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Drosophila simulans Cu-Zn superoxide dismutase gene sequence

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The sequence of 1793 bp given below, isolated from a lambda EMBL4 genomic library of Drosophila simulans, codes for Cu-Zn superoxide dismutase (SOD). This sequence is very similar to that of D. melanogaster (1,2). The putative regulatory sequences found in D. melanogaster sequence are identifiable in homologous positions in D. simulans. These include the TATA box starting at position -26 and a polyadenylation signal at 1400. An open reading frame and a termination codon start at positions 69 and 1258, respectively. The overall identity of the sequence herein to the D. melanogaster SOD sequence from a Canton S strain (2) is 93.8%, but 4 and 10 gaps, constituting 95 nucleotides in all (the largest one of 28 nucleotides), are introduced in the D. melanogaster and D. simulans sequences, respectively. The transcribed region (capitalized; inferred by analogy with the D. melanogaster one) displays 95.3% identity. The coding region consists of two exons; the 729bp-long intron, spanning from position 135 to 864, separates the codons for amino acids 22 and 23, similarly as for D. melanogaster. The coding region is 97.6% identical in the two species (i.e., 11 substitutions out of 459 sites). The inferred sequence of 153 amino acids is the same as in D. melanogaster.

gattccccgatttcgttttttttttttgcacccattggaattttccgacct
-270 gtcattggaaatcagtggaacgcttccacgtagccaccctgatttcgtttccacgctccacccggtgacctgattttgaccgtgacccaaa
-180 tttccgcttttccacatttgcattttctgatttttcgcttccacccgacccccccttcgcttgcattttccacgctttctctcc
-90 cgtaccgggaaatcagtggaacgcttccacgtagccaccctgacctccagctccacgctttccctgaaattttccacgcttctctc
1 ACACCTTAAAGATACCTGGAAAGTCTCAACTTTTTCTGCTTTTATTAATTTATTAATTCATTCGAAATGTTTAAAGCTGTCTGG
H V K A V C
91 TAATTAACGGCRATCCCAAGGGCAGCGTTTTCTTCCAAACAAGTGAAGTAAATCCAAATCATTGAACTTCTCTCTCCGCAAAATATAC
V I H B D A K G T V F F E Q E
181 GAAAAACAAGTCTAAAGGTCAAAATACCCGCAAGCCACCCGGCCCTCTTCCACTTCAAAATGCTGTTTAAATGCTTCAAGCAATT
271 TCAATTAAGTCCGATTTGAATTTACGCTTACGACCAAGGTGCACCTTTATATTTATATAAGCCGCAAAAATGGCCATATATGTA
361 TGTCCCTCAAGTCCCTACCAAGGAGGTCAAGCAATTAAGTACTGCTCGTAAAAGGCGTTAAGTATAAAGCTCTTTCATCACTTTGTA
451 TAAAGTACGTTAAATCAACAAATGTTTGTTTAAATAATCATTAGCAATATTGCAATAATAGAAATGATGTTGTTTCATCAATTAAT
541 TGTACATCAAGTAAAGCAGCCATGTCAATTTGCAATTAAGCAATATTAACTTTGATTACAGGTTATGTTTAAAGTGTCCGAGAAATTA
631 TGTTTTAAATCTATAAAGATAACCAAAATGTTTATTAAAGCCGCTAAAAAATATTCCATTTGACGTGTCTTATTAAACAATGTTAACTT
721 TATAATAACCTATTAAACATAAAGTGTGCCCACTGATTTATCATAATCATTCACTACTATACACAACTTTGTTCTTACGATTTGAG
811 TATAATCTGAAGCCTTGGCTTAATTTGAACCAATCCCTTCATCCGCCCCAGCAGCCGCTACCCCGTGAAGGTCTCCGGTGGAGTG
S S G T P V K V S G E V
901 TCCGCTTGGCCAAAGGCTCTCCAGGATTCACGTGCACGAGTTTGCAGACAACACCAATGCTGCATGTCGTCCGACCCCACTTCAAT
C G L A K G L H G F H V H E F G D H T H G C H S S G P H F H
991 CCGTATGGCAAGGACCGGCTCCCGTCCAGCAAGCCCTCACTGGCCGATTTGGCAACATTCAGGTCACAGCCGACTGCCGACCA
P Y G K E D G A P V D E D H L G D L G H I E A T G D C P T
1001 AAGTCAACATCACCGACTCCAAGATCAGGCTCTTCCGCGCCAGCAGCATCATCCGACCCGCTTGTCTCCGACGCGGATGCCGATGAT
K V D I T D S K I T L F G A D S I I G R T V V W H A D A D
1171 CTCCGACGCTGACACAGCTGAGCAAGTCAACGCTCAACGCTGGTCCGCGCATCCGCTGCGGCTTATTGGCATTCGCAAGGCTTAA
L G G G S G H E L S T G B A G A R I G C G V I G I A K V *
1261 CCRATAATCTATTCCCATGTCGCGCACTGTGCTEATCTACTCTATTATTACCACTACCCCACTGGAGATATGCAAAACGATATACTTCTACACA
1351 TAATTTATACCTGTGCTGTTGATGATGCAACCACTTTGAGGTTCAATGATGTTGTTTGAATTCGCCCAACCAACcaatctata
1441 tccatctatctcttctgttcgattgattc

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REFERENCES:

1. Seto, N.O.L., Hayashi, S. and Toner, G.M. (1987) Nucl. Acids Res. 15, 10601.
2. Kwiatowski, J., Patel, M. and Ayala, F.J. (1989) Nucl. Acids Res. 17, 1264.

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