



A novel protein interacting with the insulin receptor substrate 1 in mice muscle and skeletal muscle fibroblasts

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ABSTRACT

In this study, we report a novel interaction between the insulin receptor substrate 1 (IRS-1) and a membrane protein, named IBS-1, in mouse muscle and skeletal muscle fibroblasts. IRS-1 is a key player in insulin signaling, whereas IBS-1 is a membrane protein involved in glucose homeostasis. We show that IRS-1 and IBS-1 colocalize at the plasma membrane and interact physically. This interaction is mediated by the IRS-1 C-terminal domain and the IBS-1 extracellular domain. The interaction is dependent on the phosphorylation of IRS-1 at Ser309 and Ser316. Moreover, IRS-1 and IBS-1 are both expressed in muscle tissue, and IRS-1 is highly expressed in skeletal muscle. Our results suggest that IRS-1 and IBS-1 may play a role in glucose homeostasis in muscle tissue.

1. Introduction

The hypothalamic–pituitary–adrenal axis (HPA) axis is a major regulator of stress responses. It involves the release of adrenocorticotrophic hormone (ACTH) from the pituitary gland, which stimulates the adrenal cortex to release cortisol. Cortisol has various physiological effects, including regulation of blood glucose levels, metabolism, and immune function. In addition, cortisol can affect the central nervous system, leading to changes in mood and behavior. The HPA axis is also involved in the regulation of other hormones, such as growth hormone and thyroid hormone. These hormones have important roles in growth, development, and metabolism. The HPA axis is controlled by various factors, including stressors, circadian rhythms, and feedback loops. The HPA axis is a complex system that requires coordination between multiple organs and tissues to maintain homeostasis.

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Dysregulation of P-glycoprotein (P-gp) is a key driver of resistance to various chemotherapeutics. P-gp is a membrane protein that actively transports drugs out of cells, reducing their intracellular concentration. It is encoded by the ABCB1 gene and is found in high concentrations in the apical membrane of intestinal epithelial cells, mammary gland, and blood-brain barrier.

In this study, we investigated the effect of a novel P-gp inhibitor, LHMH-1, on the absorption and distribution of doxorubicin (Dox) in mice. We found that LHMH-1 significantly increased the bioavailability of Dox in mice, resulting in higher concentrations in the liver and spleen. This suggests that LHMH-1 may be a promising candidate for the treatment of Dox-resistant cancers.

We also evaluated the pharmacokinetic properties of LHMH-1 in mice. The drug showed a half-life of approximately 12 hours and a bioavailability of about 20%. The pharmacokinetic parameters were estimated using non-compartmental analysis. The results indicate that LHMH-1 has a low clearance rate and a long half-life, making it a potential candidate for once-daily administration.

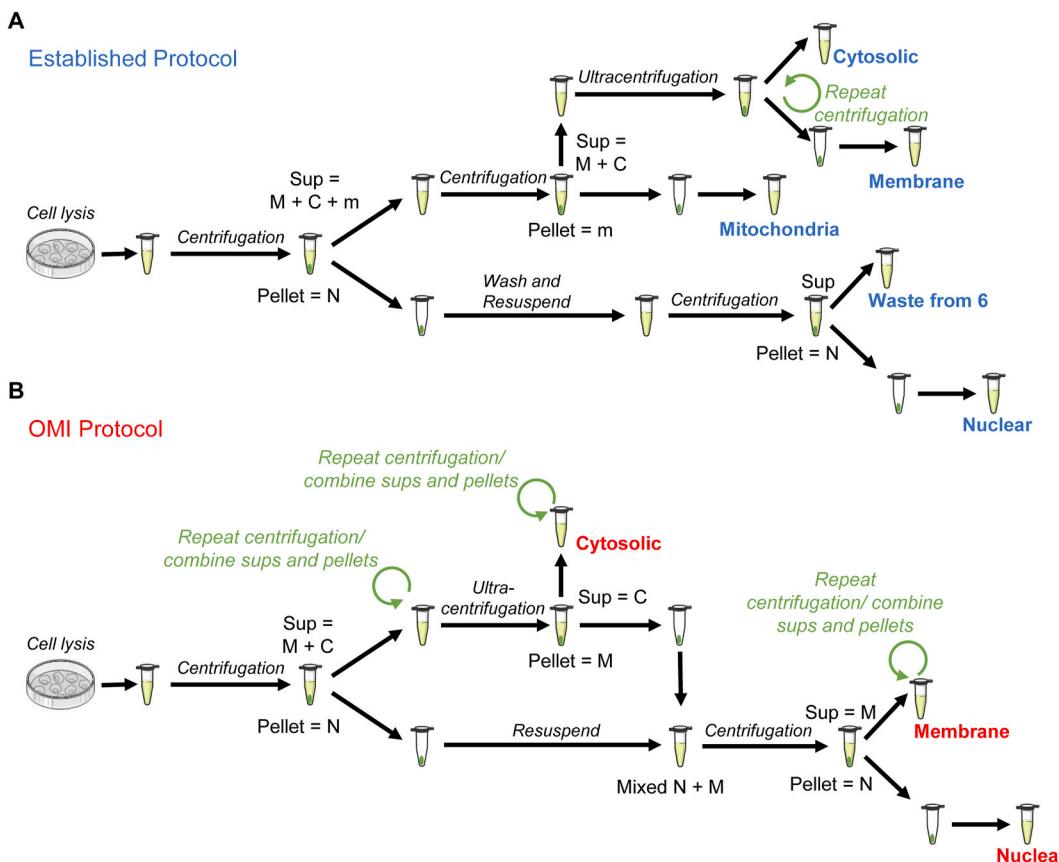
The pharmacokinetic parameters of LHMH-1 were found to be similar to those of other P-gp inhibitors, such as cyclosporine A and verapamil. These drugs have been shown to increase the bioavailability of Dox in cancer patients. Our results suggest that LHMH-1 may have similar therapeutic potential. Further studies are needed to confirm these findings and to determine the optimal dosing regimen for LHMH-1 in cancer patients.

Overall, our results demonstrate that LHMH-1 is a promising P-gp inhibitor with potential therapeutic value in cancer treatment. Further research is needed to fully understand its mechanism of action and to develop it as a new treatment option for cancer patients.

2. Materials and Methods

2.1. Structure

The chemical structure of LHMH-1 is shown in Figure 1. It consists of a core molecule (2-(4-chlorophenoxy)-N,N-dimethyl-N-(2-methoxyethyl)acetamide) substituted with a 4-hydroxyphenyl group at the 2-position. The hydroxyl group is further substituted with a 4-(2-hydroxyethyl)phenyl group. The entire molecule is linked to a 4-hydroxyphenyl ring via a methylene bridge.



F i g . S c h e m a f t h e s t a b l a i n s d u b c e l f l r a l c a r i p n e t b (A) o l l t h e s t a b l p i r s o h e s t a c o m p a r e l e s y s f e a d l I d y c e e d n t r i f t u g a t i o n p r o d a p e l d e r t a i t h e n g l f e r a r c a t h o p e r n c o a t n a t h a m e i m b g a c y e t , o s a o n l d i c t , o c h o p n r d a t i d h e s u c l p e a l r l s v a s h v e d t h f r a c t i b o a f i e c o n t r i a f g u a g o p e r n f a r t a m t t e n t r i f s t u g e a p t i s s o c n a (r W a e s d t r e n g) n t h e u c l p e a l r l e s t u s p e h s e p e r n a t a n t f r o t h n e i t e a t r i f o u g h j p t s w o n o d e r t w e n t r i f a g j a c t i r e g f s o n t c o g e l l t e n t i t o c h o f n r d a i f a d b h d y t e h e m b r a n e f r a c t h e e m a i s u p r e n i a s t h y t o o f o l a i c (B) l o r h G M p r o t o s a c o m p a r e l e s y s a e n d t h e e n t r i f p u g e e d t u l p e r n c o a t n a t h a n g m e m b r a n e d y t o p o l i t e m a p s e l w i e t h u c l p e a r o t t h e s p e r n i a s t u a n t h e r o c e v s i s a t d r a c e n t t r o l f t u g h a c y i t o n s o l a c t r i a b n p e l d e r t a i m b g a t h e s m b r a n e d l f e r a r c a t r i e s c o m b f i n l e d b y c e e d n t r i f t u g b a t t a h o n e c l a e n d r e m b r a n e a c t i o n s . M = m e m b r a n e , c y t o s o l b r i u c g l a m i t o c h o n d r i a .

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2. F.I ocytometry

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2. Signals and signs

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2. **P**er la relazione con Amministratore di EnergiA11n munoprecipitati incendi erano stati emessi dallo stesso giorno 10 aprile.

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was performed on membrane fractions obtained from the myocardium of rats with or without myocardial infarction. The membrane fraction was isolated by differential centrifugation and the membrane proteinome was characterized by SDS-PAGE and mass spectrometry. A total of 100 proteins were identified, including 34 unique proteins that were differentially expressed between the two groups. The most abundant protein in the membrane fraction was Na⁺/K⁺-ATPase, followed by p84 and GAPDH. The membrane proteinome was found to be significantly altered in the myocardium of rats with myocardial infarction, with a higher proportion of proteins being upregulated and a lower proportion being downregulated. The most significant changes were observed in the Na⁺/K⁺-ATPase, p84, and GAPDH levels. These results suggest that the membrane proteinome is significantly altered in the myocardium of rats with myocardial infarction, and that this alteration may be related to the pathophysiology of the disease.

Materials and methods

Animals and experimental design

Male Wistar rats (200–220 g) were used in this study. They were housed under standard conditions (temperature 22°C, humidity 55%) and fed a standard diet. All procedures were approved by the Animal Care and Use Committee of the University of Valencia. The animals were randomly assigned to two groups: control (n=10) and myocardial infarction (OMI) (n=10). Myocardial infarction was induced in the OMI group by ligation of the left coronary artery for 30 min. After 24 h, the animals were killed and their hearts were removed. The myocardium was homogenized in ice-cold buffer containing 20 mM Tris-HCl (pH 7.4), 150 mM NaCl, 1 mM EGTA, 1 mM PMSF, and 1% Triton X-100. The homogenate was centrifuged at 10,000 × g for 30 min at 4°C. The supernatant was collected and used for protein extraction.

3. Results

3.1. Identification of membrane proteins

Total membrane proteins were isolated from rat myocardium using a modified protocol (Fig. 1A). The protocol involved three steps: lysis of the tissue in a buffer containing Triton X-100, centrifugation at 10,000 × g for 30 min, and collection of the supernatant. The supernatant was then passed through a column packed with Q-Sepharose 6B (Pharmacia Biotech) to remove membrane proteins. The eluted proteins were then resolved by SDS-PAGE and stained with Coomassie Blue R-250. The membrane was scanned and the protein bands were analyzed using a Bio-Rad ImageQuant software. The protein bands were excised and digested with trypsin, and the resulting peptides were analyzed by LC-MS/MS. The identified proteins were then compared between the control and OMI groups. A total of 100 proteins were identified, including 34 unique proteins that were differentially expressed between the two groups. The most abundant protein in the membrane fraction was Na⁺/K⁺-ATPase, followed by p84 and GAPDH. The membrane proteinome was found to be significantly altered in the myocardium of rats with myocardial infarction, with a higher proportion of proteins being upregulated and a lower proportion being downregulated. The most significant changes were observed in the Na⁺/K⁺-ATPase, p84, and GAPDH levels. These results suggest that the membrane proteinome is significantly altered in the myocardium of rats with myocardial infarction, and that this alteration may be related to the pathophysiology of the disease.

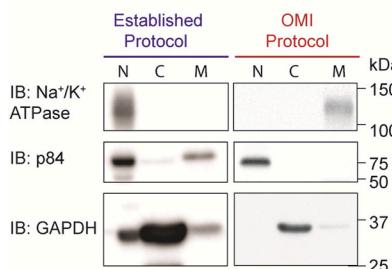
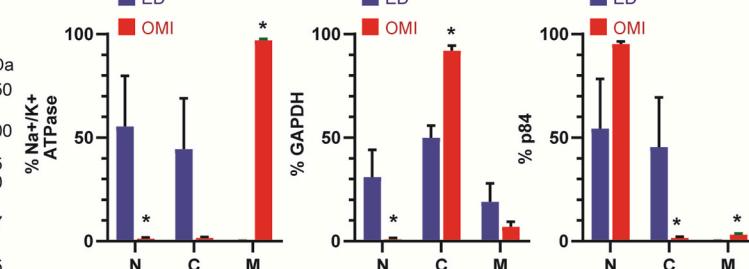
A**B**

Fig. 1. Optimization of the membrane proteinome analysis. Panel A shows Western blots for Na⁺/K⁺-ATPase, p84, and GAPDH under Established Protocol (N, C, M) and OMI Protocol (N, C, M). Panel B shows the relative levels of Na⁺/K⁺-ATPase, GAPDH, and p84 in the three groups. * indicates significant difference from control (C).

3.2. Insulin promotes GLUT1 translocation to the membrane in 2C3 cells. Insulin increases the expression of GLUT1 in 2C3 cells and induces its translocation to the membrane. Using a coimmunoprecipitation assay, we found that GLUT1 interacts with the insulin receptor in 2C3 cells. Immunoprecipitation of the insulin receptor with anti-insulin receptor antibody followed by immunoblotting with anti-GLUT1 antibody revealed that GLUT1 is present in the insulin receptor complex. Conversely, GLUT1 was present in the insulin receptor complex, as shown by coimmunoprecipitation of GLUT1 with the insulin receptor. These results indicate that GLUT1 is associated with the insulin receptor in 2C3 cells. Furthermore, GLUT1 is phosphorylated at Ser 654 by the insulin receptor kinase, which is required for its translocation to the membrane. Our findings suggest that GLUT1 is a target of the insulin signaling pathway in 2C3 cells.

Top article 6: *Influence of insulin on GLUT1 translocation in 2C3 cells*. Surprisingly, we found that insulin promotes GLUT1 translocation to the membrane in 2C3 cells. This finding suggests that GLUT1 is a target of the insulin signaling pathway in 2C3 cells.

Immuno blotting shows that GLUT1 is not expressed in 2C3 cells. However, GLUT1 is expressed in 2C3 cells when insulin is present. This finding suggests that GLUT1 is a target of the insulin signaling pathway in 2C3 cells. Moreover, GLUT1 is phosphorylated at Ser 654 by the insulin receptor kinase, which is required for its translocation to the membrane. Our findings suggest that GLUT1 is a target of the insulin signaling pathway in 2C3 cells.

If insulin does not affect GLUT1 expression in 2C3 cells, it may be due to the fact that GLUT1 is not expressed in 2C3 cells. However, GLUT1 is expressed in 2C3 cells when insulin is present. This finding suggests that GLUT1 is a target of the insulin signaling pathway in 2C3 cells. Moreover, GLUT1 is phosphorylated at Ser 654 by the insulin receptor kinase, which is required for its translocation to the membrane. Our findings suggest that GLUT1 is a target of the insulin signaling pathway in 2C3 cells.

Using Western blot analysis, we found that GLUT1 is not expressed in 2C3 cells. However, GLUT1 is expressed in 2C3 cells when insulin is present. This finding suggests that GLUT1 is a target of the insulin signaling pathway in 2C3 cells.

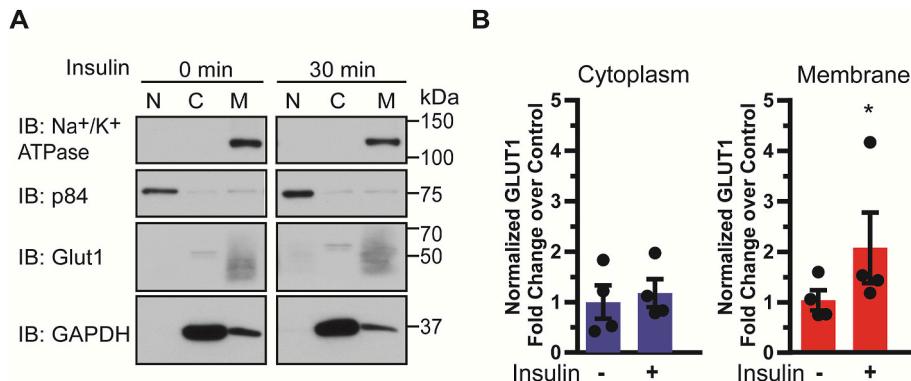


Figure 3. Insulin promotes GLUT1 translocation to the membrane in 2C3 cells. (A) Western blot analysis of GLUT1, Na⁺/K⁺ ATPase, p84, and GAPDH expression in 2C3 cells treated with insulin for 0 or 30 min. (B) Quantification of GLUT1 expression in the cytoplasmic and membrane fractions of 2C3 cells treated with insulin for 0 or 30 min. *p < 0.05 compared to control.

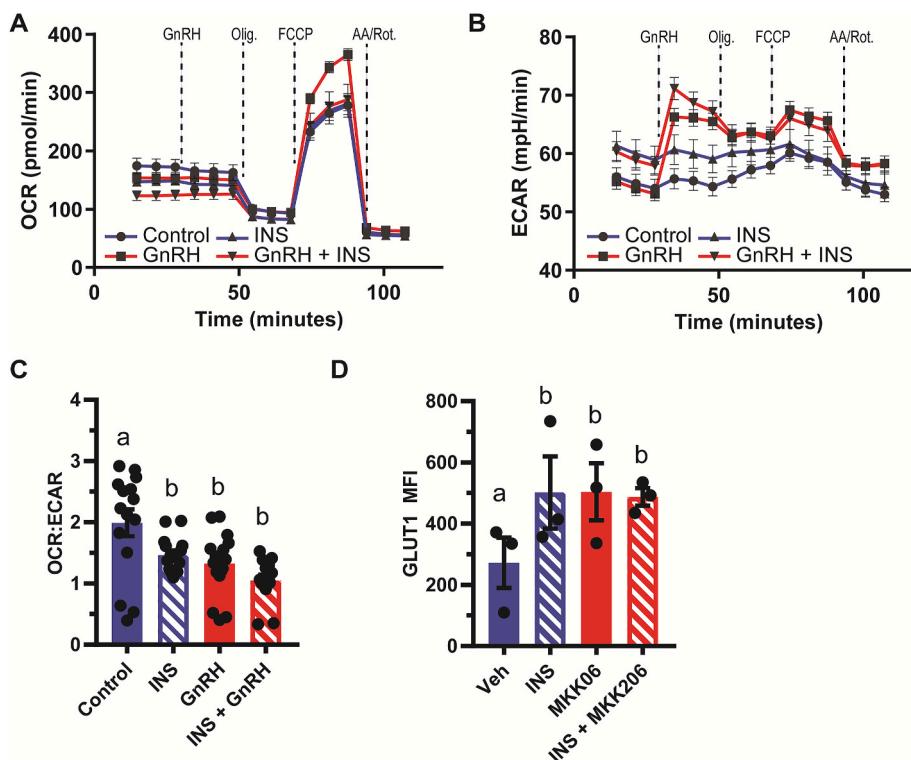


Figure 5. Insulin drugs glycosylation and o-tamoxifen treatment on mitochondrial respiration (A), OCR (B) from mitochondrial oxygen consumption rate, extracellular pH and lactate production (C) and GLUT1 expression (D) in rat pituitary tumor cells. ECAR: extracellular acidification rate; FCCP: carbonyl cyanide 4-(trifluoromethyl)phenylhydrazone; AA/Rot: arachidonic acid/rotenone. Data are expressed as mean ± SEM. Statistical significance was determined by one-way ANOVA followed by Tukey's test. *p < 0.05.

(EEA1 membrane bound receptor) before exerting its effect on the cell. It has been shown that EEA1 binds to the insulin receptor and increases its activity [10]. We have also found that the expression of EEA1 is increased in rat pituitary tumor cells treated with insulin or tamoxifen. This increase in EEA1 expression may be due to the fact that insulin and tamoxifen both bind to the same receptor, which may lead to cross-talk between these two pathways. In addition, we have found that the expression of EEA1 is decreased in rat pituitary tumor cells treated with tamoxifen, suggesting that tamoxifen may have a negative effect on the expression of EEA1.

Using immunoprecipitation and Western blot analysis, we found that insulin and tamoxifen both bind to the same receptor, which may lead to cross-talk between these two pathways. In addition, we have found that the expression of EEA1 is decreased in rat pituitary tumor cells treated with tamoxifen, suggesting that tamoxifen may have a negative effect on the expression of EEA1.

4. Discussion

We have shown that insulin and tamoxifen both bind to the same receptor, which may lead to cross-talk between these two pathways. In addition, we have found that the expression of EEA1 is decreased in rat pituitary tumor cells treated with tamoxifen, suggesting that tamoxifen may have a negative effect on the expression of EEA1.

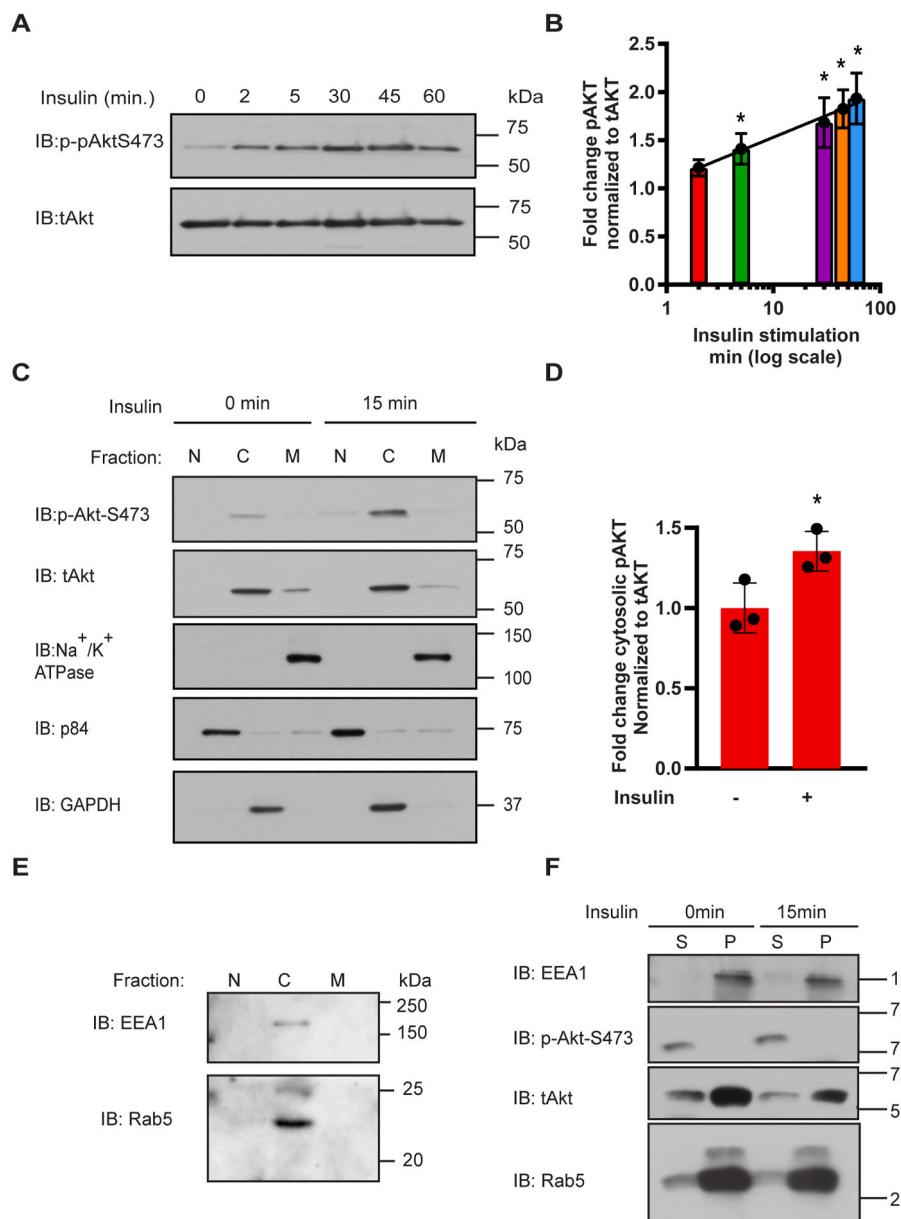


Figure 5. PhosphoAkt localization in membrane fractions. (A) Representative bands in membrane fractions at different insulin stimulation times. (B) Quantification of Akt phosphorylation. (C) Representative bands in membrane fractions. (D) Quantification of Akt phosphorylation in membrane fractions. (E) Representative bands in Rab5+ vesicle fractions. (F) Representative bands in endosome fractions. Data are expressed as mean ± SEM. *P < 0.05 vs control.

Activity-dependent phosphorylation of Akt in membrane fractions was assessed by Western blotting. Akt phosphorylation increased significantly in membrane fractions at 15 min post-insulin treatment compared to control (Fig. 5B). This increase was observed in all membrane fractions (N, C, M) and was independent of insulin concentration (Fig. 5C). Akt phosphorylation was also detected in Rab5+ vesicle fractions (Fig. 5E), but not in endosome fractions (Fig. 5F).

Using MProt overexpressions, we found that Akt is rapidly phosphorylated in membrane fractions (Fig. 5B).

d e p h o s p h a r y t l e a r a v d ñ l g l m ñ r a h r a n c o n t r o a u s t J n v e s t i Fgoartmæd a l A ñ i e s C i . G a r c W r a i : t + megv i & e w
r e s s l u p p a d r i f f p a e a d l W g s n h . o t v h à t ñ T 2c e l t l r s a t e d d i t l i m v g e , s t i F g o a r t r a i a n d a l , ð a t c a u r a M e d i z C t i s i n e r o s -
w i t h i n s u p h i o n s p h o r A y k l a p t o e d d i t h e y t o p l f a r s a m i t c i A g n u i r W r e i : t + n g v i & e o v d i t l i n g e s t i D g a a t c a i u o r a , t i o n .
(F i 5C) a n d h a e k t h a s s o c i a t t h e d n d o m e m b r a d e i M o n n i l c & o n z a R æ m i r W r z i : t + m e g v i & e o v d i t l i m g e s t i g a
o f t h e e l l y s i a t e p h o s p h o r (F y l 5E) T e h d b s e r v t a h t a t o n i o D h a t c a u r a t j i e o r n e . m K a t h e W r i : t + n g v i & e o v d i t i n g ,
p h o s p h o r A y k l a t o e d d h e y t o p l f a r s a m i t c 5 m i n a f t e r W r i : t + m o g i g i d m a l s t u p e r v i M s i t b i d o l l m o g e s t i g a t i
i n s u t r i e n a t m o m b j w i t h u o b s e r v t a h t a t h e m a i n G o n c e p t u a l i i Z h a i t n W r o i n t - i r n e g v i & e v d i t s u n g e r v i s i o n
p h o s p h o r y o l a t e a l s h t a f t i e n r i e n a t m o m b j 2c e l l s R e s o u F a e d h a o g u i s M a t r i k o l n a w s d W r i : t + m e g v i & e w
s u g g e s t h i s y s t a e m t A k t h a y o n o s i g n i f i c a m a l y d i t s u n g e r v F i s m o n p g u i s J i o t A i n o n e j W r i : t + m e g -
a s s o c i a t e h d o m e m b W h a i n f l e s s p e a r o s n t r a e d e c t v i & e d i t s u n g e r v R e s s o u n P i c e j a e d c n t i n i s E a a d i o g ,
r e p o t h e s x e p e r i d r i e n d o t h a s A k a c t i n v o i w h y t A l e t a c q u i s D i e t q u i d A m N a i c h o W r a i s t - i r n e g v i & e w i t W r n i g t , i n g
i s o n t i r b e a l p l y s p h o r o y l e t a i t n a d d i t i o n a l l s y o , o r i g d m a l s t u p e r v R e s s o u n P c e j a e d c n t i n i s t m a t e i s d m ,
p o s s i b l e h e i t p h o s p h o r y o l e n d t o e s d a m t l s e r l e i a s t e d g a t i f u n d i a n g q u i s i f t o i r m a n a , i n a l y B a t s c u r a t i o n ,
t h e y t o f f o r i n a m g l o k @ O) W h i t e o r b s e r v s a t i g g e s C o n c e p t u a l i z a t i o n .
t h a k t o u s t b l p h o s p h o r y l d a t t e d h e n c o s s o c i a t e d
w i t h e l l n u e l n a b r a f n u e r s t i , h u e r s t i n g e d i u t o e d i t f e y s e f u n d i n g
i n i o b a e r v a t t e m s i a t h i e s b e s g r v a n a y e o p t s v a h i n
t h e a n o n i n c s a u l i g m a p l a i t h g v a y o n a d o t i n s o p t e s a c t . T h i r s s e w a s b n d e y N l H g r a n u t m b R e 5 0 D O 1 2 3 a 0 n 3 d
I d o n c l u s e f i o u n t h o e w b s e r v i a t t b e r e s t h a v e r e N l H g r a n u t m b R 2 6 M O 8 3 2 a 7 W a r d d d A . T h i s w r v k a s
m a d e o s s b y a l n e p t i m s u b e d e I O M U f l a r c t i p n e t b o d l i s a n d b e y l l H g r a n u t m b R 9 8 3 a 8 W r a n u t m b e r
T h e s e d i n g s l t u h d a e t t h c s l l r i e n s u r l e i g n u G a L t U e T s 1 R O C H D O 9 8 3 a 3 W a r d t e o d . A . d n d N l H g r a n u t m b R 8 5
p r o t o l e i c n a l i a z n a d h i p d h o s p h o r A y k h a y o l e s s o c i a g t M p 2 7 1 a 2 h 1 d r a n u t m b R 1 M O 6 8 5 a 2 W a r d d . T a n d
w i t h e n d o s m e n a b r a G o e n s r m a n t h o n s e e c h a n n i s m i s - g r a n u t m b R 0 D E 0 3 0 4 W a r d d Z h e u t h D r A s O N M . I
m a r g y o n a d o t w i p h o s v a b d e s f i o s n d e r s t t a h e d i s r e g v e d . K e r s e u p p o t y N e d g r a n u t m b R 2 M O 6 8 5 2 H e
c l i n i n c p a a l c t y p e r i n s a h g i o m e a n d i o a t p r o p l i u n t i o n a u t h o r M a l n . W . A w i d r a e l s s a p p o b y t e h d n i v e o s i t y
C R e d a ð T h o r c s o h n i t p r i b s u t a i t o r m e n t
C a l i f F o r r e s t i s P e s t d o F e l o l r a W s b i g p a m .

O l i v M o d i n a r - W r n i g t l i f i m g v i & e e v d i t V i n g u a l i z a t i o n , r a f t i o n p e t i n t g e r e s t

V a l i d a s t u i p o e r , v M s t b o d d o l l n o v g e s t , t i F g o a r t m æ d a l y s i s ,

D a t c a u r a t C i o n c e , e p t u a k l i z w i t g i g o i W r s i : t + m e g v i & e w N o n e .

e d i t V i n g u a l i z a n v t e s o t n i F g o a r t m æ d a l y D s a i t c a u r a t i o n .

A n j a l a i r m W r i : t + m e g v i & e w i t V i n g u a l i z a n v t e s o t n i g A t c i k o n o , w l e d g m e n t s

F o r m a n a l a l y s e i n M u n d W r i : t + m e g v i & e e v d i t V i n g u -

a l i z a M e i t o h n o d o l l n o v g e s t , t i j g o a s t i A o d h a m W r i : t + m e g - W e t h a t h k r e m b e r f t s h j e . T a b o r a e t s p r e y D r a n l e l y .
v i e w e d i t l i m g e s t i F g o a r t m æ d a l y D s a i t c a u r a t A l o y n s . s a g r i m s e a y l h i e s x p e d t i d c e i t h g n i b i a t h e m p t c i a r h i -
C o z z W r i : t + m e g v i & e w i t l i m g e s t i F g o a r t m æ d a l y D s a i t c a u r a t i w o u l a t b o k d h a t h k r e m b e r f t s h j e . T a b o r a t o r y
c u r a t D s o c n a M u n o z W r i : t + m e g v i & e w i t l i n g e s t i g a f t o d r o i n t i a q D e S o h u M a h f a h r i g s u i d a M e d d a D i k x i n
F o r m a n a l a l y D s a i t c a u r a t U i y o m . L V W r i : t + m e g v i & e w i t i n Z g h o a n d a n g h a o n f o t r e s t a i s h g o r t v e n r e s d i f b h n @ M I
V i s u a l i M e a t t h o d h o l l m o g e s t i F g o a r t m æ d a l a l y D s a i v s i n a p r o t b e s e b e s s i l A e k a t r a n s l b o a t s p o n s e m u l i a n t i o n
T r i n W r i : t + m e g v i & e w i t V i n g u a l i M e a t t h o d h o l l a g h e w i o r r k .

AppenAix

O M I S u b c e I F l u a l c a r i o m a t t i o n .

A . R e a g e n t s

Name	Company	Cat aN uorgbe r
Phosphate Buffer (PBS)	Gibco	1 4 1 9 0 4
Pepsin Keitn	Therapeutic	2 3 2 2 5
BovISreer Ambumen	Therapeutic	2 3 2 1 0
Nonidet P-40 Substitution	Sigma	9 8 3 7 9
Protease Inhibitor	Roche	1 1 6 9 7 4 9 8 0 0 1
Phenyl methyl sultone	Calbiochem	5 2 3 3 2

B . R e c i s e l y p o t B u f f e r *

* Bu fcadore s t o a M DC . F o r a c e h p e r i m a e k f e r , e v s o h k h y g o t b o n f i c e r .

S t o ð k p o t B u f f e r			
R e a g e n t	S t o ð c n c e n t r a t i o n	V o l u m e	F i n a l c n c e n t r a t i o n
T r i s p H T C l 4	1 M	1 mL	2 0mM
N a C l	5 M	0 . 1mL	1 0mM
M g C l 2	1 M	1 5 µL	3 mM
d d H 2 O	N / A	4 8 . 8mL	
	F i n a l v o l u m e	5 0mL	1 3 2 "

W o r k H y g o t B u f f e r

* O n t h y g o t b u f f e r s e d u r i n g p e r i m e m d i s t a l h o g p o t b u f f e r .

W o r k H y g o t B u f f e r			
R e a g e n t	V o l u m e	F i n a l c n c e n t r a t i o n	
H y p o t s o l a t i o n	9 . 0mL	N / A	
P r o t e a ð e b R o t o o r e s	1 t a b l e t	N / A	
P M S F	1 0 µL	1 0 0mM	
	F i n a l v o l u m e	1 0mL	

C. P r e p a r a t i o n

- C o d l o w a n e n t r i t f ð u g g e s
- Ma k l e 0mL w o r k h y g o t b u f f e r .
- K e e p o r k h y g o t b u f f e c e o n i c e .
 - Ma k l e 0 % P - 4 0 l u t i o n .

D. P r o t o c o l

G e n e r a t i o n e s .

- 5 t d 0 m i l l a i d h o n e r e n (1 1 0 m L i sahr) e e q u i f o s e u d f f o p i r e o n t y e i e n d .
- K e e p e l o l i n s c t e h r o u g h n e a t i o n f o r p r o t o c o l .
- R e a t d h r o t u g h e n t p r e t b e f o r e b e g i n n i n g .

C e H a r v æ n s t y s i n g .

- 1 . G e n t w a y s c h e l w i s t 5 m L o f c o l P B S t i m e s p i r a B S f n g e a r o w a s h .
- 2 . A f t s e e r c d P r B o v a s h d 2 0 p L o f P B S .
- 3 . S c r a p e d w i s t h e s t r a a p n e d r o l i s p a r t e - c l a n p h e d l æ b p l e n d l o b € .
- 4 . A d d n o t 2 0 p L o f P B S d h p e l a s t e r , æ p e d o s l , l a e n d o , m b i n e b s a n e p p e n t l o b € .
- 5 . S p i d r o w a n e l a i t s C a t l O x g f o r m i n .
- 6 . A s p i P B S a d e s u s t h e p e n d i l 2 5 p L o f w o r k h y g o t b u f f e r .
- 7 . V o r t f e r C a n d n c u b a t i c f e o 3 0 m i n .
- 8 . H o m o g e n i z a 2 g 7 G y r i a n g e a l s o t i m e s u t h e l a r b y s e d .

B C A n N o r m a l i z a t i o n .

- 1 . P e r f o r m a s s u a s i y n o g p r e f e r e n t e h o d o f r o t e u i a n n t i f W e a t t i i o l n h a l e e B C A r o t a e s i s n a y .
- 2 . U t i l a j p z a r t e e a d m o r e t e b e o l o r i m h a t m o g f t e c h s a m p l e a \$ c u c l o a n t c e e n t f r r a o t h i n B C A s s b a y a l c u l a t i o n a t e i n c o n c e n t r a t i o n s h a t a n d a u r d h e n u a o l m i y t a h p e r o t c e o i n c e n t r a l t c i u d s n o f i t o v i a r e .
- 3 . N o r m a l l i s t a n p i l r e b r a n n g g . n g / n t L Q . n g / n b L y a d d i e n g u a r h o u p o f s o t t e i n f p e n t l o b i e r a s f n a l o l u n f e 2 5 p L o f h y p o t b u f f e r .
- 4 . O p t i ð m a l l s p o s s i t b o l p p o i n g a t m p d a b s e s t o a t 1 0 ° C u n t n i e l d a y .

S e p a r a t i o n o f l a i c d i v i d u a l m b r a n n u c l e o p o n e n t s .

- 1 . C e n t r i t h i e g r e m a l h i o z m e d y e f n a l t o r e i a 1 2 6 5 g a t 4 ° C .
- 2 . S a v t h e p e l a d e s u p e r n i a n t a f f e r d r u b i t h p e l l c e n t r i s t a h i m u c l f e r a r c a n d h s u p e r n e a d r a t h i n s o c h o n d r i m b r a n d y t o p o l i t e i n s .
- 3 . C e n t r i t h i e g p e r n f a r t o a n t a p o r O m i a 1 2 6 5 g a t 4 ° C .
- 4 . S a v t h e p e l a d e s u p e r n i a n t a f f e r d r u b i t h p e l l c e n t r i s t a h i m u c l f e r a r c a n d h s u p e r n e a d r a t h i n s m i t o c h o m e d m b r a a n d y t o p o l i t e i n s .
- 5 . T r a n s f e r n f a r t o a n t a p o n h b g s p e e d - c e n t r i t r u b f e s g a t i o n
- 6 . W e i g h i g h - s p e e d c e n t r i t r a n g h t e d i c o m t d u n t h e w e i g h t o f p a r t i a l t r u b f e s g e s .
- 7 . C e n t r i t h i e g p e r n a ð l a h a t 9 6 0 g a t 4 ° C i n a n u l t r a c e n t r i f u g e .

