA hydratase/isomerase [Burkholderia cenocepacia AU 1054]		x		
67101448	>gi|67101448|gb|EAM18589.1| Enoyl-CoA hydratase/isomerase [Burkholderia cenocepacia HI2424]		x		
67093996	>gi|67093996|gb|EAM11533.1| Enoyl-CoA hydratase/isomerase [Burkholderia cenocepacia AU 1054]		x		
56178986	>gi|56178986|gb|AAV81708.1| Enoyl-CoA hydratase/isomerase family protein [Idiomarina loihiensis L2TR]		x		
56459976	>gi|56459976|ref|YP_155257.1| Enoyl-CoA hydratase/isomerase family protein [Idiomarina loihiensis L2TR]		x		
74016895	>gi|74016895|ref|ZP_00687520.1| Enoyl-CoA hydratase/isomerase [Burkholderia ambifaria AMMD]		x		
72610366	>gi|72610366|gb|EAO46313.1| Enoyl-CoA hydratase/isomerase [Burkholderia ambifaria AMMD]		x		
6320241	>gi|6320241|ref|NP_010321.1| Protein of unconfirmed function, plays an indirect role in endocytic membrane trafficking, member of a family of enoyl-CoA hydratase/isomerases; Ehd3p [Saccharomyces cerevisiae]		x		
78368178	>gi|78368178|ref|ZP_00838423.1| Enoyl-CoA hydratase/isomerase [Shewanella sp. PV-4]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
78359757	>gi|78359757|gb|EAP01609.1| Enoyl-CoA hydratase/isomerase [Shewanella sp. PV-4]		x		
83374669	>gi|83374669|ref|ZP_00919439.1| enoyl-CoA hydratase/isomerase family protein [Rhodobacter sphaeroides ATCC 17029]		x		
83364040	>gi|83364040|gb|EAP67533.1| enoyl-CoA hydratase/isomerase family protein [Rhodobacter sphaeroides ATCC 17029]		x		
77388142	>gi|77388142|gb|ABA79327.1| enoyl-CoA hydratase [Rhodobacter sphaeroides 2.4.1]		x		
77463724	>gi|77463724|ref|YP_353228.1| enoyl-CoA hydratase [Rhodobacter sphaeroides 2.4.1]		x		
68547274	>gi|68547274|ref|ZP_00586813.1| Enoyl-CoA hydratase/isomerase [Shewanella amazonensis SB2B]		x		
68515049	>gi|68515049|gb|EAN38771.1| Enoyl-CoA hydratase/isomerase [Shewanella amazonensis SB2B]		x		
83368357	>gi|83368357|ref|ZP_00913221.1| enoyl-CoA hydratase/isomerase family protein [Rhodobacter sphaeroides ATCC 17025]		x		
83362070	>gi|83362070|gb|EAP65582.1| enoyl-CoA hydratase/isomerase family protein [Rhodobacter sphaeroides ATCC 17025]		x		
85703747	>gi|85703747|ref|ZP_01034851.1| enoyl-CoA hydratase/isomerase family protein [Roseovarius sp. 217]		x		
85672675	>gi|85672675|gb|EAQ27532.1| enoyl-CoA hydratase/isomerase family protein [Roseovarius sp. 217]		x		
83643530	>gi|83643530|ref|YP_431965.1| Enoyl-CoA hydratase/carnithine racemase [Hahella chejuensis KCTC 2396]		x		
83631573	>gi|83631573|gb|ABC27540.1| Enoyl-CoA hydratase/carnithine racemase [Hahella chejuensis KCTC 2396]		x		
41325144	>gi|41325144|emb|CAF19625.1| Enoyl-CoA hydratase/carnithine racemase [Corynebacterium glutamicum ATCC 13032]		x		
21323685	>gi|21323685|dbj|BAB98312.1| Enoyl-CoA hydratase/carnithine racemase [Corynebacterium glutamicum ATCC 13032]		x		
62389809	>gi|62389809|ref|YP_225211.1| enoyl-CoA hydratase [Corynebacterium glutamicum ATCC 13032]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
19552145	>gi|19552145|ref|NP_600147.1| enoyl-CoA hydratase [Corynebacterium glutamicum ATCC 13032]		x		
7270084	>gi|7270084|emb|CAB79899.1| enoyl-CoA hydratase-like protein [Arabidopsis thaliana]		x		
4584520	>gi|4584520|emb|CAB40751.1| enoyl-CoA hydratase-like protein [Arabidopsis thaliana]		x		
62423100	>gi|62423100|ref|ZP_00378271.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Brevibacterium linens BL2]		x		
67906936	>gi|67906936|ref|ZP_00505341.1| Enoyl-CoA hydratase/isomerase [Polaromonas sp. JS666]		x		
67780586	>gi|67780586|gb|EAM40201.1| Enoyl-CoA hydratase/isomerase [Polaromonas sp. JS666]		x		
23492819	>gi|23492819|dbj|BAC17791.1| putative enoyl-CoA hydratase [Corynebacterium efficiens YS-314]		x		
25027537	>gi|25027537|ref|NP_737591.1| enoyl-CoA hydratase [Corynebacterium efficiens YS-314]		x		
6014701	>gi|6014701|gb|AAF01467.1| enoyl-CoA-hydratase [Avicennia marina]		x		
69949474	>gi|69949474|ref|ZP_00637471.1| Enoyl-CoA hydratase/isomerase [Shewanella frigidimarina NCIMB 400]		x		
69166698	>gi|69166698|gb|EAN75657.1| Enoyl-CoA hydratase/isomerase [Shewanella frigidimarina NCIMB 400]		x		
33576045	>gi|33576045|emb|CAE33124.1| enoly-CoA hydratase [Bordetella bronchiseptica RB50]		x		
33572190	>gi|33572190|emb|CAE41736.1| enoly-CoA hydratase [Bordetella pertussis Tohama I]		x		
33592544	>gi|33592544|ref|NP_880188.1| enoly-CoA hydratase [Bordetella pertussis Tohama I]		x		
33601608	>gi|33601608|ref|NP_889168.1| enoly-CoA hydratase [Bordetella bronchiseptica RB50]		x		
33573200	>gi|33573200|emb|CAE36855.1| enoly-CoA hydratase [Bordetella parapertussis]		x		
33596197	>gi|33596197|ref|NP_883840.1| enoly-CoA hydratase [Bordetella parapertussis 12822]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
69157802	>gi|69157802|gb|EAN70011.1| Enoyl-CoA hydratase/isomerase [Shewanella denitrificans OS217]		x		
69944036	>gi|69944036|ref|ZP_00635507.1| Enoyl-CoA hydratase/isomerase [Shewanella denitrificans OS-217]		x		
83952652	>gi|83952652|ref|ZP_00961382.1| enoyl-CoA hydratase/isomerase family protein [Roseovarius nubinhibens ISM]		x		
83835787	>gi|83835787|gb|EAP75086.1| enoyl-CoA hydratase/isomerase family protein [Roseovarius nubinhibens ISM]		x		
57899600	>gi|57899600|dbj|BAD87179.1| putative enoyl-CoA-hydratase [Oryza sativa (japonica cultivar-group)]		x		
57899161	>gi|57899161|dbj|BAD87104.1| putative enoyl-CoA-hydratase [Oryza sativa (japonica cultivar-group)]		x		
67676057	>gi|67676057|ref|ZP_00472809.1| Enoyl-CoA hydratase/isomerase [Chromohalobacter salexigens DSM 3043]		x		
67519819	>gi|67519819|gb|EAM23767.1| Enoyl-CoA hydratase/isomerase [Chromohalobacter salexigens DSM 3043]		x		
34497537	>gi|34497537|ref|NP_901752.1| enoyl-CoA hydratase [Chromobacterium violaceum ATCC 12472]		x		
34331002	>gi|34331002|gb|AAQ59754.2| enoyl-CoA hydratase [Chromobacterium violaceum ATCC 12472]		x		
46916211	>gi|46916211|emb|CAG22980.1| putative enoyl-CoA hydratase [Photobacterium profundum SS9]		x		
54302787	>gi|54302787|ref|YP_132780.1| putative enoyl-CoA hydratase [Photobacterium profundum SS9]		x		
76875312	>gi|76875312|emb|CAI86533.1| Enoyl-CoA hydratase/isomerase family protein [Pseudoalteromonas haloplanktis TAC125]		x		
77360401	>gi|77360401|ref|YP_339976.1| Enoyl-CoA hydratase/isomerase protein [Pseudoalteromonas haloplanktis TAC125]		x		
86138797	>gi|86138797|ref|ZP_01057369.1| enoyl-CoA hydratase/isomerase family protein [Roseobacter sp. MED193]		x		
85824444	>gi|85824444|gb|EAQ44647.1| enoyl-CoA hydratase/isomerase family protein [Roseobacter sp. MED193]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
69936390	>gi|69936390|ref|ZP_00631216.1| Enoyl-CoA hydratase/isomerase [Paracoccus denitrificans PD1222]		x		
69152327	>gi|69152327|gb|EAN65494.1| Enoyl-CoA hydratase/isomerase [Paracoccus denitrificans PD1222]		x		
56678812	>gi|56678812|gb|AAV95478.1| enoyl-CoA hydratase/isomerase family protein [Silicibacter pomeroyi DSS-3]		x		
56697075	>gi|56697075|ref|YP_167438.1| enoyl-CoA hydratase/isomerase family protein [Silicibacter pomeroyi DSS-3]		x		
84503053	>gi|84503053|ref|ZP_01001149.1| enoyl-CoA hydratase/isomerase family protein [Oceanicola batsensis HTCC2597]		x		
84388597	>gi|84388597|gb|EAQ01469.1| enoyl-CoA hydratase/isomerase family protein [Oceanicola batsensis HTCC2597]		x		
69297921	>gi|69297921|ref|ZP_00620217.1| Enoyl-CoA hydratase/isomerase [Silicibacter sp. TM1040]		x		
69135458	>gi|69135458|gb|EAN58652.1| Enoyl-CoA hydratase/isomerase [Silicibacter sp. TM1040]		x		
49475616	>gi|49475616|ref|YP_033657.1| enoyl-CoA hydratase [Bartonella henselae str. Houston-1]		x		
83954344	>gi|83954344|ref|ZP_00963064.1| enoyl-CoA hydratase/isomerase family protein [Sulfitobacter sp. NAS-14.1]		x		
83841381	>gi|83841381|gb|EAP80551.1| enoyl-CoA hydratase/isomerase family protein [Sulfitobacter sp. NAS-14.1]		x		
83943209	>gi|83943209|ref|ZP_00955669.1| enoyl-CoA hydratase/isomerase family protein [Sulfitobacter sp. EE-36]		x		
83846217	>gi|83846217|gb|EAP84094.1| enoyl-CoA hydratase/isomerase family protein [Sulfitobacter sp. EE-36]		x		
56909818	>gi|56909818|dbj|BAD64345.1| enoyl-CoA hydratase [Bacillus clausii KSM-K16]		x		
56963575	>gi|56963575|ref|YP_175306.1| enoyl-CoA hydratase [Bacillus clausii KSM-K16]		x		
74024885	>gi|74024885|ref|ZP_00695362.1| Enoyl-CoA hydratase/isomerase [Rhodoferax ferrireducens DSM 15236]		x		

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>72602406</td><td>>gi|72602406|gb|EAO38501.1| Enoyl-CoA hydratase/isomerase [Rhodoferax ferrireducens DSM 15236]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>84684712</td><td>>gi|84684712|ref|ZP_01012612.1| enoyl-CoA hydratase/isomerase family protein [Rhodobacterales bacterium HTCC2654]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>84667047</td><td>>gi|84667047|gb|EAQ13517.1| enoyl-CoA hydratase/isomerase family protein [Rhodobacterales bacterium HTCC2654]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>70880810</td><td>>gi|70880810|gb|EAN93883.1| enoyl-CoA hydratase/isomerase family protein, putative [Trypanosoma cruzi]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>71654220</td><td>>gi|71654220|ref|XP_815734.1| enoyl-CoA hydratase/isomerase family protein [Trypanosoma cruzi]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>76793726</td><td>>gi|76793726|ref|ZP_00776209.1| Enoyl-CoA hydratase/isomerase [Pseudoalteromonas atlantica T6c]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>76591044</td><td>>gi|76591044|gb|EAO67251.1| Enoyl-CoA hydratase/isomerase [Pseudoalteromonas atlantica T6c]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>68182426</td><td>>gi|68182426|ref|ZP_00555406.1| Enoyl-CoA hydratase/isomerase [Jannaschia sp. CCS1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>67977530</td><td>>gi|67977530|gb|EAM67150.1| Enoyl-CoA hydratase/isomerase [Jannaschia sp. CCS1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>71147946</td><td>>gi|71147946|gb|AAZ28419.1| enoyl-CoA hydratase/isomerase family protein [Colwellia psychrerythraea 34H]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>71282206</td><td>>gi|71282206|ref|YP_267406.1| enoyl-CoA hydratase/isomerase family protein [Colwellia psychrerythraea 34H]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>23008652</td><td>>gi|23008652|ref|ZP_00050010.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Magnetospirillum magnetotacticum MS-1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>71147469</td><td>>gi|71147469|gb|AAZ27942.1| enoyl-CoA hydratase/isomerase family protein [Colwellia psychrerythraea 34H]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>71281729</td><td>>gi|71281729|ref|YP_268349.1| enoyl-CoA hydratase/isomerase family protein [Colwellia psychrerythraea 34H]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>78700594</td><td>>gi|78700594|ref|ZP_00865050.1| enoyl-CoA hydratase [Alkalilimnicola ehrlichei MLHE-1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>78522081</td><td>>gi|78522081|gb|EAP35332.1| enoyl-CoA hydratase [Alkalilimnicola ehrlichei MLHE-1]</td><td></td><td>x</td><td></td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
86164753	>gi|86164753|gb|EAQ66022.1| enoyl-CoA hydratase/isomerase family protein [Marinomonas sp. MED121]		x		
71366013	>gi|71366013|ref|ZP_00656561.1| Enoyl-CoA hydratase/isomerase [Nocardioides sp. JS614]		x		
71158317	>gi|71158317|gb|EAO08696.1| Enoyl-CoA hydratase/isomerase [Nocardioides sp. JS614]		x		
24461673	>gi|24461673|gb|AAN62242.1| putative enoyl-CoA hydratase [Pseudomonas aeruginosa]		x		
84515560	>gi|84515560|ref|ZP_01002922.1| enoyl-CoA hydratase/isomerase family protein [Loktanella vestfoldensis SKA53]		x		
84510843	>gi|84510843|gb|EAQ07298.1| enoyl-CoA hydratase/isomerase family protein [Loktanella vestfoldensis SKA53]		x		
70835091	>gi|70835091|gb|EAN80593.1| enoyl-CoA hydratase/isomerase family protein, putative [Trypanosoma brucei]		x		
74026278	>gi|74026278|ref|XP_829705.1| enoyl-CoA hydratase/isomerase family protein [Trypanosoma brucei]		x		
70876097	>gi|70876097|gb|EAN89582.1| enoyl-CoA hydratase/isomerase family protein, putative [Trypanosoma cruzi]		x		
71420280	>gi|71420280|ref|XP_811433.1| enoyl-CoA hydratase/isomerase family protein [Trypanosoma cruzi]		x		
77952157	>gi|77952157|ref|ZP_00816574.1| enoyl-CoA hydratase/isomerase family protein [Marinobacter aquaeolei VT8]		x		
77868964	>gi|77868964|gb|EAP00230.1| enoyl-CoA hydratase/isomerase family protein [Marinobacter aquaeolei VT8]		x		
70880811	>gi|70880811|gb|EAN93884.1| enoyl-CoA hydratase/isomerase family protein, putative [Trypanosoma cruzi]		x		
71654222	>gi|71654222|ref|XP_815735.1| enoyl-CoA hydratase/isomerase family protein [Trypanosoma cruzi]		x		
70876098	>gi|70876098|gb|EAN89583.1| enoyl-CoA hydratase/isomerase family protein, putative [Trypanosoma cruzi]		x		
71420282	>gi|71420282|ref|XP_811434.1| enoyl-CoA hydratase/isomerase family protein [Trypanosoma cruzi]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
38233482	>gi|38233482|ref|NP_939249.1| enoyl-CoA hydratase [Corynebacterium diphtheriae NCTC 13129]		x		
68264188	>gi|68264188|emb|CAI37676.1| enoyl-CoA hydratase [Corynebacterium jeikeium K411]		x		
68536589	>gi|68536589|ref|YP_251294.1| enoyl-CoA hydratase [Corynebacterium jeikeium K411]		x		
2462733	>gi|2462733|gb|AAB71952.1| Putative enoyl-CoA hydratase/isomerase [Arabidopsis thaliana]		x		
30696431	>gi|30696431|ref|NP_176255.2| catalytic/ naphthoate synthase [Arabidopsis thaliana]		x		
26450042	>gi|26450042|dbj|BAC42141.1| putative enoyl-CoA hydratase/isomerase [Arabidopsis thaliana]		x		
37198045	>gi|37198045|dbj|BAC93882.1| dihydroxynaphthoic acid synthase [Vibrio vulnificus YJ016]		x		
37679302	>gi|37679302|ref|NP_933911.1| naphthoate synthase [Vibrio vulnificus YJ016]		x		
77975453	>gi|77975453|ref|ZP_00830988.1| COG0447: Dihydroxynaphthoic acid synthase [Yersinia frederiksenii ATCC 33641]		x		
34912078	>gi|34912078|ref|NP_917386.1| putative naphthoate synthase [Oryza sativa (japonica cultivar-group)]		x		
20521224	>gi|20521224|dbj|BAB91741.1| putative naphthoate synthase menB [Oryza sativa (japonica cultivar-group)]		x		
62463996	>gi|62463996|ref|ZP_00383301.1| COG0447: Dihydroxynaphthoic acid synthase [Lactococcus lactis subsp. cremoris SK11]		x		
21647863	>gi|21647863|gb|AAM73066.1| naphthoate synthase [Chlorobium tepidum TLS]		x		
21674659	>gi|21674659|ref|NP_662724.1| naphthoate synthase [Chlorobium tepidum TLS]		x		
9656513	>gi|9656513|gb|AAF95121.1| naphthoate synthase [Vibrio cholerae O1 biovar eltor str. N16961]		x		
15641975	>gi|15641975|ref|NP_231607.1| naphthoate synthase [Vibrio cholerae O1 biovar eltor str. N16961]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
28805918	>gi|28805918|dbj|BAC59194.1| naphthoate synthase [Vibrio parahaemolyticus RIMD 2210633]		x		
28897705	>gi|28897705|ref|NP_797310.1| naphthoate synthase [Vibrio parahaemolyticus RIMD 2210633]		x		
23467877	>gi|23467877|ref|ZP_00123454.1| COG0447: Dihydroxynaphthoic acid synthase [Haemophilus somnus 129PT]		x		
15602961	>gi|15602961|ref|NP_246033.1| naphthoate synthase [Pasteurella multocida subsp. multocida str. Pm70]		x		
18202821	>gi|18202821|sp|Q9CLV5|MENB_PASMU Naphthoate synthase (Dihydroxynaphthoic acid synthetase) (DHNA synthetase)		x		
27362632	>gi|27362632|gb|AAO11486.1| Dihydroxynaphthoic acid synthase [Vibrio vulnificus CMCP6]		x		
27366431	>gi|27366431|ref|NP_761959.1| naphthoate synthase [Vibrio vulnificus CMCP6]		x		
32029562	>gi|32029562|ref|ZP_00132565.1| COG0447: Dihydroxynaphthoic acid synthase [Haemophilus somnus 2336]		x		
75854298	>gi|75854298|ref|ZP_00762000.1| COG0447: Dihydroxynaphthoic acid synthase [Vibrio sp. Ex25]		x		
68057754	>gi|68057754|gb|AAX88007.1| naphthoate synthase [Haemophilus influenzae 86-028NP]		x		
68249555	>gi|68249555|ref|YP_248667.1| naphthoate synthase [Haemophilus influenzae 86-028NP]		x		
42631290	>gi|42631290|ref|ZP_00156828.1| COG0447: Dihydroxynaphthoic acid synthase [Haemophilus influenzae R2866]		x		
46129093	>gi|46129093|ref|ZP_00155738.2| COG0447: Dihydroxynaphthoic acid synthase [Haemophilus influenzae R2846]		x		
16272905	>gi|16272905|ref|NP_439129.1| naphthoate synthase [Haemophilus influenzae Rd KW20]		x		
1573991	>gi|1573991|gb|AAC22625.1| naphthoate synthase (menB) [Haemophilus influenzae Rd KW20]		x		
1074008	>gi|1074008|pir||B64105 naphthoate synthase (EC 4.1.3.36) menB - Haemophilus influenzae (strain Rd KW20)		x		

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>1170915</td><td>>gi|1170915|sp|P44960|MENB_HAEIN Naphthoate synthase (Dihydroxynaphthoic acid synthetase) (DHNA synthetase)</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>21958459</td><td>>gi|21958459|gb|AAM85231.1| dihydroxynaphtoic acid synthetase [Yersinia pestis KIM]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>22125557</td><td>>gi|22125557|ref|NP_668980.1| naphthoate synthase [Yersinia pestis KIM]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>75830780</td><td>>gi|75830780|ref|ZP_00760052.1| COG0447: Dihydroxynaphthoic acid synthase [Vibrio cholerae MO10]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>75827286</td><td>>gi|75827286|ref|ZP_00756721.1| COG0447: Dihydroxynaphthoic acid synthase [Vibrio cholerae O395]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>75815077</td><td>>gi|75815077|ref|ZP_00745605.1| COG0447: Dihydroxynaphthoic acid synthase [Vibrio cholerae V52]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>62180877</td><td>>gi|62180877|ref|YP_217294.1| naphthoate synthase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>62128510</td><td>>gi|62128510|gb|AAX66213.1| dihydroxynaphtoic acid synthetase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>75818948</td><td>>gi|75818948|ref|ZP_00749057.1| COG0447: Dihydroxynaphthoic acid synthase [Vibrio cholerae V51]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>24052699</td><td>>gi|24052699|gb|AAN43855.1| dihydroxynaphtoic acid synthetase [Shigella flexneri 2a str. 301]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>30041948</td><td>>gi|30041948|gb|AAP17674.1| dihydroxynaphtoic acid synthetase [Shigella flexneri 2a str. 2457T]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>30063693</td><td>>gi|30063693|ref|NP_837864.1| naphthoate synthase [Shigella flexneri 2a str. 2457T]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>24113638</td><td>>gi|24113638|ref|NP_708148.1| naphthoate synthase [Shigella flexneri 2a str. 301]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>16503532</td><td>>gi|16503532|emb|CAD07540.1| naphthoate synthase [Salmonella enterica subsp. enterica serovar Typhi]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>16420847</td><td>>gi|16420847|gb|AAL21208.1| dihydroxynaphtoic acid synthetase [Salmonella typhimurium LT2]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>56127052</td><td>>gi|56127052|gb|AAV76558.1| naphthoate synthase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]</td><td></td><td>x</td><td></td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
29136697	>gi|29136697|gb|AAO68262.1| naphthoate synthase [Salmonella enterica subsp. enterica serovar Typhi Ty2]		x		
16765634	>gi|16765634|ref|NP_461249.1| naphthoate synthase [Salmonella typhimurium LT2]		x		
56412795	>gi|56412795|ref|YP_149870.1| naphthoate synthase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]		x		
16761233	>gi|16761233|ref|NP_456850.1| naphthoate synthase [Salmonella enterica subsp. enterica serovar Typhi str. CT18]		x		
29141071	>gi|29141071|ref|NP_804413.1| naphthoate synthase [Salmonella enterica subsp. enterica serovar Typhi Ty2]		x		
25291829	>gi|25291829|pir||AB0795 naphthoate synthase (EC 4.1.3.36) [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)		x		
75512740	>gi|75512740|ref|ZP_00735242.1| COG0447: Dihydroxynaphthoic acid synthase [Escherichia coli 53638]		x		
75259726	>gi|75259726|ref|ZP_00731028.1| COG0447: Dihydroxynaphthoic acid synthase [Escherichia coli E22]		x		
75243078	>gi|75243078|ref|ZP_00726784.1| COG0447: Dihydroxynaphthoic acid synthase [Escherichia coli F11]		x		
75238051	>gi|75238051|ref|ZP_00722056.1| COG0447: Dihydroxynaphthoic acid synthase [Escherichia coli E110019]		x		
75211671	>gi|75211671|ref|ZP_00711750.1| COG0447: Dihydroxynaphthoic acid synthase [Escherichia coli B171]		x		
75196305	>gi|75196305|ref|ZP_00706375.1| COG0447: Dihydroxynaphthoic acid synthase [Escherichia coli HS]		x		
75187049	>gi|75187049|ref|ZP_00700316.1| COG0447: Dihydroxynaphthoic acid synthase [Escherichia coli E24377A]		x		
1788597	>gi|1788597|gb|AAC75322.1| dihydroxynaphtoic acid synthetase [Escherichia coli K12]		x		
1799616	>gi|1799616|dbj|BAA16086.1| dihydroxynaphthoic acid synthetase [Escherichia coli W3110]		x		
26109056	>gi|26109056|gb|AAN81259.1| Naphthoate synthase [Escherichia coli CFT073]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
16130197	>gi|16130197|ref|NP_416765.1| naphthoate synthase [Escherichia coli K12]		x		
83588249	>gi|83588249|ref|ZP_00926874.1| COG0447: Dihydroxynaphthoic acid synthase [Escherichia coli 101-1]		x		
78100380	>gi|78100380|sp|P0ABU0|MENB_ECOLI Naphthoate synthase (Dihydroxynaphthoic acid synthetase) (DHNA synthetase)		x		
78100379	>gi|78100379|sp|P0ABU1|MENB_ECOL6 Naphthoate synthase (Dihydroxynaphthoic acid synthetase) (DHNA synthetase)		x		
26248651	>gi|26248651|ref|NP_754691.1| naphthoate synthase [Escherichia coli CFT073]		x		
145740	>gi|145740|gb|AAA23682.1| DHNA synthase		x		
52425847	>gi|52425847|ref|YP_088984.1| naphthoate synthase [Mannheimia succiniciproducens MBEL55E]		x		
75230351	>gi|75230351|ref|ZP_00716841.1| COG0447: Dihydroxynaphthoic acid synthase [Escherichia coli B7A]		x		
75177945	>gi|75177945|ref|ZP_00698007.1| COG0447: Dihydroxynaphthoic acid synthase [Shigella boydii BS512]		x		
13362620	>gi|13362620|dbj|BAB36573.1| dihydroxynaphtoic acid synthetase [Escherichia coli O157:H7]		x		
82544744	>gi|82544744|ref|YP_408691.1| dihydroxynaphtoic acid synthetase [Shigella boydii Sb227]		x		
15832404	>gi|15832404|ref|NP_311177.1| naphthoate synthase [Escherichia coli O157:H7]		x		
74312784	>gi|74312784|ref|YP_311203.1| naphthoate synthase [Shigella sonnei Ss046]		x		
81246155	>gi|81246155|gb|ABB66863.1| dihydroxynaphtoic acid synthetase [Shigella boydii Sb227]		x		
73856261	>gi|73856261|gb|AAZ88968.1| dihydroxynaphtoic acid synthetase [Shigella sonnei Ss046]		x		
77976637	>gi|77976637|ref|ZP_00832115.1| COG0447: Dihydroxynaphthoic acid synthase [Yersinia intermedia ATCC 29909]		x		
82777671	>gi|82777671|ref|YP_404020.1| dihydroxynaphtoic acid synthetase [Shigella dysenteriae Sd197]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
81241819	>gi|81241819|gb|ABB62529.1| dihydroxynaphtoic acid synthetase [Shigella dysenteriae Sd197]		x		
77636598	>gi|77636598|ref|ZP_00798671.1| COG0447: Dihydroxynaphthoic acid synthase [Yersinia pestis Angola]		x		
77629611	>gi|77629611|ref|ZP_00792197.1| COG0447: Dihydroxynaphthoic acid synthase [Yersinia pseudotuberculosis IP 31758]		x		
45436989	>gi|45436989|gb|AAS62542.1| naphthoate synthase [Yersinia pestis biovar Medievalis str. 91001]		x		
51590159	>gi|51590159|emb|CAH21796.1| naphthoate synthase [Yersinia pseudotuberculosis IP 32953]		x		
15980517	>gi|15980517|emb|CAC91328.1| naphthoate synthase [Yersinia pestis CO92]		x		
51596877	>gi|51596877|ref|YP_071068.1| naphthoate synthase [Yersinia pseudotuberculosis IP 32953]		x		
45442126	>gi|45442126|ref|NP_993665.1| naphthoate synthase [Yersinia pestis biovar Medievalis str. 91001]		x		
16122744	>gi|16122744|ref|NP_406057.1| naphthoate synthase [Yersinia pestis CO92]		x		
12516610	>gi|12516610|gb|AAG57395.1| dihydroxynaphtoic acid synthetase [Escherichia coli O157:H7 EDL933]		x		
15802813	>gi|15802813|ref|NP_288840.1| naphthoate synthase [Escherichia coli O157:H7 EDL933]		x		
49610678	>gi|49610678|emb|CAG74123.1| naphthoate synthase [Erwinia carotovora subsp. atroseptica SCRI1043]		x		
50120152	>gi|50120152|ref|YP_049319.1| naphthoate synthase [Erwinia carotovora subsp. atroseptica SCRI1043]		x		
71673659	>gi|71673659|ref|ZP_00671407.1| Naphthoate synthase [Trichodesmium erythraeum IMS101]		x		
71672907	>gi|71672907|gb|EAO29569.1| Naphthoate synthase [Trichodesmium erythraeum IMS101]		x		
46143479	>gi|46143479|ref|ZP_00135155.2| COG0447: Dihydroxynaphthoic acid synthase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
77957629	>gi|77957629|ref|ZP_00821680.1| COG0447: Dihydroxynaphthoic acid synthase [Yersinia bercovieri ATCC 43970]		x		
77961209	>gi|77961209|ref|ZP_00825053.1| COG0447: Dihydroxynaphthoic acid synthase [Yersinia mollaretii ATCC 43969]		x		
75823557	>gi|75823557|ref|ZP_00753050.1| COG0447: Dihydroxynaphthoic acid synthase [Vibrio cholerae RC385]		x		
75429737	>gi|75429737|ref|ZP_00732399.1| dihydroxynaphthoic acid synthase [Actinobacillus succinogenes 130Z]		x		
74276945	>gi|74276945|gb|EAO50532.1| dihydroxynaphthoic acid synthase [Actinobacillus succinogenes 130Z]		x		
33149130	>gi|33149130|gb|AAP96647.1| napthoate synthetase [Haemophilus ducreyi 35000HP]		x		
33152905	>gi|33152905|ref|NP_874258.1| naphthoate synthase [Haemophilus ducreyi 35000HP]		x		
75762877	>gi|75762877|ref|ZP_00742690.1| Naphthoate synthase [Bacillus thuringiensis serovar israelensis ATCC 35646]		x		
74489636	>gi|74489636|gb|EAO53039.1| Naphthoate synthase [Bacillus thuringiensis serovar israelensis ATCC 35646]		x		
36786392	>gi|36786392|emb|CAE15445.1| naphthoate synthase (dihydroxynaphthoic acid synthetase) (DHNA synthetase) [Photorhabdus luminescens subsp. laumondii TTO1]		x		
37526959	>gi|37526959|ref|NP_930303.1| naphthoate synthase [Photorhabdus luminescens subsp. laumondii TTO1]		x		
86148508	>gi|86148508|ref|ZP_01066796.1| naphthoate synthase [Vibrio sp. MED222]		x		
85833699	>gi|85833699|gb|EAQ51869.1| naphthoate synthase [Vibrio sp. MED222]		x		
84387749	>gi|84387749|ref|ZP_00990765.1| naphthoate synthase [Vibrio splendidus 12B01]		x		
84377432	>gi|84377432|gb|EAP94299.1| naphthoate synthase [Vibrio splendidus 12B01]		x		
56381250	>gi|56381250|dbj|BAD77158.1| dihydroxynapthoic acid synthetase [Geobacillus kaustophilus HTA426]		x		

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>56421408</td><td>>gi|56421408|ref|YP_148726.1| naphthoate synthase [Geobacillus kaustophilus HTA426]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>23126174</td><td>>gi|23126174|ref|ZP_00108078.1| COG0447: Dihydroxynaphthoic acid synthase [Nostoc punctiforme PCC 73102]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>75700116</td><td>>gi|75700116|gb|ABA19792.1| Naphthoate synthase [Anabaena variabilis ATCC 29413]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>75906391</td><td>>gi|75906391|ref|YP_320687.1| naphthoate synthase [Anabaena variabilis ATCC 29413]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>67987855</td><td>>gi|67987855|gb|EAM75641.1| Naphthoate synthase [Kineococcus radiotolerans SRS30216]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>69284895</td><td>>gi|69284895|ref|ZP_00616594.1| Naphthoate synthase [Kineococcus radiotolerans SRS30216]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>52004777</td><td>>gi|52004777|gb|AAU24719.1| dihydroxynapthoic acid synthetase [Bacillus licheniformis ATCC 14580]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>52081566</td><td>>gi|52081566|ref|YP_080357.1| naphthoate synthase [Bacillus licheniformis ATCC 14580]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>52786944</td><td>>gi|52786944|ref|YP_092773.1| naphthoate synthase [Bacillus licheniformis ATCC 14580]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>68548715</td><td>>gi|68548715|ref|ZP_00588184.1| Naphthoate synthase [Pelodictyon phaeoclathratiforme BU-1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>68244273</td><td>>gi|68244273|gb|EAN26465.1| Naphthoate synthase [Pelodictyon phaeoclathratiforme BU-1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>42784059</td><td>>gi|42784059|ref|NP_981306.1| naphthoate synthase [Bacillus cereus ATCC 10987]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>42739990</td><td>>gi|42739990|gb|AAS43914.1| naphthoate synthase [Bacillus cereus ATCC 10987]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>65322221</td><td>>gi|65322221|ref|ZP_00395180.1| COG0447: Dihydroxynaphthoic acid synthase [Bacillus anthracis str. A2012]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>49330350</td><td>>gi|49330350|gb|AAT60996.1| naphthoate synthase [Bacillus thuringiensis serovar konkukian str. 97-27]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>47505559</td><td>>gi|47505559|gb|AAT34235.1| naphthoate synthase [Bacillus anthracis str. 'Ames Ancestor']</td><td></td><td>x</td><td></td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
49181666	>gi|49181666|gb|AAT57042.1| naphthoate synthase [Bacillus anthracis str. Sterne]		x		
49187739	>gi|49187739|ref|YP_030992.1| naphthoate synthase [Bacillus anthracis str. Sterne]		x		
49478794	>gi|49478794|ref|YP_038898.1| naphthoate synthase [Bacillus thuringiensis serovar konkukian str. 97-27]		x		
30259593	>gi|30259593|gb|AAP28781.1| naphthoate synthase [Bacillus anthracis str. Ames]		x		
47530411	>gi|47530411|ref|YP_021760.1| naphthoate synthase [Bacillus anthracis str. 'Ames Ancestor']		x		
30264918	>gi|30264918|ref|NP_847295.1| naphthoate synthase [Bacillus anthracis str. Ames]		x		
51974114	>gi|51974114|gb|AAU15664.1| naphthoate synthase [Bacillus cereus E33L]		x		
52140645	>gi|52140645|ref|YP_086183.1| naphthoate synthase [Bacillus cereus E33L]		x		
68054686	>gi|68054686|ref|ZP_00538836.1| Naphthoate synthase [Exiguobacterium sp. 255-15]		x		
68008603	>gi|68008603|gb|EAM87827.1| Naphthoate synthase [Exiguobacterium sp. 255-15]		x		
17131439	>gi|17131439|dbj|BAB74046.1| naphthoate synthase [Nostoc sp. PCC 7120]		x		
17229839	>gi|17229839|ref|NP_486387.1| naphthoate synthase [Nostoc sp. PCC 7120]		x		
22778008	>gi|22778008|dbj|BAC14279.1| naphthoate synthase [Oceanobacillus iheyensis HTE831]		x		
23099778	>gi|23099778|ref|NP_693244.1| naphthoate synthase [Oceanobacillus iheyensis HTE831]		x		
29898480	>gi|29898480|gb|AAP11753.1| Naphthoate synthase [Bacillus cereus ATCC 14579]		x		
30022921	>gi|30022921|ref|NP_834552.1| naphthoate synthase [Bacillus cereus ATCC 14579]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
2635564	>gi|2635564|emb|CAB15058.1| dihydroxynapthoic acid synthetase [Bacillus subtilis subsp. subtilis str. 168]		x		
20141516	>gi|20141516|sp|P23966|MENB_BACSU Naphthoate synthase (Dihydroxynaphthoic acid synthetase) (DHNA synthetase)		x		
2293148	>gi|2293148|gb|AAC00226.1| dihydroxynaphthoate synthase [Bacillus subtilis]		x		
16080132	>gi|16080132|ref|NP_390958.1| naphthoate synthase [Bacillus subtilis subsp. subtilis str. 168]		x		
67921527	>gi|67921527|ref|ZP_00515045.1| Naphthoate synthase [Crocosphaera watsonii WH 8501]		x		
67856639	>gi|67856639|gb|EAM51880.1| Naphthoate synthase [Crocosphaera watsonii WH 8501]		x		
45478466	>gi|45478466|gb|AAS66445.1| 1,4 dihydroxy-2-naphthaote synthase [Synechococcus sp. PCC 7002]		x		
67938338	>gi|67938338|ref|ZP_00530865.1| Naphthoate synthase [Chlorobium phaeobacteroides BS1]		x		
67915446	>gi|67915446|gb|EAM64767.1| Naphthoate synthase [Chlorobium phaeobacteroides BS1]		x		
68208072	>gi|68208072|ref|ZP_00560208.1| Naphthoate synthase [Desulfitobacterium hafniense DCB-2]		x		
68168051	>gi|68168051|gb|EAM96001.1| Naphthoate synthase [Desulfitobacterium hafniense DCB-2]		x		
71481155	>gi|71481155|ref|ZP_00660863.1| Naphthoate synthase [Prosthecochloris vibrioformis DSM 265]		x		
71284015	>gi|71284015|gb|EAO15836.1| Naphthoate synthase [Prosthecochloris vibrioformis DSM 265]		x		
22296185	>gi|22296185|dbj|BAC10009.1| naphthoate synthase [Thermosynechococcus elongatus BP-1]		x		
22300000	>gi|22300000|ref|NP_683247.1| naphthoate synthase [Thermosynechococcus elongatus BP-1]		x		
78166118	>gi|78166118|gb|ABB23216.1| Naphthoate synthase [Pelodictyon luteolum DSM 273]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
78186216	>gi|78186216|ref|YP_374259.1| naphthoate synthase [Pelodictyon luteolum DSM 273]		x		
47568032	>gi|47568032|ref|ZP_00238738.1| naphthoate synthase [Bacillus cereus G9241]		x		
47555335	>gi|47555335|gb|EAL13680.1| naphthoate synthase [Bacillus cereus G9241]		x		
1652614	>gi|1652614|dbj|BAA17535.1| naphthoate synthase [Synechocystis sp. PCC 6803]		x		
16330127	>gi|16330127|ref|NP_440855.1| naphthoate synthase [Synechocystis sp. PCC 6803]		x		
78171874	>gi|78171874|gb|ABB28970.1| Naphthoate synthase [Chlorobium chlorochromatii CaD3]		x		
78189675	>gi|78189675|ref|YP_380013.1| naphthoate synthase [Chlorobium chlorochromatii CaD3]		x		
12723642	>gi|12723642|gb|AAK04827.1| dihydroxynaphthonic acid synthase (EC 4.1.3.36) [Lactococcus lactis subsp. lactis Il1403]		x		
15672711	>gi|15672711|ref|NP_266885.1| naphthoate synthase [Lactococcus lactis subsp. lactis Il1403]		x		
49244328	>gi|49244328|emb|CAG42756.1| putative naphthoate synthase [Staphylococcus aureus subsp. aureus MSSA476]		x		
21204096	>gi|21204096|dbj|BAB94794.1| naphthoate synthase [Staphylococcus aureus subsp. aureus MW2]		x		
49485885	>gi|49485885|ref|YP_043106.1| naphthoate synthase [Staphylococcus aureus subsp. aureus MSSA476]		x		
21282658	>gi|21282658|ref|NP_645746.1| naphthoate synthase [Staphylococcus aureus subsp. aureus MW2]		x		
49241340	>gi|49241340|emb|CAG40023.1| putative naphthoate synthase [Staphylococcus aureus subsp. aureus MRSA252]		x		
57284425	>gi|57284425|gb|AAW36519.1| naphthoate synthase [Staphylococcus aureus subsp. aureus COL]		x		
57650239	>gi|57650239|ref|YP_185919.1| naphthoate synthase [Staphylococcus aureus subsp. aureus COL]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
49483211	>gi|49483211|ref|YP_040435.1| naphthoate synthase [Staphylococcus aureus subsp. aureus MRSA252]		x		
68447642	>gi|68447642|dbj|BAE05226.1| naphthoate synthase [Staphylococcus haemolyticus JCSC1435]		x		
70726918	>gi|70726918|ref|YP_253832.1| naphthoate synthase [Staphylococcus haemolyticus JCSC1435]		x		
68551552	>gi|68551552|ref|ZP_00590947.1| Naphthoate synthase [Prosthecochloris aestuarii DSM 271]		x		
68241486	>gi|68241486|gb|EAN23752.1| Naphthoate synthase [Prosthecochloris aestuarii DSM 271]		x		
67784005	>gi|67784005|gb|EAM43385.1| Naphthoate synthase [Chlorobium limicola DSM 245]		x		
67918349	>gi|67918349|ref|ZP_00511948.1| Naphthoate synthase [Chlorobium limicola DSM 245]		x		
14246815	>gi|14246815|dbj|BAB57207.1| naphthoate synthase [Staphylococcus aureus subsp. aureus Mu50]		x		
13700847	>gi|13700847|dbj|BAB42143.1| naphthoate synthase [Staphylococcus aureus subsp. aureus N315]		x		
15926632	>gi|15926632|ref|NP_374165.1| naphthoate synthase [Staphylococcus aureus subsp. aureus N315]		x		
15924035	>gi|15924035|ref|NP_371569.1| naphthoate synthase [Staphylococcus aureus subsp. aureus Mu50]		x		
67935849	>gi|67935849|ref|ZP_00528866.1| Naphthoate synthase [Chlorobium phaeobacteroides DSM 266]		x		
67775244	>gi|67775244|gb|EAM34913.1| Naphthoate synthase [Chlorobium phaeobacteroides DSM 266]		x		
82750657	>gi|82750657|ref|YP_416398.1| naphthoate synthase [Staphylococcus aureus RF122]		x		
82656188	>gi|82656188|emb|CAI80600.1| naphthoate synthase [Staphylococcus aureus RF122]		x		
72495570	>gi|72495570|dbj|BAE18891.1| dihydroxynaphthoic acid synthase [Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
73663055	>gi|73663055|ref|YP_301836.1| naphthoate synthase [Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305]		x		
86605247	>gi|86605247|ref|YP_474010.1| naphthoate synthase [Cyanobacteria bacterium Yellowstone A-Prime]		x		
86553789	>gi|86553789|gb|ABC98747.1| naphthoate synthase [Cyanobacteria bacterium Yellowstone A-Prime]		x		
46907904	>gi|46907904|ref|YP_014293.1| naphthoate synthase [Listeria monocytogenes str. 4b F2365]		x		
47093552	>gi|47093552|ref|ZP_00231312.1| naphthoate synthase [Listeria monocytogenes str. 4b H7858]		x		
47018066	>gi|47018066|gb|EAL08839.1| naphthoate synthase [Listeria monocytogenes str. 4b H7858]		x		
46881173	>gi|46881173|gb|AAT04470.1| naphthoate synthase [Listeria monocytogenes str. 4b F2365]		x		
16803713	>gi|16803713|ref|NP_465198.1| naphthoate synthase [Listeria monocytogenes EGD-e]		x		
47096746	>gi|47096746|ref|ZP_00234330.1| naphthoate synthase [Listeria monocytogenes str. 1/2a F6854]		x		
47014878	>gi|47014878|gb|EAL05827.1| naphthoate synthase [Listeria monocytogenes str. 1/2a F6854]		x		
16800849	>gi|16800849|ref|NP_471117.1| naphthoate synthase [Listeria innocua Clip11262]		x		
56685894	>gi|56685894|dbj|BAD79116.1| naphthoate synthase [Synechococcus elongatus PCC 6301]		x		
56750935	>gi|56750935|ref|YP_171636.1| naphthoate synthase [Synechococcus elongatus PCC 6301]		x		
57866511	>gi|57866511|ref|YP_188217.1| naphthoate synthase [Staphylococcus epidermidis RP62A]		x		
57637169	>gi|57637169|gb|AAW53957.1| naphthoate synthase [Staphylococcus epidermidis RP62A]		x		
41324695	>gi|41324695|emb|CAF19177.1| DIHYDROXYNAPHTHONIC ACID SYNTHASE [Corynebacterium glutamicum ATCC 13032]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
21323228	>gi|21323228|dbj|BAB97856.1| Dihydroxynaphthoic acid synthase [Corynebacterium glutamicum ATCC 13032]		x		
62389361	>gi|62389361|ref|YP_224763.1| naphthoate synthase [Corynebacterium glutamicum ATCC 13032]		x		
19551706	>gi|19551706|ref|NP_599708.1| naphthoate synthase [Corynebacterium glutamicum ATCC 13032]		x		
27315208	>gi|27315208|gb|AAO04343.1| naphthoate synthase [Staphylococcus epidermidis ATCC 12228]		x		
27467664	>gi|27467664|ref|NP_764301.1| naphthoate synthase [Staphylococcus epidermidis ATCC 12228]		x		
76260425	>gi|76260425|ref|ZP_00768061.1| Naphthoate synthase [Chloroflexus aurantiacus J-10-fl]		x		
76164674	>gi|76164674|gb|EAO58818.1| Naphthoate synthase [Chloroflexus aurantiacus J-10-fl]		x		
81299408	>gi|81299408|ref|YP_399616.1| naphthoate synthase [Synechococcus elongatus PCC 7942]		x		
81168289	>gi|81168289|gb|ABB56629.1| naphthoate synthase [Synechococcus elongatus PCC 7942]		x		
55377678	>gi|55377678|ref|YP_135529.1| naphthoate synthase [Haloarcula marismortui ATCC 43049]		x		
55230403	>gi|55230403|gb|AAV45822.1| enoyl-CoA hydratase [Haloarcula marismortui ATCC 43049]		x		
86608057	>gi|86608057|ref|YP_476819.1| naphthoate synthase [Cyanobacteria bacterium Yellowstone B-Prime]		x		
86556599	>gi|86556599|gb|ABD01556.1| naphthoate synthase [Cyanobacteria bacterium Yellowstone B-Prime]		x		
23492311	>gi|23492311|dbj|BAC17285.1| putative naphthoate synthase [Corynebacterium efficiens YS-314]		x		
25027031	>gi|25027031|ref|NP_737085.1| naphthoate synthase [Corynebacterium efficiens YS-314]		x		
72001734	>gi|72001734|gb|AAZ57536.1| naphthoate synthase [Prochlorococcus marinus str. NATL2A]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
72381884	>gi|72381884|ref|YP_291239.1| naphthoate synthase [Prochlorococcus marinus str. NATL2A]		x		
33634594	>gi|33634594|emb|CAE20580.1| Naphthoate synthase [Prochlorococcus marinus str. MIT 9313]		x		
33862678	>gi|33862678|ref|NP_894238.1| Naphthoate synthase [Prochlorococcus marinus str. MIT 9313]		x		
84517892	>gi|84517892|ref|ZP_01005241.1| Naphthoate synthase [Prochlorococcus marinus str. MIT 9211]		x		
84512641	>gi|84512641|gb|EAQ08979.1| Naphthoate synthase [Prochlorococcus marinus str. MIT 9211]		x		
33632701	>gi|33632701|emb|CAE07513.1| Naphthoate synthase [Synechococcus sp. WH 8102]		x		
33865532	>gi|33865532|ref|NP_897091.1| Naphthoate synthase [Synechococcus sp. WH 8102]		x		
78169200	>gi|78169200|gb|ABB26297.1| Naphthoate synthase [Synechococcus sp. CC9902]		x		
78184906	>gi|78184906|ref|YP_377341.1| Naphthoate synthase [Synechococcus sp. CC9902]		x		
86167773	>gi|86167773|gb|EAQ69031.1| Naphthoate synthase [Synechococcus sp. RS9917]		x		
71915545	>gi|71915545|gb|AAZ55447.1| naphthoate synthase [Thermobifida fusca YX]		x		
72161813	>gi|72161813|ref|YP_289470.1| naphthoate synthase [Thermobifida fusca YX]		x		
13880083	>gi|13880083|gb|AAK44795.1| naphthoate synthase [Mycobacterium tuberculosis CDC1551]		x		
31791730	>gi|31791730|ref|NP_854223.1| naphthoate synthase [Mycobacterium bovis AF2122/97]		x		
15607688	>gi|15607688|ref|NP_215062.1| naphthoate synthase [Mycobacterium tuberculosis H37Rv]		x		
15839944	>gi|15839944|ref|NP_334981.1| naphthoate synthase [Mycobacterium tuberculosis CDC1551]		x		
143186	>gi|143186|gb|AAC37016.1| dihydroxynapthoic acid (DHNA) synthetase		x		

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>557492</td><td>>gi|557492|gb|AAA50401.1| dihydroxynapthoic acid (DHNA) synthetase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>78197115</td><td>>gi|78197115|gb|ABB34880.1| naphthoate synthase [Synechococcus sp. CC9605]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>78212656</td><td>>gi|78212656|ref|YP_381435.1| naphthoate synthase [Synechococcus sp. CC9605]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>29342535</td><td>>gi|29342535|gb|AAO80300.1| naphthoate synthase [Enterococcus faecalis V583]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>29375076</td><td>>gi|29375076|ref|NP_814229.1| naphthoate synthase [Enterococcus faecalis V583]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>33639897</td><td>>gi|33639897|emb|CAE19067.1| Napthoate synthase [Prochlorococcus marinus subsp. pastoris str. CCMP1986]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>33861165</td><td>>gi|33861165|ref|NP_892726.1| Napthoate synthase [Prochlorococcus marinus subsp. pastoris str. CCMP1986]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>732732</td><td>>gi|732732|emb|CAA59693.1| naphthoate synthase [Haemophilus parahaemolyticus]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>68544606</td><td>>gi|68544606|ref|ZP_00584236.1| Naphthoate synthase [Shewanella baltica OS155]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>68517691</td><td>>gi|68517691|gb|EAN41322.1| Naphthoate synthase [Shewanella baltica OS155]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>33238031</td><td>>gi|33238031|gb|AAQ00098.1| Dihydroxynaphthoic acid synthase [Prochlorococcus marinus subsp. marinus str. CCMP1375]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>33240503</td><td>>gi|33240503|ref|NP_875445.1| Dihydroxynaphthoic acid synthase [Prochlorococcus marinus subsp. marinus str. CCMP1375]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>15790175</td><td>>gi|15790175|ref|NP_279999.1| naphthoate synthase [Halobacterium sp. NRC-1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>41410142</td><td>>gi|41410142|ref|NP_962978.1| naphthoate synthase [Mycobacterium avium subsp. paratuberculosis K-10]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>68264562</td><td>>gi|68264562|emb|CAI38050.1| naphthoate synthase [Corynebacterium jeikeium K411]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>68536963</td><td>>gi|68536963|ref|YP_251668.1| naphthoate synthase [Corynebacterium jeikeium K411]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>48856485</td><td>>gi|48856485|ref|ZP_00310642.1| COG0447: Dihydroxynaphthoic acid synthase [Cytophaga hutchinsonii]</td><td></td><td>x</td><td></td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
60492255	>gi|60492255|emb|CAH07020.1| putative naphthoate synthase [Bacteroides fragilis NCTC 9343]		x		
52215475	>gi|52215475|dbj|BAD48068.1| dihydroxynapthoic acid synthetase [Bacteroides fragilis YCH46]		x		
53712610	>gi|53712610|ref|YP_098602.1| dihydroxynapthoic acid synthetase [Bacteroides fragilis YCH46]		x		
60680821	>gi|60680821|ref|YP_210965.1| putative naphthoate synthase [Bacteroides fragilis NCTC 9343]		x		
48866139	>gi|48866139|ref|ZP_00319996.1| COG0447: Dihydroxynaphthoic acid synthase [Oenococcus oeni PSU-1]		x		
78712492	>gi|78712492|gb|ABB49669.1| naphthoate synthase [Prochlorococcus marinus str. MIT 9312]		x		
78778993	>gi|78778993|ref|YP_397105.1| naphthoate synthase [Prochlorococcus marinus str. MIT 9312]		x		
29350110	>gi|29350110|ref|NP_813613.1| dihydroxynapthoic acid synthetase [Bacteroides thetaiotaomicron VPI-5482]		x		
29342022	>gi|29342022|gb|AAO79807.1| dihydroxynapthoic acid synthetase [Bacteroides thetaiotaomicron VPI-5482]		x		
71366728	>gi|71366728|ref|ZP_00657266.1| Naphthoate synthase [Nocardioides sp. JS614]		x		
71157539	>gi|71157539|gb|EAO07928.1| Naphthoate synthase [Nocardioides sp. JS614]		x		
39577055	>gi|39577055|emb|CAE78284.1| Naphthoate synthase [Bdellovibrio bacteriovorus HD100]		x		
42524845	>gi|42524845|ref|NP_970225.1| naphthoate synthase [Bdellovibrio bacteriovorus HD100]		x		
28410416	>gi|28410416|emb|CAD66802.1| naphthoate synthase [Tropheryma whipplei TW08/27]		x		
28476117	>gi|28476117|gb|AAO44207.1| naphthoate synthase [Tropheryma whipplei str. Twist]		x		
28572285	>gi|28572285|ref|NP_789065.1| naphthoate synthase [Tropheryma whipplei TW08/27]		x		

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>28493077</td><td>>gi|28493077|ref|NP_787238.1| naphthoate synthase [Tropheryma whipplei str. Twist]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>69953506</td><td>>gi|69953506|ref|ZP_00640617.1| Naphthoate synthase [Shewanella frigidimarina NCIMB 400]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>69163491</td><td>>gi|69163491|gb|EAN72634.1| Naphthoate synthase [Shewanella frigidimarina NCIMB 400]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>77813712</td><td>>gi|77813712|ref|ZP_00812985.1| Naphthoate synthase [Shewanella putrefaciens CN-32]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>77811218</td><td>>gi|77811218|gb|EAO95591.1| Naphthoate synthase [Shewanella putrefaciens CN-32]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>82742522</td><td>>gi|82742522|ref|ZP_00905212.1| Naphthoate synthase [Shewanella sp. W3-18-1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>82720140</td><td>>gi|82720140|gb|EAP55016.1| Naphthoate synthase [Shewanella sp. W3-18-1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>50950517</td><td>>gi|50950517|gb|AAT88218.1| naphthoate synthase [Leifsonia xyli subsp. xyli str. CTCB07]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>50954035</td><td>>gi|50954035|ref|YP_061323.1| naphthoate synthase [Leifsonia xyli subsp. xyli str. CTCB07]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>24376211</td><td>>gi|24376211|ref|NP_720255.1| naphthoate synthase [Shewanella oneidensis MR-1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>24351268</td><td>>gi|24351268|gb|AAN57698.1| naphthoate synthase [Shewanella oneidensis MR-1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>78691283</td><td>>gi|78691283|ref|ZP_00855907.1| Naphthoate synthase [Shewanella sp. MR-7]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>78687815</td><td>>gi|78687815|ref|ZP_00852551.1| Naphthoate synthase [Shewanella sp. ANA-3]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>78509337</td><td>>gi|78509337|gb|EAP22735.1| Naphthoate synthase [Shewanella sp. MR-7]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>78504426</td><td>>gi|78504426|gb|EAP17983.1| Naphthoate synthase [Shewanella sp. ANA-3]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>86143133</td><td>>gi|86143133|ref|ZP_01061555.1| naphthoate synthase [Flavobacterium sp. MED217]</td><td></td><td>x</td><td></td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
85830578	>gi|85830578|gb|EAQ49037.1| naphthoate synthase [Flavobacterium sp. MED217]		x		
78367711	>gi|78367711|ref|ZP_00837975.1| Naphthoate synthase [Shewanella sp. PV-4]		x		
78360257	>gi|78360257|gb|EAP02097.1| Naphthoate synthase [Shewanella sp. PV-4]		x		
68548540	>gi|68548540|ref|ZP_00588034.1| Naphthoate synthase [Shewanella amazonensis SB2B]		x		
68513759	>gi|68513759|gb|EAN37526.1| Naphthoate synthase [Shewanella amazonensis SB2B]		x		
86133839	>gi|86133839|ref|ZP_01052421.1| naphthoate synthase [Tenacibaculum sp. MED152]		x		
85820702	>gi|85820702|gb|EAQ41849.1| naphthoate synthase [Tenacibaculum sp. MED152]		x		
86132721	>gi|86132721|ref|ZP_01051313.1| naphthoate synthase [Cellulophaga sp. MED134]		x		
85816675	>gi|85816675|gb|EAQ37861.1| naphthoate synthase [Cellulophaga sp. MED134]		x		
13093764	>gi|13093764|emb|CAC31219.1| naphthoate synthase [Mycobacterium leprae]		x		
15828210	>gi|15828210|ref|NP_302473.1| naphthoate synthase [Mycobacterium leprae TN]		x		
54018620	>gi|54018620|dbj|BAD59990.1| putative dihydroxynaphtoic acid synthetase [Nocardia farcinica IFM 10152]		x		
54027112	>gi|54027112|ref|YP_121354.1| naphthoate synthase [Nocardia farcinica IFM 10152]		x		
82498032	>gi|82498032|ref|ZP_00883549.1| Naphthoate synthase [Shewanella sp. MR-4]		x		
82403949	>gi|82403949|gb|EAP44653.1| Naphthoate synthase [Shewanella sp. MR-4]		x		
38199294	>gi|38199294|emb|CAE48925.1| Putative naphthoate synthase [Corynebacterium diphtheriae]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
38233035	>gi|38233035|ref|NP_938802.1| naphthoate synthase [Corynebacterium diphtheriae NCTC 13129]		x		
84494963	>gi|84494963|ref|ZP_00994082.1| putative naphthoate synthase [Janibacter sp. HTCC2649]		x		
84384456	>gi|84384456|gb|EAQ00336.1| putative naphthoate synthase [Janibacter sp. HTCC2649]		x		
83857229	>gi|83857229|ref|ZP_00950757.1| naphthoate synthase [Croceibacter atlanticus HTCC2559]		x		
83848596	>gi|83848596|gb|EAP86465.1| naphthoate synthase [Croceibacter atlanticus HTCC2559]		x		
62425059	>gi|62425059|ref|ZP_00380197.1| COG0447: Dihydroxynaphthoic acid synthase [Brevibacterium linens BL2]		x		
85860722	>gi|85860722|ref|YP_462924.1| dihydroxynaphthoic acid synthase [Syntrophus aciditrophicus SB]		x		
85723813	>gi|85723813|gb|ABC78756.1| dihydroxynaphthoic acid synthase [Syntrophus aciditrophicus SB]		x		
83815505	>gi|83815505|ref|YP_446858.1| naphthoate synthase [Salinibacter ruber DSM 13855]		x		
83756899	>gi|83756899|gb|ABC45012.1| naphthoate synthase [Salinibacter ruber DSM 13855]		x		
23024048	>gi|23024048|ref|ZP_00063272.1| COG0447: Dihydroxynaphthoic acid synthase [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]		x		
71846868	>gi|71846868|gb|AAZ46364.1| Naphthoate synthase [Dechloromonas aromatica RCB]		x		
71907247	>gi|71907247|ref|YP_284834.1| Naphthoate synthase [Dechloromonas aromatica RCB]		x		
76557872	>gi|76557872|emb|CAI49456.1| naphthoate synthase (EC 4.1.3.36) [Natronomonas pharaonis DSM 2160]		x		
76802007	>gi|76802007|ref|YP_327015.1| naphthoate synthase [Natronomonas pharaonis DSM 2160]		x		
76785837	>gi|76785837|ref|ZP_00773001.1| COG0447: Dihydroxynaphthoic acid synthase [Mycobacterium tuberculosis F11]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
81255561	>gi|81255561|ref|ZP_00880035.1| COG0447: Dihydroxynaphthoic acid synthase [Mycobacterium tuberculosis C]		x		
34541185	>gi|34541185|ref|NP_905664.1| naphthoate synthase [Porphyromonas gingivalis W83]		x		
34397501	>gi|34397501|gb|AAQ66563.1| naphthoate synthase [Porphyromonas gingivalis W83]		x		
30409237	>gi|30409237|dbj|BAC76186.1| naphthoate synthase [Cyanidioschyzon merolae]		x		
30468137	>gi|30468137|ref|NP_849024.1| naphthoate synthase [Cyanidioschyzon merolae strain 10D]		x		
68562468	>gi|68562468|ref|ZP_00601726.1| Naphthoate synthase [Rubrobacter xylanophilus DSM 9941]		x		
68511353	>gi|68511353|gb|EAN35202.1| Naphthoate synthase [Rubrobacter xylanophilus DSM 9941]		x		
66966063	>gi|66966063|ref|ZP_00413626.1| Naphthoate synthase [Arthrobacter sp. FB24]		x		
66868115	>gi|66868115|gb|EAL95488.1| Naphthoate synthase [Arthrobacter sp. FB24]		x		
83638332	>gi|83638332|gb|ABC33866.1| naphthoate synthase [Rhodococcus sp. T104]		x		
6466406	>gi|6466406|gb|AAF12988.1| unknown; naphthoate synthase [Cyanidium caldarium]		x		
11465502	>gi|11465502|ref|NP_045107.1| naphthoate synthase [Cyanidium caldarium]		x		
14423764	>gi|14423764|sp|Q9TM10|MENB_CYACA Naphthoate synthase (Dihydroxynaphthoic acid synthetase) (DHNA synthetase)		x		
50842391	>gi|50842391|ref|YP_055618.1| naphthoate synthase [Propionibacterium acnes KPA171202]		x		
48428779	>gi|48428779|gb|AAT42427.1| L-alanine-DL-glutamate epimerase [Collimonas fungivorans]		x		
66045229	>gi|66045229|ref|YP_235070.1| Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Pseudomonas syringae pv. syringae B728a]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
63255936	>gi|63255936|gb|AAY37032.1| Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Pseudomonas syringae pv. syringae B728a]		x		
77968208	>gi|77968208|gb|ABB09588.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia sp. 383]		x		
78067463	>gi|78067463|ref|YP_370232.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia sp. 383]		x		
67663959	>gi|67663959|ref|ZP_00461237.1| Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Burkholderia cenocepacia HI2424]		x		
67102475	>gi|67102475|gb|EAM19607.1| Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Burkholderia cenocepacia HI2424]		x		
74014271	>gi|74014271|ref|ZP_00684900.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia ambifaria AMMD]		x		
72612873	>gi|72612873|gb|EAO48816.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia ambifaria AMMD]		x		
67549010	>gi|67549010|ref|ZP_00426886.1| Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Burkholderia vietnamiensis G4]		x		
67529663	>gi|67529663|gb|EAM26522.1| Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Burkholderia vietnamiensis G4]		x		
77384347	>gi|77384347|gb|ABA75860.1| Mandelate racemase/muconate lactonizing enzyme [Pseudomonas fluorescens PfO-1]		x		
77460344	>gi|77460344|ref|YP_349851.1| Mandelate racemase/muconate lactonizing enzyme [Pseudomonas fluorescens PfO-1]		x		
74024396	>gi|74024396|ref|ZP_00694948.1| Mandelate racemase/muconate lactonizing enzyme [Rhodoferax ferrireducens DSM 15236]		x		
72602896	>gi|72602896|gb|EAO38916.1| Mandelate racemase/muconate lactonizing enzyme [Rhodoferax ferrireducens DSM 15236]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
67158311	>gi|67158311|ref|ZP_00419302.1| Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Azotobacter vinelandii AvOP]		x		
67084806	>gi|67084806|gb|EAM04285.1| Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Azotobacter vinelandii AvOP]		x		
67661240	>gi|67661240|ref|ZP_00458560.1| Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Burkholderia cenocepacia AU 1054]		x		
67091168	>gi|67091168|gb|EAM08757.1| Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Burkholderia cenocepacia AU 1054]		x		
52005569	>gi|52005569|gb|AAU25511.1| Mandelate racemase/muconate lactonizing enzyme,Mandelate racemase/muconate lactonizing enzyme [Bacillus licheniformis ATCC 14580]		x		
52082358	>gi|52082358|ref|YP_081149.1| Mandelate racemase/muconate lactonizing enzyme,Mandelate racemase/muconate lactonizing enzyme [Bacillus licheniformis ATCC 14580]		x		
21112838	>gi|21112838|gb|AAM41037.1| 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-deoxyphosphogluconate aldolase [Xanthomonas campestris pv. campestris str. ATCC 33913]		x		
66574128	>gi|66574128|gb|AAY49538.1| 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-deoxyphosphogluconate aldolase [Xanthomonas campestris pv. campestris str. 8004]		x		
66768796	>gi|66768796|ref|YP_243558.1| 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-deoxyphosphogluconate aldolase [Xanthomonas campestris pv. campestris str. 8004]		x		
21231196	>gi|21231196|ref|NP_637113.1| 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-deoxyphosphogluconate aldolase [Xanthomonas campestris pv. campestris str. ATCC 33913]		x		
66799010	>gi|66799010|ref|ZP_00397752.1| Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Deinococcus geothermalis DSM 11300]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
66780648	>gi|66780648|gb|EAL81630.1| Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Deinococcus geothermalis DSM 11300]		x		
84368366	>gi|84368366|dbj|BAE69524.1| 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-deoxyphosphogluconate aldolase [Xanthomonas oryzae pv. oryzae MAFF 311018]		x		
84624426	>gi|84624426|ref|YP_451798.1| 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-deoxyphosphogluconate aldolase [Xanthomonas oryzae pv. oryzae MAFF 311018]		x		
58582542	>gi|58582542|ref|YP_201558.1| 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-deoxyphosphogluconate aldolase [Xanthomonas oryzae pv. oryzae KACC10331]		x		
58427136	>gi|58427136|gb|AAW76173.1| 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-deoxyphosphogluconate aldolase [Xanthomonas oryzae pv. oryzae KACC10331]		x		
21107962	>gi|21107962|gb|AAM36629.1| 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-deoxyphosphogluconate aldolase [Xanthomonas axonopodis pv. citri str. 306]		x		
21242511	>gi|21242511|ref|NP_642093.1| 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-deoxyphosphogluconate aldolase [Xanthomonas axonopodis pv. citri str. 306]		x		
57229094	>gi|57229094|gb|AAW45528.1| mandelate racemase/muconate lactonizing enzyme, putative [Cryptococcus neoformans var. neoformans JEC21]		x		
58271358	>gi|58271358|ref|XP_572835.1| mandelate racemase/muconate lactonizing enzyme [Cryptococcus neoformans var. neoformans JEC21]		x		
77964602	>gi|77964602|gb|ABB05983.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia sp. 383]		x		
78060052	>gi|78060052|ref|YP_366627.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia sp. 383]		x		
67677415	>gi|67677415|ref|ZP_00474151.1| Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Chromohalobacter salexigens DSM 3043]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
67518584	>gi|67518584|gb|EAM22550.1| Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Chromohalobacter salexigens DSM 3043]		x		
6469462	>gi|6469462|emb|CAB61799.1| putative isomerase [Streptomyces coelicolor A3(2)]		x		
21221899	>gi|21221899|ref|NP_627678.1| isomerase [Streptomyces coelicolor A3(2)]		x		
77383946	>gi|77383946|gb|ABA75459.1| Mandelate racemase/muconate lactonizing enzyme [Pseudomonas fluorescens PfO-1]		x		
77459943	>gi|77459943|ref|YP_349450.1| Mandelate racemase/muconate lactonizing enzyme [Pseudomonas fluorescens PfO-1]		x		
67547730	>gi|67547730|ref|ZP_00425630.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia vietnamiensis G4]		x		
67531011	>gi|67531011|gb|EAM27836.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia vietnamiensis G4]		x		
67664329	>gi|67664329|ref|ZP_00461604.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia cenocepacia HI2424]		x		
67657983	>gi|67657983|ref|ZP_00455358.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia cenocepacia AU 1054]		x		
67102115	>gi|67102115|gb|EAM19250.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia cenocepacia HI2424]		x		
67094410	>gi|67094410|gb|EAM11944.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia cenocepacia AU 1054]		x		
77966492	>gi|77966492|gb|ABB07872.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia sp. 383]		x		
78065747	>gi|78065747|ref|YP_368516.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia sp. 383]		x		
74015769	>gi|74015769|ref|ZP_00686396.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia ambifaria AMMD]		x		
72611198	>gi|72611198|gb|EAO47143.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia ambifaria AMMD]		x		
52001952	>gi|52001952|gb|AAU21894.1| Mandelate racemase/muconate lactonizing enzyme [Bacillus licheniformis ATCC 14580]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
52078741	>gi|52078741|ref|YP_077532.1| Mandelate racemase/muconate lactonizing enzyme [Bacillus licheniformis ATCC 14580]		x		
67932686	>gi|67932686|ref|ZP_00525824.1| Mandelate racemase/muconate lactonizing enzyme [Solibacter usitatus Ellin6076]		x		
67860101	>gi|67860101|gb|EAM55157.1| Mandelate racemase/muconate lactonizing enzyme [Solibacter usitatus Ellin6076]		x		
46914221	>gi|46914221|emb|CAG21001.1| putative o-succinylbenzoate-CoA synthase [Photobacterium profundum SS9]		x		
1573992	>gi|1573992|gb|AAC22626.1| O-succinylbenzoate-CoA synthase (menC) [Haemophilus influenzae Rd KW20]		x		
23492313	>gi|23492313|dbj|BAC17287.1| putative muconate cycloisomerase [Corynebacterium efficiens YS-314]		x		
45436988	>gi|45436988|gb|AAS62541.1| putative O-succinylbenzoate-CoA synthase [Yersinia pestis biovar Medievalis str. 91001]		x		
15980516	>gi|15980516|emb|CAC91327.1| putative O-succinylbenzoate-CoA synthase [Yersinia pestis CO92]		x		
21958460	>gi|21958460|gb|AAM85232.1| o-succinylbenzoyl-CoA synthase [Yersinia pestis KIM]		x		
49610679	>gi|49610679|emb|CAG74124.1| O-succinylbenzoate-CoA synthase [Erwinia carotovora subsp. atroseptica SCRI1043]		x		
51590158	>gi|51590158|emb|CAH21795.1| putative O-succinylbenzoate-CoA synthase [Yersinia pseudotuberculosis IP 32953]		x		
28805919	>gi|28805919|dbj|BAC59195.1| o-succinylbenzoate-CoA synthase [Vibrio parahaemolyticus RIMD 2210633]		x		
24351060	>gi|24351060|gb|AAN57535.1| O-succinylbenzoate-CoA synthase [Shewanella oneidensis MR-1]		x		
2635562	>gi|2635562|emb|CAB15056.1| O-succinylbenzoate-CoA synthase [Bacillus subtilis subsp. subtilis str. 168]		x		
16080130	>gi|16080130|ref|NP_390956.1| O-succinylbenzoate-CoA synthase [Bacillus subtilis subsp. subtilis str. 168]		x		
9656512	>gi|9656512|gb|AAF95120.1| o-succinylbenzoate-CoA synthase [Vibrio cholerae O1 biovar eltor str. N16961]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
1788596	>gi|1788596|gb|AAC75321.1| o-succinylbenzoyl-CoA synthase; conversion of chorismate to 2-o-succinylbenzoyl-CoA [Escherichia coli K12]		x		
85675330	>gi|85675330|dbj|BAA16085.2| o-succinylbenzoyl-CoA synthase [Escherichia coli W3110]		x		
82777670	>gi|82777670|ref|YP_404019.1| o-succinylbenzoyl-CoA synthase [Shigella dysenteriae Sd197]		x		
81241818	>gi|81241818|gb|ABB62528.1| o-succinylbenzoyl-CoA synthase [Shigella dysenteriae Sd197]		x		
73856260	>gi|73856260|gb|AAZ88967.1| O-succinylbenzoyl-CoA synthase [Shigella sonnei Ss046]		x		
13362619	>gi|13362619|dbj|BAB36572.1| o-succinylbenzoyl-CoA synthase [Escherichia coli O157:H7]		x		
12516609	>gi|12516609|gb|AAG57394.1| o-succinylbenzoyl-CoA synthase; conversion of chorismate to 2-o-succinylbenzoyl-CoA [Escherichia coli O157:H7 EDL933]		x		
26109055	>gi|26109055|gb|AAN81258.1| O-succinylbenzoate-CoA synthase [Escherichia coli CFT073]		x		
16420846	>gi|16420846|gb|AAL21207.1| o-succinylbenzoyl-CoA synthase [Salmonella typhimurium LT2]		x		
62128509	>gi|62128509|gb|AAX66212.1| o-succinylbenzoyl-CoA synthase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]		x		
24052698	>gi|24052698|gb|AAN43854.1| O-succinylbenzoyl-CoA synthase [Shigella flexneri 2a str. 301]		x		
30041947	>gi|30041947|gb|AAP17673.1| O-succinylbenzoyl-CoA synthase [Shigella flexneri 2a str. 2457T]		x		
82544743	>gi|82544743|ref|YP_408690.1| o-succinylbenzoyl-CoA synthase [Shigella boydii Sb227]		x		
81246154	>gi|81246154|gb|ABB66862.1| o-succinylbenzoyl-CoA synthase [Shigella boydii Sb227]		x		
56127053	>gi|56127053|gb|AAV76559.1| O-succinylbenzoate-CoA synthase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
16503531	>gi|16503531|emb|CAD07539.1| O-succinylbenzoate-CoA synthase [Salmonella enterica subsp. enterica serovar Typhi]		x		
29136698	>gi|29136698|gb|AAO68263.1| O-succinylbenzoate-CoA synthase [Salmonella enterica subsp. enterica serovar Typhi Ty2]		x		
25357724	>gi|25357724|pir||AI0794 O-succinylbenzoate-CoA synthase [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)		x		
33148409	>gi|33148409|gb|AAP95929.1| O-succinylbenzoate-CoA synthase [Haemophilus ducreyi 35000HP]		x		
68208070	>gi|68208070|ref|ZP_00560206.1| Mandelate racemase/muconate lactonizing enzyme [Desulfitobacterium hafniense DCB-2]		x		
68168049	>gi|68168049|gb|EAM95999.1| Mandelate racemase/muconate lactonizing enzyme [Desulfitobacterium hafniense DCB-2]		x		
13093906	>gi|13093906|emb|CAC31784.1| putative isomerase/racemase [Mycobacterium leprae]		x		
41324698	>gi|41324698|emb|CAF19180.1| similar to o-succinylbenzoate-coa synthase [Corynebacterium glutamicum ATCC 13032]		x		
52004775	>gi|52004775|gb|AAU24717.1| O-succinylbenzoate-CoA synthase [Bacillus licheniformis ATCC 14580]		x		
52081564	>gi|52081564|ref|YP_080355.1| O-succinylbenzoate-CoA synthase [Bacillus licheniformis ATCC 14580]		x		
12723640	>gi|12723640|gb|AAK04825.1| racemase [Lactococcus lactis subsp. lactis Il1403]		x		
15672709	>gi|15672709|ref|NP_266883.1| racemase [Lactococcus lactis subsp. lactis Il1403]		x		
50950516	>gi|50950516|gb|AAT88217.1| O-succinylbenzoate-CoA synthase [Leifsonia xyli subsp. xyli str. CTCB07]		x		
82497160	>gi|82497160|ref|ZP_00882719.1| O-succinylbenzoate-CoA synthase [Shewanella sp. MR-4]		x		
82404873	>gi|82404873|gb|EAP45554.1| O-succinylbenzoate-CoA synthase [Shewanella sp. MR-4]		x		
78684421	>gi|78684421|ref|ZP_00849205.1| O-succinylbenzoate-CoA synthase [Shewanella sp. ANA-3]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
78507753	>gi|78507753|gb|EAP21262.1| O-succinylbenzoate-CoA synthase [Shewanella sp. ANA-3]		x		
68054688	>gi|68054688|ref|ZP_00538838.1| Mandelate racemase/muconate lactonizing enzyme [Exiguobacterium sp. 255-15]		x		
68008605	>gi|68008605|gb|EAM87829.1| Mandelate racemase/muconate lactonizing enzyme [Exiguobacterium sp. 255-15]		x		
78689221	>gi|78689221|ref|ZP_00853885.1| O-succinylbenzoate-CoA synthase [Shewanella sp. MR-7]		x		
78511378	>gi|78511378|gb|EAP24736.1| O-succinylbenzoate-CoA synthase [Shewanella sp. MR-7]		x		
21647864	>gi|21647864|gb|AAM73067.1| o-succinylbenzoate-CoA synthase [Chlorobium tepidum TLS]		x		
21674660	>gi|21674660|ref|NP_662725.1| O-succinylbenzoate-CoA synthase [Chlorobium tepidum TLS]		x		
13880091	>gi|13880091|gb|AAK44802.1| muconate cycloisomerase I, putative [Mycobacterium tuberculosis CDC1551]		x		
3261782	>gi|3261782|emb|CAB08964.1| PROBABLE MUCONATE CYCLOISOMERASE MENC (CIS,CIS-MUCONATE LACTONIZING ENZYME) (MLE) [Mycobacterium tuberculosis H37Rv]		x		
31617321	>gi|31617321|emb|CAD93430.1| PROBABLE MUCONATE CYCLOISOMERASE MENC (CIS,CIS-MUCONATE LACTONIZING ENZYME) (MLE) [Mycobacterium bovis AF2122/97]		x		
50839988	>gi|50839988|gb|AAT82655.1| O-succinylbenzoate-CoA synthase [Propionibacterium acnes KPA171202]		x		
71915546	>gi|71915546|gb|AAZ55448.1| o-succinylbenzoate-CoA synthase [Thermobifida fusca YX]		x		
38199295	>gi|38199295|emb|CAE48926.1| Putative O-succinylbenzoate-CoA synthase [Corynebacterium diphtheriae]		x		
29350111	>gi|29350111|ref|NP_813614.1| chloromuconate cycloisomerase [Bacteroides thetaiotaomicron VPI-5482]		x		
29342023	>gi|29342023|gb|AAO79808.1| chloromuconate cycloisomerase [Bacteroides thetaiotaomicron VPI-5482]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
67987856	>gi|67987856|gb|EAM75642.1| Mandelate racemase/muconate lactonizing enzyme [Kineococcus radiotolerans SRS30216]		x		
69284896	>gi|69284896|ref|ZP_00616595.1| Mandelate racemase/muconate lactonizing enzyme [Kineococcus radiotolerans SRS30216]		x		
66966163	>gi|66966163|ref|ZP_00413725.1| Mandelate racemase/muconate lactonizing enzyme [Arthrobacter sp. FB24]		x		
66868003	>gi|66868003|gb|EAL95377.1| Mandelate racemase/muconate lactonizing enzyme [Arthrobacter sp. FB24]		x		
68562469	>gi|68562469|ref|ZP_00601727.1| Mandelate racemase/muconate lactonizing enzyme [Rubrobacter xylanophilus DSM 9941]		x		
68511354	>gi|68511354|gb|EAN35203.1| Mandelate racemase/muconate lactonizing enzyme [Rubrobacter xylanophilus DSM 9941]		x		
33237177	>gi|33237177|gb|AAP99246.1| O-succinylbenzoate-CoA synthase [Prochlorococcus marinus subsp. marinus str. CCMP1375]		x		
33239652	>gi|33239652|ref|NP_874594.1| O-succinylbenzoate-CoA synthase [Prochlorococcus marinus subsp. marinus str. CCMP1375]		x		
84494961	>gi|84494961|ref|ZP_00994080.1| O-succinylbenzoate-CoA synthase [Janibacter sp. HTCC2649]		x		
84384454	>gi|84384454|gb|EAQ00334.1| O-succinylbenzoate-CoA synthase [Janibacter sp. HTCC2649]		x		
77814934	>gi|77814934|ref|ZP_00814184.1| O-succinylbenzoate-CoA synthase [Shewanella putrefaciens CN-32]		x		
77810108	>gi|77810108|gb|EAO94493.1| O-succinylbenzoate-CoA synthase [Shewanella putrefaciens CN-32]		x		
68542839	>gi|68542839|ref|ZP_00582561.1| O-succinylbenzoate-CoA synthase [Shewanella baltica OS155]		x		
68519432	>gi|68519432|gb|EAN42965.1| O-succinylbenzoate-CoA synthase [Shewanella baltica OS155]		x		
82741684	>gi|82741684|ref|ZP_00904400.1| O-succinylbenzoate-CoA synthase [Shewanella sp. W3-18-1]		x		
60492256	>gi|60492256|emb|CAH07021.1| putative muconate cycloisomerase [Bacteroides fragilis NCTC 9343]		x		

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>60680822</td><td>>gi|60680822|ref|YP_210966.1| putative muconate cycloisomerase [Bacteroides fragilis NCTC 9343]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>71846867</td><td>>gi|71846867|gb|AAZ46363.1| Mandelate racemase/muconate lactonizing enzyme [Dechloromonas aromatica RCB]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>71907246</td><td>>gi|71907246|ref|YP_284833.1| Mandelate racemase/muconate lactonizing enzyme [Dechloromonas aromatica RCB]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>52215476</td><td>>gi|52215476|dbj|BAD48069.1| chloromuconate cycloisomerase [Bacteroides fragilis YCH46]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>53712611</td><td>>gi|53712611|ref|YP_098603.1| chloromuconate cycloisomerase [Bacteroides fragilis YCH46]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>71369872</td><td>>gi|71369872|ref|ZP_00660277.1| Mandelate racemase/muconate lactonizing enzyme [Nocardioides sp. JS614]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>71154410</td><td>>gi|71154410|gb|EAO04932.1| Mandelate racemase/muconate lactonizing enzyme [Nocardioides sp. JS614]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>76261333</td><td>>gi|76261333|ref|ZP_00768947.1| Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Chloroflexus aurantiacus J-10-fl]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>76163761</td><td>>gi|76163761|gb|EAO57927.1| Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Chloroflexus aurantiacus J-10-fl]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>14021703</td><td>>gi|14021703|dbj|BAB48315.1| probable muconate cycloisomerase [Mesorhizobium loti MAFF303099]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>13470960</td><td>>gi|13470960|ref|NP_102529.1| probable muconate cycloisomerase [Mesorhizobium loti MAFF303099]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>68193420</td><td>>gi|68193420|gb|EAN08072.1| Mandelate racemase/muconate lactonizing enzyme [Mesorhizobium sp. BNC1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>69274980</td><td>>gi|69274980|ref|ZP_00610892.1| Mandelate racemase/muconate lactonizing enzyme [Mesorhizobium sp. BNC1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>49612565</td><td>>gi|49612565|emb|CAG76015.1| putative mandelate racemase/muconate lactonizing enzyme [Erwinia carotovora subsp. atroseptica SCRI1043]</td><td></td><td>x</td><td></td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
50122039	>gi|50122039|ref|YP_051206.1| putative mandelate racemase/muconate lactonizing enzyme [Erwinia carotovora subsp. atroseptica SCRI1043]		x		
82699869	>gi|82699869|ref|YP_414443.1| Mandelate racemase/muconate lactonizing enzyme [Brucella melitensis biovar Abortus 2308]		x		
82615970	>gi|82615970|emb|CAJ10993.1| Mandelate racemase/muconate lactonizing enzyme [Brucella melitensis biovar Abortus]		x		
17982924	>gi|17982924|gb|AAL52147.1| MUCONATE CYCLOISOMERASE I [Brucella melitensis 16M]		x		
17987249	>gi|17987249|ref|NP_539883.1| MUCONATE CYCLOISOMERASE I [Brucella melitensis 16M]		x		
39650882	>gi|39650882|emb|CAE29405.1| putative muconate cycloisomerase [Rhodopseudomonas palustris CGA009]		x		
39937025	>gi|39937025|ref|NP_949301.1| putative muconate cycloisomerase [Rhodopseudomonas palustris CGA009]		x		
69928950	>gi|69928950|ref|ZP_00625964.1| Mandelate racemase/muconate lactonizing enzyme [Nitrobacter hamburgensis X14]		x		
69142115	>gi|69142115|gb|EAN60680.1| Mandelate racemase/muconate lactonizing enzyme [Nitrobacter hamburgensis X14]		x		
77386731	>gi|77386731|gb|ABA77916.1| Mandelate racemase / muconate lactonizing enzyme [Rhodobacter sphaeroides 2.4.1]		x		
77462313	>gi|77462313|ref|YP_351817.1| Mandelate racemase / muconate lactonizing enzyme [Rhodobacter sphaeroides 2.4.1]		x		
78495713	>gi|78495713|ref|ZP_00847932.1| Mandelate racemase/muconate lactonizing enzyme [Rhodopseudomonas palustris BisB18]		x		
78387141	>gi|78387141|gb|EAP10208.1| Mandelate racemase/muconate lactonizing enzyme [Rhodopseudomonas palustris BisB18]		x		
29137654	>gi|29137654|gb|AAO69216.1| putative mandelate racemase [Salmonella enterica subsp. enterica serovar Typhi Ty2]		x		
86571778	>gi|86571778|gb|ABD06335.1| Mandelate racemase/muconate lactonizing enzyme [Rhodopseudomonas palustris HaA2]		x		
22778653	>gi|22778653|dbj|BAC14921.1| muconate cycloisomerase [Oceanobacillus iheyensis HTE831]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
23100420	>gi|23100420|ref|NP_693887.1| muconate cycloisomerase [Oceanobacillus iheyensis HTE831]		x		
85715012	>gi|85715012|ref|ZP_01045997.1| mandelate racemase/muconate lactonizing enzyme [Nitrobacter sp. Nb-311A]		x		
85698209	>gi|85698209|gb|EAQ36081.1| mandelate racemase/muconate lactonizing enzyme [Nitrobacter sp. Nb-311A]		x		
62180244	>gi|62180244|ref|YP_216661.1| putative chloromuconate cycloisomerase (muconate cycloisomerase) [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]		x		
62127877	>gi|62127877|gb|AAX65580.1| putative chloromuconate cycloisomerase (muconate cycloisomerase) [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]		x		
16420208	>gi|16420208|gb|AAL20598.1| putative chloromuconate cycloisomerase; muconate cycloisomerase [Salmonella typhimurium LT2]		x		
16765024	>gi|16765024|ref|NP_460639.1| putative chloromuconate cycloisomerase [Salmonella typhimurium LT2]		x		
56383430	>gi|56383430|gb|AAN42937.2| putative muconate cycloisomerase I [Shigella flexneri 2a str. 301]		x		
30041091	>gi|30041091|gb|AAP16821.1| putative muconate cycloisomerase I [Shigella flexneri 2a str. 2457T]		x		
30062843	>gi|30062843|ref|NP_837014.1| putative muconate cycloisomerase I [Shigella flexneri 2a str. 2457T]		x		
56479879	>gi|56479879|ref|NP_707230.2| putative muconate cycloisomerase I [Shigella flexneri 2a str. 301]		x		
82776689	>gi|82776689|ref|YP_403038.1| putative muconate cycloisomerase I [Shigella dysenteriae Sd197]		x		
81240837	>gi|81240837|gb|ABB61547.1| putative muconate cycloisomerase I [Shigella dysenteriae Sd197]		x		
13361369	>gi|13361369|dbj|BAB35327.1| putative muconate cycloisomerase I [Escherichia coli O157:H7]		x		
38703962	>gi|38703962|ref|NP_309931.2| putative muconate cycloisomerase I [Escherichia coli O157:H7]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
77689340	>gi|77689340|ref|ZP_00804522.1| Mandelate racemase/muconate lactonizing enzyme [Rhodopseudomonas palustris BisB5]		x		
77654347	>gi|77654347|gb|EAO86088.1| Mandelate racemase/muconate lactonizing enzyme [Rhodopseudomonas palustris BisB5]		x		
19712800	>gi|19712800|gb|AAL93701.1| O-succinylbenzoate-CoA synthase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]		x		
19704907	>gi|19704907|ref|NP_602402.1| O-succinylbenzoate-CoA synthase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]		x		
15801845	>gi|15801845|ref|NP_287863.1| putative muconate cycloisomerase I [Escherichia coli O157:H7 EDL933]		x		
86357965	>gi|86357965|ref|YP_469857.1| probable muconate cycloisomerase I protein [Rhizobium etli CFN 42]		x		
86282067	>gi|86282067|gb|ABC91130.1| probable muconate cycloisomerase I protein [Rhizobium etli CFN 42]		x		
45436784	>gi|45436784|gb|AAS62337.1| putative mandelate racemase / muconate lactonizing protein [Yersinia pestis biovar Medievalis str. 91001]		x		
51589866	>gi|51589866|emb|CAH21498.1| putative mandelate racemase / muconate lactonizing protein [Yersinia pseudotuberculosis IP 32953]		x		
15980338	>gi|15980338|emb|CAC91146.1| putative mandelate racemase / muconate lactonizing protein [Yersinia pestis CO92]		x		
21958818	>gi|21958818|gb|AAM85557.1| putative muconate cycloisomerase I [Yersinia pestis KIM]		x		
22125883	>gi|22125883|ref|NP_669306.1| muconate cycloisomerase I [Yersinia pestis KIM]		x		
51596584	>gi|51596584|ref|YP_070775.1| putative mandelate racemase / muconate lactonizing protein [Yersinia pseudotuberculosis IP 32953]		x		
45441921	>gi|45441921|ref|NP_993460.1| putative mandelate racemase / muconate lactonizing protein [Yersinia pestis biovar Medievalis str. 91001]		x		
16122565	>gi|16122565|ref|NP_405878.1| putative mandelate racemase / muconate lactonizing protein [Yersinia pestis CO92]		x		

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>83593891</td><td>>gi|83593891|ref|YP_427643.1| Mandelate racemase/muconate lactonizing enzyme [Rhodospirillum rubrum ATCC 11170]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>83576805</td><td>>gi|83576805|gb|ABC23356.1| Mandelate racemase/muconate lactonizing enzyme [Rhodospirillum rubrum ATCC 11170]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>74420148</td><td>>gi|74420148|gb|ABA04347.1| mandelate racemase/muconate lactonizing enzyme [Nitrobacter winogradskyi Nb-255]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>75675278</td><td>>gi|75675278|ref|YP_317699.1| mandelate racemase/muconate lactonizing enzyme [Nitrobacter winogradskyi Nb-255]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>77739092</td><td>>gi|77739092|ref|ZP_00807584.1| IMP dehydrogenase/GMP reductase:Mandelate racemase/muconate lactonizing enzyme [Rhodopseudomonas palustris BisA53]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>77700902</td><td>>gi|77700902|gb|EAO92041.1| IMP dehydrogenase/GMP reductase:Mandelate racemase/muconate lactonizing enzyme [Rhodopseudomonas palustris BisA53]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>56127654</td><td>>gi|56127654|gb|AAV77160.1| putative mandelate racemase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>56413397</td><td>>gi|56413397|ref|YP_150472.1| putative mandelate racemase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>21110264</td><td>>gi|21110264|gb|AAM38704.1| chloromuconate cycloisomerase [Xanthomonas axonopodis pv. citri str. 306]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>21244586</td><td>>gi|21244586|ref|NP_644168.1| chloromuconate cycloisomerase [Xanthomonas axonopodis pv. citri str. 306]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>46913516</td><td>>gi|46913516|emb|CAG20302.1| Hypothetical muconate cycloisomerase I [Photobacterium profundum SS9]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>54309084</td><td>>gi|54309084|ref|YP_130104.1| Hypothetical muconate cycloisomerase I [Photobacterium profundum SS9]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>15023023</td><td>>gi|15023023|gb|AAK78174.1| Similar to chloromuconate cycloisomerase [Clostridium acetobutylicum ATCC 824]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>15893485</td><td>>gi|15893485|ref|NP_346834.1| Similar to chloromuconate cycloisomerase [Clostridium acetobutylicum ATCC 824]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>10581283</td><td>>gi|10581283|gb|AAG20045.1| chloromuconate cycloisomerase; YkfB1 [Halobacterium sp. NRC-1]</td><td></td><td>x</td><td></td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
21115078	>gi|21115078|gb|AAM43053.1| chloromuconate cycloisomerase [Xanthomonas campestris pv. campestris str. ATCC 33913]		x		
21233235	>gi|21233235|ref|NP_639152.1| chloromuconate cycloisomerase [Xanthomonas campestris pv. campestris str. ATCC 33913]		x		
78037966	>gi|78037966|emb|CAJ25711.1| putative chloromuconate cycloisomerase [Xanthomonas campestris pv. vesicatoria str. 85-10]		x		
78049536	>gi|78049536|ref|YP_365711.1| putative chloromuconate cycloisomerase [Xanthomonas campestris pv. vesicatoria str. 85-10]		x		
28808495	>gi|28808495|dbj|BAC61672.1| putative muconate cycloisomerase I [Vibrio parahaemolyticus RIMD 2210633]		x		
28900184	>gi|28900184|ref|NP_799839.1| putative muconate cycloisomerase I [Vibrio parahaemolyticus RIMD 2210633]		x		
51976131	>gi|51976131|gb|AAU17681.1| mandelate racemase/muconate lactonizing enzyme [Bacillus cereus E33L]		x		
52142662	>gi|52142662|ref|YP_084167.1| mandelate racemase/muconate lactonizing enzyme [Bacillus cereus E33L]		x		
17132665	>gi|17132665|dbj|BAB75231.1| muconate cycloisomerase [Nostoc sp. PCC 7120]		x		
17231024	>gi|17231024|ref|NP_487572.1| muconate cycloisomerase [Nostoc sp. PCC 7120]		x		
66575509	>gi|66575509|gb|AAY50919.1| chloromuconate cycloisomerase [Xanthomonas campestris pv. campestris str. 8004]		x		
66770177	>gi|66770177|ref|YP_244939.1| chloromuconate cycloisomerase [Xanthomonas campestris pv. campestris str. 8004]		x		
68192448	>gi|68192448|gb|EAN07102.1| Mandelate racemase/muconate lactonizing enzyme [Mesorhizobium sp. BNC1]		x		
69276542	>gi|69276542|ref|ZP_00612136.1| Mandelate racemase/muconate lactonizing enzyme [Mesorhizobium sp. BNC1]		x		
75703443	>gi|75703443|gb|ABA23119.1| Mandelate racemase/muconate lactonizing enzyme [Anabaena variabilis ATCC 29413]		x		
75909718	>gi|75909718|ref|YP_324014.1| Mandelate racemase/muconate lactonizing enzyme [Anabaena variabilis ATCC 29413]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
69300394	>gi|69300394|ref|ZP_00621959.1| Mandelate racemase/muconate lactonizing enzyme [Silicibacter sp. TM1040]		x		
69132915	>gi|69132915|gb|EAN56189.1| Mandelate racemase/muconate lactonizing enzyme [Silicibacter sp. TM1040]		x		
32446038	>gi|32446038|emb|CAD75867.1| chloromuconate cycloisomerase YkfB1 [Rhodopirellula baltica SH 1]		x		
32475496	>gi|32475496|ref|NP_868490.1| chloromuconate cycloisomerase YkfB1 [Rhodopirellula baltica SH 1]		x		
82544227	>gi|82544227|ref|YP_408174.1| putative muconate cycloisomerase I [Shigella boydii Sb227]		x		
81245638	>gi|81245638|gb|ABB66346.1| putative muconate cycloisomerase I [Shigella boydii Sb227]		x		
49330647	>gi|49330647|gb|AAT61293.1| mandelate racemase/muconate lactonizing enzyme [Bacillus thuringiensis serovar konkukian str. 97-27]		x		
49479091	>gi|49479091|ref|YP_036935.1| mandelate racemase/muconate lactonizing enzyme [Bacillus thuringiensis serovar konkukian str. 97-27]		x		
84369475	>gi|84369475|dbj|BAE70633.1| chloromuconate cycloisomerase [Xanthomonas oryzae pv. oryzae MAFF 311018]		x		
84625535	>gi|84625535|ref|YP_452907.1| chloromuconate cycloisomerase [Xanthomonas oryzae pv. oryzae MAFF 311018]		x		
58583725	>gi|58583725|ref|YP_202741.1| chloromuconate cycloisomerase [Xanthomonas oryzae pv. oryzae KACC10331]		x		
58428319	>gi|58428319|gb|AAW77356.1| chloromuconate cycloisomerase [Xanthomonas oryzae pv. oryzae KACC10331]		x		
77966567	>gi|77966567|gb|ABB07947.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia sp. 383]		x		
78065822	>gi|78065822|ref|YP_368591.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia sp. 383]		x		
84515760	>gi|84515760|ref|ZP_01003121.1| Mandelate racemase / muconate lactonizing enzyme [Loktanella vestfoldensis SKA53]		x		
84510202	>gi|84510202|gb|EAQ06658.1| Mandelate racemase / muconate lactonizing enzyme [Loktanella vestfoldensis SKA53]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
10175628	>gi|10175628|dbj|BAB06725.1| muconate cycloisomerase [Bacillus halodurans C-125]		x		
15615568	>gi|15615568|ref|NP_243872.1| muconate cycloisomerase [Bacillus halodurans C-125]		x		
68180729	>gi|68180729|ref|ZP_00553712.1| Mandelate racemase/muconate lactonizing enzyme [Jannaschia sp. CCS1]		x		
67979088	>gi|67979088|gb|EAM68705.1| Mandelate racemase/muconate lactonizing enzyme [Jannaschia sp. CCS1]		x		
77684669	>gi|77684669|ref|ZP_00800093.1| Mandelate racemase/muconate lactonizing enzyme [Alkaliphilus metalliredigenes QYMF]		x		
77639548	>gi|77639548|gb|EAO81912.1| Mandelate racemase/muconate lactonizing enzyme [Alkaliphilus metalliredigenes QYMF]		x		
74312308	>gi|74312308|ref|YP_310727.1| putative muconate cycloisomerase I [Shigella sonnei Ss046]		x		
73855785	>gi|73855785|gb|AAZ88492.1| putative muconate cycloisomerase I [Shigella sonnei Ss046]		x		
84389418	>gi|84389418|ref|ZP_00991224.1| putative muconate cycloisomerase I [Vibrio splendidus 12B01]		x		
84376933	>gi|84376933|gb|EAP93806.1| putative muconate cycloisomerase I [Vibrio splendidus 12B01]		x		
52003007	>gi|52003007|gb|AAU22949.1| putative muconate cycloisomerase [Bacillus subtilis phage PBSX]		x		
52079796	>gi|52079796|ref|YP_078587.1| putative muconate cycloisomerase [Bacillus licheniformis ATCC 14580]		x		
86145024	>gi|86145024|ref|ZP_01063356.1| putative muconate cycloisomerase I [Vibrio sp. MED222]		x		
85837923	>gi|85837923|gb|EAQ56035.1| putative muconate cycloisomerase I [Vibrio sp. MED222]		x		
68560641	>gi|68560641|ref|ZP_00599952.1| Mandelate racemase/muconate lactonizing enzyme [Rubrobacter xylanophilus DSM 9941]		x		
68513172	>gi|68513172|gb|EAN36968.1| Mandelate racemase/muconate lactonizing enzyme [Rubrobacter xylanophilus DSM 9941]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
76792916	>gi|76792916|ref|ZP_00775410.1| Mandelate racemase/muconate lactonizing enzyme [Pseudoalteromonas atlantica T6c]		x		
76591735	>gi|76591735|gb|EAO67931.1| Mandelate racemase/muconate lactonizing enzyme [Pseudoalteromonas atlantica T6c]		x		
76557748	>gi|76557748|emb|CAI49331.1| mandelate racemase homolog / muconate lactonizing enzyme homolog [Natronomonas pharaonis DSM 2160]		x		
76801883	>gi|76801883|ref|YP_326891.1| mandelate racemase homolog / muconate lactonizing enzyme homolog [Natronomonas pharaonis DSM 2160]		x		
72123620	>gi|72123620|gb|AAZ65763.1| Mandelate racemase/muconate lactonizing enzyme [Ralstonia eutropha JMP134]		x		
72384267	>gi|72384267|ref|YP_293620.1| Mandelate racemase/muconate lactonizing enzyme [Ralstonia eutropha JMP134]		x		
41326584	>gi|41326584|emb|CAF21066.1| CHLOROMUCONATE CYCLOISOMERASE [Corynebacterium glutamicum ATCC 13032]		x		
62391244	>gi|62391244|ref|YP_226646.1| CHLOROMUCONATE CYCLOISOMERASE [Corynebacterium glutamicum ATCC 13032]		x		
23308936	>gi|23308936|ref|NP_601602.2| putative chloromuconate cycloisomerase [Corynebacterium glutamicum ATCC 13032]		x		
57223758	>gi|57223758|gb|AAW41801.1| mandelate racemase/muconate lactonizing enzyme, putative [Cryptococcus neoformans var. neoformans JEC21]		x		
58263396	>gi|58263396|ref|XP_569108.1| mandelate racemase/muconate lactonizing enzyme [Cryptococcus neoformans var. neoformans JEC21]		x		
77969357	>gi|77969357|gb|ABB10736.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia sp. 383]		x		
78061472	>gi|78061472|ref|YP_371380.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia sp. 383]		x		
74018423	>gi|74018423|ref|ZP_00689044.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia ambifaria AMMD]		x		
72608955	>gi|72608955|gb|EAO44906.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia ambifaria AMMD]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
67663584	>gi|67663584|ref|ZP_00460865.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia cenocepacia HI2424]		x		
67655301	>gi|67655301|ref|ZP_00452688.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia cenocepacia AU 1054]		x		
67102866	>gi|67102866|gb|EAM19995.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia cenocepacia HI2424]		x		
67097439	>gi|67097439|gb|EAM14961.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia cenocepacia AU 1054]		x		
45436138	>gi|45436138|gb|AAS61694.1| O-succinylbenzoate synthase and related enzymes [Yersinia pestis biovar Medievalis str. 91001]		x		
45441278	>gi|45441278|ref|NP_992817.1| O-succinylbenzoate synthase and related enzyme [Yersinia pestis biovar Medievalis str. 91001]		x		
17983732	>gi|17983732|gb|AAL52888.1| MANDELATE RACEMASE [Brucella melitensis 16M]		x		
17987990	>gi|17987990|ref|NP_540624.1| MANDELATE RACEMASE [Brucella melitensis 16M]		x		
82699152	>gi|82699152|ref|YP_413726.1| Mandelate racemase/muconate lactonizing enzyme [Brucella melitensis biovar Abortus 2308]		x		
82615253	>gi|82615253|emb|CAJ10204.1| Mandelate racemase/muconate lactonizing enzyme [Brucella melitensis biovar Abortus]		x		
67543243	>gi|67543243|ref|ZP_00421176.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia vietnamiensis G4]		x		
67535422	>gi|67535422|gb|EAM32154.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia vietnamiensis G4]		x		
86360704	>gi|86360704|ref|YP_472592.1| probable mandelate racemase protein [Rhizobium etli CFN 42]		x		
86284806	>gi|86284806|gb|ABC93865.1| probable mandelate racemase protein [Rhizobium etli CFN 42]		x		
67777516	>gi|67777516|gb|EAM37143.1| Mandelate racemase/muconate lactonizing enzyme [Polaromonas sp. JS666]		x		
67910349	>gi|67910349|ref|ZP_00508740.1| Mandelate racemase/muconate lactonizing enzyme [Polaromonas sp. JS666]		x		

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
74020687	>gi|74020687|ref|ZP_00691276.1| Mandelate racemase/muconate lactonizing enzyme [Rhodoferax ferrireducens DSM 15236]		x		
72606701	>gi|72606701|gb|EAO42684.1| Mandelate racemase/muconate lactonizing enzyme [Rhodoferax ferrireducens DSM 15236]		x		
29610948	>gi|29610948|dbj|BAC74993.1| putative mandelate racemase [Streptomyces avermitilis MA-4680]		x		
29833824	>gi|29833824|ref|NP_828458.1| putative mandelate racemase [Streptomyces avermitilis MA-4680]		x		
68562552	>gi|68562552|ref|ZP_00601806.1| Mandelate racemase/muconate lactonizing enzyme [Rubrobacter xylanophilus DSM 9941]		x		
68511291	>gi|68511291|gb|EAN35144.1| Mandelate racemase/muconate lactonizing enzyme [Rubrobacter xylanophilus DSM 9941]		x		
76651806	>gi|76651806|ref|XP_871913.1| PREDICTED: similar to rTS beta protein isoform 2 [Bos taurus]		x		
67675856	>gi|67675856|ref|ZP_00472610.1| Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Chromohalobacter salexigens DSM 3043]		x		
67520125	>gi|67520125|gb|EAM24071.1| Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Chromohalobacter salexigens DSM 3043]		x		
78038273	>gi|78038273|emb|CAJ26018.1| putative mandelate racemase/muconate lactonizing enzyme [Xanthomonas campestris pv. vesicatoria str. 85-10]		x		
78049843	>gi|78049843|ref|YP_366018.1| putative mandelate racemase/muconate lactonizing enzyme [Xanthomonas campestris pv. vesicatoria str. 85-10]		x		
67986809	>gi|67986809|gb|EAM74620.1| Mandelate racemase/muconate lactonizing enzyme [Kineococcus radiotolerans SRS30216]		x		
69286820	>gi|69286820|ref|ZP_00617628.1| Mandelate racemase/muconate lactonizing enzyme [Kineococcus radiotolerans SRS30216]		x		
73961860	>gi|73961860|ref|XP_848625.1| PREDICTED: similar to rTS beta protein isoform 2 isoform 3 [Canis familiaris]		x		

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>32398341</td><td>>gi|32398341|emb|CAD61030.1| putative mandelate racemase/muconate lactonizing enzyme [Arthrobacter ilicis]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>69300569</td><td>>gi|69300569|ref|ZP_00622134.1| Mandelate racemase/muconate lactonizing enzyme [Silicibacter sp. TM1040]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>69133090</td><td>>gi|69133090|gb|EAN56364.1| Mandelate racemase/muconate lactonizing enzyme [Silicibacter sp. TM1040]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>51589196</td><td>>gi|51589196|emb|CAH20816.1| putative racemase [Yersinia pseudotuberculosis IP 32953]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>15979607</td><td>>gi|15979607|emb|CAC90389.1| putative racemase [Yersinia pestis CO92]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>51595914</td><td>>gi|51595914|ref|YP_070105.1| putative racemase [Yersinia pseudotuberculosis IP 32953]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>16121837</td><td>>gi|16121837|ref|NP_405150.1| putative racemase [Yersinia pestis CO92]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>68182765</td><td>>gi|68182765|ref|ZP_00555743.1| Mandelate racemase/muconate lactonizing enzyme [Jannaschia sp. CCS1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>67976928</td><td>>gi|67976928|gb|EAM66550.1| Mandelate racemase/muconate lactonizing enzyme [Jannaschia sp. CCS1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>66963668</td><td>>gi|66963668|ref|ZP_00411239.1| Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Arthrobacter sp. FB24]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>66870116</td><td>>gi|66870116|gb|EAL97481.1| Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Arthrobacter sp. FB24]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>67676304</td><td>>gi|67676304|ref|ZP_00473054.1| Mandelate racemase/muconate lactonizing enzyme [Chromohalobacter salexigens DSM 3043]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>67519629</td><td>>gi|67519629|gb|EAM23581.1| Mandelate racemase/muconate lactonizing enzyme [Chromohalobacter salexigens DSM 3043]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>19917838</td><td>>gi|19917838|gb|AAM07119.1| acylneuraminate cytidylyltransferase [Methanosarcina acetivorans C2A]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>20092564</td><td>>gi|20092564|ref|NP_618639.1| acylneuraminate cytidylyltransferase [Methanosarcina acetivorans C2A]</td><td></td><td>x</td><td></td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>56313239</td><td>>gi|56313239|emb|CAI07884.1| Phenylphosphate carboxylase, gamma subunit [Azoarcus sp. EbN1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>56477196</td><td>>gi|56477196|ref|YP_158785.1| phenylphosphate carboxylase, gamma subunit [Azoarcus sp. EbN1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>27359576</td><td>>gi|27359576|gb|AAO08520.1| Predicted phosphatase/phosphohexomutase [Vibrio vulnificus CMCP6]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>27368003</td><td>>gi|27368003|ref|NP_763530.1| Predicted phosphatase/phosphohexomutase [Vibrio vulnificus CMCP6]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>75856018</td><td>>gi|75856018|ref|ZP_00763654.1| COG0637: Predicted phosphatase/phosphohexomutase [Vibrio sp. Ex25]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>32041351</td><td>>gi|32041351|ref|ZP_00138934.1| COG0637: Predicted phosphatase/phosphohexomutase [Pseudomonas aeruginosa UCBPP-PA14]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>84328248</td><td>>gi|84328248|ref|ZP_00976255.1| COG0637: Predicted phosphatase/phosphohexomutase [Pseudomonas aeruginosa 2192]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>84321922</td><td>>gi|84321922|ref|ZP_00970273.1| COG0637: Predicted phosphatase/phosphohexomutase [Pseudomonas aeruginosa C3719]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>75831515</td><td>>gi|75831515|ref|ZP_00760778.1| COG0637: Predicted phosphatase/phosphohexomutase [Vibrio cholerae MO10]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>75825431</td><td>>gi|75825431|ref|ZP_00754867.1| COG0637: Predicted phosphatase/phosphohexomutase [Vibrio cholerae O395]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>75817213</td><td>>gi|75817213|ref|ZP_00747666.1| COG0637: Predicted phosphatase/phosphohexomutase [Vibrio cholerae V52]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>75818497</td><td>>gi|75818497|ref|ZP_00748652.1| COG0637: Predicted phosphatase/phosphohexomutase [Vibrio cholerae V51]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>75821624</td><td>>gi|75821624|ref|ZP_00751452.1| COG0637: Predicted phosphatase/phosphohexomutase [Vibrio cholerae RC385]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>16418937</td><td>>gi|16418937|gb|AAL19386.1| 2-aminoethylphosphonate transport [Salmonella typhimurium LT2]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>16763812</td><td>>gi|16763812|ref|NP_459427.1| 2-aminoethylphosphonate transport [Salmonella typhimurium LT2]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>62179043</td><td>>gi|62179043|ref|YP_215460.1| 2-aminoethylphosphonate transport [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]</td><td></td><td>x</td><td></td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
62126676	>gi|62126676|gb|AAX64379.1| 2-aminoethylphosphonate transport [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]		x		
84394244	>gi|84394244|ref|ZP_00992971.1| Predicted phosphatase/phosphohexomutase [Vibrio splendidus 12B01]		x		
84375119	>gi|84375119|gb|EAP92039.1| Predicted phosphatase/phosphohexomutase [Vibrio splendidus 12B01]		x		
86144390	>gi|86144390|ref|ZP_01062722.1| Predicted phosphatase/phosphohexomutase [Vibrio sp. MED222]		x		
85837289	>gi|85837289|gb|EAQ55401.1| Predicted phosphatase/phosphohexomutase [Vibrio sp. MED222]		x		
65318692	>gi|65318692|ref|ZP_00391651.1| COG0637: Predicted phosphatase/phosphohexomutase [Bacillus anthracis str. A2012]		x		
34013301	>gi|34013301|dbj|BAC81974.1| haloacetate dehalogenase H-2 [Delftia acidovorans]		x		
18916607	>gi|18916607|dbj|BAB85580.1| haloacetate dehalogenase H-2 [Delftia acidovorans]		x		
18916600	>gi|18916600|dbj|BAB85577.1| haloacetate dehalogenase H-2 [Delftia acidovorans]		x		
216775	>gi|216775|dbj|BAA14413.1| haloacetate dehalogenase H-2 [Moraxella sp. B]		x		
34500480	>gi|34500480|ref|NP_904251.1| haloacetate dehalogenase H-2 [Delftia acidovorans]		x		
461926	>gi|461926|sp|Q01399|DEH2_MORSB Haloacetate dehalogenase H-2		x		
348433	>gi|348433|pir||B44856 haloacetate dehalogenase (EC 3.8.1.3) H-2 - Moraxella sp. plasmid pUO1		x		
52211788	>gi|52211788|emb|CAH37787.1| putative amino acid dioxygenase [Burkholderia pseudomallei K96243]		x		
53721374	>gi|53721374|ref|YP_110359.1| putative amino acid dioxygenase [Burkholderia pseudomallei K96243]		x		
76582500	>gi|76582500|gb|ABA51974.1| putative amino acid dioxygenase [Burkholderia pseudomallei 1710b]		x		
76818027	>gi|76818027|ref|YP_337051.1| putative amino acid dioxygenase [Burkholderia pseudomallei 1710b]		x		

Table L-1. GenBank NR Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>77381551</td><td>>gi|77381551|gb|ABA73064.1| Glyoxalase/bleomycin resistance protein/dioxygenase [Pseudomonas fluorescens PfO-1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>77457548</td><td>>gi|77457548|ref|YP_347053.1| Glyoxalase/bleomycin resistance protein/dioxygenase [Pseudomonas fluorescens PfO-1]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>32041139</td><td>>gi|32041139|ref|ZP_00138722.1| COG0346: Lactoylglutathione lyase and related lyases [Pseudomonas aeruginosa UCBPP-PA14]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>84328603</td><td>>gi|84328603|ref|ZP_00976607.1| COG0346: Lactoylglutathione lyase and related lyases [Pseudomonas aeruginosa 2192]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>84322124</td><td>>gi|84322124|ref|ZP_00970469.1| COG0346: Lactoylglutathione lyase and related lyases [Pseudomonas aeruginosa C3719]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>86169225</td><td>>gi|86169225|gb|EAQ70481.1| Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily protein [Synechococcus sp. RS9917]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>68178628</td><td>>gi|68178628|ref|ZP_00551741.1| IMP dehydrogenase/GMP reductase:Amidohydrolase [Desulfuromonas acetoxidans DSM 684]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>67981316</td><td>>gi|67981316|gb|EAM70759.1| IMP dehydrogenase/GMP reductase:Amidohydrolase [Desulfuromonas acetoxidans DSM 684]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>22776497</td><td>>gi|22776497|dbj|BAC12773.1| enoyl-CoA hydratase (3-hydroxybutyryl-CoA dehydratase) [Oceanobacillus iheyensis HTE831]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>60492114</td><td>>gi|60492114|emb|CAH06877.1| putative heme-binding enolase [Bacteroides fragilis NCTC 9343]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>29839251</td><td>>gi|29839251|sp|Q8KNX9|ENO_BACFR Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Heme uptake protein A)</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>49613860</td><td>>gi|49613860|emb|CAG77312.1| DgoA protein [includes: 2-dehydro-3-deoxyphosphogalactonate aldolase; galactonate dehydratase] [Erwinia carotovora subsp. atroseptica SCRI1043]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>50123334</td><td>>gi|50123334|ref|YP_052501.1| DgoA protein [includes: 2-dehydro-3-deoxyphosphogalactonate aldolase; galactonate dehydratase] [Erwinia carotovora subsp. atroseptica SCRI1043]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>16422401</td><td>>gi|16422401|gb|AAL22687.1| galactonate dehydratase; 2-oxo-3-deoxygalactonate 6-phosphate aldolase [Salmonella typhimurium LT2]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>16767113</td><td>>gi|16767113|ref|NP_462728.1| 2-oxo-3-deoxygalactonate 6-phosphate aldolase/galactonate dehydratase [Salmonella typhimurium LT2]</td><td>x</td><td></td><td></td><td></td></tr>
</table>

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
36786391	>gi|36786391|emb|CAE15444.1| O-succinylbenzoate-CoA synthase (OSB synthase) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) [Photorhabdus luminescens subsp. laumondii TTO1]	x			
79043126	>gi|79043126|ref|ZP_00873779.1| Mandelate racemase/muconate lactonizing enzyme [Novosphingobium aromaticivorans DSM 12444]	x			
78772597	>gi|78772597|gb|EAP36290.1| Mandelate racemase/muconate lactonizing enzyme [Novosphingobium aromaticivorans DSM 12444]	x			
77382555	>gi|77382555|gb|ABA74068.1| Mandelate racemase/muconate lactonizing enzyme [Pseudomonas fluorescens PfO-1]	x			
77458552	>gi|77458552|ref|YP_348057.1| Mandelate racemase/muconate lactonizing enzyme [Pseudomonas fluorescens PfO-1]	x			
72121566	>gi|72121566|gb|AAZ63752.1| Mandelate racemase/muconate lactonizing enzyme [Ralstonia eutropha JMP134]	x			
73538229	>gi|73538229|ref|YP_298596.1| Mandelate racemase/muconate lactonizing enzyme [Ralstonia eutropha JMP134]	x			
68556131	>gi|68556131|ref|ZP_00595474.1| Mandelate racemase/muconate lactonizing enzyme [Ralstonia metallidurans CH34]	x			
68529304	>gi|68529304|gb|EAN52267.1| Mandelate racemase/muconate lactonizing enzyme [Ralstonia metallidurans CH34]	x			
607908	>gi|607908|gb|AAA66202.1| muconate lactonizing enzyme	x			
77383191	>gi|77383191|gb|ABA74704.1| Mandelate racemase/muconate lactonizing enzyme [Pseudomonas fluorescens PfO-1]	x			
77459188	>gi|77459188|ref|YP_348694.1| Mandelate racemase/muconate lactonizing enzyme [Pseudomonas fluorescens PfO-1]	x			
72118791	>gi|72118791|gb|AAZ61054.1| Mandelate racemase/muconate lactonizing enzyme [Ralstonia eutropha JMP134]	x			
73541378	>gi|73541378|ref|YP_295898.1| Mandelate racemase/muconate lactonizing enzyme [Ralstonia eutropha JMP134]	x			
77964708	>gi|77964708|gb|ABB06089.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia sp. 383]	x			
78060158	>gi|78060158|ref|YP_366733.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia sp. 383]	x			

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
74017902	>gi|74017902|ref|ZP_00688524.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia ambifaria AMMD]	x			
72609078	>gi|72609078|gb|EAO45028.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia ambifaria AMMD]	x			
74015085	>gi|74015085|ref|ZP_00685713.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia ambifaria AMMD]	x			
72611888	>gi|72611888|gb|EAO47832.1| Mandelate racemase/muconate lactonizing enzyme [Burkholderia ambifaria AMMD]	x			
32030885	>gi|32030885|ref|ZP_00133620.1| COG1778: Low specificity phosphatase (HAD superfamily) [Haemophilus somnus 2336]	x			
23467284	>gi|23467284|ref|ZP_00122867.1| COG1778: Low specificity phosphatase (HAD superfamily) [Haemophilus somnus 129PT]	x			
42629027	>gi|42629027|ref|ZP_00154577.1| COG1778: Low specificity phosphatase (HAD superfamily) [Haemophilus influenzae R2846]	x			
42631907	>gi|42631907|ref|ZP_00157445.1| COG1778: Low specificity phosphatase (HAD superfamily) [Haemophilus influenzae R2866]	x			
84323010	>gi|84323010|ref|ZP_00971087.1| COG1778: Low specificity phosphatase (HAD superfamily) [Pseudomonas aeruginosa 2192]	x			
84316989	>gi|84316989|ref|ZP_00965446.1| COG1778: Low specificity phosphatase (HAD superfamily) [Pseudomonas aeruginosa C3719]	x			
32039674	>gi|32039674|ref|ZP_00137946.1| COG1778: Low specificity phosphatase (HAD superfamily) [Pseudomonas aeruginosa UCBPP-PA14]	x			
32035568	>gi|32035568|ref|ZP_00135499.1| COG1778: Low specificity phosphatase (HAD superfamily) [Actinobacillus pleuropneumoniae serovar 1 str. 4074]	x			
82699462	>gi|82699462|ref|YP_414036.1| Haloacid dehalogenase/epoxide hydrolase:Haloacid dehalogenase-like hydrolase:HAD-superfamily hydrolase, subfamily IA, variant 2 [Brucella melitensis biovar Abortus 2308]	x			
82615563	>gi|82615563|emb|CAJ10546.1| Haloacid dehalogenase/epoxide hydrolase:Haloacid dehalogenase-like hydrolase:HAD-superfamily hydrolase, subfamily IA, variant 2 [Brucella melitensis biovar Abortus]	x			

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
23023945	>gi|23023945|ref|ZP_00063172.1| COG0637: Predicted phosphatase/phosphohexomutase [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]	x			
23023302	>gi|23023302|ref|ZP_00062539.1| COG0637: Predicted phosphatase/phosphohexomutase [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]	x			
68196414	>gi|68196414|gb|EAN10842.1| HAD-superfamily hydrolase, subfamily IA, variant 3:Beta-phosphoglucomutase:Beta-phosphoglucomutase hydrolase [Enterococcus faecium DO]	x			
69244473	>gi|69244473|ref|ZP_00602889.1| HAD-superfamily hydrolase, subfamily IA, variant 3:Beta-phosphoglucomutase:Beta-phosphoglucomutase hydrolase [Enterococcus faecium DO]	x			
48866179	>gi|48866179|ref|ZP_00320036.1| COG0637: Predicted phosphatase/phosphohexomutase [Oenococcus oeni PSU-1]	x			
20515793	>gi|20515793|gb|AAM24059.1| predicted phosphatase/phosphohexomutase [Thermoanaerobacter tengcongensis MB4]	x			
20807284	>gi|20807284|ref|NP_622455.1| predicted phosphatase/phosphohexomutase [Thermoanaerobacter tengcongensis MB4]	x			
76795835	>gi|76795835|ref|ZP_00778206.1| HAD-superfamily hydrolase, subfamily IA, variant 3:Beta-phosphoglucomutase:Beta-phosphoglucomutase hydrolase [Thermoanaerobacter ethanolicus ATCC 33223]	x			
76588820	>gi|76588820|gb|EAO65221.1| HAD-superfamily hydrolase, subfamily IA, variant 3:Beta-phosphoglucomutase:Beta-phosphoglucomutase hydrolase [Thermoanaerobacter ethanolicus ATCC 33223]	x			
62463248	>gi|62463248|ref|ZP_00382589.1| COG0637: Predicted phosphatase/phosphohexomutase [Lactococcus lactis subsp. cremoris SK11]	x			
75242116	>gi|75242116|ref|ZP_00725910.1| COG0637: Predicted phosphatase/phosphohexomutase [Escherichia coli F11]	x			
75259429	>gi|75259429|ref|ZP_00730748.1| COG0637: Predicted phosphatase/phosphohexomutase [Escherichia coli E22]	x			

Table L-1. GenBank NR Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
75212757	>gi|75212757|ref|ZP_00712755.1| COG0637: Predicted phosphatase/phosphohexomutase [Escherichia coli B171]	x			
75190403	>gi|75190403|ref|ZP_00703670.1| COG0637: Predicted phosphatase/phosphohexomutase [Escherichia coli E24377A]	x			
75515063	>gi|75515063|ref|ZP_00737267.1| COG0637: Predicted phosphatase/phosphohexomutase [Escherichia coli 53638]	x			
75195466	>gi|75195466|ref|ZP_00705536.1| COG0637: Predicted phosphatase/phosphohexomutase [Escherichia coli HS]	x			
83587457	>gi|83587457|ref|ZP_00926085.1| COG0637: Predicted phosphatase/phosphohexomutase [Escherichia coli 101-1]	x			
68195257	>gi|68195257|gb|EAN09710.1| HAD-superfamily hydrolase, subfamily IA, variant 3:Beta-phosphoglucomutase:Beta-phosphoglucomutase hydrolase [Enterococcus faecium DO]	x			
69246454	>gi|69246454|ref|ZP_00603949.1| HAD-superfamily hydrolase, subfamily IA, variant 3:Beta-phosphoglucomutase:Beta-phosphoglucomutase hydrolase [Enterococcus faecium DO]	x			
75240037	>gi|75240037|ref|ZP_00723998.1| COG0637: Predicted phosphatase/phosphohexomutase [Escherichia coli E110019]	x			
75231885	>gi|75231885|ref|ZP_00718226.1| COG0637: Predicted phosphatase/phosphohexomutase [Escherichia coli B7A]	x			
83569459	>gi|83569459|ref|ZP_00920912.1| COG0637: Predicted phosphatase/phosphohexomutase [Shigella dysenteriae 1012]	x			
68055676	>gi|68055676|ref|ZP_00539819.1| HAD-superfamily hydrolase, subfamily IA, variant 3:Beta-phosphoglucomutase:Beta-phosphoglucomutase hydrolase [Exiguobacterium sp. 255-15]	x			
68007811	>gi|68007811|gb|EAM87055.1| HAD-superfamily hydrolase, subfamily IA, variant 3:Beta-phosphoglucomutase:Beta-phosphoglucomutase hydrolase [Exiguobacterium sp. 255-15]	x			
83749409	>gi|83749409|ref|ZP_00946403.1| 3-dehydroshikimate dehydratase / 4-hydroxyphenylpyruvate dioxygenase [Ralstonia solanacearum UW551]	x			
83723936	>gi|83723936|gb|EAP71120.1| 3-dehydroshikimate dehydratase / 4-hydroxyphenylpyruvate dioxygenase [Ralstonia solanacearum UW551]	x			

L.2. Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>Q8FKG9_ECOL6</td><td>>gnl|tr|Q8FKG9_ECOL6 (Q8FKG9) Cytosine deaminase (EC 3.5.4.1)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q53ZC8_ECOLI</td><td>>gnl|tr|Q53ZC8_ECOLI (Q53ZC8) Cytosine deaminase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q57JD4_SALCH</td><td>>gnl|tr|Q57JD4_SALCH (Q57JD4) Putative cytosine deaminase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q8ZJE7_YERPE</td><td>>gnl|tr|Q8ZJE7_YERPE (Q8ZJE7) Cytosine deaminase (EC 3.5.4.1)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q8X690_ECO57</td><td>>gnl|tr|Q8X690_ECO57 (Q8X690) Cytosine deaminase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q5PLF4_SALPA</td><td>>gnl|tr|Q5PLF4_SALPA (Q5PLF4) Cytosine deaminase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q8Z3F3_SALTI</td><td>>gnl|tr|Q8Z3F3_SALTI (Q8Z3F3) Cytosine deaminase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q8ZLR0_SALTY</td><td>>gnl|tr|Q8ZLR0_SALTY (Q8ZLR0) Putative cytosine deaminase (EC 3.5.4.1)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q6Q8Q1_ECOLI</td><td>>gnl|tr|Q6Q8Q1_ECOLI (Q6Q8Q1) Cytosine deaminase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q664N0_YERPS</td><td>>gnl|tr|Q664N0_YERPS (Q664N0) Cytosine deaminase (EC 3.5.4.1)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q66ZJ3_9CARY</td><td>>gnl|tr|Q66ZJ3_9CARY (Q66ZJ3) Cytosine deaminase (Fragment)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q9I680_PSEAE</td><td>>gnl|tr|Q9I680_PSEAE (Q9I680) Cytosine deaminase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q92XH0_RHIME</td><td>>gnl|tr|Q92XH0_RHIME (Q92XH0) Putative CodA1 cytosine deaminase (EC 3.5.4.1)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q5E7H0_VIBF1</td><td>>gnl|tr|Q5E7H0_VIBF1 (Q5E7H0) Cytosine deaminase (EC 3.5.4.1)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q87GS2_VIBPA</td><td>>gnl|tr|Q87GS2_VIBPA (Q87GS2) Putative cytosine deaminase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q8D5W3_VIBVU</td><td>>gnl|tr|Q8D5W3_VIBVU (Q8D5W3) Cytosine deaminase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q7MCY1_VIBVY</td><td>>gnl|tr|Q7MCY1_VIBVY (Q7MCY1) Cytosine deaminase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q6LHI8_PHOPR</td><td>>gnl|tr|Q6LHI8_PHOPR (Q6LHI8) Putative cytosine deaminase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q8XZ12_RALSO</td><td>>gnl|tr|Q8XZ12_RALSO (Q8XZ12) PROBABLE CYTOSINE DEAMINASE (CYTOSINE AMINOHYDROLASE) PROTEIN (EC 3.5.4.1)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q8XMD3_CLOPE</td><td>>gnl|tr|Q8XMD3_CLOPE (Q8XMD3) Cytosine deaminase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q4J633_AZOVI</td><td>>gnl|tr|Q4J633_AZOVI (Q4J633) Cytosine deaminase (EC 3.5.4.1)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q6W266_RHISN</td><td>>gnl|tr|Q6W266_RHISN (Q6W266) Cytosine deaminase (EC 3.5.4.1)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q8G870_BIFLO</td><td>>gnl|tr|Q8G870_BIFLO (Q8G870) Cytosine deaminase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q3RTW7_RALME</td><td>>gnl|tr|Q3RTW7_RALME (Q3RTW7) Amidohydrolase</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>Q3J118_RHOS4</td><td>>gnl|tr|Q3J118_RHOS4 (Q3J118) Cytosine deaminase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q3L5C3_BIFBR</td><td>>gnl|tr|Q3L5C3_BIFBR (Q3L5C3) Cytosine deaminase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q893E4_CLOTE</td><td>>gnl|tr|Q893E4_CLOTE (Q893E4) Cytosine deaminase (EC 3.5.4.1)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q4K9F3_PSEF5</td><td>>gnl|tr|Q4K9F3_PSEF5 (Q4K9F3) Cytosine deaminase (EC 3.5.4.1)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q5WAP7_BACSK</td><td>>gnl|tr|Q5WAP7_BACSK (Q5WAP7) Cytosine deaminase (EC 3.5.4.1)</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q96XW5_SULTO	>gnl|tr|Q96XW5_SULTO (Q96XW5) 412aa long hypothetical cytosine deaminase			x	
Q2XIC1_PSEPU	>gnl|tr|Q2XIC1_PSEPU (Q2XIC1) Cytosine deaminase			x	
Q4AZB6_9BURK	>gnl|tr|Q4AZB6_9BURK (Q4AZB6) Cytosine deaminase (EC 3.5.4.1)			x	
Q88I13_PSEPK	>gnl|tr|Q88I13_PSEPK (Q88I13) Cytosine deaminase			x	
Q97V65_SULSO	>gnl|tr|Q97V65_SULSO (Q97V65) Cytosine deaminase (CodA) (EC 3.5.4.1)			x	
Q3JG17_BURP1	>gnl|tr|Q3JG17_BURP1 (Q3JG17) Cytosine deaminase (EC 3.5.4.1)			x	
Q4LTU9_9BURK	>gnl|tr|Q4LTU9_9BURK (Q4LTU9) Cytosine deaminase (EC 3.5.4.1)			x	
Q63M99_BURPS	>gnl|tr|Q63M99_BURPS (Q63M99) Cytosine deaminase (EC 3.5.4.1)			x	
Q62D65_BURMA	>gnl|tr|Q62D65_BURMA (Q62D65) Cytosine deaminase (EC 3.5.4.1)			x	
Q2T4R6_BURTH	>gnl|tr|Q2T4R6_BURTH (Q2T4R6) Cytosine deaminase			x	
Q2SBZ7_9GAMM	>gnl|tr|Q2SBZ7_9GAMM (Q2SBZ7) Cytosine deaminase and related metal-dependent Hydrolase			x	x
Q5LPP2_SILPO	>gnl|tr|Q5LPP2_SILPO (Q5LPP2) Cytosine deaminase, putative			x	
Q8NU64_CORGL	>gnl|tr|Q8NU64_CORGL (Q8NU64) Cytosine deaminase and related metal-dependent hydrolases (EC 3.5.4.21)			x	
Q7NHK7_GLOVI	>gnl|tr|Q7NHK7_GLOVI (Q7NHK7) Cytosine deaminase			x	
Q3X5C2_9ACTN	>gnl|tr|Q3X5C2_9ACTN (Q3X5C2) Cytosine deaminase (EC 3.5.4.1)			x	
Q4J9V1_SULAC	>gnl|tr|Q4J9V1_SULAC (Q4J9V1) Cytosine deaminase (EC 3.5.4.1)			x	
Q8FLL9_COREF	>gnl|tr|Q8FLL9_COREF (Q8FLL9) Putative cytosine deaminase			x	
Q3Z1X8_SHISS	>gnl|tr|Q3Z1X8_SHISS (Q3Z1X8) Adenosine deaminase			x	
Q57PH5_SALCH	>gnl|tr|Q57PH5_SALCH (Q57PH5) Adenosine deaminase			x	
Q32FF0_SHIDS	>gnl|tr|Q32FF0_SHIDS (Q32FF0) Adenosine deaminase			x	
Q320Y0_SHIBS	>gnl|tr|Q320Y0_SHIBS (Q320Y0) Adenosine deaminase			x	
Q365P4_9GAMM	>gnl|tr|Q365P4_9GAMM (Q365P4) Adenosine deaminase (EC 3.5.4.4)			x	
Q3E0Q9_CHLAU	>gnl|tr|Q3E0Q9_CHLAU (Q3E0Q9) Adenosine deaminase			x	
Q35VI2_9GAMM	>gnl|tr|Q35VI2_9GAMM (Q35VI2) Adenosine deaminase (EC 3.5.4.4)			x	
Q2Z4Z4_9GAMM	>gnl|tr|Q2Z4Z4_9GAMM (Q2Z4Z4) Adenosine deaminase (EC 3.5.4.4)			x	
Q2ZM92_SHEPU	>gnl|tr|Q2ZM92_SHEPU (Q2ZM92) Adenosine deaminase (EC 3.5.4.4)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q2WZZ7_9GAMM	>gnl|tr|Q2WZZ7_9GAMM (Q2WZZ7) Adenosine deaminase (EC 3.5.4.4)			x	
Q33P63_9GAMM	>gnl|tr|Q33P63_9GAMM (Q33P63) Adenosine deaminase (EC 3.5.4.4)			x	
Q3Q260_9GAMM	>gnl|tr|Q3Q260_9GAMM (Q3Q260) Adenosine deaminase (EC 3.5.4.4)			x	
Q6LLR1_PHOPR	>gnl|tr|Q6LLR1_PHOPR (Q6LLR1) Putative adenosine deaminase			x	
Q3P429_9GAMM	>gnl|tr|Q3P429_9GAMM (Q3P429) Adenosine deaminase (EC 3.5.4.4)			x	
Q3QEL7_9GAMM	>gnl|tr|Q3QEL7_9GAMM (Q3QEL7) Adenosine deaminase (EC 3.5.4.4)			x	
Q3NNU5_SHEFR	>gnl|tr|Q3NNU5_SHEFR (Q3NNU5) Adenosine deaminase (EC 3.5.4.4)			x	
Q66AF0_YERPS	>gnl|tr|Q66AF0_YERPS (Q66AF0) Adenosine deaminase (EC 3.5.4.4)			x	
Q4ZZD7_PSEU2	>gnl|tr|Q4ZZD7_PSEU2 (Q4ZZD7) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)			x	
Q3KID9_PSEPF	>gnl|tr|Q3KID9_PSEPF (Q3KID9) Amidohydrolase			x	x
Q48PG1_PSE14	>gnl|tr|Q48PG1_PSE14 (Q48PG1) N-acyl-D-amino acid deacylase family protein			x	x
Q8XQN5_RALSO	>gnl|tr|Q8XQN5_RALSO (Q8XQN5) PROBABLE N-ACYL-D-GLUTAMATE DEACYLASE PROTEIN (EC 3.5.1.82)			x	
Q3RUN2_RALME	>gnl|tr|Q3RUN2_RALME (Q3RUN2) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)			x	
Q87V24_PSESM	>gnl|tr|Q87V24_PSESM (Q87V24) N-acyl-D-amino acid deacylase family protein			x	x
Q9AGH8_ALCFA	>gnl|tr|Q9AGH8_ALCFA (Q9AGH8) D-aminoacylase (EC 3.5.1.81)			x	
Q2T146_BURTH	>gnl|tr|Q2T146_BURTH (Q2T146) N-acyl-D-amino-acid deacylase family protein			x	x
Q3JW03_BURP1	>gnl|tr|Q3JW03_BURP1 (Q3JW03) D-aminoacylase (EC 3.5.1.81)			x	
Q63XA6_BURPS	>gnl|tr|Q63XA6_BURPS (Q63XA6) D-aminoacylase (EC 3.5.1.81)			x	
Q4BEP1_BURVI	>gnl|tr|Q4BEP1_BURVI (Q4BEP1) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q4KIM1_PSEF5	>gnl|tr|Q4KIM1_PSEF5 (Q4KIM1) N-acyl-D-amino acid deacylase family protein			x	x
Q3FJ43_9BURK	>gnl|tr|Q3FJ43_9BURK (Q3FJ43) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)			x	
Q46U08_RALEJ	>gnl|tr|Q46U08_RALEJ (Q46U08) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)			x	
Q4LJF1_9BURK	>gnl|tr|Q4LJF1_9BURK (Q4LJF1) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)			x	
Q451H6_9BURK	>gnl|tr|Q451H6_9BURK (Q451H6) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)			x	
Q39D04_BURS3	>gnl|tr|Q39D04_BURS3 (Q39D04) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)			x	
Q62MQ0_BURMA	>gnl|tr|Q62MQ0_BURMA (Q62MQ0) N-acyl-D-amino-acid deacylase family protein			x	x
Q3RIZ4_RALME	>gnl|tr|Q3RIZ4_RALME (Q3RIZ4) N-acyl-D-amino-acid deacylase (EC 3.5.1.81)			x	
Q9F465_ARTAU	>gnl|tr|Q9F465_ARTAU (Q9F465) L-hydantoinase HyuH			x	
Q92MZ3_RHIME	>gnl|tr|Q92MZ3_RHIME (Q92MZ3) PUTATIVE D-HYDANTOINASE (DIHYDROPYRIMIDINASE) PROTEIN (EC 3.5.2.2)			x	
Q3J1I0_RHOS4	>gnl|tr|Q3J1I0_RHOS4 (Q3J1I0) Putative D-hydantoinase (Dihydropyrimidinase) (EC 3.5.2.2)			x	
Q98K55_RHILO	>gnl|tr|Q98K55_RHILO (Q98K55) Dihydropyrimidinase			x	x
Q8UCU7_AGRT5	>gnl|tr|Q8UCU7_AGRT5 (Q8UCU7) Dihydropyrimidinase			x	x
Q3QXR4_9RHOB	>gnl|tr|Q3QXR4_9RHOB (Q3QXR4) Dihydropyrimidinase (EC 3.5.2.2)			x	x
Q8G2P0_BRUSU	>gnl|tr|Q8G2P0_BRUSU (Q8G2P0) D-hydantoinase (EC 3.5.2.2)			x	
Q5LSI5_SILPO	>gnl|tr|Q5LSI5_SILPO (Q5LSI5) D-hydantoinase (EC 3.5.2.2)			x	
Q8YF78_BRUME	>gnl|tr|Q8YF78_BRUME (Q8YF78) D-HYDANTOINASE (EC 3.5.2.2)			x	
Q3KAM5_PSEPF	>gnl|tr|Q3KAM5_PSEPF (Q3KAM5) D-hydantoinase (EC 3.5.2.2)			x	
Q4KDM8_PSEF5	>gnl|tr|Q4KDM8_PSEF5 (Q4KDM8) Dihydropyrimidinase (EC 3.5.2.2)			x	x
Q2X8L4_PSEPU	>gnl|tr|Q2X8L4_PSEPU (Q2X8L4) D-hydantoinase			x	
Q6TTR0_PSEPU	>gnl|tr|Q6TTR0_PSEPU (Q6TTR0) D-hydantoinase			x	
Q9I676_PSEAE	>gnl|tr|Q9I676_PSEAE (Q9I676) Dihydropyrimidinase			x	x

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q94J90_ORYSA	>gnl|tr|Q94J90_ORYSA (Q94J90) Putative dihydropyrimidine amidohydrolase			x	x
Q5L028_GEOKA	>gnl|tr|Q5L028_GEOKA (Q5L028) Dihydropyrimidinase (D-hydantoinase) (EC 3.5.2.2)			x	
Q3PBX6_PARDE	>gnl|tr|Q3PBX6_PARDE (Q3PBX6) Dihydropyrimidinase (EC 3.5.2.2)			x	x
Q400N7_9PSED	>gnl|tr|Q400N7_9PSED (Q400N7) Hydantoinase			x	x
Q3F3U2_9BURK	>gnl|tr|Q3F3U2_9BURK (Q3F3U2) Amidohydrolase			x	x
Q4BSJ1_BURVI	>gnl|tr|Q4BSJ1_BURVI (Q4BSJ1) Amidohydrolase			x	x
Q39PA8_BURS3	>gnl|tr|Q39PA8_BURS3 (Q39PA8) D-hydantoinase (EC 3.5.2.2)			x	
Q44Y56_9BURK	>gnl|tr|Q44Y56_9BURK (Q44Y56) Amidohydrolase			x	x
Q4LI60_9BURK	>gnl|tr|Q4LI60_9BURK (Q4LI60) Dihydropyrimidinase (EC 3.5.2.2)			x	x
Q3WTB1_9RHIZ	>gnl|tr|Q3WTB1_9RHIZ (Q3WTB1) Dihydropyrimidinase (EC 3.5.2.2)			x	x
Q9FMP3_ARATH	>gnl|tr|Q9FMP3_ARATH (Q9FMP3) Dihydropyrimidinase (Dihydropyrimidine amidohydrolase) (EC 3.5.2.2)			x	x
Q89D30_BRAJA	>gnl|tr|Q89D30_BRAJA (Q89D30) Dihydropyrimidinase			x	x
Q47WW0_COLP3	>gnl|tr|Q47WW0_COLP3 (Q47WW0) D-hydantoinase (EC 3.5.2.2)			x	
Q56S49_9BACI	>gnl|tr|Q56S49_9BACI (Q56S49) Dihydropyrimidinase			x	x
Q4ACX3_9BACI	>gnl|tr|Q4ACX3_9BACI (Q4ACX3) Hydantoinase			x	x
Q35GJ0_9BRAD	>gnl|tr|Q35GJ0_9BRAD (Q35GJ0) D-hydantoinase (EC 3.5.2.2)			x	
Q409E0_9RHOB	>gnl|tr|Q409E0_9RHOB (Q409E0) Dihydropyrimidinase (EC 3.5.2.2)			x	x
Q3RN52_RALME	>gnl|tr|Q3RN52_RALME (Q3RN52) Dihydropyrimidinase (EC 3.5.2.2)			x	x
Q82LR1_STRAW	>gnl|tr|Q82LR1_STRAW (Q82LR1) Putative dihydropyrimidinase			x	x
Q5DLU2_9BACI	>gnl|tr|Q5DLU2_9BACI (Q5DLU2) D-hydantoinase (EC 3.5.2.2)			x	
Q3IWL8_RHOS4	>gnl|tr|Q3IWL8_RHOS4 (Q3IWL8) Putative D-hydantoinase dihydropyrimidinase			x	
Q8FE90_ECOL6	>gnl|tr|Q8FE90_ECOL6 (Q8FE90) Hypothetical hydrolase ygeZ (EC 3.-.-.-)			x	x
Q5WBE6_BACSK	>gnl|tr|Q5WBE6_BACSK (Q5WBE6) D-hydantoinase (EC 3.5.2.2)			x	
Q2MKJ8_9RHIZ	>gnl|tr|Q2MKJ8_9RHIZ (Q2MKJ8) D-hydantoinase			x	
Q400N8_AGRSK	>gnl|tr|Q400N8_AGRSK (Q400N8) Hydantoinase			x	x
Q846U5_9BACL	>gnl|tr|Q846U5_9BACL (Q846U5) Dihydropyrimidinase			x	x
Q8VT66_9RHIZ	>gnl|tr|Q8VT66_9RHIZ (Q8VT66) D-hydantoinase			x	
Q477K6_RALEJ	>gnl|tr|Q477K6_RALEJ (Q477K6) D-hydantoinase (EC 3.5.2.2)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q4ARF3_9BURK	>gnl|tr|Q4ARF3_9BURK (Q4ARF3) Dihydropyrimidinase (EC 3.5.2.2)			x	x
Q3X0C6_9ACTN	>gnl|tr|Q3X0C6_9ACTN (Q3X0C6) Dihydropyrimidinase (EC 3.5.2.2)			x	x
Q43N94_SOLUS	>gnl|tr|Q43N94_SOLUS (Q43N94) Dihydropyrimidinase (EC 3.5.2.2)			x	x
Q86LT2_DICDI	>gnl|tr|Q86LT2_DICDI (Q86LT2) Dihydropyrimidine amidohydrolase (EC 3.5.2.2)			x	x
Q893N3_CLOTE	>gnl|tr|Q893N3_CLOTE (Q893N3) D-hydantoinase (EC 3.5.2.2)			x	
Q3X5B8_9ACTN	>gnl|tr|Q3X5B8_9ACTN (Q3X5B8) Dihydropyrimidinase (EC 3.5.2.2)			x	x
Q40YU6_KINRA	>gnl|tr|Q40YU6_KINRA (Q40YU6) Dihydropyrimidinase precursor (EC 3.5.2.2)			x	x
Q35K56_9BRAD	>gnl|tr|Q35K56_9BRAD (Q35K56) D-hydantoinase (EC 3.5.2.2)			x	
Q3PG89_PARDE	>gnl|tr|Q3PG89_PARDE (Q3PG89) Dihydropyrimidinase (EC 3.5.2.2)			x	x
Q89Q35_BRAJA	>gnl|tr|Q89Q35_BRAJA (Q89Q35) D-hydantoinase (EC 3.5.2.2)			x	
Q4ARU7_9BURK	>gnl|tr|Q4ARU7_9BURK (Q4ARU7) Dihydropyrimidinase (EC 3.5.2.2)			x	x
Q3W890_9ACTO	>gnl|tr|Q3W890_9ACTO (Q3W890) Amidohydrolase			x	x
Q86LT3_DROME	>gnl|tr|Q86LT3_DROME (Q86LT3) Dihydropyrimidine amidohydrolase (EC 3.5.2.2)			x	x
Q4LYM7_9BURK	>gnl|tr|Q4LYM7_9BURK (Q4LYM7) Dihydropyrimidinase (EC 3.5.2.2)			x	x
Q45BR0_9BURK	>gnl|tr|Q45BR0_9BURK (Q45BR0) Dihydropyrimidinase (EC 3.5.2.2)			x	x
Q2WNG4_CLOBE	>gnl|tr|Q2WNG4_CLOBE (Q2WNG4) D-hydantoinase			x	
Q35NL8_9BRAD	>gnl|tr|Q35NL8_9BRAD (Q35NL8) D-hydantoinase (EC 3.5.2.2)			x	
Q89PZ7_BRAJA	>gnl|tr|Q89PZ7_BRAJA (Q89PZ7) D-hydantoinase (EC 3.5.2.2)			x	
Q84FR6_9MICC	>gnl|tr|Q84FR6_9MICC (Q84FR6) D-hydantoinase			x	
Q949H4_SOYBN	>gnl|tr|Q949H4_SOYBN (Q949H4) Leaf ubiquitous urease (EC 3.5.1.5)			x	
Q93X19_SOLTU	>gnl|tr|Q93X19_SOLTU (Q93X19) Urease (EC 3.5.1.5)			x	
Q8W3L6_ORYSA	>gnl|tr|Q8W3L6_ORYSA (Q8W3L6) Urease (EC 3.5.1.5)			x	
Q93WI8_SOLTU	>gnl|tr|Q93WI8_SOLTU (Q93WI8) Urease (EC 3.5.1.5)			x	
Q9SR52_ARATH	>gnl|tr|Q9SR52_ARATH (Q9SR52) Putative urease			x	
Q7XAC5_SOYBN	>gnl|tr|Q7XAC5_SOYBN (Q7XAC5) Embryo-specific urease (EC 3.5.1.5)			x	
O14420_COCPO	>gnl|tr|O14420_COCPO (O14420) Urease (EC 3.5.1.5)			x	
Q2UKB4_ASPOR	>gnl|tr|Q2UKB4_ASPOR (Q2UKB4) Urea amidohydrolase			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q7SFW8_NEUCR	>gnl|tr|Q7SFW8_NEUCR (Q7SFW8) Hypothetical protein (Probable urease)			x	
Q948Z6_SOLTU	>gnl|tr|Q948Z6_SOLTU (Q948Z6) Urease (EC 3.5.1.5) (Fragment)			x	
Q8H6V8_CANEN	>gnl|tr|Q8H6V8_CANEN (Q8H6V8) Urease JBURE-II			x	
Q34RK6_RHOPA	>gnl|tr|Q34RK6_RHOPA (Q34RK6) Urease (EC 3.5.1.5)			x	
Q3XRS1_9PROT	>gnl|tr|Q3XRS1_9PROT (Q3XRS1) Urease			x	
Q4ZN06_PSEU2	>gnl|tr|Q4ZN06_PSEU2 (Q4ZN06) Urease (EC 3.5.1.5)			x	
Q48DE6_PSE14	>gnl|tr|Q48DE6_PSE14 (Q48DE6) Urease, alpha subunit (EC 3.5.1.5)			x	
Q87VP0_PSESM	>gnl|tr|Q87VP0_PSESM (Q87VP0) Urease, alpha subunit			x	
O52305_SYNP2	>gnl|tr|O52305_SYNP2 (O52305) Urease alpha subunit			x	
Q4IXD2_AZOVI	>gnl|tr|Q4IXD2_AZOVI (Q4IXD2) Urease (EC 3.5.1.5)			x	
Q3M712_ANAVT	>gnl|tr|Q3M712_ANAVT (Q3M712) Urease, alpha subunit (EC 3.5.1.5)			x	
Q4KJ10_PSEF5	>gnl|tr|Q4KJ10_PSEF5 (Q4KJ10) Urease, alpha subunit (EC 3.5.1.5)			x	
Q8YQZ0_ANASP	>gnl|tr|Q8YQZ0_ANASP (Q8YQZ0) Urease alpha subunit			x	
Q3KIT2_PSEPF	>gnl|tr|Q3KIT2_PSEPF (Q3KIT2) Urease, alpha subunit			x	
Q3FBA4_9BURK	>gnl|tr|Q3FBA4_9BURK (Q3FBA4) Urease (EC 3.5.1.5)			x	
Q4LNH4_9BURK	>gnl|tr|Q4LNH4_9BURK (Q4LNH4) Urease (EC 3.5.1.5)			x	
Q454M1_9BURK	>gnl|tr|Q454M1_9BURK (Q454M1) Urease (EC 3.5.1.5)			x	
Q3RWB6_RALME	>gnl|tr|Q3RWB6_RALME (Q3RWB6) Urease (EC 3.5.1.5)			x	
Q39IW3_BURS3	>gnl|tr|Q39IW3_BURS3 (Q39IW3) Urease, alpha subunit (EC 3.5.1.5)			x	
Q8DMV6_SYNEL	>gnl|tr|Q8DMV6_SYNEL (Q8DMV6) Urease alpha subunit			x	
Q3HBC3_TRIER	>gnl|tr|Q3HBC3_TRIER (Q3HBC3) Urease (EC 3.5.1.5)			x	
O30337_RALEU	>gnl|tr|O30337_RALEU (O30337) Urease, structural subunit			x	
Q9KG59_BACHD	>gnl|tr|Q9KG59_BACHD (Q9KG59) Urease alpha subunit (EC 3.5.1.5)			x	
Q473Q9_RALEJ	>gnl|tr|Q473Q9_RALEJ (Q473Q9) Urease, alpha subunit			x	
Q4BIH6_BURVI	>gnl|tr|Q4BIH6_BURVI (Q4BIH6) Urease (EC 3.5.1.5)			x	
Q34XU6_9GAMM	>gnl|tr|Q34XU6_9GAMM (Q34XU6) Urease, alpha subunit (EC 3.5.1.5)			x	
Q8XXT1_RALSO	>gnl|tr|Q8XXT1_RALSO (Q8XXT1) PROBABLE UREASE (ALPHA SUBUNIT) PROTEIN (EC 3.5.1.5)			x	
Q2SDQ1_9GAMM	>gnl|tr|Q2SDQ1_9GAMM (Q2SDQ1) Urease, alpha subunit (EC 3.5.1.5)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q63RL3_BURPS	>gnl|tr|Q63RL3_BURPS (Q63RL3) Urease alpha subunit (EC 3.5.1.5)			x	
Q62HS0_BURMA	>gnl|tr|Q62HS0_BURMA (Q62HS0) Urease, alpha subunit (EC 3.5.1.5)			x	
Q9HUU5_PSEAE	>gnl|tr|Q9HUU5_PSEAE (Q9HUU5) Urease alpha subunit			x	
Q3WT92_9RHIZ	>gnl|tr|Q3WT92_9RHIZ (Q3WT92) Urease			x	
Q8RPY2_RHILV	>gnl|tr|Q8RPY2_RHILV (Q8RPY2) UreC			x	
Q47G55_DECAR	>gnl|tr|Q47G55_DECAR (Q47G55) Urease, alpha subunit			x	
Q3J770_NITOC	>gnl|tr|Q3J770_NITOC (Q3J770) Urease, alpha subunit (EC 3.5.1.5)			x	
Q98CY9_RHILO	>gnl|tr|Q98CY9_RHILO (Q98CY9) Urease alpha subunit			x	
Q3AVR1_SYNS9	>gnl|tr|Q3AVR1_SYNS9 (Q3AVR1) Urease, alpha subunit (EC 3.5.1.5)			x	
Q3JPJ6_BURP1	>gnl|tr|Q3JPJ6_BURP1 (Q3JPJ6) Urease, alpha subunit (EC 3.5.1.5)			x	
Q8UCT2_AGRT5	>gnl|tr|Q8UCT2_AGRT5 (Q8UCT2) Urease alpha subunit (AGR_C_4357p)			x	
Q7V3V2_PROMM	>gnl|tr|Q7V3V2_PROMM (Q7V3V2) Urease alpha subunit (EC 3.5.1.5)			x	
Q3AGD0_SYNSC	>gnl|tr|Q3AGD0_SYNSC (Q3AGD0) Urease, alpha subunit (EC 3.5.1.5)			x	
Q2SYF7_BURTH	>gnl|tr|Q2SYF7_BURTH (Q2SYF7) Urease, alpha subunit (EC 3.5.1.5)			x	
Q374G2_RHOPA	>gnl|tr|Q374G2_RHOPA (Q374G2) Urease, alpha subunit (EC 3.5.1.5)			x	
Q5KYM1_GEOKA	>gnl|tr|Q5KYM1_GEOKA (Q5KYM1) Urease alpha subunit (Urea amidohydrolase) (EC 3.5.1.5)			x	
Q3X7H8_METFL	>gnl|tr|Q3X7H8_METFL (Q3X7H8) Urease (EC 3.5.1.5)			x	
Q36I62_MARHY	>gnl|tr|Q36I62_MARHY (Q36I62) Urease, alpha subunit			x	
Q7U3I3_SYNPX	>gnl|tr|Q7U3I3_SYNPX (Q7U3I3) Urease alpha subunit (EC 3.5.1.5)			x	
Q89UG0_BRAJA	>gnl|tr|Q89UG0_BRAJA (Q89UG0) Urease alpha subunit			x	
Q35RD7_9BRAD	>gnl|tr|Q35RD7_9BRAD (Q35RD7) Urease, alpha subunit (EC 3.5.1.5)			x	
O87402_SYNPV	>gnl|tr|O87402_SYNPV (O87402) Urease alpha subunit (EC 3.5.1.5)			x	
Q46IY3_PROMT	>gnl|tr|Q46IY3_PROMT (Q46IY3) Urease, alpha subunit (EC 3.5.1.5)			x	
Q349U1_RHOPA	>gnl|tr|Q349U1_RHOPA (Q349U1) Urease, alpha subunit			x	
Q4CHE3_CLOTM	>gnl|tr|Q4CHE3_CLOTM (Q4CHE3) Urease (EC 3.5.1.5)			x	
Q44DF6_CHRSL	>gnl|tr|Q44DF6_CHRSL (Q44DF6) Urease (EC 3.5.1.5)			x	
Q93T81_BRUAB	>gnl|tr|Q93T81_BRUAB (Q93T81) Urease alpha subunit UreC (UreC-1, urease, alpha subunit)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q2YPD5_BRUA2	>gnl|tr|Q2YPD5_BRUA2 (Q2YPD5) Urease:Amidohydrolase (EC 3.5.1.5)			x	
Q8G2P8_BRUSU	>gnl|tr|Q8G2P8_BRUSU (Q8G2P8) Urease, alpha subunit (EC 3.5.1.5)			x	
Q7V1B6_PROMP	>gnl|tr|Q7V1B6_PROMP (Q7V1B6) Urease alpha subunit (EC 3.5.1.5)			x	
Q9L644_PROMA	>gnl|tr|Q9L644_PROMA (Q9L644) UreC			x	
Q6FD83_ACIAD	>gnl|tr|Q6FD83_ACIAD (Q6FD83) Urease alpha subunit (EC 3.5.1.5)			x	
Q31B49_PROM9	>gnl|tr|Q31B49_PROM9 (Q31B49) Urease, alpha subunit (EC 3.5.1.5)			x	
Q6N3N3_RHOPA	>gnl|tr|Q6N3N3_RHOPA (Q6N3N3) Urease alpha subunit (EC 3.5.1.5)			x	
Q5LSQ2_SILPO	>gnl|tr|Q5LSQ2_SILPO (Q5LSQ2) Urease, alpha subunit (EC 3.5.1.5)			x	
Q8YF72_BRUME	>gnl|tr|Q8YF72_BRUME (Q8YF72) UREASE ALPHA SUBUNIT (EC 3.5.1.5)			x	
Q9AQT4_RHOCA	>gnl|tr|Q9AQT4_RHOCA (Q9AQT4) Alpha subunit of urease (EC 3.5.1.5)			x	
Q37N01_RHOPA	>gnl|tr|Q37N01_RHOPA (Q37N01) Urease, alpha subunit (EC 3.5.1.5)			x	
Q3J154_RHOS4	>gnl|tr|Q3J154_RHOS4 (Q3J154) Urea amidohydrolase (Urease) alpha subunit (EC 3.5.1.5)			x	
Q8XAG0_ECO57	>gnl|tr|Q8XAG0_ECO57 (Q8XAG0) Putative urease structural subunit C (Alpha) (Urease alpha subunit)			x	
Q3QUL3_9RHOB	>gnl|tr|Q3QUL3_9RHOB (Q3QUL3) Urease			x	
Q5E728_VIBF1	>gnl|tr|Q5E728_VIBF1 (Q5E728) Urease alpha subunit (EC 3.5.1.5)			x	
Q3GRG7_9GAMM	>gnl|tr|Q3GRG7_9GAMM (Q3GRG7) Urease (EC 3.5.1.5)			x	
Q9FAS5_VIBPA	>gnl|tr|Q9FAS5_VIBPA (Q9FAS5) UreC			x	
Q733J6_BACC1	>gnl|tr|Q733J6_BACC1 (Q733J6) Urease alpha subunit (EC 3.5.1.5)			x	
Q8RJJ9_9GAMM	>gnl|tr|Q8RJJ9_9GAMM (Q8RJJ9) Urea amidohydrolase alpha subunit			x	
Q4NKR4_9MICC	>gnl|tr|Q4NKR4_9MICC (Q4NKR4) Urease (EC 3.5.1.5)			x	
Q40BI2_9RHOB	>gnl|tr|Q40BI2_9RHOB (Q40BI2) Urease			x	
Q4QN09_HAEI8	>gnl|tr|Q4QN09_HAEI8 (Q4QN09) Urease alpha subunit (EC 3.5.1.5)			x	
Q88J04_PSEPK	>gnl|tr|Q88J04_PSEPK (Q88J04) Urease, alpha subunit			x	
Q2Y9M7_NITMU	>gnl|tr|Q2Y9M7_NITMU (Q2Y9M7) Urease, alpha subunit (EC 3.5.1.5)			x	
Q8GH75_9PROT	>gnl|tr|Q8GH75_9PROT (Q8GH75) UreC			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q6Y3X2_9PROT	>gnl|tr|Q6Y3X2_9PROT (Q6Y3X2) Urease C			x	
Q2XLA8_PSEPU	>gnl|tr|Q2XLA8_PSEPU (Q2XLA8) Urease, alpha subunit			x	
Q3FXN9_9BURK	>gnl|tr|Q3FXN9_9BURK (Q3FXN9) Urease (EC 3.5.1.5)			x	
Q9RYJ4_DEIRA	>gnl|tr|Q9RYJ4_DEIRA (Q9RYJ4) Urease, alpha subunit			x	
Q6WVG4_9PROT	>gnl|tr|Q6WVG4_9PROT (Q6WVG4) Urease C subunit			x	
Q6Y9S4_9PROT	>gnl|tr|Q6Y9S4_9PROT (Q6Y9S4) Urease subunit C			x	
Q3GSR3_9GAMM	>gnl|tr|Q3GSR3_9GAMM (Q3GSR3) Urease (EC 3.5.1.5)			x	
Q93PJ4_HELHP	>gnl|tr|Q93PJ4_HELHP (Q93PJ4) Urease beta subunit UreB (EC 3.5.1.5)			x	
Q4AW22_9BURK	>gnl|tr|Q4AW22_9BURK (Q4AW22) Peptidase M38, urease (EC 3.5.1.5)			x	
Q3IH68_PSEHT	>gnl|tr|Q3IH68_PSEHT (Q3IH68) Urease, alpha subunit (EC 3.5.1.5)			x	
Q6YCI8_9PROT	>gnl|tr|Q6YCI8_9PROT (Q6YCI8) Urea amidohydrolase alpha subunit			x	
Q7VUD3_BORPE	>gnl|tr|Q7VUD3_BORPE (Q7VUD3) Urease alpha subunit (EC 3.5.1.5)			x	
Q7W417_BORPA	>gnl|tr|Q7W417_BORPA (Q7W417) Urease alpha subunit (EC 3.5.1.5)			x	
Q492E9_BLOPB	>gnl|tr|Q492E9_BLOPB (Q492E9) Putative urease structural subunit C (Alpha)			x	
Q8GH97_HELBI	>gnl|tr|Q8GH97_HELBI (Q8GH97) Urease B			x	
Q9S0Q5_HELPY	>gnl|tr|Q9S0Q5_HELPY (Q9S0Q5) Urease B			x	
Q38Q64_HELPY	>gnl|tr|Q38Q64_HELPY (Q38Q64) Urease B (Fragment)			x	
Q7X3W5_HELPY	>gnl|tr|Q7X3W5_HELPY (Q7X3W5) Urease B			x	
Q9AFB1_HELPY	>gnl|tr|Q9AFB1_HELPY (Q9AFB1) Urease B			x	
Q9Z369_ACTNA	>gnl|tr|Q9Z369_ACTNA (Q9Z369) Urease alpha subunit UreC			x	
Q64EY3_HELPY	>gnl|tr|Q64EY3_HELPY (Q64EY3) UreB			x	
Q7VRS6_BLOFL	>gnl|tr|Q7VRS6_BLOFL (Q7VRS6) Putative urease structural subunit C (Alpha) (EC 3.5.1.5)			x	
Q84F75_HELPY	>gnl|tr|Q84F75_HELPY (Q84F75) Urease beta (EC 3.5.1.5)			x	
Q6T368_9PROT	>gnl|tr|Q6T368_9PROT (Q6T368) UreC			x	
Q3PBN3_PARDE	>gnl|tr|Q3PBN3_PARDE (Q3PBN3) Urease			x	
Q4A0J5_STAS1	>gnl|tr|Q4A0J5_STAS1 (Q4A0J5) Urease alpha subunit			x	
Q2YYQ6_STAAB	>gnl|tr|Q2YYQ6_STAAB (Q2YYQ6) Urease alpha subunit (EC 3.5.1.5)			x	
Q8RNU6_HELPY	>gnl|tr|Q8RNU6_HELPY (Q8RNU6) Urease B subunit			x	
Q8FQX2_COREF	>gnl|tr|Q8FQX2_COREF (Q8FQX2) Urease alpha subunit (EC 3.5.1.5)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q5YWR8_NOCFA	>gnl|tr|Q5YWR8_NOCFA (Q5YWR8) Putative urease alpha subunit			x	
Q79VJ3_CORGL	>gnl|tr|Q79VJ3_CORGL (Q79VJ3) Urea amidohydrolase (Urease) alpha subunit (EC 3.5.1.5) (UREASE ALPHA SUBUNIT)			x	
Q5FB23_CAMLA	>gnl|tr|Q5FB23_CAMLA (Q5FB23) Urease B subunit			x	
Q3S3T8_9STRE	>gnl|tr|Q3S3T8_9STRE (Q3S3T8) Urease alpha subunit			x	
Q6UB24_STRTR	>gnl|tr|Q6UB24_STRTR (Q6UB24) UreC protein			x	
Q5M607_STRT2	>gnl|tr|Q5M607_STRT2 (Q5M607) Urea amidohydrolase (Urease) alpha subunit			x	
Q5M1G6_STRT1	>gnl|tr|Q5M1G6_STRT1 (Q5M1G6) Urea amidohydrolase (Urease) alpha subunit			x	
Q6UR42_YERMO	>gnl|tr|Q6UR42_YERMO (Q6UR42) UreC			x	
Q84I83_STRTR	>gnl|tr|Q84I83_STRTR (Q84I83) UreC			x	
Q6UR51_YERKR	>gnl|tr|Q6UR51_YERKR (Q6UR51) UreC			x	
Q6UR84_YERAL	>gnl|tr|Q6UR84_YERAL (Q6UR84) UreC			x	
Q6UR68_YERFR	>gnl|tr|Q6UR68_YERFR (Q6UR68) UreC			x	
Q6UR60_YERIN	>gnl|tr|Q6UR60_YERIN (Q6UR60) UreC			x	
Q6UR76_YERBE	>gnl|tr|Q6UR76_YERBE (Q6UR76) UreC			x	
Q6UR33_YERRO	>gnl|tr|Q6UR33_YERRO (Q6UR33) UreC			x	
Q826R9_STRAW	>gnl|tr|Q826R9_STRAW (Q826R9) Putative urease alpha subunit			x	
Q9FCD3_STRCO	>gnl|tr|Q9FCD3_STRCO (Q9FCD3) Urease alpha subunit			x	
Q84ED2_STRTR	>gnl|tr|Q84ED2_STRTR (Q84ED2) UreC protein			x	
Q2ZGT0_CALSA	>gnl|tr|Q2ZGT0_CALSA (Q2ZGT0) Urease, alpha subunit			x	
Q7N4Y7_PHOLL	>gnl|tr|Q7N4Y7_PHOLL (Q7N4Y7) Urease alpha subunit			x	
Q3VZP2_9ACTO	>gnl|tr|Q3VZP2_9ACTO (Q3VZP2) Urease (EC 3.5.1.5)			x	
Q437T6_9ACTO	>gnl|tr|Q437T6_9ACTO (Q437T6) Urease (EC 3.5.1.5)			x	
Q8FZW2_BRUSU	>gnl|tr|Q8FZW2_BRUSU (Q8FZW2) Urease, alpha subunit (EC 3.5.1.5)			x	
Q8YHZ8_BRUME	>gnl|tr|Q8YHZ8_BRUME (Q8YHZ8) UREASE ALPHA SUBUNIT (EC 3.5.1.5)			x	
Q2YQD8_BRUA2	>gnl|tr|Q2YQD8_BRUA2 (Q2YQD8) Urease:Amidohydrolase (EC 3.5.1.5)			x	
Q57CE8_BRUAB	>gnl|tr|Q57CE8_BRUAB (Q57CE8) UreC-2, urease, alpha subunit			x	
Q9S6F6_LACFE	>gnl|tr|Q9S6F6_LACFE (Q9S6F6) Urease alpha subunit			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q4ZUD2_PSEU2	>gnl|tr|Q4ZUD2_PSEU2 (Q4ZUD2) Urease (EC 3.5.1.5)			x	
Q35P05_9BRAD	>gnl|tr|Q35P05_9BRAD (Q35P05) Urease, alpha subunit (EC 3.5.1.5)			x	
Q3IRZ5_NATPD	>gnl|tr|Q3IRZ5_NATPD (Q3IRZ5) Urease (EC 3.5.1.5), alpha subunit (EC 3.5.1.5)			x	
Q75ZQ5_HALMA	>gnl|tr|Q75ZQ5_HALMA (Q75ZQ5) Urease alpha subunit UreC (EC 3.5.1.5)			x	
Q6JHP2_9PSEU	>gnl|tr|Q6JHP2_9PSEU (Q6JHP2) Urease alpha subunit			x	
Q6I6I3_CAMLA	>gnl|tr|Q6I6I3_CAMLA (Q6I6I3) Urease beta subunit (Fragment)			x	
Q6I6I9_CAMLA	>gnl|tr|Q6I6I9_CAMLA (Q6I6I9) Urease beta subunit (Fragment)			x	
Q6I6H3_CAMLA	>gnl|tr|Q6I6H3_CAMLA (Q6I6H3) Urease beta subunit (Fragment)			x	
Q6I6J1_CAMLA	>gnl|tr|Q6I6J1_CAMLA (Q6I6J1) Urease beta subunit (Fragment)			x	
Q6I6H5_CAMLA	>gnl|tr|Q6I6H5_CAMLA (Q6I6H5) Urease beta subunit (Fragment)			x	
Q6I6I5_CAMLA	>gnl|tr|Q6I6I5_CAMLA (Q6I6I5) Urease beta subunit (Fragment)			x	
Q6I6H7_CAMLA	>gnl|tr|Q6I6H7_CAMLA (Q6I6H7) Urease beta subunit (Fragment)			x	
Q6I6I1_CAMLA	>gnl|tr|Q6I6I1_CAMLA (Q6I6I1) Urease beta subunit (Fragment)			x	
Q6I6H1_CAMLA	>gnl|tr|Q6I6H1_CAMLA (Q6I6H1) Urease beta subunit (Fragment)			x	
Q972W0_SULTO	>gnl|tr|Q972W0_SULTO (Q972W0) 493aa long hypothetical urease alpha subunit			x	
Q6I6H9_CAMLA	>gnl|tr|Q6I6H9_CAMLA (Q6I6H9) Urease beta subunit (Fragment)			x	
O86508_STRCO	>gnl|tr|O86508_STRCO (O86508) Urease alpha subunit			x	
Q82JN9_STRAW	>gnl|tr|Q82JN9_STRAW (Q82JN9) Putative urease alpha subunit			x	
Q35JE7_9BRAD	>gnl|tr|Q35JE7_9BRAD (Q35JE7) Urease, alpha subunit (EC 3.5.1.5)			x	
Q40VS0_KINRA	>gnl|tr|Q40VS0_KINRA (Q40VS0) Urease (EC 3.5.1.5)			x	
Q8KT25_HELBI	>gnl|tr|Q8KT25_HELBI (Q8KT25) Urease UreB (Fragment)			x	
Q8KT24_HELFE	>gnl|tr|Q8KT24_HELFE (Q8KT24) Urease UreB (Fragment)			x	
Q8KT12_HELPY	>gnl|tr|Q8KT12_HELPY (Q8KT12) Urease UreB (Fragment)			x	
Q8KT33_HELPY	>gnl|tr|Q8KT33_HELPY (Q8KT33) Urease UreB (Fragment)			x	
Q8KT29_HELHE	>gnl|tr|Q8KT29_HELHE (Q8KT29) Urease UreB (Fragment)			x	
Q8KT26_HELBI	>gnl|tr|Q8KT26_HELBI (Q8KT26) Urease UreB (Fragment)			x	
Q6UK70_HELPY	>gnl|tr|Q6UK70_HELPY (Q6UK70) UreB (Fragment)			x	
Q6UK72_HELPY	>gnl|tr|Q6UK72_HELPY (Q6UK72) UreB (Fragment)			x	
Q6UK82_HELFE	>gnl|tr|Q6UK82_HELFE (Q6UK82) UreB (Fragment)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>ath:At1g67550</td><td>>gnl|kg|ath:At1g67550 F12B7.10; urease, putative / urea amidohydrolase, putative [EC:3.5.1.5] [KO:K01428 K01429 K01430]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>spo:SPAC1952.11c</td><td>>gnl|kg|spo:SPAC1952.11c ure1; urease (EC 3.5.1.5) [EC:3.5.1.5] [KO:K01428 K01429 K01430]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>cne:CNH01900</td><td>>gnl|kg|cne:CNH01900 urease [EC:3.5.1.5] [KO:K01428 K01429 K01430]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>psb:Psyr_4436</td><td>>gnl|kg|psb:Psyr_4436 urease [EC:3.5.1.5] [KO:K01428]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>psp:PSPPH_4479</td><td>>gnl|kg|psp:PSPPH_4479 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01428]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>pst:PSPTO4895</td><td>>gnl|kg|pst:PSPTO4895 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01428]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ava:Ava_3618</td><td>>gnl|kg|ava:Ava_3618 urease, alpha subunit [EC:3.5.1.5] [KO:K01427]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>pfl:PFL_0631</td><td>>gnl|kg|pfl:PFL_0631 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01428]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ana:alr3670</td><td>>gnl|kg|ana:alr3670 urease alpha subunit [EC:3.5.1.5] [KO:K01428]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>pfo:Pfl_0580</td><td>>gnl|kg|pfo:Pfl_0580 urease, alpha subunit</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>syn:sll1750</td><td>>gnl|kg|syn:sll1750 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bur:Bcep18194_A4006</td><td>>gnl|kg|bur:Bcep18194_A4006 urease, alpha subunit [EC:3.5.1.5] [KO:K01427]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>tel:tlr0005</td><td>>gnl|kg|tel:tlr0005 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bha:BH0254</td><td>>gnl|kg|bha:BH0254 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>reu:Reut_A0995</td><td>>gnl|kg|reu:Reut_A0995 urease, alpha subunit [EC:3.5.1.5] [KO:K01428]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sme:SMc01837</td><td>>gnl|kg|sme:SMc01837 ureC; urease alpha subunit protein [EC:3.5.1.5] [KO:K01428]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>rso:RSc2032</td><td>>gnl|kg|rso:RSc2032 ureC, RS02789; probable urease (alpha subunit) protein [EC:3.5.1.5] [KO:K01428]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>hch:HCH_04523</td><td>>gnl|kg|hch:HCH_04523 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01427]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
bps:BPSL2659	>gnl|kg|bps:BPSL2659 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
bma:BMA2184	>gnl|kg|bma:BMA2184 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
pae:PA4868	>gnl|kg|pae:PA4868 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
dar:Daro_1427	>gnl|kg|dar:Daro_1427 urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
ret:RHE_CH03305	>gnl|kg|ret:RHE_CH03305 ureC; urease (UreA amidohydrolase) alpha subunit protein [EC:3.5.1.5] [KO:K01427]			x	
cyb:CYB_0023	>gnl|kg|cyb:CYB_0023 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x	
noc:Noc_2880	>gnl|kg|noc:Noc_2880 urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x	
mlo:mll4940	>gnl|kg|mlo:mll4940 urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
sye:Syncc9902_2257	>gnl|kg|sye:Syncc9902_2257 urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x	
pm:BURPS1710b_313	>gnl|kg|bpm:BURPS1710b_3135 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x	
atc:AGR_C_4357	>gnl|kg|atc:AGR_C_4357 ureA; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
atu:Atu2401	>gnl|kg|atu:Atu2401 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
pmt:PMT2236	>gnl|kg|pmt:PMT2236 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
syd:Syncc9605_2627	>gnl|kg|syd:Syncc9605_2627 urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x	
bte:BTH_I1496	>gnl|kg|bte:BTH_I1496 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x	
gka:GK1930	>gnl|kg|gka:GK1930 ureC; urease alpha subunit (urea amidohydrolase) [EC:3.5.1.5] [KO:K01428]			x	
syw:SYNW2449	>gnl|kg|syw:SYNW2449 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
bja:blr1457	>gnl|kg|bja:blr1457 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
pmn:PMN2A_1055	>gnl|kg|pmn:PMN2A_1055 urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
bms:BR0270	>gnl|kg|bms:BR0270 ureC-1; urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
bmb:BruAb1_0296	>gnl|kg|bmb:BruAb1_0296 ureC-1; UreC-1, urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
bmf:BAB1_0300	>gnl|kg|bmf:BAB1_0300 ureC-1; urease:amidohydrolase [EC:3.5.1.5] [KO:K01427]			x	
pmm:PMM0963	>gnl|kg|pmm:PMM0963 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
aci:ACIAD1091	>gnl|kg|aci:ACIAD1091 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
pmi:PMT9312_0836	>gnl|kg|pmi:PMT9312_0836 urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x	
rpa:RPA3660	>gnl|kg|rpa:RPA3660 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
sil:SPO1714	>gnl|kg|sil:SPO1714 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
bme:BMEI1652	>gnl|kg|bme:BMEI1652 urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
rsp:RSP_6111	>gnl|kg|rsp:RSP_6111 ureC; UreA amidohydrolase (urease) alpha subunit [EC:3.5.1.5] [KO:K01427]			x	
ecs:ECs1324	>gnl|kg|ecs:ECs1324 urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
ece:Z1145	>gnl|kg|ece:Z1145 ureC; putative urease structural subunit C (alpha) [EC:3.5.1.5] [KO:K01428]			x	
ece:Z1584	>gnl|kg|ece:Z1584 ureC_2; putative urease structural subunit C (alpha) [EC:3.5.1.5] [KO:K01428]			x	
rpb:RPB_1803	>gnl|kg|rpb:RPB_1803 urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x	
vfi:VF0673	>gnl|kg|vfi:VF0673 urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
bca:BCE3662	>gnl|kg|bca:BCE3662 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
hit:NTHI0665	>gnl|kg|hit:NTHI0665 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
ppu:PP2845	>gnl|kg|ppu:PP2845 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
nmu:Nmul_A1241	>gnl|kg|nmu:Nmul_A1241 urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x	
bsu:BG11983	>gnl|kg|bsu:BG11983 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
hin:HI0539	>gnl|kg|hin:HI0539 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
dra:DRA0318	>gnl|kg|dra:DRA0318 urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
hhe:HH0408	>gnl|kg|hhe:HH0408 ureB; urease [EC:3.5.1.5] [KO:K01428]			x	
pha:PSHAa1759	>gnl|kg|pha:PSHAa1759 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x	
cya:CYA_0603	>gnl|kg|cya:CYA_0603 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x	
bpe:BP3168	>gnl|kg|bpe:BP3168 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
bbr:BB4323	>gnl|kg|bbr:BB4323 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
bpa:BPP3855	>gnl|kg|bpa:BPP3855 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
bpn:BPEN_542	>gnl|kg|bpn:BPEN_542 ureC; putative urease structural subunit C (alpha) [EC:3.5.1.5] [KO:K01428]			x	
hpy:HP0072	>gnl|kg|hpy:HP0072 ureB; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
hpj:jhp0067	>gnl|kg|hpj:jhp0067 ureB; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
bfl:Bfl523	>gnl|kg|bfl:Bfl523 ureC; putative urease structural subunit C (alpha) [EC:3.5.1.5] [KO:K01428]			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
saa:SAUSA300_2240	>gnl|kg|saa:SAUSA300_2240 ureC; urease, alpha subunit [EC:3.5.1.5]			x	
sas:SAS2180	>gnl|kg|sas:SAS2180 urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
sau:SA2084	>gnl|kg|sau:SA2084 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
sav:SAV2290	>gnl|kg|sav:SAV2290 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
sac:SACOL2282	>gnl|kg|sac:SACOL2282 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
sam:MW2208	>gnl|kg|sam:MW2208 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
sep:SE1863	>gnl|kg|sep:SE1863 urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
ser:SERP1871	>gnl|kg|ser:SERP1871 ureC; urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
sar:SAR2374	>gnl|kg|sar:SAR2374 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
ssp:SSP0263	>gnl|kg|ssp:SSP0263 urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
sab:SAB2162	>gnl|kg|sab:SAB2162 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01427]			x	
uur:UU432	>gnl|kg|uur:UU432 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
cef:CE0995	>gnl|kg|cef:CE0995 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
nfa:nfa25260	>gnl|kg|nfa:nfa25260 ureC; putative urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
cgb:cg0115	>gnl|kg|cgb:cg0115 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
cgl:NCgl0085	>gnl|kg|cgl:NCgl0085 Cgl0086; urea amidohydrolase (urease) alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
mtu:Rv1850	>gnl|kg|mtu:Rv1850 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
mbo:Mb1881	>gnl|kg|mbo:Mb1881 ureC; urease alpha subunit UreC (urea amidohydrolase) [EC:3.5.1.5] [KO:K01428]			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
mtc:MT1898	>gnl|kg|mtc:MT1898 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
stl:stu0283	>gnl|kg|stl:stu0283 ureC; urea amidohydrolase (urease) alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
stc:str0283	>gnl|kg|stc:str0283 ureC; urea amidohydrolase (urease) alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
ype:YPO2667	>gnl|kg|ype:YPO2667 ureC, yeuC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
yps:YPTB2942	>gnl|kg|yps:YPTB2942 ureC, yeuC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
sma:SAV7106	>gnl|kg|sma:SAV7106 ureC1; putative urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
ypm:YP2468	>gnl|kg|ypm:YP2468 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
sco:SCO1234	>gnl|kg|sco:SCO1234 2SCG1.09c, ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
plu:plu2173	>gnl|kg|plu:plu2173 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
fra:Francci3_0832	>gnl|kg|fra:Francci3_0832 urease, alpha subunit [EC:3.5.1.5] [KO:K01427]			x	
bms:BR1358	>gnl|kg|bms:BR1358 ureC-2; urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
bme:BMEI0647	>gnl|kg|bme:BMEI0647 urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
bmf:BAB1_1378	>gnl|kg|bmf:BAB1_1378 urease:amidohydrolase [EC:3.5.1.5] [KO:K01427]			x	
bmb:BruAb1_1355	>gnl|kg|bmb:BruAb1_1355 ureC-2; UreC-2, urease, alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
psb:Psyr_2197	>gnl|kg|psb:Psyr_2197 urease [EC:3.5.1.5] [KO:K01428]			x	
ypk:y1239	>gnl|kg|ypk:y1239 ureC; urease (urea amidohydrolase) alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
nph:NP2010A	>gnl|kg|nph:NP2010A ureA; urease , alpha subunit [EC:3.5.1.5] [KO:K01428]			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
hma:pNG7124	>gnl|kg|hma:pNG7124 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
sto:ST1028	>gnl|kg|sto:ST1028 urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
sco:SCO5526	>gnl|kg|sco:SCO5526 ureC; urease alpha subunit [EC:3.5.1.5] [KO:K01428]			x	
sma:SAV2715	>gnl|kg|sma:SAV2715 ureC2; putative urease subunit alpha [EC:3.5.1.5] [KO:K01428]			x	
Q8XB98_ECO57	>gnl|tr|Q8XB98_ECO57 (Q8XB98) Isoaspartyl dipeptidase			x	
Q83P79_SHIFL	>gnl|tr|Q83P79_SHIFL (Q83P79) Isoaspartyl dipeptidase			x	
Q659Y9_ECOLI	>gnl|tr|Q659Y9_ECOLI (Q659Y9) Isoaspartyl dipeptidase yadA			x	
Q31T14_SHIBS	>gnl|tr|Q31T14_SHIBS (Q31T14) Isoaspartyl dipeptidase			x	
Q8FA99_ECOL6	>gnl|tr|Q8FA99_ECOL6 (Q8FA99) Isoaspartyl dipeptidase (EC 3.4.19.-)			x	
Q57G89_SALCH	>gnl|tr|Q57G89_SALCH (Q57G89) Isoaspartyl dipeptidase			x	
Q5PM50_SALPA	>gnl|tr|Q5PM50_SALPA (Q5PM50) Probable isoaspartyl dipeptidase			x	
Q8Z0X6_SALTI	>gnl|tr|Q8Z0X6_SALTI (Q8Z0X6) Probable isoaspartyl dipeptidase (EC 3.4.19.-)			x	
Q8QZV3_MOUSE	>gnl|tr|Q8QZV3_MOUSE (Q8QZV3) Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase) (Dci protein) (0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833445A04 product:dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-			x	
Q9DBN7_MOUSE	>gnl|tr|Q9DBN7_MOUSE (Q9DBN7) Adult male liver cDNA, RIKEN full-length enriched library, clone:1300001E07 product:dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase), full insert sequence			x	
Q68G41_RAT	>gnl|tr|Q68G41_RAT (Q68G41) Dodecenoyl-coenzyme A delta isomerase			x	
Q7Z2L7_HUMAN	>gnl|tr|Q7Z2L7_HUMAN (Q7Z2L7) Dodecenoyl-Coenzyme A delta isomerase,			x	
Q5M8Y6_XENTR	>gnl|tr|Q5M8Y6_XENTR (Q5M8Y6) Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q88FQ7_PSEPK	>gnl|tr|Q88FQ7_PSEPK (Q88FQ7) Enoyl-CoA hydratase/isomerase family protein			x	x
Q2X8K8_PSEPU	>gnl|tr|Q2X8K8_PSEPU (Q2X8K8) Enoyl-CoA hydratase/isomerase family protein			x	x
Q882B0_PSESM	>gnl|tr|Q882B0_PSESM (Q882B0) Enoyl-CoA hydratase/isomerase family protein			x	x
Q4KBL1_PSEF5	>gnl|tr|Q4KBL1_PSEF5 (Q4KBL1) Enoyl-CoA hydratase/isomerase family protein			x	x
Q48IH9_PSE14	>gnl|tr|Q48IH9_PSE14 (Q48IH9) Enoyl-CoA hydratase/isomerase family protein (EC 5.3.3.-)			x	x
Q9AB78_CAUCR	>gnl|tr|Q9AB78_CAUCR (Q9AB78) Enoyl-CoA hydratase/isomerase family protein			x	x
Q8WZH4_NEUCR	>gnl|tr|Q8WZH4_NEUCR (Q8WZH4) Probable DELTA3, 5-DELTA2, 4-DIENOYL-COA ISOMERASE (ECH1)			x	
Q4WYW7_ASPFU	>gnl|tr|Q4WYW7_ASPFU (Q4WYW7) Enoyl-CoA hydratase/isomerase family protein			x	x
Q36PW7_MARHY	>gnl|tr|Q36PW7_MARHY (Q36PW7) Enoyl-CoA hydratase/isomerase family protein			x	x
Q5Z2W6_NOCFA	>gnl|tr|Q5Z2W6_NOCFA (Q5Z2W6) Putative enoyl-CoA hydratase/isomerase family protein			x	x
Q31WH7_SHIBS	>gnl|tr|Q31WH7_SHIBS (Q31WH7) Putative enzyme			x	x
Q8XD14_ECO57	>gnl|tr|Q8XD14_ECO57 (Q8XD14) Putative enzyme			x	x
Q83JT8_SHIFL	>gnl|tr|Q83JT8_SHIFL (Q83JT8) Putative enzyme			x	x
Q3YXV3_SHISS	>gnl|tr|Q3YXV3_SHISS (Q3YXV3) Putative enzyme			x	x
Q53GA8_HUMAN	>gnl|tr|Q53GA8_HUMAN (Q53GA8) 3-hydroxyisobutyryl-Coenzyme A hydrolase isoform 1 variant (Fragment)			x	
Q53GF2_HUMAN	>gnl|tr|Q53GF2_HUMAN (Q53GF2) 3-hydroxyisobutyryl-Coenzyme A hydrolase isoform 1 variant (Fragment)			x	
Q6NVY1_HUMAN	>gnl|tr|Q6NVY1_HUMAN (Q6NVY1) 3-hydroxyisobutyryl-Coenzyme A hydrolase, isoform 1			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q8QZS1_MOUSE	>gnl|tr|Q8QZS1_MOUSE (Q8QZS1) 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610509I15 product:similar to 3-HYDROXYISOBUTYRYL-COENZYME A HYDROLASE			x	x
Q58EB4_BRARE	>gnl|tr|Q58EB4_BRARE (Q58EB4) 3-hydroxyisobutyryl-Coenzyme A hydrolase			x	
Q92931_HUMAN	>gnl|tr|Q92931_HUMAN (Q92931) 3-hydroxyisobutyryl-coenzyme A hydrolase			x	
Q9LKJ1_ARATH	>gnl|tr|Q9LKJ1_ARATH (Q9LKJ1) CoA-thioester hydrolase CHY1 (3-hydroxyisobutyryl-coenzyme A hydrolase)			x	
O49331_ARATH	>gnl|tr|O49331_ARATH (O49331) 3-hydroxyisobutyryl-coenzyme A hydrolase			x	
O49330_ARATH	>gnl|tr|O49330_ARATH (O49330) 3-hydroxyisobutyryl-coenzyme A hydrolase			x	
Q81DR3_BACCR	>gnl|tr|Q81DR3_BACCR (Q81DR3) 3-hydroxyisobutyryl-coenzyme A hydrolase (EC 3.1.2.4)			x	
Q983C3_RHILO	>gnl|tr|Q983C3_RHILO (Q983C3) 3-hydroxyisobutyryl-Coenzyme A hydrolase			x	
Q9LK08_ARATH	>gnl|tr|Q9LK08_ARATH (Q9LK08) 3-hydroxyisobutyryl-coenzyme A hydrolase-like protein			x	x
Q9T0K7_ARATH	>gnl|tr|Q9T0K7_ARATH (Q9T0K7) 3-hydroxyisobutyryl-coenzyme A hydrolase-like protein (AT4g13360/T9E8_100)			x	x
Q4WVP0_ASPFU	>gnl|tr|Q4WVP0_ASPFU (Q4WVP0) Mitochondrial 3-hydroxyisobutyryl-CoA hydrolase, putative			x	
Q63TV7_BURPS	>gnl|tr|Q63TV7_BURPS (Q63TV7) Putative hydratase			x	x
Q56XU5_ARATH	>gnl|tr|Q56XU5_ARATH (Q56XU5) 3-hydroxyisobutyryl-coenzyme A hydrolase (At1g06550)			x	
Q2QUG4_ORYSA	>gnl|tr|Q2QUG4_ORYSA (Q2QUG4) 3-hydroxyisobutyryl-coenzyme A hydrolase, putative			x	
Q2QUG3_ORYSA	>gnl|tr|Q2QUG3_ORYSA (Q2QUG3) 3-hydroxyisobutyryl-coenzyme A hydrolase, putative			x	
Q69UF2_ORYSA	>gnl|tr|Q69UF2_ORYSA (Q69UF2) Putative 3-hydroxyisobutyryl-coenzyme A hydrolase			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q6G3D0_BARHE	>gnl|tr|Q6G3D0_BARHE (Q6G3D0) 3-hydroxyisobutyryl-coenzyme A hydrolase			x	
Q5XIE6_RAT	>gnl|tr|Q5XIE6_RAT (Q5XIE6) 3-hydroxyisobutyryl-Coenzyme A hydrolase (Predicted)			x	
Q6NI92_CORDI	>gnl|tr|Q6NI92_CORDI (Q6NI92) Putative hydrolase			x	x
O85078_9MICC	>gnl|tr|O85078_9MICC (O85078) 4-chlorobenzoyl CoA dehalogenase			x	
Q7BI35_ARTGO	>gnl|tr|Q7BI35_ARTGO (Q7BI35) 4-chlorobenzoate Co-A dehalogenase			x	
Q7BUZ5_9MICC	>gnl|tr|Q7BUZ5_9MICC (Q7BUZ5) 4-chlorobenzoyl CoA dehalogenase			x	
Q99QJ6_9MICC	>gnl|tr|Q99QJ6_9MICC (Q99QJ6) 4-CBA-CoA dehalogenase			x	
Q9LCU3_9MICC	>gnl|tr|Q9LCU3_9MICC (Q9LCU3) 4-chlorobenzoyl CoA dehalogenase			x	
O68600_9PROT	>gnl|tr|O68600_9PROT (O68600) 4-chlorobenzoyl CoA dehalogenase			x	
Q8GN87_9BURK	>gnl|tr|Q8GN87_9BURK (Q8GN87) 4-chlorobenzoyl CoA dehalogenase			x	
Q84RL9_DUNSA	>gnl|tr|Q84RL9_DUNSA (Q84RL9) Enolase			x	
Q6FHV6_HUMAN	>gnl|tr|Q6FHV6_HUMAN (Q6FHV6) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x	
Q4YQJ5_PLABE	>gnl|tr|Q4YQJ5_PLABE (Q4YQJ5) Enolase, putative			x	
Q3CFC7_THEET	>gnl|tr|Q3CFC7_THEET (Q3CFC7) Enolase (EC 4.2.1.11)			x	
Q545V3_MOUSE	>gnl|tr|Q545V3_MOUSE (Q545V3) Adult male brain cDNA, RIKEN full-length enriched library, clone:0710008M22 product:enolase 2, gamma neuronal, full insert sequence (Adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1520403G13 product:enolase 2,			x	
Q5NJY7_LACPL	>gnl|tr|Q5NJY7_LACPL (Q5NJY7) Enolase (EC 4.2.1.11)			x	
Q53FT9_HUMAN	>gnl|tr|Q53FT9_HUMAN (Q53FT9) Enolase 1 variant (Fragment)			x	
Q3UJ20_MOUSE	>gnl|tr|Q3UJ20_MOUSE (Q3UJ20) 17 days embryo heart cDNA, RIKEN full-length enriched library, clone:I920038O04 product:enolase 2, gamma neuronal, full insert sequence			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q5FW97_MOUSE	>gnl|tr|Q5FW97_MOUSE (Q5FW97) Hypothetical protein LOC433182 (Melanocyte cDNA, RIKEN full-length enriched library, clone:G270128I15 product:enolase 1, alpha non-neuron, full insert sequence) (Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone			x	
Q53HR3_HUMAN	>gnl|tr|Q53HR3_HUMAN (Q53HR3) Enolase 1 variant (Fragment)			x	
Q5EB49_RAT	>gnl|tr|Q5EB49_RAT (Q5EB49) Enolase 1, alpha			x	
Q7XAS6_CYNDA	>gnl|tr|Q7XAS6_CYNDA (Q7XAS6) Pollen 2-phosphoglycerate dehydrogenase 2			x	
Q5XIV3_RAT	>gnl|tr|Q5XIV3_RAT (Q5XIV3) Enolase 3, beta			x	
Q4R5L2_MACFA	>gnl|tr|Q4R5L2_MACFA (Q4R5L2) Brain cDNA, clone: QccE-14518, similar to human enolase 1, (alpha) (ENO1),			x	x
Q2SSR3_MYCCA	>gnl|tr|Q2SSR3_MYCCA (Q2SSR3) Enolase (EC 4.2.1.11)			x	
Q9LEK6_EUGGR	>gnl|tr|Q9LEK6_EUGGR (Q9LEK6) Chloroplast enolase precursor (EC 4.2.1.11) (Fragment)			x	
Q3AFC8_CARHZ	>gnl|tr|Q3AFC8_CARHZ (Q3AFC8) Enolase (EC 4.2.1.11)			x	
Q3XX08_ENTFC	>gnl|tr|Q3XX08_ENTFC (Q3XX08) Enolase (EC 4.2.1.11)			x	
Q5SX58_MOUSE	>gnl|tr|Q5SX58_MOUSE (Q5SX58) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x	
Q7XBE4_ORYSA	>gnl|tr|Q7XBE4_ORYSA (Q7XBE4) Enolase (EC 4.2.1.11)			x	
Q8VYG4_ARATH	>gnl|tr|Q8VYG4_ARATH (Q8VYG4) Putative enolase (2-phospho-D-glycerate hydroylase)			x	
Q65EN2_BACLD	>gnl|tr|Q65EN2_BACLD (Q65EN2) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x	
Q4MQ53_BACCE	>gnl|tr|Q4MQ53_BACCE (Q4MQ53) Enolase (EC 4.2.1.11)			x	
Q5R6Y1_PONPY	>gnl|tr|Q5R6Y1_PONPY (Q5R6Y1) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x	
Q4U8Y7_THEAN	>gnl|tr|Q4U8Y7_THEAN (Q4U8Y7) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x	
Q6PC12_BRARE	>gnl|tr|Q6PC12_BRARE (Q6PC12) Enolase 1, (Alpha)			x	
Q2RLT8_MOOTH	>gnl|tr|Q2RLT8_MOOTH (Q2RLT8) Enolase (EC 4.2.1.11)			x	
Q6IQP5_BRARE	>gnl|tr|Q6IQP5_BRARE (Q6IQP5) Enolase 1, (Alpha)			x	
Q9LEE0_SPIOL	>gnl|tr|Q9LEE0_SPIOL (Q9LEE0) Enolase (EC 4.2.1.11)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q3EMP6_BACTI	>gnl|tr|Q3EMP6_BACTI (Q3EMP6) Enolase (EC 4.2.1.11)			x	
Q6P8E1_XENTR	>gnl|tr|Q6P8E1_XENTR (Q6P8E1) Enolase (2-phosphoglycerate dehydratase)			x	
Q4N1N2_THEPA	>gnl|tr|Q4N1N2_THEPA (Q4N1N2) Enolase, putative (EC 4.2.1.11)			x	
Q9LEK7_EUGGR	>gnl|tr|Q9LEK7_EUGGR (Q9LEK7) Enolase (EC 4.2.1.11)			x	
Q5VNT9_ORYSA	>gnl|tr|Q5VNT9_ORYSA (Q5VNT9) Putative enolase			x	
Q6WB92_GOSBA	>gnl|tr|Q6WB92_GOSBA (Q6WB92) Enolase			x	
Q8RWM8_ARATH	>gnl|tr|Q8RWM8_ARATH (Q8RWM8) Enolase (2-phospho-D-glycerate hydroylase)			x	
Q6TH14_BRARE	>gnl|tr|Q6TH14_BRARE (Q6TH14) Enolase 1, (Alpha)			x	
Q3ATQ5_CHLCH	>gnl|tr|Q3ATQ5_CHLCH (Q3ATQ5) Enolase (EC 4.2.1.11)			x	
Q39T27_GEOMG	>gnl|tr|Q39T27_GEOMG (Q39T27) Enolase			x	
Q8GDZ5_HELMO	>gnl|tr|Q8GDZ5_HELMO (Q8GDZ5) Enolase (EC 4.2.1.11) (Fragment)			x	
Q3VI98_9CHLB	>gnl|tr|Q3VI98_9CHLB (Q3VI98) Enolase (EC 4.2.1.11)			x	
Q9M434_LUPLU	>gnl|tr|Q9M434_LUPLU (Q9M434) Enolase			x	
Q568G3_BRARE	>gnl|tr|Q568G3_BRARE (Q568G3) Enolase 3, (Beta, muscle)			x	
Q38Y18_LACSS	>gnl|tr|Q38Y18_LACSS (Q38Y18) Phosphopyruvate hydratase (EC 4.2.1.11)			x	
Q5ISQ0_MACFA	>gnl|tr|Q5ISQ0_MACFA (Q5ISQ0) Enolase 2 (Fragment)			x	
Q3GIP3_CHLVI	>gnl|tr|Q3GIP3_CHLVI (Q3GIP3) Enolase (EC 4.2.1.11)			x	
Q5LG64_BACFN	>gnl|tr|Q5LG64_BACFN (Q5LG64) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x	
Q6W7E8_BRACM	>gnl|tr|Q6W7E8_BRACM (Q6W7E8) Enolase			x	
Q3B1G7_PELLD	>gnl|tr|Q3B1G7_PELLD (Q3B1G7) Enolase (EC 4.2.1.11)			x	
Q41AA9_9BACI	>gnl|tr|Q41AA9_9BACI (Q41AA9) Enolase (EC 4.2.1.11)			x	
Q4H8Q9_9DEIO	>gnl|tr|Q4H8Q9_9DEIO (Q4H8Q9) Enolase (EC 4.2.1.11)			x	
Q967U0_TRISP	>gnl|tr|Q967U0_TRISP (Q967U0) Enolase			x	
Q3XPP9_9PROT	>gnl|tr|Q3XPP9_9PROT (Q3XPP9) Enolase (EC 4.2.1.11)			x	
Q6RIB7_SOYBN	>gnl|tr|Q6RIB7_SOYBN (Q6RIB7) Enolase (EC 2.3.1.16)			x	
Q4EEP6_LISMO	>gnl|tr|Q4EEP6_LISMO (Q4EEP6) Enolase (EC 4.2.1.11)			x	
Q44T71_CHLLI	>gnl|tr|Q44T71_CHLLI (Q44T71) Enolase (EC 4.2.1.11)			x	
Q3FZA1_9DELT	>gnl|tr|Q3FZA1_9DELT (Q3FZA1) Enolase (EC 4.2.1.11)			x	
Q5NJZ3_LACSK	>gnl|tr|Q5NJZ3_LACSK (Q5NJZ3) Enolase			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q3SEA7_PARTE	>gnl|tr|Q3SEA7_PARTE (Q3SEA7) Enolase, putative			x	
Q58WU7_9BACT	>gnl|tr|Q58WU7_9BACT (Q58WU7) Enolase			x	
Q6A4N1_CAEEL	>gnl|tr|Q6A4N1_CAEEL (Q6A4N1) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x	
Q3VWM9_PROAE	>gnl|tr|Q3VWM9_PROAE (Q3VWM9) Enolase (EC 4.2.1.11)			x	
Q6W7E7_BRANA	>gnl|tr|Q6W7E7_BRANA (Q6W7E7) Enolase			x	
Q4J257_AZOVI	>gnl|tr|Q4J257_AZOVI (Q4J257) Enolase (EC 4.2.1.11)			x	
Q3A578_PELCD	>gnl|tr|Q3A578_PELCD (Q3A578) Enolase			x	
Q6GQM9_BRARE	>gnl|tr|Q6GQM9_BRARE (Q6GQM9) Enolase 2			x	
Q3SL43_THIDA	>gnl|tr|Q3SL43_THIDA (Q3SL43) Enolase (Phosphopyruvate hydratase) (EC 4.2.1.11)			x	
Q2RT60_RHORU	>gnl|tr|Q2RT60_RHORU (Q2RT60) Phosphopyruvate hydratase (EC 4.2.1.11)			x	
Q4IUV7_AZOVI	>gnl|tr|Q4IUV7_AZOVI (Q4IUV7) Enolase precursor (EC 4.2.1.11)			x	
Q3SEB6_PARTE	>gnl|tr|Q3SEB6_PARTE (Q3SEB6) Enolase, putative			x	
Q316Q0_DESDG	>gnl|tr|Q316Q0_DESDG (Q316Q0) Enolase (EC 4.2.1.11)			x	
Q3CTJ0_ALTAT	>gnl|tr|Q3CTJ0_ALTAT (Q3CTJ0) Enolase (EC 4.2.1.11)			x	
Q4IV38_AZOVI	>gnl|tr|Q4IV38_AZOVI (Q4IV38) Enolase (EC 4.2.1.11)			x	
O96656_PENMO	>gnl|tr|O96656_PENMO (O96656) Phosphopyruvate hydratase			x	
Q40LS9_DESAC	>gnl|tr|Q40LS9_DESAC (Q40LS9) Enolase (EC 4.2.1.11)			x	
Q43J81_9CHLB	>gnl|tr|Q43J81_9CHLB (Q43J81) Enolase (EC 4.2.1.11)			x	
Q5XXS5_9HEMI	>gnl|tr|Q5XXS5_9HEMI (Q5XXS5) Enolase			x	
Q4BXE8_CROWT	>gnl|tr|Q4BXE8_CROWT (Q4BXE8) Enolase (EC 4.2.1.11)			x	
Q4AFG0_9CHLB	>gnl|tr|Q4AFG0_9CHLB (Q4AFG0) Enolase (EC 4.2.1.11)			x	
Q4JU51_CORJK	>gnl|tr|Q4JU51_CORJK (Q4JU51) Eno protein (EC 4.2.1.11)			x	
Q2WQ80_CLOBE	>gnl|tr|Q2WQ80_CLOBE (Q2WQ80) Enolase			x	
Q4NII0_9MICC	>gnl|tr|Q4NII0_9MICC (Q4NII0) Enolase (EC 4.2.1.11)			x	
Q3MZ86_9DELT	>gnl|tr|Q3MZ86_9DELT (Q3MZ86) Enolase (EC 4.2.1.11)			x	
Q4AJ21_9CHLB	>gnl|tr|Q4AJ21_9CHLB (Q4AJ21) Enolase (EC 4.2.1.11)			x	
Q37RX0_SPHAR	>gnl|tr|Q37RX0_SPHAR (Q37RX0) Enolase (EC 4.2.1.11)			x	
Q4QLX6_HAEI8	>gnl|tr|Q4QLX6_HAEI8 (Q4QLX6) Enolase (EC 4.2.1.11)			x	
Q48UF7_STRPM	>gnl|tr|Q48UF7_STRPM (Q48UF7) Enolase (EC 4.2.1.11)			x	
Q3DFV3_STRAG	>gnl|tr|Q3DFV3_STRAG (Q3DFV3) Enolase (EC 4.2.1.11)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q47DI1_DECAR	>gnl|tr|Q47DI1_DECAR (Q47DI1) Enolase			x	
Q2XUR0_CORGL	>gnl|tr|Q2XUR0_CORGL (Q2XUR0) Enolase			x	
Q3K2B2_STRA1	>gnl|tr|Q3K2B2_STRA1 (Q3K2B2) Enolase (EC 4.2.1.11)			x	
Q3D1D7_STRAG	>gnl|tr|Q3D1D7_STRAG (Q3D1D7) Enolase (EC 4.2.1.11)			x	
Q3DRQ3_STRAG	>gnl|tr|Q3DRQ3_STRAG (Q3DRQ3) Enolase (EC 4.2.1.11)			x	
Q36RG6_MARHY	>gnl|tr|Q36RG6_MARHY (Q36RG6) Enolase			x	
Q8RP81_STRAG	>gnl|tr|Q8RP81_STRAG (Q8RP81) Enolase			x	
Q2YSE8_STAAB	>gnl|tr|Q2YSE8_STAAB (Q2YSE8) Enolase 2-phosphoglycerate dehydratase (EC 4.2.1.11)			x	
Q935W7_STRPN	>gnl|tr|Q935W7_STRPN (Q935W7) Alpha-enolase			x	
Q8VVB4_STRTR	>gnl|tr|Q8VVB4_STRTR (Q8VVB4) 2-phosphoglycerate dehydratase			x	
Q3LFH7_PROFR	>gnl|tr|Q3LFH7_PROFR (Q3LFH7) Enolase 1 (EC 4.2.1.11)			x	
Q3E6B9_CHLAU	>gnl|tr|Q3E6B9_CHLAU (Q3E6B9) Enolase			x	
Q31G68_THICR	>gnl|tr|Q31G68_THICR (Q31G68) Enolase (EC 4.2.1.11)			x	
Q4L4K7_STAHJ	>gnl|tr|Q4L4K7_STAHJ (Q4L4K7) Enolase			x	
Q3DK41_STRAG	>gnl|tr|Q3DK41_STRAG (Q3DK41) Enolase (EC 4.2.1.11)			x	
Q2XF58_PSEPU	>gnl|tr|Q2XF58_PSEPU (Q2XF58) Enolase			x	
Q3XBL7_METFL	>gnl|tr|Q3XBL7_METFL (Q3XBL7) Enolase (EC 4.2.1.11)			x	
Q32CD6_SHIDS	>gnl|tr|Q32CD6_SHIDS (Q32CD6) Enolase			x	
Q31XL1_SHIBS	>gnl|tr|Q31XL1_SHIBS (Q31XL1) Enolase			x	
Q4UTP2_XANC8	>gnl|tr|Q4UTP2_XANC8 (Q4UTP2) Enolase			x	
Q4IN62_GIBZE	>gnl|tr|Q4IN62_GIBZE (Q4IN62) ENO_ALTAL Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Major allergen Alt a 11) (Alt a XI)			x	
Q2SKX0_9GAMM	>gnl|tr|Q2SKX0_9GAMM (Q2SKX0) Enolase (EC 4.2.1.11)			x	
Q845Q5_9STRE	>gnl|tr|Q845Q5_9STRE (Q845Q5) Enolase			x	
Q3ZX11_DEHSC	>gnl|tr|Q3ZX11_DEHSC (Q3ZX11) Enolase (EC 4.2.1.11)			x	
Q3BUT0_XANC5	>gnl|tr|Q3BUT0_XANC5 (Q3BUT0) Enolase (EC 4.2.1.11)			x	
Q3YY77_SHISS	>gnl|tr|Q3YY77_SHISS (Q3YY77) Enolase			x	
Q8MU59_ANISI	>gnl|tr|Q8MU59_ANISI (Q8MU59) Enolase (EC 4.2.1.11)			x	
Q48F79_PSE14	>gnl|tr|Q48F79_PSE14 (Q48F79) Enolase (EC 4.2.1.11)			x	
Q3RW22_RALME	>gnl|tr|Q3RW22_RALME (Q3RW22) Enolase (EC 4.2.1.11)			x	
Q4ZWQ8_PSEU2	>gnl|tr|Q4ZWQ8_PSEU2 (Q4ZWQ8) Enolase (EC 4.2.1.11)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q4IXV2_AZOVI	>gnl|tr|Q4IXV2_AZOVI (Q4IXV2) Enolase (EC 4.2.1.11)			x	
Q5B135_EMENI	>gnl|tr|Q5B135_EMENI (Q5B135) ENO_ASPOR Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
Q4A740_MYCS5	>gnl|tr|Q4A740_MYCS5 (Q4A740) Enolase (EC 4.2.1.11)			x	
Q47SV1_THEFY	>gnl|tr|Q47SV1_THEFY (Q47SV1) Enolase (EC 4.2.1.11)			x	
Q45RT9_BIFAN	>gnl|tr|Q45RT9_BIFAN (Q45RT9) Alpha-enolase			x	
Q3Z8W4_DEHE1	>gnl|tr|Q3Z8W4_DEHE1 (Q3Z8W4) Enolase (EC 4.2.1.11)			x	
Q4KHF6_PSEF5	>gnl|tr|Q4KHF6_PSEF5 (Q4KHF6) Enolase (EC 4.2.1.11)			x	
Q44G15_CHRSL	>gnl|tr|Q44G15_CHRSL (Q44G15) Enolase (EC 4.2.1.11)			x	
Q3Q3U6_9GAMM	>gnl|tr|Q3Q3U6_9GAMM (Q3Q3U6) Enolase (EC 4.2.1.11)			x	
Q2P1K8_XANOR	>gnl|tr|Q2P1K8_XANOR (Q2P1K8) Enolase			x	
Q43KU5_SOLUS	>gnl|tr|Q43KU5_SOLUS (Q43KU5) Enolase (EC 4.2.1.11)			x	
Q473G4_RALEJ	>gnl|tr|Q473G4_RALEJ (Q473G4) Enolase (EC 4.2.1.11)			x	
Q3GWD8_9ACTO	>gnl|tr|Q3GWD8_9ACTO (Q3GWD8) Enolase (EC 4.2.1.11)			x	
Q2NJ39_9MOLU	>gnl|tr|Q2NJ39_9MOLU (Q2NJ39) Enolase (EC 4.2.1.11)			x	
Q57KH0_SALCH	>gnl|tr|Q57KH0_SALCH (Q57KH0) Enolase			x	
Q3KH92_PSEPF	>gnl|tr|Q3KH92_PSEPF (Q3KH92) Phosphopyruvate hydratase (EC 4.2.1.11)			x	
Q40BD7_9RHOB	>gnl|tr|Q40BD7_9RHOB (Q40BD7) Enolase (EC 4.2.1.11)			x	
Q3QH16_9GAMM	>gnl|tr|Q3QH16_9GAMM (Q3QH16) Enolase (EC 4.2.1.11)			x	
Q2X6H4_9GAMM	>gnl|tr|Q2X6H4_9GAMM (Q2X6H4) Enolase (EC 4.2.1.11)			x	
Q2ZQF5_SHEPU	>gnl|tr|Q2ZQF5_SHEPU (Q2ZQF5) Enolase (EC 4.2.1.11)			x	
Q3FSQ4_9BURK	>gnl|tr|Q3FSQ4_9BURK (Q3FSQ4) Enolase (EC 4.2.1.11)			x	
Q34CZ0_RHOPA	>gnl|tr|Q34CZ0_RHOPA (Q34CZ0) Enolase			x	
Q3QVK8_9RHOB	>gnl|tr|Q3QVK8_9RHOB (Q3QVK8) Enolase (EC 4.2.1.11)			x	
Q5KLA7_CRYNE	>gnl|tr|Q5KLA7_CRYNE (Q5KLA7) Phosphopyruvate hydratase, putative			x	
Q3RGV0_XYLFA	>gnl|tr|Q3RGV0_XYLFA (Q3RGV0) Enolase (EC 4.2.1.11)			x	
Q2NAQ1_9SPHN	>gnl|tr|Q2NAQ1_9SPHN (Q2NAQ1) Enolase			x	
Q36D71_9GAMM	>gnl|tr|Q36D71_9GAMM (Q36D71) Enolase (EC 4.2.1.11)			x	
Q35US6_9GAMM	>gnl|tr|Q35US6_9GAMM (Q35US6) Enolase (EC 4.2.1.11)			x	
Q2Z3H6_9GAMM	>gnl|tr|Q2Z3H6_9GAMM (Q2Z3H6) Enolase (EC 4.2.1.11)			x	
Q54RK5_DICDI	>gnl|tr|Q54RK5_DICDI (Q54RK5) Phosphopyruvate hydratase			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q33Y02_9GAMM	>gnl|tr|Q33Y02_9GAMM (Q33Y02) Enolase (EC 4.2.1.11)			x	
Q2XG84_PSEPU	>gnl|tr|Q2XG84_PSEPU (Q2XG84) Enolase			x	
Q35JB8_9BRAD	>gnl|tr|Q35JB8_9BRAD (Q35JB8) Enolase (EC 4.2.1.11)			x	
Q3DBB1_STRAG	>gnl|tr|Q3DBB1_STRAG (Q3DBB1) Enolase (EC 4.2.1.11) (Fragment)			x	
Q8H716_PHYIN	>gnl|tr|Q8H716_PHYIN (Q8H716) Enolase			x	
Q49W03_STAS1	>gnl|tr|Q49W03_STAS1 (Q49W03) Enolase			x	
Q84FY9_METEX	>gnl|tr|Q84FY9_METEX (Q84FY9) Enolase			x	
Q3NL87_SHEFR	>gnl|tr|Q3NL87_SHEFR (Q3NL87) Enolase (EC 4.2.1.11)			x	
Q3F8V7_9BURK	>gnl|tr|Q3F8V7_9BURK (Q3F8V7) Enolase (EC 4.2.1.11)			x	
Q2NVN7_SODGL	>gnl|tr|Q2NVN7_SODGL (Q2NVN7) Enolase			x	
Q39EV9_BURS3	>gnl|tr|Q39EV9_BURS3 (Q39EV9) Phosphopyruvate hydratase (EC 4.2.1.11)			x	
Q3R8C7_XYLFA	>gnl|tr|Q3R8C7_XYLFA (Q3R8C7) Enolase (EC 4.2.1.11)			x	
Q37IT6_RHOPA	>gnl|tr|Q37IT6_RHOPA (Q37IT6) Enolase (EC 4.2.1.11)			x	
Q4LMD0_9BURK	>gnl|tr|Q4LMD0_9BURK (Q4LMD0) Enolase (EC 4.2.1.11)			x	
Q457U5_9BURK	>gnl|tr|Q457U5_9BURK (Q457U5) Enolase (EC 4.2.1.11)			x	
Q4B7M9_BURVI	>gnl|tr|Q4B7M9_BURVI (Q4B7M9) Enolase (EC 4.2.1.11)			x	
Q4ARP8_9BURK	>gnl|tr|Q4ARP8_9BURK (Q4ARP8) Enolase (EC 4.2.1.11)			x	
Q3GKS6_9GAMM	>gnl|tr|Q3GKS6_9GAMM (Q3GKS6) Enolase (EC 4.2.1.11)			x	
Q4NT46_9DELT	>gnl|tr|Q4NT46_9DELT (Q4NT46) Enolase (EC 4.2.1.11)			x	
Q7P791_FUSNV	>gnl|tr|Q7P791_FUSNV (Q7P791) Enolase (EC 4.2.1.11)			x	
Q5CRP8_CRYPV	>gnl|tr|Q5CRP8_CRYPV (Q5CRP8) Enolase (2-phosphoglycerate dehydratase) (Fragment)			x	
Q2YPV0_BRUA2	>gnl|tr|Q2YPV0_BRUA2 (Q2YPV0) Enolase (EC 4.2.1.11)			x	
Q2UMC4_ASPOR	>gnl|tr|Q2UMC4_ASPOR (Q2UMC4) Enolase			x	
Q57D07_BRUAB	>gnl|tr|Q57D07_BRUAB (Q57D07) Enolase			x	
Q3PK04_PARDE	>gnl|tr|Q3PK04_PARDE (Q3PK04) Enolase (EC 4.2.1.11)			x	
Q36Y92_RHOPA	>gnl|tr|Q36Y92_RHOPA (Q36Y92) Enolase (EC 4.2.1.11)			x	
Q50QB0_ENTHI	>gnl|tr|Q50QB0_ENTHI (Q50QB0) Enolase, putative			x	
Q34UX9_9GAMM	>gnl|tr|Q34UX9_9GAMM (Q34UX9) Enolase (EC 4.2.1.11)			x	
Q3VBY9_9SPHN	>gnl|tr|Q3VBY9_9SPHN (Q3VBY9) Enolase (EC 4.2.1.11)			x	
Q3WWV7_9RHIZ	>gnl|tr|Q3WWV7_9RHIZ (Q3WWV7) Enolase (EC 4.2.1.11)			x	
Q438Q7_9ACTO	>gnl|tr|Q438Q7_9ACTO (Q438Q7) Enolase (EC 4.2.1.11)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q4FR74_PSYAR	>gnl|tr|Q4FR74_PSYAR (Q4FR74) Enolase (EC 4.2.1.11)			x	
Q2W698_MAGSA	>gnl|tr|Q2W698_MAGSA (Q2W698) Enolase			x	
Q3M7B2_ANAVT	>gnl|tr|Q3M7B2_ANAVT (Q3M7B2) Enolase (EC 4.2.1.11)			x	
Q3JQQ6_BURP1	>gnl|tr|Q3JQQ6_BURP1 (Q3JQQ6) Phosphopyruvate hydratase (EC 4.2.1.11)			x	
Q3P3W1_9GAMM	>gnl|tr|Q3P3W1_9GAMM (Q3P3W1) Enolase (EC 4.2.1.11)			x	
Q47WR1_COLP3	>gnl|tr|Q47WR1_COLP3 (Q47WR1) Enolase (EC 4.2.1.11)			x	
Q38BV6_9TRYP	>gnl|tr|Q38BV6_9TRYP (Q38BV6) Enolase (EC 4.2.1.11)			x	
Q9NDH8_TRYBB	>gnl|tr|Q9NDH8_TRYBB (Q9NDH8) Enolase (EC 4.2.1.11)			x	
Q3IDM2_PSEHT	>gnl|tr|Q3IDM2_PSEHT (Q3IDM2) Enolase (EC 4.2.1.11)			x	
Q2SXC5_BURTH	>gnl|tr|Q2SXC5_BURTH (Q2SXC5) Enolase (EC 4.2.1.11)			x	
Q3W1G4_9ACTO	>gnl|tr|Q3W1G4_9ACTO (Q3W1G4) Enolase (EC 4.2.1.11)			x	
Q9C9C4_ARATH	>gnl|tr|Q9C9C4_ARATH (Q9C9C4) Putative enolase; 31277-33713 (Putative enolase)			x	
Q31QJ8_SYNP7	>gnl|tr|Q31QJ8_SYNP7 (Q31QJ8) Enolase (EC 4.2.1.11)			x	
Q6SGG1_9BACT	>gnl|tr|Q6SGG1_9BACT (Q6SGG1) Enolase (EC 4.2.1.11)			x	
Q3HGQ2_TRIER	>gnl|tr|Q3HGQ2_TRIER (Q3HGQ2) Enolase (EC 4.2.1.11)			x	
Q34LT3_RHOPA	>gnl|tr|Q34LT3_RHOPA (Q34LT3) Phosphopyruvate hydratase (EC 4.2.1.11)			x	
Q3X3P9_9ACTN	>gnl|tr|Q3X3P9_9ACTN (Q3X3P9) Enolase (EC 4.2.1.11)			x	
Q3PU04_NITHA	>gnl|tr|Q3PU04_NITHA (Q3PU04) Enolase (EC 4.2.1.11)			x	
Q3J3H9_RHOS4	>gnl|tr|Q3J3H9_RHOS4 (Q3J3H9) Enolase (EC 4.2.1.11)			x	
Q415I2_KINRA	>gnl|tr|Q415I2_KINRA (Q415I2) Enolase (EC 4.2.1.11)			x	
Q4DZ98_TRYCR	>gnl|tr|Q4DZ98_TRYCR (Q4DZ98) Enolase, putative (EC 4.2.1.11)			x	
Q5WQL5_HETTR	>gnl|tr|Q5WQL5_HETTR (Q5WQL5) Enolase (Fragment)			x	
Q2S4F8_9SPHI	>gnl|tr|Q2S4F8_9SPHI (Q2S4F8) Phosphopyruvate hydratase (EC 4.2.1.11)			x	
Q7SHD6_NEUCR	>gnl|tr|Q7SHD6_NEUCR (Q7SHD6) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x	
O44101_DROSU	>gnl|tr|O44101_DROSU (O44101) Enolase (Fragment)			x	
Q2Y9P0_NITMU	>gnl|tr|Q2Y9P0_NITMU (Q2Y9P0) Enolase (EC 4.2.1.11)			x	
Q6SET0_9BACT	>gnl|tr|Q6SET0_9BACT (Q6SET0) Enolase (EC 4.2.1.11)			x	
Q7YZX3_ONCVO	>gnl|tr|Q7YZX3_ONCVO (Q7YZX3) Enolase			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q3AVW5_SYNS9	>gnl|tr|Q3AVW5_SYNS9 (Q3AVW5) Enolase (EC 4.2.1.11)			x	
Q31CX3_PROM9	>gnl|tr|Q31CX3_PROM9 (Q31CX3) Enolase (EC 4.2.1.11)			x	
Q56RP2_DROPS	>gnl|tr|Q56RP2_DROPS (Q56RP2) Enolase (Fragment)			x	
Q3SRK4_NITWN	>gnl|tr|Q3SRK4_NITWN (Q3SRK4) Enolase (EC 4.2.1.11)			x	
Q3HL75_LEIME	>gnl|tr|Q3HL75_LEIME (Q3HL75) Enolase (EC 4.2.1.11)			x	
Q4EBA7_9RICK	>gnl|tr|Q4EBA7_9RICK (Q4EBA7) Enolase (EC 4.2.1.11)			x	
Q33AR4_ORYSA	>gnl|tr|Q33AR4_ORYSA (Q33AR4) Enolase			x	
Q30P06_THIDN	>gnl|tr|Q30P06_THIDN (Q30P06) Phosphopyruvate hydratase (EC 4.2.1.11)			x	
O44100_DROPS	>gnl|tr|O44100_DROPS (O44100) Enolase (Fragment)			x	
Q56RN2_DROMI	>gnl|tr|Q56RN2_DROMI (Q56RN2) Enolase (Fragment)			x	
Q4QFL8_LEIMA	>gnl|tr|Q4QFL8_LEIMA (Q4QFL8) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x	
Q3AGS4_SYNSC	>gnl|tr|Q3AGS4_SYNSC (Q3AGS4) Enolase (EC 4.2.1.11)			x	
Q46HG5_PROMT	>gnl|tr|Q46HG5_PROMT (Q46HG5) Enolase (EC 4.2.1.11)			x	
Q3ND54_9PROT	>gnl|tr|Q3ND54_9PROT (Q3ND54) Enolase (EC 4.2.1.11)			x	
Q55F83_DICDI	>gnl|tr|Q55F83_DICDI (Q55F83) Phosphopyruvate hydratase			x	
Q4ZWE0_PSEU2	>gnl|tr|Q4ZWE0_PSEU2 (Q4ZWE0) Enolase (EC 4.2.1.11)			x	
Q3JCT1_NITOC	>gnl|tr|Q3JCT1_NITOC (Q3JCT1) Phosphopyruvate hydratase (EC 4.2.1.11)			x	
Q33AR3_ORYSA	>gnl|tr|Q33AR3_ORYSA (Q33AR3) Enolase			x	
Q8MVR9_CLOSI	>gnl|tr|Q8MVR9_CLOSI (Q8MVR9) Enolase			x	
Q8LM12_ORYSA	>gnl|tr|Q8LM12_ORYSA (Q8LM12) Putative enolase (2-phospho-D-glycerate hydroylase)			x	
Q33I06_METHU	>gnl|tr|Q33I06_METHU (Q33I06) Enolase (EC 4.2.1.11)			x	
Q5UU97_HETTR	>gnl|tr|Q5UU97_HETTR (Q5UU97) Enolase 2 (Fragment)			x	
Q8WP40_GIALA	>gnl|tr|Q8WP40_GIALA (Q8WP40) Enolase (EC 4.2.1.11)			x	
Q5KG11_CRYNE	>gnl|tr|Q5KG11_CRYNE (Q5KG11) Enolase 1, putative			x	
Q4HE43_CAMCO	>gnl|tr|Q4HE43_CAMCO (Q4HE43) Enolase (EC 4.2.1.11)			x	
Q5L4S5_CHLAB	>gnl|tr|Q5L4S5_CHLAB (Q5L4S5) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x	
Q33EG2_METHU	>gnl|tr|Q33EG2_METHU (Q33EG2) Enolase (EC 4.2.1.11)			x	
Q4AA88_MYCHJ	>gnl|tr|Q4AA88_MYCHJ (Q4AA88) Enolase (EC 4.2.1.11)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q4A8B5_MYCH7	>gnl|tr|Q4A8B5_MYCH7 (Q4A8B5) Enolase (EC 4.2.1.11)			x	
Q468E2_METBA	>gnl|tr|Q468E2_METBA (Q468E2) Phosphopyruvate hydratase			x	
O93873_PNECA	>gnl|tr|O93873_PNECA (O93873) Enolase			x	
Q9PTX5_LAMRE	>gnl|tr|Q9PTX5_LAMRE (Q9PTX5) Enolase-2 (Fragment)			x	
Q4HR03_CAMUP	>gnl|tr|Q4HR03_CAMUP (Q4HR03) Enolase (EC 4.2.1.11)			x	
Q5GTG4_WOLTR	>gnl|tr|Q5GTG4_WOLTR (Q5GTG4) Enolase			x	
Q4HLW3_CAMLA	>gnl|tr|Q4HLW3_CAMLA (Q4HLW3) Enolase (EC 4.2.1.11)			x	
Q421L5_DESHA	>gnl|tr|Q421L5_DESHA (Q421L5) Enolase (EC 4.2.1.11)			x	
Q5EFD8_TRIVA	>gnl|tr|Q5EFD8_TRIVA (Q5EFD8) Enolase			x	
Q302C2_STRSU	>gnl|tr|Q302C2_STRSU (Q302C2) Enolase (EC 4.2.1.11) (Fragment)			x	
Q41NP7_METBU	>gnl|tr|Q41NP7_METBU (Q41NP7) Enolase (EC 4.2.1.11)			x	
Q9U5F7_EPTBU	>gnl|tr|Q9U5F7_EPTBU (Q9U5F7) Enolase (Fragment)			x	
Q2VCI5_SOLTU	>gnl|tr|Q2VCI5_SOLTU (Q2VCI5) Enolase-like			x	x
Q5K117_9LACO	>gnl|tr|Q5K117_9LACO (Q5K117) Alpha-enolase (EC 4.2.1.11)			x	
Q648E0_9ARCH	>gnl|tr|Q648E0_9ARCH (Q648E0) Phosphopyruvate hydratase enolase			x	
Q76DW2_9EUKA	>gnl|tr|Q76DW2_9EUKA (Q76DW2) Enolase			x	
Q9PTX6_LAMRE	>gnl|tr|Q9PTX6_LAMRE (Q9PTX6) Enolase-1 (Fragment)			x	
Q3KLB0_CHLTA	>gnl|tr|Q3KLB0_CHLTA (Q3KLB0) Enolase (EC 4.2.1.11)			x	
Q493N5_BLOPB	>gnl|tr|Q493N5_BLOPB (Q493N5) Enolase			x	
Q3RVQ1_RALME	>gnl|tr|Q3RVQ1_RALME (Q3RVQ1) Enolase (EC 4.2.1.11)			x	
Q5PAS6_ANAMM	>gnl|tr|Q5PAS6_ANAMM (Q5PAS6) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x	
Q9NG68_9MYRI	>gnl|tr|Q9NG68_9MYRI (Q9NG68) Enolase (Fragment)			x	
Q3YRX9_EHRCJ	>gnl|tr|Q3YRX9_EHRCJ (Q3YRX9) Enolase (EC 4.2.1.11)			x	
Q5HB46_EHRRW	>gnl|tr|Q5HB46_EHRRW (Q5HB46) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x	
Q4H4A4_9DINO	>gnl|tr|Q4H4A4_9DINO (Q4H4A4) Enolase 3 (Fragment)			x	
Q9W6D2_TRASC	>gnl|tr|Q9W6D2_TRASC (Q9W6D2) Alpha enolase (Fragment)			x	
Q9W6D3_9SAUR	>gnl|tr|Q9W6D3_9SAUR (Q9W6D3) Alpha enolase (Fragment)			x	
Q9NG67_9HEXA	>gnl|tr|Q9NG67_9HEXA (Q9NG67) Enolase (Fragment)			x	
Q5FH95_EHRRG	>gnl|tr|Q5FH95_EHRRG (Q5FH95) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q9W6D1_EUMIN	>gnl|tr|Q9W6D1_EUMIN (Q9W6D1) Alpha enolase (Fragment)			x	
Q40JH5_EHRCH	>gnl|tr|Q40JH5_EHRCH (Q40JH5) Enolase (EC 4.2.1.11)			x	
Q4H4B0_KARBR	>gnl|tr|Q4H4B0_KARBR (Q4H4B0) Enolase 3 (Fragment)			x	
Q5WQL6_9STRA	>gnl|tr|Q5WQL6_9STRA (Q5WQL6) Enolase (Fragment)			x	
Q9W6C9_CAICR	>gnl|tr|Q9W6C9_CAICR (Q9W6C9) Alpha enolase (Fragment)			x	
Q56RN9_DROMI	>gnl|tr|Q56RN9_DROMI (Q56RN9) Enolase (Fragment)			x	
Q5WQM2_9STRA	>gnl|tr|Q5WQM2_9STRA (Q5WQM2) Enolase (Fragment)			x	
Q5WQL7_9EUKA	>gnl|tr|Q5WQL7_9EUKA (Q5WQL7) Enolase (Fragment)			x	
Q5WQM3_9STRA	>gnl|tr|Q5WQM3_9STRA (Q5WQM3) Enolase 2 (Fragment)			x	
Q5WQM4_9STRA	>gnl|tr|Q5WQM4_9STRA (Q5WQM4) Enolase 1 (Fragment)			x	
Q95WB0_9HYMN	>gnl|tr|Q95WB0_9HYMN (Q95WB0) Enolase (Fragment)			x	
Q9W6D0_SPHPU	>gnl|tr|Q9W6D0_SPHPU (Q9W6D0) Alpha enolase (Fragment)			x	
Q9DDG7_SALTR	>gnl|tr|Q9DDG7_SALTR (Q9DDG7) Alpha-1 enolase-1 (Fragment)			x	
Q9NG69_9MYRI	>gnl|tr|Q9NG69_9MYRI (Q9NG69) Enolase (Fragment)			x	
Q5WQL8_9STRA	>gnl|tr|Q5WQL8_9STRA (Q5WQL8) Enolase (Fragment)			x	
Q967N8_9CUCU	>gnl|tr|Q967N8_9CUCU (Q967N8) Enolase (Fragment)			x	
Q4H4A2_9DINO	>gnl|tr|Q4H4A2_9DINO (Q4H4A2) Enolase 3 (Fragment)			x	
Q95WA9_TETTH	>gnl|tr|Q95WA9_TETTH (Q95WA9) Enolase (Fragment)			x	
Q9DDH0_NEOFS	>gnl|tr|Q9DDH0_NEOFS (Q9DDH0) Beta enolase-1 (Fragment)			x	
Q95WA8_9HYMN	>gnl|tr|Q95WA8_9HYMN (Q95WA8) Enolase (Fragment)			x	
Q95WB1_PARTE	>gnl|tr|Q95WB1_PARTE (Q95WB1) Enolase (Fragment)			x	
Q5WQM1_ISOGA	>gnl|tr|Q5WQM1_ISOGA (Q5WQM1) Enolase (Fragment)			x	
Q9DDH1_LEPPA	>gnl|tr|Q9DDH1_LEPPA (Q9DDH1) Beta enolase-1 (Fragment)			x	
Q9DDH5_AMICA	>gnl|tr|Q9DDH5_AMICA (Q9DDH5) Beta enolase-1 (Fragment)			x	
Q6QWQ0_9ARAC	>gnl|tr|Q6QWQ0_9ARAC (Q6QWQ0) 2-phospho-D-glycerate hydrolase (Fragment)			x	
Q6QWP3_9SCOR	>gnl|tr|Q6QWP3_9SCOR (Q6QWP3) 2-phospho-D-glycerate hydrolase (Fragment)			x	
Q9DDH6_AMICA	>gnl|tr|Q9DDH6_AMICA (Q9DDH6) Alpha enolase-1 (Fragment)			x	
Q947A1_PRILA	>gnl|tr|Q947A1_PRILA (Q947A1) Enolase 1 (Fragment)			x	
Q9DDG8_CHIPU	>gnl|tr|Q9DDG8_CHIPU (Q9DDG8) Beta enolase-1 (Fragment)			x	
Q9DDH4_LATCH	>gnl|tr|Q9DDH4_LATCH (Q9DDH4) Alpha enolase-1 (Fragment)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q8SUA4_ENCCU	>gnl|tr|Q8SUA4_ENCCU (Q8SUA4) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x	
Q9DDG6_SALTR	>gnl|tr|Q9DDG6_SALTR (Q9DDG6) Alpha-2 enolase-1 (Fragment)			x	
Q5WQL9_PHATR	>gnl|tr|Q5WQL9_PHATR (Q5WQL9) Enolase (Fragment)			x	
Q6QWP8_9CRUS	>gnl|tr|Q6QWP8_9CRUS (Q6QWP8) 2-phospho-D-glycerate hydrolase (Fragment)			x	
Q4FM37_PELUB	>gnl|tr|Q4FM37_PELUB (Q4FM37) Enolase (EC 4.2.1.11)			x	
Q947A3_9FLOR	>gnl|tr|Q947A3_9FLOR (Q947A3) Enolase 1 (Fragment)			x	
Q6QWP6_CALSI	>gnl|tr|Q6QWP6_CALSI (Q6QWP6) 2-phospho-D-glycerate hydrolase (Fragment)			x	
Q6JKT5_9EUKA	>gnl|tr|Q6JKT5_9EUKA (Q6JKT5) Enolase (Fragment)			x	
Q3LFH6_PROFR	>gnl|tr|Q3LFH6_PROFR (Q3LFH6) Enolase 2 (EC 4.2.1.11)			x	
Q6QWQ2_9MYRI	>gnl|tr|Q6QWQ2_9MYRI (Q6QWQ2) 2-phospho-D-glycerate hydrolase (Fragment)			x	
Q6QWP7_9CRUS	>gnl|tr|Q6QWP7_9CRUS (Q6QWP7) 2-phospho-D-glycerate hydrolase (Fragment)			x	
Q9DDG9_CHIPU	>gnl|tr|Q9DDG9_CHIPU (Q9DDG9) Alpha enolase-1 (Fragment)			x	
Q6JKT8_9EUKA	>gnl|tr|Q6JKT8_9EUKA (Q6JKT8) Enolase (Fragment)			x	
Q6QWQ1_9MYRI	>gnl|tr|Q6QWQ1_9MYRI (Q6QWQ1) 2-phospho-D-glycerate hydrolase (Fragment)			x	
Q947A0_PRILA	>gnl|tr|Q947A0_PRILA (Q947A0) Enolase 2 (Fragment)			x	
Q6JKT4_9EUKA	>gnl|tr|Q6JKT4_9EUKA (Q6JKT4) Enolase (Fragment)			x	
Q6JKT7_9EUKA	>gnl|tr|Q6JKT7_9EUKA (Q6JKT7) Enolase (Fragment)			x	
Q9NDF5_9TRYP	>gnl|tr|Q9NDF5_9TRYP (Q9NDF5) Enolase (EC 4.2.1.11) (Fragment)			x	
Q6JKT9_9EUKA	>gnl|tr|Q6JKT9_9EUKA (Q6JKT9) Enolase (Fragment)			x	
Q4H4A8_KARBR	>gnl|tr|Q4H4A8_KARBR (Q4H4A8) Enolase 3 (Fragment)			x	
Q2NG02_9EURY	>gnl|tr|Q2NG02_9EURY (Q2NG02) Enolase (EC 4.2.1.11)			x	
Q6QWP5_9ANNE	>gnl|tr|Q6QWP5_9ANNE (Q6QWP5) 2-phospho-D-glycerate hydrolase (Fragment)			x	
Q6QWP9_LIMPO	>gnl|tr|Q6QWP9_LIMPO (Q6QWP9) 2-phospho-D-glycerate hydrolase (Fragment)			x	
Q6QWP4_9CRUS	>gnl|tr|Q6QWP4_9CRUS (Q6QWP4) 2-phospho-D-glycerate hydrolase (Fragment)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q3IQT0_NATPD	>gnl|tr|Q3IQT0_NATPD (Q3IQT0) Phosphopyruvate hydratase (EC 4.2.1.11) (Enolase) (EC 4.2.1.11)			x	
Q6JKT2_9EUKA	>gnl|tr|Q6JKT2_9EUKA (Q6JKT2) Enolase (Fragment)			x	
Q6JKU0_9EUKA	>gnl|tr|Q6JKU0_9EUKA (Q6JKU0) Enolase (Fragment)			x	
Q6JKT3_9EUKA	>gnl|tr|Q6JKT3_9EUKA (Q6JKT3) Enolase (Fragment)			x	
Q947A2_9FLOR	>gnl|tr|Q947A2_9FLOR (Q947A2) Enolase 2 (Fragment)			x	
Q4H4A5_9DINO	>gnl|tr|Q4H4A5_9DINO (Q4H4A5) Enolase 2 (Fragment)			x	
Q6JKT6_9EUKA	>gnl|tr|Q6JKT6_9EUKA (Q6JKT6) Enolase (Fragment)			x	
Q4H4B1_KARBR	>gnl|tr|Q4H4B1_KARBR (Q4H4B1) Enolase 2 (Fragment)			x	
Q41RU7_FERAC	>gnl|tr|Q41RU7_FERAC (Q41RU7) Phosphopyruvate hydratase (EC 4.2.1.11)			x	
Q33G47_METHU	>gnl|tr|Q33G47_METHU (Q33G47) Enolase (EC 4.2.1.11)			x	
Q4H4B2_KARBR	>gnl|tr|Q4H4B2_KARBR (Q4H4B2) Enolase 2 (Fragment)			x	
Q703Y8_THETE	>gnl|tr|Q703Y8_THETE (Q703Y8) Enolase (EC 4.2.1.11)			x	
Q6KZN3_PICTO	>gnl|tr|Q6KZN3_PICTO (Q6KZN3) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)			x	
Q9NDF6_TRIVA	>gnl|tr|Q9NDF6_TRIVA (Q9NDF6) Enolase 5 (EC 4.2.1.11) (Fragment)			x	
Q9NDF9_TRIVA	>gnl|tr|Q9NDF9_TRIVA (Q9NDF9) Enolase 2 (EC 4.2.1.11) (Fragment)			x	
Q9NDG0_TRIVA	>gnl|tr|Q9NDG0_TRIVA (Q9NDG0) Enolase 1 (EC 4.2.1.11) (Fragment)			x	
Q9NDF8_TRIVA	>gnl|tr|Q9NDF8_TRIVA (Q9NDF8) Enolase 3 (EC 4.2.1.11) (Fragment)			x	
Q9NDF7_TRIVA	>gnl|tr|Q9NDF7_TRIVA (Q9NDF7) Enolase 4 (EC 4.2.1.11) (Fragment)			x	
Q6WP07_9EUKA	>gnl|tr|Q6WP07_9EUKA (Q6WP07) Enolase (Fragment)			x	
Q9NDG2_9EUKA	>gnl|tr|Q9NDG2_9EUKA (Q9NDG2) Enolase 2 (EC 4.2.1.11) (Fragment)			x	
Q6WP08_TRIFO	>gnl|tr|Q6WP08_TRIFO (Q6WP08) Enolase (Fragment)			x	
Q92W53_RHIME	>gnl|tr|Q92W53_RHIME (Q92W53) Probable galactonate dehydratase protein (EC 4.2.1.6)			x	
Q884B6_PSESM	>gnl|tr|Q884B6_PSESM (Q884B6) Mandelate racemase/muconate lactonizing enzyme family protein			x	x
Q48K93_PSE14	>gnl|tr|Q48K93_PSE14 (Q48K93) Galactonate dehydratase (EC 4.2.1.6)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q63X38_BURPS	>gnl|tr|Q63X38_BURPS (Q63X38) Putative galactonate dehydratase protein			x	
Q7MC07_VIBVY	>gnl|tr|Q7MC07_VIBVY (Q7MC07) Probable galactonate dehydratase protein			x	
Q5KYJ6_GEOKA	>gnl|tr|Q5KYJ6_GEOKA (Q5KYJ6) Galactonate dehydratase (EC 4.2.1.6)			x	
Q8XVS8_RALSO	>gnl|tr|Q8XVS8_RALSO (Q8XVS8) PUTATIVE GALACTONATE DEHYDRATASE PROTEIN (EC 4.2.1.6)			x	
Q5WKP1_BACSK	>gnl|tr|Q5WKP1_BACSK (Q5WKP1) Galactonate dehydratase (EC 4.2.1.6)			x	
Q57I11_SALCH	>gnl|tr|Q57I11_SALCH (Q57I11) Galactonate dehydratase			x	
Q3BUN6_XANC5	>gnl|tr|Q3BUN6_XANC5 (Q3BUN6) Galactonate dehydratase (EC 4.2.1.6)			x	
Q2ULT5_ASPOR	>gnl|tr|Q2ULT5_ASPOR (Q2ULT5) L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily			x	x
Q47NZ8_THEFY	>gnl|tr|Q47NZ8_THEFY (Q47NZ8) Mandelate racemase/muconate lactonizing enzyme family			x	x
Q5UY67_HALMA	>gnl|tr|Q5UY67_HALMA (Q5UY67) Mandelate racemase/muconate lactonizing enzyme family			x	x
Q4WJL9_ASPFU	>gnl|tr|Q4WJL9_ASPFU (Q4WJL9) Mandelate racemase/muconate lactonizing enzyme family protein			x	x
Q2X863_PSEPU	>gnl|tr|Q2X863_PSEPU (Q2X863) Glucarate dehydratase			x	
Q4ZRS0_PSEU2	>gnl|tr|Q4ZRS0_PSEU2 (Q4ZRS0) Glucarate dehydratase (EC 4.2.1.40)			x	
Q88DR6_PSEPK	>gnl|tr|Q88DR6_PSEPK (Q88DR6) Glucarate dehydratase			x	
Q87ZY7_PSESM	>gnl|tr|Q87ZY7_PSESM (Q87ZY7) Glucarate dehydratase			x	
Q6D173_ERWCT	>gnl|tr|Q6D173_ERWCT (Q6D173) Glucarate dehydratase (EC 4.2.1.40)			x	
Q3RWP4_RALME	>gnl|tr|Q3RWP4_RALME (Q3RWP4) Glucarate dehydratase (EC 4.2.1.40)			x	
Q46UW1_RALEJ	>gnl|tr|Q46UW1_RALEJ (Q46UW1) Glucarate dehydratase (EC 4.2.1.40)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q8ZMD9_SALTY	>gnl|tr|Q8ZMD9_SALTY (Q8ZMD9) D-glucarate dehydratase (EC 4.2.1.40)			x	
Q57KF6_SALCH	>gnl|tr|Q57KF6_SALCH (Q57KF6) D-glucarate dehydratase			x	
Q8EMK6_OCEIH	>gnl|tr|Q8EMK6_OCEIH (Q8EMK6) Glucarate dehydratase (EC 4.2.1.40)			x	
Q8Z443_SALTI	>gnl|tr|Q8Z443_SALTI (Q8Z443) Probable glucarate dehydratase 1 (EC 4.2.1.40)			x	
Q8Y0G5_RALSO	>gnl|tr|Q8Y0G5_RALSO (Q8Y0G5) PROBABLE GLUCARATE DEHYDRATASE PROTEIN (EC 4.2.1.40)			x	
Q3EIQ9_ACTSC	>gnl|tr|Q3EIQ9_ACTSC (Q3EIQ9) Glucarate dehydratase (EC 4.2.1.40)			x	
Q83QD4_SHIFL	>gnl|tr|Q83QD4_SHIFL (Q83QD4) Putative glucarate dehydratase			x	
Q31XK3_SHIBS	>gnl|tr|Q31XK3_SHIBS (Q31XK3) Putative glucarate dehydratase			x	
Q2T252_BURTH	>gnl|tr|Q2T252_BURTH (Q2T252) Glucarate dehydratase (EC 4.2.1.40)			x	
Q5PEJ1_SALPA	>gnl|tr|Q5PEJ1_SALPA (Q5PEJ1) Probable glucarate dehydratase 1			x	
Q4AUW2_9BURK	>gnl|tr|Q4AUW2_9BURK (Q4AUW2) Glucarate dehydratase (EC 4.2.1.40)			x	
Q3YY69_SHISS	>gnl|tr|Q3YY69_SHISS (Q3YY69) Putative glucarate dehydratase			x	
Q89HW7_BRAJA	>gnl|tr|Q89HW7_BRAJA (Q89HW7) Glucarate dehydratase (EC 4.2.1.40)			x	
Q4UY48_XANC8	>gnl|tr|Q4UY48_XANC8 (Q4UY48) Glucarate hydratase			x	
Q8P5U3_XANCP	>gnl|tr|Q8P5U3_XANCP (Q8P5U3) Glucarate hydratase			x	
Q35KA8_9BRAD	>gnl|tr|Q35KA8_9BRAD (Q35KA8) Glucarate dehydratase (EC 4.2.1.40)			x	
Q6FFQ2_ACIAD	>gnl|tr|Q6FFQ2_ACIAD (Q6FFQ2) D-glucarate dehydratase (EC 4.2.1.40)			x	
Q39KL8_BURS3	>gnl|tr|Q39KL8_BURS3 (Q39KL8) Glucarate dehydratase (EC 4.2.1.40)			x	
Q44TQ7_9BURK	>gnl|tr|Q44TQ7_9BURK (Q44TQ7) Glucarate dehydratase (EC 4.2.1.40)			x	
Q4LLI4_9BURK	>gnl|tr|Q4LLI4_9BURK (Q4LLI4) Glucarate dehydratase (EC 4.2.1.40)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q3F2Y9_9BURK	>gnl|tr|Q3F2Y9_9BURK (Q3F2Y9) Glucarate dehydratase (EC 4.2.1.40)			x	
Q4B8L5_BURVI	>gnl|tr|Q4B8L5_BURVI (Q4B8L5) Glucarate dehydratase (EC 4.2.1.40)			x	
Q8XRK2_RALSO	>gnl|tr|Q8XRK2_RALSO (Q8XRK2) PROBABLE GLUCARATE DEHYDRATASE PROTEIN (EC 4.2.1.40)			x	
Q426I1_DESHA	>gnl|tr|Q426I1_DESHA (Q426I1) Methylaspartate ammonia-lyase (EC 4.3.1.2)			x	
O66145_CITAM	>gnl|tr|O66145_CITAM (O66145) 3-methylaspartate ammonia-lyase			x	
Q8X990_ECO57	>gnl|tr|Q8X990_ECO57 (Q8X990) Putative methylaspartate ammonia-lyase (3-methylaspartate ammonia-lyase)			x	
Q32IJ6_SHIDS	>gnl|tr|Q32IJ6_SHIDS (Q32IJ6) Putative methylaspartate ammonia-lyase			x	
Q98A98_RHILO	>gnl|tr|Q98A98_RHILO (Q98A98) 3-methylaspartate ammonia-lyase			x	
Q890S3_CLOTE	>gnl|tr|Q890S3_CLOTE (Q890S3) Methylaspartate ammonia-lyase (EC 4.3.1.2)			x	
Q9HN19_HALSA	>gnl|tr|Q9HN19_HALSA (Q9HN19) Methylaspartate ammonia-lyase			x	
Q7MMF3_VIBVY	>gnl|tr|Q7MMF3_VIBVY (Q7MMF3) O-succinylbenzoate synthase			x	
Q8D823_VIBVU	>gnl|tr|Q8D823_VIBVU (Q8D823) O-succinylbenzoate synthase			x	
Q4QLT9_HAEI8	>gnl|tr|Q4QLT9_HAEI8 (Q4QLT9) O-succinylbenzoate synthase (EC 4.2.1.-)			x	
Q3EGU2_ACTSC	>gnl|tr|Q3EGU2_ACTSC (Q3EGU2) O-succinylbenzoate synthase and related enzymes			x	x
Q6HC30_BACHK	>gnl|tr|Q6HC30_BACHK (Q6HC30) Enolase superfamily protein; possible N-acylamino acid racemase, mandelate racemase/muconate lactonizing enzyme, or o-succinylbenzoate synthase			x	x
Q81K98_BACAN	>gnl|tr|Q81K98_BACAN (Q81K98) N-acylamino acid racemase			x	
Q632I6_BACCZ	>gnl|tr|Q632I6_BACCZ (Q632I6) Possible N-acylamino acid racemase; possible O-succinylbenzoate synthase (EC 4.2.1.-)			x	x
Q5E484_VIBF1	>gnl|tr|Q5E484_VIBF1 (Q5E484) O-succinylbenzoate synthase (EC 4.2.1.-)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q8NT44_CORGL	>gnl|tr|Q8NT44_CORGL (Q8NT44) O-succinylbenzoate synthase and related enzymes (Similar to o-succinylbenzoate-coa synthase)			x	x
Q838J7_ENTFA	>gnl|tr|Q838J7_ENTFA (Q838J7) Mandelate racemase/muconate lactonizing enzyme family protein			x	x
Q6ARP5_DESPS	>gnl|tr|Q6ARP5_DESPS (Q6ARP5) Related to N-acylamino acid racemase (MenC)			x	x
Q4MNA0_BACCE	>gnl|tr|Q4MNA0_BACCE (Q4MNA0) O-succinylbenzoic acid (OSB) synthetase (EC 4.2.1.-)			x	
Q7MUJ1_PORGI	>gnl|tr|Q7MUJ1_PORGI (Q7MUJ1) Mandelate racemase/muconate lactonizing enzyme family protein			x	x
Q3M9T7_ANAVT	>gnl|tr|Q3M9T7_ANAVT (Q3M9T7) O-succinylbenzoic acid synthase			x	
Q8Z0Q6_ANASP	>gnl|tr|Q8Z0Q6_ANASP (Q8Z0Q6) O-succinylbenzoic acid synthase			x	
Q5L1G9_GEOKA	>gnl|tr|Q5L1G9_GEOKA (Q5L1G9) N-acylamino acid racemase			x	
Q7U3X1_SYNPX	>gnl|tr|Q7U3X1_SYNPX (Q7U3X1) Putative O-succinylbenzoate synthase (EC 4.2.1.-)			x	
Q3HJR0_TRIER	>gnl|tr|Q3HJR0_TRIER (Q3HJR0) Similar to L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily			x	x
Q7A4Z3_STAAN	>gnl|tr|Q7A4Z3_STAAN (Q7A4Z3) O-succinylbenzoic acid synthetase			x	
Q99T74_STAAM	>gnl|tr|Q99T74_STAAM (Q99T74) O-succinylbenzoic acid synthetase			x	
Q53635_STAAU	>gnl|tr|Q53635_STAAU (Q53635) O-succinylbenzoic acid (OSB) synthetase			x	
Q5HEY3_STAAC	>gnl|tr|Q5HEY3_STAAC (Q5HEY3) O-succinylbenzoic acid (OSB) synthetase, putative			x	
Q8EMX7_OCEIH	>gnl|tr|Q8EMX7_OCEIH (Q8EMX7) N-acylamino acid racemase			x	
Q8NVZ5_STAAW	>gnl|tr|Q8NVZ5_STAAW (Q8NVZ5) O-succinylbenzoic acid synthetase			x	
Q7V4A4_PROMM	>gnl|tr|Q7V4A4_PROMM (Q7V4A4) Putative O-succinylbenzoate synthase (EC 4.2.1.-)			x	
Q2YTP1_STAAB	>gnl|tr|Q2YTP1_STAAB (Q2YTP1) O-succinylbenzoic acid synthetase (EC 4.2.1.-)			x	
Q8CNT4_STAES	>gnl|tr|Q8CNT4_STAES (Q8CNT4) O-succinylbenzoic acid (OSB) synthetase			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q5HNB3_STAEQ	>gnl|tr|Q5HNB3_STAEQ (Q5HNB3) O-succinylbenzoic acid synthetase, putative			x	
Q57DB1_BRUAB	>gnl|tr|Q57DB1_BRUAB (Q57DB1) Mandelate racemase/muconate lactonizing enzyme family protein			x	x
Q8UEV6_AGRT5	>gnl|tr|Q8UEV6_AGRT5 (Q8UEV6) Mandelate racemase/muconate lactonizing enzyme family protein (AGR_C_3037p)			x	x
Q313B8_DESDG	>gnl|tr|Q313B8_DESDG (Q313B8) L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily-like			x	x
Q9A3T9_CAUCR	>gnl|tr|Q9A3T9_CAUCR (Q9A3T9) Mandelate racemase/muconate lactonizing enzyme family protein			x	x
Q81CC3_BACCR	>gnl|tr|Q81CC3_BACCR (Q81CC3) Mandelate racemase/muconate lactonizing enzyme family protein			x	x
Q3ESE4_BACTI	>gnl|tr|Q3ESE4_BACTI (Q3ESE4) L-Ala-D/L-Glu racemase (EC 5.1.1.-)			x	
Q81PF7_BACAN	>gnl|tr|Q81PF7_BACAN (Q81PF7) Mandelate racemase/muconate lactonizing enzyme family protein			x	x
Q5LMF7_SILPO	>gnl|tr|Q5LMF7_SILPO (Q5LMF7) Mandelate racemase/muconate lactonizing enzyme family protein			x	x
Q736M2_BACC1	>gnl|tr|Q736M2_BACC1 (Q736M2) Mandelate racemase/muconate lactonizing enzyme family protein			x	x
Q4MP89_BACCE	>gnl|tr|Q4MP89_BACCE (Q4MP89) Mandelate racemase/muconate lactonizing enzyme family protein			x	x
Q6DAW3_ERWCT	>gnl|tr|Q6DAW3_ERWCT (Q6DAW3) Putative mandelate racemase / muconate lactonizing enzyme family protein			x	x
Q3IRB2_NATPD	>gnl|tr|Q3IRB2_NATPD (Q3IRB2) Mandelate racemase homolog / muconate lactonizing enzyme homolog			x	x
Q8GFH9_ALCXX	>gnl|tr|Q8GFH9_ALCXX (Q8GFH9) Chloromuconate cycloisomerase (EC 5.5.1.7)			x	
Q9RHQ8_VARPD	>gnl|tr|Q9RHQ8_VARPD (Q9RHQ8) Chloromuconate cycloisomerase			x	
Q7BV50_BURCE	>gnl|tr|Q7BV50_BURCE (Q7BV50) Chloromuconate cycloisomerase			x	
Q93UZ6_9BURK	>gnl|tr|Q93UZ6_9BURK (Q93UZ6) Chloromuconate cycloisomerase (EC 5.5.1.7)			x	
Q706U0_PSEPU	>gnl|tr|Q706U0_PSEPU (Q706U0) Chloromuconate cycloisomerase			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q9RPB4_PSEAE	>gnl|tr|Q9RPB4_PSEAE (Q9RPB4) Chloromuconate cycloisomerase			x	
Q9RPF7_PSEAE	>gnl|tr|Q9RPF7_PSEAE (Q9RPF7) Chloromuconate cycloisomerase			x	
O87609_PSEAE	>gnl|tr|O87609_PSEAE (O87609) Chloromuconate cycloisomerase			x	
Q8G9L1_RHOOP	>gnl|tr|Q8G9L1_RHOOP (Q8G9L1) Chloromuconate cycloisomerase			x	
O67985_RHOOP	>gnl|tr|O67985_RHOOP (O67985) Chloromuconate cycloisomerase			x	
Q8GAZ7_BURST	>gnl|tr|Q8GAZ7_BURST (Q8GAZ7) Cis,cis-muconate lactonizing enzyme			x	
Q9AQQ3_9PSED	>gnl|tr|Q9AQQ3_9PSED (Q9AQQ3) Cis,cis-muconate cycloisomerase CatB			x	
Q9EV42_RALEU	>gnl|tr|Q9EV42_RALEU (Q9EV42) Putative muconate cycloisomerase (EC 5.5.1.1)			x	
Q9AEQ3_PSEPU	>gnl|tr|Q9AEQ3_PSEPU (Q9AEQ3) Cis,cis-muconate lactonizing enzyme			x	
Q88GK6_PSEPK	>gnl|tr|Q88GK6_PSEPK (Q88GK6) Muconate cycloisomerase			x	
Q2XL31_PSEPU	>gnl|tr|Q2XL31_PSEPU (Q2XL31) Muconate cycloisomerase			x	
Q9AQS7_9BURK	>gnl|tr|Q9AQS7_9BURK (Q9AQS7) Muconate cycloisomerase (EC 5.5.1.1)			x	
Q51958_PSEPU	>gnl|tr|Q51958_PSEPU (Q51958) Muconate lactonizing enzyme			x	
Q9Z9Y6_9GAMM	>gnl|tr|Q9Z9Y6_9GAMM (Q9Z9Y6) Muconate cycloisomerase (EC 5.5.1.1)			x	
Q7WWT7_RALEU	>gnl|tr|Q7WWT7_RALEU (Q7WWT7) Putative muconate cycloisomerase			x	
Q8GAY8_BURST	>gnl|tr|Q8GAY8_BURST (Q8GAY8) Cis,cis-muconate lactonizing enzyme			x	
Q9Z9Y1_9GAMM	>gnl|tr|Q9Z9Y1_9GAMM (Q9Z9Y1) Muconate cycloisomerase (EC 5.5.1.1)			x	
Q93SR2_PSEPU	>gnl|tr|Q93SR2_PSEPU (Q93SR2) Putative muconate cycloisomerase I CatB			x	
Q4K9X1_PSEF5	>gnl|tr|Q4K9X1_PSEF5 (Q4K9X1) Muconate cycloisomerase (EC 5.5.1.1)			x	
Q9I0X3_PSEAE	>gnl|tr|Q9I0X3_PSEAE (Q9I0X3) Muconate cycloisomerase I			x	
Q7WWU8_RALEU	>gnl|tr|Q7WWU8_RALEU (Q7WWU8) Putative muconate cycloisomerase			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q3PBR5_PARDE	>gnl|tr|Q3PBR5_PARDE (Q3PBR5) Muconate cycloisomerase (EC 5.5.1.1)			x	
Q393C7_BURS3	>gnl|tr|Q393C7_BURS3 (Q393C7) Muconate cycloisomerase (EC 5.5.1.1)			x	
Q4LPX1_9BURK	>gnl|tr|Q4LPX1_9BURK (Q4LPX1) Muconate cycloisomerase (EC 5.5.1.1)			x	
Q458I5_9BURK	>gnl|tr|Q458I5_9BURK (Q458I5) Muconate cycloisomerase (EC 5.5.1.1)			x	
Q2T814_BURTH	>gnl|tr|Q2T814_BURTH (Q2T814) Muconate cycloisomerase			x	
Q5NTR1_9BACT	>gnl|tr|Q5NTR1_9BACT (Q5NTR1) Muconate lactonizing enzyme I			x	
Q63J25_BURPS	>gnl|tr|Q63J25_BURPS (Q63J25) Muconate cycloisomerase I (EC 5.5.1.1)			x	
Q62E51_BURMA	>gnl|tr|Q62E51_BURMA (Q62E51) Muconate cycloisomerase (EC 5.5.1.1)			x	
Q3JJV9_BURP1	>gnl|tr|Q3JJV9_BURP1 (Q3JJV9) Muconate cycloisomerase (EC 5.5.1.1)			x	
Q8FN45_COREF	>gnl|tr|Q8FN45_COREF (Q8FN45) Putative muconate cycloisomerase			x	
Q8NN12_CORGL	>gnl|tr|Q8NN12_CORGL (Q8NN12) O-succinylbenzoate synthase and related enzymes (EC 5.5.1.1) (CHLOROMUCONATE CYCLOISOMERASE) (EC 5.5.1.7)			x	x
Q8G2R9_BRUSU	>gnl|tr|Q8G2R9_BRUSU (Q8G2R9) Mandelate racemase/muconate lactonizing enzyme domain protein			x	x
Q57FD7_BRUAB	>gnl|tr|Q57FD7_BRUAB (Q57FD7) Mandelate racemase/muconate lactonizing enzyme domain protein			x	x
Q2XLC2_PSEPU	>gnl|tr|Q2XLC2_PSEPU (Q2XLC2) Mandelate racemase/muconate lactonizing enzyme family protein			x	x
Q2TZZ6_ASPOR	>gnl|tr|Q2TZZ6_ASPOR (Q2TZZ6) L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily			x	x
Q88J18_PSEPK	>gnl|tr|Q88J18_PSEPK (Q88J18) Mandelate racemase/muconate lactonizing enzyme family protein			x	x
Q4X1I9_ASPFU	>gnl|tr|Q4X1I9_ASPFU (Q4X1I9) Mandelate racemase/muconate lactonizing enzyme family protein			x	x

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q48EB9_PSE14	>gnl|tr|Q48EB9_PSE14 (Q48EB9) Phosphatase, YrbI family			x	x
Q87WU4_PSESM	>gnl|tr|Q87WU4_PSESM (Q87WU4) Phosphatase, YrbI family			x	x
Q3KI02_PSEPF	>gnl|tr|Q3KI02_PSEPF (Q3KI02) Phosphatase kdsC (EC 3.1.3.45)			x	
Q88P96_PSEPK	>gnl|tr|Q88P96_PSEPK (Q88P96) Phosphatase, YrbI family			x	x
Q4QJR5_HAEI8	>gnl|tr|Q4QJR5_HAEI8 (Q4QJR5) 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45)			x	
Q2XJN8_PSEPU	>gnl|tr|Q2XJN8_PSEPU (Q2XJN8) HAD-superfamily hydrolase subfamily IIIA:Phosphatase kdsC			x	x
Q4KI83_PSEF5	>gnl|tr|Q4KI83_PSEF5 (Q4KI83) 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45)			x	
Q4IYC4_AZOVI	>gnl|tr|Q4IYC4_AZOVI (Q4IYC4) HAD-superfamily hydrolase, subfamily IIIA:Phosphatase YrbI			x	x
Q4ZNU9_PSEU2	>gnl|tr|Q4ZNU9_PSEU2 (Q4ZNU9) HAD-superfamily hydrolase, subfamily IIIA:Phosphatase YrbI (EC 3.1.3.45)			x	x
Q7U9R7_SYNPX	>gnl|tr|Q7U9R7_SYNPX (Q7U9R7) Possible phosphatase			x	x
Q3EFA0_ACTSC	>gnl|tr|Q3EFA0_ACTSC (Q3EFA0) 3-deoxy-manno-octulosonate-8-phosphatase (EC 3.1.3.45)			x	
Q3AN74_SYNSC	>gnl|tr|Q3AN74_SYNSC (Q3AN74) Phosphatase kdsC			x	x
Q3B0E3_SYNS9	>gnl|tr|Q3B0E3_SYNS9 (Q3B0E3) Phosphatase kdsC			x	x
Q7MF46_VIBVY	>gnl|tr|Q7MF46_VIBVY (Q7MF46) Phosphonoacetaldehyde phosphonohydrolase			x	
Q8RSQ3_PSEPU	>gnl|tr|Q8RSQ3_PSEPU (Q8RSQ3) 2-phosphonoacetaldehyde hydrolase			x	
Q3K9Y2_PSEPF	>gnl|tr|Q3K9Y2_PSEPF (Q3K9Y2) Phosphonoacetaldehyde hydrolase			x	
Q4K9L7_PSEF5	>gnl|tr|Q4K9L7_PSEF5 (Q4K9L7) 2-phosphonoacetaldehyde hydrolase (EC 3.11.1.1)			x	
Q9I433_PSEAE	>gnl|tr|Q9I433_PSEAE (Q9I433) 2-phosphonoacetaldehyde hydrolase			x	
Q51386_PSEAE	>gnl|tr|Q51386_PSEAE (Q51386) 2-phosphonoacetaldehyde hydrolase			x	
Q2XEK9_PSEPU	>gnl|tr|Q2XEK9_PSEPU (Q2XEK9) Phosphonoacetaldehyde hydrolase:HAD-superfamily hydrolase subfamily IA, variant 3			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q88KT1_PSEPK	>gnl|tr|Q88KT1_PSEPK (Q88KT1) 2-phosphonoacetaldehyde hydrolase			x	
Q9KLY5_VIBCH	>gnl|tr|Q9KLY5_VIBCH (Q9KLY5) Phosphonoacetaldehyde phosphonohydrolase			x	
Q87JL6_VIBPA	>gnl|tr|Q87JL6_VIBPA (Q87JL6) Phosphonoacetaldehyde phosphonohydrolase			x	
Q8Z8W5_SALTI	>gnl|tr|Q8Z8W5_SALTI (Q8Z8W5) Phosphonoacetaldehyde phosphonohydrolase			x	
Q5PFR1_SALPA	>gnl|tr|Q5PFR1_SALPA (Q5PFR1) Phosphonoacetaldehyde phosphonohydrolase			x	
O31156_BACCE	>gnl|tr|O31156_BACCE (O31156) Phosphonoacetaldehyde hydrolase			x	
Q73BH9_BACC1	>gnl|tr|Q73BH9_BACC1 (Q73BH9) Phosphonoacetaldehyde phosphonohydrolase (EC 3.11.1.1)			x	
Q81TE1_BACAN	>gnl|tr|Q81TE1_BACAN (Q81TE1) Phosphonoacetaldehyde phosphonohydrolase			x	
Q6HLM1_BACHK	>gnl|tr|Q6HLM1_BACHK (Q6HLM1) Possible phosphonoacetaldehyde hydrolase (EC 3.11.1.1)			x	
Q63E46_BACCZ	>gnl|tr|Q63E46_BACCZ (Q63E46) Possible phosphonoacetaldehyde hydrolase (EC 3.11.1.1)			x	
Q4MSF0_BACCE	>gnl|tr|Q4MSF0_BACCE (Q4MSF0) Phosphonoacetaldehyde phosphonohydrolase VCA0606			x	
Q88YN8_LACPL	>gnl|tr|Q88YN8_LACPL (Q88YN8) Phosphonoacetaldehyde hydrolase (EC 3.11.1.1)			x	
Q6N251_RHOPA	>gnl|tr|Q6N251_RHOPA (Q6N251) Putative 2-haloacid halidohydrolase Iva			x	
Q89D82_BRAJA	>gnl|tr|Q89D82_BRAJA (Q89D82) 2-haloalkanoic acid dehalogenase (EC 3.8.1.2)			x	
Q8XZN3_RALSO	>gnl|tr|Q8XZN3_RALSO (Q8XZN3) PUTATIVE 2-HALOALKANOIC ACID DEHALOGENASE PROTEIN (EC 3.8.1.2)			x	
Q3RK08_RALME	>gnl|tr|Q3RK08_RALME (Q3RK08) HAD-superfamily hydrolase, subfamily IA, variant 2 (EC 3.8.1.2)			x	
Q9Z3Z3_PSEPU	>gnl|tr|Q9Z3Z3_PSEPU (Q9Z3Z3) Haloalkanoic acid dehalogenase			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q3JQZ5_BURP1	>gnl|tr|Q3JQZ5_BURP1 (Q3JQZ5) Haloacid dehalogenase, type II (EC 3.8.1.2)			x	
Q62J90_BURMA	>gnl|tr|Q62J90_BURMA (Q62J90) Haloacid dehalogenase, type II (EC 3.8.1.2)			x	
Q63SY0_BURPS	>gnl|tr|Q63SY0_BURPS (Q63SY0) Putative dehalogenase			x	x
Q46ZW7_RALEJ	>gnl|tr|Q46ZW7_RALEJ (Q46ZW7) Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2 (EC 3.8.1.2)			x	
Q2SX30_BURTH	>gnl|tr|Q2SX30_BURTH (Q2SX30) Haloacid dehalogenase, type II (EC 3.8.1.2)			x	
Q3F8P8_9BURK	>gnl|tr|Q3F8P8_9BURK (Q3F8P8) HAD-superfamily hydrolase, subfamily IA, variant 2 (EC 3.8.1.2)			x	
Q985K5_RHILO	>gnl|tr|Q985K5_RHILO (Q985K5) 2-haloacid halidohydrolase Iva			x	
Q4LN60_9BURK	>gnl|tr|Q4LN60_9BURK (Q4LN60) HAD-superfamily hydrolase, subfamily IA, variant 2 (EC 3.8.1.2)			x	
Q450N4_9BURK	>gnl|tr|Q450N4_9BURK (Q450N4) HAD-superfamily hydrolase, subfamily IA, variant 2 (EC 3.8.1.2)			x	
Q4B9E0_BURVI	>gnl|tr|Q4B9E0_BURVI (Q4B9E0) HAD-superfamily hydrolase, subfamily IA, variant 2 (EC 3.8.1.2)			x	
Q39F12_BURS3	>gnl|tr|Q39F12_BURS3 (Q39F12) Haloacid dehalogenase, type II (EC 3.8.1.2)			x	
Q59I43_9BURK	>gnl|tr|Q59I43_9BURK (Q59I43) L-2-haloacid dehalogenase (EC 3.8.1.2)			x	
Q92RC4_RHIME	>gnl|tr|Q92RC4_RHIME (Q92RC4) PUTATIVE ALPHA-HALOCARBOXYLIC ACID DEHALOGENASE PROTEIN (EC 3.8.1.-)			x	x
Q57EG9_BRUAB	>gnl|tr|Q57EG9_BRUAB (Q57EG9) Haloacid dehalogenase			x	
Q2YMR7_BRUA2	>gnl|tr|Q2YMR7_BRUA2 (Q2YMR7) Haloacid dehalogenase/epoxide hydrolase:Haloacid dehalogenase-like hydrolase:HAD-superfamily hydrolase, subfamily IA, variant 2			x	x
Q8G1Y6_BRUSU	>gnl|tr|Q8G1Y6_BRUSU (Q8G1Y6) Haloacid dehalogenase, type II (EC 3.8.1.2)			x	
Q4ASX7_9BURK	>gnl|tr|Q4ASX7_9BURK (Q4ASX7) HAD-superfamily hydrolase, subfamily IA, variant 2 (EC 3.8.1.2)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q4B1A0_9BURK	>gnl|tr|Q4B1A0_9BURK (Q4B1A0) HAD-superfamily hydrolase, subfamily IA, variant 2 (EC 3.8.1.2)			x	
Q5P813_AZOSE	>gnl|tr|Q5P813_AZOSE (Q5P813) Putative 2-haloalkanoic acid dehalogenase (EC 3.8.1.2)			x	
Q3WKR9_9RHIZ	>gnl|tr|Q3WKR9_9RHIZ (Q3WKR9) HAD-superfamily hydrolase, subfamily IA, variant 2 (EC 3.8.1.2)			x	
Q2W483_MAGSA	>gnl|tr|Q2W483_MAGSA (Q2W483) 2-haloalkanoic acid dehalogenase I			x	
Q3E2N8_CHLAU	>gnl|tr|Q3E2N8_CHLAU (Q3E2N8) Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2			x	
Q4NUL1_9DELT	>gnl|tr|Q4NUL1_9DELT (Q4NUL1) HAD-superfamily hydrolase, subfamily IA, variant 2			x	x
Q9ZA67_BURCE	>gnl|tr|Q9ZA67_BURCE (Q9ZA67) Cryptic haloacid dehalogenase 1			x	
Q890I4_LACPL	>gnl|tr|Q890I4_LACPL (Q890I4) Beta-phosphoglucomutase (EC 5.4.2.6)			x	
Q3Y2T0_ENTFC	>gnl|tr|Q3Y2T0_ENTFC (Q3Y2T0) HAD-superfamily hydrolase, subfamily IA, variant 3:Beta-phosphoglucomutase:Beta-phosphoglucomutase hydrolase			x	
O87773_LACSN	>gnl|tr|O87773_LACSN (O87773) Beta-phosphoglucomutase			x	
Q9K108_NEIMB	>gnl|tr|Q9K108_NEIMB (Q9K108) Beta-phosphoglucomutase (EC 5.4.2.6)			x	
Q890F6_LACPL	>gnl|tr|Q890F6_LACPL (Q890F6) Beta-phosphoglucomutase (EC 5.4.2.6)			x	
Q9JSX3_NEIMA	>gnl|tr|Q9JSX3_NEIMA (Q9JSX3) Beta-phosphoglucomutase (EC 5.4.2.6)			x	
Q3CJ79_THEET	>gnl|tr|Q3CJ79_THEET (Q3CJ79) HAD-superfamily hydrolase, subfamily IA, variant 3:Beta-phosphoglucomutase:Beta-phosphoglucomutase hydrolase			x	
Q8X8K2_ECO57	>gnl|tr|Q8X8K2_ECO57 (Q8X8K2) Putative beta-phosphoglucomutase			x	
Q83RK7_SHIFL	>gnl|tr|Q83RK7_SHIFL (Q83RK7) Putative beta-phosphoglucomutase			x	
Q4ENF6_LISMO	>gnl|tr|Q4ENF6_LISMO (Q4ENF6) Beta-phosphoglucomutase (EC 5.4.2.6)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q71VT0_LISMF	>gnl|tr|Q71VT0_LISMF (Q71VT0) Beta-phosphoglucomutase (EC 5.4.2.6)			x	
Q4EH91_LISMO	>gnl|tr|Q4EH91_LISMO (Q4EH91) Beta-phosphoglucomutase (EC 5.4.2.6)			x	
Q8FHR4_ECOL6	>gnl|tr|Q8FHR4_ECOL6 (Q8FHR4) Putative beta-phosphoglucomutase (EC 5.4.2.6)			x	
Q9JSW9_NEIMA	>gnl|tr|Q9JSW9_NEIMA (Q9JSW9) Beta-phosphoglucomutase (EC 5.4.2.6)			x	
Q3XZS0_ENTFC	>gnl|tr|Q3XZS0_ENTFC (Q3XZS0) HAD-superfamily hydrolase, subfamily IA, variant 3:Beta-phosphoglucomutase:Beta-phosphoglucomutase hydrolase			x	
Q3Z162_SHISS	>gnl|tr|Q3Z162_SHISS (Q3Z162) Putative beta-phosphoglucomutase			x	
Q836Y8_ENTFA	>gnl|tr|Q836Y8_ENTFA (Q836Y8) Beta-phosphoglucomutase			x	
Q41CC8_9BACI	>gnl|tr|Q41CC8_9BACI (Q41CC8) HAD-superfamily hydrolase, subfamily IA, variant 3:Beta-phosphoglucomutase:Beta-phosphoglucomutase hydrolase			x	
Q98PT4_MYCPU	>gnl|tr|Q98PT4_MYCPU (Q98PT4) BETA-PHOSPHOGLUCOMUTASE (BETA-PGM) (EC 5.4.2.6)			x	
O65323_CAPAN	>gnl|tr|O65323_CAPAN (O65323) Sesquiterpene cyclase			x	x
Q84LF1_9SOLA	>gnl|tr|Q84LF1_9SOLA (Q84LF1) 5-epi-aristolochene synthase 34			x	
Q84LF0_9SOLA	>gnl|tr|Q84LF0_9SOLA (Q84LF0) 5-epi-aristolochene synthase 37			x	
Q84LG0_9SOLA	>gnl|tr|Q84LG0_9SOLA (Q84LG0) 5-epi-aristolochene synthase			x	
Q84LF2_9SOLA	>gnl|tr|Q84LF2_9SOLA (Q84LF2) 5-epi-aristolochene synthase 12			x	
Q82IY4_STRAW	>gnl|tr|Q82IY4_STRAW (Q82IY4) Pentalenene synthase			x	
Q748E3_GEOSL	>gnl|tr|Q748E3_GEOSL (Q748E3) Squalene-hopene cyclase (EC 5.4.99.17)			x	
Q74FC1_GEOSL	>gnl|tr|Q74FC1_GEOSL (Q74FC1) Squalene-hopene cyclase (EC 5.4.99.17)			x	
Q39YL2_GEOMG	>gnl|tr|Q39YL2_GEOMG (Q39YL2) Terpene synthase:Squalene cyclase			x	
Q9X7V9_STRCO	>gnl|tr|Q9X7V9_STRCO (Q9X7V9) Putative squalene-hopene cyclase			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q39RT6_GEOMG	>gnl|tr|Q39RT6_GEOMG (Q39RT6) Terpene synthase:Squalene cyclase			x	
Q37GN6_RHOPA	>gnl|tr|Q37GN6_RHOPA (Q37GN6) Terpene synthase:Squalene cyclase			x	
O69790_RHOPA	>gnl|tr|O69790_RHOPA (O69790) Squalene-hopene cyclase			x	
Q6N3F4_RHOPA	>gnl|tr|Q6N3F4_RHOPA (Q6N3F4) Squalene-hopene-cyclase (EC 5.4.99.7)			x	
Q82ML0_STRAW	>gnl|tr|Q82ML0_STRAW (Q82ML0) Squalene-hopene cyclase			x	
Q8DGK8_SYNEL	>gnl|tr|Q8DGK8_SYNEL (Q8DGK8) Squalene-hopene-cyclase			x	
Q8YYS1_ANASP	>gnl|tr|Q8YYS1_ANASP (Q8YYS1) Squalene-hopene-cyclase			x	
Q34RT4_RHOPA	>gnl|tr|Q34RT4_RHOPA (Q34RT4) Squalene-hopene-cyclase			x	
Q3M418_ANAVT	>gnl|tr|Q3M418_ANAVT (Q3M418) Terpene synthase (EC 5.4.99.17)			x	
P73914_SYNY3	>gnl|tr|P73914_SYNY3 (P73914) Squalene-hopene-cyclase			x	
Q34E48_RHOPA	>gnl|tr|Q34E48_RHOPA (Q34E48) Terpene synthase:Squalene cyclase			x	
Q7NE23_GLOVI	>gnl|tr|Q7NE23_GLOVI (Q7NE23) Squalene-hopene cyclase			x	
Q60AN5_METCA	>gnl|tr|Q60AN5_METCA (Q60AN5) Squalene-hopene cyclase (EC 5.4.99.-)			x	x
Q3G6F5_9DELT	>gnl|tr|Q3G6F5_9DELT (Q3G6F5) Terpene synthase (EC 5.4.99.17)			x	
O69446_METCA	>gnl|tr|O69446_METCA (O69446) Squalene-hopene cyclase			x	
Q3PXP7_NITHA	>gnl|tr|Q3PXP7_NITHA (Q3PXP7) Terpene synthase (EC 5.4.99.17)			x	
Q3SQB8_NITWN	>gnl|tr|Q3SQB8_NITWN (Q3SQB8) Terpene synthase/Squalene cyclase (EC 5.4.99.17)			x	
Q59080_9BACL	>gnl|tr|Q59080_9BACL (Q59080) Squalene-hopene cyclase (EC 5.4.99.7)			x	
Q4CA42_CROWT	>gnl|tr|Q4CA42_CROWT (Q4CA42) Terpene synthase			x	x
Q63HT1_BURPS	>gnl|tr|Q63HT1_BURPS (Q63HT1) Squalene--hopene cyclase (EC 5.4.99.17)			x	
Q3A7E3_PELCD	>gnl|tr|Q3A7E3_PELCD (Q3A7E3) Squalene-hopene cyclase			x	
Q2T2Q3_BURTH	>gnl|tr|Q2T2Q3_BURTH (Q2T2Q3) Squalene-hopene cyclase (EC 5.4.99.17)			x	
Q3JIF6_BURP1	>gnl|tr|Q3JIF6_BURP1 (Q3JIF6) Squalene-hopene cyclase (EC 5.4.99.17)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q629M5_BURMA	>gnl|tr|Q629M5_BURMA (Q629M5) Squalene-hopene cyclase (EC 5.4.99.17)			x	
Q45EI7_9BURK	>gnl|tr|Q45EI7_9BURK (Q45EI7) Terpene synthase precursor (EC 5.4.99.17)			x	
Q4LRR6_9BURK	>gnl|tr|Q4LRR6_9BURK (Q4LRR6) Terpene synthase precursor (EC 5.4.99.17)			x	
Q3HBE6_TRIER	>gnl|tr|Q3HBE6_TRIER (Q3HBE6) Terpene synthase			x	x
Q3F5Y2_9BURK	>gnl|tr|Q3F5Y2_9BURK (Q3F5Y2) Terpene synthase (EC 5.4.99.17)			x	
Q4BML1_BURVI	>gnl|tr|Q4BML1_BURVI (Q4BML1) Terpene synthase (EC 5.4.99.17)			x	
Q39BM5_BURS3	>gnl|tr|Q39BM5_BURS3 (Q39BM5) Terpene synthase/Squalene cyclase (EC 5.4.99.17)			x	
Q46RD2_RALEJ	>gnl|tr|Q46RD2_RALEJ (Q46RD2) Terpene synthase:Squalene cyclase			x	
Q3RZT4_RALME	>gnl|tr|Q3RZT4_RALME (Q3RZT4) Terpene synthase precursor (EC 5.4.99.17)			x	
Q3G291_9DELT	>gnl|tr|Q3G291_9DELT (Q3G291) Terpene synthase			x	x
Q5FNQ3_GLUOX	>gnl|tr|Q5FNQ3_GLUOX (Q5FNQ3) Squalene-hopene cyclase			x	
Q3JBH8_NITOC	>gnl|tr|Q3JBH8_NITOC (Q3JBH8) Terpene synthase/Squalene cyclase (EC 5.4.99.17)			x	
Q733T6_BACC1	>gnl|tr|Q733T6_BACC1 (Q733T6) Squalene-hopene cyclase (EC 5.4.99.-)			x	x
Q81AK6_BACCR	>gnl|tr|Q81AK6_BACCR (Q81AK6) Squalene--hopene cyclase (EC 5.4.99.-)			x	x
Q796C3_BACSU	>gnl|tr|Q796C3_BACSU (Q796C3) Squalene-hopene cyclase (EC 5.4.99.-)			x	x
Q3MYE8_9DELT	>gnl|tr|Q3MYE8_9DELT (Q3MYE8) Terpene synthase (EC 5.4.99.17)			x	
Q4MKR1_BACCE	>gnl|tr|Q4MKR1_BACCE (Q4MKR1) Squalene--hopene cyclase			x	
Q2RYC8_RHORU	>gnl|tr|Q2RYC8_RHORU (Q2RYC8) Terpene synthase, squalene cyclase (EC 5.4.99.17)			x	
Q3N6T0_9PROT	>gnl|tr|Q3N6T0_9PROT (Q3N6T0) Terpene synthase (EC 5.4.99.17)			x	
Q6HFN9_BACHK	>gnl|tr|Q6HFN9_BACHK (Q6HFN9) Squalene-hopene cyclase (EC 5.4.99.-)			x	x
Q81YD8_BACAN	>gnl|tr|Q81YD8_BACAN (Q81YD8) Squalene-hopene cyclase			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q637R6_BACCZ	>gnl|tr|Q637R6_BACCZ (Q637R6) Squalene-hopene cyclase (EC 5.4.99.-)			x	x
Q2Y5X6_NITMU	>gnl|tr|Q2Y5X6_NITMU (Q2Y5X6) Squalene cyclase			x	
Q3W869_9ACTO	>gnl|tr|Q3W869_9ACTO (Q3W869) Terpene synthase			x	x
Q3W9E9_9ACTO	>gnl|tr|Q3W9E9_9ACTO (Q3W9E9) Terpene synthase (EC 5.4.99.17)			x	
Q437S7_9ACTO	>gnl|tr|Q437S7_9ACTO (Q437S7) Terpene synthase			x	x
Q3RN02_RALME	>gnl|tr|Q3RN02_RALME (Q3RN02) Terpene synthase (EC 5.4.99.17)			x	
Q3FA06_9BURK	>gnl|tr|Q3FA06_9BURK (Q3FA06) Terpene synthase (EC 5.4.99.17)			x	
Q39LV3_BURS3	>gnl|tr|Q39LV3_BURS3 (Q39LV3) Terpene synthase/Squalene cyclase (EC 5.4.99.17)			x	
Q4LM82_9BURK	>gnl|tr|Q4LM82_9BURK (Q4LM82) Terpene synthase (EC 5.4.99.17)			x	
Q459N5_9BURK	>gnl|tr|Q459N5_9BURK (Q459N5) Terpene synthase (EC 5.4.99.17)			x	
Q5NM88_ZYMMO	>gnl|tr|Q5NM88_ZYMMO (Q5NM88) Squalene--hopene cyclase (EC 5.4.99.17)			x	
Q3A7M9_PELCD	>gnl|tr|Q3A7M9_PELCD (Q3A7M9) Squalene--hopene cyclase			x	
Q3MZV5_9DELT	>gnl|tr|Q3MZV5_9DELT (Q3MZV5) Terpene synthase (EC 5.4.99.17)			x	
Q7LJS4_FUSMI	>gnl|tr|Q7LJS4_FUSMI (Q7LJS4) Trichodiene synthase			x	
Q7LJT2_FUSAS	>gnl|tr|Q7LJT2_FUSAS (Q7LJT2) Trichodiene synthase			x	
Q96W88_GIBZE	>gnl|tr|Q96W88_GIBZE (Q96W88) Trichodiene synthase			x	
Q76PE4_GIBZE	>gnl|tr|Q76PE4_GIBZE (Q76PE4) Trichodiene synthase			x	
Q7LJL9_FUSAU	>gnl|tr|Q7LJL9_FUSAU (Q7LJL9) Trichodiene synthase			x	
Q7LJL3_GIBZE	>gnl|tr|Q7LJL3_GIBZE (Q7LJL3) Trichodiene synthase			x	
Q8NJH2_FUSLU	>gnl|tr|Q8NJH2_FUSLU (Q8NJH2) Trichodiene synthase			x	
Q8NJU9_GIBZE	>gnl|tr|Q8NJU9_GIBZE (Q8NJU9) Trichodiene synthetase			x	
Q7LP67_FUSSP	>gnl|tr|Q7LP67_FUSSP (Q7LP67) Trichodiene synthase			x	
Q7Z8B9_FUSPO	>gnl|tr|Q7Z8B9_FUSPO (Q7Z8B9) Trichodiene synthase			x	
Q8NJV0_GIBZE	>gnl|tr|Q8NJV0_GIBZE (Q8NJV0) Trichodiene synthetase			x	
Q7Z8C0_FUSSP	>gnl|tr|Q7Z8C0_FUSSP (Q7Z8C0) Trichodiene synthase			x	
Q71RX9_STACH	>gnl|tr|Q71RX9_STACH (Q71RX9) Trichodiene synthase			x	
Q9UR08_ASPTE	>gnl|tr|Q9UR08_ASPTE (Q9UR08) Aristolochene synthase			x	
Q7NZF3_CHRVO	>gnl|tr|Q7NZF3_CHRVO (Q7NZF3) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q63PY5_BURPS	>gnl|tr|Q63PY5_BURPS (Q63PY5) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q3JYB9_BURP1	>gnl|tr|Q3JYB9_BURP1 (Q3JYB9) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q62GQ1_BURMA	>gnl|tr|Q62GQ1_BURMA (Q62GQ1) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q2STZ8_BURTH	>gnl|tr|Q2STZ8_BURTH (Q2STZ8) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q4B831_BURVI	>gnl|tr|Q4B831_BURVI (Q4B831) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q8XUT2_RALSO	>gnl|tr|Q8XUT2_RALSO (Q8XUT2) PROBABLE 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE OXIDOREDUCTASE PROTEIN (EC 1.13.11.27)			x	
Q4LIA5_9BURK	>gnl|tr|Q4LIA5_9BURK (Q4LIA5) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q44U09_9BURK	>gnl|tr|Q44U09_9BURK (Q44U09) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q3F1S4_9BURK	>gnl|tr|Q3F1S4_9BURK (Q3F1S4) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q39KJ4_BURS3	>gnl|tr|Q39KJ4_BURS3 (Q39KJ4) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q9RCH2_VIBCH	>gnl|tr|Q9RCH2_VIBCH (Q9RCH2) P-hydroxyphenylpyruvate dioxygenase (4-hydroxyphenylpyruvate dioxygenase)			x	
Q8VQC4_VIBAN	>gnl|tr|Q8VQC4_VIBAN (Q8VQC4) 4-hydroxyphenylpyruvate dioxygenase			x	
Q9I576_PSEAE	>gnl|tr|Q9I576_PSEAE (Q9I576) 4-hydroxyphenylpyruvate dioxygenase			x	
Q87Q01_VIBPA	>gnl|tr|Q87Q01_VIBPA (Q87Q01) 4-hydroxyphenylpyruvate dioxygenase			x	
Q983J0_RHILO	>gnl|tr|Q983J0_RHILO (Q983J0) 4-hydroxyphenylpyruvate dioxygenase			x	
Q3KC47_PSEPF	>gnl|tr|Q3KC47_PSEPF (Q3KC47) 4-hydroxyphenylpyruvate dioxygenase			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>Q4ZR60_PSEU2</td><td>>gnl|tr|Q4ZR60_PSEU2 (Q4ZR60) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q89XH5_BRAJA</td><td>>gnl|tr|Q89XH5_BRAJA (Q89XH5) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q4KB91_PSEF5</td><td>>gnl|tr|Q4KB91_PSEF5 (Q4KB91) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q88HC7_PSEPK</td><td>>gnl|tr|Q88HC7_PSEPK (Q88HC7) 4-hydroxyphenylpyruvate dioxygenase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q4AZW6_9BURK</td><td>>gnl|tr|Q4AZW6_9BURK (Q4AZW6) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q87Z77_PSESM</td><td>>gnl|tr|Q87Z77_PSESM (Q87Z77) 4-hydroxyphenylpyruvate dioxygenase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q48GS3_PSE14</td><td>>gnl|tr|Q48GS3_PSE14 (Q48GS3) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q2XKA2_PSEPU</td><td>>gnl|tr|Q2XKA2_PSEPU (Q2XKA2) 4-hydroxyphenylpyruvate dioxygenase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q6EMJ1_PSEPU</td><td>>gnl|tr|Q6EMJ1_PSEPU (Q6EMJ1) P-hydroxyphenylpyruvate dioxygenase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q35KQ1_9BRAD</td><td>>gnl|tr|Q35KQ1_9BRAD (Q35KQ1) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q3RV34_RALME</td><td>>gnl|tr|Q3RV34_RALME (Q3RV34) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q37XY1_SPHAR</td><td>>gnl|tr|Q37XY1_SPHAR (Q37XY1) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q92LT1_RHIME</td><td>>gnl|tr|Q92LT1_RHIME (Q92LT1) PUTATIVE 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE PROTEIN (EC 1.13.11.27)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q46SN3_RALEJ</td><td>>gnl|tr|Q46SN3_RALEJ (Q46SN3) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q4J186_AZOVI</td><td>>gnl|tr|Q4J186_AZOVI (Q4J186) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q6NDU9_RHOPA</td><td>>gnl|tr|Q6NDU9_RHOPA (Q6NDU9) 4-hydroxyphenylpyruvate dioxygenase</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q3JB70_NITOC	>gnl|tr|Q3JB70_NITOC (Q3JB70) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q3WTX8_9RHIZ	>gnl|tr|Q3WTX8_9RHIZ (Q3WTX8) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q2SND1_9GAMM	>gnl|tr|Q2SND1_9GAMM (Q2SND1) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q8PQ76_XANAC	>gnl|tr|Q8PQ76_XANAC (Q8PQ76) 4-hydroxyphenylpyruvate dioxygenase			x	
Q6LI28_PHOPR	>gnl|tr|Q6LI28_PHOPR (Q6LI28) Putative 4-hydroxyphenylpyruvate dioxygenase			x	
Q3BYF0_XANC5	>gnl|tr|Q3BYF0_XANC5 (Q3BYF0) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q3V924_9SPHN	>gnl|tr|Q3V924_9SPHN (Q3V924) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q4UZJ1_XANC8	>gnl|tr|Q4UZJ1_XANC8 (Q4UZJ1) 4-hydroxyphenylpyruvate dioxygenase			x	
Q8PDA4_XANCP	>gnl|tr|Q8PDA4_XANCP (Q8PDA4) 4-hydroxyphenylpyruvate dioxygenase			x	
Q2NAB6_9SPHN	>gnl|tr|Q2NAB6_9SPHN (Q2NAB6) 4-hydroxyphenylpyruvate dioxygenase			x	
Q3PHY1_PARDE	>gnl|tr|Q3PHY1_PARDE (Q3PHY1) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q5GVE8_XANOR	>gnl|tr|Q5GVE8_XANOR (Q5GVE8) 4-hydroxyphenylpyruvate dioxygenase			x	
Q5WUG4_LEGPL	>gnl|tr|Q5WUG4_LEGPL (Q5WUG4) 4-hydroxyphenylpyruvate dioxygenase (Legiolysin)			x	
Q2NYM6_XANOR	>gnl|tr|Q2NYM6_XANOR (Q2NYM6) 4-hydroxyphenylpyruvate dioxygenase			x	
Q3CWI1_ALTAT	>gnl|tr|Q3CWI1_ALTAT (Q3CWI1) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q5X304_LEGPA	>gnl|tr|Q5X304_LEGPA (Q5X304) 4-hydroxyphenylpyruvate dioxygenase (Legiolysin)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q3CUY6_ALTAT	>gnl|tr|Q3CUY6_ALTAT (Q3CUY6) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q9A5B7_CAUCR	>gnl|tr|Q9A5B7_CAUCR (Q9A5B7) 4-hydroxyphenylpyruvate dioxygenase			x	
Q5R0G8_IDILO	>gnl|tr|Q5R0G8_IDILO (Q5R0G8) 4-hydroxyphenylpyruvate dioxygenase			x	
Q3GL80_9GAMM	>gnl|tr|Q3GL80_9GAMM (Q3GL80) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q4IY20_AZOVI	>gnl|tr|Q4IY20_AZOVI (Q4IY20) 4-hydroxyphenylpyruvate dioxygenase precursor (EC 1.13.11.27)			x	
Q3K6G2_PSEPF	>gnl|tr|Q3K6G2_PSEPF (Q3K6G2) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q2XM67_PSEPU	>gnl|tr|Q2XM67_PSEPU (Q2XM67) 4-hydroxyphenylpyruvate dioxygenase, putative			x	
Q88JU3_PSEPK	>gnl|tr|Q88JU3_PSEPK (Q88JU3) 4-hydroxyphenylpyruvate dioxygenase, putative			x	
Q883L0_PSESM	>gnl|tr|Q883L0_PSESM (Q883L0) 4-hydroxyphenylpyruvate dioxygenase, putative			x	
Q4ZUJ9_PSEU2	>gnl|tr|Q4ZUJ9_PSEU2 (Q4ZUJ9) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q48JV3_PSE14	>gnl|tr|Q48JV3_PSE14 (Q48JV3) 4-hydroxyphenylpyruvate dioxygenase, putative			x	
Q40C79_9RHOB	>gnl|tr|Q40C79_9RHOB (Q40C79) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q4K5N0_PSEF5	>gnl|tr|Q4K5N0_PSEF5 (Q4K5N0) 4-hydroxyphenylpyruvate dioxygenase, putative			x	
Q3QWK3_9RHOB	>gnl|tr|Q3QWK3_9RHOB (Q3QWK3) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q7X4L3_9BACT	>gnl|tr|Q7X4L3_9BACT (Q7X4L3) 4-hydroxyphenylpyruvate dioxygenase			x	
Q33PL8_9GAMM	>gnl|tr|Q33PL8_9GAMM (Q33PL8) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q2ZNE8_SHEPU	>gnl|tr|Q2ZNE8_SHEPU (Q2ZNE8) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q8L7E8_ARATH	>gnl|tr|Q8L7E8_ARATH (Q8L7E8) 4-hydroxyphenylpyruvate dioxygenase HPD			x	
Q5LTI8_SILPO	>gnl|tr|Q5LTI8_SILPO (Q5LTI8) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q2X680_9GAMM	>gnl|tr|Q2X680_9GAMM (Q2X680) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q3Q520_9GAMM	>gnl|tr|Q3Q520_9GAMM (Q3Q520) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q8EFK9_SHEON	>gnl|tr|Q8EFK9_SHEON (Q8EFK9) 4-hydroxyphenylpyruvate dioxygenase			x	
Q35TW0_9GAMM	>gnl|tr|Q35TW0_9GAMM (Q35TW0) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q2Z830_9GAMM	>gnl|tr|Q2Z830_9GAMM (Q2Z830) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q36BK6_9GAMM	>gnl|tr|Q36BK6_9GAMM (Q36BK6) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q4IUU1_AZOVI	>gnl|tr|Q4IUU1_AZOVI (Q4IUU1) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q3QEM4_9GAMM	>gnl|tr|Q3QEM4_9GAMM (Q3QEM4) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q3NQQ8_SHEFR	>gnl|tr|Q3NQQ8_SHEFR (Q3NQQ8) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q3P045_9GAMM	>gnl|tr|Q3P045_9GAMM (Q3P045) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q8XF91_RALSO	>gnl|tr|Q8XF91_RALSO (Q8XF91) PROBABLE 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE OXIDOREDUCTASE PROTEIN (EC 1.13.11.27)			x	
Q3IET4_PSEHT	>gnl|tr|Q3IET4_PSEHT (Q3IET4) 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) (EC 1.13.11.27)			x	
Q2S2T7_9SPHI	>gnl|tr|Q2S2T7_9SPHI (Q2S2T7) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
O82449_ARATH	>gnl|tr|O82449_ARATH (O82449) P-hydroxyphenylpyruvate dioxygenase			x	
Q4LSN2_9BURK	>gnl|tr|Q4LSN2_9BURK (Q4LSN2) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q45B07_9BURK	>gnl|tr|Q45B07_9BURK (Q45B07) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q395X2_BURS3	>gnl|tr|Q395X2_BURS3 (Q395X2) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q6MHJ8_BDEBA	>gnl|tr|Q6MHJ8_BDEBA (Q6MHJ8) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q37V98_SPHAR	>gnl|tr|Q37V98_SPHAR (Q37V98) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q56H33_MEDTR	>gnl|tr|Q56H33_MEDTR (Q56H33) 4-hydroxyphenylpyruvate dioxygenase			x	
Q3FD81_9BURK	>gnl|tr|Q3FD81_9BURK (Q3FD81) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q4BSU0_BURVI	>gnl|tr|Q4BSU0_BURVI (Q4BSU0) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q35GS2_9BRAD	>gnl|tr|Q35GS2_9BRAD (Q35GS2) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q4MPU8_BACCE	>gnl|tr|Q4MPU8_BACCE (Q4MPU8) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q3EW31_BACTI	>gnl|tr|Q3EW31_BACTI (Q3EW31) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q81IU6_BACCR	>gnl|tr|Q81IU6_BACCR (Q81IU6) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q73EU8_BACC1	>gnl|tr|Q73EU8_BACC1 (Q73EU8) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q81VG6_BACAN	>gnl|tr|Q81VG6_BACAN (Q81VG6) 4-hydroxyphenylpyruvate dioxygenase			x	
Q6HPF2_BACHK	>gnl|tr|Q6HPF2_BACHK (Q6HPF2) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q63GY1_BACCZ	>gnl|tr|Q63GY1_BACCZ (Q63GY1) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q47YG2_COLP3	>gnl|tr|Q47YG2_COLP3 (Q47YG2) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q2T5Y1_BURTH	>gnl|tr|Q2T5Y1_BURTH (Q2T5Y1) 4-hydroxyphenylpyruvate dioxygenase			x	
Q442A4_SOLUS	>gnl|tr|Q442A4_SOLUS (Q442A4) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q3F6R6_9BURK	>gnl|tr|Q3F6R6_9BURK (Q3F6R6) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q45CM2_9BURK	>gnl|tr|Q45CM2_9BURK (Q45CM2) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q4LJW9_9BURK	>gnl|tr|Q4LJW9_9BURK (Q4LJW9) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q7ZUY6_BRARE	>gnl|tr|Q7ZUY6_BRARE (Q7ZUY6) Similar to 4-hydroxyphenylpyruvate dioxygenase			x	x
Q3DXR8_CHLAU	>gnl|tr|Q3DXR8_CHLAU (Q3DXR8) 4-hydroxyphenylpyruvate dioxygenase			x	
Q6BG80_PARTE	>gnl|tr|Q6BG80_PARTE (Q6BG80) 4-hydroxyphenylpyruvate dioxygenase, putative			x	
Q62CM9_BURMA	>gnl|tr|Q62CM9_BURMA (Q62CM9) Putative 4-hydroxyphenylpyruvate dioxygenase			x	
Q39AQ2_BURS3	>gnl|tr|Q39AQ2_BURS3 (Q39AQ2) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q63NG0_BURPS	>gnl|tr|Q63NG0_BURPS (Q63NG0) Putative amino acid dioxygenase			x	x
Q3JHA2_BURP1	>gnl|tr|Q3JHA2_BURP1 (Q3JHA2) Putative amino acid dioxygenase			x	x
Q4BU52_BURVI	>gnl|tr|Q4BU52_BURVI (Q4BU52) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q3W6Y0_9ACTO	>gnl|tr|Q3W6Y0_9ACTO (Q3W6Y0) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	
Q3H2J4_9ACTO	>gnl|tr|Q3H2J4_9ACTO (Q3H2J4) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>Q6H4V1_ORYSA</td><td>>gnl|tr|Q6H4V1_ORYSA (Q6H4V1) Putative 4-hydroxyphenylpyruvate dioxygenase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q2T3K2_BURTH</td><td>>gnl|tr|Q2T3K2_BURTH (Q2T3K2) 4-hydroxyphenylpyruvate dioxygenase, putative</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q46R58_RALEJ</td><td>>gnl|tr|Q46R58_RALEJ (Q46R58) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q46R51_RALEJ</td><td>>gnl|tr|Q46R51_RALEJ (Q46R51) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q5YPF8_NOCFA</td><td>>gnl|tr|Q5YPF8_NOCFA (Q5YPF8) Putative 4-hydroxyphenylpyruvate dioxygenase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q3WKZ6_9RHIZ</td><td>>gnl|tr|Q3WKZ6_9RHIZ (Q3WKZ6) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q2UM50_ASPOR</td><td>>gnl|tr|Q2UM50_ASPOR (Q2UM50) Glyoxalase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q4WN17_ASPFU</td><td>>gnl|tr|Q4WN17_ASPFU (Q4WN17) Lactoylglutathione lyase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q696X2_PHANO</td><td>>gnl|tr|Q696X2_PHANO (Q696X2) Glyoxylase I (EC 4.4.1.5)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q870H6_PARBR</td><td>>gnl|tr|Q870H6_PARBR (Q870H6) Glyoxalase I (EC 4.4.1.5)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q4YS97_PLABE</td><td>>gnl|tr|Q4YS97_PLABE (Q4YS97) Glyoxalase I, putative</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q7RRI6_PLAYO</td><td>>gnl|tr|Q7RRI6_PLAYO (Q7RRI6) Lactoylglutathione lyase, putative</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q71KM3_PLAFA</td><td>>gnl|tr|Q71KM3_PLAFA (Q71KM3) Glyoxalase I</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q8IIM5_PLAF7</td><td>>gnl|tr|Q8IIM5_PLAF7 (Q8IIM5) Glyoxalase I, putative</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q6BIM5_DEBHA</td><td>>gnl|tr|Q6BIM5_DEBHA (Q6BIM5) Similar to CA4918|CaGLO1 Candida albicans CaGLO1 Glyoxalase I</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>Q4X4Q2_PLACH</td><td>>gnl|tr|Q4X4Q2_PLACH (Q4X4Q2) Glyoxalase I, putative</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q9XGF2_WHEAT</td><td>>gnl|tr|Q9XGF2_WHEAT (Q9XGF2) Putative glyoxalase I (EC 4.4.1.5) (Fragment)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q6ES23_ORYSA</td><td>>gnl|tr|Q6ES23_ORYSA (Q6ES23) Putative glyoxalase I</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q8LEY7_ARATH</td><td>>gnl|tr|Q8LEY7_ARATH (Q8LEY7) Glyoxalase I, putative</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q75GB0_ORYSA</td><td>>gnl|tr|Q75GB0_ORYSA (Q75GB0) Putative glyoxalase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q6XC06_MAIZE</td><td>>gnl|tr|Q6XC06_MAIZE (Q6XC06) Glyoxalase I (EC 4.4.1.5)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>O65398_ARATH</td><td>>gnl|tr|O65398_ARATH (O65398) F12F1.32 protein (Protein At1g11840) (Glyoxalase I homolog) (At1g11840/F12F1_32) (Lactoylglutathione lyase-like protein)</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>Q9ZS21_SOYBN</td><td>>gnl|tr|Q9ZS21_SOYBN (Q9ZS21) Glyoxalase I (EC 4.4.1.5)</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q3KC41_PSEPF	>gnl|tr|Q3KC41_PSEPF (Q3KC41) Glyoxalase I			x	
Q9AXH1_AVIMR	>gnl|tr|Q9AXH1_AVIMR (Q9AXH1) Glyoxalase I			x	
Q940A4_ARATH	>gnl|tr|Q940A4_ARATH (Q940A4) Putative lactoylglutathione lyase			x	
Q59EL0_HUMAN	>gnl|tr|Q59EL0_HUMAN (Q59EL0) Glyoxalase I variant (Fragment)			x	
Q88GF8_PSEPK	>gnl|tr|Q88GF8_PSEPK (Q88GF8) Lactoylglutathione lyase			x	
Q4KB85_PSEF5	>gnl|tr|Q4KB85_PSEF5 (Q4KB85) Lactoylglutathione lyase (EC 4.4.1.5)			x	
Q48JF2_PSE14	>gnl|tr|Q48JF2_PSE14 (Q48JF2) Lactoylglutathione lyase (EC 4.4.1.5)			x	
Q4ZS65_PSEU2	>gnl|tr|Q4ZS65_PSEU2 (Q4ZS65) Glyoxalase I (EC 4.4.1.5)			x	
Q2XL87_PSEPU	>gnl|tr|Q2XL87_PSEPU (Q2XL87) Glyoxalase I			x	
Q880P8_PSESM	>gnl|tr|Q880P8_PSESM (Q880P8) Lactoylglutathione lyase			x	
Q6P696_BRARE	>gnl|tr|Q6P696_BRARE (Q6P696) Glyoxalase 1			x	
Q8PCX6_XANCP	>gnl|tr|Q8PCX6_XANCP (Q8PCX6) Lactoylglutathione lyase			x	
Q4UQH4_XANC8	>gnl|tr|Q4UQH4_XANC8 (Q4UQH4) Lactoylglutathione lyase			x	
Q87DQ2_XYLFT	>gnl|tr|Q87DQ2_XYLFT (Q87DQ2) Lactoylglutathione lyase			x	
Q6MJD2_BDEBA	>gnl|tr|Q6MJD2_BDEBA (Q6MJD2) Lactoylglutathione lyase (EC 4.4.1.5)			x	
Q9PDI0_XYLFA	>gnl|tr|Q9PDI0_XYLFA (Q9PDI0) Lactoylglutathione lyase			x	
Q3RBN2_XYLFA	>gnl|tr|Q3RBN2_XYLFA (Q3RBN2) Glyoxalase I (EC 4.4.1.5)			x	
Q3R2G4_XYLFA	>gnl|tr|Q3R2G4_XYLFA (Q3R2G4) Glyoxalase I (EC 4.4.1.5)			x	
Q3RH69_XYLFA	>gnl|tr|Q3RH69_XYLFA (Q3RH69) Glyoxalase I (EC 4.4.1.5)			x	
Q9HU72_PSEAE	>gnl|tr|Q9HU72_PSEAE (Q9HU72) Lactoylglutathione lyase			x	
Q3BP33_XANC5	>gnl|tr|Q3BP33_XANC5 (Q3BP33) Lactoylglutathione lyase (EC 4.4.1.5)			x	
Q36NB0_MARHY	>gnl|tr|Q36NB0_MARHY (Q36NB0) Glyoxalase I			x	
Q8PGI4_XANAC	>gnl|tr|Q8PGI4_XANAC (Q8PGI4) Lactoylglutathione lyase			x	
Q2P7N8_XANOR	>gnl|tr|Q2P7N8_XANOR (Q2P7N8) Lactoylglutathione lyase			x	
Q5H4W2_XANOR	>gnl|tr|Q5H4W2_XANOR (Q5H4W2) Lactoylglutathione lyase			x	
Q3IGQ9_PSEHT	>gnl|tr|Q3IGQ9_PSEHT (Q3IGQ9) Lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase) (EC 4.4.1.5)			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q44K51_CHRSL	>gnl|tr|Q44K51_CHRSL (Q44K51) Glyoxalase I (EC 4.4.1.5)			x	
Q451L0_9BURK	>gnl|tr|Q451L0_9BURK (Q451L0) Glyoxalase I (EC 4.4.1.5)			x	
Q4LU31_9BURK	>gnl|tr|Q4LU31_9BURK (Q4LU31) Glyoxalase I (EC 4.4.1.5)			x	
Q3FJ10_9BURK	>gnl|tr|Q3FJ10_9BURK (Q3FJ10) Glyoxalase I (EC 4.4.1.5)			x	
Q4BES9_BURVI	>gnl|tr|Q4BES9_BURVI (Q4BES9) Glyoxalase I (EC 4.4.1.5)			x	
Q3CV50_ALTAT	>gnl|tr|Q3CV50_ALTAT (Q3CV50) Glyoxalase I (EC 4.4.1.5)			x	
Q39D39_BURS3	>gnl|tr|Q39D39_BURS3 (Q39D39) Glyoxalase I (EC 4.4.1.5)			x	
Q8YUM0_ANASP	>gnl|tr|Q8YUM0_ANASP (Q8YUM0) Lactoylglutathione lyase			x	
Q2T112_BURTH	>gnl|tr|Q2T112_BURTH (Q2T112) Lactoylglutathione lyase (EC 4.4.1.5)			x	
Q3MGX1_ANAVT	>gnl|tr|Q3MGX1_ANAVT (Q3MGX1) Glyoxalase I (EC 4.4.1.5)			x	
Q3H8N5_TRIER	>gnl|tr|Q3H8N5_TRIER (Q3H8N5) Glyoxalase I (EC 4.4.1.5)			x	
Q62MM1_BURMA	>gnl|tr|Q62MM1_BURMA (Q62MM1) Lactoylglutathione lyase (EC 4.4.1.5)			x	
Q3JVW4_BURP1	>gnl|tr|Q3JVW4_BURP1 (Q3JVW4) Lactoylglutathione lyase (EC 4.4.1.5)			x	
Q63X74_BURPS	>gnl|tr|Q63X74_BURPS (Q63X74) Lactoylglutathione lyase (EC 4.4.1.5)			x	
Q5QZJ8_IDILO	>gnl|tr|Q5QZJ8_IDILO (Q5QZJ8) Lactoylglutathione lyase			x	
Q3Z207_SHISS	>gnl|tr|Q3Z207_SHISS (Q3Z207) Lactoylglutathione lyase			x	
Q32FB9_SHIDS	>gnl|tr|Q32FB9_SHIDS (Q32FB9) Lactoylglutathione lyase			x	
Q5E6C3_VIBF1	>gnl|tr|Q5E6C3_VIBF1 (Q5E6C3) Lactoylglutathione lyase (EC 4.4.1.5)			x	
Q8FH76_ECOL6	>gnl|tr|Q8FH76_ECOL6 (Q8FH76) Lactoylglutathione lyase (EC 4.4.1.5)			x	
Q5P269_AZOSE	>gnl|tr|Q5P269_AZOSE (Q5P269) Lactoylglutathione lyase (EC 4.4.1.5)			x	
Q6FAA3_ACIAD	>gnl|tr|Q6FAA3_ACIAD (Q6FAA3) Lactoylglutathione lyase (EC 4.4.1.5)			x	
Q7NXG6_CHRVO	>gnl|tr|Q7NXG6_CHRVO (Q7NXG6) Lactoylglutathione lyase (EC 4.4.1.5)			x	
Q9HY85_PSEAE	>gnl|tr|Q9HY85_PSEAE (Q9HY85) Lactoylglutathione lyase			x	
Q57PK1_SALCH	>gnl|tr|Q57PK1_SALCH (Q57PK1) Glyoxalase I, nickel isomerase			x	

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>Q5PH08_SALPA</td><td>>gnl|tr|Q5PH08_SALPA (Q5PH08) Lactoylglutathione lyase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q321A6_SHIBS</td><td>>gnl|tr|Q321A6_SHIBS (Q321A6) Lactoylglutathione lyase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q6D5V9_ERWCT</td><td>>gnl|tr|Q6D5V9_ERWCT (Q6D5V9) Lactoylglutathione lyase (EC 4.4.1.5)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q3EF41_ACTSC</td><td>>gnl|tr|Q3EF41_ACTSC (Q3EF41) Lactoylglutathione lyase (EC 4.4.1.5)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q7W4K1_BORPA</td><td>>gnl|tr|Q7W4K1_BORPA (Q7W4K1) Lactoylglutathione lyase (EC 4.4.1.5)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q7W0Q1_BORPE</td><td>>gnl|tr|Q7W0Q1_BORPE (Q7W0Q1) Lactoylglutathione lyase (EC 4.4.1.5)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q3J7R2_NITOC</td><td>>gnl|tr|Q3J7R2_NITOC (Q3J7R2) Glyoxalase I (EC 4.4.1.5)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q7WG26_BORBR</td><td>>gnl|tr|Q7WG26_BORBR (Q7WG26) Lactoylglutathione lyase (EC 4.4.1.5)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q8D0L9_YERPE</td><td>>gnl|tr|Q8D0L9_YERPE (Q8D0L9) Lactoylglutathione lyase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q31QJ9_SYNP7</td><td>>gnl|tr|Q31QJ9_SYNP7 (Q31QJ9) Glyoxalase I (EC 4.4.1.5)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q5N3P3_SYNP6</td><td>>gnl|tr|Q5N3P3_SYNP6 (Q5N3P3) Lactoylglutathione lyase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q4IWB5_AZOVI</td><td>>gnl|tr|Q4IWB5_AZOVI (Q4IWB5) Glyoxalase I (EC 4.4.1.5)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q7MM88_VIBVY</td><td>>gnl|tr|Q7MM88_VIBVY (Q7MM88) Lactoylglutathione lyase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q4C9S5_CROWT</td><td>>gnl|tr|Q4C9S5_CROWT (Q4C9S5) Glyoxalase I (EC 4.4.1.5)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q4AT89_9BURK</td><td>>gnl|tr|Q4AT89_9BURK (Q4AT89) Glyoxalase I (EC 4.4.1.5)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q82UQ5_NITEU</td><td>>gnl|tr|Q82UQ5_NITEU (Q82UQ5) Possible gloA; lactoylglutathione lyase (EC 4.4.1.5)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q7VDY1_PROMA</td><td>>gnl|tr|Q7VDY1_PROMA (Q7VDY1) Lactoylglutathione lyase family enzyme</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>Q7N3W1_PHOLL</td><td>>gnl|tr|Q7N3W1_PHOLL (Q7N3W1) Lactoylglutathione lyase (Methylglyoxalase) (S-D-lactolyglutathione methylglyoxal lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q66A37_YERPS</td><td>>gnl|tr|Q66A37_YERPS (Q66A37) Lactoylglutathione lyase (EC 4.4.1.5)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q8ZE09_YERPE</td><td>>gnl|tr|Q8ZE09_YERPE (Q8ZE09) Lactoylglutathione lyase (EC 4.4.1.5)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q3N8V3_9PROT</td><td>>gnl|tr|Q3N8V3_9PROT (Q3N8V3) Glyoxalase I (EC 4.4.1.5)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q3XB57_METFL</td><td>>gnl|tr|Q3XB57_METFL (Q3XB57) Glyoxalase I (EC 4.4.1.5)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>Q475P8_RALEJ</td><td>>gnl|tr|Q475P8_RALEJ (Q475P8) Glyoxalase I (EC 4.4.1.5)</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q4NTS9_9DELT	>gnl|tr|Q4NTS9_9DELT (Q4NTS9) Glyoxalase I (EC 4.4.1.5)			x	
Q2Y5Q9_NITMU	>gnl|tr|Q2Y5Q9_NITMU (Q2Y5Q9) Glyoxalase I (EC 4.4.1.5)			x	
Q47A63_DECAR	>gnl|tr|Q47A63_DECAR (Q47A63) Glyoxalase I			x	
Q2SDH5_9GAMM	>gnl|tr|Q2SDH5_9GAMM (Q2SDH5) Lactoylglutathione lyase (EC 4.4.1.5)			x	
Q7U3T2_SYNPX	>gnl|tr|Q7U3T2_SYNPX (Q7U3T2) Lactoylglutathione lyase (EC 4.4.1.5)			x	
Q4QNL6_HAEI8	>gnl|tr|Q4QNL6_HAEI8 (Q4QNL6) Lactoylglutathione lyase (EC 4.4.1.5)			x	
Q87I32_VIBPA	>gnl|tr|Q87I32_VIBPA (Q87I32) Lactoylglutathione lyase			x	
Q2RQL0_RHORU	>gnl|tr|Q2RQL0_RHORU (Q2RQL0) N-isopropylammelide isopropylaminohydrolase (EC 3.5.99.4)		x		
Q46U35_RALEJ	>gnl|tr|Q46U35_RALEJ (Q46U35) TatD-related deoxyribonuclease		x		
Q98BZ6_RHILO	>gnl|tr|Q98BZ6_RHILO (Q98BZ6) Creatinine deaminase		x		
Q3K9N7_PSEPF	>gnl|tr|Q3K9N7_PSEPF (Q3K9N7) N-isopropylammelide isopropylaminohydrolase (EC 3.5.99.4)		x		
Q399E7_BURS3	>gnl|tr|Q399E7_BURS3 (Q399E7) N-isopropylammelide isopropylaminohydrolase (EC 3.5.99.4)		x		
Q3FD23_9BURK	>gnl|tr|Q3FD23_9BURK (Q3FD23) N-isopropylammelide isopropylaminohydrolase (EC 3.5.99.4)		x		
Q4BSP0_BURVI	>gnl|tr|Q4BSP0_BURVI (Q4BSP0) N-isopropylammelide isopropylaminohydrolase (EC 3.5.99.4)		x		
Q45AU2_9BURK	>gnl|tr|Q45AU2_9BURK (Q45AU2) N-isopropylammelide isopropylaminohydrolase (EC 3.5.99.4)		x		
Q405V4_9RHOB	>gnl|tr|Q405V4_9RHOB (Q405V4) N-isopropylammelide isopropylaminohydrolase (EC 3.5.99.4)		x		
Q6M8S4_CORGL	>gnl|tr|Q6M8S4_CORGL (Q6M8S4) CREATININE DEAMINASE (EC 3.5.4.21)		x		
O32386_BACSP	>gnl|tr|O32386_BACSP (O32386) Creatinine deaminase (EC 3.5.4.21)		x		
Q84FJ3_9BURK	>gnl|tr|Q84FJ3_9BURK (Q84FJ3) Methylenediurea deiminase large subunit (EC 3.5.3.21) (Fragment)		x		

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>Q5M8P6_MOUSE</td><td>>gnl|tr|Q5M8P6_MOUSE (Q5M8P6) Enoyl coenzyme A hydratase 1, peroxisomal</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q3KC82_PSEPF</td><td>>gnl|tr|Q3KC82_PSEPF (Q3KC82) Enoyl-CoA hydratase/isomerase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q4ZTN1_PSEU2</td><td>>gnl|tr|Q4ZTN1_PSEU2 (Q4ZTN1) Enoyl-CoA hydratase/isomerase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q9I2S4_PSEAE</td><td>>gnl|tr|Q9I2S4_PSEAE (Q9I2S4) Probable enoyl-CoA hydratase/isomerase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q6DJA5_XENTR</td><td>>gnl|tr|Q6DJA5_XENTR (Q6DJA5) Enoyl Coenzyme A hydratase 1, peroxisomal</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q9FHR8_ARATH</td><td>>gnl|tr|Q9FHR8_ARATH (Q9FHR8) Enoyl CoA hydratase-like protein</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q3Y5G5_PIG</td><td>>gnl|tr|Q3Y5G5_PIG (Q3Y5G5) Peroxisomal enoyl coenzyme A hydratase 1 (Fragment)</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q8RUL6_ORYSA</td><td>>gnl|tr|Q8RUL6_ORYSA (Q8RUL6) Enoyl CoA hydratase-like protein (Putative enoyl coenzyme A hydratase 1, peroxisomal)</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q7TVP7_MYCBO</td><td>>gnl|tr|Q7TVP7_MYCBO (Q7TVP7) PUTATIVE ENOYL-COA HYDRATASE ECHA21 (ENOYL HYDRASE) (UNSATURATED ACYL-COA HYDRATASE) (CROTONASE) (EC 4.2.1.17)</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q9CD94_MYCLE</td><td>>gnl|tr|Q9CD94_MYCLE (Q9CD94) Putative enoyl-CoA hydratase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q8F7B6_LEPIN</td><td>>gnl|tr|Q8F7B6_LEPIN (Q8F7B6) Enoyl-CoA hydratase (EC 4.2.1.17)</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q2SLF3_9GAMM</td><td>>gnl|tr|Q2SLF3_9GAMM (Q2SLF3) Enoyl-CoA hydratase/carnithine racemase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q3FRA8_9BURK</td><td>>gnl|tr|Q3FRA8_9BURK (Q3FRA8) Enoyl-CoA hydratase/isomerase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q47AT2_DECAR</td><td>>gnl|tr|Q47AT2_DECAR (Q47AT2) Enoyl-CoA hydratase/isomerase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q2U862_ASPOR</td><td>>gnl|tr|Q2U862_ASPOR (Q2U862) Enoyl-CoA isomerase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q3CT36_ALTAT</td><td>>gnl|tr|Q3CT36_ALTAT (Q3CT36) Enoyl-CoA hydratase/isomerase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q3NN78_SHEFR</td><td>>gnl|tr|Q3NN78_SHEFR (Q3NN78) Enoyl-CoA hydratase/isomerase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q72P47_LEPIC</td><td>>gnl|tr|Q72P47_LEPIC (Q72P47) Enoyl-CoA hydratase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q7NV60_CHRVO</td><td>>gnl|tr|Q7NV60_CHRVO (Q7NV60) Probable enoyl-CoA hydratase (EC 4.2.1.17)</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q3W381_9ACTO</td><td>>gnl|tr|Q3W381_9ACTO (Q3W381) Enoyl-CoA hydratase/isomerase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>O74188_AGABI</td><td>>gnl|tr|O74188_AGABI (O74188) Putative peroxisomal enoyl-CoA hydratase (Fragment)</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q9M208_ARATH</td><td>>gnl|tr|Q9M208_ARATH (Q9M208) Enoyl-CoA-hydratase-like protein</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q3KCA0_PSEPF</td><td>>gnl|tr|Q3KCA0_PSEPF (Q3KCA0) Enoyl-CoA hydratase/isomerase</td><td></td><td>x</td><td></td><td></td></tr>
</table>

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q4KC65_PSEF5	>gnl|tr|Q4KC65_PSEF5 (Q4KC65) Enoly-coenzyme A hydratase/isomerase family protein		x		
Q88H70_PSEPK	>gnl|tr|Q88H70_PSEPK (Q88H70) Enoly-coenzyme A hydratase/isomerase family protein		x		
Q3RPS1_RALME	>gnl|tr|Q3RPS1_RALME (Q3RPS1) Enoyl-CoA hydratase/isomerase		x		
Q4IX56_AZOVI	>gnl|tr|Q4IX56_AZOVI (Q4IX56) Enoyl-CoA hydratase/isomerase		x		
Q4ZVK4_PSEU2	>gnl|tr|Q4ZVK4_PSEU2 (Q4ZVK4) Enoyl-CoA hydratase/isomerase		x		
Q87YT7_PSESM	>gnl|tr|Q87YT7_PSESM (Q87YT7) Enoly-CoA hydratase/isomerase family protein		x		
Q8UA69_AGRT5	>gnl|tr|Q8UA69_AGRT5 (Q8UA69) Enoyl-CoA hydratase		x		
Q48KW7_PSE14	>gnl|tr|Q48KW7_PSE14 (Q48KW7) Enoly-CoA hydratase/isomerase family protein (EC 4.2.1.17)		x		
Q2XKF3_PSEPU	>gnl|tr|Q2XKF3_PSEPU (Q2XKF3) Enoly-coenzyme A hydratase/isomerase family protein		x		
Q6N492_RHOPA	>gnl|tr|Q6N492_RHOPA (Q6N492) Putative enoyl-CoA hydratase/isomerase (EC 4.2.1.17)		x		
Q2RTB1_RHORU	>gnl|tr|Q2RTB1_RHORU (Q2RTB1) Enoyl-CoA hydratase/isomerase (EC 4.2.1.17)		x		
Q8XS34_RALSO	>gnl|tr|Q8XS34_RALSO (Q8XS34) PUTATIVE ENOYL-COENZYME A HYDRATASE PROTEIN (EC 4.2.1.17)		x		
Q8EGC3_SHEON	>gnl|tr|Q8EGC3_SHEON (Q8EGC3) Enoyl-CoA hydratase/isomerase family protein		x		
Q2W188_MAGSA	>gnl|tr|Q2W188_MAGSA (Q2W188) Enoyl-CoA hydratase/carnithine racemase		x		
Q9C251_NEUCR	>gnl|tr|Q9C251_NEUCR (Q9C251) Related to enoyl-CoA-hydratase		x		
Q2Z8W1_9GAMM	>gnl|tr|Q2Z8W1_9GAMM (Q2Z8W1) Enoyl-CoA hydratase/isomerase family protein		x		
Q36DS6_9GAMM	>gnl|tr|Q36DS6_9GAMM (Q36DS6) Enoyl-CoA hydratase/isomerase family protein		x		
Q4J4W9_AZOVI	>gnl|tr|Q4J4W9_AZOVI (Q4J4W9) Enoyl-CoA hydratase/isomerase		x		
Q35U53_9GAMM	>gnl|tr|Q35U53_9GAMM (Q35U53) Enoyl-CoA hydratase/isomerase family protein		x		
Q37AX1_RHOPA	>gnl|tr|Q37AX1_RHOPA (Q37AX1) Enoyl-CoA hydratase/isomerase		x		

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q2XLE9_PSEPU	>gnl|tr|Q2XLE9_PSEPU (Q2XLE9) Enoly-coenzyme A hydratase/isomerase family protein		x		
Q51969_PSEPU	>gnl|tr|Q51969_PSEPU (Q51969) Enoly-coenzyme A hydratase (Enoyl-CoA hydratase)		x		
Q92TQ6_RHIME	>gnl|tr|Q92TQ6_RHIME (Q92TQ6) Putative enoyl-CoA hydratase protein (EC 4.2.1.17)		x		
Q37MG0_RHOPA	>gnl|tr|Q37MG0_RHOPA (Q37MG0) Enoyl-CoA hydratase/isomerase		x		
Q8YGG3_BRUME	>gnl|tr|Q8YGG3_BRUME (Q8YGG3) ENOYL-COA HYDRATASE (EC 4.2.1.17)		x		
Q8G1F8_BRUSU	>gnl|tr|Q8G1F8_BRUSU (Q8G1F8) Enoyl-CoA hydratase/isomerase family protein		x		
Q3PXC2_NITHA	>gnl|tr|Q3PXC2_NITHA (Q3PXC2) Enoyl-CoA hydratase/isomerase		x		
Q3Q6G5_9GAMM	>gnl|tr|Q3Q6G5_9GAMM (Q3Q6G5) Enoyl-CoA hydratase/isomerase		x		
Q89N86_BRAJA	>gnl|tr|Q89N86_BRAJA (Q89N86) Enoyl-CoA hydratase		x		
Q2YNA1_BRUA2	>gnl|tr|Q2YNA1_BRUA2 (Q2YNA1) Enoyl-CoA hydratase/isomerase (EC 4.2.1.17)		x		
Q57DZ1_BRUAB	>gnl|tr|Q57DZ1_BRUAB (Q57DZ1) Enoyl-CoA hydratase/isomerase family protein		x		
Q3BVW6_XANC5	>gnl|tr|Q3BVW6_XANC5 (Q3BVW6) Enoyl-CoA hydratase/isomerase family protein (EC 4.2.1.17)		x		
Q34UE3_RHOPA	>gnl|tr|Q34UE3_RHOPA (Q34UE3) Putative enoyl-CoA hydratase/isomerase		x		
Q2ZWZ5_SHEPU	>gnl|tr|Q2ZWZ5_SHEPU (Q2ZWZ5) Enoyl-CoA hydratase/isomerase		x		
Q8PMW0_XANAC	>gnl|tr|Q8PMW0_XANAC (Q8PMW0) Enoyl-CoA hydratase		x		
Q738L0_BACC1	>gnl|tr|Q738L0_BACC1 (Q738L0) Enoyl-CoA hydratase/isomerase family protein		x		
Q9FWQ0_ORYSA	>gnl|tr|Q9FWQ0_ORYSA (Q9FWQ0) Putative enoyl-CoA-hydratase		x		
Q336U0_ORYSA	>gnl|tr|Q336U0_ORYSA (Q336U0) Enoyl-CoA-hydratase, putative		x		
Q9A8K1_CAUCR	>gnl|tr|Q9A8K1_CAUCR (Q9A8K1) Enoyl-CoA hydratase/isomerase family protein		x		
Q81QR3_BACAN	>gnl|tr|Q81QR3_BACAN (Q81QR3) Enoyl-CoA hydratase/isomerase family protein		x		

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
O53419_MYCTU	>gnl|tr|O53419_MYCTU (O53419) POSSIBLE ENOYL-CoA HYDRATASE ECHA9 (ENOYL HYDRASE) (UNSATURATED ACYL-CoA HYDRATASE) (CROTONASE) (EC 4.2.1.17) (Enoyl-CoA hydratase/isomerase family protein)		x		
Q7U0Q8_MYCBO	>gnl|tr|Q7U0Q8_MYCBO (Q7U0Q8) POSSIBLE ENOYL-COA HYDRATASE ECHA9 (ENOYL HYDRASE) (UNSATURATED ACYL-COA HYDRATASE) (CROTONASE) (EC 4.2.1.17)		x		
Q4USE7_XANC8	>gnl|tr|Q4USE7_XANC8 (Q4USE7) Enoyl-CoA hydratase		x		
Q2X1B4_9GAMM	>gnl|tr|Q2X1B4_9GAMM (Q2X1B4) Enoyl-CoA hydratase/isomerase family protein		x		
Q8RXN4_ARATH	>gnl|tr|Q8RXN4_ARATH (Q8RXN4) Putative enoyl-CoA hydratase		x		
Q4MU30_BACCE	>gnl|tr|Q4MU30_BACCE (Q4MU30) Enoly-CoA hydratase/isomerase family protein		x		
Q5H1S2_XANOR	>gnl|tr|Q5H1S2_XANOR (Q5H1S2) Enoyl-CoA hydratase		x		
Q2P4N1_XANOR	>gnl|tr|Q2P4N1_XANOR (Q2P4N1) Enoyl-CoA hydratase		x		
Q34DB6_RHOPA	>gnl|tr|Q34DB6_RHOPA (Q34DB6) Enoyl-CoA hydratase/isomerase		x		
Q37X83_SPHAR	>gnl|tr|Q37X83_SPHAR (Q37X83) Enoyl-CoA hydratase/isomerase family protein		x		
Q3F6U7_9BURK	>gnl|tr|Q3F6U7_9BURK (Q3F6U7) Enoyl-CoA hydratase/isomerase		x		
Q3SQN0_NITWN	>gnl|tr|Q3SQN0_NITWN (Q3SQN0) Enoyl-CoA hydratase/isomerase (EC 4.2.1.17)		x		
Q8PB61_XANCP	>gnl|tr|Q8PB61_XANCP (Q8PB61) Enoyl-CoA hydratase		x		
Q2N893_9SPHN	>gnl|tr|Q2N893_9SPHN (Q2N893) Enoyl-CoA hydratase/isomerase family protein		x		
Q2W460_MAGSA	>gnl|tr|Q2W460_MAGSA (Q2W460) Enoyl-CoA hydratase/carnithine racemase		x		
O07138_MYCLE	>gnl|tr|O07138_MYCLE (O07138) B1306.06c protein (Putative enoyl-CoA hydratase/isomerase)		x		
Q399M8_BURS3	>gnl|tr|Q399M8_BURS3 (Q399M8) Enoyl-CoA hydratase/isomerase (EC 4.2.1.17)		x		
Q46ZQ0_RALEJ	>gnl|tr|Q46ZQ0_RALEJ (Q46ZQ0) Enoyl-CoA hydratase/isomerase		x		
Q35HL2_9BRAD	>gnl|tr|Q35HL2_9BRAD (Q35HL2) Enoyl-CoA hydratase		x		
Q4BR18_BURVI	>gnl|tr|Q4BR18_BURVI (Q4BR18) Enoyl-CoA hydratase/isomerase		x		

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q63MM8_BURPS	>gnl|tr|Q63MM8_BURPS (Q63MM8) Enoyl-CoA hydratase/isomerase family		x		
Q3JGG9_BURP1	>gnl|tr|Q3JGG9_BURP1 (Q3JGG9) Enoyl-CoA hydratase/isomerase family		x		
Q2X8G8_PSEPU	>gnl|tr|Q2X8G8_PSEPU (Q2X8G8) Enoyl-CoA hydratase/isomerase family protein		x		
Q3VBJ9_9SPHN	>gnl|tr|Q3VBJ9_9SPHN (Q3VBJ9) Enoyl-CoA hydratase/isomerase		x		
Q9I5I5_PSEAE	>gnl|tr|Q9I5I5_PSEAE (Q9I5I5) Probable enoyl-CoA hydratase/isomerase		x		
Q88N06_PSEPK	>gnl|tr|Q88N06_PSEPK (Q88N06) Enoyl-CoA hydratase/isomerase family protein		x		
Q8D6N8_VIBVU	>gnl|tr|Q8D6N8_VIBVU (Q8D6N8) Enoyl-CoA hydratase/carnithine racemase		x		
Q44VC8_9BURK	>gnl|tr|Q44VC8_9BURK (Q44VC8) Enoyl-CoA hydratase/isomerase		x		
Q4LHB9_9BURK	>gnl|tr|Q4LHB9_9BURK (Q4LHB9) Enoyl-CoA hydratase/isomerase		x		
Q2SVM5_BURTH	>gnl|tr|Q2SVM5_BURTH (Q2SVM5) Enoyl-CoA hydratase/isomerase family protein		x		
Q2T4A7_BURTH	>gnl|tr|Q2T4A7_BURTH (Q2T4A7) Enoyl-CoA hydratase/isomerase family		x		
Q7MDJ7_VIBVY	>gnl|tr|Q7MDJ7_VIBVY (Q7MDJ7) Putative enoyl-CoA hydratase/isomerase		x		
Q87H46_VIBPA	>gnl|tr|Q87H46_VIBPA (Q87H46) Putative enoyl-CoA hydratase/isomerase		x		
Q62K52_BURMA	>gnl|tr|Q62K52_BURMA (Q62K52) Enoyl-CoA hydratase/isomerase family protein		x		
Q3JSS2_BURP1	>gnl|tr|Q3JSS2_BURP1 (Q3JSS2) Enoyl-CoA hydratase/isomerase family protein		x		
Q87II2_VIBPA	>gnl|tr|Q87II2_VIBPA (Q87II2) Putative enoyl-CoA hydratase/isomerase		x		
Q5Z107_NOCFA	>gnl|tr|Q5Z107_NOCFA (Q5Z107) Putative enoyl-CoA hydratase/isomerase family protein		x		
Q46TC0_RALEJ	>gnl|tr|Q46TC0_RALEJ (Q46TC0) Enoyl-CoA hydratase/isomerase		x		
Q2U621_ASPOR	>gnl|tr|Q2U621_ASPOR (Q2U621) Enoyl-CoA hydratase		x		

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q4B2Y2_9BURK	>gnl|tr|Q4B2Y2_9BURK (Q4B2Y2) Enoyl-CoA hydratase/isomerase		x		
Q3W1N1_9ACTO	>gnl|tr|Q3W1N1_9ACTO (Q3W1N1) Enoyl-CoA hydratase/isomerase		x		
Q65IX3_BACLD	>gnl|tr|Q65IX3_BACLD (Q65IX3) Hypothetical protein (EC 4.2.1.17) (Enoyl-CoA hydratase/isomerase)		x		
Q39GW9_BURS3	>gnl|tr|Q39GW9_BURS3 (Q39GW9) Enoyl-CoA hydratase/isomerase (EC 4.2.1.17)		x		
Q4NL92_9MICC	>gnl|tr|Q4NL92_9MICC (Q4NL92) Enoyl-CoA hydratase/isomerase		x		
Q4BCD7_BURVI	>gnl|tr|Q4BCD7_BURVI (Q4BCD7) Enoyl-CoA hydratase/isomerase		x		
Q3WQZ5_9RHIZ	>gnl|tr|Q3WQZ5_9RHIZ (Q3WQZ5) Enoyl-CoA hydratase/isomerase		x		
Q4KGS1_PSEF5	>gnl|tr|Q4KGS1_PSEF5 (Q4KGS1) Enoyl-CoA hydratase/isomerase family protein		x		
Q3KGL5_PSEPF	>gnl|tr|Q3KGL5_PSEPF (Q3KGL5) Enoyl-CoA hydratase/isomerase		x		
Q4LRG6_9BURK	>gnl|tr|Q4LRG6_9BURK (Q4LRG6) Enoyl-CoA hydratase/isomerase		x		
Q452D0_9BURK	>gnl|tr|Q452D0_9BURK (Q452D0) Enoyl-CoA hydratase/isomerase		x		
Q5QW21_IDILO	>gnl|tr|Q5QW21_IDILO (Q5QW21) Enoyl-CoA hydratase/isomerase family protein		x		
Q3FBF4_9BURK	>gnl|tr|Q3FBF4_9BURK (Q3FBF4) Enoyl-CoA hydratase/isomerase		x		
Q33R76_9GAMM	>gnl|tr|Q33R76_9GAMM (Q33R76) Enoyl-CoA hydratase/isomerase		x		
Q3J1K7_RHOS4	>gnl|tr|Q3J1K7_RHOS4 (Q3J1K7) Enoyl-CoA hydratase (EC 4.2.1.17)		x		
Q3QFV9_9GAMM	>gnl|tr|Q3QFV9_9GAMM (Q3QFV9) Enoyl-CoA hydratase/isomerase		x		
Q2SP84_9GAMM	>gnl|tr|Q2SP84_9GAMM (Q2SP84) Enoyl-CoA hydratase/carnithine racemase		x		
Q8NRX2_CORGL	>gnl|tr|Q8NRX2_CORGL (Q8NRX2) Enoyl-CoA hydratase/carnithine racemase (EC 4.2.1.17)		x		
Q9SZ48_ARATH	>gnl|tr|Q9SZ48_ARATH (Q9SZ48) Enoyl-CoA hydratase-like protein		x		
Q4B2U1_9BURK	>gnl|tr|Q4B2U1_9BURK (Q4B2U1) Enoyl-CoA hydratase/isomerase		x		
Q8FQY6_COREF	>gnl|tr|Q8FQY6_COREF (Q8FQY6) Putative enoyl-CoA hydratase		x		
Q9SE41_AVIMR	>gnl|tr|Q9SE41_AVIMR (Q9SE41) Enoyl-CoA-hydratase		x		
Q3NUX3_SHEFR	>gnl|tr|Q3NUX3_SHEFR (Q3NUX3) Enoyl-CoA hydratase/isomerase		x		
Q7VYA4_BORPE	>gnl|tr|Q7VYA4_BORPE (Q7VYA4) Enoly-CoA hydratase		x		
Q7WJ69_BORBR	>gnl|tr|Q7WJ69_BORBR (Q7WJ69) Enoly-CoA hydratase		x		
Q7WA37_BORPA	>gnl|tr|Q7WA37_BORPA (Q7WA37) Enoly-CoA hydratase		x		
Q3P0I4_9GAMM	>gnl|tr|Q3P0I4_9GAMM (Q3P0I4) Enoyl-CoA hydratase/isomerase		x		

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q5JMX9_ORYSA	>gnl|tr|Q5JMX9_ORYSA (Q5JMX9) Putative enoyl-CoA-hydratase		x		
Q44GK6_CHRSL	>gnl|tr|Q44GK6_CHRSL (Q44GK6) Enoyl-CoA hydratase/isomerase		x		
Q7NWA8_CHRVO	>gnl|tr|Q7NWA8_CHRVO (Q7NWA8) Enoyl-CoA hydratase (EC 4.2.1.17) (EC 5.3.3.8)		x		
Q6LIA0_PHOPR	>gnl|tr|Q6LIA0_PHOPR (Q6LIA0) Putative enoyl-CoA hydratase		x		
Q3IGC8_PSEHT	>gnl|tr|Q3IGC8_PSEHT (Q3IGC8) Enoyl-CoA hydratase/isomerase family protein (EC 4.2.1.17)		x		
Q3PCS1_PARDE	>gnl|tr|Q3PCS1_PARDE (Q3PCS1) Enoyl-CoA hydratase/isomerase		x		
Q5LRB7_SILPO	>gnl|tr|Q5LRB7_SILPO (Q5LRB7) Enoyl-CoA hydratase/isomerase family protein		x		
Q3QWM2_9RHOB	>gnl|tr|Q3QWM2_9RHOB (Q3QWM2) Enoyl-CoA hydratase/isomerase		x		
Q6CA37_YARLI	>gnl|tr|Q6CA37_YARLI (Q6CA37) Similar to tr|Q9C251 Neurospora crassa Related to enoyl-CoA-hydratase		x		
Q5WH10_BACSK	>gnl|tr|Q5WH10_BACSK (Q5WH10) Enoyl-CoA hydratase (EC 4.2.1.17)		x		
Q3FK72_9BURK	>gnl|tr|Q3FK72_9BURK (Q3FK72) Enoyl-CoA hydratase/isomerase		x		
Q4DMX9_TRYCR	>gnl|tr|Q4DMX9_TRYCR (Q4DMX9) Enoyl-CoA hydratase/isomerase family protein, putative (EC 4.2.1.17)		x		
Q3CPX4_ALTAT	>gnl|tr|Q3CPX4_ALTAT (Q3CPX4) Enoyl-CoA hydratase/isomerase		x		
Q40B25_9RHOB	>gnl|tr|Q40B25_9RHOB (Q40B25) Enoyl-CoA hydratase/isomerase		x		
Q488V8_COLP3	>gnl|tr|Q488V8_COLP3 (Q488V8) Enoyl-CoA hydratase/isomerase family protein		x		
Q485B6_COLP3	>gnl|tr|Q485B6_COLP3 (Q485B6) Enoyl-CoA hydratase/isomerase family protein		x		
Q351Q9_9GAMM	>gnl|tr|Q351Q9_9GAMM (Q351Q9) Enoyl-CoA hydratase		x		
Q3H3V4_9ACTO	>gnl|tr|Q3H3V4_9ACTO (Q3H3V4) Enoyl-CoA hydratase/isomerase		x		
Q381D8_9TRYP	>gnl|tr|Q381D8_9TRYP (Q381D8) Enoyl-CoA hydratase/isomerase family protein, putative		x		
Q4DAM8_TRYCR	>gnl|tr|Q4DAM8_TRYCR (Q4DAM8) Enoyl-CoA hydratase/isomerase family protein, putative		x		
Q36TB7_MARHY	>gnl|tr|Q36TB7_MARHY (Q36TB7) Enoyl-CoA hydratase/isomerase family protein		x		

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q4DMX8_TRYCR	>gnl|tr|Q4DMX8_TRYCR (Q4DMX8) Enoyl-CoA hydratase/isomerase family protein, putative		x		
Q4DAM7_TRYCR	>gnl|tr|Q4DAM7_TRYCR (Q4DAM7) Enoyl-CoA hydratase/isomerase family protein, putative (EC 4.2.1.17)		x		
Q4JU31_CORJK	>gnl|tr|Q4JU31_CORJK (Q4JU31) Enoyl-CoA hydratase (EC 4.2.1.17)		x		
O22696_ARATH	>gnl|tr|O22696_ARATH (O22696) Putative enoyl-CoA hydratase/isomerase		x		
Q8GYN9_ARATH	>gnl|tr|Q8GYN9_ARATH (Q8GYN9) Putative enoyl-CoA hydratase/isomerase		x		
Q7MMF4_VIBVY	>gnl|tr|Q7MMF4_VIBVY (Q7MMF4) Dihydroxynaphthoic acid synthase		x		
Q8KBE2_CHLTE	>gnl|tr|Q8KBE2_CHLTE (Q8KBE2) Naphthoate synthase (EC 4.1.3.36)		x		
Q9KQM5_VIBCH	>gnl|tr|Q9KQM5_VIBCH (Q9KQM5) Naphthoate synthase		x		
Q87R67_VIBPA	>gnl|tr|Q87R67_VIBPA (Q87R67) Naphthoate synthase		x		
Q8D822_VIBVU	>gnl|tr|Q8D822_VIBVU (Q8D822) Dihydroxynaphthoic acid synthase		x		
Q4QLU0_HAEI8	>gnl|tr|Q4QLU0_HAEI8 (Q4QLU0) Naphthoate synthase (EC 4.1.3.36)		x		
Q8D0S4_YERPE	>gnl|tr|Q8D0S4_YERPE (Q8D0S4) Dihydroxynaphtoic acid synthetase		x		
Q57M49_SALCH	>gnl|tr|Q57M49_SALCH (Q57M49) Dihydroxynaphtoic acid synthetase		x		
Q83QT5_SHIFL	>gnl|tr|Q83QT5_SHIFL (Q83QT5) Dihydroxynaphtoic acid synthetase		x		
Q8XFL0_SALTI	>gnl|tr|Q8XFL0_SALTI (Q8XFL0) Naphthoate synthase (EC 4.1.3.36)		x		
Q7CQ56_SALTY	>gnl|tr|Q7CQ56_SALTY (Q7CQ56) Dihydroxynaphtoic acid synthetase (EC 4.1.3.36)		x		
Q5PN74_SALPA	>gnl|tr|Q5PN74_SALPA (Q5PN74) Naphthoate synthase		x		
Q7AC18_ECO57	>gnl|tr|Q7AC18_ECO57 (Q7AC18) Dihydroxynaphtoic acid synthetase		x		
Q31YJ5_SHIBS	>gnl|tr|Q31YJ5_SHIBS (Q31YJ5) Dihydroxynaphtoic acid synthetase		x		
Q3YZU4_SHISS	>gnl|tr|Q3YZU4_SHISS (Q3YZU4) Dihydroxynaphtoic acid synthetase		x		
Q32DS6_SHIDS	>gnl|tr|Q32DS6_SHIDS (Q32DS6) Dihydroxynaphtoic acid synthetase		x		
Q669C9_YERPS	>gnl|tr|Q669C9_YERPS (Q669C9) Naphthoate synthase (EC 4.1.3.36)		x		

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q8ZDN6_YERPE	>gnl|tr|Q8ZDN6_YERPE (Q8ZDN6) Naphthoate synthase (EC 4.1.3.36)		x		
Q8XDY1_ECO57	>gnl|tr|Q8XDY1_ECO57 (Q8XDY1) Dihydroxynaphtoic acid synthetase		x		
Q6D7W2_ERWCT	>gnl|tr|Q6D7W2_ERWCT (Q6D7W2) Naphthoate synthase (EC 4.1.3.36)		x		
Q3HJS9_TRIER	>gnl|tr|Q3HJS9_TRIER (Q3HJS9) Naphthoate synthase		x		
Q3EGU1_ACTSC	>gnl|tr|Q3EGU1_ACTSC (Q3EGU1) Dihydroxynaphthoic acid synthase		x		
Q7VKI1_HAEDU	>gnl|tr|Q7VKI1_HAEDU (Q7VKI1) Napthoate synthetase		x		
Q3ENZ9_BACTI	>gnl|tr|Q3ENZ9_BACTI (Q3ENZ9) Naphthoate synthase (EC 4.1.3.36)		x		
Q7N2K5_PHOLL	>gnl|tr|Q7N2K5_PHOLL (Q7N2K5) Naphthoate synthase (Dihydroxynaphthoic acid synthetase) (DHNA synthetase)		x		
Q5KVX8_GEOKA	>gnl|tr|Q5KVX8_GEOKA (Q5KVX8) Dihydroxynapthoic acid synthetase (EC 4.1.3.36)		x		
Q3MGU4_ANAVT	>gnl|tr|Q3MGU4_ANAVT (Q3MGU4) Naphthoate synthase (EC 4.1.3.36)		x		
Q414A8_KINRA	>gnl|tr|Q414A8_KINRA (Q414A8) Naphthoate synthase		x		
Q3VQI3_9CHLB	>gnl|tr|Q3VQI3_9CHLB (Q3VQI3) Naphthoate synthase		x		
Q6HC28_BACHK	>gnl|tr|Q6HC28_BACHK (Q6HC28) Naphthoate synthase (EC 4.1.3.36)		x		
Q81K96_BACAN	>gnl|tr|Q81K96_BACAN (Q81K96) Naphthoate synthase		x		
Q72YK8_BACC1	>gnl|tr|Q72YK8_BACC1 (Q72YK8) Naphthoate synthase (EC 4.1.3.36)		x		
Q632I4_BACCZ	>gnl|tr|Q632I4_BACCZ (Q632I4) Naphthoate synthase (EC 4.1.3.36)		x		
Q41F61_9BACI	>gnl|tr|Q41F61_9BACI (Q41F61) Naphthoate synthase		x		
Q8YUJ9_ANASP	>gnl|tr|Q8YUJ9_ANASP (Q8YUJ9) Naphthoate synthase		x		
Q8ENZ6_OCEIH	>gnl|tr|Q8ENZ6_OCEIH (Q8ENZ6) Naphthoate synthase (EC 4.1.3.36)		x		
Q816H9_BACCR	>gnl|tr|Q816H9_BACCR (Q816H9) Naphthoate synthase (EC 4.1.3.36)		x		
Q4C6T8_CROWT	>gnl|tr|Q4C6T8_CROWT (Q4C6T8) Naphthoate synthase		x		
Q6Q301_SYNP2	>gnl|tr|Q6Q301_SYNP2 (Q6Q301) 1,4 dihydroxy-2-naphthaote synthase		x		
Q4ANX2_9CHLB	>gnl|tr|Q4ANX2_9CHLB (Q4ANX2) Naphthoate synthase		x		

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q41Z99_DESHA	>gnl|tr|Q41Z99_DESHA (Q41Z99) Naphthoate synthase		x		
Q3GJH0_CHLVI	>gnl|tr|Q3GJH0_CHLVI (Q3GJH0) Naphthoate synthase		x		
Q8DG66_SYNEL	>gnl|tr|Q8DG66_SYNEL (Q8DG66) Naphthoate synthase		x		
Q3B615_PELLD	>gnl|tr|Q3B615_PELLD (Q3B615) Naphthoate synthase		x		
Q4MN98_BACCE	>gnl|tr|Q4MN98_BACCE (Q4MN98) Naphthoate synthase (EC 4.1.3.36)		x		
P73495_SYNY3	>gnl|tr|P73495_SYNY3 (P73495) Naphthoate synthase		x		
Q3APV5_CHLCH	>gnl|tr|Q3APV5_CHLCH (Q3APV5) Naphthoate synthase (EC 4.1.3.36)		x		
Q9CHK2_LACLA	>gnl|tr|Q9CHK2_LACLA (Q9CHK2) Dihydroxynaphthonic acid synthase (EC 4.1.3.36)		x		
Q8NXA0_STAAW	>gnl|tr|Q8NXA0_STAAW (Q8NXA0) Naphthoate synthase		x		
Q6GAG7_STAAS	>gnl|tr|Q6GAG7_STAAS (Q6GAG7) Putative naphthoate synthase (EC 4.1.3.36)		x		
Q5HH38_STAAC	>gnl|tr|Q5HH38_STAAC (Q5HH38) Naphthoate synthase (EC 4.1.3.36)		x		
Q6GI37_STAAR	>gnl|tr|Q6GI37_STAAR (Q6GI37) Putative naphthoate synthase (EC 4.1.3.36)		x		
Q4L549_STAHJ	>gnl|tr|Q4L549_STAHJ (Q4L549) Naphthoate synthase		x		
Q3VX36_PROAE	>gnl|tr|Q3VX36_PROAE (Q3VX36) Naphthoate synthase		x		
Q44QP5_CHLLI	>gnl|tr|Q44QP5_CHLLI (Q44QP5) Naphthoate synthase		x		
Q7A6A9_STAAN	>gnl|tr|Q7A6A9_STAAN (Q7A6A9) Naphthoate synthase		x		
Q99V48_STAAM	>gnl|tr|Q99V48_STAAM (Q99V48) Naphthoate synthase		x		
Q43GZ6_9CHLB	>gnl|tr|Q43GZ6_9CHLB (Q43GZ6) Naphthoate synthase		x		
Q2YX28_STAAB	>gnl|tr|Q2YX28_STAAB (Q2YX28) Naphthoate synthase (EC 4.1.3.36)		x		
Q49WG8_STAS1	>gnl|tr|Q49WG8_STAS1 (Q49WG8) Dihydroxynaphthoic acid synthase		x		
Q71YZ4_LISMF	>gnl|tr|Q71YZ4_LISMF (Q71YZ4) Naphthoate synthase		x		
Q4EQ39_LISMO	>gnl|tr|Q4EQ39_LISMO (Q4EQ39) Naphthoate synthase		x		
Q4EGC9_LISMO	>gnl|tr|Q4EGC9_LISMO (Q4EGC9) Naphthoate synthase		x		
Q5N3K4_SYNP6	>gnl|tr|Q5N3K4_SYNP6 (Q5N3K4) Naphthoate synthase		x		

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q5HQC3_STAEQ	>gnl|tr|Q5HQC3_STAEQ (Q5HQC3) Naphthoate synthase (EC 4.1.3.36)		x		
Q8NT47_CORGL	>gnl|tr|Q8NT47_CORGL (Q8NT47) Dihydroxynaphthoic acid synthase (EC 4.1.3.36) (DIHYDROXYNAPHTHONIC ACID SYNTHASE)		x		
Q8CPQ4_STAES	>gnl|tr|Q8CPQ4_STAES (Q8CPQ4) Naphthoate synthase		x		
Q3DZE4_CHLAU	>gnl|tr|Q3DZE4_CHLAU (Q3DZE4) Naphthoate synthase		x		
Q31QP0_SYNP7	>gnl|tr|Q31QP0_SYNP7 (Q31QP0) Naphthoate synthase		x		
Q5V3S9_HALMA	>gnl|tr|Q5V3S9_HALMA (Q5V3S9) Enoyl-CoA hydratase (EC 4.2.1.17)		x		
Q8FSB9_COREF	>gnl|tr|Q8FSB9_COREF (Q8FSB9) Putative naphthoate synthase		x		
Q46LU2_PROMT	>gnl|tr|Q46LU2_PROMT (Q46LU2) Naphthoate synthase		x		
Q7V8E8_PROMM	>gnl|tr|Q7V8E8_PROMM (Q7V8E8) Naphthoate synthase (EC 4.1.3.36)		x		
Q7U7I4_SYNPX	>gnl|tr|Q7U7I4_SYNPX (Q7U7I4) Naphthoate synthase (EC 4.1.3.36)		x		
Q3AVF7_SYNS9	>gnl|tr|Q3AVF7_SYNS9 (Q3AVF7) Naphthoate synthase		x		
Q47Q22_THEFY	>gnl|tr|Q47Q22_THEFY (Q47Q22) Naphthoate synthase		x		
O06414_MYCTU	>gnl|tr|O06414_MYCTU (O06414) PROBABLE NAPHTHOATE SYNTHASE MENB (DIHYDROXYNAPHTHOIC ACID SYNTHETASE) (DHNA SYNTHETASE) (EC 4.1.3.36) (Naphthoate synthase)		x		
Q7U1T0_MYCBO	>gnl|tr|Q7U1T0_MYCBO (Q7U1T0) PROBABLE NAPHTHOATE SYNTHASE MENB (DIHYDROXYNAPHTHOIC ACID SYNTHETASE) (DHNA SYNTHETASE) (EC 4.1.3.36)		x		
Q3AKK2_SYNSC	>gnl|tr|Q3AKK2_SYNSC (Q3AKK2) Naphthoate synthase		x		
Q838K2_ENTFA	>gnl|tr|Q838K2_ENTFA (Q838K2) Naphthoate synthase		x		
Q7V276_PROMP	>gnl|tr|Q7V276_PROMP (Q7V276) Napthoate synthase (EC 4.1.3.36)		x		
Q59464_HAEPH	>gnl|tr|Q59464_HAEPH (Q59464) Naphthoate synthase (EC 4.1.3.36) (Fragment)		x		
Q3Q0N0_9GAMM	>gnl|tr|Q3Q0N0_9GAMM (Q3Q0N0) Naphthoate synthase		x		
Q7VBN9_PROMA	>gnl|tr|Q7VBN9_PROMA (Q7VBN9) Dihydroxynaphthoic acid synthase		x		
Q9HQN4_HALSA	>gnl|tr|Q9HQN4_HALSA (Q9HQN4) Dihydroxynaphthoic acid synthase		x		
Q4JT07_CORJK	>gnl|tr|Q4JT07_CORJK (Q4JT07) Naphthoate synthase (EC 4.1.3.36)		x		

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q5LFS3_BACFN	>gnl|tr|Q5LFS3_BACFN (Q5LFS3) Putative naphthoate synthase (EC 4.1.3.36)		x		
Q64WQ8_BACFR	>gnl|tr|Q64WQ8_BACFR (Q64WQ8) Dihydroxynapthoic acid synthetase		x		
Q31BS6_PROM9	>gnl|tr|Q31BS6_PROM9 (Q31BS6) Naphthoate synthase		x		
Q89YM9_BACTN	>gnl|tr|Q89YM9_BACTN (Q89YM9) Dihydroxynapthoic acid synthetase		x		
Q3H1V1_9ACTO	>gnl|tr|Q3H1V1_9ACTO (Q3H1V1) Naphthoate synthase		x		
Q6MHP8_BDEBA	>gnl|tr|Q6MHP8_BDEBA (Q6MHP8) Naphthoate synthase		x		
Q83GX0_TROWT	>gnl|tr|Q83GX0_TROWT (Q83GX0) Naphthoate synthase (EC 4.1.3.36)		x		
Q83IB8_TROW8	>gnl|tr|Q83IB8_TROW8 (Q83IB8) Naphthoate synthase (EC 4.1.3.36)		x		
Q3NKX7_SHEFR	>gnl|tr|Q3NKX7_SHEFR (Q3NKX7) Naphthoate synthase		x		
Q2ZUS8_SHEPU	>gnl|tr|Q2ZUS8_SHEPU (Q2ZUS8) Naphthoate synthase		x		
Q2X1G3_9GAMM	>gnl|tr|Q2X1G3_9GAMM (Q2X1G3) Naphthoate synthase		x		
Q6AHC7_LEIXX	>gnl|tr|Q6AHC7_LEIXX (Q6AHC7) Naphthoate synthase		x		
Q8E8C7_SHEON	>gnl|tr|Q8E8C7_SHEON (Q8E8C7) Naphthoate synthase		x		
Q366R3_9GAMM	>gnl|tr|Q366R3_9GAMM (Q366R3) Naphthoate synthase		x		
Q35V57_9GAMM	>gnl|tr|Q35V57_9GAMM (Q35V57) Naphthoate synthase		x		
Q33SG7_9GAMM	>gnl|tr|Q33SG7_9GAMM (Q33SG7) Naphthoate synthase		x		
Q3QCE2_9GAMM	>gnl|tr|Q3QCE2_9GAMM (Q3QCE2) Naphthoate synthase		x		
Q9CBB5_MYCLE	>gnl|tr|Q9CBB5_MYCLE (Q9CBB5) Naphthoate synthase		x		
Q5YPA1_NOCFA	>gnl|tr|Q5YPA1_NOCFA (Q5YPA1) Putative dihydroxynaphtoic acid synthetase		x		
Q6NJI0_CORDI	>gnl|tr|Q6NJI0_CORDI (Q6NJI0) Putative naphthoate synthase		x		
Q2Z4E1_9GAMM	>gnl|tr|Q2Z4E1_9GAMM (Q2Z4E1) Naphthoate synthase		x		
Q6ARP4_DESPS	>gnl|tr|Q6ARP4_DESPS (Q6ARP4) Probable naphthoate synthase (MenB)		x		
Q2RYX3_9SPHI	>gnl|tr|Q2RYX3_9SPHI (Q2RYX3) Naphthoate synthase (EC 4.1.3.36)		x		
Q47FL7_DECAR	>gnl|tr|Q47FL7_DECAR (Q47FL7) Naphthoate synthase		x		
Q3IQY8_NATPD	>gnl|tr|Q3IQY8_NATPD (Q3IQY8) Naphthoate synthase (EC 4.1.3.36) (EC 4.1.3.36)		x		
Q7MUJ0_PORGI	>gnl|tr|Q7MUJ0_PORGI (Q7MUJ0) Naphthoate synthase		x		

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>Q85G05_CYAME</td><td>>gnl|tr|Q85G05_CYAME (Q85G05) Naphthoate synthase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q3X033_9ACTN</td><td>>gnl|tr|Q3X033_9ACTN (Q3X033) Naphthoate synthase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q4NDX0_9MICC</td><td>>gnl|tr|Q4NDX0_9MICC (Q4NDX0) Naphthoate synthase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q2PQY7_9NOCA</td><td>>gnl|tr|Q2PQY7_9NOCA (Q2PQY7) Naphthoate synthase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q6A9A6_PROAC</td><td>>gnl|tr|Q6A9A6_PROAC (Q6A9A6) Naphthoate synthase MenB (EC 4.1.3.36)</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q6J674_9BURK</td><td>>gnl|tr|Q6J674_9BURK (Q6J674) L-alanine-DL-glutamate epimerase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q4ZUZ0_PSEU2</td><td>>gnl|tr|Q4ZUZ0_PSEU2 (Q4ZUZ0) Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q4LU69_9BURK</td><td>>gnl|tr|Q4LU69_9BURK (Q4LU69) Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q3FIX4_9BURK</td><td>>gnl|tr|Q3FIX4_9BURK (Q3FIX4) Mandelate racemase/muconate lactonizing enzyme</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q4B9K4_BURVI</td><td>>gnl|tr|Q4B9K4_BURVI (Q4B9K4) Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q3K8P4_PSEPF</td><td>>gnl|tr|Q3K8P4_PSEPF (Q3K8P4) Mandelate racemase/muconate lactonizing enzyme</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q3FLD4_9BURK</td><td>>gnl|tr|Q3FLD4_9BURK (Q3FLD4) Mandelate racemase/muconate lactonizing enzyme</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q4IU35_AZOVI</td><td>>gnl|tr|Q4IU35_AZOVI (Q4IU35) Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q44TM9_9BURK</td><td>>gnl|tr|Q44TM9_9BURK (Q44TM9) Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q8P9V1_XANCP</td><td>>gnl|tr|Q8P9V1_XANCP (Q8P9V1) 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-deoxyphosphogluconate aldolase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q4UTT5_XANC8</td><td>>gnl|tr|Q4UTT5_XANC8 (Q4UTT5) 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-deoxyphosphogluconate aldolase</td><td></td><td>x</td><td></td><td></td></tr>
</table>

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q4H5S5_9DEIO	>gnl|tr|Q4H5S5_9DEIO (Q4H5S5) Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme		x		
Q2P1Q3_XANOR	>gnl|tr|Q2P1Q3_XANOR (Q2P1Q3) 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-deoxyphosphogluconate aldolase		x		
Q5GYP8_XANOR	>gnl|tr|Q5GYP8_XANOR (Q5GYP8) 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-deoxyphosphogluconate aldolase		x		
Q8PLN0_XANAC	>gnl|tr|Q8PLN0_XANAC (Q8PLN0) 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-deoxyphosphogluconate aldolase		x		
Q5KBM5_CRYNE	>gnl|tr|Q5KBM5_CRYNE (Q5KBM5) Mandelate racemase/muconate lactonizing enzyme, putative		x		
Q39NI3_BURS3	>gnl|tr|Q39NI3_BURS3 (Q39NI3) Mandelate racemase/muconate lactonizing enzyme (EC 4.1.2.21)		x		
Q44CR8_CHRSL	>gnl|tr|Q44CR8_CHRSL (Q44CR8) Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme		x		
Q9RKG2_STRCO	>gnl|tr|Q9RKG2_STRCO (Q9RKG2) Putative isomerase		x		
Q3K9U5_PSEPF	>gnl|tr|Q3K9U5_PSEPF (Q3K9U5) Mandelate racemase/muconate lactonizing enzyme		x		
Q4BD61_BURVI	>gnl|tr|Q4BD61_BURVI (Q4BD61) Mandelate racemase/muconate lactonizing enzyme		x		
Q453Y0_9BURK	>gnl|tr|Q453Y0_9BURK (Q453Y0) Mandelate racemase/muconate lactonizing enzyme		x		
Q4LT53_9BURK	>gnl|tr|Q4LT53_9BURK (Q4LT53) Mandelate racemase/muconate lactonizing enzyme		x		
Q3FEL8_9BURK	>gnl|tr|Q3FEL8_9BURK (Q3FEL8) Mandelate racemase/muconate lactonizing enzyme		x		
Q43QN0_SOLUS	>gnl|tr|Q43QN0_SOLUS (Q43QN0) Mandelate racemase/muconate lactonizing enzyme		x		
Q6LNX5_PHOPR	>gnl|tr|Q6LNX5_PHOPR (Q6LNX5) Putative o-succinylbenzoate-CoA synthase		x		
Q8FSB7_COREF	>gnl|tr|Q8FSB7_COREF (Q8FSB7) Putative muconate cycloisomerase		x		

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q6D7W1_ERWCT	>gnl|tr|Q6D7W1_ERWCT (Q6D7W1) O-succinylbenzoate-CoA synthase (EC 4.2.1.-)		x		
Q669D0_YERPS	>gnl|tr|Q669D0_YERPS (Q669D0) Putative O-succinylbenzoate-CoA synthase (EC 4.2.1.-)		x		
Q87R66_VIBPA	>gnl|tr|Q87R66_VIBPA (Q87R66) O-succinylbenzoate-CoA synthase		x		
Q8E8T2_SHEON	>gnl|tr|Q8E8T2_SHEON (Q8E8T2) O-succinylbenzoate-CoA synthase		x		
Q32DS7_SHIDS	>gnl|tr|Q32DS7_SHIDS (Q32DS7) O-succinylbenzoyl-CoA synthase		x		
Q3YZU5_SHISS	>gnl|tr|Q3YZU5_SHISS (Q3YZU5) O-succinylbenzoyl-CoA synthase		x		
Q8FFL4_ECOL6	>gnl|tr|Q8FFL4_ECOL6 (Q8FFL4) O-succinylbenzoate-CoA synthase (EC 4.2.1.-)		x		
Q83QT6_SHIFL	>gnl|tr|Q83QT6_SHIFL (Q83QT6) O-succinylbenzoyl-CoA synthase		x		
Q57M50_SALCH	>gnl|tr|Q57M50_SALCH (Q57M50) O-succinylbenzoyl-CoA synthase		x		
Q31YJ6_SHIBS	>gnl|tr|Q31YJ6_SHIBS (Q31YJ6) O-succinylbenzoyl-CoA synthase		x		
Q5PN73_SALPA	>gnl|tr|Q5PN73_SALPA (Q5PN73) O-succinylbenzoate-CoA synthase		x		
Q7VMC8_HAEDU	>gnl|tr|Q7VMC8_HAEDU (Q7VMC8) O-succinylbenzoate-CoA synthase		x		
Q41ZA1_DESHA	>gnl|tr|Q41ZA1_DESHA (Q41ZA1) Mandelate racemase/muconate lactonizing enzyme		x		
Q9CHK4_LACLA	>gnl|tr|Q9CHK4_LACLA (Q9CHK4) Racemase		x		
Q6AHC8_LEIXX	>gnl|tr|Q6AHC8_LEIXX (Q6AHC8) O-succinylbenzoate-CoA synthase		x		
Q2Z6R9_9GAMM	>gnl|tr|Q2Z6R9_9GAMM (Q2Z6R9) O-succinylbenzoate-CoA synthase		x		
Q36H56_9GAMM	>gnl|tr|Q36H56_9GAMM (Q36H56) O-succinylbenzoate-CoA synthase		x		
Q41F59_9BACI	>gnl|tr|Q41F59_9BACI (Q41F59) Mandelate racemase/muconate lactonizing enzyme		x		
Q361H8_9GAMM	>gnl|tr|Q361H8_9GAMM (Q361H8) O-succinylbenzoate-CoA synthase		x		
Q8KBE1_CHLTE	>gnl|tr|Q8KBE1_CHLTE (Q8KBE1) O-succinylbenzoate-CoA synthase (EC 5.3.99.-)		x		
Q6A9B1_PROAC	>gnl|tr|Q6A9B1_PROAC (Q6A9B1) O-succinylbenzoate-CoA synthase (EC 4.2.1.-)		x		
Q47Q21_THEFY	>gnl|tr|Q47Q21_THEFY (Q47Q21) O-succinylbenzoate-CoA synthase		x		
Q6NJH9_CORDI	>gnl|tr|Q6NJH9_CORDI (Q6NJH9) Putative O-succinylbenzoate-CoA synthase		x		
Q89YM8_BACTN	>gnl|tr|Q89YM8_BACTN (Q89YM8) Chloromuconate cycloisomerase		x		

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>Q414A6_KINRA</td><td>>gnl|tr|Q414A6_KINRA (Q414A6) Mandelate racemase/muconate lactonizing enzyme</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q4NDM1_9MICC</td><td>>gnl|tr|Q4NDM1_9MICC (Q4NDM1) Mandelate racemase/muconate lactonizing enzyme</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q3X032_9ACTN</td><td>>gnl|tr|Q3X032_9ACTN (Q3X032) Mandelate racemase/muconate lactonizing enzyme</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q7VE14_PROMA</td><td>>gnl|tr|Q7VE14_PROMA (Q7VE14) O-succinylbenzoate-CoA synthase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q2ZRD0_SHEPU</td><td>>gnl|tr|Q2ZRD0_SHEPU (Q2ZRD0) O-succinylbenzoate-CoA synthase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q3Q5F5_9GAMM</td><td>>gnl|tr|Q3Q5F5_9GAMM (Q3Q5F5) O-succinylbenzoate-CoA synthase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q2X3S4_9GAMM</td><td>>gnl|tr|Q2X3S4_9GAMM (Q2X3S4) O-succinylbenzoate-CoA synthase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q5LFS2_BACFN</td><td>>gnl|tr|Q5LFS2_BACFN (Q5LFS2) Putative muconate cycloisomerase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q47FL8_DECAR</td><td>>gnl|tr|Q47FL8_DECAR (Q47FL8) Mandelate racemase/muconate lactonizing enzyme</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q64WQ7_BACFR</td><td>>gnl|tr|Q64WQ7_BACFR (Q64WQ7) Chloromuconate cycloisomerase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q3GT94_9ACTO</td><td>>gnl|tr|Q3GT94_9ACTO (Q3GT94) Mandelate racemase/muconate lactonizing enzyme precursor</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q3DWV9_CHLAU</td><td>>gnl|tr|Q3DWV9_CHLAU (Q3DWV9) Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q98LZ8_RHILO</td><td>>gnl|tr|Q98LZ8_RHILO (Q98LZ8) Probable muconate cycloisomerase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q3WX47_9RHIZ</td><td>>gnl|tr|Q3WX47_9RHIZ (Q3WX47) Mandelate racemase/muconate lactonizing enzyme</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q6D2H9_ERWCT</td><td>>gnl|tr|Q6D2H9_ERWCT (Q6D2H9) Putative mandelate racemase/muconate lactonizing enzyme</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q2YQ53_BRUA2</td><td>>gnl|tr|Q2YQ53_BRUA2 (Q2YQ53) Mandelate racemase/muconate lactonizing enzyme</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>Q8YH38_BRUME</td><td>>gnl|tr|Q8YH38_BRUME (Q8YH38) MUCONATE CYCLOISOMERASE I (EC 5.5.1.1)</td><td></td><td>x</td><td></td><td></td></tr>
</table>

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q6N2T4_RHOPA	>gnl|tr|Q6N2T4_RHOPA (Q6N2T4) Putative muconate cycloisomerase (EC 5.5.1.1)		x		
Q3PSS2_NITHA	>gnl|tr|Q3PSS2_NITHA (Q3PSS2) Mandelate racemase/muconate lactonizing enzyme		x		
Q3J5L8_RHOS4	>gnl|tr|Q3J5L8_RHOS4 (Q3J5L8) Mandelate racemase / muconate lactonizing enzyme (EC 5.1.2.2) (EC 5.5.1.1)		x		
Q343J3_RHOPA	>gnl|tr|Q343J3_RHOPA (Q343J3) Mandelate racemase/muconate lactonizing enzyme		x		
Q8Z7A7_SALTI	>gnl|tr|Q8Z7A7_SALTI (Q8Z7A7) Putative mandelate racemase		x		
Q34S34_RHOPA	>gnl|tr|Q34S34_RHOPA (Q34S34) Putative muconate cycloisomerase		x		
Q8EM93_OCEIH	>gnl|tr|Q8EM93_OCEIH (Q8EM93) Muconate cycloisomerase		x		
Q57NY1_SALCH	>gnl|tr|Q57NY1_SALCH (Q57NY1) Putative chloromuconate cycloisomerase (Muconate cycloisomerase)		x		
Q8ZP66_SALTY	>gnl|tr|Q8ZP66_SALTY (Q8ZP66) Putative chloromuconate cycloisomerase (EC 5.5.-.-)		x		
Q83LB1_SHIFL	>gnl|tr|Q83LB1_SHIFL (Q83LB1) Putative muconate cycloisomerase I		x		
Q32GK8_SHIDS	>gnl|tr|Q32GK8_SHIDS (Q32GK8) Putative muconate cycloisomerase I (EC 5.5.-.-)		x		
Q7AEG8_ECO57	>gnl|tr|Q7AEG8_ECO57 (Q7AEG8) Putative muconate cycloisomerase I		x		
Q37J85_RHOPA	>gnl|tr|Q37J85_RHOPA (Q37J85) Mandelate racemase/muconate lactonizing enzyme		x		
Q8RIK3_FUSNN	>gnl|tr|Q8RIK3_FUSNN (Q8RIK3) O-succinylbenzoate-CoA synthase		x		
Q8X8L8_ECO57	>gnl|tr|Q8X8L8_ECO57 (Q8X8L8) Putative muconate cycloisomerase I (EC 5.5.-.-)		x		
Q66A72_YERPS	>gnl|tr|Q66A72_YERPS (Q66A72) Putative mandelate racemase / muconate lactonizing protein		x		
Q8ZE43_YERPE	>gnl|tr|Q8ZE43_YERPE (Q8ZE43) Putative mandelate racemase / muconate lactonizing protein (Putative muconate cycloisomerase I) (EC 5.5.-.-)		x		

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q2RR89_RHORU	>gnl|tr|Q2RR89_RHORU (Q2RR89) Mandelate racemase/muconate lactonizing enzyme (EC 5.5.1.1)		x		
Q3STP4_NITWN	>gnl|tr|Q3STP4_NITWN (Q3STP4) Mandelate racemase/muconate lactonizing enzyme (EC 5.5.1.1)		x		
Q37AH7_RHOPA	>gnl|tr|Q37AH7_RHOPA (Q37AH7) IMP dehydrogenase/GMP reductase:Mandelate racemase/muconate lactonizing enzyme		x		
Q5PHP6_SALPA	>gnl|tr|Q5PHP6_SALPA (Q5PHP6) Putative mandelate racemase		x		
Q8PFW0_XANAC	>gnl|tr|Q8PFW0_XANAC (Q8PFW0) Chloromuconate cycloisomerase		x		
Q6LQX4_PHOPR	>gnl|tr|Q6LQX4_PHOPR (Q6LQX4) Hypothetical muconate cycloisomerase I		x		
Q97MK4_CLOAB	>gnl|tr|Q97MK4_CLOAB (Q97MK4) Similar to chloromuconate cycloisomerase		x		
Q9HP25_HALSA	>gnl|tr|Q9HP25_HALSA (Q9HP25) Chloromuconate cycloisomerase		x		
Q8P4A3_XANCP	>gnl|tr|Q8P4A3_XANCP (Q8P4A3) Chloromuconate cycloisomerase		x		
Q3BNF2_XANC5	>gnl|tr|Q3BNF2_XANC5 (Q3BNF2) Putative chloromuconate cycloisomerase (EC 5.5.1.7)		x		
Q87JC4_VIBPA	>gnl|tr|Q87JC4_VIBPA (Q87JC4) Putative muconate cycloisomerase I		x		
Q63AA0_BACCZ	>gnl|tr|Q63AA0_BACCZ (Q63AA0) Mandelate racemase/muconate lactonizing enzyme (EC 5.1.2.2)		x		
Q8YRB6_ANASP	>gnl|tr|Q8YRB6_ANASP (Q8YRB6) Muconate cycloisomerase		x		
Q4UPV4_XANC8	>gnl|tr|Q4UPV4_XANC8 (Q4UPV4) Chloromuconate cycloisomerase		x		
Q3WTQ1_9RHIZ	>gnl|tr|Q3WTQ1_9RHIZ (Q3WTQ1) Mandelate racemase/muconate lactonizing enzyme		x		
Q3M7B7_ANAVT	>gnl|tr|Q3M7B7_ANAVT (Q3M7B7) Mandelate racemase/muconate lactonizing enzyme (EC 5.5.1.1)		x		
Q3QRU3_9RHOB	>gnl|tr|Q3QRU3_9RHOB (Q3QRU3) Mandelate racemase/muconate lactonizing enzyme		x		
Q7UMP9_RHOBA	>gnl|tr|Q7UMP9_RHOBA (Q7UMP9) Chloromuconate cycloisomerase YkfB1 (EC 5.5.1.7)		x		
Q320B2_SHIBS	>gnl|tr|Q320B2_SHIBS (Q320B2) Putative muconate cycloisomerase I (EC 5.5.-.-)		x		

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q6HHP1_BACHK	>gnl|tr|Q6HHP1_BACHK (Q6HHP1) Mandelate racemase/muconate lactonizing enzyme (EC 5.1.2.2)		x		
Q5GVB7_XANOR	>gnl|tr|Q5GVB7_XANOR (Q5GVB7) Chloromuconate cycloisomerase		x		
Q2NYJ4_XANOR	>gnl|tr|Q2NYJ4_XANOR (Q2NYJ4) Chloromuconate cycloisomerase		x		
Q39HW9_BURS3	>gnl|tr|Q39HW9_BURS3 (Q39HW9) Mandelate racemase/muconate lactonizing enzyme (EC 5.5.1.1)		x		
Q9K8K0_BACHD	>gnl|tr|Q9K8K0_BACHD (Q9K8K0) Muconate cycloisomerase		x		
Q40FR6_9RHOB	>gnl|tr|Q40FR6_9RHOB (Q40FR6) Mandelate racemase/muconate lactonizing enzyme		x		
Q3CAC9_9CLOT	>gnl|tr|Q3CAC9_9CLOT (Q3CAC9) Mandelate racemase/muconate lactonizing enzyme		x		
Q3Z170_SHISS	>gnl|tr|Q3Z170_SHISS (Q3Z170) Putative muconate cycloisomerase I (EC 5.5.-.-)		x		
Q3X528_9ACTN	>gnl|tr|Q3X528_9ACTN (Q3X528) Mandelate racemase/muconate lactonizing enzyme		x		
Q3CS75_ALTAT	>gnl|tr|Q3CS75_ALTAT (Q3CS75) Mandelate racemase/muconate lactonizing enzyme		x		
Q5NN58_ZYMMO	>gnl|tr|Q5NN58_ZYMMO (Q5NN58) Mandelate racemase (EC 5.1.2.2)		x		
Q3V963_9SPHN	>gnl|tr|Q3V963_9SPHN (Q3V963) Mandelate racemase/muconate lactonizing enzyme		x		
Q5UX71_HALMA	>gnl|tr|Q5UX71_HALMA (Q5UX71) Chloromuconate cycloisomerase		x		
Q5KMP0_CRYNE	>gnl|tr|Q5KMP0_CRYNE (Q5KMP0) Mandelate racemase/muconate lactonizing enzyme, putative		x		
Q399X5_BURS3	>gnl|tr|Q399X5_BURS3 (Q399X5) Mandelate racemase/muconate lactonizing enzyme (EC 5.1.2.2)		x		
Q3F714_9BURK	>gnl|tr|Q3F714_9BURK (Q3F714) Mandelate racemase/muconate lactonizing enzyme		x		
Q4LV88_9BURK	>gnl|tr|Q4LV88_9BURK (Q4LV88) Mandelate racemase/muconate lactonizing enzyme		x		
Q45D30_9BURK	>gnl|tr|Q45D30_9BURK (Q45D30) Mandelate racemase/muconate lactonizing enzyme		x		

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q8CKY6_YERPE	>gnl|tr|Q8CKY6_YERPE (Q8CKY6) Hypothetical (O-succinylbenzoate synthase and related enzymes)		x		
Q8YF20_BRUME	>gnl|tr|Q8YF20_BRUME (Q8YF20) MANDELATE RACEMASE (EC 5.1.2.2)		x		
Q2YP88_BRUA2	>gnl|tr|Q2YP88_BRUA2 (Q2YP88) Mandelate racemase/muconate lactonizing enzyme		x		
Q4BQW7_BURVI	>gnl|tr|Q4BQW7_BURVI (Q4BQW7) Mandelate racemase/muconate lactonizing enzyme		x		
Q4AT53_9BURK	>gnl|tr|Q4AT53_9BURK (Q4AT53) Mandelate racemase/muconate lactonizing enzyme		x		
Q3FWV8_9BURK	>gnl|tr|Q3FWV8_9BURK (Q3FWV8) Mandelate racemase/muconate lactonizing enzyme		x		
Q826B1_STRAW	>gnl|tr|Q826B1_STRAW (Q826B1) Putative mandelate racemase		x		
Q3WZU8_9ACTN	>gnl|tr|Q3WZU8_9ACTN (Q3WZU8) Mandelate racemase/muconate lactonizing enzyme		x		
Q44H55_CHRSL	>gnl|tr|Q44H55_CHRSL (Q44H55) Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme		x		
Q3BMJ5_XANC5	>gnl|tr|Q3BMJ5_XANC5 (Q3BMJ5) Putative mandelate racemase/muconate lactonizing enzyme		x		
Q40ZX4_KINRA	>gnl|tr|Q40ZX4_KINRA (Q40ZX4) Mandelate racemase/muconate lactonizing enzyme		x		
Q7WSS0_9MICC	>gnl|tr|Q7WSS0_9MICC (Q7WSS0) Putative mandelate racemase/muconate lactonizing enzyme		x		
Q3QRA6_9RHOB	>gnl|tr|Q3QRA6_9RHOB (Q3QRA6) Mandelate racemase/muconate lactonizing enzyme		x		
Q8ZFW0_YERPE	>gnl|tr|Q8ZFW0_YERPE (Q8ZFW0) Putative racemase		x		
Q66C33_YERPS	>gnl|tr|Q66C33_YERPS (Q66C33) Putative racemase		x		
Q40A42_9RHOB	>gnl|tr|Q40A42_9RHOB (Q40A42) Mandelate racemase/muconate lactonizing enzyme		x		
Q4NKQ5_9MICC	>gnl|tr|Q4NKQ5_9MICC (Q4NKQ5) Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme		x		

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q44FW6_CHRSL	>gnl|tr|Q44FW6_CHRSL (Q44FW6) Mandelate racemase/muconate lactonizing enzyme		x		
Q8TJL6_METAC	>gnl|tr|Q8TJL6_METAC (Q8TJL6) Acylneuraminate cytidylyltransferase		x		
Q5P479_AZOSE	>gnl|tr|Q5P479_AZOSE (Q5P479) Phenylphosphate carboxylase, gamma subunit		x		
Q8D3M6_VIBVU	>gnl|tr|Q8D3M6_VIBVU (Q8D3M6) Predicted phosphatase/phosphohexomutase		x		
Q7ZAP3_SALTY	>gnl|tr|Q7ZAP3_SALTY (Q7ZAP3) 2-aminoethylphosphonate transport (EC 3.1.3.18)		x		
Q57SD2_SALCH	>gnl|tr|Q57SD2_SALCH (Q57SD2) 2-aminoethylphosphonate transport		x		
Q7DI63_COMAC	>gnl|tr|Q7DI63_COMAC (Q7DI63) Haloacetate dehalogenase H-2		x		
Q40NU8_DESAC	>gnl|tr|Q40NU8_DESAC (Q40NU8) IMP dehydrogenase/GMP reductase:Amidohydrolase	x			
Q8ZJZ8_SALTY	>gnl|tr|Q8ZJZ8_SALTY (Q8ZJZ8) Isoaspartyl dipeptidase (EC 3.4.19.5)	x			
P75019_MYCTU	>gnl|tr|P75019_MYCTU (P75019) POSSIBLE ENOYL-CoA HYDRATASE ECHA21 (ENOYL HYDRASE) (UNSATURATED ACYL-CoA HYDRATASE) (CROTONASE) (EC 4.2.1.17) (Enoyl-CoA hydratase/isomerase family protein) (Enoyl-CoA hydratase)	x			
Q8XZU7_RALSO	>gnl|tr|Q8XZU7_RALSO (Q8XZU7) PROBABLE ENOYL(3-HYDROXYISOBUTYRYL)-COENZYME A HYDRATASE PROTEIN (EC 4.2.1.17)	x			
Q8ES26_OCEIH	>gnl|tr|Q8ES26_OCEIH (Q8ES26) Enoyl-CoA hydratase (3-hydroxybutyryl-CoA dehydratase) (EC 4.2.1.17)	x			
Q63BK8_BACCZ	>gnl|tr|Q63BK8_BACCZ (Q63BK8) 3-hydroxyisobutyryl-coenzyme A hydrolase (EC 4.2.1.17)	x			
Q6HJ17_BACHK	>gnl|tr|Q6HJ17_BACHK (Q6HJ17) 3-hydroxyisobutyryl-coenzyme A hydrolase (EC 4.2.1.17)	x			
Q5ZX62_LEGPH	>gnl|tr|Q5ZX62_LEGPH (Q5ZX62) 3-hydroxyisobutyryl Coenzyme A hydrolase (EC 4.2.1.17)	x			

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>Q8LR33_ORYSA</td><td>>gnl|tr|Q8LR33_ORYSA (Q8LR33) Putative naphthoate synthase menB</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>Q65FT4_BACLD</td><td>>gnl|tr|Q65FT4_BACLD (Q65FT4) MenB (Dihydroxynapthoic acid synthetase)</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>Q6MCB1_PARUW</td><td>>gnl|tr|Q6MCB1_PARUW (Q6MCB1) Probable naphthoate synthase, menB</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>Q39D78_BURS3</td><td>>gnl|tr|Q39D78_BURS3 (Q39D78) Mandelate racemase/muconate lactonizing enzyme (EC 4.2.1.6)</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>Q6CYT9_ERWCT</td><td>>gnl|tr|Q6CYT9_ERWCT (Q6CYT9) DgoA protein (EC 4.1.2.21) [Includes: 2-dehydro-3-deoxyphosphogalactonate aldolase; galactonate dehydratase]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>Q65DI1_BACLD</td><td>>gnl|tr|Q65DI1_BACLD (Q65DI1) Hypothetical protein (EC 4.2.1.6) (Mandelate racemase/muconate lactonizing enzyme,Mandelate racemase/muconate lactonizing enzyme)</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>Q8ZKZ1_SALTY</td><td>>gnl|tr|Q8ZKZ1_SALTY (Q8ZKZ1) Galactonate dehydratase (EC 4.1.2.21) (EC 4.2.1.6)</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>Q39I44_BURS3</td><td>>gnl|tr|Q39I44_BURS3 (Q39I44) Mandelate racemase/muconate lactonizing enzyme (EC 4.2.1.40)</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>Q7N2K6_PHOLL</td><td>>gnl|tr|Q7N2K6_PHOLL (Q7N2K6) O-succinylbenzoate-CoA synthase (OSB synthase) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase)</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>Q65FT6_BACLD</td><td>>gnl|tr|Q65FT6_BACLD (Q65FT6) MenC (O-succinylbenzoate-CoA synthase)</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>Q8G0R9_BRUSU</td><td>>gnl|tr|Q8G0R9_BRUSU (Q8G0R9) Mandelate racemase/muconate lactonizing enzyme family protein (EC 5.5.1.7)</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>Q65KW2_BACLD</td><td>>gnl|tr|Q65KW2_BACLD (Q65KW2) YkfB (Putative muconate cycloisomerase)</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>Q37R07_SPHAR</td><td>>gnl|tr|Q37R07_SPHAR (Q37R07) Mandelate racemase/muconate lactonizing enzyme</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>Q3KDT8_PSEPF</td><td>>gnl|tr|Q3KDT8_PSEPF (Q3KDT8) Mandelate racemase/muconate lactonizing enzyme</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>Q46SY2_RALEJ</td><td>>gnl|tr|Q46SY2_RALEJ (Q46SY2) Mandelate racemase/muconate lactonizing enzyme</td><td>x</td><td></td><td></td><td></td></tr>
</table>

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>Q3RUY7_RALME</td><td>>gnl|tr|Q3RUY7_RALME (Q3RUY7) Mandelate racemase/muconate lactonizing enzyme</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>Q3KC01_PSEPF</td><td>>gnl|tr|Q3KC01_PSEPF (Q3KC01) Mandelate racemase/muconate lactonizing enzyme</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>Q470X9_RALEJ</td><td>>gnl|tr|Q470X9_RALEJ (Q470X9) Mandelate racemase/muconate lactonizing enzyme</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>Q39N77_BURS3</td><td>>gnl|tr|Q39N77_BURS3 (Q39N77) Mandelate racemase/muconate lactonizing enzyme (EC 5.5.1.1)</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>Q3F8J8_9BURK</td><td>>gnl|tr|Q3F8J8_9BURK (Q3F8J8) Mandelate racemase/muconate lactonizing enzyme</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>Q3FGJ2_9BURK</td><td>>gnl|tr|Q3FGJ2_9BURK (Q3FGJ2) Mandelate racemase/muconate lactonizing enzyme</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>Q4BGR5_BURVI</td><td>>gnl|tr|Q4BGR5_BURVI (Q4BGR5) Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>Q35PU6_9BRAD</td><td>>gnl|tr|Q35PU6_9BRAD (Q35PU6) Haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2:HAD-superfamily hydrolase, subfamily IA, variant 1 (EC 3.8.1.2)</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>Q8RBL4_THETN</td><td>>gnl|tr|Q8RBL4_THETN (Q8RBL4) Predicted phosphatase/phosphohexomutase</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>Q65MW1_BACLD</td><td>>gnl|tr|Q65MW1_BACLD (Q65MW1) PgcM (Beta-phosphoglucomutase and glucose-1-phosphate phosphodismutase)</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td></td></tr>
</table>

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q83AM7_COXBU	>gnl|tr|Q83AM7_COXBU (Q83AM7) Enoyl-CoA hydratase/isomerase family protein				
Q36P54_MARHY	>gnl|tr|Q36P54_MARHY (Q36P54) Enoyl-CoA hydratase/isomerase family protein				

Table L-2. UniProtKB/TrEMBL Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
Q65UR4_MANSM	>gnl|tr|Q65UR4_MANSM (Q65UR4) DgoA protein				
Q72YL0_BACC1	>gnl|tr|Q72YL0_BACC1 (Q72YL0) N-acylamino acid racemase				
Q4EMY8_LISMO	>gnl|tr|Q4EMY8_LISMO (Q4EMY8) N-acylamino acid racemase				
Q71WQ8_LISMF	>gnl|tr|Q71WQ8_LISMF (Q71WQ8) N-acylamino acid racemase				

L.3. Table L-3. KEGG Data (Chapter 3)

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
aci:ACIAD1446	>gnl|kg|aci:ACIAD1446 catB; muconate cycloisomerase I (cis,cis-muconate lactonizing enzyme I) (MLE) [EC:5.5.1.1] [KO:K01856]			x	
ecc:c0456	>gnl|kg|ecc:c0456 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
eco:b0337	>gnl|kg|eco:b0337 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
ecj:JW0328	>gnl|kg|ecj:JW0328 codA; Cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
sec:SC3272	>gnl|kg|sec:SC3272 codA; putative cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
ece:Z0433	>gnl|kg|ece:Z0433 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
ypm:YP0164	>gnl|kg|ypm:YP0164 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
ecs:ECs0390	>gnl|kg|ecs:ECs0390 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
ypk:y3946	>gnl|kg|ypk:y3946 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
ype:YPO0162	>gnl|kg|ype:YPO0162 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
spt:SPA3202	>gnl|kg|spt:SPA3202 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
stt:t3251	>gnl|kg|stt:t3251 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
sty:STY3514	>gnl|kg|sty:STY3514 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
stm:STM3334	>gnl|kg|stm:STM3334 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
yps:YPTB3739	>gnl|kg|yps:YPTB3739 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
pmu:PM0565	>gnl|kg|pmu:PM0565 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
pae:PA0437	>gnl|kg|pae:PA0437 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
sme:SMa2371	>gnl|kg|sme:SMa2371 codA1; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
vfi:VF0531	>gnl|kg|vfi:VF0531 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
vpa:VPA1243	>gnl|kg|vpa:VPA1243 putative cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
vvu:VV20789	>gnl|kg|vvu:VV20789 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
vvy:VVA1255	>gnl|kg|vvy:VVA1255 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
ppr:PBPRB1375	>gnl|kg|ppr:PBPRB1375 putative cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
rso:RSc1594	>gnl|kg|rso:RSc1594 codA, RS03956; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
cpe:CPE0756	>gnl|kg|cpe:CPE0756 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
blo:BL0011	>gnl|kg|blo:BL0011 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
ret:RHE_PB00107	>gnl|kg|ret:RHE_PB00107 codAb; cytosine deaminase protein [EC:3.5.4.1] [KO:K01485]			x	
rsp:RSP_0341	>gnl|kg|rsp:RSP_0341 cytosine deaminase			x	
ctc:CTC01883	>gnl|kg|ctc:CTC01883 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
cya:CYA_1587	>gnl|kg|cya:CYA_1587 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
pfl:PFL_4033	>gnl|kg|pfl:PFL_4033 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
bcl:ABC4032	>gnl|kg|bcl:ABC4032 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
cyb:CYB_0393	>gnl|kg|cyb:CYB_0393 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
sto:ST2403	>gnl|kg|sto:ST2403 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
ppu:PP3189	>gnl|kg|ppu:PP3189 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
sso:SSO2770	>gnl|kg|sso:SSO2770 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
bpm:BURPS1710b_A2335	>gnl|kg|bpm:BURPS1710b_A2335 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
bps:BPSS0761	>gnl|kg|bps:BPSS0761 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
bma:BMAA0603	>gnl|kg|bma:BMAA0603 codA; cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
bte:BTH_II1639	>gnl|kg|bte:BTH_II1639 cytosine deaminase			x	
hch:HCH_05147	>gnl|kg|hch:HCH_05147 cytosine deaminase and related metal-dependent hydrolase			x	x
sil:SPO2806	>gnl|kg|sil:SPO2806 cytosine deaminase, putative [EC:3.5.4.1] [KO:K01485]			x	
cgl:NCgl0075	>gnl|kg|cgl:NCgl0075 Cgl0076; cytosine deaminase or related metal-dependent hydrolase [EC:3.5.4.21] [KO:K03365]			x	x
gvi:gll2528	>gnl|kg|gvi:gll2528 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
sai:Saci_1072	>gnl|kg|sai:Saci_1072 cytosine deaminase [EC:3.5.4.1] [KO:K01485]			x	
cef:CE2849	>gnl|kg|cef:CE2849 putative cytosine deaminase			x	
bta:280712	>gnl|kg|bta:280712 ADA; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x	
hsa:100	>gnl|kg|hsa:100 ADA; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x	
mmu:11486	>gnl|kg|mmu:11486 Ada; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x	
rno:24165	>gnl|kg|rno:24165 Ada; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x	
vch:VC2751	>gnl|kg|vch:VC2751 adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x	
stt:t1331	>gnl|kg|stt:t1331 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x	
sty:STY1658	>gnl|kg|sty:STY1658 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x	
ssn:SSO_1535	>gnl|kg|ssn:SSO_1535 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
sec:SC1480	>gnl|kg|sec:SC1480 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x	
ecc:c2015	>gnl|kg|ecc:c2015 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x	
eco:b1623	>gnl|kg|eco:b1623 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x	
ecj:JW1615	>gnl|kg|ecj:JW1615 add; Adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x	
stm:STM1463	>gnl|kg|stm:STM1463 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x	
ecs:ECs2331	>gnl|kg|ecs:ECs2331 adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x	
ece:Z2628	>gnl|kg|ece:Z2628 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x	
sfl:SF1648	>gnl|kg|sfl:SF1648 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x	
sfx:S1780	>gnl|kg|sfx:S1780 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x	
sdy:SDY_1846	>gnl|kg|sdy:SDY_1846 add; adenosine deaminase			x	
sbo:SBO_1511	>gnl|kg|sbo:SBO_1511 add; adenosine deaminase			x	
son:SO4731	>gnl|kg|son:SO4731 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x	
vpa:VP0116	>gnl|kg|vpa:VP0116 adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x	
ppr:PBPRA3496	>gnl|kg|ppr:PBPRA3496 putative adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x	
xtr:496434	>gnl|kg|xtr:496434 ada-prov; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x	
yps:YPTB2180	>gnl|kg|yps:YPTB2180 add; adenosine deaminase [EC:3.5.4.4] [KO:K01488]			x	
xla:444167	>gnl|kg|xla:444167 MGC80635; MGC80635 protein [EC:3.5.4.4] [KO:K01488]			x	

Table L-3. KEGG Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>psb:Psyr_0415</td><td>>gnl|kg|psb:Psyr_0415 N-acyl-D-amino-acid deacylase [EC:3.5.1.82]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>pfo:Pfl_0723</td><td>>gnl|kg|pfo:Pfl_0723 amidohydrolase</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>psp:PSPPH_0405</td><td>>gnl|kg|psp:PSPPH_0405 N-acyl-D-amino acid deacylase family protein [EC:3.5.1.82]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>rso:RSp1187</td><td>>gnl|kg|rso:RSp1187 ndeD, RS03131; probable N-acyl-D-glutamate deacylase protein [EC:3.5.1.82]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>pst:PSPTO5117</td><td>>gnl|kg|pst:PSPTO5117 N-acyl-D-amino acid deacylase family protein [EC:3.5.1.82]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>bte:BTH_I0546</td><td>>gnl|kg|bte:BTH_I0546 N-acyl-D-amino-acid deacylase family protein</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>bpm:BURPS1710b_0837</td><td>>gnl|kg|bpm:BURPS1710b_0837 D-aminoacylase [EC:3.5.1.81]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bps:BPSL0630</td><td>>gnl|kg|bps:BPSL0630 dan; D-aminoacylase [EC:3.5.1.81]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>pfl:PFL_0775</td><td>>gnl|kg|pfl:PFL_0775 N-acyl-D-amino acid deacylase family protein [EC:3.5.1.82]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>reu:Reut_B4020</td><td>>gnl|kg|reu:Reut_B4020 N-acyl-D-amino-acid deacylase [EC:3.5.1.81]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bur:Bcep18194_A6068</td><td>>gnl|kg|bur:Bcep18194_A6068 N-acyl-D-amino-acid deacylase [EC:3.5.1.81]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bma:BMA0178</td><td>>gnl|kg|bma:BMA0178 N-acyl-D-amino-acid deacylase family protein [EC:3.5.1.81]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>sme:SMc01821</td><td>>gnl|kg|sme:SMc01821 dht; dihydropyrimidinase [EC:3.5.2.2] [KO:K01464]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>rsp:RSP_0183</td><td>>gnl|kg|rsp:RSP_0183 dht; dihydropyrimidinase [EC:3.5.2.2] [KO:K01464]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>mlo:mll1629</td><td>>gnl|kg|mlo:mll1629 dihydropyrimidinase [EC:3.5.2.2] [KO:K01464]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>atu:Atu2386</td><td>>gnl|kg|atu:Atu2386 dht; dihydropyrimidinase [EC:3.5.2.2] [KO:K01464]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>atc:AGR_C_4328</td><td>>gnl|kg|atc:AGR_C_4328 dihydropyrimidinase [EC:3.5.2.2] [KO:K01464]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>bms:BR0278</td><td>>gnl|kg|bms:BR0278 dhT; D-hydantoinase [EC:3.5.2.2] [KO:K01464]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sil:SPO1783</td><td>>gnl|kg|sil:SPO1783 hydA; D-hydantoinase [EC:3.5.2.2] [KO:K01464]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-3. KEGG Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>bme:BMEI1644</td><td>>gnl|kg|bme:BMEI1644 dihydropyrimidinase [EC:3.5.2.2] [KO:K01464]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>pfo:Pfl_3441</td><td>>gnl|kg|pfo:Pfl_3441 D-hydantoinase [EC:3.5.2.2] [KO:K01464]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>pfl:PFL_2548</td><td>>gnl|kg|pfl:PFL_2548 hydA; dihydropyrimidinase [EC:3.5.2.2] [KO:K01464]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>pae:PA0441</td><td>>gnl|kg|pae:PA0441 dihydropyrimidinase [EC:3.5.2.2] [KO:K01464]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>osa:P0702B09.7</td><td>>gnl|kg|osa:P0702B09.7 putative dihydropyrimidinase</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>gka:GK1423</td><td>>gnl|kg|gka:GK1423 dihydropyrimidinase [EC:3.5.2.2] [KO:K01464]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>bur:Bcep18194_C6658</td><td>>gnl|kg|bur:Bcep18194_C6658 D-hydantoinase [EC:3.5.2.2] [KO:K01464]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bja:blr7615</td><td>>gnl|kg|bja:blr7615 dht; dihydropyrimidinase [EC:3.5.2.2] [KO:K01464]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>cps:CPS_4055</td><td>>gnl|kg|cps:CPS_4055 dht; dihydropyrimidinase [EC:3.5.2.2] [KO:K01464]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>sco:SCO6415</td><td>>gnl|kg|sco:SCO6415 SC1A6.04; putative D-hydantoinase [EC:3.5.2.2] [KO:K01464]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sma:SAV1949</td><td>>gnl|kg|sma:SAV1949 dht; putative dihydropyrimidinase [EC:3.5.2.2] [KO:K01464]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>ecs:ECs3746</td><td>>gnl|kg|ecs:ECs3746 dihydropyrimidinase</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>ece:Z4212</td><td>>gnl|kg|ece:Z4212 dihydropyrimidinase</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>rsp:RSP_3462</td><td>>gnl|kg|rsp:RSP_3462 dihydropyrimidinase</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>ecc:c3451</td><td>>gnl|kg|ecc:c3451 ygeZ; dihydropyrimidinase [EC:3.-.-.-]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>bcl:ABC3783</td><td>>gnl|kg|bcl:ABC3783 dihydropyrimidinase [EC:3.5.2.2] [KO:K01464]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>reu:Reut_A0045</td><td>>gnl|kg|reu:Reut_A0045 D-hydantoinase [EC:3.5.2.2] [KO:K01464]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>cfa:475067</td><td>>gnl|kg|cfa:475067 LOC475067; similar to Dihydropyrimidinase (DHPase) (Hydantoinase) (DHP)</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>ddi:DDB0191172</td><td>>gnl|kg|ddi:DDB0191172 pyd2; hypothetical protein [EC:3.5.2.2] [KO:K01464]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>gga:420266</td><td>>gnl|kg|gga:420266 LOC420266; similar to dihydropyrimidinase</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>hsa:1807</td><td>>gnl|kg|hsa:1807 DPYS; dihydropyrimidinase [EC:3.5.2.2] [KO:K01464]</td><td></td><td></td><td>x</td><td>x</td></tr>
</table>

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
ctc:CTC01781	>gnl|kg|ctc:CTC01781 dihydropyrimidinase [EC:3.5.2.2] [KO:K01464]			x	x
rno:65135	>gnl|kg|rno:65135 Dpys; dihydropyrimidinase [EC:3.5.2.2] [KO:K01464]			x	x
mmu:64705	>gnl|kg|mmu:64705 Dpys; dihydropyrimidinase [EC:3.5.2.2] [KO:K01464]			x	x
ppr:PBPRA1991	>gnl|kg|ppr:PBPRA1991 ygeZ; hypothetical hydrolase ygeZ [EC:3.-.-.-]			x	x
xla:495311	>gnl|kg|xla:495311 LOC495311; hypothetical LOC495311 [EC:3.5.2.2] [KO:K01464]			x	x
bta:509241	>gnl|kg|bta:509241 LOC509241; similar to Dihydropyrimidinase (DHPase) (Hydantoinase) (DHP)			x	x
cel:C47E12.8	>gnl|kg|cel:C47E12.8 dhp-2; Hypothetical protein C47E12.8 [EC:3.5.2.2] [KO:K01464]			x	x
bja:blr3295	>gnl|kg|bja:blr3295 dihydropyrimidinase [EC:3.5.2.2] [KO:K01464]			x	x
sbo:SBO_4379	>gnl|kg|sbo:SBO_4379 iadA; isoaspartyl dipeptidase			x	
mmu:13177	>gnl|kg|mmu:13177 Dci; dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase) [EC:5.3.3.8] [KO:K01825]			x	
hsa:1632	>gnl|kg|hsa:1632 DCI; dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase) [EC:5.3.3.8] [KO:K01825]			x	
rno:29740	>gnl|kg|rno:29740 Dci; dodecenoyl-coenzyme A delta isomerase [EC:5.3.3.8] [KO:K01825]			x	
dme:CG4598-PA	>gnl|kg|dme:CG4598-PA CG4598; CG4598 gene product from transcript CG4598-RA [EC:5.3.3.8] [KO:K01825]			x	
dme:CG4594-PA	>gnl|kg|dme:CG4594-PA CG4594; CG4594 gene product from transcript CG4594-RA [EC:5.3.3.8] [KO:K01825]			x	
xtr:496654	>gnl|kg|xtr:496654 dci-prov; dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase) [EC:5.3.3.8] [KO:K01825]			x	
xla:432103	>gnl|kg|xla:432103 MGC82167; hypothetical protein MGC82167 [EC:5.3.3.8] [KO:K01825]			x	
cfa:490059	>gnl|kg|cfa:490059 LOC490059; similar to dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)			x	x

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
pfo:Pfl_2882	>gnl|kg|pfo:Pfl_2882 enoyl-CoA hydratase/isomerase			x	x
psp:PSPPH_2608	>gnl|kg|psp:PSPPH_2608 enoyl-CoA hydratase/isomerase family protein [EC:5.3.3.-]			x	x
ath:At5g43280	>gnl|kg|ath:At5g43280 MNL12.10; enoyl-CoA hydratase/isomerase family [EC:5.3.3.-]			x	x
sfl:SF2904	>gnl|kg|sfl:SF2904 ygfG; putative enzyme			x	x
eco:b2919	>gnl|kg|eco:b2919 ygfG; methylmalonyl-CoA decarboxylase, biotin-independent			x	
sfx:S3104	>gnl|kg|sfx:S3104 ygfG; putative enzyme			x	x
ece:Z4256	>gnl|kg|ece:Z4256 ygfG; putative enzyme			x	x
sbo:SBO_3075	>gnl|kg|sbo:SBO_3075 ygfG; putative enzyme			x	x
ssn:SSO_3070	>gnl|kg|ssn:SSO_3070 ygfG; putative enzyme			x	x
hsa:26275	>gnl|kg|hsa:26275 HIBCH; 3-hydroxyisobutyryl-Coenzyme A hydrolase			x	
mmu:227095	>gnl|kg|mmu:227095 Hibch; 3-hydroxyisobutyryl-Coenzyme A hydrolase			x	
gga:423979	>gnl|kg|gga:423979 LOC423979; similar to 3-hydroxyisobutyryl-Coenzyme A hydrolase isoform 1			x	x
ath:At5g65940	>gnl|kg|ath:At5g65940 K14B20.11; 3-hydroxyisobutyryl-coenzyme A hydrolase (CoA-thioester hydrolase) (CHY1)			x	
bta:535883	>gnl|kg|bta:535883 LOC535883; similar to 3-hydroxyisobutyryl-Coenzyme A hydrolase isoform 1			x	x
ath:At2g30660	>gnl|kg|ath:At2g30660 T11J7.5; 3-hydroxyisobutyryl-coenzyme A hydrolase, putative / CoA-thioester hydrolase, putative			x	
ath:At2g30650	>gnl|kg|ath:At2g30650 T11J7.4; 3-hydroxyisobutyryl-coenzyme A hydrolase, putative / CoA-thioester hydrolase, putative			x	
bce:BC2292	>gnl|kg|bce:BC2292 3-hydroxyisobutyryl-coenzyme A hydrolase [EC:4.2.1.17] [KO:K01692]			x	
cfa:478841	>gnl|kg|cfa:478841 LOC478841; similar to 3-hydroxyisobutyryl-Coenzyme A hydrolase isoform 1			x	x
rno:301384	>gnl|kg|rno:301384 Hibch_predicted; 3-hydroxyisobutyryl-Coenzyme A hydrolase (predicted)			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
gka:GK3054	>gnl|kg|gka:GK3054 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
cte:CT0145	>gnl|kg|cte:CT0145 eno-2; enolase [EC:4.2.1.11] [KO:K01689]			x	
gga:396017	>gnl|kg|gga:396017 LOC396017; enolase [EC:4.2.1.11] [KO:K01689]			x	
dme:CG17654-PB	>gnl|kg|dme:CG17654-PB CG17654; CG17654 gene product from transcript CG17654-RB CG17654 gene product from transcript CG17654-RC [EC:4.2.1.11] [KO:K01689]			x	
mfl:Mfl468	>gnl|kg|mfl:Mfl468 enolase [EC:4.2.1.11] [KO:K01689]			x	
pfa:PF10_0155	>gnl|kg|pfa:PF10_0155 enolase [EC:4.2.1.11] [KO:K01689]			x	
tte:TTE1759	>gnl|kg|tte:TTE1759 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
hsa:2026	>gnl|kg|hsa:2026 ENO2; enolase 2 (gamma, neuronal) [EC:4.2.1.11] [KO:K01689]			x	
xla:380298	>gnl|kg|xla:380298 eno1-prov; enolase 1, alpha [EC:4.2.1.11] [KO:K01689]			x	
rno:24334	>gnl|kg|rno:24334 Eno2; enolase 2, gamma [EC:4.2.1.11] [KO:K01689]			x	
gga:395689	>gnl|kg|gga:395689 LOC395689; gamma-subunit of enolase			x	
cfa:477709	>gnl|kg|cfa:477709 LOC477709; similar to Gamma enolase (2-phospho-D-glycerate hydro-lyase) (Neural enolase) (NSE) (Enolase 2)			x	
mmu:13807	>gnl|kg|mmu:13807 Eno2; enolase 2, gamma neuronal [EC:4.2.1.11] [KO:K01689]			x	
lpl:lp_0792	>gnl|kg|lpl:lp_0792 enoA1; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
hsa:2023	>gnl|kg|hsa:2023 ENO1; enolase 1, (alpha) [EC:4.2.1.11] [KO:K01689]			x	
dre:393668	>gnl|kg|dre:393668 enolase [EC:4.2.1.11] [KO:K01689]			x	
hsa:2027	>gnl|kg|hsa:2027 ENO3; enolase 3 (beta, muscle) [EC:4.2.1.11] [KO:K01689]			x	
zma:ENO2	>gnl|kg|zma:ENO2 eno2; enolase 2 (2-phosphoglycerate dehydratase 2) (2-phospho- d-glycerate hydro-lyase 2). [EC:4.2.1.11] [SP:ENO2_MAIZE]			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
cfa:479469	>gnl|kg|cfa:479469 LOC479469; similar to Enolase 3, beta			x	
bta:540303	>gnl|kg|bta:540303 MGC128156; similar to Beta enolase (2-phospho-D-glycerate hydro-lyase) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase) (Enolase 3)			x	
xla:380038	>gnl|kg|xla:380038 eno3-prov; enolase 3, beta muscle [EC:4.2.1.11] [KO:K01689]			x	
mcp:MCAP_0213	>gnl|kg|mcp:MCAP_0213 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
ljo:LJ0875	>gnl|kg|ljo:LJ0875 enolase [EC:4.2.1.11] [KO:K01689]			x	
chy:CHY_0284	>gnl|kg|chy:CHY_0284 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
mmu:13806	>gnl|kg|mmu:13806 Eno1; enolase 1, alpha non-neuron [EC:4.2.1.11] [KO:K01689]			x	
bsu:BG10899	>gnl|kg|bsu:BG10899 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
mmu:13808	>gnl|kg|mmu:13808 Eno3; enolase 3, beta muscle [EC:4.2.1.11] [KO:K01689]			x	
bcz:BCZK4824	>gnl|kg|bcz:BCZK4824 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
ptr:457913	>gnl|kg|ptr:457913 ENO1; enolase 1			x	
bli:BL03468	>gnl|kg|bli:BL03468 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
bld:BLi03661	>gnl|kg|bld:BLi03661 eno; enolase; RBL03415 [EC:4.2.1.11] [KO:K01689]			x	
bha:BH3556	>gnl|kg|bha:BH3556 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
ath:At2g36530	>gnl|kg|ath:At2g36530 F1O11.16; enolase [EC:4.2.1.11] [KO:K01689]			x	
ban:BA5364	>gnl|kg|ban:BA5364 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
baa:BA_0223	>gnl|kg|baa:BA_0223 enolase [EC:4.2.1.11] [KO:K01689]			x	
bar:GBAA5364	>gnl|kg|bar:GBAA5364 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
btk:BT9727_4814	>gnl|kg|btk:BT9727_4814 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
bat:BAS4985	>gnl|kg|bat:BAS4985 enolase [EC:4.2.1.11] [KO:K01689]			x	
xla:379079	>gnl|kg|xla:379079 MGC53543; similar to enolase 1, alpha non-neuron [EC:4.2.1.11] [KO:K01689]			x	
efa:EF1961	>gnl|kg|efa:EF1961 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
bca:BCE5238	>gnl|kg|bca:BCE5238 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
tan:TA10425	>gnl|kg|tan:TA10425 enolase, putative			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
mmy:MSC_0253	>gnl|kg|mmy:MSC_0253 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
dre:334116	>gnl|kg|dre:334116 enolase [EC:4.2.1.11] [KO:K01689]			x	
mta:Moth_0266	>gnl|kg|mta:Moth_0266 enolase [EC:4.2.1.11] [KO:K01689]			x	
bce:BC5135	>gnl|kg|bce:BC5135 enolase [EC:4.2.1.11] [KO:K01689]			x	
xtr:394749	>gnl|kg|xtr:394749 MGC75746; Enolase (2-phosphoglycerate dehydratase) [EC:4.2.1.11] [KO:K01689]			x	
rno:24333	>gnl|kg|rno:24333 Eno1; enolase 1, alpha [EC:4.2.1.11] [KO:K01689]			x	
tpv:TP04_0700	>gnl|kg|tpv:TP04_0700 enolase [EC:4.2.1.11] [KO:K01689]			x	
tma:TM0877	>gnl|kg|tma:TM0877 enolase [EC:4.2.1.11] [KO:K01689]			x	
dre:378963	>gnl|kg|dre:378963 eno3; enolase 3, (beta, muscle) [EC:4.2.1.11] [KO:K01689]			x	
bcl:ABC3017	>gnl|kg|bcl:ABC3017 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
cch:Cag_0347	>gnl|kg|cch:Cag_0347 enolase [EC:4.2.1.11] [KO:K01689]			x	
gme:Gmet_2372	>gnl|kg|gme:Gmet_2372 enolase			x	
bga:BG0338	>gnl|kg|bga:BG0338 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
aae:aq_484	>gnl|kg|aae:aq_484 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
gsu:GSU2286	>gnl|kg|gsu:GSU2286 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
bth:BT4572	>gnl|kg|bth:BT4572 enolase [EC:4.2.1.11] [KO:K01689]			x	
lsa:LSA0607	>gnl|kg|lsa:LSA0607 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
ctc:CTC00382	>gnl|kg|ctc:CTC00382 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
bbu:BB0337	>gnl|kg|bbu:BB0337 eno; enolase (eno) [EC:4.2.1.11] [KO:K01689]			x	
bfr:BF1188	>gnl|kg|bfr:BF1188 enolase [EC:4.2.1.11] [KO:K01689]			x	
bfs:BF1155	>gnl|kg|bfs:BF1155 eno, hupA; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
plt:Plut_1972	>gnl|kg|plt:Plut_1972 enolase [EC:4.2.1.11] [KO:K01689]			x	
cac:CAC0713	>gnl|kg|cac:CAC0713 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
pcu:pc0143	>gnl|kg|pcu:pc0143 eno; probable phosphopyruvate hydratase (enolase) [EC:4.2.1.11] [KO:K01689]			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
bta:526006	>gnl|kg|bta:526006 LOC526006; similar to Gamma enolase (2-phospho-D-glycerate hydro-lyase) (Neural enolase) (Neuron-specific enolase) (NSE) (Enolase 2)			x	x
lmo:lmo2455	>gnl|kg|lmo:lmo2455 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
lin:lin2549	>gnl|kg|lin:lin2549 eno; highly similar to enolase [EC:4.2.1.11] [KO:K01689]			x	x
lmf:LMOf2365_2428	>gnl|kg|lmf:LMOf2365_2428 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
cal:orf19.395	>gnl|kg|cal:orf19.395 ENO1; enolase I [EC:4.2.1.11] [KO:K01689]			x	
pac:PPA0545	>gnl|kg|pac:PPA0545 phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
ago:AER294C	>gnl|kg|ago:AER294C AER294Cp; enolase (ENO2) (ENO1) [EC:4.2.1.11] [KO:K01689]			x	
tde:TDE0949	>gnl|kg|tde:TDE0949 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
sth:STH249	>gnl|kg|sth:STH249 enolase [EC:4.2.1.11] [KO:K01689]			x	
zma:ENO1	>gnl|kg|zma:ENO1 eno1, pgh1; enolase 1 (2-phosphoglycerate dehydratase 1) (2-phospho- d-glycerate hydro-lyase 1). [EC:4.2.1.11] [SP:ENO1_MAIZE]			x	
mpu:MYPU_5180	>gnl|kg|mpu:MYPU_5180 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
oih:OB2434	>gnl|kg|oih:OB2434 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
dvu:DVU0322	>gnl|kg|dvu:DVU0322 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
sce:YGR254W	>gnl|kg|sce:YGR254W ENO1; enolase I [EC:4.2.1.11] [KO:K01689]			x	
pca:Pcar_1230	>gnl|kg|pca:Pcar_1230 enolase			x	
pab:PAB1126	>gnl|kg|pab:PAB1126 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
dre:402874	>gnl|kg|dre:402874 eno2; enolase 2			x	
tbd:Tbd_0621	>gnl|kg|tbd:Tbd_0621 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
rru:Rru_A1885	>gnl|kg|rru:Rru_A1885 phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
ttj:TTHA0002	>gnl|kg|ttj:TTHA0002 enolase (2-phosphoglycerate dehydratase) [EC:4.2.1.11] [KO:K01689]			x	
tth:TTC1610	>gnl|kg|tth:TTC1610 enolase [EC:4.2.1.11] [KO:K01689]			x	
dde:Dde_0295	>gnl|kg|dde:Dde_0295 enolase [EC:4.2.1.11] [KO:K01689]			x	

Table L-3. KEGG Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>rno:25438</td><td>>gnl|kg|rno:25438 Eno3; enolase 3, beta [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>cjk:jk1483</td><td>>gnl|kg|cjk:jk1483 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>dra:DR2637</td><td>>gnl|kg|dra:DR2637 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>zmo:ZMO1608</td><td>>gnl|kg|zmo:ZMO1608 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>cdi:DIP0917</td><td>>gnl|kg|cdi:DIP0917 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sce:YHR174W</td><td>>gnl|kg|sce:YHR174W ENO2; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>cef:CE1042</td><td>>gnl|kg|cef:CE1042 putative enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>blo:BL1022</td><td>>gnl|kg|blo:BL1022 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>mja:MJ0232</td><td>>gnl|kg|mja:MJ0232 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>spn:SP1128</td><td>>gnl|kg|spn:SP1128 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>hin:HI0932</td><td>>gnl|kg|hin:HI0932 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>spr:spr1036</td><td>>gnl|kg|spr:spr1036 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>nar:Saro_2223</td><td>>gnl|kg|nar:Saro_2223 phosphopyruvate hydratase [EC:4.2.1.11]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>hit:NTHI1103</td><td>>gnl|kg|hit:NTHI1103 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>msu:MS0256</td><td>>gnl|kg|msu:MS0256 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>cpe:CPE1299</td><td>>gnl|kg|cpe:CPE1299 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>tko:TK2106</td><td>>gnl|kg|tko:TK2106 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>spm:spyM18_0798</td><td>>gnl|kg|spm:spyM18_0798 eno; putative enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>spb:M28_Spy0535</td><td>>gnl|kg|spb:M28_Spy0535 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>spg:SpyM3_0479</td><td>>gnl|kg|spg:SpyM3_0479 eno; putative enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sps:SPs1375</td><td>>gnl|kg|sps:SPs1375 putative enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>spy:SPy0731</td><td>>gnl|kg|spy:SPy0731 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>dar:Daro_2364</td><td>>gnl|kg|dar:Daro_2364 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>cgb:cg1111</td><td>>gnl|kg|cgb:cg1111 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>cgl:NCgl0935</td><td>>gnl|kg|cgl:NCgl0935 Cgl0974; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>san:gbs0608</td><td>>gnl|kg|san:gbs0608 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sak:SAK_0713</td><td>>gnl|kg|sak:SAK_0713 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sag:SAG0628</td><td>>gnl|kg|sag:SAG0628 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-3. KEGG Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>bta:281141</td><td>>gnl|kg|bta:281141 ENO1; enolase 1 [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>mle:ML0255</td><td>>gnl|kg|mle:ML0255 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>aci:ACIAD2001</td><td>>gnl|kg|aci:ACIAD2001 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>stl:stu0635</td><td>>gnl|kg|stl:stu0635 eno; 2-phosphoglycerate dehydratase, enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>stc:str0635</td><td>>gnl|kg|stc:str0635 eno; 2-phosphoglycerate dehydratase, enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sab:SAB0732</td><td>>gnl|kg|sab:SAB0732 eno; enolase 2-phosphoglycerate dehydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sav:SAV0776</td><td>>gnl|kg|sav:SAV0776 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sau:SA0731</td><td>>gnl|kg|sau:SA0731 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sac:SACOL0842</td><td>>gnl|kg|sac:SACOL0842 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>saa:SAUSA300_0760</td><td>>gnl|kg|saa:SAUSA300_0760 eno; phosphopyruvate hydratase [EC:4.2.1.11]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sam:MW0738</td><td>>gnl|kg|sam:MW0738 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sar:SAR0832</td><td>>gnl|kg|sar:SAR0832 eno; putative enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sas:SAS0742</td><td>>gnl|kg|sas:SAS0742 putative enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>pmu:PM1871</td><td>>gnl|kg|pmu:PM1871 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>mlo:mlr0378</td><td>>gnl|kg|mlo:mlr0378 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>smu:SMU.1247</td><td>>gnl|kg|smu:SMU.1247 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>tcx:Tcr_1260</td><td>>gnl|kg|tcx:Tcr_1260 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>pae:PA3635</td><td>>gnl|kg|pae:PA3635 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sha:SH2109</td><td>>gnl|kg|sha:SH2109 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>pho:PH1942</td><td>>gnl|kg|pho:PH1942 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sep:SE0561</td><td>>gnl|kg|sep:SE0561 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ser:SERP0446</td><td>>gnl|kg|ser:SERP0446 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>poy:PAM284</td><td>>gnl|kg|poy:PAM284 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sbo:SBO_2660</td><td>>gnl|kg|sbo:SBO_2660 eno; enolase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sfx:S2988</td><td>>gnl|kg|sfx:S2988 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sdy:SDY_2996</td><td>>gnl|kg|sdy:SDY_2996 eno; enolase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ecs:ECs3639</td><td>>gnl|kg|ecs:ECs3639 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
ecc:c3344	>gnl|kg|ecc:c3344 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
ecj:JW2750	>gnl|kg|ecj:JW2750 eno; Enolase (2-phosphoglycerate dehydratase) (2-phospho-d- glycerate hydro-lyase). [EC:4.2.1.11] [KO:K01689]			x	
eco:b2779	>gnl|kg|eco:b2779 eno, eno'; enolase [EC:4.2.1.11] [KO:K01689]			x	
sfl:SF2794	>gnl|kg|sfl:SF2794 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
ngo:NGO0617	>gnl|kg|ngo:NGO0617 putative enolase (2-phosphoglycerate dehydratase) [EC:4.2.1.11] [KO:K01689]			x	
xcc:XCC1700	>gnl|kg|xcc:XCC1700 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
xcb:XC_2531	>gnl|kg|xcb:XC_2531 enolase [EC:4.2.1.11] [KO:K01689]			x	
mpa:MAP0990	>gnl|kg|mpa:MAP0990 eno; putative enolase [EC:4.2.1.11] [KO:K01689]			x	
xoo:XOO2963	>gnl|kg|xoo:XOO2963 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
xac:XAC1719	>gnl|kg|xac:XAC1719 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
ype:YPO3376	>gnl|kg|ype:YPO3376 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
ypk:y0814	>gnl|kg|ypk:y0814 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
vvy:VV2818	>gnl|kg|vvy:VV2818 enolase [EC:4.2.1.11] [KO:K01689]			x	
yps:YPTB0755	>gnl|kg|yps:YPTB0755 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
ypm:YP0310	>gnl|kg|ypm:YP0310 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
ppr:PBPRA3079	>gnl|kg|ppr:PBPRA3079 eno; putative enolase [EC:4.2.1.11] [KO:K01689]			x	
nma:NMA1495	>gnl|kg|nma:NMA1495 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
nme:NMB1285	>gnl|kg|nme:NMB1285 enolase [EC:4.2.1.11] [KO:K01689]			x	
ece:Z4094	>gnl|kg|ece:Z4094 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
ilo:IL0772	>gnl|kg|ilo:IL0772 enolase [EC:4.2.1.11] [KO:K01689]			x	
gga:396016	>gnl|kg|gga:396016 LOC396016; enolase			x	
pfu:PF0215	>gnl|kg|pfu:PF0215 enolase [EC:4.2.1.11] [KO:K01689]			x	
hch:HCH_01867	>gnl|kg|hch:HCH_01867 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
xfa:XF1291	>gnl|kg|xfa:XF1291 enolase [EC:4.2.1.11] [KO:K01689]			x	
plu:plu0913	>gnl|kg|plu:plu0913 eno; enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) [EC:4.2.1.11] [KO:K01689]			x	

Table L-3. KEGG Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>sco:SCO3096</td><td>>gnl|kg|sco:SCO3096 eno, SCE41.05c; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>deh:cbdb_A573</td><td>>gnl|kg|deh:cbdb_A573 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>tpa:TP0817</td><td>>gnl|kg|tpa:TP0817 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ssn:SSO_2936</td><td>>gnl|kg|ssn:SSO_2936 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>xcv:XCV1752</td><td>>gnl|kg|xcv:XCV1752 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>psp:PSPPH_3820</td><td>>gnl|kg|psp:PSPPH_3820 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>dps:DP1799</td><td>>gnl|kg|dps:DP1799 probable enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>psb:Psyr_1363</td><td>>gnl|kg|psb:Psyr_1363 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>msy:MS53_0009</td><td>>gnl|kg|msy:MS53_0009 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>vpa:VP2561</td><td>>gnl|kg|vpa:VP2561 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>spo:SPBC1815.01</td><td>>gnl|kg|spo:SPBC1815.01 eno1; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>tfu:Tfu_0428</td><td>>gnl|kg|tfu:Tfu_0428 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>rba:RB12381</td><td>>gnl|kg|rba:RB12381 eno; enolase (2-phosphoglycerate dehydratase) [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>det:DET0593</td><td>>gnl|kg|det:DET0593 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>pfl:PFL_1196</td><td>>gnl|kg|pfl:PFL_1196 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>mtc:MT1051</td><td>>gnl|kg|mtc:MT1051 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>mtu:Rv1023</td><td>>gnl|kg|mtu:Rv1023 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sma:SAV3533</td><td>>gnl|kg|sma:SAV3533 eno; putative enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>atc:AGR_C_2631</td><td>>gnl|kg|atc:AGR_C_2631 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>reu:Reut_A1091</td><td>>gnl|kg|reu:Reut_A1091 enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>mka:MK1647</td><td>>gnl|kg|mka:MK1647 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>hdu:HD0477</td><td>>gnl|kg|hdu:HD0477 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ayw:AYWB_437</td><td>>gnl|kg|ayw:AYWB_437 eno; enolase [EC:4.2.1.11] [KO:K01689]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
stm:STM2952	>gnl|kg|stm:STM2952 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
sty:STY3081	>gnl|kg|sty:STY3081 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
stt:t2853	>gnl|kg|stt:t2853 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
spt:SPA2809	>gnl|kg|spt:SPA2809 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
sec:SC2886	>gnl|kg|sec:SC2886 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
pfo:Pfl_1121	>gnl|kg|pfo:Pfl_1121 phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
eca:ECA3566	>gnl|kg|eca:ECA3566 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
mbo:Mb1051	>gnl|kg|mbo:Mb1051 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
mga:MGA_0209	>gnl|kg|mga:MGA_0209 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
vvu:VV11579	>gnl|kg|vvu:VV11579 enolase [EC:4.2.1.11] [KO:K01689]			x	
vch:VC2447	>gnl|kg|vch:VC2447 enolase [EC:4.2.1.11] [KO:K01689]			x	
spz:M5005_Spy_0556	>gnl|kg|spz:M5005_Spy_0556 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
bja:bll4794	>gnl|kg|bja:bll4794 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
cne:CNC00160	>gnl|kg|cne:CNC00160 phosphopyruvate hydratase, putative [EC:4.2.1.11] [KO:K01689]			x	
cte:CT1962	>gnl|kg|cte:CT1962 eno-1; enolase [EC:4.2.1.11] [KO:K01689]			x	
sme:SMc01028	>gnl|kg|sme:SMc01028 eno; probable enolase protein [EC:4.2.1.11] [KO:K01689]			x	
eli:ELI_05740	>gnl|kg|eli:ELI_05740 enolase			x	
nfa:nfa48590	>gnl|kg|nfa:nfa48590 eno; putative enolase [EC:4.2.1.11] [KO:K01689]			x	
hpj:jhp0142	>gnl|kg|hpj:jhp0142 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
vfi:VF2075	>gnl|kg|vfi:VF2075 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
fnu:FN1764	>gnl|kg|fnu:FN1764 enolase [EC:4.2.1.11] [KO:K01689]			x	
lxx:Lxx17200	>gnl|kg|lxx:Lxx17200 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
ddi:DDB0231355	>gnl|kg|ddi:DDB0231355 enoA; 2-phospho-D-glycerate hydrolase [EC:4.2.1.11] [KO:K01689]			x	
pgi:PG1824	>gnl|kg|pgi:PG1824 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
xft:PD0543	>gnl|kg|xft:PD0543 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
ppu:PP1612	>gnl|kg|ppu:PP1612 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
mmp:MMP0396	>gnl|kg|mmp:MMP0396 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
pst:PSPTO1554	>gnl|kg|pst:PSPTO1554 eno-1; enolase [EC:4.2.1.11] [KO:K01689]			x	
ssp:SSP1912	>gnl|kg|ssp:SSP1912 enolase [EC:4.2.1.11] [KO:K01689]			x	
lic:LIC11954	>gnl|kg|lic:LIC11954 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
lil:LA1951	>gnl|kg|lil:LA1951 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
rso:RSc1129	>gnl|kg|rso:RSc1129 eno, RS04624; enolase [EC:4.2.1.11] [KO:K01689]			x	
cme:CMK131C	>gnl|kg|cme:CMK131C enolase [EC:4.2.1.11] [KO:K01689]			x	
sil:SPO2474	>gnl|kg|sil:SPO2474 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
lla:L0007	>gnl|kg|lla:L0007 enoA; enolase [EC:4.2.1.11] [KO:K01689]			x	
cpa:CP1071	>gnl|kg|cpa:CP1071 enolase [EC:4.2.1.11] [KO:K01689]			x	
cpj:CPj0800	>gnl|kg|cpj:CPj0800 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
ftu:FTT0709	>gnl|kg|ftu:FTT0709 eno; enolase (2-phosphoglycerate dehydratase) [EC:4.2.1.11] [KO:K01689]			x	
bur:Bcep18194_A5413	>gnl|kg|bur:Bcep18194_A5413 phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
sgl:SG0513	>gnl|kg|sgl:SG0513 enolase			x	
cpn:CPn0800	>gnl|kg|cpn:CPn0800 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
cpt:CpB0829	>gnl|kg|cpt:CpB0829 enolase [EC:4.2.1.11] [KO:K01689]			x	
ret:RHE_CH01931	>gnl|kg|ret:RHE_CH01931 eno; 2-phosphoglycerate dehydratase (enolase) protein [EC:4.2.1.11] [KO:K01689]			x	
cpv:cgd5_1960	>gnl|kg|cpv:cgd5_1960 enolase (2-phosphoglycerate dehydratase) [EC:4.2.1.11] [KO:K01689]			x	
bmf:BAB1_1155	>gnl|kg|bmf:BAB1_1155 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
bmb:BruAb1_1138	>gnl|kg|bmb:BruAb1_1138 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
bms:BR1132	>gnl|kg|bms:BR1132 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
ana:all3538	>gnl|kg|ana:all3538 enolase [EC:4.2.1.11] [KO:K01689]			x	
bhe:BH05720	>gnl|kg|bhe:BH05720 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
hpy:HP0154	>gnl|kg|hpy:HP0154 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
rpa:RPA2874	>gnl|kg|rpa:RPA2874 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
bpa:BPP3252	>gnl|kg|bpa:BPP3252 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
bbr:BB3703	>gnl|kg|bbr:BB3703 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
bpe:BP2386	>gnl|kg|bpe:BP2386 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
bqu:BQ04880	>gnl|kg|bqu:BQ04880 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
ehi:337.t00001	>gnl|kg|ehi:337.t00001 enolase, putative [EC:4.2.1.11] [KO:K01689]			x	
bme:BMEI0851	>gnl|kg|bme:BMEI0851 enolase [EC:4.2.1.11] [KO:K01689]			x	
fra:Francci3_3923	>gnl|kg|fra:Francci3_3923 phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
mag:amb1823	>gnl|kg|mag:amb1823 enolase			x	
par:Psyc_1636	>gnl|kg|par:Psyc_1636 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
ava:Ava_3517	>gnl|kg|ava:Ava_3517 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
bpm:BURPS1710b_2711	>gnl|kg|bpm:BURPS1710b_2711 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
bps:BPSL2270	>gnl|kg|bps:BPSL2270 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
bma:BMA1689	>gnl|kg|bma:BMA1689 enolase [EC:4.2.1.11] [KO:K01689]			x	
sco:SCO7638	>gnl|kg|sco:SCO7638 eno2, SC10F4.11c; enolase [EC:4.2.1.11] [KO:K01689]			x	
ccr:CC1724	>gnl|kg|ccr:CC1724 enolase [EC:4.2.1.11] [KO:K01689]			x	
gvi:gll2121	>gnl|kg|gvi:gll2121 enolase [EC:4.2.1.11] [KO:K01689]			x	
cps:CPS_4106	>gnl|kg|cps:CPS_4106 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
tbr:Tb10.70.4740	>gnl|kg|tbr:Tb10.70.4740 enolase [EC:4.2.1.11] [KO:K01689]			x	
tel:tlr0658	>gnl|kg|tel:tlr0658 enolase [EC:4.2.1.11] [KO:K01689]			x	
pha:PSHAa0742	>gnl|kg|pha:PSHAa0742 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
bte:BTH_I1894	>gnl|kg|bte:BTH_I1894 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
ath:At1g74030	>gnl|kg|ath:At1g74030 F2P9.10; enolase, putative [EC:4.2.1.11] [KO:K01689]			x	
syc:syc0886_c	>gnl|kg|syc:syc0886_c eno; enolase [EC:4.2.1.11] [KO:K01689]			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
syf:Synpcc7942_0639	>gnl|kg|syf:Synpcc7942_0639 enolase [EC:4.2.1.11] [KO:K01689]			x	
gox:GOX2279	>gnl|kg|gox:GOX2279 enolase [EC:4.2.1.11] [KO:K01689]			x	
mca:MCA2515	>gnl|kg|mca:MCA2515 eno-2; enolase [EC:4.2.1.11] [KO:K01689]			x	
rpb:RPB_2778	>gnl|kg|rpb:RPB_2778 enolase [EC:4.2.1.11] [KO:K01689]			x	
rsp:RSP_2491	>gnl|kg|rsp:RSP_2491 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
mpe:MYPE3750	>gnl|kg|mpe:MYPE3750 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
syn:slr0752	>gnl|kg|syn:slr0752 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
tcr:504105.140	>gnl|kg|tcr:504105.140 enolase [EC:4.2.1.11] [KO:K01689]			x	
mmo:MMOB1800	>gnl|kg|mmo:MMOB1800 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
sru:SRU_0787	>gnl|kg|sru:SRU_0787 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
eba:ebA6162	>gnl|kg|eba:ebA6162 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
mpn:MPN606	>gnl|kg|mpn:MPN606 eno, C12_orf456; enolase [EC:4.2.1.11] [KO:K01689]			x	
pmm:PMM0208	>gnl|kg|pmm:PMM0208 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
nmu:Nmul_A1228	>gnl|kg|nmu:Nmul_A1228 enolase [EC:4.2.1.11] [KO:K01689]			x	
lpl:lp_1920	>gnl|kg|lpl:lp_1920 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
sye:Syncc9902_2161	>gnl|kg|sye:Syncc9902_2161 enolase [EC:4.2.1.11] [KO:K01689]			x	
pmt:PMT2083	>gnl|kg|pmt:PMT2083 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
pmi:PMT9312_0210	>gnl|kg|pmi:PMT9312_0210 enolase [EC:4.2.1.11] [KO:K01689]			x	
lpf:lpl2015	>gnl|kg|lpf:lpl2015 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
wsu:WS1494	>gnl|kg|wsu:WS1494 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
nwi:Nwi_1827	>gnl|kg|nwi:Nwi_1827 enolase [EC:4.2.1.11] [KO:K01689]			x	
cya:CYA_2554	>gnl|kg|cya:CYA_2554 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
syw:SYNW2348	>gnl|kg|syw:SYNW2348 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
cbu:CBU_1674	>gnl|kg|cbu:CBU_1674 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
pma:Pro0235	>gnl|kg|pma:Pro0235 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
tdn:Tmden_2001	>gnl|kg|tdn:Tmden_2001 phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
lpn:lpg2037	>gnl|kg|lpn:lpg2037 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
bba:Bd0796	>gnl|kg|bba:Bd0796 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
lma:LmjF14.1160	>gnl|kg|lma:LmjF14.1160 enolase [EC:4.2.1.11] [KO:K01689]			x	
syd:Syncc9605_2476	>gnl|kg|syd:Syncc9605_2476 enolase [EC:4.2.1.11] [KO:K01689]			x	
pmn:PMN2A_1575	>gnl|kg|pmn:PMN2A_1575 enolase [EC:4.2.1.11] [KO:K01689]			x	
bfl:Bfl157	>gnl|kg|bfl:Bfl157 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
lpp:lpp2020	>gnl|kg|lpp:lpp2020 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
hhe:HH0631	>gnl|kg|hhe:HH0631 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
ddi:DDB0231356	>gnl|kg|ddi:DDB0231356 enoB; 2-phospho-D-glycerate hydrolase [EC:4.2.1.11] [KO:K01689]			x	
psb:Psyr_1482	>gnl|kg|psb:Psyr_1482 enolase [EC:4.2.1.11] [KO:K01689]			x	
noc:Noc_0852	>gnl|kg|noc:Noc_0852 phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
pst:PSPTO4616	>gnl|kg|pst:PSPTO4616 eno-2; enolase [EC:4.2.1.11] [KO:K01689]			x	
cyb:CYB_2531	>gnl|kg|cyb:CYB_2531 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
neu:NE1044	>gnl|kg|neu:NE1044 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
twh:TWT783	>gnl|kg|twh:TWT783 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
cje:Cj1672c	>gnl|kg|cje:Cj1672c eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
wol:WD0494	>gnl|kg|wol:WD0494 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
cne:CNE00040	>gnl|kg|cne:CNE00040 enolase 1, putative [EC:4.2.1.11] [KO:K01689]			x	
cne:CNE05250	>gnl|kg|cne:CNE05250 enolase 1, putative			x	
sce:YMR323W	>gnl|kg|sce:YMR323W Hypothetical ORF [EC:4.2.1.11] [KO:K01689]			x	
cjr:CJE1844	>gnl|kg|cjr:CJE1844 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
sce:YPL281C	>gnl|kg|sce:YPL281C ERR2; enolase-related subtelomeric sequence (ERR1 and ERR2 code for identical proteins)			x	x
sce:YOR393W	>gnl|kg|sce:YOR393W ERR1; Protein of unknown function, has similarity to enolases [EC:4.2.1.11] [KO:K01689]			x	x
tws:TW793	>gnl|kg|tws:TW793 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
lla:L0008	>gnl|kg|lla:L0008 enoB; 2-phosphoglycerate dehydratase [EC:4.2.1.11] [KO:K01689]			x	
buc:BU417	>gnl|kg|buc:BU417 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
bab:bbp377	>gnl|kg|bab:bbp377 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
cca:CCA00963	>gnl|kg|cca:CCA00963 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
cab:CAB932	>gnl|kg|cab:CAB932 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
mhy:mhp129	>gnl|kg|mhy:mhp129 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
mhj:MHJ_0242	>gnl|kg|mhj:MHJ_0242 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
mca:MCA1933	>gnl|kg|mca:MCA1933 eno-1; enolase [EC:4.2.1.11] [KO:K01689]			x	
mhp:MHP7448_0250	>gnl|kg|mhp:MHP7448_0250 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
uur:UU184	>gnl|kg|uur:UU184 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
ape:APE2458	>gnl|kg|ape:APE2458 enolase [EC:4.2.1.11] [KO:K01689]			x	
bas:BUsg400	>gnl|kg|bas:BUsg400 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
mba:Mbar_A2850	>gnl|kg|mba:Mbar_A2850 phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
wbm:Wbm0119	>gnl|kg|wbm:Wbm0119 enolase [EC:4.2.1.11] [KO:K01689]			x	
lac:LBA0889	>gnl|kg|lac:LBA0889 2-phosphoglycerate dehydratase [EC:4.2.1.11] [KO:K01689]			x	
mge:MG407	>gnl|kg|mge:MG407 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
cmu:TC0876	>gnl|kg|cmu:TC0876 enolase [EC:4.2.1.11] [KO:K01689]			x	
mac:MA1672	>gnl|kg|mac:MA1672 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
ljo:LJ1416	>gnl|kg|ljo:LJ1416 enolase [EC:4.2.1.11] [KO:K01689]			x	
mma:MM2836	>gnl|kg|mma:MM2836 enolase [EC:4.2.1.11] [KO:K01689]			x	
ctr:CT587	>gnl|kg|ctr:CT587 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
cta:CTA_0637	>gnl|kg|cta:CTA_0637 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
atu:Atu1426	>gnl|kg|atu:Atu1426 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
bpn:BPEN_162	>gnl|kg|bpn:BPEN_162 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
ama:AM600	>gnl|kg|ama:AM600 eno; Enolase 1 (2-phosphoglycerate dehydratase 1) [EC:4.2.1.11] [KO:K01689]			x	
ljo:LJ1246	>gnl|kg|ljo:LJ1246 enolase [EC:4.2.1.11] [KO:K01689]			x	
son:SO3440	>gnl|kg|son:SO3440 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
ecn:Ecaj_0489	>gnl|kg|ecn:Ecaj_0489 enolase [EC:4.2.1.11] [KO:K01689]			x	
eru:Erum4840	>gnl|kg|eru:Erum4840 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
erw:ERWE_CDS_05060	>gnl|kg|erw:ERWE_CDS_05060 eno; enolase (2-phosphoglycerate dehydratase) [EC:4.2.1.11] [KO:K01689]			x	
ptr:454457	>gnl|kg|ptr:454457 LOC454457; similar to enolase 3; enolase-3, beta, muscle; muscle specific enolase; beta enolase; skeletal muscle enolase; 2-phospho-D-glycerate hydrolyase			x	x
wbr:WGLp353	>gnl|kg|wbr:WGLp353 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
erg:ERGA_CDS_04960	>gnl|kg|erg:ERGA_CDS_04960 eno; enolase (2-phosphoglycerate dehydratase) [EC:4.2.1.11] [KO:K01689]			x	
mth:MTH43	>gnl|kg|mth:MTH43 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
rno:310585	>gnl|kg|rno:310585 LOC310585; similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1)			x	
sso:SSO0913	>gnl|kg|sso:SSO0913 enolase [EC:4.2.1.11] [KO:K01689]			x	
ecu:ECU10_1690	>gnl|kg|ecu:ECU10_1690 10_1690, ENOLASE, ENO_FASHE, gene found by Glimmer [EC:4.2.1.11] [KO:K01689]			x	
pub:SAR11_0939	>gnl|kg|pub:SAR11_0939 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
sto:ST1212	>gnl|kg|sto:ST1212 enolase [EC:4.2.1.11] [KO:K01689]			x	
mst:Msp_0862	>gnl|kg|mst:Msp_0862 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
hma:rrnAC0069	>gnl|kg|hma:rrnAC0069 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
nph:NP2846A	>gnl|kg|nph:NP2846A eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
sai:Saci_1377	>gnl|kg|sai:Saci_1377 eno; enolase [EC:4.2.1.11] [KO:K01689]			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
pai:PAE0812	>gnl|kg|pai:PAE0812 enolase [EC:4.2.1.11] [KO:K01689]			x	
afu:AF1132	>gnl|kg|afu:AF1132 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
hal:VNG1142G	>gnl|kg|hal:VNG1142G eno; enolase [EC:4.2.1.11] [KO:K01689]			x	
tac:Ta0882	>gnl|kg|tac:Ta0882 enolase [EC:4.2.1.11] [KO:K01689]			x	
tvo:TVN0981	>gnl|kg|tvo:TVN0981 enolase [EC:4.2.1.11] [KO:K01689]			x	
pto:PTO1234	>gnl|kg|pto:PTO1234 eno; phosphopyruvate hydratase [EC:4.2.1.11] [KO:K01689]			x	
sme:SMb20510	>gnl|kg|sme:SMb20510 dgoA; probable galactonate dehydratase protein [EC:4.2.1.6] [KO:K01684]			x	
pst:PSPTO2179	>gnl|kg|pst:PSPTO2179 mandelate racemase/muconate lactonizing enzyme family protein [EC:4.2.1.6] [KO:K01684]			x	x
psp:PSPPH_1958	>gnl|kg|psp:PSPPH_1958 dgoD; galactonate dehydratase [EC:4.2.1.6] [KO:K01684]			x	
oih:OB2215	>gnl|kg|oih:OB2215 putative galactonate dehydratase [EC:4.2.1.6] [KO:K01684]			x	
bps:BPSL0699	>gnl|kg|bps:BPSL0699 putative galactonate dehydratase protein [EC:4.2.1.6] [KO:K01684]			x	
vvy:VVA1580	>gnl|kg|vvy:VVA1580 probable galactonate dehydratase protein [EC:4.2.1.6] [KO:K01684]			x	
gka:GK1955	>gnl|kg|gka:GK1955 galactonate dehydratase [EC:4.2.1.6] [KO:K01684]			x	
eco:b4478	>gnl|kg|eco:b4478 dgoD; galactonate dehydratase [EC:4.2.1.6] [KO:K01684]			x	
bcl:ABC0524	>gnl|kg|bcl:ABC0524 galactonate dehydratase [EC:4.2.1.6] [KO:K01684]			x	
bld:BLi04070	>gnl|kg|bld:BLi04070 hypothetical protein [EC:4.2.1.6] [KO:K01684]			x	
xcv:XCV1796	>gnl|kg|xcv:XCV1796 dgoD; galactonate dehydratase [EC:4.2.1.6] [KO:K01684]			x	
sco:SCO3475	>gnl|kg|sco:SCO3475 SCE65.11c; putative galactonate dehydratase protein [EC:4.2.1.6] [KO:K01684]			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
psb:Psyr_3120	>gnl|kg|psb:Psyr_3120 glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x	
ppu:PP4757	>gnl|kg|ppu:PP4757 glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x	
pst:PSPTO3285	>gnl|kg|pst:PSPTO3285 gudD; glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x	
bsu:BG11161	>gnl|kg|bsu:BG11161 ycbF; glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x	
eca:ECA3575	>gnl|kg|eca:ECA3575 gudD; glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x	
reu:Reut_B3715	>gnl|kg|reu:Reut_B3715 glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x	
msu:MS0689	>gnl|kg|msu:MS0689 dgoA; O-succinylbenzoate synthase and related enzymes [EC:4.2.1.40] [KO:K01706]			x	x
stm:STM2960	>gnl|kg|stm:STM2960 gudD; D-glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x	
sec:SC2900	>gnl|kg|sec:SC2900 gudD; D-glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x	
oih:OB2836	>gnl|kg|oih:OB2836 glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x	
sty:STY3098	>gnl|kg|sty:STY3098 ygcX; probable glucarate dehydratase 1 [EC:4.2.1.40] [KO:K01706]			x	
stt:t2869	>gnl|kg|stt:t2869 ygcX; probable glucarate dehydratase 1 [EC:4.2.1.40] [KO:K01706]			x	
rso:RSc1079	>gnl|kg|rso:RSc1079 gudD1, RS04108; probable glucarate dehydratase protein [EC:4.2.1.40] [KO:K01706]			x	
ecj:JW2758	>gnl|kg|ecj:JW2758 ygcX; Probable glucarate dehydrogenase 1 (GDH) [EC:4.2.1.40] [KO:K01706]			x	
ecs:ECs3647	>gnl|kg|ecs:ECs3647 putative glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x	
eco:b2787	>gnl|kg|eco:b2787 gudD, ygcX, gdh1; (D)-glucarate dehydratase 1 [EC:4.2.1.40] [KO:K01706]			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
sfl:SF2800	>gnl|kg|sfl:SF2800 ygcX; putative glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x	
sfx:S2994	>gnl|kg|sfx:S2994 ygcX; putative glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x	
ece:Z4102	>gnl|kg|ece:Z4102 ygcX; putative glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x	
sbo:SBO_2668	>gnl|kg|sbo:SBO_2668 ygcX; putative glucarate dehydratase			x	
bte:BTH_I0189	>gnl|kg|bte:BTH_I0189 glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x	
spt:SPA2825	>gnl|kg|spt:SPA2825 ygcX; probable glucarate dehydratase 1 [EC:4.2.1.40] [KO:K01706]			x	
bld:BLi00287	>gnl|kg|bld:BLi00287 ycbF; similar to glucarate dehydratase; RBL01496 [EC:4.2.1.40] [KO:K01706]			x	x
ssn:SSO_2944	>gnl|kg|ssn:SSO_2944 ygcX; putative glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x	
bja:blr5872	>gnl|kg|bja:blr5872 gudD; glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x	
xcc:XCC3242	>gnl|kg|xcc:XCC3242 tcbD; glucarate hydratase [EC:4.2.1.40] [KO:K01706]			x	
xcb:XC_0951	>gnl|kg|xcb:XC_0951 glucarate hydratase [EC:4.2.1.40] [KO:K01706]			x	
aci:ACIAD0128	>gnl|kg|aci:ACIAD0128 gudD; D-glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x	
bur:Bcep18194_A3396	>gnl|kg|bur:Bcep18194_A3396 glucarate dehydratase [EC:4.2.1.40] [KO:K01706]			x	
rso:RSp0829	>gnl|kg|rso:RSp0829 gudD2, RS05366; probable glucarate dehydratase protein [EC:4.2.1.40] [KO:K01706]			x	
ece:Z0892	>gnl|kg|ece:Z0892 putative methylaspartate ammonia-lyase [EC:4.3.1.2] [KO:K04835]			x	
ecs:ECs0761	>gnl|kg|ecs:ECs0761 3-methylaspartate ammonia-lyase [EC:4.3.1.2] [KO:K04835]			x	
sdy:SDY_0673	>gnl|kg|sdy:SDY_0673 putative methylaspartate ammonia-lyase			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
mlo:mlr6095	>gnl|kg|mlo:mlr6095 3-methylaspartate ammonia-lyase [EC:4.3.1.2] [KO:K04835]			x	
ctc:CTC02563	>gnl|kg|ctc:CTC02563 methylaspartate ammonia-lyase [EC:4.3.1.2] [KO:K04835]			x	
hal:VNG2289G	>gnl|kg|hal:VNG2289G mal; methylaspartate ammonia-lyase [EC:4.3.1.2] [KO:K04835]			x	
msu:MS1791	>gnl|kg|msu:MS1791 dgoA; O-succinylbenzoate synthase and related enzymes [EC:4.2.1.-] [KO:K02549]			x	x
bsu:BG13847	>gnl|kg|bsu:BG13847 menC, ytfD; o-succinylbenzoate synthase [EC:4.2.1.-] [KO:K02549]			x	
vvy:VV1119	>gnl|kg|vvy:VV1119 O-succinylbenzoate synthase [EC:4.2.1.-] [KO:K02549]			x	
hit:NTHI1142	>gnl|kg|hit:NTHI1142 menC; O-succinylbenzoate synthase [EC:4.2.1.-] [KO:K02549]			x	
btk:BT9727_4584	>gnl|kg|btk:BT9727_4584 enolase superfamily protein; possible N-acylamino acid racemase, mandelate racemase/muconate lactonizing enzyme, or o-succinylbenzoate synthase [EC:4.2.1.-] [KO:K02549]			x	x
ban:BA5107	>gnl|kg|ban:BA5107 N-acylamino acid racemase [EC:4.2.1.-] [KO:K02549]			x	
bat:BAS4746	>gnl|kg|bat:BAS4746 N-acylamino acid racemase [EC:4.2.1.-] [KO:K02549]			x	
bar:GBAA5107	>gnl|kg|bar:GBAA5107 N-acylamino acid racemase [EC:4.2.1.-] [KO:K02549]			x	
bcz:BCZK4606	>gnl|kg|bcz:BCZK4606 menC; possible N-acylamino acid racemase; possible O-succinylbenzoate synthase [EC:4.2.1.-] [KO:K02549]			x	x
bca:BCE5011	>gnl|kg|bca:BCE5011 N-acylamino acid racemase [EC:4.2.1.-] [KO:K02549]			x	
vfi:VF1667	>gnl|kg|vfi:VF1667 O-succinylbenzoate synthase [EC:4.2.1.-] [KO:K02549]			x	
cgl:NCgl0449	>gnl|kg|cgl:NCgl0449 Cgl0466; O-succinylbenzoate synthase or related enzyme [EC:4.2.1.-] [KO:K02549]			x	x

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
efa:EF0450	>gnl|kg|efa:EF0450 mandelate racemase/muconate lactonizing enzyme family protein [EC:4.2.1.-] [KO:K02549]			x	x
dps:DP0251	>gnl|kg|dps:DP0251 menC; similar to N-acylamino acid racemase (MenC)			x	
pgi:PG1522	>gnl|kg|pgi:PG1522 mandelate racemase/muconate lactonizing enzyme family protein			x	x
ava:Ava_2635	>gnl|kg|ava:Ava_2635 O-succinylbenzoate synthase [EC:4.2.1.-] [KO:K02549]			x	
ana:alr0034	>gnl|kg|ana:alr0034 menC; O-succinylbenzoic acid synthase [EC:4.2.1.-] [KO:K02549]			x	
gka:GK0926	>gnl|kg|gka:GK0926 N-acylamino acid racemase [EC:4.2.1.-] [KO:K02549]			x	
syw:SYNW2306	>gnl|kg|syw:SYNW2306 menC; putative O-succinylbenzoate synthase [EC:4.2.1.-] [KO:K02549]			x	
sav:SAV1796	>gnl|kg|sav:SAV1796 menC; o-succinylbenzoic acid synthetase [EC:4.2.1.-] [KO:K02549]			x	
sau:SA1614	>gnl|kg|sau:SA1614 menC; o-succinylbenzoic acid (OSB) synthetase [EC:4.2.1.-] [KO:K02549]			x	
sac:SACOL1843	>gnl|kg|sac:SACOL1843 O-succinylbenzoic acid (OSB) synthetase, putative [EC:4.2.1.-] [KO:K02549]			x	
saa:SAUSA300_1735	>gnl|kg|saa:SAUSA300_1735 menC; O-succinylbenzoic acid synthetase [EC:4.2.1.-]			x	
oih:OB2713	>gnl|kg|oih:OB2713 N-acylamino acid racemase [EC:4.2.1.-] [KO:K02549]			x	
sam:MW1734	>gnl|kg|sam:MW1734 menC; O-succinylbenzoic acid synthetase [EC:4.2.1.-] [KO:K02549]			x	
pmt:PMT2058	>gnl|kg|pmt:PMT2058 menC; putative O-succinylbenzoate synthase [EC:4.2.1.-] [KO:K02549]			x	
sab:SAB1650c	>gnl|kg|sab:SAB1650c O-succinylbenzoic acid synthetase [EC:4.2.1.-]			x	
lmf:LMOf2365_2493	>gnl|kg|lmf:LMOf2365_2493 N-acylamino acid racemase [EC:4.2.1.-] [KO:K02549]			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
sep:SE1463	>gnl|kg|sep:SE1463 o-succinylbenzoic acid (OSB) synthetase [EC:4.2.1.-] [KO:K02549]			x	
ser:SERP1357	>gnl|kg|ser:SERP1357 O-succinylbenzoic acid synthetase, putative [EC:4.2.1.-] [KO:K02549]			x	
bmb:BruAb1_1023	>gnl|kg|bmb:BruAb1_1023 mandelate racemase/muconate lactonizing enzyme family protein			x	x
atu:Atu1648	>gnl|kg|atu:Atu1648 mandelate racemase/muconate lactonizing enzyme family protein			x	x
dde:Dde_1177	>gnl|kg|dde:Dde_1177 L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily-like			x	x
sty:STY1382	>gnl|kg|sty:STY1382 putative mandelate racemase / muconate lactonizing enzyme family protein			x	x
stt:t1585	>gnl|kg|stt:t1585 muconate lactonizing enzyme family protein			x	x
eco:b1325	>gnl|kg|eco:b1325 ycjG, ycjH; L-Ala-D/L-Glu epimerase, a muconate lactonizing enzyme			x	x
ccr:CC3113	>gnl|kg|ccr:CC3113 mandelate racemase/muconate lactonizing enzyme family protein			x	x
bce:BC2850	>gnl|kg|bce:BC2850 mandelate racemase/muconate lactonizing enzyme family protein			x	x
ban:BA2850	>gnl|kg|ban:BA2850 mandelate racemase/muconate lactonizing enzyme family protein			x	x
bat:BAS2659	>gnl|kg|bat:BAS2659 mandelate racemase/muconate lactonizing enzyme family protein			x	x
bar:GBAA2850	>gnl|kg|bar:GBAA2850 mandelate racemase/muconate lactonizing enzyme family protein			x	x
sil:SPO3606	>gnl|kg|sil:SPO3606 mandelate racemase/muconate lactonizing enzyme family protein			x	x
bca:BCE2879	>gnl|kg|bca:BCE2879 mandelate racemase/muconate lactonizing enzyme family protein			x	x
eca:ECA0139	>gnl|kg|eca:ECA0139 putative mandelate racemase / muconate lactonizing enzyme family protein			x	x
nph:NP2480A	>gnl|kg|nph:NP2480A mandelate racemase homolog / muconate lactonizing enzyme homolog			x	x

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
ppu:PP3715	>gnl|kg|ppu:PP3715 catB; muconate cycloisomerase			x	
pfl:PFL_3862	>gnl|kg|pfl:PFL_3862 catB; muconate cycloisomerase [EC:5.5.1.1] [KO:K01856]			x	
pae:PA2509	>gnl|kg|pae:PA2509 catB; muconate cycloisomerase I [EC:5.5.-.-]			x	
bur:Bcep18194_B2328	>gnl|kg|bur:Bcep18194_B2328 muconate cycloisomerase [EC:5.5.1.1] [KO:K01856]			x	
bte:BTH_II0485	>gnl|kg|bte:BTH_II0485 muconate cycloisomerase			x	
bps:BPSS1891	>gnl|kg|bps:BPSS1891 catB; muconate cycloisomerase I [EC:5.5.1.1] [KO:K01856]			x	
bma:BMAA0200	>gnl|kg|bma:BMAA0200 catB; muconate cycloisomerase [EC:5.5.1.1] [KO:K01856]			x	
bpm:BURPS1710b_A0986	>gnl|kg|bpm:BURPS1710b_A0986 catB; muconate cycloisomerase [EC:5.5.1.1] [KO:K01856]			x	
cef:CE2303	>gnl|kg|cef:CE2303 putative muconate cycloisomerase			x	
bms:BR0245	>gnl|kg|bms:BR0245 mandelate racemase/muconate lactonizing enzyme domain protein			x	x
bmb:BruAb1_0240	>gnl|kg|bmb:BruAb1_0240 mandelate racemase/muconate lactonizing enzyme domain protein			x	x
hsa:55556	>gnl|kg|hsa:55556 ENOSF1; enolase superfamily member 1			x	x
ppu:PP2831	>gnl|kg|ppu:PP2831 mandelate racemase/muconate lactonizing enzyme family protein			x	x
pmu:PM0524	>gnl|kg|pmu:PM0524 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]			x	
psp:PSPPH_4147	>gnl|kg|psp:PSPPH_4147 phosphatase, YrbI family [EC:3.1.3.45] [KO:K03270]			x	
pst:PSPTO4449	>gnl|kg|pst:PSPTO4449 phosphatase, YrbI family [EC:3.1.3.45] [KO:K03270]			x	
hin:HI1679	>gnl|kg|hin:HI1679 yrbI; putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]			x	
pfo:Pfl_0861	>gnl|kg|pfo:Pfl_0861 kdsC; phosphatase KdsC [EC:3.1.3.45] [KO:K03270]			x	
ppu:PP0956	>gnl|kg|ppu:PP0956 phosphatase, YrbI family [EC:3.1.3.45] [KO:K03270]			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
hit:NTHI1982	>gnl|kg|hit:NTHI1982 yrbI; 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]			x	
pae:PA4458	>gnl|kg|pae:PA4458 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]			x	
nme:NMB0353	>gnl|kg|nme:NMB0353 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]			x	
pfl:PFL_0919	>gnl|kg|pfl:PFL_0919 kdsC; 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]			x	
msu:MS0995	>gnl|kg|msu:MS0995 uncharacterized proteins of HAD superfamily, CMP-Neu5Ac similarity [EC:3.1.3.45] [KO:K03270]			x	x
ngo:NGO1608	>gnl|kg|ngo:NGO1608 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (KDO 8-P phosphatase) [EC:3.1.3.45] [KO:K03270]			x	
nma:NMA2134	>gnl|kg|nma:NMA2134 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]			x	
psb:Psyr_4143	>gnl|kg|psb:Psyr_4143 yrbI; HAD-superfamily hydrolase, subfamily IIIA:phosphatase YrbI [EC:3.1.3.45] [KO:K03270]			x	
syw:SYNW0186	>gnl|kg|syw:SYNW0186 possible phosphatase [EC:3.1.3.45] [KO:K03270]			x	x
hpj:jhp1478	>gnl|kg|hpj:jhp1478 putative [EC:3.1.3.45] [KO:K03270]			x	
syd:Syncc9605_0182	>gnl|kg|syd:Syncc9605_0182 kdsC; phosphatase KdsC			x	x
hpy:HP1570	>gnl|kg|hpy:HP1570 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]			x	
sye:Syncc9902_0210	>gnl|kg|sye:Syncc9902_0210 kdsC; phosphatase KdsC			x	x
aae:aq_2171	>gnl|kg|aae:aq_2171 putative 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [EC:3.1.3.45] [KO:K03270]			x	
vvy:VVA0474	>gnl|kg|vvy:VVA0474 phosphonoacetaldehyde phosphonohydrolase			x	
pfo:Pfl_3684	>gnl|kg|pfo:Pfl_3684 phosphonoacetaldehyde hydrolase			x	
pfl:PFL_3966	>gnl|kg|pfl:PFL_3966 phnX; 2-phosphonoacetaldehyde hydrolase [EC:3.11.1.1] [KO:K05306]			x	
pae:PA1311	>gnl|kg|pae:PA1311 phnX; 2-phosphonoacetaldehyde hydrolase			x	
ppu:PP2208	>gnl|kg|ppu:PP2208 phnX; 2-phosphonoacetaldehyde hydrolase			x	
vch:VCA0606	>gnl|kg|vch:VCA0606 phosphonoacetaldehyde phosphonohydrolase			x	

Table L-3. KEGG Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>vpa:VPA0233</td><td>>gnl|kg|vpa:VPA0233 phosphonoacetaldehyde phosphonohydrolase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>stm:STM0432</td><td>>gnl|kg|stm:STM0432 phnX; 2-aminoethylphosphonate transport</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sty:STY0471</td><td>>gnl|kg|sty:STY0471 phnX; phosphonoacetaldehyde phosphonohydrolase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>stt:t2431</td><td>>gnl|kg|stt:t2431 phnX; phosphonoacetaldehyde phosphonohydrolase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>spt:SPA2291</td><td>>gnl|kg|spt:SPA2291 phnX; phosphonoacetaldehyde phosphonohydrolase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bca:BCE1439</td><td>>gnl|kg|bca:BCE1439 phnX; phosphonoacetaldehyde phosphonohydrolase [EC:3.11.1.1] [KO:K05306]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bat:BAS1239</td><td>>gnl|kg|bat:BAS1239 phosphonoacetaldehyde phosphonohydrolase [EC:3.11.1.1] [KO:K05306]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ban:BA1340</td><td>>gnl|kg|ban:BA1340 phnX; phosphonoacetaldehyde phosphonohydrolase [EC:3.11.1.1] [KO:K05306]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>baa:BA_1865</td><td>>gnl|kg|baa:BA_1865 haloacid dehalogenase-like hydrolase [EC:3.11.1.1] [KO:K05306]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>bar:GBAA1340</td><td>>gnl|kg|bar:GBAA1340 phnX; phosphonoacetaldehyde phosphonohydrolase [EC:3.11.1.1] [KO:K05306]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>btk:BT9727_1215</td><td>>gnl|kg|btk:BT9727_1215 phnX; possible phosphonoacetaldehyde hydrolase [EC:3.11.1.1] [KO:K05306]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bcz:BCZK1217</td><td>>gnl|kg|bcz:BCZK1217 phnX; possible phosphonoacetaldehyde hydrolase [EC:3.11.1.1] [KO:K05306]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>lpl:lp_0711</td><td>>gnl|kg|lpl:lp_0711 phnX; phosphonoacetaldehyde hydrolase [EC:3.11.1.1] [KO:K05306]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>rpa:RPA4199</td><td>>gnl|kg|rpa:RPA4199 putative 2-haloacid halidohydrolase Iva [EC:3.8.1.2] [KO:K01560]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bja:blr7560</td><td>>gnl|kg|bja:blr7560 dhlB; 2-haloalkanoic acid dehalogenase [EC:3.8.1.2] [KO:K01560]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>rso:RSc1362</td><td>>gnl|kg|rso:RSc1362 RS04644; putative 2-haloalkanoic acid dehalogenase protein [EC:3.8.1.2] [KO:K01560]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bpm:BURPS1710b_2616</td><td>>gnl|kg|bpm:BURPS1710b_2616 dehII; haloacid dehalogenase, type II [EC:3.8.1.2] [KO:K01560]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-3. KEGG Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>bps:BPSL2191</td><td>>gnl|kg|bps:BPSL2191 putative dehalogenase [EC:3.8.1.2] [KO:K01560]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bma:BMA1589</td><td>>gnl|kg|bma:BMA1589 dheII; haloacid dehalogenase, type II [EC:3.8.1.2] [KO:K01560]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>reu:Reut_A1952</td><td>>gnl|kg|reu:Reut_A1952 haloacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2 [EC:3.8.1.2] [KO:K01560]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bte:BTH_I1995</td><td>>gnl|kg|bte:BTH_I1995 dehII-1; haloacid dehalogenase, type II [EC:3.8.1.2] [KO:K01560]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>mlo:mll7634</td><td>>gnl|kg|mlo:mll7634 2-haloacid halidohydrolase Iva</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bur:Bcep18194_A5360</td><td>>gnl|kg|bur:Bcep18194_A5360 haloacid dehalogenase, type II [EC:3.8.1.2] [KO:K01560]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sme:SMc00103</td><td>>gnl|kg|sme:SMc00103 dhe; putative alpha-halocarboxylic acid dehalogenase protein [EC:3.8.1.-]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>bmb:BruAb1_0587</td><td>>gnl|kg|bmb:BruAb1_0587 haloacid dehalogenase [EC:3.8.1.2] [KO:K01560]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bms:BR0565</td><td>>gnl|kg|bms:BR0565 haloacid dehalogenase, type II [EC:3.8.1.2] [KO:K01560]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>eba:ebA812</td><td>>gnl|kg|eba:ebA812 putative 2-haloalkanoic acid dehalogenase [EC:3.8.1.2] [KO:K01560]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>mag:amb2538</td><td>>gnl|kg|mag:amb2538 2-haloalkanoic acid dehalogenase I</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bsu:BG12422</td><td>>gnl|kg|bsu:BG12422 yvdM; putative beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>lpl:lp_0027</td><td>>gnl|kg|lpl:lp_0027 pgmB1; beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>nme:NMB0391</td><td>>gnl|kg|nme:NMB0391 beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>lla:L0001</td><td>>gnl|kg|lla:L0001 pgmB; beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>lpl:lp_0066</td><td>>gnl|kg|lpl:lp_0066 pgmB2; beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>nma:NMA2093</td><td>>gnl|kg|nma:NMA2093 pgm2; beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-3. KEGG Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>lin:lin2964</td><td>>gnl|kg|lin:lin2964 similar to phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>ecs:ECs1896</td><td>>gnl|kg|ecs:ECs1896 putative beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ece:Z2465</td><td>>gnl|kg|ece:Z2465 ycjU; putative beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sfl:SF1323</td><td>>gnl|kg|sfl:SF1323 ycjU; putative beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sfx:S1406</td><td>>gnl|kg|sfx:S1406 ycjU; putative beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>lmf:LMOf2365_2822</td><td>>gnl|kg|lmf:LMOf2365_2822 beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>lmo:lmo2831</td><td>>gnl|kg|lmo:lmo2831 putative beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>nma:NMA2097</td><td>>gnl|kg|nma:NMA2097 pgm1; beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ecc:c1789</td><td>>gnl|kg|ecc:c1789 ycjU; putative beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>eco:b1317</td><td>>gnl|kg|eco:b1317 ycjU, pgmB; putative beta phosphoglucomutase, contains a phophatase-like domain [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ecj:JW1310</td><td>>gnl|kg|ecj:JW1310 ycjU; Putative beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ssn:SSO_1823</td><td>>gnl|kg|ssn:SSO_1823 ycjU; putative beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>efa:EF0956</td><td>>gnl|kg|efa:EF0956 pgmB; beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>mpu:MYPU_6350</td><td>>gnl|kg|mpu:MYPU_6350 pgmB; beta-phosphoglucomutase [EC:5.4.2.6] [KO:K01838]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sma:SAV2998</td><td>>gnl|kg|sma:SAV2998 ptlA; pentalenene synthase [EC:4.2.3.7]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>gsu:GSU3061</td><td>>gnl|kg|gsu:GSU3061 shc-2; squalene-hopene cyclase [EC:5.4.99.17]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
gsu:GSU0688	>gnl|kg|gsu:GSU0688 shc-1; squalene-hopene cyclase [EC:5.4.99.17]			x	
gme:Gmet_0419	>gnl|kg|gme:Gmet_0419 terpene synthase:squalene cyclase			x	
sco:SCO6764	>gnl|kg|sco:SCO6764 SC6A5.13; putative squalene-hopene cyclase			x	
gme:Gmet_2820	>gnl|kg|gme:Gmet_2820 terpene synthase:squalene cyclase			x	
rpa:RPA3740	>gnl|kg|rpa:RPA3740 sqhC; squalene-hopene-cyclase [EC:5.4.99.7] [KO:K01852]			x	
sma:SAV1650	>gnl|kg|sma:SAV1650 hopA; squalene-hopene cyclase			x	
tel:tlr2309	>gnl|kg|tel:tlr2309 shc; squalene-hopene-cyclase			x	
bja:blr3004	>gnl|kg|bja:blr3004 shc; squalene-hopene cyclase [EC:5.4.99.-]			x	x
ana:all0775	>gnl|kg|ana:all0775 squalene-hopene-cyclase			x	
zmo:ZMO0872	>gnl|kg|zmo:ZMO0872 shc; squalene--hopene cyclase [EC:5.4.99.17]			x	
rpb:RPB_1726	>gnl|kg|rpb:RPB_1726 squalene cyclase			x	
ava:Ava_4671	>gnl|kg|ava:Ava_4671 terpene synthase [EC:5.4.99.17]			x	
syn:slr2089	>gnl|kg|syn:slr2089 shc; squalene-hopene-cyclase			x	
gvi:glr4057	>gnl|kg|gvi:glr4057 shc; squalene-hopene cyclase			x	
mca:MCA0812	>gnl|kg|mca:MCA0812 sqhC; squalene-hopene cyclase [EC:5.4.99.-]			x	x
nwi:Nwi_2269	>gnl|kg|nwi:Nwi_2269 terpene synthase/squalene cyclase [EC:5.4.99.17]			x	
bps:BPSS2339	>gnl|kg|bps:BPSS2339 shc; squalene--hopene cyclase [EC:5.4.99.17]			x	
pca:Pcar_0441	>gnl|kg|pca:Pcar_0441 squalene-hopene cyclase			x	
bte:BTH_II2359	>gnl|kg|bte:BTH_II2359 shc; squalene-hopene cyclase [EC:5.4.99.17]			x	
bpm:BURPS1710b_A1490	>gnl|kg|bpm:BURPS1710b_A1490 shc; squalene-hopene cyclase [EC:5.4.99.17]			x	
bma:BMAA2100	>gnl|kg|bma:BMAA2100 shc; squalene-hopene cyclase [EC:5.4.99.17]			x	
bur:Bcep18194_B0019	>gnl|kg|bur:Bcep18194_B0019 terpene synthase/squalene cyclase [EC:5.4.99.17]			x	

Table L-3. KEGG Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>reu:Reut_B4954</td><td>>gnl|kg|reu:Reut_B4954 terpene synthase:squalene cyclase [EC:5.4.99.17]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>gox:GOX2260</td><td>>gnl|kg|gox:GOX2260 squalene-hopene cyclase [EC:5.4.99.17]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>noc:Noc_1320</td><td>>gnl|kg|noc:Noc_1320 terpene synthase/squalene cyclase [EC:5.4.99.17]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bca:BCE3572</td><td>>gnl|kg|bca:BCE3572 squalene-hopene cyclase [EC:5.4.99.-]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>bce:BC3557</td><td>>gnl|kg|bce:BC3557 squalene--hopene cyclase [EC:5.4.99.-]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>bsu:BG12679</td><td>>gnl|kg|bsu:BG12679 sqhC; squalene-hopene cyclase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>rru:Rru_A0062</td><td>>gnl|kg|rru:Rru_A0062 terpene synthase, squalene cyclase [EC:5.4.99.17]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>neu:NE1168</td><td>>gnl|kg|neu:NE1168 prenyltransferase and squalene oxidase repeats [EC:5.4.99.-]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>btk:BT9727_3315</td><td>>gnl|kg|btk:BT9727_3315 sqhC; squalene-hopene cyclase [EC:5.4.99.-]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bat:BAS3351</td><td>>gnl|kg|bat:BAS3351 squalene-hopene cyclase [EC:5.4.99.-]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>baa:BA_4104</td><td>>gnl|kg|baa:BA_4104 prenyltrans, prenyltransferase and squalene oxidase repeat [EC:5.4.99.-]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>bar:GBAA3612</td><td>>gnl|kg|bar:GBAA3612 squalene-hopene cyclase [EC:5.4.99.-]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>ban:BA3612</td><td>>gnl|kg|ban:BA3612 squalene-hopene cyclase [EC:5.4.99.-]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>bcz:BCZK3265</td><td>>gnl|kg|bcz:BCZK3265 sqhC; squalene-hopene cyclase [EC:5.4.99.-]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>nmu:Nmul_A2556</td><td>>gnl|kg|nmu:Nmul_A2556 squalene cyclase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>fra:Francci3_0823</td><td>>gnl|kg|fra:Francci3_0823 squalene cyclase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bur:Bcep18194_C7519</td><td>>gnl|kg|bur:Bcep18194_C7519 terpene synthase/squalene cyclase [EC:5.4.99.17]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>zmo:ZMO1548</td><td>>gnl|kg|zmo:ZMO1548 shc; squalene--hopene cyclase [EC:5.4.99.17]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>pca:Pcar_0355</td><td>>gnl|kg|pca:Pcar_0355 squalene--hopene cyclase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>hsa:84693</td><td>>gnl|kg|hsa:84693 MCEE; methylmalonyl CoA epimerase [EC:5.1.99.1] [KO:K05606]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ptr:459310</td><td>>gnl|kg|ptr:459310 LOC459310; similar to Methylmalonyl-CoA epimerase, mitochondrial precursor (DL-methylmalonyl-CoA racemase)</td><td></td><td></td><td>x</td><td>x</td></tr>
</table>

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
cfa:479018	>gnl|kg|cfa:479018 LOC479018; similar to Methylmalonyl-CoA epimerase, mitochondrial precursor (DL-methylmalonyl-CoA racemase)			x	x
bta:508170	>gnl|kg|bta:508170 LOC508170; similar to methylmalonyl-CoA epimerase			x	x
mmu:73724	>gnl|kg|mmu:73724 Mcee; methylmalonyl CoA epimerase [EC:5.1.99.1] [KO:K05606]			x	
rno:293829	>gnl|kg|rno:293829 Mcee_predicted; methylmalonyl CoA epimerase (predicted) [EC:5.1.99.1] [KO:K05606]			x	
cvi:CV0969	>gnl|kg|cvi:CV0969 hpd; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
bpm:BURPS1710b_0016	>gnl|kg|bpm:BURPS1710b_0016 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
bma:BMA2582	>gnl|kg|bma:BMA2582 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
bps:BPSL3239	>gnl|kg|bps:BPSL3239 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
bpa:BPP3767	>gnl|kg|bpa:BPP3767 bllY; putative hemolysin [EC:1.13.11.27] [KO:K00457]			x	
bbr:BB4213	>gnl|kg|bbr:BB4213 bllY; putative hemolysin [EC:1.13.11.27] [KO:K00457]			x	
bte:BTH_I3106	>gnl|kg|bte:BTH_I3106 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
rso:RSc3103	>gnl|kg|rso:RSc3103 RS00556; probable 4-hydroxyphenylpyruvate dioxygenase oxidoreductase protein [EC:1.13.11.27] [KO:K00457]			x	
bur:Bcep18194_A3420	>gnl|kg|bur:Bcep18194_A3420 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
bpe:BP3040	>gnl|kg|bpe:BP3040 bllY; putative hemolysin [EC:1.13.11.27] [KO:K00457]			x	
vvu:VV12768	>gnl|kg|vvu:VV12768 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
vvy:VV1495	>gnl|kg|vvy:VV1495 putitive hemolysin [EC:1.13.11.27] [KO:K00457]			x	

Table L-3. KEGG Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>vch:VC1344</td><td>>gnl|kg|vch:VC1344 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>pae:PA0865</td><td>>gnl|kg|pae:PA0865 hpd; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>vpa:VP1349</td><td>>gnl|kg|vpa:VP1349 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>mlo:mll8309</td><td>>gnl|kg|mlo:mll8309 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>pfo:Pfl_2917</td><td>>gnl|kg|pfo:Pfl_2917 4-hydroxyphenylpyruvate dioxygenase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>psb:Psyr_3330</td><td>>gnl|kg|psb:Psyr_3330 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bja:bll0339</td><td>>gnl|kg|bja:bll0339 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>pfl:PFL_3387</td><td>>gnl|kg|pfl:PFL_3387 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ppu:PP3433</td><td>>gnl|kg|ppu:PP3433 hpd; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>pst:PSPTO3553</td><td>>gnl|kg|pst:PSPTO3553 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>psp:PSPPH_3250</td><td>>gnl|kg|psp:PSPPH_3250 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>nar:Saro_0597</td><td>>gnl|kg|nar:Saro_0597 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>sme:SMc03211</td><td>>gnl|kg|sme:SMc03211 putative 4-hydroxyphenylpyruvate dioxygenase protein [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>reu:Reut_B4501</td><td>>gnl|kg|reu:Reut_B4501 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>rpa:RPA0005</td><td>>gnl|kg|rpa:RPA0005 hpd; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ret:RHE_CH01745</td><td>>gnl|kg|ret:RHE_CH01745 probable 4-hydroxyphenylpyruvate dioxygenase protein [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>noc:Noc_1437</td><td>>gnl|kg|noc:Noc_1437 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
hch:HCH_00955	>gnl|kg|hch:HCH_00955 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
xac:XAC0452	>gnl|kg|xac:XAC0452 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
ppr:PBPRB1180	>gnl|kg|ppr:PBPRB1180 putative 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
xcv:XCV0482	>gnl|kg|xcv:XCV0482 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
xcb:XC_0450	>gnl|kg|xcb:XC_0450 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
xcc:XCC0436	>gnl|kg|xcc:XCC0436 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
eli:ELI_06415	>gnl|kg|eli:ELI_06415 4-hydroxyphenylpyruvate dioxygenase			x	
lpn:lpg2278	>gnl|kg|lpn:lpg2278 hpd; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
xoo:XOO4071	>gnl|kg|xoo:XOO4071 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
lpf:lpl2204	>gnl|kg|lpf:lpl2204 lly; 4-hydroxyphenylpyruvate dioxygenase (legiolysin) [EC:1.13.11.27] [KO:K00457]			x	
lpp:lpp2232	>gnl|kg|lpp:lpp2232 lly; 4-hydroxyphenylpyruvate dioxygenase (legiolysin) [EC:1.13.11.27] [KO:K00457]			x	
ccr:CC2533	>gnl|kg|ccr:CC2533 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
ilo:IL0722	>gnl|kg|ilo:IL0722 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
pfo:Pfl_4905	>gnl|kg|pfo:Pfl_4905 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
pae:PA0242	>gnl|kg|pae:PA0242 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
ppu:PP2554	>gnl|kg|ppu:PP2554 4-hydroxyphenylpyruvate dioxygenase, putative [EC:1.13.11.27] [KO:K00457]			x	
pst:PSPTO2346	>gnl|kg|pst:PSPTO2346 4-hydroxyphenylpyruvate dioxygenase, putative [EC:1.13.11.27] [KO:K00457]			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
psb:Psyr_2130	>gnl|kg|psb:Psyr_2130 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
psp:PSPPH_2105	>gnl|kg|psp:PSPPH_2105 4-hydroxyphenylpyruvate dioxygenase, putative [EC:1.13.11.27] [KO:K00457]			x	
ptr:473296	>gnl|kg|ptr:473296 HPD; 4-hydroxyphenylpyruvate dioxygenase			x	
pfl:PFL_5385	>gnl|kg|pfl:PFL_5385 4-hydroxyphenylpyruvate dioxygenase, putative [EC:1.13.11.27] [KO:K00457]			x	
hsa:3242	>gnl|kg|hsa:3242 HPD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
mmu:15445	>gnl|kg|mmu:15445 Hpd; 4-hydroxyphenylpyruvic acid dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
bta:516058	>gnl|kg|bta:516058 HPD; 4-hydroxyphenylpyruvate dioxygenase			x	
rno:29531	>gnl|kg|rno:29531 Hpd; 4-hydroxyphenylpyruvic acid dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
sil:SPO1426	>gnl|kg|sil:SPO1426 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
ath:At1g06570	>gnl|kg|ath:At1g06570 F12K11.9; 4-hydroxyphenylpyruvate dioxygenase (HPD) [EC:1.13.11.27] [KO:K00457]			x	
son:SO1962	>gnl|kg|son:SO1962 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
sco:SCO2927	>gnl|kg|sco:SCO2927 SCE19A.27c; putative 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
ssc:397443	>gnl|kg|ssc:397443 HPD; 4-hydroxyphenylpyruvic acid dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
bja:bll1053	>gnl|kg|bja:bll1053 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
sma:SAV5149	>gnl|kg|sma:SAV5149 hpd; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
rso:RS04776	>gnl|kg|rso:RS04776 RSp1347; probable 4-hydroxyphenylpyruvate dioxygenase oxidoreductase protein [EC:1.13.11.27] [KO:K00457]			x	
rso:RS05661	>gnl|kg|rso:RS05661 RSp1316; probable 4-hydroxyphenylpyruvate dioxygenase oxidoreductase protein [EC:1.13.11.27] [KO:K00457]			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
rso:RS02058	>gnl|kg|rso:RS02058 RSp1400; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
pha:PSHAa2168	>gnl|kg|pha:PSHAa2168 melA; 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) [EC:1.13.11.27] [KO:K00457]			x	
atc:AGR_L_678	>gnl|kg|atc:AGR_L_678 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
atu:Atu4529	>gnl|kg|atu:Atu4529 putative 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
xla:495029	>gnl|kg|xla:495029 LOC495029; hypothetical LOC495029 [EC:1.13.11.27] [KO:K00457]			x	
sru:SRU_1370	>gnl|kg|sru:SRU_1370 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
bur:Bcep18194_B1625	>gnl|kg|bur:Bcep18194_B1625 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
bba:Bd3543	>gnl|kg|bba:Bd3543 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
nar:Saro_1586	>gnl|kg|nar:Saro_1586 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27]			x	
bce:BC0252	>gnl|kg|bce:BC0252 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
ban:BA0240	>gnl|kg|ban:BA0240 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
baa:BA_0807	>gnl|kg|baa:BA_0807 glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily [EC:1.13.11.27] [KO:K00457]			x	x
btk:BT9727_0213	>gnl|kg|btk:BT9727_0213 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
bcz:BCZK0215	>gnl|kg|bcz:BCZK0215 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
bar:GBAA0240	>gnl|kg|bar:GBAA0240 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	
bat:BAS0226	>gnl|kg|bat:BAS0226 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]			x	

Table L-3. KEGG Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>bca:BCE0260</td><td>>gnl|kg|bca:BCE0260 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>cps:CPS_3484</td><td>>gnl|kg|cps:CPS_3484 hppD; 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bte:BTH_II1222</td><td>>gnl|kg|bte:BTH_II1222 4-hydroxyphenylpyruvate dioxygenase</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bma:BMAA0848</td><td>>gnl|kg|bma:BMAA0848 4-hydroxyphenylpyruvate dioxygenase, putative [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bur:Bcep18194_B0343</td><td>>gnl|kg|bur:Bcep18194_B0343 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bps:BPSS0339</td><td>>gnl|kg|bps:BPSS0339 putative amino acid dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>bpm:BURPS1710b_A1894</td><td>>gnl|kg|bpm:BURPS1710b_A1894 putative amino acid dioxygenase</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>ret:RHE_PC00215</td><td>>gnl|kg|ret:RHE_PC00215 putative 4-hydroxyphenylpyruvate dioxygenase protein [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>cel:T21C12.2</td><td>>gnl|kg|cel:T21C12.2 hpd-1; Hypothetical protein T21C12.2 [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bte:BTH_II2059</td><td>>gnl|kg|bte:BTH_II2059 4-hydroxyphenylpyruvate dioxygenase, putative</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>reu:Reut_B5028</td><td>>gnl|kg|reu:Reut_B5028 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>dme:CG11796-PA</td><td>>gnl|kg|dme:CG11796-PA CG11796; CG11796 gene product from transcript CG11796-RA [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>reu:Reut_B5035</td><td>>gnl|kg|reu:Reut_B5035 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ddi:DDB0203373</td><td>>gnl|kg|ddi:DDB0203373 hypothetical protein [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>nfa:nfa50810</td><td>>gnl|kg|nfa:nfa50810 putative 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>cme:CMI063C</td><td>>gnl|kg|cme:CMI063C 4-hydroxyphenylpyruvate dioxygenase, 4HPPD [EC:1.13.11.27] [KO:K00457]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>pae:PA1129</td><td>>gnl|kg|pae:PA1129 probable fosfomycin resistance protein</td><td></td><td></td><td>x</td><td>x</td></tr>
</table>

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
ath:At1g08110	>gnl|kg|ath:At1g08110 T6D22.20; lactoylglutathione lyase, putative / glyoxalase I, putative [EC:4.4.1.5] [KO:K01759]			x	
ath:At1g11840	>gnl|kg|ath:At1g11840 F12F1.32; lactoylglutathione lyase, putative / glyoxalase I, putative [EC:4.4.1.5] [KO:K01759]			x	
sce:YML004C	>gnl|kg|sce:YML004C GLO1; Regulated by HOG (high osmolarity glycerol)-MAP (mitogen-activated protein) kinase pathway in osmotic stress response [EC:4.4.1.5] [KO:K01759]			x	
spo:SPBC12C2.12c	>gnl|kg|spo:SPBC12C2.12c lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
pfa:PF11_0145	>gnl|kg|pfa:PF11_0145 glyoxalase I, putative [EC:4.4.1.5] [KO:K01759]			x	
cal:orf19.6058	>gnl|kg|cal:orf19.6058 GLO1; glyoxalase I [EC:4.4.1.5] [KO:K01759]			x	
ath:At1g67280	>gnl|kg|ath:At1g67280 F1N21.10; lactoylglutathione lyase, putative / glyoxalase I, putative			x	
gga:421428	>gnl|kg|gga:421428 LOC421428; similar to glyoxylase 1; glyoxalase 1			x	x
pfo:Pfl_2923	>gnl|kg|pfo:Pfl_2923 glyoxalase I			x	
rno:294320	>gnl|kg|rno:294320 Glo1; glyoxylase 1			x	
mmu:109801	>gnl|kg|mmu:109801 Glo1; glyoxalase 1 [EC:4.4.1.5] [KO:K01759]			x	
ppu:PP3766	>gnl|kg|ppu:PP3766 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
hsa:2739	>gnl|kg|hsa:2739 GLO1; glyoxalase I [EC:4.4.1.5] [KO:K01759]			x	
dme:CG1707-PA	>gnl|kg|dme:CG1707-PA CG1707; CG1707 gene product from transcript CG1707-RA [EC:4.4.1.5] [KO:K01759]			x	
pfl:PFL_3393	>gnl|kg|pfl:PFL_3393 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
psp:PSPPH_2267	>gnl|kg|psp:PSPPH_2267 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
psb:Psyr_2973	>gnl|kg|psb:Psyr_2973 glyoxalase I [EC:4.4.1.5] [KO:K01759]			x	
xla:446359	>gnl|kg|xla:446359 MGC82317; MGC82317 protein [EC:4.4.1.5] [KO:K01759]			x	

Table L-3. KEGG Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>pst:PSPTO3106</td><td>>gnl|kg|pst:PSPTO3106 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>cfa:474894</td><td>>gnl|kg|cfa:474894 LOC474894; similar to glyoxylase 1</td><td></td><td></td><td>x</td><td>x</td></tr>
<tr><td>xla:447401</td><td>>gnl|kg|xla:447401 MGC84827; MGC84827 protein [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>dre:368213</td><td>>gnl|kg|dre:368213 glo1; glyoxalase 1</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>xcb:XC_3658</td><td>>gnl|kg|xcb:XC_3658 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>xcc:XCC0575</td><td>>gnl|kg|xcc:XCC0575 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>xft:PD0629</td><td>>gnl|kg|xft:PD0629 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>bba:Bd2848</td><td>>gnl|kg|bba:Bd2848 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>xfa:XF1399</td><td>>gnl|kg|xfa:XF1399 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>pae:PA5111</td><td>>gnl|kg|pae:PA5111 gloA3; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>xcv:XCV3749</td><td>>gnl|kg|xcv:XCV3749 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>xac:XAC3632</td><td>>gnl|kg|xac:XAC3632 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>xoo:XOO0754</td><td>>gnl|kg|xoo:XOO0754 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>pha:PSHAa1601</td><td>>gnl|kg|pha:PSHAa1601 gloA; lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase) [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>syn:slr0381</td><td>>gnl|kg|syn:slr0381 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>vch:VC1010</td><td>>gnl|kg|vch:VC1010 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
bur:Bcep18194_A6033	>gnl|kg|bur:Bcep18194_A6033 glyoxalase I [EC:4.4.1.5] [KO:K01759]			x	
ana:alr2321	>gnl|kg|ana:alr2321 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
bte:BTH_I0580	>gnl|kg|bte:BTH_I0580 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
ava:Ava_0139	>gnl|kg|ava:Ava_0139 glyoxalase I [EC:4.4.1.5] [KO:K01759]			x	
nma:NMA2147	>gnl|kg|nma:NMA2147 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
nme:NMB0340	>gnl|kg|nme:NMB0340 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
bpm:BURPS1710b_0876	>gnl|kg|bpm:BURPS1710b_0876 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
bps:BPSL0663	>gnl|kg|bps:BPSL0663 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
bma:BMA0213	>gnl|kg|bma:BMA0213 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
ilo:IL2633	>gnl|kg|ilo:IL2633 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
ecs:ECs2360	>gnl|kg|ecs:ECs2360 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
sfx:S1810	>gnl|kg|sfx:S1810 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
eco:b1651	>gnl|kg|eco:b1651 gloA; glyoxalase I, nickel isomerase [EC:4.4.1.5] [KO:K01759]			x	
ssn:SSO_1505	>gnl|kg|ssn:SSO_1505 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
ecj:JW1643	>gnl|kg|ecj:JW1643 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
ece:Z2669	>gnl|kg|ece:Z2669 gloA; hypothetical protein [EC:4.4.1.5] [KO:K01759]			x	
sdy:SDY_1877	>gnl|kg|sdy:SDY_1877 gloA; lactoylglutathione lyase			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
sfl:SF1678	>gnl|kg|sfl:SF1678 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
vfi:VF0928	>gnl|kg|vfi:VF0928 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
ecc:c2044	>gnl|kg|ecc:c2044 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
eba:ebB148	>gnl|kg|eba:ebB148 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
aci:ACIAD2213	>gnl|kg|aci:ACIAD2213 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
vpa:VP2109	>gnl|kg|vpa:VP2109 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
cvi:CV1660	>gnl|kg|cvi:CV1660 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
pae:PA3524	>gnl|kg|pae:PA3524 gloA1; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
stt:t1303	>gnl|kg|stt:t1303 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
sty:STY1687	>gnl|kg|sty:STY1687 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
sec:SC1454	>gnl|kg|sec:SC1454 gloA; glyoxalase I, nickel isomerase [EC:4.4.1.5] [KO:K01759]			x	
spt:SPA1418	>gnl|kg|spt:SPA1418 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
stm:STM1435	>gnl|kg|stm:STM1435 gloA; glyoxalase I, nickel isomerase [EC:4.4.1.5] [KO:K01759]			x	
sbo:SBO_1484	>gnl|kg|sbo:SBO_1484 gloA; lactoylglutathione lyase			x	
eca:ECA1929	>gnl|kg|eca:ECA1929 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
cya:CYA_1244	>gnl|kg|cya:CYA_1244 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
noc:Noc_2681	>gnl|kg|noc:Noc_2681 glyoxalase I [EC:4.4.1.5] [KO:K01759]			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
bbr:BB4094	>gnl|kg|bbr:BB4094 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
bpe:BP0038	>gnl|kg|bpe:BP0038 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
bpa:BPP3659	>gnl|kg|bpa:BPP3659 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
msu:MS0703	>gnl|kg|msu:MS0703 gloA; lactoylglutathione lyase and related lyases [EC:4.4.1.5] [KO:K01759]			x	x
ypk:y1957	>gnl|kg|ypk:y1957 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
ypm:YP2167	>gnl|kg|ypm:YP2167 gloA1; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
syf:Synpcc7942_0638	>gnl|kg|syf:Synpcc7942_0638 glyoxalase I [EC:4.4.1.5] [KO:K01759]			x	
syc:syc0887_d	>gnl|kg|syc:syc0887_d gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
vvy:VV1185	>gnl|kg|vvy:VV1185 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
pmu:PM0987	>gnl|kg|pmu:PM0987 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
neu:NE1427	>gnl|kg|neu:NE1427 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
plu:plu2602	>gnl|kg|plu:plu2602 gloA; lactoylglutathione lyase (methylglyoxalase) (S-D-lactolyglutathione methylglyoxal lyase) [EC:4.4.1.5] [KO:K01759]			x	
pma:Pro0234	>gnl|kg|pma:Pro0234 gloA; lactoylglutathione lyase family enzyme [EC:4.4.1.5] [KO:K01759]			x	x
ype:YPO2381	>gnl|kg|ype:YPO2381 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
yps:YPTB2295	>gnl|kg|yps:YPTB2295 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
reu:Reut_A0503	>gnl|kg|reu:Reut_A0503 glyoxalase I [EC:4.4.1.5] [KO:K01759]			x	
nmu:Nmul_A2625	>gnl|kg|nmu:Nmul_A2625 glyoxalase I [EC:4.4.1.5] [KO:K01759]			x	

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
dar:Daro_3539	>gnl|kg|dar:Daro_3539 glyoxalase I [EC:4.4.1.5] [KO:K01759]			x	
hch:HCH_04598	>gnl|kg|hch:HCH_04598 gloA2; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
syw:SYNW2347	>gnl|kg|syw:SYNW2347 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
hit:NTHI0441	>gnl|kg|hit:NTHI0441 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
hin:HI0323	>gnl|kg|hin:HI0323 gloA; lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
vpa:VPA0774	>gnl|kg|vpa:VPA0774 lactoylglutathione lyase [EC:4.4.1.5] [KO:K01759]			x	
rru:Rru_A2788	>gnl|kg|rru:Rru_A2788 N-isopropylammelide isopropylaminohydrolase [EC:3.5.99.4]		x		
pfo:Pfl_3779	>gnl|kg|pfo:Pfl_3779 N-isopropylammelide isopropylaminohydrolase [EC:3.5.99.4]		x		
bur:Bcep18194_B0800	>gnl|kg|bur:Bcep18194_B0800 N-isopropylammelide isopropylaminohydrolase [EC:3.5.99.4]		x		
cgb:cg0104	>gnl|kg|cgb:cg0104 codA; creatinine deaminase [EC:3.5.4.21] [KO:K03365]		x		
rno:64526	>gnl|kg|rno:64526 Ech1; enoyl coenzyme A hydratase 1, peroxisomal [EC:5.3.3.-]		x		
mmu:51798	>gnl|kg|mmu:51798 Ech1; enoyl coenzyme A hydratase 1, peroxisomal [EC:5.3.3.-]		x		
hsa:1891	>gnl|kg|hsa:1891 ECH1; enoyl Coenzyme A hydratase 1, peroxisomal [EC:5.3.3.-]		x		
xtr:448218	>gnl|kg|xtr:448218 ech1-prov; enoyl Coenzyme A hydratase 1, peroxisomal [EC:5.3.3.-]		x		
osa:B1033B05.16	>gnl|kg|osa:B1033B05.16 enoyl CoA hydratase-like protein		x		
mbo:Mb3803	>gnl|kg|mbo:Mb3803 echA21; enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]		x		
mle:ML0120	>gnl|kg|mle:ML0120 echA1; putative enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]		x		

Table L-3. KEGG Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>lil:LA1032</td><td>>gnl|kg|lil:LA1032 ech3; enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>hch:HCH_01668</td><td>>gnl|kg|hch:HCH_01668 enoyl-CoA hydratase/carnithine racemase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>dar:Daro_3320</td><td>>gnl|kg|dar:Daro_3320 enoyl-CoA hydratase/isomerase [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>lic:LIC12629</td><td>>gnl|kg|lic:LIC12629 ech3; enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>cvi:CV2485</td><td>>gnl|kg|cvi:CV2485 enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>pfo:Pfl_2864</td><td>>gnl|kg|pfo:Pfl_2864 enoyl-CoA hydratase/isomerase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>pfl:PFL_3062</td><td>>gnl|kg|pfl:PFL_3062 echA9; enoly-coenzyme A hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>atc:AGR_L_2647</td><td>>gnl|kg|atc:AGR_L_2647 probable enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>ppu:PP3491</td><td>>gnl|kg|ppu:PP3491 enoly-coenzyme A hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>psb:Psyr_1770</td><td>>gnl|kg|psb:Psyr_1770 enoyl-CoA hydratase/isomerase [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>pst:PSPTO3705</td><td>>gnl|kg|pst:PSPTO3705 enoly-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>atu:Atu3505</td><td>>gnl|kg|atu:Atu3505 enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>psp:PSPPH_1721</td><td>>gnl|kg|psp:PSPPH_1721 enoly-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>cbu:CBU_1856</td><td>>gnl|kg|cbu:CBU_1856 enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>rso:RSc1298</td><td>>gnl|kg|rso:RSc1298 RS02820; enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>rpa:RPA3447</td><td>>gnl|kg|rpa:RPA3447 enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>rru:Rru_A1834</td><td>>gnl|kg|rru:Rru_A1834 enoyl-CoA hydratase/isomerase [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>rso:RS05575</td><td>>gnl|kg|rso:RS05575 RSp0647; putative enoyl-coenzyme A hydratase protein [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
</table>

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
son:SO1681	>gnl|kg|son:SO1681 enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]		x		
mag:amb3583	>gnl|kg|mag:amb3583 enoyl-CoA hydratase/carnithine racemase		x		
sme:SMb20752	>gnl|kg|sme:SMb20752 enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]		x		
bme:BMEI1196	>gnl|kg|bme:BMEI1196 enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]		x		
bms:BR0758	>gnl|kg|bms:BR0758 enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]		x		
oih:OB0817	>gnl|kg|oih:OB0817 enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]		x		
bja:blr3956	>gnl|kg|bja:blr3956 enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]		x		
bmb:BruAb1_0775	>gnl|kg|bmb:BruAb1_0775 enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]		x		
bmf:BAB1_0781	>gnl|kg|bmf:BAB1_0781 enoyl-CoA hydratase/isomerase [EC:4.2.1.17] [KO:K01692]		x		
xcv:XCV1366	>gnl|kg|xcv:XCV1366 enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]		x		
rpb:RPB_2121	>gnl|kg|rpb:RPB_2121 enoyl-CoA hydratase/isomerase		x		
ath:At3g60510	>gnl|kg|ath:At3g60510 T8B10.170; enoyl-CoA hydratase/isomerase family protein		x		
xac:XAC1315	>gnl|kg|xac:XAC1315 enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]		x		
bca:BCE2384	>gnl|kg|bca:BCE2384 enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]		x		
bcz:BCZK2118	>gnl|kg|bcz:BCZK2118 phaB; enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]		x		
btk:BT9727_2132	>gnl|kg|btk:BT9727_2132 phaB; enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]		x		
ccr:CC1352	>gnl|kg|ccr:CC1352 enoyl-CoA hydratase/isomerase family protein		x		
bar:GBAA2356	>gnl|kg|bar:GBAA2356 enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]		x		

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
bat:BAS2195	>gnl|kg|bat:BAS2195 enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]		x		
ban:BA2356	>gnl|kg|ban:BA2356 enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]		x		
mtu:Rv1071c	>gnl|kg|mtu:Rv1071c echA9 [EC:4.2.1.17] [KO:K01692]		x		
mbo:Mb1100c	>gnl|kg|mbo:Mb1100c echA9; enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]		x		
mtc:MT1101	>gnl|kg|mtc:MT1101 enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]		x		
xcb:XC_2978	>gnl|kg|xcb:XC_2978 enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]		x		
mlo:mlr8392	>gnl|kg|mlo:mlr8392 enoyl-CoA hydratase		x		
ath:At4g31810	>gnl|kg|ath:At4g31810 F11C18.10; enoyl-CoA hydratase/isomerase family protein		x		
baa:BA_2850	>gnl|kg|baa:BA_2850 enoyl-CoA hydratase/isomerase family [EC:4.2.1.17] [KO:K01692]		x		
xoo:XOO1845	>gnl|kg|xoo:XOO1845 enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]		x		
ath:At3g24360	>gnl|kg|ath:At3g24360 K7M2.21; enoyl-CoA hydratase/isomerase family protein		x		
ath:At4g13360	>gnl|kg|ath:At4g13360 T9E8.100; enoyl-CoA hydratase/isomerase family protein		x		
nar:Saro_0859	>gnl|kg|nar:Saro_0859 enoyl-CoA hydratase/isomerase		x		
nwi:Nwi_2157	>gnl|kg|nwi:Nwi_2157 enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]		x		
xcc:XCC1263	>gnl|kg|xcc:XCC1263 enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]		x		
mpa:MAP1018c	>gnl|kg|mpa:MAP1018c echA9; putative enoyl-CoA hydratase/isomerase [EC:4.2.1.17] [KO:K01692]		x		
eli:ELI_10030	>gnl|kg|eli:ELI_10030 enoyl-CoA hydratase/isomerase family protein		x		
mag:amb2561	>gnl|kg|mag:amb2561 enoyl-CoA hydratase/carnithine racemase		x		

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
mle:ML2401	>gnl|kg|mle:ML2401 putative enoyl-CoA hydratase/isomerase [EC:4.2.1.17] [KO:K01692]		x		
bur:Bcep18194_B0719	>gnl|kg|bur:Bcep18194_B0719 enoyl-CoA hydratase/isomerase [EC:4.2.1.17] [KO:K01692]		x		
reu:Reut_A2019	>gnl|kg|reu:Reut_A2019 enoyl-CoA hydratase/isomerase [EC:4.2.1.17] [KO:K01692]		x		
bpm:BURPS1710b_A2183	>gnl|kg|bpm:BURPS1710b_A2183 enoyl-CoA hydratase/isomerase family		x		
bps:BPSS0622	>gnl|kg|bps:BPSS0622 enoyl-CoA hydratase/isomerase family [EC:4.2.1.17] [KO:K01692]		x		
ret:RHE_CH00571	>gnl|kg|ret:RHE_CH00571 probable enoyl-CoA hydratase protein [EC:4.2.1.17] [KO:K01692]		x		
pae:PA0744	>gnl|kg|pae:PA0744 probable enoyl-CoA hydratase/isomerase [EC:4.2.1.17] [KO:K01692]		x		
ppu:PP1412	>gnl|kg|ppu:PP1412 enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]		x		
vvu:VV20490	>gnl|kg|vvu:VV20490 enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]		x		
bte:BTH_I2504	>gnl|kg|bte:BTH_I2504 enoyl-CoA hydratase/isomerase family protein		x		
bte:BTH_II1798	>gnl|kg|bte:BTH_II1798 enoyl-CoA hydratase/isomerase family		x		
vvy:VVA1039	>gnl|kg|vvy:VVA1039 putative enoyl-CoA hydratase/isomerase [EC:4.2.1.17] [KO:K01692]		x		
vpa:VPA1119	>gnl|kg|vpa:VPA1119 putative enoyl-CoA hydratase/isomerase [EC:4.2.1.17] [KO:K01692]		x		
bma:BMA1244	>gnl|kg|bma:BMA1244 enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]		x		
bpm:BURPS1710b_1985	>gnl|kg|bpm:BURPS1710b_1985 paaG; enoyl-CoA hydratase/isomerase family protein		x		
vpa:VPA0624	>gnl|kg|vpa:VPA0624 putative enoyl-CoA hydratase/isomerase [EC:4.2.1.17] [KO:K01692]		x		
nfa:nfa10390	>gnl|kg|nfa:nfa10390 putative enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]		x		

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
reu:Reut_B4261	>gnl|kg|reu:Reut_B4261 enoyl-CoA hydratase/isomerase [EC:4.2.1.17] [KO:K01692]		x		
bps:BPSL1860	>gnl|kg|bps:BPSL1860 putative hydratase [EC:4.2.1.17] [KO:K01692]		x		
bli:BL00295	>gnl|kg|bli:BL00295 enoyl-CoA hydratase/isomerase [EC:4.2.1.17] [KO:K01692]		x		
bld:BLi02102	>gnl|kg|bld:BLi02102 enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]		x		
bur:Bcep18194_A4702	>gnl|kg|bur:Bcep18194_A4702 enoyl-CoA hydratase/isomerase [EC:4.2.1.17] [KO:K01692]		x		
pfl:PFL_1434	>gnl|kg|pfl:PFL_1434 echA9; enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]		x		
ath:At1g06550	>gnl|kg|ath:At1g06550 F12K11.12; enoyl-CoA hydratase/isomerase family protein		x		
pfo:Pfl_1348	>gnl|kg|pfo:Pfl_1348 enoyl-CoA hydratase/isomerase		x		
ilo:IL0868	>gnl|kg|ilo:IL0868 enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]		x		
sce:YDR036C	>gnl|kg|sce:YDR036C EHD3, MRP5; Protein of unconfirmed function, plays an indirect role in endocytic membrane trafficking, member of a family of enoyl-CoA hydratase/isomerases		x		
lpf:lpl0902	>gnl|kg|lpf:lpl0902 enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]		x		
spo:SPBC2D10.09	>gnl|kg|spo:SPBC2D10.09 3-hydroxyisobutyryl-coenzyme a hydrolase; Enoyl-CoA isomerase family		x		
rsp:RSP_0155	>gnl|kg|rsp:RSP_0155 enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]		x		
lpp:lpp0933	>gnl|kg|lpp:lpp0933 enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]		x		
cgb:cg1049	>gnl|kg|cgb:cg1049 enoyl-CoA hydratase/carnithine racemase [EC:4.2.1.17] [KO:K01692]		x		
cgl:NCgl0882	>gnl|kg|cgl:NCgl0882 Cgl0919; enoyl-CoA hydratase/carnithine racemase [EC:4.2.1.17] [KO:K01692]		x		
hch:HCH_00639	>gnl|kg|hch:HCH_00639 enoyl-CoA hydratase/carnithine racemase		x		

Table L-3. KEGG Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>cef:CE0981</td><td>>gnl|kg|cef:CE0981 putative enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>bpe:BP1446</td><td>>gnl|kg|bpe:BP1446 enoly-CoA hydratase [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>bbr:BB2631</td><td>>gnl|kg|bbr:BB2631 enoly-CoA hydratase [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>bpa:BPP1553</td><td>>gnl|kg|bpa:BPP1553 enoly-CoA hydratase [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>cvi:CV2082</td><td>>gnl|kg|cvi:CV2082 paaG; enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>ppr:PBPRB1108</td><td>>gnl|kg|ppr:PBPRB1108 paaG; putative enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>pha:PSHAa1458</td><td>>gnl|kg|pha:PSHAa1458 enoyl-CoA hydratase/isomerase protein [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>sil:SPO2212</td><td>>gnl|kg|sil:SPO2212 enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>bcl:ABC1810</td><td>>gnl|kg|bcl:ABC1810 enoyl-CoA hydratase [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>tcr:511529.160</td><td>>gnl|kg|tcr:511529.160 enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>cps:CPS_0656</td><td>>gnl|kg|cps:CPS_0656 enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>cps:CPS_1607</td><td>>gnl|kg|cps:CPS_1607 enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>tbr:Tb11.01.8200</td><td>>gnl|kg|tbr:Tb11.01.8200 enoyl-CoA hydratase/isomerase family protein</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>tcr:506727.90</td><td>>gnl|kg|tcr:506727.90 enoyl-CoA hydratase/isomerase family protein</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>tcr:511529.170</td><td>>gnl|kg|tcr:511529.170 enoyl-CoA hydratase/isomerase family protein</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>tcr:506727.100</td><td>>gnl|kg|tcr:506727.100 enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>cdi:DIP0885</td><td>>gnl|kg|cdi:DIP0885 putative hydrolase [EC:4.2.1.17] [KO:K01692]</td><td></td><td>x</td><td></td><td></td></tr>
</table>

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
cjk:jk1503	>gnl|kg|cjk:jk1503 echA5; enoyl-CoA hydratase/carnithine racemase [EC:4.2.1.17] [KO:K01692]		x		
ath:At1g60550	>gnl|kg|ath:At1g60550 F8A5.9; naphthoate synthase, putative / dihydroxynaphthoic acid synthetase, putative / DHNA synthetase, putative [EC:4.1.3.36] [KO:K01661]		x		
vvy:VV1118	>gnl|kg|vvy:VV1118 dihydroxynaphthoic acid synthase [EC:4.1.3.36] [KO:K01661]		x		
osa:P0671D01.18	>gnl|kg|osa:P0671D01.18 putative naphthoate synthase		x		
vch:VC1973	>gnl|kg|vch:VC1973 naphthoate synthase [EC:4.1.3.36] [KO:K01661]		x		
vpa:VP0931	>gnl|kg|vpa:VP0931 naphthoate synthase [EC:4.1.3.36] [KO:K01661]		x		
vvu:VV13170	>gnl|kg|vvu:VV13170 naphthoate synthase [EC:4.1.3.36] [KO:K01661]		x		
ecs:ECs3150	>gnl|kg|ecs:ECs3150 dihydroxynaphtoic acid synthetase [EC:4.1.3.36] [KO:K01661]		x		
gka:GK2873	>gnl|kg|gka:GK2873 naphthoate synthase [EC:4.1.3.36] [KO:K01661]		x		
ava:Ava_0166	>gnl|kg|ava:Ava_0166 naphthoate synthase [EC:4.1.3.36] [KO:K01661]		x		
bat:BAS4748	>gnl|kg|bat:BAS4748 naphthoate synthase [EC:4.1.3.36] [KO:K01661]		x		
baa:BA_5527	>gnl|kg|baa:BA_5527 enoyl-CoA hydratase/isomerase family [EC:4.1.3.36] [KO:K01661]		x		
ana:all2347	>gnl|kg|ana:all2347 naphthoate synthase [EC:4.1.3.36] [KO:K01661]		x		
oih:OB2323	>gnl|kg|oih:OB2323 naphthoate synthase [EC:4.1.3.36] [KO:K01661]		x		
bce:BC4853	>gnl|kg|bce:BC4853 naphthoate synthase [EC:4.1.3.36] [KO:K01661]		x		
plt:Plut_0328	>gnl|kg|plt:Plut_0328 naphthoate synthase		x		
cch:Cag_1719	>gnl|kg|cch:Cag_1719 naphthoate synthase [EC:4.1.3.36] [KO:K01661]		x		

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
sas:SAS0981	>gnl|kg|sas:SAS0981 naphthoate synthase [EC:4.1.3.36] [KO:K01661]		x		
ssp:SSP1746	>gnl|kg|ssp:SSP1746 dihydroxynaphthoic acid synthase [EC:4.1.3.36] [KO:K01661]		x		
cgl:NCgl0446	>gnl|kg|cgl:NCgl0446 Cgl0463; dihydroxynaphthoic acid synthase [EC:4.1.3.36] [KO:K01661]		x		
sep:SE0746	>gnl|kg|sep:SE0746 naphthoate synthase [EC:4.1.3.36] [KO:K01661]		x		
syf:Synpcc7942_0597	>gnl|kg|syf:Synpcc7942_0597 naphthoate synthase		x		
hma:rrnAC0841	>gnl|kg|hma:rrnAC0841 ech1; naphthoate synthase [EC:4.2.1.17] [KO:K01692]		x		
cef:CE0475	>gnl|kg|cef:CE0475 putative naphthoate synthase [EC:4.1.3.36] [KO:K01661]		x		
pmn:PMN2A_0044	>gnl|kg|pmn:PMN2A_0044 naphthoate synthase [EC:4.1.3.36] [KO:K01661]		x		
sye:Syncc9902_1333	>gnl|kg|sye:Syncc9902_1333 naphthoate synthase		x		
tfu:Tfu_1409	>gnl|kg|tfu:Tfu_1409 naphthoate synthase [EC:4.1.3.36] [KO:K01661]		x		
syd:Syncc9605_1123	>gnl|kg|syd:Syncc9605_1123 naphthoate synthase		x		
bfr:BF1318	>gnl|kg|bfr:BF1318 dihydroxynapthoic acid synthetase [EC:4.1.3.36] [KO:K01661]		x		
pmi:PMT9312_0608	>gnl|kg|pmi:PMT9312_0608 naphthoate synthase		x		
bth:BT4702	>gnl|kg|bth:BT4702 dihydroxynapthoic acid synthetase [EC:4.1.3.36] [KO:K01661]		x		
dar:Daro_1616	>gnl|kg|dar:Daro_1616 naphthoate synthase [EC:4.1.3.36] [KO:K01661]		x		
cme:CMV113C	>gnl|kg|cme:CMV113C naphthoate synthase		x		
pac:PPA0907	>gnl|kg|pac:PPA0907 naphthoate synthase [EC:4.1.3.36] [KO:K01661]		x		
pfo:Pfl_4123	>gnl|kg|pfo:Pfl_4123 mandelate racemase/muconate lactonizing enzyme		x		
bur:Bcep18194_C6937	>gnl|kg|bur:Bcep18194_C6937 mandelate racemase/muconate lactonizing enzyme [EC:4.1.2.21] [KO:K01631]		x		

Table L-3. KEGG Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>pfo:Pfl_3721</td><td>>gnl|kg|pfo:Pfl_3721 mandelate racemase/muconate lactonizing enzyme</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>pmu:PM1094</td><td>>gnl|kg|pmu:PM1094 menC; O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>ppr:PBPRA2622</td><td>>gnl|kg|ppr:PBPRA2622 menC; putative o-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>cef:CE0477</td><td>>gnl|kg|cef:CE0477 putative muconate cycloisomerase [EC:4.2.1.-] [KO:K02549]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>hin:HI0969</td><td>>gnl|kg|hin:HI0969 menC; O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>ypm:YP2335</td><td>>gnl|kg|ypm:YP2335 menC; putative O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>ype:YPO2524</td><td>>gnl|kg|ype:YPO2524 menC; O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>ypk:y1663</td><td>>gnl|kg|ypk:y1663 menC; O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>eca:ECA1214</td><td>>gnl|kg|eca:ECA1214 menC; O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>yps:YPTB2557</td><td>>gnl|kg|yps:YPTB2557 menC; putative O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>vpa:VP0932</td><td>>gnl|kg|vpa:VP0932 o-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>son:SO4575</td><td>>gnl|kg|son:SO4575 menC; O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>vch:VC1972</td><td>>gnl|kg|vch:VC1972 O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>vvu:VV13169</td><td>>gnl|kg|vvu:VV13169 O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>eco:b2261</td><td>>gnl|kg|eco:b2261 menC; o-succinylbenzoyl-CoA synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>sdy:SDY_2457</td><td>>gnl|kg|sdy:SDY_2457 menC; O-succinylbenzoyl-CoA synthase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>ecj:JW2256</td><td>>gnl|kg|ecj:JW2256 menC; O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]</td><td></td><td>x</td><td></td><td></td></tr>
</table>

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
ssn:SSO_2322	>gnl|kg|ssn:SSO_2322 menC; O-succinylbenzoyl-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
ecs:ECs3149	>gnl|kg|ecs:ECs3149 O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
ece:Z3521	>gnl|kg|ece:Z3521 menC; o-succinylbenzoyl-CoA synthase; conversion of chorismate to 2-o-succinylbenzoyl-CoA [EC:4.2.1.-] [KO:K02549]		x		
ecc:c2804	>gnl|kg|ecc:c2804 menC; O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
sfx:S2474	>gnl|kg|sfx:S2474 menC; O-succinylbenzoyl-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
sfl:SF2340	>gnl|kg|sfl:SF2340 menC; O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
stm:STM2306	>gnl|kg|stm:STM2306 menC; O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
sec:SC2306	>gnl|kg|sec:SC2306 menC; O-succinylbenzoyl-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
sbo:SBO_2298	>gnl|kg|sbo:SBO_2298 menC; O-succinylbenzoyl-CoA synthase		x		
spt:SPA0557	>gnl|kg|spt:SPA0557 menC; O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
sty:STY2536	>gnl|kg|sty:STY2536 menC; O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
stt:t0557	>gnl|kg|stt:t0557 menC; O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
hdu:HD1055	>gnl|kg|hdu:HD1055 menC; O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
baa:BA_5525	>gnl|kg|baa:BA_5525 mandelate racemase / muconate lactonizing enzyme, C-terminal domain [EC:4.2.1.-] [KO:K02549]		x		
mle:ML2268	>gnl|kg|mle:ML2268 putative O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
cgb:cg0551	>gnl|kg|cgb:cg0551 menC; similar to O-succinylbenzoate-coa synthase [EC:4.2.1.-] [KO:K02549]		x		

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
bli:BL02404	>gnl|kg|bli:BL02404 menC; O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
bld:BLi03218	>gnl|kg|bld:BLi03218 menC; O-succinylbenzoate-CoA synthase; RBL03386 [EC:4.2.1.-] [KO:K02549]		x		
lla:L131805	>gnl|kg|lla:L131805 yhdB; O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
lxx:Lxx01430	>gnl|kg|lxx:Lxx01430 menC; O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
cte:CT1847	>gnl|kg|cte:CT1847 menC; O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
mbo:Mb0568	>gnl|kg|mbo:Mb0568 menC; probable muconate cycloisomerase MenC (cis,cis-muconate lactonizing enzyme) (MLE) [EC:4.2.1.-] [KO:K02549]		x		
mtu:Rv0553	>gnl|kg|mtu:Rv0553 menC; O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
mtc:MT0579	>gnl|kg|mtc:MT0579 O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
pac:PPA0902	>gnl|kg|pac:PPA0902 O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
mpa:MAP4050	>gnl|kg|mpa:MAP4050 menC; O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
tfu:Tfu_1410	>gnl|kg|tfu:Tfu_1410 O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
cdi:DIP0422	>gnl|kg|cdi:DIP0422 menC; putative O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
bth:BT4703	>gnl|kg|bth:BT4703 chloromuconate cycloisomerase		x		
pma:Pro0200	>gnl|kg|pma:Pro0200 menC; O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
syn:sll0409	>gnl|kg|syn:sll0409 menC; O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
sas:SAS1716	>gnl|kg|sas:SAS1716 O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
bfs:BF1304	>gnl|kg|bfs:BF1304 putative muconate cycloisomerase		x		

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
dar:Daro_1615	>gnl|kg|dar:Daro_1615 mandelate racemase/muconate lactonizing enzyme		x		
bfr:BF1319	>gnl|kg|bfr:BF1319 chloromuconate cycloisomerase		x		
sar:SAR1876	>gnl|kg|sar:SAR1876 O-succinylbenzoate-CoA synthase [EC:4.2.1.-] [KO:K02549]		x		
mlo:mlr0803	>gnl|kg|mlo:mlr0803 probable muconate cycloisomerase		x		
eca:ECA3116	>gnl|kg|eca:ECA3116 putative mandelate racemase/muconate lactonizing enzyme		x		
bmf:BAB1_1037	>gnl|kg|bmf:BAB1_1037 mandelate racemase/muconate lactonizing enzyme		x		
atc:AGR_C_3037	>gnl|kg|atc:AGR_C_3037 putative muconate cycloisomerase I		x		
bme:BMEI0966	>gnl|kg|bme:BMEI0966 muconate cycloisomerase I [EC:5.5.1.1] [KO:K01856]		x		
rpa:RPA3964	>gnl|kg|rpa:RPA3964 putative muconate cycloisomerase [EC:5.5.1.1] [KO:K01856]		x		
rsp:RSP_1769	>gnl|kg|rsp:RSP_1769 mandelate racemase / muconate lactonizing enzyme [EC:5.1.2.2 5.5.1.1] [KO:K01781 K01856]		x		
rpb:RPB_1626	>gnl|kg|rpb:RPB_1626 mandelate racemase/muconate lactonizing enzyme		x		
oih:OB2965	>gnl|kg|oih:OB2965 muconate cycloisomerase		x		
sec:SC1674	>gnl|kg|sec:SC1674 ycjG; putative chloromuconate cycloisomerase (muconate cycloisomerase)		x		
stm:STM1681	>gnl|kg|stm:STM1681 ycjG; putative chloromuconate cycloisomerase (muconate cycloisomerase)		x		
sfl:SF1331	>gnl|kg|sfl:SF1331 ycjG; putative muconate cycloisomerase I [EC:5.5.-.-]		x		
sfx:S1414	>gnl|kg|sfx:S1414 ycjG; putative muconate cycloisomerase I		x		
ecs:ECs1904	>gnl|kg|ecs:ECs1904 putative muconate cycloisomerase I		x		
fnu:FN1586	>gnl|kg|fnu:FN1586 O-succinylbenzoate-CoA synthase		x		
bsu:BG13232	>gnl|kg|bsu:BG13232 ykfB; similar to chloromuconate cycloisomerase		x		
ece:Z2450	>gnl|kg|ece:Z2450 ycjG; putative muconate cycloisomerase I		x		

Table L-3. KEGG Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>ret:RHE_CH02350</td><td>>gnl|kg|ret:RHE_CH02350 probable muconate cycloisomerase I protein</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>ypm:YP2128</td><td>>gnl|kg|ypm:YP2128 dgoA2; putative mandelate racemase / muconate lactonizing protein</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>yps:YPTB2260</td><td>>gnl|kg|yps:YPTB2260 putative mandelate racemase / muconate lactonizing protein</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>ype:YPO2341</td><td>>gnl|kg|ype:YPO2341 putative mandelate racemase / muconate lactonizing protein</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>rru:Rru_A2556</td><td>>gnl|kg|rru:Rru_A2556 mandelate racemase/muconate lactonizing enzyme [EC:5.5.1.1] [KO:K01856]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>nwi:Nwi_1085</td><td>>gnl|kg|nwi:Nwi_1085 mandelate racemase/muconate lactonizing enzyme [EC:5.5.1.1] [KO:K01856]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>spt:SPA1203</td><td>>gnl|kg|spt:SPA1203 ycjG; putative mandelate racemase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>xac:XAC3862</td><td>>gnl|kg|xac:XAC3862 tcbD; chloromuconate cycloisomerase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>ppr:PBPRA1898</td><td>>gnl|kg|ppr:PBPRA1898 hypothetical muconate cycloisomerase I</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>cac:CAC0192</td><td>>gnl|kg|cac:CAC0192 similar to chloromuconate cycloisomerase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>xcv:XCV3980</td><td>>gnl|kg|xcv:XCV3980 tcbD; putative chloromuconate cycloisomerase [EC:5.5.1.7] [KO:K01860]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>xcc:XCC3807</td><td>>gnl|kg|xcc:XCC3807 tcbD; chloromuconate cycloisomerase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>vpa:VPA0329</td><td>>gnl|kg|vpa:VPA0329 putative muconate cycloisomerase I</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>bcz:BCZK2578</td><td>>gnl|kg|bcz:BCZK2578 ykfB; mandelate racemase/muconate lactonizing enzyme [EC:5.1.2.2] [KO:K01781]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>xcb:XC_3879</td><td>>gnl|kg|xcb:XC_3879 chloromuconate cycloisomerase</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>ava:Ava_3512</td><td>>gnl|kg|ava:Ava_3512 mandelate racemase/muconate lactonizing enzyme [EC:5.5.1.1] [KO:K01856]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>rba:RB8686</td><td>>gnl|kg|rba:RB8686 ykfB; chloromuconate cycloisomerase YkfB1 [EC:5.5.1.7] [KO:K01860]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>sbo:SBO_1745</td><td>>gnl|kg|sbo:SBO_1745 ycjG; putative muconate cycloisomerase I [EC:5.5.-.-]</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>btk:BT9727_2610</td><td>>gnl|kg|btk:BT9727_2610 ykfB; mandelate racemase/muconate lactonizing enzyme</td><td></td><td>x</td><td></td><td></td></tr>
<tr><td>baa:BA_3373</td><td>>gnl|kg|baa:BA_3373 MR_MLE, mandelate racemase / muconate lactonizing enzyme, C-terminal domain</td><td></td><td>x</td><td></td><td></td></tr>
</table>

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
xoo:XOO4102	>gnl|kg|xoo:XOO4102 tcbD; chloromuconate cycloisomerase		x		
bur:Bcep18194_A4351	>gnl|kg|bur:Bcep18194_A4351 mandelate racemase/muconate lactonizing enzyme [EC:5.5.1.1] [KO:K01856]		x		
bha:BH3006	>gnl|kg|bha:BH3006 muconate cycloisomerase		x		
ssn:SSO_1813	>gnl|kg|ssn:SSO_1813 ycjG; putative muconate cycloisomerase I		x		
bli:BL03765	>gnl|kg|bli:BL03765 putative muconate cycloisomerase		x		
reu:Reut_D6465	>gnl|kg|reu:Reut_D6465 mandelate racemase/muconate lactonizing enzyme [EC:5.5.1.1] [KO:K01856]		x		
cgb:cg2635	>gnl|kg|cgb:cg2635 catB; chloromuconate cycloisomerase [EC:5.5.1.7] [KO:K01860]		x		
cgl:NCgl2318	>gnl|kg|cgl:NCgl2318 Cgl2401; putative chloromuconate cycloisomerase		x		
cne:CNB01020	>gnl|kg|cne:CNB01020 mandelate racemase/muconate lactonizing enzyme, putative		x		
bur:Bcep18194_B0622	>gnl|kg|bur:Bcep18194_B0622 mandelate racemase/muconate lactonizing enzyme [EC:5.1.2.2] [KO:K01781]		x		
ypm:YP1455	>gnl|kg|ypm:YP1455 dgoA1; O-succinylbenzoate synthase and related enzyme		x		
bme:BMEI1707	>gnl|kg|bme:BMEI1707 mandelate racemase [EC:5.1.2.2] [KO:K01781]		x		
bmf:BAB1_0248	>gnl|kg|bmf:BAB1_0248 mandelate racemase/muconate lactonizing enzyme		x		
ret:RHE_PE00430	>gnl|kg|ret:RHE_PE00430 probable mandelate racemase protein		x		
sma:SAV7282	>gnl|kg|sma:SAV7282 menC; putative mandelate racemase		x		
xcv:XCV4287	>gnl|kg|xcv:XCV4287 putative mandelate racemase/muconate lactonizing enzyme		x		
ype:YPO1567	>gnl|kg|ype:YPO1567 putative racemase		x		
yps:YPTB1577	>gnl|kg|yps:YPTB1577 putative racemase		x		
vvu:VV21662	>gnl|kg|vvu:VV21662 predicted phosphatase/phosphohexomutase		x		
sec:SC0473	>gnl|kg|sec:SC0473 phnX; 2-aminoethylphosphonate transport		x		
reu:Reut_B3993	>gnl|kg|reu:Reut_B3993 TatD-related deoxyribonuclease [EC:3.5.4.1] [KO:K01485]	x			

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
mlo:mlr5363	>gnl|kg|mlo:mlr5363 creatinine deaminase [EC:3.5.4.1] [KO:K01485]	x			
ret:RHE_CH03292	>gnl|kg|ret:RHE_CH03292 dht; dihydropyrimidinase protein [EC:3.5.2.3 3.5.2.2] [KO:K01464 K01465]	x			
eco:b4328	>gnl|kg|eco:b4328 iadA, yjiF; isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]	x			
ecj:JW4291	>gnl|kg|ecj:JW4291 iadA; isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]	x			
ecs:ECs5286	>gnl|kg|ecs:ECs5286 isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]	x			
ece:Z5927	>gnl|kg|ece:Z5927 iadA; isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]	x			
sfl:SF4190	>gnl|kg|sfl:SF4190 iadA; isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]	x			
sfx:S4446	>gnl|kg|sfx:S4446 iadA; isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]	x			
ecc:c5408	>gnl|kg|ecc:c5408 iadA; isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]	x			
sec:SC4367	>gnl|kg|sec:SC4367 iadA; isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]	x			
spt:SPA4332	>gnl|kg|spt:SPA4332 iadA; probable isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]	x			
stm:STM4512	>gnl|kg|stm:STM4512 iadA; isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]	x			
stt:t4562	>gnl|kg|stt:t4562 iadA; probable isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]	x			
sty:STY4868	>gnl|kg|sty:STY4868 iadA; probable isoaspartyl dipeptidase [EC:3.4.19.5] [KO:K01305]	x			
ppu:PP4030	>gnl|kg|ppu:PP4030 enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]	x			
pst:PSPTO2719	>gnl|kg|pst:PSPTO2719 enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]	x			

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
psb:Psyr_2452	>gnl|kg|psb:Psyr_2452 enoyl-CoA hydratase/isomerase [EC:4.2.1.17] [KO:K01692]	x			
pfl:PFL_3267	>gnl|kg|pfl:PFL_3267 fad-1; enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]	x			
pae:PA1821	>gnl|kg|pae:PA1821 probable enoyl-CoA hydratase/isomerase [EC:4.2.1.17] [KO:K01692]	x			
ccr:CC0353	>gnl|kg|ccr:CC0353 enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]	x			
mtc:MT3883	>gnl|kg|mtc:MT3883 enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]	x			
mtu:Rv3774	>gnl|kg|mtu:Rv3774 echA21; enoyl-CoA hydratase/isomerase superfamily [EC:4.2.1.17] [KO:K01692]	x			
nfa:nfa3830	>gnl|kg|nfa:nfa3830 echA1; putative enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]	x			
mpa:MAP0249c	>gnl|kg|mpa:MAP0249c echA21; enoyl-CoA hydratase/isomerase family protein [EC:4.2.1.17] [KO:K01692]	x			
lpn:lpg0870	>gnl|kg|lpn:lpg0870 3-hydroxyisobutyryl Coenzyme A hydrolase [EC:4.2.1.17] [KO:K01692]	x			
bhe:BH08520	>gnl|kg|bhe:BH08520 3-hydroxyisobutyryl-coenzyme A hydrolase [EC:4.2.1.17] [KO:K01692]	x			
cte:CT1846	>gnl|kg|cte:CT1846 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
pmu:PM1096	>gnl|kg|pmu:PM1096 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
hit:NTHI1141	>gnl|kg|hit:NTHI1141 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
hin:HI0968	>gnl|kg|hin:HI0968 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
ypk:y1662	>gnl|kg|ypk:y1662 menB; dihydroxynaphtoic acid synthetase [EC:4.1.3.36] [KO:K01661]	x			
sec:SC2307	>gnl|kg|sec:SC2307 menB; dihydroxynaphtoic acid synthetase [EC:4.1.3.36] [KO:K01661]	x			

Table L-3. KEGG Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>sfl:SF2341</td><td>>gnl|kg|sfl:SF2341 menB; dihydroxynaphtoic acid synthetase [EC:4.1.3.36] [KO:K01661]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>sfx:S2475</td><td>>gnl|kg|sfx:S2475 menB; dihydroxynaphtoic acid synthetase [EC:4.1.3.36] [KO:K01661]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>stt:t0556</td><td>>gnl|kg|stt:t0556 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>stm:STM2307</td><td>>gnl|kg|stm:STM2307 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>spt:SPA0556</td><td>>gnl|kg|spt:SPA0556 menB; naphthoate synthase</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>sty:STY2537</td><td>>gnl|kg|sty:STY2537 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>ecj:JW2257</td><td>>gnl|kg|ecj:JW2257 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>eco:b2262</td><td>>gnl|kg|eco:b2262 menB; dihydroxynaphthoic acid synthetase [EC:4.1.3.36] [KO:K01661]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>ecc:c2805</td><td>>gnl|kg|ecc:c2805 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>msu:MS1792</td><td>>gnl|kg|msu:MS1792 menB; dihydroxynaphthoic acid synthase [EC:4.1.3.36] [KO:K01661]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>sbo:SBO_2299</td><td>>gnl|kg|sbo:SBO_2299 menB; dihydroxynaphtoic acid synthetase</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>ssn:SSO_2323</td><td>>gnl|kg|ssn:SSO_2323 menB; dihydroxynaphtoic acid synthetase [EC:4.1.3.36] [KO:K01661]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>sdy:SDY_2458</td><td>>gnl|kg|sdy:SDY_2458 menB; dihydroxynaphtoic acid synthetase</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>yps:YPTB2558</td><td>>gnl|kg|yps:YPTB2558 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>ypm:YP2336</td><td>>gnl|kg|ypm:YP2336 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>ype:YPO2525</td><td>>gnl|kg|ype:YPO2525 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>ece:Z3522</td><td>>gnl|kg|ece:Z3522 menB; dihydroxynaphtoic acid synthetase [EC:4.1.3.36] [KO:K01661]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>eca:ECA1213</td><td>>gnl|kg|eca:ECA1213 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]</td><td>x</td><td></td><td></td><td></td></tr>
</table>

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
hdu:HD1925	>gnl|kg|hdu:HD1925 menB; napthoate synthetase [EC:4.1.3.36] [KO:K01661]	x			
plu:plu3071	>gnl|kg|plu:plu3071 menB; naphthoate synthase (dihydroxynaphthoic acid synthetase) (DHNA synthetase) [EC:4.1.3.36] [KO:K01661]	x			
bli:BL02406	>gnl|kg|bli:BL02406 menB; dihydroxynapthoic acid synthetase [EC:4.1.3.36] [KO:K01661]	x			
bld:BLi03220	>gnl|kg|bld:BLi03220 menB; dihydroxynapthoic acid synthetase; RBL03382 [EC:4.1.3.36] [KO:K01661]	x			
bca:BCE5013	>gnl|kg|bca:BCE5013 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
ban:BA5109	>gnl|kg|ban:BA5109 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
btk:BT9727_4586	>gnl|kg|btk:BT9727_4586 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
bar:GBAA5109	>gnl|kg|bar:GBAA5109 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
bcz:BCZK4608	>gnl|kg|bcz:BCZK4608 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
bsu:BG10686	>gnl|kg|bsu:BG10686 menB; dihydroxynapthoic acid synthetase [EC:4.1.3.36] [KO:K01661]	x			
tel:tll2458	>gnl|kg|tel:tll2458 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
syn:sll1127	>gnl|kg|syn:sll1127 menB; 1,4-dihydroxy-2-naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
lla:L0171	>gnl|kg|lla:L0171 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
sam:MW0929	>gnl|kg|sam:MW0929 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
sac:SACOL1054	>gnl|kg|sac:SACOL1054 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
sar:SAR1019	>gnl|kg|sar:SAR1019 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
saa:SAUSA300_0948	>gnl|kg|saa:SAUSA300_0948 menB; naphthoate synthase [EC:4.1.3.36]	x			
sha:SH1917	>gnl|kg|sha:SH1917 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
sau:SA0898	>gnl|kg|sau:SA0898 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
sav:SAV1045	>gnl|kg|sav:SAV1045 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
sab:SAB0912	>gnl|kg|sab:SAB0912 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
cya:CYA_0530	>gnl|kg|cya:CYA_0530 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
lmo:lmo1673	>gnl|kg|lmo:lmo1673 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
lin:lin1781	>gnl|kg|lin:lin1781 menB; similar to dihydroxynapthoic acid synthetase [EC:4.1.3.36] [KO:K01661]	x			
lmf:LMOf2365_1697	>gnl|kg|lmf:LMOf2365_1697 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
syc:syc0926_d	>gnl|kg|syc:syc0926_d menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
ser:SERP0632	>gnl|kg|ser:SERP0632 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
cgb:cg0548	>gnl|kg|cgb:cg0548 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
cyb:CYB_0565	>gnl|kg|cyb:CYB_0565 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
pmt:PMT0405	>gnl|kg|pmt:PMT0405 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
syw:SYNW0998	>gnl|kg|syw:SYNW0998 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
pcu:pc1064	>gnl|kg|pcu:pc1064 menB; probable naphthoate synthase, menB [EC:4.1.3.36] [KO:K01661]	x			

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
mtc:MT0573	>gnl|kg|mtc:MT0573 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
mtu:Rv0548c	>gnl|kg|mtu:Rv0548c menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
mbo:Mb0562c	>gnl|kg|mbo:Mb0562c menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
efa:EF0445	>gnl|kg|efa:EF0445 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
pmm:PMM0608	>gnl|kg|pmm:PMM0608 menB; napthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
pma:Pro1053	>gnl|kg|pma:Pro1053 menB; dihydroxynaphthoic acid synthase [EC:4.1.3.36] [KO:K01661]	x			
hal:VNG1079G	>gnl|kg|hal:VNG1079G menB; dihydroxynaphthoic acid synthase [EC:4.1.3.36] [KO:K01661]	x			
mpa:MAP4044c	>gnl|kg|mpa:MAP4044c menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
cjk:jk1870	>gnl|kg|cjk:jk1870 menB; dihydroxynaphthoic acid synthase [EC:4.1.3.36] [KO:K01661]	x			
bfs:BF1303	>gnl|kg|bfs:BF1303 menB; putative naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
bba:Bd3492	>gnl|kg|bba:Bd3492 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
tws:TW120	>gnl|kg|tws:TW120 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
twh:TWT110	>gnl|kg|twh:TWT110 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
lxx:Lxx01440	>gnl|kg|lxx:Lxx01440 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
son:SO4739	>gnl|kg|son:SO4739 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
mle:ML2263	>gnl|kg|mle:ML2263 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
nfa:nfa51380	>gnl|kg|nfa:nfa51380 menB; putative dihydroxynaphtoic acid synthetase [EC:4.1.3.36] [KO:K01661]	x			
cdi:DIP0421	>gnl|kg|cdi:DIP0421 menB; putative naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
dps:DP0252	>gnl|kg|dps:DP0252 menB; probable naphthoate synthase (MenB) [EC:4.1.3.36] [KO:K01661]	x			
sru:SRU_2766	>gnl|kg|sru:SRU_2766 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
nph:NP2730A	>gnl|kg|nph:NP2730A menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
pgi:PG1523	>gnl|kg|pgi:PG1523 menB; naphthoate synthase [EC:4.1.3.36] [KO:K01661]	x			
psb:Psyr_1989	>gnl|kg|psb:Psyr_1989 mandelate racemase/muconate lactonizing enzyme:mandelate racemase/muconate lactonizing enzyme [EC:4.2.1.6] [KO:K01684]	x			
bur:Bcep18194_A5994	>gnl|kg|bur:Bcep18194_A5994 mandelate racemase/muconate lactonizing enzyme [EC:4.2.1.6] [KO:K01684]	x			
eca:ECA4416	>gnl|kg|eca:ECA4416 dgoA1, dgoD2; DgoA protein [includes: 2-dehydro-3-deoxyphosphogalactonate aldolase; galactonate dehydratase] [EC:4.1.2.21 4.2.1.6] [KO:K01631 K01684]	x			
bli:BL03851	>gnl|kg|bli:BL03851 mandelate racemase/muconate lactonizing enzyme,mandelate racemase/muconate lactonizing enzyme [EC:4.2.1.6] [KO:K01684]	x			
stm:STM3828	>gnl|kg|stm:STM3828 dgoA; 2-oxo-3-deoxygalactonate 6-phosphate aldolase/galactonate dehydratase [EC:4.1.2.21 4.2.1.6] [KO:K01631 K01684]	x			
xcc:XCC1746	>gnl|kg|xcc:XCC1746 dgoA; 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-deoxyphosphogluconate aldolase [EC:4.2.1.6] [KO:K01684]	x			
xcb:XC_2488	>gnl|kg|xcb:XC_2488 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-deoxyphosphogluconate aldolase [EC:4.2.1.6] [KO:K01684]	x			

Table L-3. KEGG Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>xoo:XOO2919</td><td>>gnl|kg|xoo:XOO2919 dgoA; 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-deoxyphosphogluconate aldolase [EC:4.2.1.6] [KO:K01684]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>xac:XAC1765</td><td>>gnl|kg|xac:XAC1765 dgoA; 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-deoxyphosphogluconate aldolase [EC:4.2.1.6] [KO:K01684]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>cne:CNI02060</td><td>>gnl|kg|cne:CNI02060 mandelate racemase/muconate lactonizing enzyme, putative [EC:4.2.1.6] [KO:K01684]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>tfu:Tfu_1786</td><td>>gnl|kg|tfu:Tfu_1786 mandelate racemase/muconate lactonizing enzyme family [EC:4.2.1.6] [KO:K01684]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>hma:rrnAC3069</td><td>>gnl|kg|hma:rrnAC3069 dgoA3; mandelate racemase/muconate lactonizing enzyme family [EC:4.2.1.6] [KO:K01684]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>bur:Bcep18194_A4275</td><td>>gnl|kg|bur:Bcep18194_A4275 mandelate racemase/muconate lactonizing enzyme [EC:4.2.1.40] [KO:K01706]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>bli:BL01649</td><td>>gnl|kg|bli:BL01649 gudD; mandelate racemase/muconate lactonizing enzyme [EC:4.2.1.40] [KO:K01706]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>plu:plu3070</td><td>>gnl|kg|plu:plu3070 menC; O-succinylbenzoate-CoA synthase (OSB synthase) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) [EC:4.2.1.-] [KO:K02549]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>lmo:lmo2520</td><td>>gnl|kg|lmo:lmo2520 similar to B. subtilis O-succinylbenzoate-CoA synthase (MenC) [EC:4.2.1.-] [KO:K02549]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>lin:lin2664</td><td>>gnl|kg|lin:lin2664 similar to B. subtilis O-succinylbenzoate-CoA synthase (MenC) [EC:4.2.1.-] [KO:K02549]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>bms:BR1018</td><td>>gnl|kg|bms:BR1018 mandelate racemase/muconate lactonizing enzyme family protein [EC:5.5.1.7] [KO:K01860]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>sdy:SDY_1403</td><td>>gnl|kg|sdy:SDY_1403 ycjG; putative muconate cycloisomerase I [EC:5.5.-.-]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>ypk:y1991</td><td>>gnl|kg|ypk:y1991 muconate cycloisomerase I [EC:5.5.-.-]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>ana:all3532</td><td>>gnl|kg|ana:all3532 muconate cycloisomerase [EC:5.5.-.-]</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>pfo:Pfl_2325</td><td>>gnl|kg|pfo:Pfl_2325 mandelate racemase/muconate lactonizing enzyme</td><td>x</td><td></td><td></td><td></td></tr>
<tr><td>reu:Reut_B4400</td><td>>gnl|kg|reu:Reut_B4400 mandelate racemase/muconate lactonizing enzyme [EC:5.5.1.1] [KO:K01856]</td><td>x</td><td></td><td></td><td></td></tr>
</table>

Table L-3. KEGG Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
pfo:Pfl_2963	>gnl|kg|pfo:Pfl_2963 mandelate racemase/muconate lactonizing enzyme	x			
reu:Reut_A1689	>gnl|kg|reu:Reut_A1689 mandelate racemase/muconate lactonizing enzyme	x			
bur:Bcep18194_C7044	>gnl|kg|bur:Bcep18194_C7044 mandelate racemase/muconate lactonizing enzyme [EC:5.5.1.1] [KO:K01856]	x			
bmf:BAB1_0590	>gnl|kg|bmf:BAB1_0590 haloacid dehalogenase/epoxide hydrolase:haloacid dehalogenase-like hydrolase:HAD-superfamily hydrolase, subfamily IA, variant 2	x			
tte:TTE0802	>gnl|kg|tte:TTE0802 predicted phosphatase/phosphohexomutase [EC:5.4.2.6] [KO:K01838]	x			
bld:BLi00665	>gnl|kg|bld:BLi00665 pgcM; beta-phosphoglucomutase / glucose-1-phosphate phosphodismutase; RBL03360 [EC:5.4.2.6] [KO:K01838]	x			
bli:BL00490	>gnl|kg|bli:BL00490 pgcM; beta-phosphoglucomutase and glucose-1-phosphate phosphodismutase [EC:5.4.2.6] [KO:K01838]	x			

L.4. Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
CODA_ECOLI	>gnl|sp|CODA_ECOLI (P25524) Cytosine deaminase (EC 3.5.4.1) (Cytosine aminohydrolase)			x	
ADA_BOVIN	>gnl|sp|ADA_BOVIN (P56658) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)			x	
ADA_HUMAN	>gnl|sp|ADA_HUMAN (P00813) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)			x	
ADA_MOUSE	>gnl|sp|ADA_MOUSE (P03958) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)			x	
ADA_RAT	>gnl|sp|ADA_RAT (Q920P6) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)			x	
ADD_VIBCH	>gnl|sp|ADD_VIBCH (Q9KNI7) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)			x	
ADD_SALTI	>gnl|sp|ADD_SALTI (Q8Z6R2) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)			x	
ADD_ECOL6	>gnl|sp|ADD_ECOL6 (Q8FH99) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)			x	
ADD_ECOLI	>gnl|sp|ADD_ECOLI (P22333) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)			x	
ADD_SALTY	>gnl|sp|ADD_SALTY (Q8ZPL9) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)			x	
ADD_ECO57	>gnl|sp|ADD_ECO57 (Q8X661) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)			x	
ADD_SHIFL	>gnl|sp|ADD_SHIFL (Q83RC0) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)			x	
ADD_SHEON	>gnl|sp|ADD_SHEON (Q8E8D4) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)			x	
ADD1_VIBPA	>gnl|sp|ADD1_VIBPA (Q87TF3) Adenosine deaminase 1 (EC 3.5.4.4) (Adenosine aminohydrolase 1)			x	
ADA_XENTR	>gnl|sp|ADA_XENTR (Q63ZU0) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)			x	
ADA_XENLA	>gnl|sp|ADA_XENLA (Q6GP70) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
NDDD_ALCXX	>gnl|sp|NDDD_ALCXX (P94212) N-acyl-D-aspartate deacylase (EC 3.5.1.83) (N-acyl-D-aspartate amidohydrolase)			x	
NDAD_ALCXX	>gnl|sp|NDAD_ALCXX (P72349) D-aminoacylase (EC 3.5.1.81) (N-acyl-D-amino-acid deacylase)			x	
NDED_ALCXX	>gnl|sp|NDED_ALCXX (P94211) N-acyl-D-glutamate deacylase (EC 3.5.1.82) (N-acyl-D-glutamate amidohydrolase)			x	
HYDL_ARTAU	>gnl|sp|HYDL_ARTAU (P81006) Non-ATP-dependent L-selective hydantoinase (EC 3.5.2.2)			x	
HYDA_PSEPU	>gnl|sp|HYDA_PSEPU (Q59699) D-hydantoinase (EC 3.5.2.2) (Dihydropyrimidinase) (DHPase)			x	
HYDA_BACST	>gnl|sp|HYDA_BACST (Q45515) D-hydantoinase (EC 3.5.2.2) (Dihydropyrimidinase) (DHPase)			x	
HYDA_STRCO	>gnl|sp|HYDA_STRCO (O69809) D-hydantoinase (EC 3.5.2.2) (Dihydropyrimidinase) (DHPase)			x	
HYDA_AGRTU	>gnl|sp|HYDA_AGRTU (Q44184) D-hydantoinase (EC 3.5.2.2) (Dihydropyrimidinase) (DHPase)			x	
YGEZ_ECOLI	>gnl|sp|YGEZ_ECOLI (Q46806) Hypothetical hydrolase ygeZ (EC 3.-.-.-)			x	x
HYDA_BURPI	>gnl|sp|HYDA_BURPI (Q8VTT5) D-hydantoinase (EC 3.5.2.2) (Dihydropyrimidinase) (DHPase)			x	
DPYS_HUMAN	>gnl|sp|DPYS_HUMAN (Q14117) Dihydropyrimidinase (EC 3.5.2.2) (DHPase) (Hydantoinase) (DHP)			x	x
DPYS_RAT	>gnl|sp|DPYS_RAT (Q63150) Dihydropyrimidinase (EC 3.5.2.2) (DHPase) (Hydantoinase) (DHP)			x	x
DPYS_MOUSE	>gnl|sp|DPYS_MOUSE (Q9EQF5) Dihydropyrimidinase (EC 3.5.2.2) (DHPase) (Hydantoinase) (DHP)			x	x
DHP2_CAEBR	>gnl|sp|DHP2_CAEBR (Q61YQ1) Dihydropyrimidinase 2 (EC 3.5.2.2)			x	x
DHP2_CAEEL	>gnl|sp|DHP2_CAEEL (Q18677) Dihydropyrimidinase 2 (EC 3.5.2.2) (CeCRMP/DHP-2) (UlipA)			x	x
DHP1_CAEBR	>gnl|sp|DHP1_CAEBR (Q60Q85) Dihydropyrimidinase 1 (EC 3.5.2.2)			x	x
DHP1_CAEEL	>gnl|sp|DHP1_CAEEL (Q21773) Dihydropyrimidinase 1 (EC 3.5.2.2) (CeCRMP/DHP-1) (UlipB)			x	x
UREA_CANEN	>gnl|sp|UREA_CANEN (P07374) Urease (EC 3.5.1.5) (Urea amidohydrolase)			x	
UREA_SCHPO	>gnl|sp|UREA_SCHPO (O00084) Urease (EC 3.5.1.5) (Urea amidohydrolase)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>UREA_ASPFU</td><td>>gnl|sp|UREA_ASPFU (Q6A3P9) Urease (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>UREA_CRYNE</td><td>>gnl|sp|UREA_CRYNE (Q5KCQ6) Urease (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>UREA_CRYNV</td><td>>gnl|sp|UREA_CRYNV (O13465) Urease (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_BACSB</td><td>>gnl|sp|URE1_BACSB (Q07397) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_SYNY3</td><td>>gnl|sp|URE1_SYNY3 (P73061) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_RHIME</td><td>>gnl|sp|URE1_RHIME (P42885) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_KLEAE</td><td>>gnl|sp|URE1_KLEAE (P18314) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_PROMI</td><td>>gnl|sp|URE1_PROMI (P17086) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_PROVU</td><td>>gnl|sp|URE1_PROVU (P16122) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_BACSU</td><td>>gnl|sp|URE1_BACSU (P77837) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_HAEIN</td><td>>gnl|sp|URE1_HAEIN (P44391) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_ACTPL</td><td>>gnl|sp|URE1_ACTPL (O54420) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_BORBR</td><td>>gnl|sp|URE1_BORBR (O08400) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE2_HELPY</td><td>>gnl|sp|URE2_HELPY (P69996) Urease beta subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE2_HELPJ</td><td>>gnl|sp|URE2_HELPJ (P69997) Urease beta subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE2_HELFE</td><td>>gnl|sp|URE2_HELFE (Q08716) Urease beta subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE2_HELHE</td><td>>gnl|sp|URE2_HELHE (P42823) Urease beta subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_BACPA</td><td>>gnl|sp|URE1_BACPA (P41020) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>URE1_STAAN</td><td>>gnl|sp|URE1_STAAN (P67404) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_STAAW</td><td>>gnl|sp|URE1_STAAW (P67405) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_STAAS</td><td>>gnl|sp|URE1_STAAS (Q6G732) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_STAAM</td><td>>gnl|sp|URE1_STAAM (P67403) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_STAAC</td><td>>gnl|sp|URE1_STAAC (Q5HDR8) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_UREUR</td><td>>gnl|sp|URE1_UREUR (P17272) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_STAEQ</td><td>>gnl|sp|URE1_STAEQ (Q5HLW1) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_STAES</td><td>>gnl|sp|URE1_STAES (Q8CNC9) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_STAAR</td><td>>gnl|sp|URE1_STAAR (Q6GEE4) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_UREPA</td><td>>gnl|sp|URE1_UREPA (Q60058) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_STAXY</td><td>>gnl|sp|URE1_STAXY (P42873) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_MYCTU</td><td>>gnl|sp|URE1_MYCTU (P0A660) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_MYCBO</td><td>>gnl|sp|URE1_MYCBO (P0A661) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_CLOPE</td><td>>gnl|sp|URE1_CLOPE (P94669) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_STRSL</td><td>>gnl|sp|URE1_STRSL (P50047) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>URE1_YEREN</td><td>>gnl|sp|URE1_YEREN (P31494) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
URE1_YERPE	>gnl|sp|URE1_YERPE (Q9ZFR9) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)			x	
URE1_YERPS	>gnl|sp|URE1_YERPS (P52313) Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)			x	
URE1_LACFE	>gnl|sp|URE1_LACFE (P26929) Acid urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)			x	
IADA_ECOLI	>gnl|sp|IADA_ECOLI (P39377) Isoaspartyl dipeptidase (EC 3.4.19.-)			x	
D3D2_HUMAN	>gnl|sp|D3D2_HUMAN (P42126) 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor (EC 5.3.3.8) (Dodecenoyl-CoA isomerase) (Delta(3),delta(2)-enoyl-CoA isomerase) (D3,D2-enoyl-CoA isomerase)			x	
D3D2_RAT	>gnl|sp|D3D2_RAT (P23965) 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor (EC 5.3.3.8) (Dodecenoyl-CoA isomerase) (Delta(3),delta(2)-enoyl-CoA isomerase) (D3,D2-enoyl-CoA isomerase)			x	
D3D2_MOUSE	>gnl|sp|D3D2_MOUSE (P42125) 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor (EC 5.3.3.8) (Dodecenoyl-CoA isomerase) (Delta(3),delta(2)-enoyl-CoA isomerase) (D3,D2-enoyl-CoA isomerase)			x	
ECH1_HUMAN	>gnl|sp|ECH1_HUMAN (Q13011) Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor (EC 5.3.3.-)			x	
ECH1_RAT	>gnl|sp|ECH1_RAT (Q62651) Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor (EC 5.3.3.-)			x	
ECH1_MOUSE	>gnl|sp|ECH1_MOUSE (O35459) Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor (EC 5.3.3.-)			x	
ECH1_PONPY	>gnl|sp|ECH1_PONPY (Q5RFG0) Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor (EC 5.3.3.-)			x	
MMCD_ECOLI	>gnl|sp|MMCD_ECOLI (P52045) Methylmalonyl-CoA decarboxylase (EC 4.1.1.41) (Transcarboxylase) (MMCD)			x	
ENO_GEOKA	>gnl|sp|ENO_GEOKA (Q5KVE7) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO2_CHLTE	>gnl|sp|ENO2_CHLTE (Q8KG25) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x	
ENO_DROME	>gnl|sp|ENO_DROME (P15007) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
ENOA_CHICK	>gnl|sp|ENOA_CHICK (P51913) Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Phosphopyruvate hydratase)			x	
ENO_MESFL	>gnl|sp|ENO_MESFL (Q6F0Z7) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_PLAF7	>gnl|sp|ENO_PLAF7 (Q8IJN7) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_THETN	>gnl|sp|ENO_THETN (Q8R967) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENOG_CHICK	>gnl|sp|ENOG_CHICK (O57391) Gamma-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Neural enolase) (NSE)			x	
ENO_PLAFA	>gnl|sp|ENO_PLAFA (Q27727) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENOG_HUMAN	>gnl|sp|ENOG_HUMAN (P09104) Gamma-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Neural enolase) (Neuron-specific enolase) (NSE) (Enolase 2)			x	
ENO_LYCES	>gnl|sp|ENO_LYCES (P26300) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENOG_RAT	>gnl|sp|ENOG_RAT (P07323) Gamma-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Neural enolase) (Neuron-specific enolase) (NSE) (Enolase 2)			x	
ENO1_LACPL	>gnl|sp|ENO1_LACPL (Q88YH3) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x	
ENO_PLAFG	>gnl|sp|ENO_PLAFG (Q9UAL5) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENOA_ALLMI	>gnl|sp|ENOA_ALLMI (Q9PVK2) Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Phosphopyruvate hydratase)			x	
ENOG_MOUSE	>gnl|sp|ENOG_MOUSE (P17183) Gamma-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Neural enolase) (Neuron-specific enolase) (NSE) (Enolase 2)			x	
ENOA_RAT	>gnl|sp|ENOA_RAT (P04764) Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
ENOA_HUMAN	>gnl|sp|ENOA_HUMAN (P06733) Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1) (Phosphopyruvate hydratase) (C-myc promoter-binding protein) (MBP-1) (MPB-1) (Plasminogen-binding protein)			x	
ENOA_PYTRG	>gnl|sp|ENOA_PYTRG (Q9W7L0) Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Phosphopyruvate hydratase)			x	
ENOA_MOUSE	>gnl|sp|ENOA_MOUSE (P17182) Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1)			x	
ENO2_MAIZE	>gnl|sp|ENO2_MAIZE (P42895) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x	
ENO1_LACJO	>gnl|sp|ENO1_LACJO (Q74K78) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x	
ENO_PLAYO	>gnl|sp|ENO_PLAYO (Q7RA60) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_ENTHR	>gnl|sp|ENO_ENTHR (Q8GR70) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENOB_HUMAN	>gnl|sp|ENOB_HUMAN (P13929) Beta-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase) (Enolase 3)			x	
ENO_BACCZ	>gnl|sp|ENO_BACCZ (Q631M2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_BACHD	>gnl|sp|ENO_BACHD (Q9K717) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_ARATH	>gnl|sp|ENO_ARATH (P25696) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_BACHK	>gnl|sp|ENO_BACHK (Q6HBF3) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_BACAN	>gnl|sp|ENO_BACAN (Q81X78) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_ENTFA	>gnl|sp|ENO_ENTFA (Q9K596) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENOA_SCEUN	>gnl|sp|ENOA_SCEUN (Q9W7L2) Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Phosphopyruvate hydratase)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
ENOA_XENLA	>gnl|sp|ENOA_XENLA (P08734) Alpha-enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_BACC1	>gnl|sp|ENO_BACC1 (Q72XY5) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_MYCMS	>gnl|sp|ENO_MYCMS (Q6MTZ2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENOB_MOUSE	>gnl|sp|ENOB_MOUSE (P21550) Beta-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase) (Enolase 3)			x	
ENO_BACSU	>gnl|sp|ENO_BACSU (P37869) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_ORYSA	>gnl|sp|ENO_ORYSA (Q42971) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (OSE1)			x	
ENO_BACCR	>gnl|sp|ENO_BACCR (Q815K8) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_RICCO	>gnl|sp|ENO_RICCO (P42896) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENOB_RABIT	>gnl|sp|ENOB_RABIT (P25704) Beta-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase) (Enolase 3)			x	
ENO_THEMA	>gnl|sp|ENO_THEMA (P42848) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_BACSK	>gnl|sp|ENO_BACSK (Q5WDK9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_MESCR	>gnl|sp|ENO_MESCR (Q43130) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO2_TOXGO	>gnl|sp|ENO2_TOXGO (Q9BPL7) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x	
ENO1_HEVBR	>gnl|sp|ENO1_HEVBR (Q9LEJ0) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1) (Allergen Hev b 9)			x	
ENO_BORGA	>gnl|sp|ENO_BORGA (Q661T0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
ENO_AQUAE	>gnl|sp|ENO_AQUAE (O66778) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_GEOSL	>gnl|sp|ENO_GEOSL (Q74AR6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_BACTN	>gnl|sp|ENO_BACTN (Q89Z05) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_CLOTE	>gnl|sp|ENO_CLOTE (Q898R0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_BORBU	>gnl|sp|ENO_BORBU (O51312) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_CLOAB	>gnl|sp|ENO_CLOAB (Q97L52) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_PARUW	>gnl|sp|ENO_PARUW (Q6MEY2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_LISIN	>gnl|sp|ENO_LISIN (P64075) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_LISMO	>gnl|sp|ENO_LISMO (P64074) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_LISMF	>gnl|sp|ENO_LISMF (Q71WX1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO1_CANAL	>gnl|sp|ENO1_CANAL (P30575) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_PROAC	>gnl|sp|ENO_PROAC (Q6AAB8) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_ASHGO	>gnl|sp|ENO_ASHGO (Q756H2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_TREDE	>gnl|sp|ENO_TREDE (Q73P50) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO2_HEVBR	>gnl|sp|ENO2_HEVBR (Q9LEI9) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2) (Allergen Hev b 9)			x	
ENO_NEOFR	>gnl|sp|ENO_NEOFR (P42894) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
ENO_SYMTH	>gnl|sp|ENO_SYMTH (Q67SV9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_KLULA	>gnl|sp|ENO_KLULA (Q70CP7) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO1_MAIZE	>gnl|sp|ENO1_MAIZE (P26301) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x	
ENO_MYCPU	>gnl|sp|ENO_MYCPU (Q98Q50) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_EIMTE	>gnl|sp|ENO_EIMTE (Q967Y8) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_OCEIH	>gnl|sp|ENO_OCEIH (Q8ENP5) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_DESVH	>gnl|sp|ENO_DESVH (Q72F92) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_FASHE	>gnl|sp|ENO_FASHE (Q27655) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO2_CANGA	>gnl|sp|ENO2_CANGA (Q6FQY4) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x	
ENO_THET8	>gnl|sp|ENO_THET8 (Q5SME1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_THET2	>gnl|sp|ENO_THET2 (Q72H85) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO1_YEAST	>gnl|sp|ENO1_YEAST (P00924) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x	
ENO_CAEEL	>gnl|sp|ENO_CAEEL (Q27527) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_SCHJA	>gnl|sp|ENO_SCHJA (P33676) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_PYRAB	>gnl|sp|ENO_PYRAB (Q9UXZ0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_DEIRA	>gnl|sp|ENO_DEIRA (Q9RR60) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
ENO_ZYMMO	>gnl|sp|ENO_ZYMMO (P33675) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_CORDI	>gnl|sp|ENO_CORDI (Q6NI61) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENOB_RAT	>gnl|sp|ENOB_RAT (P15429) Beta-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase) (Enolase 3)			x	
ENO_COREF	>gnl|sp|ENO_COREF (Q8FQS7) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_BIFLO	>gnl|sp|ENO_BIFLO (Q8G5I9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_MASBA	>gnl|sp|ENO_MASBA (Q9U615) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO2_DEBHA	>gnl|sp|ENO2_DEBHA (Q6BI20) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x	
ENO_STRPN	>gnl|sp|ENO_STRPN (Q97QS2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_ALNGL	>gnl|sp|ENO_ALNGL (Q43321) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_LOLPE	>gnl|sp|ENO_LOLPE (O02654) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_STRR6	>gnl|sp|ENO_STRR6 (Q8DPS0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_MANSM	>gnl|sp|ENO_MANSM (Q65VZ7) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_CLOPE	>gnl|sp|ENO_CLOPE (Q8XKU4) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_PYRKO	>gnl|sp|ENO_PYRKO (Q5JEV6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_NEUCR	>gnl|sp|ENO_NEUCR (Q7RV85) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_CORGL	>gnl|sp|ENO_CORGL (Q8NRS1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
ENO_STRA3	>gnl|sp|ENO_STRA3 (P64080) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_STRA5	>gnl|sp|ENO_STRA5 (P64081) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO2_YEAST	>gnl|sp|ENO2_YEAST (P00925) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x	
ENO_ACIAD	>gnl|sp|ENO_ACIAD (Q6FAT9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_STRT1	>gnl|sp|ENO_STRT1 (Q5M0M5) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_STRT2	>gnl|sp|ENO_STRT2 (Q5M561) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_STAAM	>gnl|sp|ENO_STAAM (P64078) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_STAAS	>gnl|sp|ENO_STAAS (Q6GB54) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_STAAW	>gnl|sp|ENO_STAAW (P64079) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_STAAN	>gnl|sp|ENO_STAAN (P99088) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_STAAC	>gnl|sp|ENO_STAAC (Q5HHP1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_STAAR	>gnl|sp|ENO_STAAR (Q6GIL4) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_HOMGA	>gnl|sp|ENO_HOMGA (P56252) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_DESVM	>gnl|sp|ENO_DESVM (O32513) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_PASMU	>gnl|sp|ENO_PASMU (P57975) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_STRMU	>gnl|sp|ENO_STRMU (Q8DTS9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
ENO_RHILO	>gnl|sp|ENO_RHILO (Q98MZ3) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_SCHMA	>gnl|sp|ENO_SCHMA (Q27877) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_PSEAE	>gnl|sp|ENO_PSEAE (Q9HXZ5) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_MYCLE	>gnl|sp|ENO_MYCLE (Q9CD42) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_METJA	>gnl|sp|ENO_METJA (Q60173) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_STAAU	>gnl|sp|ENO_STAAU (O69174) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Laminin binding protein)			x	
ENO_CRYPA	>gnl|sp|ENO_CRYPA (Q6RG04) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_HAEIN	>gnl|sp|ENO_HAEIN (P43806) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENOA_BOVIN	>gnl|sp|ENOA_BOVIN (Q9XSJ4) Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1) (Phosphopyruvate hydratase) (HAP47)			x	
ENO_PYRHO	>gnl|sp|ENO_PYRHO (O59605) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_STRP6	>gnl|sp|ENO_STRP6 (Q5XD01) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_STAEQ	>gnl|sp|ENO_STAEQ (Q5HQV0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_STAES	>gnl|sp|ENO_STAES (Q8CPY3) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_ONYPE	>gnl|sp|ENO_ONYPE (Q6YQT9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_STRP1	>gnl|sp|ENO_STRP1 (P69949) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_STRP8	>gnl|sp|ENO_STRP8 (P69951) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
ENO_STRP3	>gnl|sp|ENO_STRP3 (P69950) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_NEIG1	>gnl|sp|ENO_NEIG1 (Q5F8Z2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO1_DEBHA	>gnl|sp|ENO1_DEBHA (Q6BTB1) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x	
ENO_XANCP	>gnl|sp|ENO_XANCP (Q8P9Z3) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_MYCPA	>gnl|sp|ENO_MYCPA (Q741U7) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_CLAHE	>gnl|sp|ENO_CLAHE (P42040) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Allergen Cla h 6) (Cla h VI)			x	
ENO_XANAC	>gnl|sp|ENO_XANAC (Q8PLS0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_YERPE	>gnl|sp|ENO_YERPE (Q8ZBN2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_YERPS	>gnl|sp|ENO_YERPS (Q66ED8) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_PHOPR	>gnl|sp|ENO_PHOPR (Q6LMT1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_NEIMA	>gnl|sp|ENO_NEIMA (Q9JU46) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_NEIMB	>gnl|sp|ENO_NEIMB (Q9JZ53) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_YARLI	>gnl|sp|ENO_YARLI (Q6C1F3) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_IDILO	>gnl|sp|ENO_IDILO (Q5R143) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_STRIT	>gnl|sp|ENO_STRIT (Q9XDS7) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_PYRFU	>gnl|sp|ENO_PYRFU (Q8U477) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
ENO_PHOLL	>gnl|sp|ENO_PHOLL (Q7N835) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO1_STRCO	>gnl|sp|ENO1_STRCO (Q9F2Q3) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x	
ENO_TREPA	>gnl|sp|ENO_TREPA (P74934) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_DESPS	>gnl|sp|ENO_DESPS (Q6AM97) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_PENCH	>gnl|sp|ENO_PENCH (Q76KF9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_SHIFL	>gnl|sp|ENO_SHIFL (P0A6Q2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_ECO57	>gnl|sp|ENO_ECO57 (P0A6Q1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_ECOL6	>gnl|sp|ENO_ECOL6 (P0A6Q0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_ECOLI	>gnl|sp|ENO_ECOLI (P0A6P9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_VIBVY	>gnl|sp|ENO_VIBVY (Q7MHQ1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_VIBPA	>gnl|sp|ENO_VIBPA (Q87LQ0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO11_SCHPO	>gnl|sp|ENO11_SCHPO (P40370) Enolase 1-1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1-1) (2-phospho-D-glycerate hydro-lyase 1-1)			x	
ENO_RHORB	>gnl|sp|ENO_RHORB (Q870B9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Allergen Rho m 1)			x	
ENO_RHOBA	>gnl|sp|ENO_RHOBA (Q7UIR2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENOB_CHICK	>gnl|sp|ENOB_CHICK (P07322) Beta-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Phosphopyruvate hydratase)			x	
ENO_STRAW	>gnl|sp|ENO_STRAW (Q82HH5) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
ENO_MYCTU	>gnl|sp|ENO_MYCTU (P96377) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_ALTAL	>gnl|sp|ENO_ALTAL (Q9HDT3) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Major allergen Alt a 6) (Alt a 11) (Alt a XI)			x	
ENO_XANOR	>gnl|sp|ENO_XANOR (Q5GYK4) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_AGRT5	>gnl|sp|ENO_AGRT5 (Q8UFH1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_METKA	>gnl|sp|ENO_METKA (Q8TUV6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_HAEDU	>gnl|sp|ENO_HAEDU (Q7VNM6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_ERWCT	>gnl|sp|ENO_ERWCT (Q6D182) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_XYLFA	>gnl|sp|ENO_XYLFA (Q9PDT8) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_MYCBO	>gnl|sp|ENO_MYCBO (Q7U0U6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_MYCGA	>gnl|sp|ENO_MYCGA (Q7NAY0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_VIBVU	>gnl|sp|ENO_VIBVU (Q8DC62) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_VIBCH	>gnl|sp|ENO_VIBCH (Q9KPC5) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_BRAJA	>gnl|sp|ENO_BRAJA (Q89KV6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO1_CHLTE	>gnl|sp|ENO1_CHLTE (Q8KB35) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x	
ENO_AERHY	>gnl|sp|ENO_AERHY (Q8GE63) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_RHIME	>gnl|sp|ENO_RHIME (Q92Q98) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
ENO_NOCFA	>gnl|sp|ENO_NOCFA (Q5YQ30) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO1_TOXGO	>gnl|sp|ENO1_TOXGO (Q9UAE6) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x	
ENO_HELPJ	>gnl|sp|ENO_HELPJ (Q9ZMS6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_VIBF1	>gnl|sp|ENO_VIBF1 (Q5E326) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_FUSNN	>gnl|sp|ENO_FUSNN (Q8RI55) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_LEIXX	>gnl|sp|ENO_LEIXX (Q6ADR6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_SALPA	>gnl|sp|ENO_SALPA (Q5PEH4) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_SALTI	>gnl|sp|ENO_SALTI (P64077) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_SALTY	>gnl|sp|ENO_SALTY (P64076) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_PORGI	>gnl|sp|ENO_PORGI (Q7MTV8) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO12_SCHPO	>gnl|sp|ENO12_SCHPO (Q8NKC2) Enolase 1-2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1-2) (2-phospho-D-glycerate hydro-lyase 1-2)			x	
ENO_ASPFU	>gnl|sp|ENO_ASPFU (Q96X30) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Allergen Asp f 22)			x	
ENO_XYLFT	>gnl|sp|ENO_XYLFT (Q87DY6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_PSEPK	>gnl|sp|ENO_PSEPK (Q88MF9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO1_PSESM	>gnl|sp|ENO1_PSESM (Q886M3) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x	
ENO_LEPIN	>gnl|sp|ENO_LEPIN (Q8F4T8) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
ENO_LEPIC	>gnl|sp|ENO_LEPIC (Q72QZ8) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_RALSO	>gnl|sp|ENO_RALSO (Q8Y0B5) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_SILPO	>gnl|sp|ENO_SILPO (Q5LQL4) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_SHEON	>gnl|sp|ENO_SHEON (Q8EBR0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO1_LACLA	>gnl|sp|ENO1_LACLA (Q9CHS7) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x	
ENO_CHLPN	>gnl|sp|ENO_CHLPN (Q9Z7A6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_FRATT	>gnl|sp|ENO_FRATT (Q5NGW8) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_METMP	>gnl|sp|ENO_METMP (Q6M075) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_BRUSU	>gnl|sp|ENO_BRUSU (Q8G0G3) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_ASPOR	>gnl|sp|ENO_ASPOR (Q12560) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_ANASP	>gnl|sp|ENO_ANASP (Q8YRB0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_BARHE	>gnl|sp|ENO_BARHE (Q8L202) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_HELPY	>gnl|sp|ENO_HELPY (P48285) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_RHOPA	>gnl|sp|ENO_RHOPA (Q6N5U6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_BORBR	>gnl|sp|ENO_BORBR (Q7WD75) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_BORPE	>gnl|sp|ENO_BORPE (Q7VW79) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
ENO_BORPA	>gnl|sp|ENO_BORPA (Q7W5N9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_BARQU	>gnl|sp|ENO_BARQU (Q6G173) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO1_ENTHI	>gnl|sp|ENO1_ENTHI (P51555) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_TUBBO	>gnl|sp|ENO_TUBBO (Q6W3C0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_BRUME	>gnl|sp|ENO_BRUME (Q8YHF0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_BURPS	>gnl|sp|ENO_BURPS (Q63SQ0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_BURMA	>gnl|sp|ENO_BURMA (Q62J10) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO2_STRCO	>gnl|sp|ENO2_STRCO (Q9F3P9) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x	
ENO_CAUCR	>gnl|sp|ENO_CAUCR (Q9A7J9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_GLOVI	>gnl|sp|ENO_GLOVI (Q7NIR1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_SYNEL	>gnl|sp|ENO_SYNEL (Q8DL40) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_PENCI	>gnl|sp|ENO_PENCI (Q96X46) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Allergen Pen c 22)			x	
ENO_SYNP6	>gnl|sp|ENO_SYNP6 (Q5N3P4) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_GLUOX	>gnl|sp|ENO_GLUOX (Q5FNN5) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO2_METCA	>gnl|sp|ENO2_METCA (Q604M4) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x	
ENO_MYCPE	>gnl|sp|ENO_MYCPE (Q8EW32) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
ENO_ALLMI	>gnl|sp|ENO_ALLMI (P42897) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Fragment)			x	
ENO_SYNY3	>gnl|sp|ENO_SYNY3 (P77972) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_MYCMO	>gnl|sp|ENO_MYCMO (Q6KIB0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO1_CANGA	>gnl|sp|ENO1_CANGA (Q6FTW6) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x	
ENO_AZOSE	>gnl|sp|ENO_AZOSE (Q5NZ69) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_MYCPN	>gnl|sp|ENO_MYCPN (P75189) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_PROMP	>gnl|sp|ENO_PROMP (Q7V377) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO2_LACPL	>gnl|sp|ENO2_LACPL (Q88VW2) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x	
ENO_PROMM	>gnl|sp|ENO_PROMM (Q7V483) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_LEGPL	>gnl|sp|ENO_LEGPL (Q5WV02) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_WOLSU	>gnl|sp|ENO_WOLSU (Q7M8Q0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_SYNPX	>gnl|sp|ENO_SYNPX (Q7U3T1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_COXBU	>gnl|sp|ENO_COXBU (Q83B44) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_PROMA	>gnl|sp|ENO_PROMA (Q7VDY0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_LEGPH	>gnl|sp|ENO_LEGPH (Q5ZTX1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_BDEBA	>gnl|sp|ENO_BDEBA (Q6MPQ2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
ENO_BLOFL	>gnl|sp|ENO_BLOFL (Q7VQH3) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_LEGPA	>gnl|sp|ENO_LEGPA (Q5X3L4) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_HELHP	>gnl|sp|ENO_HELHP (Q7VIH4) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO2_PSESM	>gnl|sp|ENO2_PSESM (Q87WD5) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x	
ENO_NITEU	>gnl|sp|ENO_NITEU (O85348) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_CAMJE	>gnl|sp|ENO_CAMJE (P42448) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_WOLPM	>gnl|sp|ENO_WOLPM (Q73HQ2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_CAMJR	>gnl|sp|ENO_CAMJR (Q5HSC1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_TROW8	>gnl|sp|ENO_TROW8 (Q83H73) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_TROWT	>gnl|sp|ENO_TROWT (Q83FF7) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO2_LACLA	>gnl|sp|ENO2_LACLA (Q9CIT0) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)			x	
ENO_BUCAI	>gnl|sp|ENO_BUCAI (P57492) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_BUCBP	>gnl|sp|ENO_BUCBP (P59566) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_CHLCV	>gnl|sp|ENO_CHLCV (Q821H7) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_MYCH2	>gnl|sp|ENO_MYCH2 (Q601S2) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO1_METCA	>gnl|sp|ENO1_METCA (Q606T2) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>ENO_UREPA</td><td>>gnl|sp|ENO_UREPA (Q9PQV9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ENO_AERPE</td><td>>gnl|sp|ENO_AERPE (Q9Y927) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ENO_BUCAP</td><td>>gnl|sp|ENO_BUCAP (Q8K9E0) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ENO_CURLU</td><td>>gnl|sp|ENO_CURLU (Q96VP4) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ENO_LACAC</td><td>>gnl|sp|ENO_LACAC (Q5FKM6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ENO_MYCGE</td><td>>gnl|sp|ENO_MYCGE (P47647) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ENO_CHLMU</td><td>>gnl|sp|ENO_CHLMU (Q9PJF3) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ENO_METAC</td><td>>gnl|sp|ENO_METAC (Q8TQ79) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ENO3_LACJO</td><td>>gnl|sp|ENO3_LACJO (Q74IV0) Enolase 3 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 3)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ENO_METMA</td><td>>gnl|sp|ENO_METMA (Q8PT81) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ENO_CHLTR</td><td>>gnl|sp|ENO_CHLTR (O84591) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ENO2_LACJO</td><td>>gnl|sp|ENO2_LACJO (Q74J64) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ENO_STRTR</td><td>>gnl|sp|ENO_STRTR (O52191) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ENO1B_HUMAN</td><td>>gnl|sp|ENO1B_HUMAN (Q05524) Alpha-enolase, lung specific (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (HLE1)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ENO_WIGBR</td><td>>gnl|sp|ENO_WIGBR (Q8D2K1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>ENO_METTH</td><td>>gnl|sp|ENO_METTH (O26149) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
ENO_SULSO	>gnl|sp|ENO_SULSO (Q97ZJ3) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_ARCFU	>gnl|sp|ENO_ARCFU (O29133) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_SULTO	>gnl|sp|ENO_SULTO (Q972B6) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_HALMA	>gnl|sp|ENO_HALMA (P29201) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_SULAC	>gnl|sp|ENO_SULAC (Q4J920) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_PYRAE	>gnl|sp|ENO_PYRAE (Q8ZYE7) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_HALSA	>gnl|sp|ENO_HALSA (Q9HQI9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_THEAC	>gnl|sp|ENO_THEAC (Q9HJT1) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
ENO_THEVO	>gnl|sp|ENO_THEVO (Q979Z9) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)			x	
DGOD_ECOLI	>gnl|sp|DGOD_ECOLI (Q6BF17) Galactonate dehydratase (EC 4.2.1.6)			x	
MANR_PSEPU	>gnl|sp|MANR_PSEPU (P11444) Mandelate racemase (EC 5.1.2.2) (MR)			x	
GUDH_BACSU	>gnl|sp|GUDH_BACSU (P42238) Probable glucarate dehydratase (EC 4.2.1.40) (GDH) (GlucD)			x	
GUDH_PSEPU	>gnl|sp|GUDH_PSEPU (P42206) Glucarate dehydratase (EC 4.2.1.40) (GDH) (GlucD)			x	
GUDH_ECO57	>gnl|sp|GUDH_ECO57 (P0AES3) Glucarate dehydratase (EC 4.2.1.40) (GDH) (GlucD)			x	
GUDH_ECOLI	>gnl|sp|GUDH_ECOLI (P0AES2) Glucarate dehydratase (EC 4.2.1.40) (GDH) (GlucD)			x	
MAAL_CLOTT	>gnl|sp|MAAL_CLOTT (Q05514) Methylaspartate ammonia-lyase (EC 4.3.1.2) (Beta-methylaspartase)			x	
MENC_PASMU	>gnl|sp|MENC_PASMU (Q9CLV7) O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>MENC_YERPE</td><td>>gnl|sp|MENC_YERPE (P58487) O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>MENC_BACSU</td><td>>gnl|sp|MENC_BACSU (O34514) O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>MENC_VIBCH</td><td>>gnl|sp|MENC_VIBCH (Q9KQM6) O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>MENC_HAEIN</td><td>>gnl|sp|MENC_HAEIN (P44961) O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>MENC_ECOLI</td><td>>gnl|sp|MENC_ECOLI (P29208) O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>MENC_ECO57</td><td>>gnl|sp|MENC_ECO57 (P58484) O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>MENC_SALTY</td><td>>gnl|sp|MENC_SALTY (P58486) O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>MENC_SALTI</td><td>>gnl|sp|MENC_SALTI (P58485) O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>MENC_MYCLE</td><td>>gnl|sp|MENC_MYCLE (Q9CBB2) Probable O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>MENC_MYCBO</td><td>>gnl|sp|MENC_MYCBO (P65426) Probable O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>MENC_MYCTU</td><td>>gnl|sp|MENC_MYCTU (P65425) Probable O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

<table>
<tr><th>Accession</th><th>Annotation</th><th>Equiv.</th><th>Incorrect</th><th>Correct</th><th>General</th></tr>
<tr><td>MENC_SYNY3</td><td>>gnl|sp|MENC_SYNY3 (Q55117) Probable O-succinylbenzoate synthase (EC 4.2.1.-) (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>TCBD_PSESQ</td><td>>gnl|sp|TCBD_PSESQ (P27099) Chloromuconate cycloisomerase (EC 5.5.1.7) (Muconate cycloisomerase II)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>TFDD_COMAC</td><td>>gnl|sp|TFDD_COMAC (Q9RNZ9) Chloromuconate cycloisomerase (EC 5.5.1.7)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>CBNB_RALEU</td><td>>gnl|sp|CBNB_RALEU (P83763) Chloromuconate cycloisomerase cbnB (EC 5.5.1.7) (Muconate cycloisomerase II cbnB)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>TFDD1_RALEJ</td><td>>gnl|sp|TFDD1_RALEJ (P05404) Chloromuconate cycloisomerase (EC 5.5.1.7) (Muconate cycloisomerase II)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>CLCB_PSEPU</td><td>>gnl|sp|CLCB_PSEPU (P11452) Chloromuconate cycloisomerase (EC 5.5.1.7) (Muconate cycloisomerase II)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>CATB1_ACILW</td><td>>gnl|sp|CATB1_ACILW (O33946) Muconate cycloisomerase I 1 (EC 5.5.1.1) (Cis,cis-muconate lactonizing enzyme I 1) (MLE 1)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>CATB_PSEPU</td><td>>gnl|sp|CATB_PSEPU (P08310) Muconate cycloisomerase I (EC 5.5.1.1) (Cis,cis-muconate lactonizing enzyme I) (MLE)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>CATB_ACIAD</td><td>>gnl|sp|CATB_ACIAD (Q43931) Muconate cycloisomerase I (EC 5.5.1.1) (Cis,cis-muconate lactonizing enzyme I) (MLE)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>CATB_RHOOP</td><td>>gnl|sp|CATB_RHOOP (P95608) Muconate cycloisomerase I (EC 5.5.1.1) (Cis,cis-muconate lactonizing enzyme I) (MLE)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>KDOP_HAEIN</td><td>>gnl|sp|KDOP_HAEIN (P45314) 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45) (KDO 8-P phosphatase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>HAD_XANAU</td><td>>gnl|sp|HAD_XANAU (Q60099) (S)-2-haloacid dehalogenase (EC 3.8.1.2) (2-haloalkanoic acid dehalogenase) (L-2-haloacid dehalogenase) (Halocarboxylic acid halidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>HAD_PSEUY</td><td>>gnl|sp|HAD_PSEUY (Q53464) (S)-2-haloacid dehalogenase (EC 3.8.1.2) (2-haloalkanoic acid dehalogenase) (L-2-haloacid dehalogenase) (Halocarboxylic acid halidohydrolase) (L-DEX)</td><td></td><td></td><td>x</td><td></td></tr>
<tr><td>HADL_PSEPU</td><td>>gnl|sp|HADL_PSEPU (Q52087) (S)-2-haloacid dehalogenase (EC 3.8.1.2) (2-haloalkanoic acid dehalogenase) (L-2-haloacid dehalogenase) (Halocarboxylic acid halidohydrolase)</td><td></td><td></td><td>x</td><td></td></tr>
</table>

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
HAD9_PSEPU	>gnl|sp|HAD9_PSEPU (Q59728) (S)-2-haloacid dehalogenase H-109 (EC 3.8.1.2) (2-haloalkanoic acid dehalogenase H-109) (L-2-haloacid dehalogenase H-109) (Halocarboxylic acid halidohydrolase H-109)			x	
HAD4_BURCE	>gnl|sp|HAD4_BURCE (Q51645) (S)-2-haloacid dehalogenase IVA (EC 3.8.1.2) (2-haloalkanoic acid dehalogenase IVA) (L-2-haloacid dehalogenase IVA) (Halocarboxylic acid halidohydrolase IVA)			x	
HAD2_PSEUC	>gnl|sp|HAD2_PSEUC (P24070) (S)-2-haloacid dehalogenase II (EC 3.8.1.2) (2-haloalkanoic acid dehalogenase II) (L-2-haloacid dehalogenase II) (Halocarboxylic acid halidohydrolase II) (DEHCII)			x	
HAD_PSEFL	>gnl|sp|HAD_PSEFL (Q59666) (S)-2-haloacid dehalogenase (EC 3.8.1.2) (2-haloalkanoic acid dehalogenase) (L-2-haloacid dehalogenase) (Halocarboxylic acid halidohydrolase)			x	
HAD1_PSEUC	>gnl|sp|HAD1_PSEUC (P24069) (S)-2-haloacid dehalogenase I (EC 3.8.1.2) (2-haloalkanoic acid dehalogenase I) (L-2-haloacid dehalogenase I) (Halocarboxylic acid halidohydrolase I) (DEHCI)			x	
HAD_AGRTR	>gnl|sp|HAD_AGRTR (P60527) 2-haloalkanoic acid dehalogenase (EC 3.8.1.2) (L-2-haloacid dehalogenase) (Halocarboxylic acid halidohydrolase) (L-DEX) (Cryptic L-isomer-specific dehalogenase) (DhlS5I)			x	
PGMB_BACSU	>gnl|sp|PGMB_BACSU (O06995) Putative beta-phosphoglucomutase (EC 5.4.2.6) (Beta-PGM)			x	
PGMB_LACLA	>gnl|sp|PGMB_LACLA (P71447) Beta-phosphoglucomutase (EC 5.4.2.6) (Beta-PGM)			x	
PGMB_ECOLI	>gnl|sp|PGMB_ECOLI (P77366) Putative beta-phosphoglucomutase (EC 5.4.2.6) (Beta-PGM)			x	
5EAS_TOBAC	>gnl|sp|5EAS_TOBAC (Q40577) Aristolchene synthase (EC 4.2.3.9) (5-epi-aristolochene synthase) (EAS)			x	
BPPS_SALOF	>gnl|sp|BPPS_SALOF (O81192) (+)-bornyl diphosphate synthase, chloroplast precursor (EC 5.5.1.8) (SBS) (BPPS)			x	
PTLS_STRS3	>gnl|sp|PTLS_STRS3 (Q55012) Pentalenene synthase (EC 4.2.3.7)			x	
SQHC_BRAJA	>gnl|sp|SQHC_BRAJA (P54924) Squalene--hopene cyclase (EC 5.4.99.17)			x	
SQHC_ZYMMO	>gnl|sp|SQHC_ZYMMO (P33990) Squalene--hopene cyclase (EC 5.4.99.17)			x	
SQHC_ALIAC	>gnl|sp|SQHC_ALIAC (P33247) Squalene--hopene cyclase (EC 5.4.99.17)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
SQHC_RHISN	>gnl|sp|SQHC_RHISN (P55348) Probable squalene--hopene cyclase (EC 5.4.99.17)			x	
TRI5_GIBPU	>gnl|sp|TRI5_GIBPU (P27679) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x	
TRI5_GIBZE	>gnl|sp|TRI5_GIBZE (Q00909) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x	
TRI5_FUSAC	>gnl|sp|TRI5_FUSAC (Q7LJR6) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x	
TRI5_FUSCU	>gnl|sp|TRI5_FUSCU (Q8NIG9) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x	
TRI5_FUSBO	>gnl|sp|TRI5_FUSBO (Q8NIH3) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x	
TRI5_FUSAS	>gnl|sp|TRI5_FUSAS (Q8NIH6) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x	
TRI5_FUSAU	>gnl|sp|TRI5_FUSAU (Q8NIH0) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x	
TRI5_FUSMI	>gnl|sp|TRI5_FUSMI (Q8NJA1) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x	
TRI5_FUSCE	>gnl|sp|TRI5_FUSCE (Q8NIC1) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x	
TRI5_FUSPS	>gnl|sp|TRI5_FUSPS (Q8NID7) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x	
TRI5_FUSPO	>gnl|sp|TRI5_FUSPO (Q00835) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x	
TRI5_FUSME	>gnl|sp|TRI5_FUSME (Q8NIC8) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x	
TRI5_FUSCO	>gnl|sp|TRI5_FUSCO (Q7LJF8) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x	
TRI5_FUSSP	>gnl|sp|TRI5_FUSSP (P13513) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x	
TRI5_STACH	>gnl|sp|TRI5_STACH (O59947) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
TRI5_MYRRO	>gnl|sp|TRI5_MYRRO (O13489) Trichodiene synthase (EC 4.2.3.6) (Sesquiterpene cyclase) (TS)			x	
ARIS_PENRO	>gnl|sp|ARIS_PENRO (Q03471) Aristolochene synthase (EC 4.2.3.9) (Sesquiterpene cyclase) (AS)			x	
MCEE_HUMAN	>gnl|sp|MCEE_HUMAN (Q96PE7) Methylmalonyl-CoA epimerase, mitochondrial precursor (EC 5.1.99.1) (DL-methylmalonyl-CoA racemase)			x	
MCEE_MOUSE	>gnl|sp|MCEE_MOUSE (Q9D1I5) Methylmalonyl-CoA epimerase, mitochondrial precursor (EC 5.1.99.1) (DL-methylmalonyl-CoA racemase)			x	
HPPD_PSEUJ	>gnl|sp|HPPD_PSEUJ (P80064) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase)			x	
LLY_LEGPH	>gnl|sp|LLY_LEGPH (Q5ZT84) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (Legiolysin)			x	
LLY_LEGPN	>gnl|sp|LLY_LEGPN (P69053) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (Legiolysin)			x	
HPPD_NEUCR	>gnl|sp|HPPD_NEUCR (Q872T7) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase)			x	
HPPD_MAGGR	>gnl|sp|HPPD_MAGGR (Q96X22) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase)			x	
HPPD_HUMAN	>gnl|sp|HPPD_HUMAN (P32754) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acide oxidase)			x	
HPPD_MOUSE	>gnl|sp|HPPD_MOUSE (P49429) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (4-hydroxyphenylpyruvic acide oxidase) (HPPDase) (F protein) (F Alloantigen)			x	
HPPD_BOVIN	>gnl|sp|HPPD_BOVIN (Q5EA20) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acide oxidase)			x	
HPPD_RAT	>gnl|sp|HPPD_RAT (P32755) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (4-hydroxyphenylpyruvic acide oxidase) (HPPDase) (F protein) (F Alloantigen)			x	
HPPD_ARATH	>gnl|sp|HPPD_ARATH (P93836) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acide oxidase)			x	
HPPD_DAUCA	>gnl|sp|HPPD_DAUCA (O23920) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acide oxidase)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
HPPD_STRCO	>gnl|sp|HPPD_STRCO (Q9S2F4) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase)			x	
HPPD_PIG	>gnl|sp|HPPD_PIG (Q02110) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acide oxidase)			x	
HPPD_STRAW	>gnl|sp|HPPD_STRAW (Q53586) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase)			x	
HPPD_SOLSC	>gnl|sp|HPPD_SOLSC (Q9ARF9) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acide oxidase)			x	
HPPD_MYCGR	>gnl|sp|HPPD_MYCGR (O42764) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase)			x	
HPPD1_ASPFU	>gnl|sp|HPPD1_ASPFU (Q4WHU1) Probable 4-hydroxyphenylpyruvate dioxygenase 1 (EC 1.13.11.27) (4HPPD 1) (HPD 1) (HPPDase 1)			x	
HPPD_BRARE	>gnl|sp|HPPD_BRARE (Q6TGZ5) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acide oxidase)			x	
HPPD_XENTR	>gnl|sp|HPPD_XENTR (Q5BKL0) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acide oxidase)			x	
HPPD_COCIM	>gnl|sp|HPPD_COCIM (Q00415) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (T-cell reactive protein)			x	
HPPD_YARLI	>gnl|sp|HPPD_YARLI (Q6CDR5) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase)			x	
HPPD_TETTH	>gnl|sp|HPPD_TETTH (Q27203) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acide oxidase) (F-antigen homolog) (TF-AG)			x	
HPPD2_ASPFU	>gnl|sp|HPPD2_ASPFU (Q4WPV8) Probable 4-hydroxyphenylpyruvate dioxygenase 2 (EC 1.13.11.27) (4HPPD 2) (HPD 2) (HPPDase 2)			x	
HPPD_CAEBR	>gnl|sp|HPPD_CAEBR (Q60Y65) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acide oxidase)			x	
HPPD_CAEEL	>gnl|sp|HPPD_CAEEL (Q22633) 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acide oxidase)			x	
FOSA_SERMA	>gnl|sp|FOSA_SERMA (Q56415) Glutathione transferase fosA (EC 2.5.1.18) (Fosfomycin resistance protein)			x	
FOSA_PSEAE	>gnl|sp|FOSA_PSEAE (Q9I4K6) Glutathione transferase fosA (EC 2.5.1.18) (Fosfomycin resistance protein)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
LGUL_YEAST	>gnl|sp|LGUL_YEAST (P50107) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
LGUL_SCHPO	>gnl|sp|LGUL_SCHPO (Q09751) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
LGUL_ORYSA	>gnl|sp|LGUL_ORYSA (Q948T6) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase) (Allergen Ory s ?) (Allergen Glb33) (PP33)			x	
LGUL_LYCES	>gnl|sp|LGUL_LYCES (Q42891) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
LGUL_BRAJU	>gnl|sp|LGUL_BRAJU (O04885) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
LGUL_CICAR	>gnl|sp|LGUL_CICAR (O49818) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
LGUL_ARATH	>gnl|sp|LGUL_ARATH (Q8H0V3) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
LGUL_RAT	>gnl|sp|LGUL_RAT (Q6P7Q4) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
LGUL_HUMAN	>gnl|sp|LGUL_HUMAN (Q04760) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
LGUL_MACFA	>gnl|sp|LGUL_MACFA (Q4R5F2) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
LGUL_MOUSE	>gnl|sp|LGUL_MOUSE (Q9CPU0) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
LGUL_PSEPU	>gnl|sp|LGUL_PSEPU (P16635) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
LGUL_BRAOG	>gnl|sp|LGUL_BRAOG (Q39366) Putative lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
LGUL_SYNY3	>gnl|sp|LGUL_SYNY3 (Q55595) Probable lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
LGUL_VIBCH	>gnl|sp|LGUL_VIBCH (Q9KT93) Probable lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
LGUL_NEIMA	>gnl|sp|LGUL_NEIMA (P0A0T2) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
LGUL_NEIMB	>gnl|sp|LGUL_NEIMB (P0A0T3) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
LGUL_SHIFL	>gnl|sp|LGUL_SHIFL (P0AC83) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
LGUL_ECO57	>gnl|sp|LGUL_ECO57 (P0AC82) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
LGUL_ECOLI	>gnl|sp|LGUL_ECOLI (P0AC81) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
LGUL_VIBPA	>gnl|sp|LGUL_VIBPA (P46235) Probable lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	

Table L-4. UniProtKB/Swiss-Prot Data (Chapter 3)

Accession	Annotation	Equiv.	Incorrect	Correct	General
LGUL_SALTY	>gnl|sp|LGUL_SALTY (P0A1Q2) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
LGUL_SALTI	>gnl|sp|LGUL_SALTI (P0A1Q3) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
LGUL_HAEIN	>gnl|sp|LGUL_HAEIN (P44638) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)			x	
MENB_PASMU	>gnl|sp|MENB_PASMU (Q9CLV5) Naphthoate synthase (EC 4.1.3.36) (Dihydroxynaphthoic acid synthetase) (DHNA synthetase)		x		
MENB_HAEIN	>gnl|sp|MENB_HAEIN (P44960) Naphthoate synthase (EC 4.1.3.36) (Dihydroxynaphthoic acid synthetase) (DHNA synthetase)		x		
MENB_ECOLI	>gnl|sp|MENB_ECOLI (P0ABU0) Naphthoate synthase (EC 4.1.3.36) (Dihydroxynaphthoic acid synthetase) (DHNA synthetase)		x		
MENB_ECOL6	>gnl|sp|MENB_ECOL6 (P0ABU1) Naphthoate synthase (EC 4.1.3.36) (Dihydroxynaphthoic acid synthetase) (DHNA synthetase)		x		
MENB_BACSU	>gnl|sp|MENB_BACSU (P23966) Naphthoate synthase (EC 4.1.3.36) (Dihydroxynaphthoic acid synthetase) (DHNA synthetase)		x		
MENB_CYACA	>gnl|sp|MENB_CYACA (Q9TM10) Naphthoate synthase (EC 4.1.3.36) (Dihydroxynaphthoic acid synthetase) (DHNA synthetase)		x		
DEH2_MORSB	>gnl|sp|DEH2_MORSB (Q01399) Haloacetate dehalogenase H-2 (EC 3.8.1.3)		x		
CATB2_ACILW	>gnl|sp|CATB2_ACILW (O33949) Muconate cycloisomerase I 2 (EC 5.5.1.1) (Cis,cis-muconate lactonizing enzyme I 2) (MLE 2)	x			

Appendix M. MLE Operon Data

M.1. ‘Old’, ‘new’ and ‘unknown’ protein accession numbers (gi) from GenBank

GI	Function
108798346	NewMLE
116670480	NewMLE
118470554	NewMLE
119715080	NewMLE
126434011	NewMLE
133913537	NewMLE
145221949	NewMLE
25990736	NewMLE
42627730	NewMLE
54025491	NewMLE
66966584	NewMLE
71365319	NewMLE
89343204	NewMLE
92911417	NewMLE
70731221	MLEIorII
141917	MLEIorII
115713	MLEIorII
2935031	MLEIorII
5915882	MLEIorII
23094408	MLEIorII
151125	MLEIorII
11270756	MLEIorII
4579699	MLEIorII

6014740	MLEIorII
23308936	MLEIorII
25028859	MLEIorII
38198158	MLEIorII
111019363	MLEIorII
77362681	MLEIorII
30698534	MLEIorII
82548049	MLEIorII
46130813	MLEIorII
1747426	MLEIorII
51243151	MLEIorII
84502279	MLEIorII
14209510	MLEIorII
150773	MLEIorII
135651	MLEIorII
116506	MLEIorII
11270764	MLEIorII
3643989	MLEIorII
48788203	MLEIorII
15026865	MLEIorII
19386505	MLEIorII
135517	MLEIorII
111616534	MLEIorII
110592574	MLEIorII
84713193	MLEIorII
118730150	MLEIorII
118051814	MLEIorII
61611869	MLEIorII
118592584	MLEIorII
85707323	MLEIorII
86139513	MLEIorII
118750314	MLEIorII
71362561	MLEIorII
118761900	MLEIorII
94414964	MLEIorII
107101955	MLEIorII
14132758	MLEIorII

15597705	MLEIorII
84320738	MLEIorII
111145985	MLEIorII
56710236	MLEIorII
115315694	MLEIorII
12862418	MLEIorII
104782198	MLEIorII
119855551	MLEIorII
13660733	MLEIorII
13399453	MLEIorII
6730036	MLEIorII
6730024	MLEIorII
607908	MLEIorII
1633161	MLEIorII
82735481	MLEIorII
26990423	MLEIorII
48729290	MLEIorII
48733237	MLEIorII
89360248	MLEIorII
12539415	MLEIorII
23491545	MLEIorII
118038923	MLEIorII
11967279	MLEIorII
38638066	MLEIorII
38638055	MLEIorII
48771790	MLEIorII
113528986	MLEIorII
53760758	MLEIorII
73538229	MLEIorII
46131202	MLEIorII
2996615	MLEIorII
50084621	MLEIorII
83749259	MLEIorII
121530931	MLEIorII
83716982	MLEIorII
67740097	MLEIorII
53716515	MLEIorII

67763500	MLEIorII
53722912	MLEIorII
67754538	MLEIorII
84358682	MLEIorII
124899758	MLEIorII
118716069	MLEIorII
44241970	MLEIorII
46316855	MLEIorII
84353826	MLEIorII
67665468	MLEIorII
118713472	MLEIorII
46323402	MLEIorII
74015085	MLEIorII
118695799	MLEIorII
118037998	MLEIorII
91783706	MLEIorII
6014742	MLEIorII
118029372	MLEIorII
23491535	MLEIorII
89358823	MLEIorII
69936817	MLEIorII
118715667	MLEIorII
74017902	MLEIorII
118696142	MLEIorII
46313897	MLEIorII
44419204	MLEIorII
113473705	MLEIorII
48848011	MLEIorII
13476122	UNK
83951128	UNK
114764387	UNK
22959025	UNK
69936829	UNK
83774494	UNK
83951697	UNK
83951694	UNK
56678215	UNK

86136102	UNK
83951693	UNK
86136103	UNK
56678216	UNK
114770232	UNK
83951695	UNK
118591613	UNK
87306973	UNK
44366874	UNK
44283290	UNK
56478651	UNK
73539613	UNK
53766361	UNK
68191996	UNK
54029967	UNK
27383232	UNK
114765516	UNK
56680224	UNK
68183493	UNK
23100298	UNK
56964777	UNK
27377950	UNK
116254727	UNK
121607611	UNK
36958607	UNK
15963874	UNK
113871165	UNK
88856058	UNK
32471785	UNK
67932993	UNK
87309493	UNK
13476121	UNK
46199775	UNK
55981793	UNK
15806871	UNK
66798121	UNK
72161364	UNK

M.2. Operons returned for ‘new’ MLEs

GI	geneName	OperonID	species	OperonType
116670479	Arth_1930	13225510	290399 Arthrobacter sp. FB24	newMLE
116670480	Arth_1931	13225510	290399 Arthrobacter sp. FB24	newMLE
116670481	Arth_1932	13225510	290399 Arthrobacter sp. FB24	newMLE
116670482	Arth_1933	13225510	290399 Arthrobacter sp. FB24	newMLE
119715079	Noca_0834	12798663	196162 Nocardioides sp. JS614	newMLE
119715080	Noca_0835	12798663	196162 Nocardioides sp. JS614	newMLE
119715081	Noca_0836	12798663	196162 Nocardioides sp. JS614	newMLE
119715082	Noca_0837	12798663	196162 Nocardioides sp. JS614	newMLE
126434010	Mjls_1408	12724298	164757 Mycobacterium sp. JLS	newMLE
126434011	Mjls_1409	12724298	164757 Mycobacterium sp. JLS	newMLE
126434012	Mjls_1410	12724298	164757 Mycobacterium sp. JLS	newMLE
126434013	Mjls_1411	12724298	164757 Mycobacterium sp. JLS	newMLE
108798345	Mmcs_1374	12720537	164756 Mycobacterium sp. MCS	newMLE
108798346	Mmcs_1375	12720537	164756 Mycobacterium sp. MCS	newMLE
108798347	Mmcs_1376	12720537	164756 Mycobacterium sp. MCS	newMLE
108798348	Mmcs_1377	12720537	164756 Mycobacterium sp. MCS	newMLE
54025490	nfa35200	12545915	37329 Nocardia farcinica	newMLE
54025491	nfa35210	12545915	37329 Nocardia farcinica	newMLE
54025492	nfa35220	12545915	37329 Nocardia farcinica	newMLE
54025493	nfa35230	12545915	37329 Nocardia farcinica	newMLE
54025494	nfa35240	12545915	37329 Nocardia farcinica	newMLE
118468666	MSMEG_1909	13001374	246196 Mycobacterium smegmatis str. MC2 155	newMLE
118470554	MSMEG_1910	13001374	246196 Mycobacterium smegmatis str. MC2 155	newMLE

118473469	MSMEG_1911	13001374	246196 Mycobacterium smegmatis str. MC2 155	newMLE
118471569	MSMEG_1912	13001374	246196 Mycobacterium smegmatis str. MC2 155	newMLE

M.3. Operons returned for ‘old’ MLEs

GI	geneName	OperonID	species	OperonType
121530925	RpicDRAFT_2992	13956227	402626 Ralstonia pickettii 12J	oldMLEs
121530926	RpicDRAFT_2993	13956227	402626 Ralstonia pickettii 12J	oldMLEs
121530927	RpicDRAFT_2994	13956227	402626 Ralstonia pickettii 12J	oldMLEs
121530928	RpicDRAFT_2995	13956227	402626 Ralstonia pickettii 12J	oldMLEs
121530929	RpicDRAFT_2996	13956227	402626 Ralstonia pickettii 12J	oldMLEs
121530930	RpicDRAFT_2997	13956227	402626 Ralstonia pickettii 12J	oldMLEs
121530931	RpicDRAFT_2998	13956227	402626 Ralstonia pickettii 12J	oldMLEs
86139509	MED193_00135	13336591	314262 Roseobacter sp. MED193	oldMLEs
86139510	MED193_00140	13336591	314262 Roseobacter sp. MED193	oldMLEs
86139511	MED193_00145	13336591	314262 Roseobacter sp. MED193	oldMLEs
86139512	MED193_00150	13336591	314262 Roseobacter sp. MED193	oldMLEs
86139513	MED193_00155	13336591	314262 Roseobacter sp. MED193	oldMLEs
26990421	PP3713	12708624	160488 Pseudomonas putida KT2440	oldMLEs
26990422	PP3714	12708624	160488 Pseudomonas putida KT2440	oldMLEs
26990423	PP3715	12708624	160488 Pseudomonas putida KT2440	oldMLEs
70731219	PFL_3860	12900123	220664 Pseudomonas fluorescens Pf-5	oldMLEs
70731220	PFL_3861	12900123	220664 Pseudomonas fluorescens Pf-5	oldMLEs
70731221	PFL_3862	12900123	220664 Pseudomonas fluorescens Pf-5	oldMLEs
118038922	BphytDRAFT_2056	13915810	398527 Burkholderia phytofirmans PsJN	oldMLEs
118038923	BphytDRAFT_2057	13915810	398527 Burkholderia phytofirmans PsJN	oldMLEs
118038924	BphytDRAFT_2058	13915810	398527 Burkholderia phytofirmans PsJN	oldMLEs
111019362	RHA1_ro02371	12657315	101510 Rhodococcus sp. RHA1	oldMLEs

161353732	RHA1_ro02372	12657315	101510	Rhodococcus sp. RHA1	oldMLEs
111019364	RHA1_ro02373	12657315	101510	Rhodococcus sp. RHA1	oldMLEs

85707323	ROS217_16450	13339812	314264	Roseovarius sp. 217	oldMLEs
85707324	ROS217_16455	13339812	314264	Roseovarius sp. 217	oldMLEs
85707325	ROS217_16460	13339812	314264	Roseovarius sp. 217	oldMLEs
85707326	ROS217_16465	13339812	314264	Roseovarius sp. 217	oldMLEs
85707327	ROS217_16470	13339812	314264	Roseovarius sp. 217	oldMLEs

118029370	BphyDRAFT_5729	13826597	391038	Burkholderia phymatum STM815	oldMLEs
118029371	BphyDRAFT_5730	13826597	391038	Burkholderia phymatum STM815	oldMLEs
118029372	BphyDRAFT_5731	13826597	391038	Burkholderia phymatum STM815	oldMLEs

118051814	CtesDRAFT_4002	13944614	399795	Comamonas testosteroni KF-1	oldMLEs

83718355	BTH_II0483	13123240	271848	Burkholderia thailandensis E264	oldMLEs
83717464	BTH_II0484	13123240	271848	Burkholderia thailandensis E264	oldMLEs
83716982	BTH_II0485	13123240	271848	Burkholderia thailandensis E264	oldMLEs

25028858	CE2302	12802734	196164	Corynebacterium efficiens YS-314	oldMLEs
161485963	CE2303	12802734	196164	Corynebacterium efficiens YS-314	oldMLEs
25028860	CE2304	12802734	196164	Corynebacterium efficiens YS-314	oldMLEs

119855551	PputW619DRAFT_4526	13812529	390235	Pseudomonas putida W619	oldMLEs
119855552	PputW619DRAFT_4527	13812529	390235	Pseudomonas putida W619	oldMLEs
119855553	PputW619DRAFT_4528	13812529	390235	Pseudomonas putida W619	oldMLEs

53722912	BPSS1891	13134770	272560	Burkholderia pseudomallei K96243	oldMLEs
53722913	BPSS1892	13134770	272560	Burkholderia pseudomallei K96243	oldMLEs
53722914	BPSS1893	13134770	272560	Burkholderia pseudomallei K96243	oldMLEs

118696140	BamMC406DRAFT_0568	13919296	398577	Burkholderia ambifaria MC40-6	oldMLEs
118696141	BamMC406DRAFT_0569	13919296	398577	Burkholderia ambifaria MC40-6	oldMLEs
118696142	BamMC406DRAFT_0570	13919296	398577	Burkholderia ambifaria MC40-6	oldMLEs

38638055	PHG394	13754051	381666	Ralstonia eutropha H16	oldMLEs

118592584	SIAM614_30761	13780933	384765	Stappia aggregata IAM 12614	oldMLEs
38638066	PHG405	13754057	381666	Ralstonia eutropha H16	oldMLEs
161611272	Reut_B4400	13054933	264198	Ralstonia eutropha JMP134	oldMLEs
104782196	PSEEN3136	13776214	384676	Pseudomonas entomophila L48	oldMLEs
104782197	PSEEN3137	13776214	384676	Pseudomonas entomophila L48	oldMLEs
104782198	PSEEN3138	13776214	384676	Pseudomonas entomophila L48	oldMLEs
118713472	Bcenmc03DRAFT_1049	14020829	406425	Burkholderia cenocepacia MC0-3	oldMLEs
84502279	OB2597_19786	13014800	252305	Oceanicola batsensis HTCC2597	oldMLEs
19553599	NCgl2317	12809828	196627	Corynebacterium glutamicum ATCC 13032	oldMLEs
23308936	NCgl2318	12809828	196627	Corynebacterium glutamicum ATCC 13032	oldMLEs
19553601	NCgl2319	12809828	196627	Corynebacterium glutamicum ATCC 13032	oldMLEs
15597703	PA2507	12870119	208964	Pseudomonas aeruginosa PAO1	oldMLEs
15597704	PA2508	12870119	208964	Pseudomonas aeruginosa PAO1	oldMLEs
15597705	PA2509	12870119	208964	Pseudomonas aeruginosa PAO1	oldMLEs
118695799	BamMC406DRAFT_5445	13919079	398577	Burkholderia ambifaria MC40-6	oldMLEs
118695800	BamMC406DRAFT_5446	13919079	398577	Burkholderia ambifaria MC40-6	oldMLEs
118695801	BamMC406DRAFT_5447	13919079	398577	Burkholderia ambifaria MC40-6	oldMLEs
118037998	BphytDRAFT_1497	13915176	398527	Burkholderia phytofirmans PsJN	oldMLEs
118037999	BphytDRAFT_1498	13915176	398527	Burkholderia phytofirmans PsJN	oldMLEs
118038000	BphytDRAFT_1499	13915176	398527	Burkholderia phytofirmans PsJN	oldMLEs
91783704	Bxe_A2110	13078271	266265	Burkholderia xenovorans LB400	oldMLEs
91783705	Bxe_A2109	13078271	266265	Burkholderia xenovorans LB400	oldMLEs
91783706	Bxe_A2108	13078271	266265	Burkholderia xenovorans LB400	oldMLEs

107101953	PaerPA_01003000	13792381	388272	Pseudomonas aeruginosa PACS2	oldMLEs
107101954	PaerPA_01003001	13792381	388272	Pseudomonas aeruginosa PACS2	oldMLEs
107101955	PaerPA_01003002	13792381	388272	Pseudomonas aeruginosa PACS2	oldMLEs
50084621	ACIAD1446	12579454	62977	Acinetobacter sp. ADP1	oldMLEs
50084622	ACIAD1447	12579454	62977	Acinetobacter sp. ADP1	oldMLEs
53716517	BMAA0198	12981119	243160	Burkholderia mallei ATCC 23344	oldMLEs
53716516	BMAA0199	12981119	243160	Burkholderia mallei ATCC 23344	oldMLEs
53716515	BMAA0200	12981119	243160	Burkholderia mallei ATCC 23344	oldMLEs

M.4. Operons returned for ‘unknown’ MLEs

GI	geneName	OperonID		species	OperonType
23100298	OB2843	12756868	182710	Oceanobacillus iheyensis	unkfuncMLE
23100299	OB2844	12756868	182710	Oceanobacillus iheyensis	unkfuncMLE
23100300	OB2845	12756868	182710	Oceanobacillus iheyensis	unkfuncMLE
87306973	DSM3645_00930	13314567	314230	Blastopirellula marina DSM 3645	unkfuncMLE
114764387	R2601_01638	13341838	314265	Roseovarius sp. HTCC2601	unkfuncMLE
72161364	Tfu_0960	13113875	269800	Thermobifida fusca YX	unkfuncMLE
56964774	ABC3010	12587029	66692	Bacillus clausii KSM-K16	unkfuncMLE
56964775	ABC3011	12587029	66692	Bacillus clausii KSM-K16	unkfuncMLE
56964776	ABC3012	12587029	66692	Bacillus clausii KSM-K16	unkfuncMLE
56964777	ABC3013	12587029	66692	Bacillus clausii KSM-K16	unkfuncMLE
56964778	ABC3014	12587029	66692	Bacillus clausii KSM-K16	unkfuncMLE
56964779	ABC3015	12587029	66692	Bacillus clausii KSM-K16	unkfuncMLE
56964780	ABC3016	12587029	66692	Bacillus clausii KSM-K16	unkfuncMLE
73539613	Reut_B5793	13055768	264198	Ralstonia eutropha JMP134	unkfuncMLE
114765516	R2601_12825	13342489	314265	Roseovarius sp. HTCC2601	unkfuncMLE
27377947	blr2836	12482458	375	Bradyrhizobium japonicum	unkfuncMLE
27377948	blr2837	12482458	375	Bradyrhizobium japonicum	unkfuncMLE
27377949	blr2838	12482458	375	Bradyrhizobium japonicum	unkfuncMLE
27377950	blr2839	12482458	375	Bradyrhizobium japonicum	unkfuncMLE
27377951	blr2840	12482458	375	Bradyrhizobium japonicum	unkfuncMLE

27377952	blr2841	12482458	375	Bradyrhizobium japonicum	unkfuncMLE
27377953	blr2842	12482458	375	Bradyrhizobium japonicum	unkfuncMLE
121607609	Veis_0615	13873692	391735	Verminephrobacter eiseniae EF01-2	unkfuncMLE
121607610	Veis_0616	13873692	391735	Verminephrobacter eiseniae EF01-2	unkfuncMLE
121607611	Veis_0617	13873692	391735	Verminephrobacter eiseniae EF01-2	unkfuncMLE
121607612	Veis_0618	13873692	391735	Verminephrobacter eiseniae EF01-2	unkfuncMLE
121607613	Veis_0619	13873692	391735	Verminephrobacter eiseniae EF01-2	unkfuncMLE
121607614	Veis_0620	13873692	391735	Verminephrobacter eiseniae EF01-2	unkfuncMLE
121607615	Veis_0621	13873692	391735	Verminephrobacter eiseniae EF01-2	unkfuncMLE
55981793	TTHA1824	13267741	300852	Thermus thermophilus HB8	unkfuncMLE
55981794	TTHA1825	13267741	300852	Thermus thermophilus HB8	unkfuncMLE
32471785	RB2166	12972319	243090	Pirellula sp. 1	unkfuncMLE
13476121	mll7352	13088816	266835	Mesorhizobium loti MAFF303099	unkfuncMLE
13476122	mll7353	13088816	266835	Mesorhizobium loti MAFF303099	unkfuncMLE
15963874	SMc04131	12486969	382	Sinorhizobium meliloti	unkfuncMLE
46199775	TTC1473	13048257	262724	Thermus thermophilus HB27	unkfuncMLE
46199776	TTC1474	13048257	262724	Thermus thermophilus HB27	unkfuncMLE
15806870	DR1870	12510659	1299	Deinococcus radiodurans	unkfuncMLE
15806871	DR1871	12510659	1299	Deinococcus radiodurans	unkfuncMLE
118591613	SIAM614_28497	13780320	384765	Stappia aggregata IAM 12614	unkfuncMLE
83951693	ISM_14060	12630760	89187	Roseovarius nubinhibens ISM	unkfuncMLE
83951694	ISM_14065	12630760	89187	Roseovarius nubinhibens ISM	unkfuncMLE
83951695	ISM_14070	12630760	89187	Roseovarius nubinhibens ISM	unkfuncMLE
83951696	ISM_14075	12630761	89187	Roseovarius nubinhibens ISM	unkfuncMLE
83951697	ISM_14080	12630761	89187	Roseovarius nubinhibens ISM	unkfuncMLE
83951698	ISM_14085	12630761	89187	Roseovarius nubinhibens ISM	unkfuncMLE

83951699	ISM_14090	12630761	89187	Roseovarius nubinhibens ISM	unkfuncMLE
83951128	ISM_08500	12630381	89187	Roseovarius nubinhibens ISM	unkfuncMLE
56478650	ebA5649	12600174	76114	Azoarcus sp. EbN1	unkfuncMLE
56478651	ebA5652	12600174	76114	Azoarcus sp. EbN1	unkfuncMLE
27383228	blr8117	12485871	375	Bradyrhizobium japonicum	unkfuncMLE
27383229	blr8118	12485871	375	Bradyrhizobium japonicum	unkfuncMLE
27383230	blr8119	12485871	375	Bradyrhizobium japonicum	unkfuncMLE
27383231	blr8120	12485871	375	Bradyrhizobium japonicum	unkfuncMLE
27383232	blr8121	12485871	375	Bradyrhizobium japonicum	unkfuncMLE
27383233	blr8122	12485871	375	Bradyrhizobium japonicum	unkfuncMLE
27383234	blr8123	12485871	375	Bradyrhizobium japonicum	unkfuncMLE
27383235	blr8124	12485871	375	Bradyrhizobium japonicum	unkfuncMLE
114770232	OM2255_1136513709296		367336	Rhodobacterales bacterium HTCC2255	unkfuncMLE
86136100	MED193_18294	13334387	314262	Roseobacter sp. MED193	unkfuncMLE
86136101	MED193_18299	13334387	314262	Roseobacter sp. MED193	unkfuncMLE
86136102	MED193_18304	13334387	314262	Roseobacter sp. MED193	unkfuncMLE
86136103	MED193_18309	13334387	314262	Roseobacter sp. MED193	unkfuncMLE
116254724	pRL100282	12890601	216596	Rhizobium leguminosarum bv. viciae 3841	unkfuncMLE
116254725	pRL100283	12890601	216596	Rhizobium leguminosarum bv. viciae 3841	unkfuncMLE
116254726	pRL100284	12890601	216596	Rhizobium leguminosarum bv. viciae 3841	unkfuncMLE
116254727	pRL100285	12890601	216596	Rhizobium leguminosarum bv. viciae 3841	unkfuncMLE
87309492	DSM3645_24360	13316731	314230	Blastopirellula marina DSM 3645	unkfuncMLE
87309493	DSM3645_24365	13316731	314230	Blastopirellula marina DSM 3645	unkfuncMLE

Publishing Agreement

It is the policy of the University to encourage the distribution of all theses and dissertations. Copies of all UCSF theses and dissertations will be routed to the library via the Graduate Division. The library will make all theses and dissertations accessible to the public and will preserve these to the best of their abilities, in perpetuity.

Please sign the following statement:

I hereby grant permission to the Graduate Division of the University of California, San Francisco to release copies of my thesis or dissertation to the Campus Library to provide access and preservation, in whole or in part, in perpetuity.

Alexandra M Schnoes

December 10, 2008

Author Signature

Date