Supplementary Table 1  Proteins reported to bind directly to 14-3-3s with relevant interaction sites indicated. A. Mammalian proteins; B. Non-mammalian animal proteins; C. Fungal proteins; D. Plant proteins; E. Bacterial and viral proteins that interact with 14-3-3s inside eukaryotic host cells.

The abstracts of 2969 papers listed with the keyword ‘14-3-3’ in PubMed (11 Jan 2010) were searched for reports of direct interactions between 14-3-3 and a target protein, and where possible relevant sites were identified in the manuscript. Often residue numbers were given with no specific amino acid sequence context, in which case these details were requested from corresponding authors, and/or deduced from the sequences of oligonucleotides used for site-directed mutagenesis of 14-3-3-binding sites. Where the precise form of a mammalian protein that had previously been studied in a publication was not specified, we assigned a sequence that contained the relevant site, choosing a human sequence where the species studied was unclear. Any sites that still could not be placed in a sequence context were omitted. 14-3-3-binding sites are indicated as lower case letters highlighted in yellow, and where more than two sites are implicated in 14-3-3 binding of a protein, these are highlighted in turquoise and not included in the Weblogo analysis in Supplementary Table 2 and Fig 1 (except for MAPT, see notes).

Caveat emptor: The data collected may include assignments that are incorrect, due to inaccuracies in the original assignments, or our interpretation of authors' intentions for which we apologise. To aid future improvements in the dataset, we ask authors to report any corrections to e.mackintosh@dundee.ac.uk.

A. Mammalian proteins reported to interact directly with 14-3-3

| Human AANAT | Serotonin N-acetyltransferase; arylalkylamine N-acetyltransferase, melatonin-synthesizing enzyme. (Swissprot = P00519) |
|-------------|-------------------------------------------------------------------------------------------------|
| 1 MLEICLKLVG CXXKGGGLSS SCSYCEALQG RPVASFDEGQ GLSEAAKNS WENS KILLAGPSE |
| 61 NDPNLVALY DFVAGDGNTL SITKGKLRV LGYHHNGEC EAQTNNQGQ VPSSNTPYN |
| 121 SELKHSWQYVL PVSNAANEYL LSSSNGSFL VRSSESSPGQ QISSLREYRG VVHRYINTAS |
| 181 DGKLYVSSES RPNTLWLRYV HSSTVADGL TLMLYPAFPR NKTFTYVSQY NDYKREWERT |
| 241 DTKMHLKLG QQGQYEVQDG KQFSTLTVY KTTLKDEMYR ESEQKAKVM KEIKHLVNLQV |
| 301 LGVCTREPP FYIITEEMTPY GNLLDLYREQ NQVEVAVVL NYLMAQISSA MEYLLKKNFI |
| 361 HRDLARNLN VGENHLLKVA FGQLSRMTG DTYTAHAGAK FFKIKTAPES LAYKFSIKS |
| 421 DWAFOAVLWL EIAITYGMSFY PGGDLQYVE LLEKDMYRRR PEQCEFERYE LRMACWQNPW |
| 481 SDPSFAPRQ INQGQVQGQVS TLLQAPFELT VTPRTSRRPE |
| 541 HRTIOTTDPN PHSKGQGQED FLDEHPAVSL LIIPKFGERPP EGMLNEDERL LPDKQXTNLF |
| 601 SALIKKXKKT APTFPKRRSS FREMDQPER RGAGEEEGRD ISGNAFAPT LTDTAPKAP |
| 661 KPSNGVVPN GALRSESSQGQ FRSPHLWKKS STIITSSRLAT GESEEEGGSGS KFRFLRSACAS |
| 721 CFPHGAKDTE WRSSVLFRDL QSTGRQDSS TSTGKHSEXK ALPKRAGEN RSDQVRTRTV |
| 781 TPPRULWKN ERADAEKVFD TMESSPGSPS PRRKTFPLGR QOTVAPASGK PFRRAEAGKGS |
| 841 ALGTPZAAEF VPTSKKGASS APGSGSKPA EESRSRRKHE ESSPSGRDGK KLRLKPFAP |
| 901 PPAASAGAKA GGGPKQPSQPS QAAGAVLGLA KTKATSULVD VNDSSAQPQG PGELKPVLF |
| 961 PATFPKRSK PKGTTSPISP VPTSLPQSS ALAGQDSLST AFISLITSTRV LRSLKQRPE |

B. Non-mammalian animal proteins

C. Fungal proteins

D. Plant proteins

E. Bacterial and viral proteins

References to 14-3-3-binding to AANAT

Obisl T, Ghihrando R, Klein DC, Ganguly S, Dyda F (2001) Crystal structure of the 14-3-3-zeta/serotonin N-acetyltransferase complex. A role for scaffolding in enzyme regulation. Cell 105:257–267

Pozdeyev N, Taylor C, Haque R, Chaurasia SS, Visser A, Thayyum A, Du Y, Fu H, Weller J, Klein DC, Iuvone PM. Photic Regulation of Arylalkylamine N-Acetyltransferase Binding to 14-3-3 Proteins in Retinal Photoreceptor Cells. J Neurosci. 2006 Sep 26;26(36):9151-63.

Ganguly S, Weller JL, Ho A, Chemineau P, Malpaux B, Klein DC (2005) Melatonin synthesis: 14-3-3-dependent activation and inhibition of arylalkylamine N-acetyltransferase mediated by phosphoryserine205. Proc Natl Acad Sci USA 102:1222–1227.

Human Abl1 Abelson murine leukemia viral oncogene homolog 1 (Tyrosine kinase) (Swissprot = P00519)

| A. | Mammalian proteins reported to interact directly with 14-3-3 |
|----|-------------------------------------------------------------|
| Human AANAT | Serotonin N-acetyltransferase; arylalkylamine N-acetyltransferase, melatonin-synthesizing enzyme. (Swissprot = P00519) |
| 1 MLEICLKLVG CXXKGGGLSS SCSYCEALQG RPVASFDEGQ GLSEAAKNS WENS KILLAGPSE |
| 61 NDPNLVALY DFVAGDGNTL SITKGKLRV LGYHHNGEC EAQTNNQGQ VPSSNTPYN |
| 121 SELKHSWQYVL PVSNAANEYL LSSSNGSFL VRSSESSPGQ QISSLREYRG VVHRYINTAS |
| 181 DGKLYVSSES RPNTLWLRYV HSSTVADGL TLMLYPAFPR NKTFTYVSQY NDYKREWERT |
| 241 DTKMHLKLG QQGQYEVQDG KQFSTLTVY KTTLKDEMYR ESEQKAKVM KEIKHLVNLQV |
| 301 LGVCTREPP FYIITEEMTPY GNLLDLYREQ NQVEVAVVL NYLMAQISSA MEYLLKKNFI |
| 361 HRDLARNLN VGENHLLKVA FGQLSRMTG DTYTAHAGAK FFKIKTAPES LAYKFSIKS |
| 421 DWAFOAVLWL EIAITYGMSFY PGGDLQYVE LLEKDMYRRR PEQCEFERYE LRMACWQNPW |
| 481 SDPSFAPRQ INQGQVQGQVS TLLQAPFELT VTPRTSRRPE |
| 541 HRTIOTTDPN PHSKGQGQED FLDEHPAVSL LIIPKFGERPP EGMLNEDERL LPDKQXTNLF |
| 601 SALIKKXKKT APTFPKRRSS FREMDQPER RGAGEEEGRD ISGNAFAPT LTDTAPKAP |
| 661 KPSNGVVPN GALRSESSQGQ FRSPHLWKKS STIITSSRLAT GESEEEGGSGS KFRFLRSACAS |
| 721 CFPHGAKDTE WRSSVLFRDL QSTGRQDSS TSTGKHSEXK ALPKRAGEN RSDQVRTRTV |
| 781 TPPRULWKN ERADAEKVFD TMESSPGSPS PRRKTFPLGR QOTVAPASGK PFRRAEAGKGS |
| 841 ALGTPZAAEF VPTSKKGASS APGSGSKPA EESRSRRKHE ESSPSGRDGK KLRLKPFAP |
| 901 PPAASAGAKA GGGPKQPSQPS QAAGAVLGLA KTKATSULVD VNDSSAQPQG PGELKPVLF |
| 961 PATFPKRSK PKGTTSPISP VPTSLPQSS ALAGQDSLST AFISLITSTRV LRSLKQRPE |

Notes

14-3-3 binding to phosphoThr31 and phosphoSer205, phosphorylated by PKA in response to light in pineal gland, activates AANAT and protects it from protein degradation.

References to 14-3-3-binding to AANAT

Obisl T, Ghihrando R, Klein DC, Ganguly S, Dyda F (2001) Crystal structure of the 14-3-3-zeta/serotonin N-acetyltransferase complex. A role for scaffolding in enzyme regulation. Cell 105:257–267

Pozdeyev N, Taylor C, Haque R, Chaurasia SS, Visser A, Thayyum A, Du Y, Fu H, Weller J, Klein DC, Iuvone PM. Photic Regulation of Arylalkylamine N-Acetyltransferase Binding to 14-3-3 Proteins in Retinal Photoreceptor Cells. J Neurosci. 2006 Sep 26;26(36):9151-63.

Ganguly S, Weller JL, Ho A, Chemineau P, Malpaux B, Klein DC (2005) Melatonin synthesis: 14-3-3-dependent activation and inhibition of arylalkylamine N-acetyltransferase mediated by phosphoryserine205. Proc Natl Acad Sci USA 102:1222–1227.

Human Abl1 Abelson murine leukemia viral oncogene homolog 1 (Tyrosine kinase) (Swissprot = P00519)
AltName: Full=Metalloproteinase

>gi|14423634|sp|P09519.1|ADAA2_HUMAN RecName: Full=Disintegrin and metalloproteinase domain-containing protein 22 (Swissprot = Q9PK01)

**Human ADAM22 Disintegrin and metalloproteinase domain-containing protein 22 (Swissprot = Q9PK01)**

3 54QAAVSVYP FLLLCLGCFL PFCRCQAGD AGLMELEKRKK ENRFESENQI VPLLIRYRSQ 61 GEDESHRDL DARVQGGLG PQLTHVDQS FXQVDAFGTIFS ILDVVNLHDL LSSIESYREHI 121 EHGKFQVEK GEECHYQVR IGKNPSQFI VLTCHGLLGMD FYHNDYTLFE PEENDTTQE 181 DHHFHYVIKS RLFEFSDLLD PSEFQVSNIT PSDKILFRPR KRSKRLQRY PRFNEVEETKY 241 IEMUVNDSLG MKKRSURLSV NTNTYASKVS NNADLYIQK LTSTRUFLVAM ETRATDNKFA 301 ISNPLELITLR EMKURYRDFII KEKSADAVLF SGQFSESSRS GAAUGYLCGK LKGQVVENNE 361 GKTDLMAVTL AQSLAHNIGI ISDKRKLA EFMKYRRDFI KEKSDAVH MFK 421 RLFEFSSLDDL PSEFQQVNIT PSDKILFRPR KRSKRLQRY PRFNEVEETKY 481 LLCCRTQCR TRQQCWYGQ KTVASSKYCY EKAIUISGTE GCNCGKGDIT IQCNQHSVLC 541 GYLLCTNIGN IPRKLGEDGE ISTDLYQQQ RTICNCGSHH KELEDVLYG WEDTPCGTCQ 601 MNLCECRHCLP VASCNPSTCL SKEKGTCSG NGVCSNLEK VCNHRWIGD OTYFPHNNDD 661 72KRGCTSGN YAGVTNIIGG IAIGTIVLW LILLITAGWY KNReRQLP GDQYVDFGKPDG 721 78QSFSDIFP GVSTNASSSS KERSNOLHS WSERFIDOTX ISIDCENGRP RSSLQONLQG 841 8QFJNNSSRKR LPSSRPS SSSNSSSQRY PMYPAPPED DMVQVQSGAR 901 LWETS1

**Notes**

Regulates cytoskeleton remodeling during cell differentiation, cell division and cell adhesion. Localizes to dynamic actin structures, and phosphorylates CRK and CRKL, DOK1, and other proteins controlling cytoskeleton dynamics. Regulates DNA repair potentially by activating the proapoptotic pathway when the DNA damage is too severe. Expression varies between both SH and SH3 domains and a nuclear localization signal (NLS) found in AβH in the cytoplasm results in cell proliferation and survival. In contrast, nuclear AβH is activated and induces apoptosis after genotoxic stress. Phosphorylated cAβH binds 14-3-3, which sequesters AβH in the cytoplasm. Upon DNA damage 14-3-3 is phosphorylated by JNK leading to dissociation from AβH and AβH translocation to the nucleus inducing apoptosis. TTK (also known as Mps1) phosphorylates c-Abl at Thr735 and this phosphorylation is of importance for the cytoplasmic sequestration of c-Abl. 14-3-3 also binds to AβH in the context of the Bcr-Abl tyrosine kinase fusion of Philadelphia chromosome (Ph1)-positive human leukemias.

**References to 14-3-3 binding to Abl**

Mancini M, Corradi V, Petta S, Martinelli G, Barbieri E, Santucci MA. mTOR inhibitor RAD001 (Everolimus) enhances the effects of imatinib in chronic myeloid leukemia by raising the nuclear expression of c-Abl. Leuk Res. 2009 Jul 28.

Yoshida K, and Miki Y. Enabling death by the Abl tyrosine kinase: mechanisms for nuclear shuttling of c-Abl in response to DNA damage. Cell Cycle. 2005 Jun;4(6):777-9.

Mancini M, Veljkovic N, Corradi V, Zuffa E, Corrado P, Pagnotta E, Martinelli G, Barbieri E, Santucci MA. 14-3-3 ligand prevents nuclear import of c-Abl protein in chronic myeloid leukemia. Traffic. 2009 Jun;10(6):637-47.

Nitra K, Taira N, Miki Y, Yoshida K. TTK/Mps1 co-activates 14-3-3 positive human leukemias. Cell Cycle. 2005 Dec;4(23):3914-21.

Dong S, Kang S, Lonial S, Khoury HJ, Viallet J, Chen J. Targeting 14-3-3 protein kinase ABL1; AltName: Full=Abelson murine leukemia viral oncogene. Leukemia. 2008 Mar;22(3):572-7.

Pendergast AM. Stress and death: breaking up the c-Abl regulatory 14-3-3 complex in apoptosis. Nat Cell Biol. 2005 Mar;7(3):213-4.

Yoshida K, Yamaguchi T, Natsume T, Kufe D, Mikj Pendergast AM. Association of the protein kinases c-Abl and c-Ras with the cytoplasm results in cell proliferation and survival. In contrast, nuclear activated c-Abl induces apoptosis after genotoxic stress. Phosphorylated cAbl binds 14-3-3, which sequesters Abl in the cytoplasm. Upon DNA damage 14-3-3 is phosphorylated by JNK leading to dissociation from Abl and Abl translocation to the nucleus inducing apoptosis. TTK (also known as Mps1) phosphorylates c-Abl at Thr735 and this phosphorylation is of importance for the cytoplasmic sequestration of c-Abl. 14-3-3 also binds to Abl in the context of the Bcr-Abl tyrosine kinase fusion of Philadelphia chromosome (Ph1)-positive human leukemias.

**References to 14-3-3 binding to Abl**

Mancini M, Corradi V, Petta S, Martinelli G, Barbieri E, Santucci MA. mTOR inhibitor RAD001 (Everolimus) enhances the effects of imatinib in chronic myeloid leukemia by raising the nuclear expression of c-Abl. Leuk Res. 2009 Jul 28.

Yoshida K, and Miki Y. Enabling death by the Abl tyrosine kinase: mechanisms for nuclear shuttling of c-Abl in response to DNA damage. Cell Cycle. 2005 Jun;4(6):777-9.

Mancini M, Veljkovic N, Corradi V, Zuffa E, Corrado P, Pagnotta E, Martinelli G, Barbieri E, Santucci MA. 14-3-3 ligand prevents nuclear import of c-Abl protein in chronic myeloid leukemia. Traffic. 2009 Jun;10(6):637-47.

Nitra K, Taira N, Miki Y, Yoshida K. TTK/Mps1 co-activates 14-3-3 positive human leukemias. Cell Cycle. 2005 Mar;7(3):213-4.

Yoshida K, Yamaguchi T, Natsume T, Kufe D, Mikj Pendergast AM. Association of the protein kinases c-Abl and c-Ras with the cytoplasm results in cell proliferation and survival. In contrast, nuclear activated c-Abl induces apoptosis after genotoxic stress. Phosphorylated cAbl binds 14-3-3, which sequesters Abl in the cytoplasm. Upon DNA damage 14-3-3 is phosphorylated by JNK leading to dissociation from Abl and Abl translocation to the nucleus inducing apoptosis. TTK (also known as Mps1) phosphorylates c-Abl at Thr735 and this phosphorylation is of importance for the cytoplasmic sequestration of c-Abl. 14-3-3 also binds to Abl in the context of the Bcr-Abl tyrosine kinase fusion of Philadelphia chromosome (Ph1)-positive human leukemias.

**References to 14-3-3 binding to Abl**

Mancini M, Corradi V, Petta S, Martinelli G, Barbieri E, Santucci MA. mTOR inhibitor RAD001 (Everolimus) enhances the effects of imatinib in chronic myeloid leukemia by raising the nuclear expression of c-Abl. Leuk Res. 2009 Jul 28.

Yoshida K, and Miki Y. Enabling death by the Abl tyrosine kinase: mechanisms for nuclear shuttling of c-Abl in response to DNA damage. Cell Cycle. 2005 Jun;4(6):777-9.

Mancini M, Veljkovic N, Corradi V, Zuffa E, Corrado P, Pagnotta E, Martinelli G, Barbieri E, Santucci MA. 14-3-3 ligand prevents nuclear import of c-Abl protein in chronic myeloid leukemia. Traffic. 2009 Jun;10(6):637-47.

Nitra K, Taira N, Miki Y, Yoshida K. TTK/Mps1 co-activates 14-3-3 positive human leukemias. Cell Cycle. 2005 Mar;7(3):213-4.

Yoshida K, Yamaguchi T, Natsume T, Kufe D, Miki Y. JNK phosphorylation of 14-3-3 protein-gramm sequesters 14-3-3 targeting of c-Abl in the cytoplasmic response to DNA damage. Nat Cell Biol. 2005 Mar;7(3):275-87.

Reuther GW, Fu H, Cripe LD, Collier RJ, Pendergast AM. Stress and death: breaking up the c-Abl regulatory 14-3-3 complex in apoptosis. Nat Cell Biol. 2005 Mar;7(3):213-4.

Yoshida K, Yamaguchi T, Natsume T, Kufe D, Miki Y. JNK phosphorylation of 14-3-3 protein-gramm sequesters 14-3-3 targeting of c-Abl in the cytoplasmic response to DNA damage. Nat Cell Biol. 2005 Mar;7(3):275-87.

Reuther GW, Fu H, Cripe LD, Collier RJ, Pendergast AM. Stress and death: breaking up the c-Abl regulatory 14-3-3 complex in apoptosis. Nat Cell Biol. 2005 Mar;7(3):275-87.
which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.

The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial Licence (http://creativecommons.org/licenses/by-nc/2.5/)

© 2010 The Author(s)

Human AKAP13

AKAP-Lbc, guanine nucleotide exchange factor (GEF) for RhoA (Swissprot = Q12802)

| AltName: Full=Protein kinase A binding auxiliary protein; binding conserved and essential for the interaction of AKAP13 with PKA. | AltName: Short=AKAP 13 | AltName: Full=Breast cancer nuclear receptor activation binding domain (BRAD) protein; binding domain for the binding of BRAD proteins. |

**References to 14-3-3 binding to Adam22**

Zhu P, Sun Y, Xu R, Sang Y, Zhao J, Liu G, Cai L, Li C, Zhao S. The interaction between ADAM22 and 14-3-3 protein family members. J Cell Sci. 2006 Aug 15;119(Pt 18):3609-16.

Gödde NJ, D'Abaco GM, Paradiso L, Novak U. Efficient ADAM22 surface expression is mediated by phosphorylation-dependent interaction with 14-3-3 protein family members. J Cell Sci. 2006 Aug 15;119(Pt 18):3609-16.

Zhu P, Yang X, Zhao J, Li C, Zhao S. The interaction between ADAM 22 and 14-3-3 beta. Sci China C Life Sci. 2002 Dec;46(6):577-82.
3β functions as a transcriptional repressor and promotes anchorage-dependent growth, tumorigenicity, and independent growth, tumorigenicity, and unscheduled cell growth in vivo. Myostatin is required for the interaction with 14-3-3 binding proteins involved in cytoskeletal regulation and cellular organization.

**Notes**

14-3-3-binding site = pser156

**PKA dependent binding to 14-3-3.**

**References to 14-3-3 binding to AKAP13**

Diviani D, Allun B, Cotecha S, Fassier L (2004) Anchoring of both PKA and 14-3-3 binding sites were converted to Ala and designated as S31A, T103A, S111A, S119A, and S131A, respectively. These mutants were inserted in FBI1 and were analyzed using the yeast two-hybrid system. All mutants did not bind to 14-3-3, suggesting that multiple 14-3-3-binding motifs of FBI1 are required for the interaction with 14-3-3. (Komiva et al 2008).” Note that Komiva et al studied the rat protein, and here the human sequence is shown. Note that Rat Ser103 is Ala in the mouse sequence and that human sequence is shown.

**References to 14-3-3 binding to AKAP13**

Macqueen DJ, Johnston IA. Evolution of the multifaceted eukaryotic akirin gene family. BMC Evol Biol. 2009 Feb 20;3:54.
Araf1 plays a role in phosphorylinsulinostil 3-kinase (PI3K)/Akt survival signaling. PRAS40 is a physiological target of in vivo insulin action. Hyperinsulinemia increases its phosphorylation in human skeletal muscle biopsies. Phosphorylated PRAS40 is predominantly localized to the nucleus. In rats fed a high-fat diet (HFD), phosphorylation of PRAS40 was markedly reduced when compared with low-fat diet-fed animals in all tissues examined. A novel mTOR binding partner that mediates Akt signals to mTOR. Binding of PRAS40 inhibits mTOR activity and suppresses constitutive activation of mTOR in cells lacking TSC2. Phosphorylation by Akt and perhaps related kinases leads to its binding to 14-3-3. Two alternatively spliced isoforms have been described. PRAS40 is a novel scaffold of Akt and is required for binding of the protein to 14-3-3. PRAS40 phosphorylation by Akt and association with 14-3-3, a cytosolic anchor protein, are crucial for insulin to stimulate mTOR. PRAS40 (C146T) and PRAS40 (T246D) could not bind 14-3-3, further indicating that PRAS40–14-3-3 interaction is important for mTOR activation. The 14-3-3 binding may lead to facilitated release of PRAS40 from mTOR, or loose association of PRAS40 with mTOR, to activate mTOR and to inactivate IRS-1 through the negative feedback regulation.

Activation of mTORC1 signalling by phorbol esters does not require PRAS40 to be phosphorylated at Thr(246), bind to 14-3-3 or be released from mTORC1. It is conceivable that phorbol esters activate mTORC1 by a distinct mechanism not involving PRAS40. Indeed, our results suggest that PRAS40 may not actually be involved in controlling mTORC1, but rather be a downstream target of mTORC1 that is regulated in response only to specific stimuli, such as insulin.

Mutation of Ser-221 to Ala reduces the interaction with 14-3-3 to the same extent as mutation of Thr-246, the Akt/kinase rich Akt substrate of 40 kDa (PRAS40) function by disrupting the PRAS40–14-3-3 interaction with Ser-221 to Ala increases the inhibitory activity of PRAS40 toward mTORC1. We propose that after mTORC1 kinase activation by upstream regulators, PRAS40 is phosphorylated directly by mTOR, thus contributing to the relief of PRAS40-mediated substrate competition.

References to 14-3-3 binding to PRAS40

Araf1 plays a role in phosphorylinsulinostil 3-kinase (PI3K)/Akt survival signaling. PRAS40 is a physiological target of in vivo insulin action. Hyperinsulinemia increases its phosphorylation in human skeletal muscle biopsies. Phosphorylated PRAS40 is predominantly localized to the nucleus. In rats fed a high-fat diet (HFD), phosphorylation of PRAS40 was markedly reduced when compared with low-fat diet-fed animals in all tissues examined. A novel mTOR binding partner that mediates Akt signals to mTOR. Binding of PRAS40 inhibits mTOR activity and suppresses constitutive activation of mTOR in cells lacking TSC2. Phosphorylation by Akt and perhaps related kinases leads to its binding to 14-3-3. Two alternatively spliced isoforms have been described. PRAS40 is a novel scaffold of Akt and is required for binding of the protein to 14-3-3. PRAS40 phosphorylation by Akt and association with 14-3-3, a cytosolic anchor protein, are crucial for insulin to stimulate mTOR. PRAS40 (C146T) and PRAS40 (T246D) could not bind 14-3-3, further indicating that PRAS40–14-3-3 interaction is important for mTOR activation. The 14-3-3 binding may lead to facilitated release of PRAS40 from mTOR, or loose association of PRAS40 with mTOR, to activate mTOR and to inactivate IRS-1 through the negative feedback regulation.

Activation of mTORC1 signalling by phorbol esters does not require PRAS40 to be phosphorylated at Thr(246), bind to 14-3-3 or be released from mTORC1. It is conceivable that phorbol esters activate mTORC1 by a distinct mechanism not involving PRAS40. Indeed, our results suggest that PRAS40 may not actually be involved in controlling mTORC1, but rather be a downstream target of mTORC1 that is regulated in response only to specific stimuli, such as insulin.

Mutation of Ser-221 to Ala reduces the interaction with 14-3-3 to the same extent as mutation of Thr-246, the Akt/kinase rich Akt substrate of 40 kDa (PRAS40) function by disrupting the PRAS40–14-3-3 interaction with Ser-221 to Ala increases the inhibitory activity of PRAS40 toward mTORC1. We propose that after mTORC1 kinase activation by upstream regulators, PRAS40 is phosphorylated directly by mTOR, thus contributing to the relief of PRAS40-mediated substrate competition.
Human ARHGEF7 (GEF-H1; Full=PAK exchange factor 7; AltName: Full=PAK)

Human ARHGEF2 (GEF-H2; Full=Proliferating cell nucleolar antigen p40; Short=GEF)

Human ARHGEF1 (GEF-H1; Full=PI3K interacting exchange factor H1; Full=Pix; AltName: Full=p85)

References to 14-3-3 binding to ARAf1 (Also see references for B RAF and C RAF)

Notes

Phosphorylation of GEF

References to 14-3-3 binding to ARAf1

Notes

Phosphorylation of GEF-H1 at Ser(885) by PAK1 induces 14-3-3 binding to relocation of ARHGEF2 (GEF binding to ARaf1)

Human ARHGEF2 (GEF-H1; Full=PI3K interacting exchange factor H1; Full=Pix; AltName: Full=p85)

Human ARHGEF1 (GEF-H1; Full=PI3K interacting exchange factor H1; Full=Pix; AltName: Full=p85)

DATA DIRECT INTERACTION BETWEEN ARHGEF7 PROTEIN AND 14-3-3, BUT SITE(S) NOT IDENTIFIED. NOT IN WEBLOGO.
Basal association between endogenous βPix and endogenous 14-3-3 was increased after forskolin stimulation and significantly inhibited by protein kinase A inhibitor, βPix(S316A, T326A). (Mutating Ser560 has no effect on 14-3-3 binding, RKE(S560)AP).

Binding of 14-3-3 inhibits dimeric βPix-GEF activity, 14-3-3 binding may either block the interaction between Rac1 and the DH domain of βPix or induce a conformational change of the DH domain that would interfere with GTP binding.

The numbering here seems to relate to MOUSE Rho guanine nucleotide exchange factor (GEF) 7 sequence NM_017402.3.

Pix(S560)AP).

1. AHTLHPFFQ1 SGSQISSOTVA SF1PSQILFPF TAHVTSVA SAGATFSFQ RSQENEYTL
2. LAMSLQISOT PGHAAEQOQ QOOQQOOQ QQOOQQQO QQOOQQQO QQOOQQQO QQOOQQQO
3. 241 PAQONQYVHI HSSHQNTGRT ASPAAPVUl HPHQTMIPHT LLGSPQNVV MVYADGSHEF
4. 301 VPRFETKAKAE SRLQQOAIQA KEVLNGEMK SRVYQPSA DLSLGKAGVG SVPHYVESHR
5. 361 VVHPSYDDSY SSRSDFVSRA SVMLPNSNT FAAPLPQOSQ THREASPSVT NDKGLHGLK
6. 421 PGRHSLALSP HTVIQHTSHA SEPLFLVPGA TAFTAQTPQ PIGVLGQQQ AITYASLQF
7. 481 HLVPQOTQPL LPVFQSTME ASAGAAPTIS SSRPAAPVPH TPTVTAPKL NENPBAPLYT
8. 541 QAAPAYPYVQ HIQLPQVQV AASAPAPIPT FYPFMKSSG QALENGLEK EDLKTEDFDQ
9. 601 SAEISDMDLK DSSTVERIED HSHGPVAVIQ FAVGHEQRA SVEVLVYPE FVPFQQGNSSC
10. 661 CPERTSQLFD LPSRKLSDVG CVDSLTQNLN KNGSVKRGQP VPASDVKLN SKADGGLSR
11. 721 HRYAEGENV NSQQAMSLNE NGELKFFKEM GLPAFLFTK IEPSKFAAAR KRGVNAFESR
12. 781 KILESTDEDEP LTLPPKLGPL QVFKCIEGR SWQG

Notes

βPix(S316A, T326A). (Mutating Ser560 has no effect on 14-3-3 binding, RKE(S560)AP).

1. PolyQ mutant in spinocerebellar ataxia 1. (Swissprot = P54253 )

© 2010 The Author(s)
which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.

© 2010 The Author(s)

© 2010 The Author(s)

Biochim Biophys Acta. 2001 Jun 11;1547(2):313

Yang H, Masters SC, Wang H, Fu H. The proapoptotic protein Bad requires binding to protein 14 Maslyar DJ, Aoki M, Vogt PK. The growth with serine 140

Masters SC, Yang H, Datta SR, Greenberg ME, Fu H. 14 140

apoptosis. Mol Cell Biol. 2003 Sep;23(18):6350

Protein phosphatase 2A dephosphorylation of phosphoserine 140

EGFR/MAPK and PI3K/Akt kinase pathways in PTEN 140

She QB, Solit DB, Ye Q, O’Reilly KE, Lobo J, Rosen N. The BAD protein integrates sur 140

sites on Bad and promote 14 140

3 protein binding. J Biol Chem. 2006 Jun 23;281(25):17321

Reversible membrane interaction of BAD requires two C 140

terminal lipid binding domains in conjunction with 14 140

3 binding to BAD 140

binding modulate 14-3-3 interaction with spliceing factors. PLoS One. 2009 Dec 23;4(12):e8372.

Human BAD (Swissprot = Q72934)

1 MFQIPEFESP EQEESASSAR GLGPSAGDDG FGSQGHHRQ APGLMDWASH QDQETSSSSHH 61 HGAGAVEIR SRSHP2ZAPGT EDEGMEGEP SFPRGRSR A PPNLAAVQRY GRELHRMSEDE 121 FVDSSFKGCLP FRRSQTATGQ MQQSSWTRV FQSQWDRNLG RGSSAPSQ

>gi|17371773|sp|Q92934.3|BAD_HUMAN RecName: Full=Bcl2 antagon 2

ataxin-3 Integrates prosurvival signals mediated by the AKT and MAPK pathways in ZNF198 140

3 binding reduces interactions with Bcl-2 & Bcl-xL. The 14-3-3 binding sites are commonly numbered as Ser112 and Ser116 according to the murine BAD (Swissprot = Q61337), which correspond to Ser75 and Ser99 in the human BAD (Q72934). Murine BAD is longer than human BAD.

References to 14-3-3 binding to BAD

Zha J, Harada H, Yang E, Jockel J, Korsmeyer SJ. Serine phosphorylation of death agonist BAD in response to 14-3-3 thereby preventing its mitochondrial translocation to induce apoptosis. The 14-3-3-binding sites that can phosphorylated by a number of protein kinases, including PKB and PAK, 14-3-3 binding reduces interactions with Bcl-2 & Bcl-xL. The 14-3-3 binding sites are commonly numbered as Ser112 and Ser116 according to the murine BAD (Swissprot = Q61337), which correspond to Ser75 and Ser99 in the human BAD (Q72934). Murine BAD is longer than human BAD.

References to 14-3-3 binding to BAD

Zha J, Harada H, Yang E, Jockel J, Korsmeyer SJ. Serine phosphorylation of death agonist BAD in response to 14-3-3 thereby preventing its mitochondrial translocation to induce apoptosis. The 14-3-3-binding sites that can phosphorylated by a number of protein kinases, including PKB and PAK, 14-3-3 binding reduces interactions with Bcl-2 & Bcl-xL. The 14-3-3 binding sites are commonly numbered as Ser112 and Ser116 according to the murine BAD (Swissprot = Q61337), which correspond to Ser75 and Ser99 in the human BAD (Q72934). Murine BAD is longer than human BAD.

References to 14-3-3 binding to BAD

Zha J, Harada H, Yang E, Jockel J, Korsmeyer SJ. Serine phosphorylation of death agonist BAD in response to 14-3-3 thereby preventing its mitochondrial translocation to induce apoptosis. The 14-3-3-binding sites that can phosphorylated by a number of protein kinases, including PKB and PAK, 14-3-3 binding reduces interactions with Bcl-2 & Bcl-xL. The 14-3-3 binding sites are commonly numbered as Ser112 and Ser116 according to the murine BAD (Swissprot = Q61337), which correspond to Ser75 and Ser99 in the human BAD (Q72934). Murine BAD is longer than human BAD.
phosphatase 2A activates the proapoptotic function of BAD in interleukin-3 dependent lymphoid cells by a mechanism requiring 14-3-3 dissociation. Blood. 2001 Mar 1;97(5):1289-97.

Lizcano JM, Morrice N, Cohen P. Regulation of BAD by CAMP-dependent protein kinase is mediated via phosphorylation of a novel site, Ser155. Biochem J. 2000 Jul 15;349(Pt 2):547-57.

Tan Y, Demeter MR, Ruan H, Comb MJ. BAD Ser-155 phosphorylation regulates BAD/Bcl-XL interaction and cell survival. J Biol Chem. 2000 Aug 18;275(33):25865-9.

Fang X, Yu S, Eder A, Mao M, Bast RC Jr, Boyd D, Mills GB. Regulation of BAD phosphorylation at serine 112 by the Ras-mitogen-activated protein kinase pathway. Oncogene. 1999 Nov 19;18(48):6635-40.

Tan Y, Ruan H, Demeter MR, Comb MJ. p90(RSK3) blocks bad-mediated cell death via a protein kinase C-dependent pathway. J Biol Chem. 1999 Dec 3;274(49):38459-67.

**Human BRAF2** (also known as IRSp53) Brain-specific angiogenesis inhibitor 1-associated protein 2 (Swissprot = Q9UQB8)

1 MSLSRSENEH RLENYVKTI MEQNPFLRNI FIAKMKYNEK ALAGVYAAK GYPDALVMGK
61 ELAESGGSK ELGDVLQFMA EVRPIQOQMLEELKSNFHE LTLQEQKVRV LDLRLSALAL
121 KRYQEQRGS GDALKRQCAE LLKLRKQSQ SNKPRQYSDK ELQIDAISSN KQSELLEYNVS
181 DQGYTAL8EE RRRPFLVEK CVCAVKNSAAA YVSHPKSHEL KLRELQWQAC AOPSKRFPERA
241 VQLMOPQRASN GATLPSALSA SKSNLISVPDG IGPAKLPVLP PELAPFVGRM QASESTPIMN
301 GTVPFGDGED SWAPDRAAQP FKLSPFQPSQ SKLSDSSYNL PVLRKSTVTPK NYASSETNKR
361 LPRSSSMGAG LERNHGRMRV AIFSHAAGDO STLLSFREGD LITLVRPEAR DGWYSEGER
421 TKMRRWFPSFS YRTVLINSGS DRLHSQQO KSSSSTGNLD KDQALAIFFPD YGAAASAPFA
481 QTASFGQKSPR YSYPVFAPQ SDLYGQASM SMFNPWAVHG KPTYTNQVR DSACSGEPRGE
541 HGDGSAPTLA GR

**Notes**

MRhR5p(S87)LISR, said to be phosphorylated by Akt/PKB, but not conventional Akt/PKB site.

**References to 14-3-3 binding to BRAF2 (IRSp53)**

Rosenberg SM, Lee YF, Ng E, Geiger E, Manser E. Regulation of IRSp53-dependent filopodial dynamics by antagonism between 14-3-3 binding and SH3-mediated localization. Mol Cell Biol. 2009 Jan 23. [Epub ahead of print]

**Human BRAF1 (BRAF) (Swissprot = P15056)**

1 MAALSSGGGG GAEPQQLFLNF GDEMEGAAG AGAAASAD PAIEPEVVNI KQMIKLQEGH
61 IEALLDXXFFG ERRNPSTYLG EAYEYTSDLK ALQQREQLLL ESLGNTDFDS VSASSAMTDVT
121 TSSSSSSSLV LVQHNPNSQD PTDVPA1RNP SDOQP1VPRP LNPKWQVTPD ARGCCVTRDS
181 LKALCMRMGL IFECCAVYRI GQOGKEKPFQ JDGDTLWGTGE ELHVELENVL PLTHNFVRK
241 TFFTLADFCD CRKLLQFGRG CTQCGYKFHQ RCSTEVPICM VNYQDQLLDF VSFKFEEHIPI
301 PQEASAILAE ALTSSSSSPS PASDISIPQ1 LTSPSPSKSI PPQIPSRPAP DDHArkRFGQQ
361 DDSSTAPNVH INTIEYNNID DLRDIQEGFR DGSTGSLGA TPSAFSLPGSL TWKNALQKSP
421 GQGRGTDHMR SSSHERNHMT LGPSRSDQDN EIPQDGIQTV QGSSGSGFST VQKGDDWNVG
481 AVKMLNVTAP TPQOLQAFKN EVGVLKRTHR VNILLYMGS TKPQAIQTV QWCEGSSLYH
541 LHIITKFEKM IKLIDIARQI3 MKDYLMXH AI3IRHDKSN NIFLHEDTLY KIFGDOCALT
601 KSRQSSQHSS EQSSLQVFA DF VQAI3RQMK NPYSFDQQSP AFVIGYVIELM TDQQFYSIIN
661 NRQDDIFNPV ROYLSLDSK VRSNFCPRM RIAMCELEKCR ARDERLFPFQ3 LSAILLELLARS
721 LPK1HRSASPE PLINRGQVLP EDSLYACAS PRTTFQAGGY GAFVPH

**Notes**

MRhR5p(S87)LISR, said to be phosphorylated by Akt/PKB, but not conventional Akt/PKB site.

**References to 14-3-3 binding to BRAF1**

Qi XJ, Wildey GM, Howe PH. Evidence that Ser87 of BimEL is phosphorylated by Akt and regulates BimEL apoptotic function. J Biol Chem. 2006 Jan 13;281(2):813-8.

**Human Braf1 (BRAF)**

See references for Araf1 and Craf.

**Human Cabin1** 
(Calcineurin-binding protein cabin-1) (Q9Y6J0)

1 MRIASONAS STIEDEHBES FSXKSTQXRE AQEEAFAF YHKALQKQD FEESEAYAH
61 ELAKEAGILVE AVSSESDKEG LKRPILGLK STYMLAQOA AQRDGAQTSN EFYELVMLD
References to 14

KLKSAILSAQSAANVRKESLCQPALEVLETSSQESSLESETDEDDDYMDI

SKAPSSGSAQPPEGHPGKPEPSRAKSRPLPNMPKLVIPSAATKFPPEITVTPPTPTLLSPKGSISEETK

EPRHSPQVKMAPTSSPAEPHCWPAEAALGTGAEPTCSQEGKLRPEPRRDGEAQEAASETQPLSSPPTAAS

DAHTKPRPALAAATTIITCPPSASASTLDQSKDPGPPRPHREPATPSMASLGPEGEELARVAEGTSFPPQ

LIKQVDEEAALEQAVKFCQVHLGAAA

APAPATTTGTRAGGHPEEPLSRSLSRKRKLLEDTESGKTLLLDAYRVWQQGQKGVAYDLGR VERIMSETYM

ESPRAGPTEPMDTVSEATVCHSDLERTPPLLPGRPARDRGPESRPTELSLEELISARQQPTPLTPAQPAP

LPGARMTTDVSHKASPEDGEGLPQPFKKPLADSGGPGGPEVGKVLGHPRVRAMDGADSSGKHRRVSSLHSTPSFLNPILLCNCNHKIKMMASLICMELDQWLQLTLL
GRSASSVFRNCMPGVRNQGFRPFPPPOTCLCDLQLQLQFSAQQLFLEDEDFRLWRYVRVYVLKFLARLQGO
MEQAILENYDCITEMGQTSTAQTVQEAEGARRDIVIRLPNLHINDSVSLEELMDKNSLQCSRLEQLRLY
EAGYDKAVHVRLLRPCLTSGDFDRAKHELLMTSTIPFAPQLLLQDSSLLKRDYQFESCDSVDAEQUOV
MVQGAVVQAVYTLQGLRSSVSSLQAGATGKDLQGATEERGKNEESLTESTEGFRAAEGVQKPAAETPASACIPGKP
AGAERRDIVIRLPNLHNSVVSLEEIDKNLKRQASLISDQKRPTEKHEPVQVQMEGRRDSMLETAKHC
FTSASAECDEEDEEHHMLYMGKVKAEQPPQTVYLYHGYHAEARYPKKHYYNHPMLEMA
LEVFRYHLASHLLKLKPDSQGAVELVNPMEKAAEFGFARGEEKTNKASEKKAELDVDSHSSGALT
QGSAPPSSIRGTPPTSPPTYPADTDYVKCKKHFQQTADFPDRDQSTDAAVSSDQQSFNEQPTNLI
PVILSSQAGATGKDLQGATEERGKNEESLTESTEGFRAAEGVQKPAAETPASACIPGKP

References to 14-3 binding to Cabin1
Pan F, Means AR, Liu JO. Calmodulin-dependent protein kinase IV regulates nuclear export of Cabin1 during T-cell activation. EMBO J. 2005 Jun 15;24(12):2104-13.
Choi SJ, Park SY, Han TH. 14-3-3tau associates with and activates the MEF2D transcription factor during muscle dependent protein kinase IV regulation.

Notes
(RA)Gp(S172)P Cabin1 is a transcriptional corepressor for myocyte enhancer factor 2
Human Cbl
E3 ubiquitin-protein ligase CBL (swissprot – P22681)

1. MAGNKVSSAGGGGSSGSGSGGLLMKDAFQFPHHNNHHSHPFGVDVKMKVCKWMVKLMKVRVLQNNFLKANSSPFYRQLPPYYRQLRNYRLTYYERMEETGSLNENEYFV;MENLMLERTKQTSLFKEGKREMYEEEFSQRNRNLTKLSIFSHLAEELGKPFSSFLQGD3RTFRAADAEWEWAERFAKGETKVRNPFSRQKALH;
2. 1P35;162(12):7095
3. Liu YC, Liu Y, Elly C, Yoshida H, Lipkowitz S, Altman A. Serine phosphorylation of Cbl induced by phorbol ester enhances its association with Cbl in T cells. J Biol Chem. 1996 Jun 14;271(24):14591-5.
4. Melander F, Andersson T, Dib K. Engagement of beta2 integrins recruits 14-3-3 proteins to Cbl and c-Src in human neutrophils. Biochem Biophys Res Commun. 2004 May 14;317(4):1000-5.
5. Subramanian RR, Masters SC, Zhang H, Fu H. Functional conservation of 14-3-3 proteins and cytoskeletal components. J Biol Chem. 1997 Apr 11;272(15):9979-86.
6. Liu YC, Elly C, Yoshida H, Bonnefoy-Berard N, Altman A. Activation-modulated association of 14-3-3 proteins with Cbl in T cells. J Biol Chem. 1996 Jun 14;271(24):14591-5.
7. Cbl; AltName: Full=Signal transduction protein CBL; AltName: Full=Proto-oncogene c-CBL; AltName: Full=Castric B-lineage lymphoma proto-oncogene 5.
8. CBL; AltName: Full=RING finger protein 55
9. CBL; AltName: Full=E3 ubiquitin binding protein (Swissprot = Q9Y3M2)
10. CBL; AltName: Full=Casitas B-lineage lymphoma proto-oncogene 1.

Notes
Mutation of Cbl serine residues 619, 623, 639, and 642 abolished the interaction between Cbl and 14-3-3 (Pedraza-Alva et al 2001). RHg(s619);LPF(s623), RLG(pS639)TF(pS642), most likely NRH(S619)LP and RLG(pS639)TF, but not certain?

References to 14-3-3 binding to Cbl
Liu YC, Elly C, Yoshida H, Bonnefoy-Berard N, Altman A. Activation-modulated association of 14-3-3 proteins with Cbl in T cells. J Biol Chem. 1996 Jun 14;271(24):14591-5.

Pedraza-Alva G, Sawadikosol S, Liu YC, Mierda LB, Cruz-Muñoz ME, Oceguera-Yañez F, Burakov SJ, Rosemberg Y. Regulation of cellular interactions by the co-receptor molecule CD43 in human T cells. J Biol Chem. 2001 Jan 5;276(1):729-37.

Chernock RD, Cherla RP, Ganju RK. SHP2 and cbl participate in alpha integrin-mediated signaling pathways. Blood. 2001 Feb 1;97(3):608-15.

Pedraza-Alva G, Sawadikosol S, Liu YC, Mierda LB, Cruz-Muñoz ME, Oceguera-Yañez F, Burakov SJ, Rosemberg Y. Regulation of cellular interactions by the co-receptor molecule CD43 in human T cells. J Biol Chem. 2001 Jan 5;276(1):729-37.

Liu Y, Liu YC, Moller N, Giampa L, Elly C, Doyle M, Altman A. Protein kinase C activation inhibits tyrosine phosphorylation of Cbl and its recruitment to Src homology 2 domain-containing proteins. J Immunol. 1999 Jun 15;162(12):7095-101.

Liu YC, Altman A. Cbl: complex formation and functional implications. Cell Signal. 1998 Jun;10(6):377-85.

Wang J, Zhang L, Liddington R, Fu H. Mutations in the hydrophobic surface of an amphipathic groove of 14-3-3 disrupt its interaction with Raf-1 kinase. J Biol Chem. 1998 Jun 26;273(26):16297-304.

Robertson H, Landon WY, Thien CB, Bowtell DD. A C-Cbl yeast two hybrid screen reveals interactions with 14-3-3 isoforms and cytoskeletal components. Biochem Biophys Res Commun. 1997 Nov 7;240(1):46-50.

Liu YC, Yu Y, Elly C, Yoshida H, Lipkovitz S, Altman A. Serine phosphorylation of Cbl induced by phorbol ester enhances its association with 14-3-3 proteins in T cells via a novel serine-rich-14-3-3 binding motif. J Biol Chem. 1997 Apr 11;272(15):9979-85.

Human CBV1 (Chibby – antagonist of β-catenin (ARPP-binding protein) (Swissprot = Q9Y3M2))

1. 1PFPQNTFSP KPPKFRKSS LNSLHLSDRS TRELVEGLG YEPTMNLADQ SLKFENGQW1
2. 1AETGVSGVD RREVQRLLRA RQQLEENNN LLKVQDLLD MLSESTAES LMEKDELIR
121 ISRRK

Notes
Chibby is a 15kDa protein evolutionarily conserved from fly to human. Cbl probably acts in concert with 14-3-3 proteins to facilitate nuclear export of beta-catenin, thereby antagonizing beta-catenin signaling. Said to be phosphorylated by Akt/PKB, but not a conventional site for this kinase.

*14-3-3 proteins specifically recognize serine 20 (RKSALS1) within the 14-3-3–binding motif of Chibby when

SITES NOT DEFINED, NOT INCLUDED IN WEBLOGO ANALYSIS.
phosphorylated by Akt kinase. Notably, 14-3-3 binding results in sequestration of Cby into the cytoplasm. Feng-Qian et al (2008).

References to 14-3-3 binding to Cibby
Takekmur A, Fischer V, Li Q. Fine-tuning of nuclear-catenin by Cibby and 14-3-3. Cell Cycle. 2009 Jan 15;8(2):210-3.

Feng-Qian Li, Adaboi Mofunanya, Kimberley Harris, and Ken-Ichi Takekmur. Cibby cooperates with 14-3-3 to regulate β-catenin subcellular distribution and signaling activity. J Cell Biol. 2008 June 30; 181(7): 1141–1154.

Li Q, Mofunanya A, Fischer V, Hall J, Takekmur KL. Nuclear-Cytoplasmic Shuttling of Cibby Controls (β)-Catenin Signaling. Mol Biol Cell. 2009 Nov 25. [Epub ahead of print]

Human Cdc25A M-phase inducer phosphatase 1 (Swissprot = P30304)

1 MELGSEPFRH BRLFLACSEPAS QSPQVKALV FASQAAGGLS PVTLTVTMD QLOGLGSDLYE
2 QPFLREVNNNS LQRMGSESST DSGCFLDSPG PLDSKENLNPNMRHLISPQ KCGLSPALK
12 RHSHSDLHDD IFQPLIDPEN KNEAEEFPEK PPVRVSRGCGL HSHQLQEKGKD LFTQORQAP
181 ARMLSNRSEN SSEEQPNSFPL FTTPSVPVTAT LSGDEGGFVD LDLGENKLN EETPSCMASL
241 WTPALVRVMT LNLDRNKLFD SPSCSLSSRT SVLRKPRERQ EEEFPSTGRR RKSMGSAQPK
301 WTPALVRVMT LAPEPQSPR TLPAGKIESPP SPKGTINEL DNREPLDGIQ GSGLYFVTRT AGEMQCKLKI
361 SPEIMASVLN GKFANLIKEW VIIDCRYPYE YEGHJKMMLV NLMVEEVED PLLKFPVPT
421 DKVRVVVFCHF CESSSERGR MCVRYSRDR LGNEYPKHLH PELYVLKKGYKEF KFMKCSQY
481 CEPPSPFMRH HEDFSDKLRK FRTSRWTAG EKSRMREYI LKLR

Notes
Phosphorylated Ser177-Cdc25A that is specific for 14.3.3 binding References to 14-3-3 binding to Cdc25A
Maldener S, Rosner M, Krieger S, Giessrigl B, Gridling M, Vo TP, Leisser C, Lackner A, Raab I, Grusch M, Anderson HA, Bergstralh DT, Kawamura T, Blauvelt A, Roche PA. Phosphorylation of the invariant chain by degradation of Cdc25A which depends on p38. Cell. 2002 Nov 15;111(4):577

O'Kelly I, Butler MH, Zilberberg N, Goldstein SA. Forward transport. 14

References to 14-3-3 binding to Cdc25A

14.3.3 binding overcomes retention in endoplasmic reticulum by dibasic signals. Cell. 2002 Nov 15;111(4):577-88.

Anderson HA, Bergstralh DT, Kawamura T, Blauvelt A, Roche PA. Phosphorylation of the invariant chain by protein kinase C regulates MHC II trafficking to antigen-processing compartments. J Immunol. 1999 Nov 15;163(10):5435-43.

Faul, C., S. Huttelmaier, J. Oh, V. Hachet, R. H. Singer, and P. Mundel. 2005. Promotion of importin α-mediated nuclear import by the phosphorylation-mediated binding of cargo protein to 14-3-3. J. Cell Biol. 169:415-424.

Human Cdc25B M-phase inducer phosphatase 2 (Swissprot = P30305)

1 MEVLQPENPPHV BAAGALLYYV GLISQDGAGL GALLSWRHFL GALLSWRHFL GALLSWRHFL GALLSWRHFL GALLSWRHFL GALLSWRHFL
2 61 DLAGLGGSETF KSVQVTLLFR SRRSLTHLSL SRRASEISLS SERRSSDAG LCMDSPSMMD
121 PMAEQTFEQ AIQAASRIRI NEFQAIRFPQ SMVQRLGHS PVLRNITSQ APGDGRKSEA
181 GSGAASGSGS KRENGDVGF MPPKTHPSHS TALAADWARQ REAPARQFS PAPDLKLSLPD
241 KRMEEVSLP LALGRFSLTP AEQVTEEGQ FDVLDISLDD KDDAVFGSME SLISAPLVLK
301 LEKEREKDLV MYSCQPELFR RPSCPCSTVR SFPLKRLRQP DQPTQVQNKR RRSTTPPEQ
361 QAEABEPKARV LRRSKSCLHDE TENLLOSDHR ELIGDYSKAQ LLQTVQDKGQ DLKYSPTM
421 VALLTQGFSN IVDKVFVIVD FYPVEEYGCH IKTAVNLPE RDAESFLKLK PIAFCSLDKR
481 VILIFHCEFSS CRMCRRSFR CRMERADVND YPSLFPYEMY LGKKGYKEF PQHNPQCEQF
541 DMRPHNHEAF KDEKLYFRLK TRSNWAGERS RELCSRLQQG

Notes
Phosphorylated Ser177-Cdc25B that is specific for 14.3.3 binding References to 14-3-3 binding to Cdc25B
Maldener S, Rosner M, Krieger S, Giessrigl B, Gridling M, Vo TP, Leisser C, Lackner A, Raab I, Grusch M, Anderson HA, Bergstralh DT, Kawamura T, Blauvelt A, Roche PA. Phosphorylation of the invariant chain by degradation of Cdc25B which depends on p38AMAPK, Chk2 and 14.3.3. Hum Mol Genet. 2009 Jun 1;18(11):1990-2000.

Conklin DS, Galaktionov K, Beach D. 14-3-3 proteins associate with cdc25 phosphatases. Proc Natl Acad Sci U S A. 1995 Aug 15;92(17):7892-9.
Notes to References 14-3-3 binding to Cdc25B

References to 14-3-3 protein binding. Oncogene. 2001 Apr 5;20(15):1839

Human Cdc25C M-phase inducer phosphate 3 (Swissprot = P30307)

Phosphorylated by CHK1 on Ser-216. This phosphorylation creates a binding site for 14-3-3 protein and inhibits the phosphatase.

References to 14-3-3 binding to Cdc25C

Telles E, Hosing AS, Kundu ST, Venkatraman P, Dalal SN. A novel pocket in 14-3-3zeta controls the cytoplasmic localization of Cdc25B: binding site preferences of 14-3-3 subtypes and the subcellular localization of Cdc25C. J Cell Sci. 2004 Jun 15;117(Pt 14):3011-20.

Bulavin DV, Higashimoto Y, Demidenko ZN, Demidenko AN, Meek S, Zhao H, Moody SA, Appella E, Fornace AJ Jr. Initiation of DNA damage response to ionizing radiation requires p38 kinase. Mol Cell. 2005 Dec 16;20(6):819-31.

Graves PR, Lovly CM, Uy GL, Piwnica-Worms H. Localization of human Cdc25C is regulated both by nuclear export and 14-3-3 protein binding. Oncogene. 2001 Apr 5;20(15):1839.
Human CDKN1B (p27Kip1)
Cyclin-dependent kinase inhibitor 1B (Swissprot = P46527)

| Accession | Name          | Description |
|-----------|---------------|-------------|
| P46527.1  | CDKN1B_HUMAN  | Cyclin-dependent kinase inhibitor p27; AltName: Full=Cyclin-dependent kinase inhibitor 1B; AltName: p27Kip1 |

**Notes**
RHRPs 11/16/07/HS = Ser11 in P2127.

**References to p27Kip1**

1. Fujita N, Sato S, Tsurow T. Phosphorylation of p27Kip1 at threonine 198 by p90 ribosomal protein S6 kinase (p90rsk) controls mitotic translation to facilitate cytokinesis. Nature. 2007 Mar 15;446(7133):32-9.

2. Fujita N, Sato S, Tsuruo T. Phosphorylation of p27Kip1 at threonine 198 by p90 ribosomal protein S6 kinase (p90rsk) controls mitotic translation to facilitate cytokinesis. Nature. 2007 Mar 15;446(7133):32-9.

**Human CENPJ (Centromere protein J)**

**References to CENPJ**

1. CENPJ (Centromere protein J) CPAP (Centrosomal Protein 4.1-Associated Protein) (Swissprot = Q9HCC7)

| Accession | Name          | Description |
|-----------|---------------|-------------|
| P46527.1  | CDKN1B_HUMAN  | Cyclin-dependent kinase inhibitor p27; AltName: Full=Cyclin-dependent kinase inhibitor 1B; AltName: p27Kip1 |

**Notes**
RHRPs 11/16/07/HS = Ser11 in P2127.

**References to CENPJ**

1. CENPJ (Centromere protein J) CPAP (Centrosomal Protein 4.1-Associated Protein) (Swissprot = Q9HCC7)
The author(s) has/have assigned this copyright to the publisher(s).
>gi|167009135|sp|Q5ETK2.1|CRTC2_HUMAN RecName: Full=Transducer of CREB; AltName: Full=Tran
der of regulat

e response element-binding protein 2; Short=TORC2; Short=Transducer of CREB

protein 2

MATS2ANGPSATASASNPRFRSEKATLQQRQAEETAAEFPVFMDGSTRLQALKLYTRSHYYYY
LPPNQVGGSSLAGEPLPILPSLDSSRTSRHGLHEVRQDFPKMVPLFRLKVRHTIDDSPSYYAVLSPPE
SSWTMRATWKGNNFAPEQLRFLSRALNRTSSDAGALTVSNNPSPQTYQFFPSILSRPGRGGLD
MMDKPKVPFAIEENLLDKKLKFDAKLKLLSSRPPPSCVPGVFINIPFSPDANVPVLPMANTGGLPLDL
THLHFPPPLFTLDPEYASPALSQGNSTLNSTTLMTHTLGRGMPLGDYPADGLPSHLPSHLSQSI
LLNQLASLSSPPQOLQSHSHPSSLASLAPLSSSSSSSTSSPVLGAFSPYAST
PGASPHHRVVLPSLGLLAGPADADARSSQOLLQKQPSMTGPSLSTSGTPQVPLDSKLSQDRKLPPYY
PSSVLQLPHTMQLPQLSQSLQSSCVQGSSQQGPQGSHYTPYTFPPGSQGNQOSYHRPMSDFNLNL
QFQMSQFASLSAVDPFGQSEQGFLGEGMPPGQDQHFTNHNQTLHCRRSHGQPGN11TQDSGSGF
SKE IAIAALGAPVGEAALGEGLEALDEMEPLFEGLEALNLSLDCAPLPDDFAEVESFRSRLQ

All papers cite phosphoSer71 as a 14-3-3 binding site, but differ in whether phosphoSer71 (Dentin et al 2008), phosphoSer358 and/or phosphoSer275 (Jansson et al 2008) provides a second 14-3-3 binding site. AMP-activated protein kinase (AMPK) and the AMP family members salicyl-inducible kinase (SIK)1 and SIK2 can phosphorylate CRTC2 at Ser 171 and thereby inhibit CRTC2 activity (Koo et al, 2005; Dentin et al, 2007). In resting cells, CRTC2 is sequestered in the cytoplasm by 14-3-3 proteins through phosphorylation at Ser70 and Ser171 by members of the AMPK family (Dentin et al, 2006). Consistent with the proposed role of O-glycosylation in blocking protein phosphorylation, alanine mutations at Ser70 and Ser171 disrupted the CRTC2:14-3-3 interaction and promoted localization of these mutant CRTC2 proteins to the nucleus (Dentin et al 2008).

TORC2 the transducer of regulated CREB protein 2 (TORC2) is a cAMP responsive coactivator that, in concert with LKB1 and AMPK, controls glucose homeostasis in the liver. Under fasting conditions, cytoplasmic TORC2 is translocated into the nucleus where it binds to CREB and stimulates gluconeogenesis. Re-feeding the liver with insulin response inhibits gluconeogenic gene transport to the nucleus (Dentin et al 2008).

TORC2 the transducer of regulated CREB protein 2 (TORC2) is a cAMP responsive coactivator that, in concert with LKB1 and AMPK, controls glucose homeostasis in the liver. Under fasting conditions, cytoplasmic TORC2 is translocated into the nucleus where it binds to CREB and stimulates gluconeogenesis. Re-feeding the liver with insulin response inhibits gluconeogenic gene transport to the nucleus (Dentin et al 2008).

References to 14-3-3 binding to CRTC2

Screaton RA, Conkright MD, Katoh Y, Best JL, Canettieri S, Guzman E, Niessen S, Yates JR 3rd, Balthasar N. A role for the CREB coactivator CRTC2 in the regulation of glucose homeostasis. J Biol Chem. 2004 Oct 1;279(33):33833-40. Epub 2004 Aug 16. PubMed.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&dopt=Abstract&list_uids=15380856

Screaton RA, Conkright MD, Katoh Y, Best JL, Canettieri S, Guzman E, Niessen S, Yates JR 3rd, Balthasar N. A role for the CREB coactivator CRTC2 in the regulation of glucose homeostasis. J Biol Chem. 2004 Oct 1;279(33):33833-40. Epub 2004 Aug 16. PubMed.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&dopt=Abstract&list_uids=15380856

Screaton RA, Balthasar N. A role for the CREB coactivator CRTC2 in the regulation of glucose homeostasis. J Biol Chem. 2004 Oct 1;279(33):33833-40. Epub 2004 Aug 16. PubMed.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&dopt=Abstract&list_uids=15380856

Screaton RA, Balthasar N. A role for the CREB coactivator CRTC2 in the regulation of glucose homeostasis. J Biol Chem. 2004 Oct 1;279(33):33833-40. Epub 2004 Aug 16. PubMed.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&dopt=Abstract&list_uids=15380856
which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.

The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial Licence (http://creativecommons.org/licenses/by-nc/2.5/)

© 2010 The Author(s)

Notes

PHER5RgLLP (Ser610). Defects in CSF2RB are a cause of congenital pulmonary alveolar proteinosis (PAP) [MIM:265210]. PAP is an autosomal recessive fatal respiratory disease.

References to 14-3-3 binding to β-Chain of GM-CSF/IL-3/IL-5 receptors

Stomski FC, Dottore M, Winnall W, Guthridge MA, Woodcock J, Bagley CJ, Thomas DT, Andrews RK, Berndt MC, Lopez AF. Identification of a 14-3-3 binding sequence in the common β chain of the granulocyte-macrophage colony-stimulating factor (GM-CSF), interleukin-3 (IL-3), and IL-5 receptors that is serine-phosphorylated by GM-CSF. Blood. 1999 Sep 15;94(6):1933-42.

Human CTNNB1 Catenin beta-1 (Beta-catenin) (Swissprot = P35222)

1 MATQADQELM DMAMEPDRKA AVSHWWQQQSYLDQGISHGATTAPASLGSKGNPEEVDVTSQVLWEYQEGFSQFSTQEOVATDCQYAMTRAQVRGAAMMETDQGQVPCSTQADAHMTNVNRQAQEMCPQMLHKNVLNYQCDDEALATREIAFLKLMDNDEQQVKNKAYQMLKSEQASHAIRMSPQMSVALIERTMNQVDRCTACTAGTJHNLSSHREGLIAIFSQGIPALVKMLGSPDSVYFLAYITTLNLLLHQEGAKMAVRLAGLQKVMLAVNKVTFLTTCDCQLIAYNGQESKILLASQGCPQVNLMTRYTTEYKELLLTTSRLVSKLSVSNSNPFAIEAVAGMQLGLHLTDPSQVLQCNLTLRLNSADAATRQGQMEGLGTLGLVQLDSQNDIVNTCAANDQQCTNYVNXNMVKQALPQVQGIGAIJVRTEFIALGERDDIEPTEFALCAHGLASHQQAEMAGAQNARLHYG6301 LQILAYNGQRNKQASEQNWANYSAEQNRMGQAGSTISNSHAQPFDFPDNLQNSSSHAKLPPQPKQGAVPQFVYIQFLKARLQQDYLSSIPWENPKRGQECV

Notes

AKT phosphorylates beta-catenin at Ser526 and enhances its interaction with 14-3-3zeta.

References to 14-3-3 binding to β CATENIN (Swissprot = P35222)

Fang D, Hawke D, Zheng Y, Xia Y, Meisenholder J, Nika H, Mills GB, Kobayashi R, Hunter T, Lu Z. Phosphorylation of beta-catenin by AKT promotes beta-catenin transcriptional activity. J Biol Chem. 2007 Apr 13;282(15):11221-9.

Takemaru K, Fischer V, Li FQ. Fine-tuning of nuclear beta-catenin transcriptional activity. J Biol Chem. 2006 Mar 2;281(10):6141-5.

Li FQ, Mofunanya A, Harris K, Takemaru K. Chibby cooperates with 14-3-3 to regulate beta-catenin subcellular distribution and signaling activity. J Cell Bio. 2008 June 30; 181(7): 1141-52.

Human Cx43 connexin43 (Swissprot = P17302)

1 MGDSALGKLDLVQAYSTA GKGWLSVLIFRILLGSTAVEWAGDEQS AFRCTNQQG6301 CENVCYKDSF PISHVRFWVL QIQFVSPVTL LYLAVHFY VKEEKLKNKE EELKVAQTGD 121 VNVMDLHIKQ EIKKFKGYIE EKHKVVRMRG LRTYIISIL FSKIFIEVAFL LIQWYNIYFGS 181 LSATVTCRDR CPHQVRQDCF SRPTEKTI IFMULVSLVS LALINIEF YVFFGVKVRDV 241 KSGDPSHAT GSAILPAKCQ SQSKAYXNG CSTPATLPS MSPQGGYUG GDRNNSCNRR 301 YNKQAEQWN ANYSAERQNI QQSTGILSNS HAQFDPPFDQ NQNSKSLAG HELQPLAIVQDRPSRSSRASSRPRDDLE1

Notes

Hexamers of connexin-43 form connexons, which form gap junctions. 14-3-3s are reported to bind to Akt-phosphorylated Ser373 in the cytoplasmic tail of Cx43 on Ser373, and GST-14-3-3 binds to Cx43 phosphorylated endogenously in EGF-treated cells (but Ser373 is not a conventional PKB consensus site).
Human DAB2IP: Disabled homolog 2-interacting protein (AIPI) ASK1-interacting protein (SwissProt = Q5VWQ8)

>gi|74753036|sp|Q9NX09.1|DDT4_HUMAN RecName: Full=DNA damage response 1; Short=REDD transcript 4 protein; AltName: Full=Prot

**Human DDBT4** DNA-damage-inducible transcript 4 protein (Redd1) (Swissprot = Q9NX09)

>gi|74753036|sp|Q9NX09.1|DDT4_HUMAN RecName: Full=DNA-damage-inducible transcript 4 protein; AltName: Full=Protein regulated in development and DNA damage response 1; Short=REDD1; AltName: Full=HIP-1 responsive protein

**References to 14-3-3 binding to connexin43**

Majoul IV, Onichtchouk D, Butkevich E, Wenzel D, Chailakhyan LM, Duden R. Limiting transport steps and novel interactions of Connexin43 along the secretory pathway. Histochem Cell Biol. 2009 Jul 22.

Park DJ, Wallick CJ, Martyn KD, Lau AF, Jin C, Wern-Cramer BJ. Akt phosphorylates Connexin43 on Ser733, a "mode binding site" for 14-3-3. Cell Commun Adhes. 2007 Sep-Oct;14(5):211-26.

Park DJ, Freitas TA, Wallick CJ, Guyette CV, Wern-Cramer BJ. Molecular dynamics and in vitro analysis of Connexin43: A new 14-3-3 mode-1 interacting protein. Protein Sci. 2006 Oct;15(10):2344-55.

**References to 14-3-3 binding to AIPI**

Zhang R, He X, Liu W, Lu M, Hsieh JT, Min W. AIP1 mediates TNF-induced desumoylation and cytoplasmic translocation of homeodomain-interacting protein kinase 1 are critical for apoptosis signal-regulating kinase 1-dependent apoptosis. J Biol Chem. 2005 Apr 15;280(15):15601-7.
Human DDT4L DNA-damage-inducible transcript 4-like protein (Redd2) (Swissprot = Q96D03)
1 MVATGSLSK NPASISELLDD CGYHPSLLS DFSDFYDVYP EPNLNIFIE ESTCNQLVMK
61 LENC5LSKQ TDLGCSKVLV PEKLRQIAQ DVRLSREP CGLRCCVMHH NLIEINNVCKK
121 LDFRCDSSV VPFTEELVTVF KQENCWSTSR DQFFFSRGRG SSFGRTLIL JSSGLRLLK
181 LSYSLITGTVI LSS
>gi|74731396|sp|Q69603.1|DDTL_HUMAN RecName: Full=DNA-damage-inducible transcript 4-like protein; AltName: Full=Protein regulated in development and DNA damage response 2; Short=DDTL; Short=DDT4L
1 MVATGSLSK NPASISELLDD CGYHPSLLS DFSDFYDVYP EPNLNIFIE ESTCNQLVMK
61 LENC5LSKQ TDLGCSKVLV PEKLRQIAQ DVRLSREP CGLRCCVMHH NLIEINNVCKK
121 LDFRCDSSV VPFTEELVTVF KQENCWSTSR DQFFFSRGRG SSFGRTLIL JSSGLRLLK
181 LSYSLITGTVI LSS

Notes
Motif scanning within this domain also supports Arg-X-X-Arg-Thr-X-Pro-binding site for 14-3-3 proteins that is conserved among mammalian orthologs of both REDD1 and the REDD1-related proteins. Of note, both Drosophila REDD1 orthologs harbor a variant of this motif with the serine residue at the +2 position relative to arginine (Arg-X-Ser-X-Arg-Thr-X-Pro).

References to REDD1 binding
DeYoung MP, Horak P, Sofer A, Sgroi D, Ellisen LW. Hypoxia regulates TSC1/2-mTOR signaling and tumor suppression through REDD1-mediated 14-3-3 shuttling. Genes Dev. 2008 Jan 15;22(2):239-51.

Human DYSK1A Dual-specificity tyrosine-phosphorylated and regulated kinase (Swissprot = Q13627)
1 MHGTGTGSAC KPSSVRALPS TFSFAAGLQQ AGQMPHSKQY SDRQPNISQFQVQALYSQD
61 Q1QQLTNPV MQDVMQLRQR MQFRDOPAT APLKXLDVL IKTYHWINEY VAKKREREQK
121 QCGDSSNHS HHFVSVMNDY DDDNYVQVX NGEKMAWRYE LSGYLGGSF DQVQVAYD
181 EQGWAVIIKII NKKKAFQQA IEVRLLEEM NKHDEMKYV IVLHRKRFM PNHLCLVFM
241 LSYNLILDR NTRNFPSVLN LTRKFAQQMC TALLLATFL LEIHSCHLKP ENLICNPRK
301 SAIKVFQDS CLSQCLQRIQ YISRFRYSP EYLMQGDYL AIDMWSLGC LVMHEWGEPL
361 FSANQEDVQM NKLVEQGLP FALHDQAPR KRFKEXLPDT GWNLKLTFRVR KGREYKFPOT
421 RKUINLGTQV TQGPDGBRAG ESGHVTADYL KFKDLILML DYFKTRQVQ RYALQNSPKK
481 KTADEGTNTS NSVQGSTUE TSSGSSSGG NSSENAGRAF TPDHQRSSHG
541 HFTAAQMDT CTHSIQVQRP QFAPFLWNSG TEAPQTVTVE THFQETFTTH VAPOQNNALHH
601 STTSSSSHHH HHHHHHHH QSQLGNRTRP RVNSPYTNS SNSQDEMVH SHHSMTSSLS
661 STTSSSSTSS TSNQKMYQAY QRFVANATL DFQOGANDM NLTVYSFNPQ ETQGIAHHTY
721 QSPNFQAPH YMTENGHTLMS QAQBREEEMP TGQCVQAPPSV ASS

>gi|3219996|sp|Q13627.2|DYSK1A_HUMAN RecName: Full=Human DYSK1A; AltName: Full=Dual specificity tyrosine-phosphorylated-regulated kinase 1A; AltName: Full=Protein kinase minibrain homolog; Short=MNHB; Short=MNBH; AltName: Full=HP56; AltName: Full=HP56-S
1 MHGTGTGSAC KPSSVRALPS TFSFAAGLQQ AGQMPHSKQY SDRQPNISQFQVQALYSQD
61 Q1QQLTNPV MQDVMQLRQR MQFRDOPAT APLKXLDVL IKTYHWINEY VAKKREREQK
121 QCGDSSNHS HHFVSVMNDY DDDNYVQVX NGEKMAWRYE LSGYLGGSF DQVQVAYD
181 EQGWAVIIKII NKKKAFQQA IEVRLLEEM NKHDEMKYV IVLHRKRFM PNHLCLVFM
241 LSYNLILDR NTRNFPSVLN LTRKFAQQMC TALLLATFL LEIHSCHLKP ENLICNPRK
301 SAIKVFQDS CLSQCLQRIQ YISRFRYSP EYLMQGDYL AIDMWSLGC LVMHEWGEPL
361 FSANQEDVQM NKLVEQGLP FALHDQAPR KRFKEXLPDT GWNLKLTFRVR KGREYKFPOT
421 RKUINLGTQV TQGPDGBRAG ESGHVTADYL KFKDLILML DYFKTRQVQ RYALQNSPKK
481 KTADEGTNTS NSVQGSTUE TSSGSSSGG NSSENAGRAF TPDHQRSSHG
541 HFTAAQMDT CTHSIQVQRP QFAPFLWNSG TEAPQTVTVE THFQETFTTH VAPOQNNALHH
601 STTSSSSHHH HHHHHHHH QSQLGNRTRP RVNSPYTNS SNSQDEMVH SHHSMTSSLS
661 STTSSSSTSS TSNQKMYQAY QRFVANATL DFQOGANDM NLTVYSFNPQ ETQGIAHHTY
721 QSPNFQAPH YMTENGHTLMS QAQBREEEMP TGQCVQAPPSV ASS

Notes
DYRK1A autophosphorylates on Ser-520 (RAR(Pro520)DP, in the PEST domain of the protein. We also show that phosphorylation of this residue, which we show is subjected to dynamic changes in vivo, mediates the interaction of DYRK1A with 14-3-3beta. A second 14-3-3 binding site is present within the N-terminal domain of the protein. In the absence of kinase activity via 14-3-3 binding, Mol Biol Cell. 2007 Apr;18(4):1167-78.

References to 14-3-3 binding to DYRK1A
Miyake M, Esser KA. REDD2 is enriched in skeletal muscle and inhibits mTOR signaling in response to leucine and stretch. Am J Physiol Cell Physiol. 2009 Mar;296(3):C583-

Human ELAVL1 (Swissprot = Q15717)
1 MN50HDEMA EDCGCG2GRT NLNLY1QPN MQDQELSLS SFSGEVSAK LIRDVQGHS
61 LGFVYVNVT AXDAERAIT NLGRLQSKT IKUVYRAPF ESVDKANLY SLGPRTMQK
121 DVEWENFSRFG RIINSPRQV QTTLGSGRVA FIPDKRSRA EEAITTFNWH KGPSGSEPTI
181 VKFAANPNQ KNFLVSLQGY HFRAGFRP VHQQARFRF SMPVDMHMSM LSQVNPQNA
241 SGQIEFNYLI YQDAEAGGIL NQFGPSFSSW THVVKRDOPN TRNCKGGFPY TMTHYEEAM
301 AIAEGLNYRL DQKLVQFPK TNSHK

Ser207 phosphorylated, but not the 14-3-3-binding site. THEREFORE NOT IN WEBLOGO ANALYSIS.
Ser202 phosphorylation occurred at the same time as 14-3-3 binding, but not functionally linked and ELAVL1 binds avidly to the AU-rich element in FOS and IL3/interleukin-3 mRNAs. In the case of the FOS AU-rich element, HUR binds to a core element of 27 nucleotides that contain AUUUA, AUUUU, and UUUUAU motifs. Interacts with ANP32A.

Here, we present evidence that HuR phosphorylation at S202 by the G2-phase kinase Cdk1 influences its subsequent subcellular distribution. In keeping with the prominently cytoplasmic location of the nonphosphorylatable point mutant HuR(S202A), phospho-HuR(S202) antibody. The enhanced cytoplasmic presence of unphosphorylated HuR was linked to its decreased association with 14-3-3 and to its heightened binding to target mRNAs.

References to 14-3-3 binding to PTPI51

Kim IH, Abdelmohsen K, Lam A, Pullmann R Jr, Yang X, Galban S, Srikanth S, Martindale JL, Brethew J, Shokat KM, Gorospe M. Nuclear HuR accumulation through phosphorylation by Cdk1. Genes Dev. 2008 Jul 1;22(13):1804-15

Gorospe M, Li L, Blethrow J, Stenzinger A, Kim HH. Cell and molecular biology of the novel protein 2; AltName: CD_antigen=CD332; Flags: Precursor

>gi|12008|sp|Q12571.2|ELAV_HUMAN RecName: Full=ELAV-like protein 1; AltName: Full=Hu-antigen R; Short=HuR

Human PTPIP51 (PTP51) Regulator of microtubule dynamics protein 3 (Protein tyrosine phosphatase-interacting protein 51) (Swissprot = Q96TC7)

>gi|174674302|sp|Q96TC7.2|RMD3_HUMAN RecName: Full=Regulator of microtubule dynamics protein 3; Short=RMD-3; AltName: Full=Protein FAM82A2; AltName: Full=Protein tyrosine phosphatase-interacting protein 51; AltName: Full=TCP5-interacting protein 51; AltName: Full=Cerebral protein 10

Human FAM82A2 (PTP51) Regulator of microtubule dynamics protein 3 (Protein tyrosine phosphatase-interacting protein 51) Only show pSer46 on WEBLOGO. Not sure whether Ser145 or 151 is the potential site. 2008). Proposed sites are 43RS(Q/S)(S46)-LP48, and either 14-6RER(pS149)DS151 or 148RSD(pS151)TG154. Proposed sites are 43RS(Q/S)(S46)-LP48, and either 14-6RER(pS149)DS151 or 148RSD(pS151)TG154.

References to 14-3-3 binding to PTPIP51

Yu C, Han W, Shi T, Lv B, He Q, Zhang Y, Li T, Zhang Y, Song Q, Wang L, Ma D. PTPIP51, a novel 14-3-3 binding, but not functionally linked and ELAVL1 binds avidly to the AU-rich element in FOS and IL3/interleukin-3 mRNAs. In the case of the FOS AU-rich element, HUR binds to a core element of 27 nucleotides that contain AUUUA, AUUUU, and UUUUAU motifs. Interacts with ANP32A.

Here, we present evidence that HuR phosphorylation at S202 by the G2-phase kinase Cdk1 influences its subsequent subcellular distribution. In keeping with the prominently cytoplasmic location of the nonphosphorylatable point mutant HuR(S202A), phospho-HuR(S202) antibody. The enhanced cytoplasmic presence of unphosphorylated HuR was linked to its decreased association with 14-3-3 and to its heightened binding to target mRNAs.

References to 14-3-3 binding to ELAVL1

Yu C, Han W, Shi T, Lv B, He Q, Zhang Y, Li T, Zhang Y, Song Q, Wang L, Ma D. PTPIP51, a novel 14-3-3 binding, but not functionally linked and ELAVL1 binds avidly to the AU-rich element in FOS and IL3/interleukin-3 mRNAs. In the case of the FOS AU-rich element, HUR binds to a core element of 27 nucleotides that contain AUUUA, AUUUU, and UUUUAU motifs. Interacts with ANP32A.

Here, we present evidence that HuR phosphorylation at S202 by the G2-phase kinase Cdk1 influences its subsequent subcellular distribution. In keeping with the prominently cytoplasmic location of the nonphosphorylatable point mutant HuR(S202A), phospho-HuR(S202) antibody. The enhanced cytoplasmic presence of unphosphorylated HuR was linked to its decreased association with 14-3-3 and to its heightened binding to target mRNAs.
which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.

© 2010 The Author(s)

Notes "FGFR2 is phosphorylated on serine 779 (KEQYSP(pS779)) in response to FGF2. S779, which lies adjacent to the phosphoacceptor glycine at 776, provides a docking site for the 14-3-3 phosphoserine-binding proteins and is essential for the full activation of the phosphatidylinositol 3-kinase and Ras/mitogen-activated protein kinase pathways" (Lonic et al 2008). Ser779 signaling is essential for promoting cell survival and proliferation in both Ba/F3 cells and BALB/c 3T3 fibroblasts.

Ser776 is conserved across mammalian species in both FGFR2 and FGFR1, and similar sites in other receptors (Lonic et al 2008).

FGFR2 (Bek)

763 NEYLLSQPLE..................QYSPSFY P21802
GM-CSF/IL-3/IL-5 receptor b subunit c 590 NQPYLGPP.........HSRLP NP_003836
FGFR1(Flg)

763 NOFYLLDSLPD..................QYSPSF P11362

ErbB4

1239 NPXX.......................WNLHP NP_005226

Low-density lipoprotein receptor-related protein 1 4470

NPTKYMEEGPDDVDGGLLADFAALPDK...KPTNTPN Q07954

Low-density lipoprotein receptor 802 NPVYQKTEDEVIIHCHN..............QDGYSYP AFA24515

Very-low-density lipoprotein receptor 834 NPYVLKTEEDLSIDIG..............RHSASVG NP_003374

Integrin beta 1 (fibronectin receptor) 780 NPY..............KSAVTVV NP_002202

Integrin beta 3 (platelet glycoprotein IIIa) 770 NPFYKAA............TSFTKNI NP_002003

Integrin beta-6 759 A30705

Integrin beta-7 775 NPLYS......................AIITTIN P26010

ErbB3

972 PPRYVL.......................KRECGP P21860

FLT3 receptor tyrosine kinase 916 EELYIMOSCWAFDS...........RRKPSFP CAA81393

Vascular endothelial growth factor receptor 2 1220 ISQYLSNQ.................KRSRP AAC16450

Granulocyte colony stimulating factor receptor 764 PGTYL...............RDSQHP NPQ99062

IL-6 receptor beta chain (glycoprotein 130) 764 HSYGHRQVPSPQVFVS............RSETQOP P40189

TrkB tyrosine kinase (BDNF/NT-3 receptor) 752 QPQWYOLSNVEIECTQVRGL.................QRPRTPC Q16620

Platelet-derived growth factor receptor alpha 608 GTAY..............GLSRQOP P16234

c-Met 1023 QVQPYLDMSGPLITSQ..............DSDSISNP P08581

Macrophage-stimulating protein receptor (p185-Ron) 1357

PATYMNLPSTSHENMVRPQFOSMPGVPNRRPRPQSEP Q04912

IGF-1R 1278 SFYSEYKENLPEEPEDELENEMVESPDL...PSAASSSLP NP_008866

TABLE 1 in Lonic et al (2008) Identification of putative conserved phosphotyrosine/serine motifs in diverse cell surface receptors. The tyrosine and serine residues in boldface in e are adjacent to the phospholipase Cgamma binding site at Y766, provides a docking site for the 14-3-3 phosphoserine-binding proteins and is essential for the full activation of the phosphatidylinositol 3-kinase and Ras/mitogen-activated protein kinase pathways" (Lonic et al 2008). Ser779 signaling is essential for promoting cell survival and proliferation in both Ba/F3 cells and BALB/c 3T3 fibroblasts.

Table 1: References to 14-3-3 binding to FGF2

Lonic A, Barry EF, Quach C, Kobe B, Saunders N, Guthridge MA. Fibroblast Growth Factor Receptor 2 Phosphorylation on Serine 779 Couples to 14-3-3 and Regulates Cell Survival and Proliferation. Mol Cell Biol. 2008;May;28(10):3372-85.

**Human FOXO1**

Forkhead box protein O1 transcription factor (FKHR) (FOXO1A)

| Accession Number | Description | Function |
|------------------|-------------|----------|
| NP_000866        | Human FOXO1 Forkhead box protein O1 transcription factor | Regulates cell survival and proliferation |

**Notes**

FOXO1 is a transcription factor of the forkhead family. Contains 1 fork-head domain. May play a role in myogenic differentiation and transcription. Localization of this gene with PAX3 has been associated with alveolar rhabdomyosarcoma. Phosphorylated FOXO1 binds 14-3-3 proteins, and co-precipitation studies with tagged proteins indicate that 14-3-3 binding involves co-operative interactions with both Thr25-26 and Ser256. Ser256 is located in the C-terminal region of the DBD, where 14-3-3 proteins may interfere both with DNA-binding and with
nuclear-localization functions. Multiple elements regulate nuclear/cytoplasmic shuttling of FOXO1: characterization of phosphorylation- and 14-3-3-dependent and -independent mechanisms. Zhao X, Gan L, Pan H, Chan D, Majeski M, Adam SA, Unterman TG.

Yuan Z, Lethinien MK, Merlo P, Villén J, Gygi S, Bonni A. Regulation of neuronal cell death by MST1-FOXO1 signaling. J Biol Chem. 2009 Apr 24;284(17):11285-92.

Yan L, Lavin VA, Moser LR, Cui Q, Kanies C, Yang E. PP2A regulates the pro-apoptotic activity of FOXO1. J Biol Chem. 2008 Mar 21;283(12):7411-20.

Koh PO. Melatonin prevents the injury-induced decline of Akt/forkhead transcription factors phosphorylation. J Pineal Res. 2008 Sep;45(2):199-203.

Won CK, Ji HH, Koh PO. Estradiol prevents the focal cerebral ischemic injury-induced decrease of forkhead transcription factors phosphorylation. Neurosci Lett. 2006 May 1;398(1-2):39-43.

Woods YL, Renia G. Effect of multiple phosphorylation events on the transcription factors FKHR, FKHL1 and AFX. Biochem Soc Trans. 2002 Aug;30(4):391-7.

Rena G, Prescott AR, Guo S, Cohen P, Unterman TG. Roles of the forkhead in rhabdomyosarcoma (FKHR) phosphorylation sites in regulating 14-3-3 binding, transactivation and nuclear targeting. Biochem J. 2001 Mar 15;354(Pt 3):559-65.

Morishita D, Katayama R, Sekimizu K, Tsuruo T, Fujita N. Pim kinases promote cell cycle progression by phosphorylating and down-regulating p27Kip1 at the transcriptional and posttranscriptional levels. Cancer Res. 2008 Jul 1;68(13):5076-85.

Yuan Z, Becker EB, Merlo P, Yamada T, DiBacco S, Konishi Y, Schaefer EM, Bonni A. Activation of FOXO1 by Cdk1 in cycling cells and postmitotic neurons. Science. 2008 Mar 21;319(5870):1665-8.

Human FOXO1 Forkhead box protein O3 (FKHR1) (FOXO3A) (Swissprot = O43524)

1 MAAEAPAPAP PSLPLELDPP EFEPQSRRRS QVPLQRRLE QASAPPRKGR TADAADDRIE
61 EDREDEDEGG GRAGSMAIG GGGGSGTLS GSLLLEDSARV LAFPGQQDFPS GATAAAGGLS
121 QGGGQGQALELQ QPLPGPQA AGGSPRQK GSRNNANWGNL SYADLTHPLTQVQGELTQNL
181 SQYIWEVMRC VYFFKDKEGDS NSSAGWNKSLRNLKSLHSMRFRVWQGLRQPKS
241 GGGSGKRAPP AVMNSKNK TKSRRGAACK KAAQLTAPES ADDPSQSLWS KGPGSTKSS
301 DELDAMTDWRT SRKSNASTV 6RGLSIMAS TELEDVQDDD APLSLMYSS ASASLSPVSK
361 FCTVSLFRTM DAMTMLNLD ALTENLMLDD LONLTLPPFS FSPSTGLMQS SSSFPYTKG
421 GCGNLSTPSS NTVGPGSSL NLSQGSPMQ IONKAPTXS SMSHYGQNL QDPIQDSLS
481 HSDVMQTSGD PLSQOASTAV AAGNSRVVMV LRNDPMMSFA AQPMSGQLVN QNHLHHQKQT
541 QGALGGSRAL SNSVSNMLGS ESLSLSGSAHK QOQSQVSQSM QTLSDDLSS GLSYTSANLP
601 VGMHEKFSPS LDDLFMGSLS ECMDSESIRS ELMDADGLDF NSDLSITQON VVGLNNGVNF
661 GAQASQSSVQ VPG >gi|8134467|sp|O43524.1|FOXO3_HUMAN RecName: Full=Forkhead box protein O3; AltName: Full=Forkhead in rhabdomyosarcoma-like 1; AltName: Full=AF6q21 protein

MAAEAPAPAP PSLPLELDPP EFEPQSRRRS QVPLQRRLE QASAPPRKGR TADAADDRIE
61 EDREDEDEGG GRAGSMAIG GGGGSGTLS GSLLLEDSARV LAFPGQQDFPS GATAAAGGLS
121 QGGGQGQALELQ QPLPGPQA AGGSPRQK GSRNNANWGNL SYADLTHPLTQVQGELTQNL
181 SQYIWEVMRC VYFFKDKEGDS NSSAGWNKSLRNLKSLHSMRFRVWQGLRQPKS
241 GGGSGKRAPP AVMNSKNK TKSRRGAACK KAAQLTAPES ADDPSQSLWS KGPGSTKSS
301 DELDAMTDWRT SRKSNASTV 6RGLSIMAS TELEDVQDDD APLSLMYSS ASASLSPVSK
361 FCTVSLFRTM DAMTMLNLD ALTENLMLDD LONLTLPPFS FSPSTGLMQS SSSFPYTKG
421 GCGNLSTPSS NTVGPGSSL NLSQGSPMQ IONKAPTXS SMSHYGQNL QDPIQDSLS
481 HSDVMQTSGD PLSQOASTAV AAGNSRVVMV LRNDPMMSFA AQPMSGQLVN QNHLHHQKQT
541 QGALGGSRAL SNSVSNMLGS ESLSLSGSAHK QOQSQVSQSM QTLSDDLSS GLSYTSANLP
601 VGMHEKFSPS LDDLFMGSLS ECMDSESIRS ELMDADGLDF NSDLSITQON VVGLNNGVNF
661 GAQASQSSVQ VPG

Notes

Higher levels of FOXO3A in the cytosol correlated with phosphorylation at Ser253, which accounted for its nuclear exclusion. FOXO4 (together with FOXO1, FOXO3a and FOXO6) belongs to a small subfamily of the forkhead transcription factors, which is designated as FOXO.

References to 14-3-3 binding to FOXO1

Shukla S, Shukla M, Macleman GT, Fu P, Gupta S. Deregluation of FOXO3A during prostate cancer progression. Int J Oncol. 2009 Jun;34(6):1613-20.

Su B, Liu H, Wang X, Chen SG, Siedlak SL, Kondo E, Choi R, Takeda A, Castellani RJ, Perry G, Smith MA, Zhu X, Lee HG. Ectopic localization of FOXO3a protein in Lewy bodies in Lewy body dementia and Parkinson's disease. Mol Neurodegener. 2009 Jul 1;4(1):23.

Yuan Z, Lethinien MK, Merlo P, Villén J, Gygi S, Bonni A. Regulation of neuronal cell death by MST1-FOXO1 signaling. J Biol Chem. 2009 Apr 24;284(17):11285-92.

Kino T, De Martino MU, Charmandari E, Ichijo T, Outas T, Chrousos GP. HIV-1 accessory protein Vpr inhibits the effect of insulin on the Foxo subfamily of forkhead transcription factors by interfering with their binding to 14-3-3 proteins: potential clinical implications regarding the insulin resistance in HIV-1-infected patients. Diabetes. 2005 Jan;54(1):23-31.

Morishita D, Katayama R, Sekimizu K, Tsuruo T, Fujita N. Pim kinases promote cell cycle progression by phosphorylating and down-regulating p27Kip1 at the transcriptional and posttranscriptional levels. Cancer Res. 2008 Jul 1;68(13):5076-85.

Chong ZZ, Maiase K. Krythropeoitin involves the phosphoryldinosiloitin 3-kinase pathway, 14-3-3 protein and FOXO3A nuclear trafficking to preserve endothelial cell integrity. Br J Pharmacol. 2009 Apr;150(7):859-60.

Mañoz-Fontela C, Marcos-Villar L, Gallego P, Arroyo J, Da Costa M, Pomeranz KM, Lam EW, Rivas C. Latent protein FOXO3 from Kaposi's sarcoma-associated herpesvirus interacts with 14-3-3 proteins and inhibits FOXO3A transcription factor. J Virol. 2007 Feb;81(3):1511-6.

Brunet A, Kanai F, Stenh J, Xu J, Srbassova D, Frangioni JV, Dalal SN, DeCaprio JA, Greenberg ME, Yaffe MB. 14-3-3 transits to the nucleus and participates in dynamic nucleo-transportal transport. J Cell Biol. 2002 Mar 4;156(5):817-28. Erratum in: J Cell Biol 2002 Apr 29;157(3):533.
Human FOXO4 Forkhead box protein O4 (AFX, AFFL, M11,T77) (Swissprot = P98177)

1 MTLNNVTMRQ GAVTVMGQQQQ RKigitDAPGRH LMVQKEPQKHQ SHNRHSATP EDHCRRSWSH
61 DCTDV516E SGGTNNYVRVL TEGQQGKYST LAFAIRQVGDI SMS0DQCVLG AETYRTDMV

Notes

“Growth factor-induced phosphorylation of Gab2 on two residues, S210 and T391, leads to recruitment of 14-3-3 proteins. Together, these events mediate negative-feedback regulation, as Gab2(S210A/T391A) exhibits sustained receptor association and signalling and promotes cell proliferation and transformation.” In human Gab2, NARSipq(S210)FQGQ and IPRNppq(T391)LAPM (conserved in Gab2 from mouse, rat, Monodelphis, Gallus, Tetraodon), but not conserved in Gab1 and Gab3.

References to 14-3-3 binding to FOXO4

(1) Bruner T, Laranje A, Zigmund MJ, Lin MZ, Jao P, Hu LS, Anderson MJ, Ardern KC, Bennis J, Greenberg ME. Akt promotes cell survival by phosphorylating and inhibiting a Forkhead transcription factor. Cell. 1999 Mar 19;96(3):857-68.

(2) Brummer T, Larance M, Herrera Abreu MT, Lyons RJ, Timpson P, Emmerich CH, Fleuren ED, Lehrbach GM, Schramek D, Guilhaus M, James DE, Daly RJ. Phosphorylation of Gab2(S210A/T391A) exhibits sustained Forkhead receptor binding and associated signaling in human Gab2. J Biol Chem. 2007 Aug 17;282(11):8265-75.

(3) Obsilova V, Vecer J, Herman P, Pabianova A, Sulc M, Teisinger J, Boura E, Obsil T. Forkhead box protein O4 (AFX, AFX1, MLLT7) (Swissprot = P98177). FEBS Lett. 2007 Dec 14;581(11):2789-95.

(4) Brunet A, Bonni A, Zigmond MJ, Lin MZ, Juo P, Greenberg ME. Akt promotes cell survival by phosphorylating and inhibiting a Forkhead transcription factor. Cell. 1999 Mar 19;96(3):857-68.
Human Gli family zinc finger 1 (Glioma associated oncogene) transcription factor (Swissprot = P08151)

1 MPNSMTFPPI SYSGEPCCCL PLPSQGAPS PS TGGELGSGP FQ CHQANLMGSP H5YPARETN
2 61 SCTEGFLPS PFLSKARKTL RALISLPSLD ASDLQTVIR TPSSSLVAFI NSRCTXPGGS
3 121 YGHSISGMTS ESOFLPFAMQ HHQFGPFAPSF VGQGDFHDASA RGGMHPFQG RGFFTPQLKR
4 181 SEUFLOWDC EERPLGFPSPSPN STGCPQIDG LPMLQMGRED LEERKKEPEP SVYFDTRWD
5 241 GCSQFPGPLS DLVHINISEH IGERKEFVCC HWGCGSREL PFKQAQMLVY HMRHTFGEK
6 301 HKCFTPGEKCR SYSLNLEKLT HLRSHTGEPK YMCEHEGSK AFNASDRK AQHRTHSNEK
7 421 PVYCLPKCCT KRYDSSSSLR KLVRKTVHGP AHVTKRRGDP GFLPRAFSPIS TVEFPRKEG
8 541 SVPPKRLSVEV VPGKMPQSF QPGQCSSCSC DHSPGASAN TDGTVMTGN AAGGTDLLS
9 639 GNECLTACTSYSLRLDLRLQVQGQ VRIYCLPKCCT KRYDSSSSLR KLVRKTVHGP AHVTKRRGDP
10 789 CLSPQGPLS DLVHINISEH IGERKEFVCC HWGCGSREL PFKQAQMLVY HMRHTFGEK

**Notes**

**Human GliAP (Gli1A)**

| 1 | MERRITTAFA RRSYSSSSEM MGVGLAPGRK LQGTPRSLILA RMPPPLPTVR DFSLAGALNA |
| 2 | 61 | GFKRETASRE AEMMELRDF ASYKIEVRML EQQQNLKAEAL LNRKQKEEPL FLTVQYNAEE |
| 3 | 121 | KELRLKLQDL TANSALVEQ RDLNQCLQATVR QKQRQDTRER LRLAEENMLA ARYQEDAEAT |
| 4 | 181 | LARLDERLZK ELEERBFRPL PKHEEEREVRLO RQLGQRQOUQ HUELDPWAFD LTAALKIFRT |
| 5 | 241 | QYEEAMSSNN HEAEERYWKR FDRLTDAAAR NAEELRQKHK EANDYRQGQ SLTCDSLR |
| 6 | 301 | GTNSESQRM REQERHVRLE AASQYELAR LEQEESGKLD EMARHLEQY DLLNVKLALD |
| 7 | 361 | IEIAYTRKLL EGEENRITIP VQFSLMLQR ETSLSDLRSV ELEQHRKGNIK VTREVMDGEV |

**Notes**

GFAP a class-I intermediate filament protein. A cell-specific marker that, during the development of the central nervous system, distinguishes astrocytes from other glial cells. Mutations in this gene cause Alexander disease, a rare disorder of astrocytes in the central nervous system. An additional transcript variant isoform has been described.14-3-3gammas associated with both soluble and filamentous GFAP in a phosphorylation- and cell-cycle-dependent manner in primary cultured astrocytes. The amount of association increases during GO/M phase due to more phosphorylated GFAP. Serine 8 in the head domain is essential for the direct association of GFAP to intermediate filaments. This data demonstrates that 14-3-3gamma associates with both soluble and filamentous GFAP in a phosphorylation-dependent manner. Overexpression of 14-3-3gamma affects dynamics and integrity of glial filaments by regulating of cell shape remodeling by regulated nuclear transport. Traffic. 2007 Sep;8(9):1164-78. Béguin P, Mahalakshmi RN, Nagashima K, Cher DH, Takahashi A, Yamada Y, Seino Y, Hunziker W. Nuclear localization of endogenous RGK like protein KIR induced T cell protein; AltName: Full=GTP-binding protein KIR

**References to 14-3-3 binding to Gli/Gem**

1. Drewes G, Kuster B, Bouwmeester T, Acker Angrand PO, Segura I, Völkel P, Ghidelli S, Terry R, Brajenovic M, Vintersten K, Klein R, Superti-Furga G, Crawford JR. transgenic mouse proteomics identifies novel proteins and modulates cell shape remodeling by regulated nuclear transport. Traffic. 2007 Sep;8(9):1164-78. Béguin P, Mahalakshmi RN, Nagashima K, Cher DH, Takahashi A, Yamada Y, Seino Y, Hunziker W. 14-3-3 and calmodulin control subcellular distribution of Gli/Gem and its regulation of cell shape and calcium channel activity. J Cell Sci. 2005 May 1;118(Pt 9):1929-34.

**Human GliAP (Gli2)**

| 1 | MERRITTAFA RRSYSSSSEM MGVGLAPGRK LQGTPRSLILA RMPPPLPTVR DFSLAGALNA |
| 2 | 61 | GFKRETASRE AEMMELRDF ASYKIEVRML EQQQNLKAEAL LNRKQKEEPL FLTVQYNAEE |
| 3 | 121 | KELRLKLQDL TANSALVEQ RDLNQCLQATVR QKQRQDTRER LRLAEENMLA ARYQEDAEAT |
| 4 | 181 | LARLDERLZK ELEERBFRPL PKHEEEREVRLO RQLGQRQOUQ HUELDPWAFD LTAALKIFRT |
| 5 | 241 | QYEEAMSSNN HEAEERYWKR FDRLTDAAAR NAEELRQKHK EANDYRQGQ SLTCDSLR |
| 6 | 301 | GTNSESQRM REQERHVRLE AASQYELAR LEQEESGKLD EMARHLEQY DLLNVKLALD |
| 7 | 361 | IEIAYTRKLL EGEENRITIP VQFSLMLQR ETSLSDLRSV ELEQHRKGNIK VTREVMDGEV |

**Notes**

GFAP a class-I intermediate filament protein. A cell-specific marker that, during the development of the central nervous system, distinguishes astrocytes from other glial cells. Mutations in this gene cause Alexander disease, a rare disorder of astrocytes in the central nervous system. An additional transcript variant isoform has been described.14-3-3gammas associated with both soluble and filamentous GFAP in a phosphorylation- and cell-cycle-dependent manner in primary cultured astrocytes. The amount of association increases during GO/M phase due to more phosphorylated GFAP. Serine 8 in the head domain is essential for the direct association of GFAP to 14-3-3gamma. 14-3-3 and calmodulin control subcellular distribution of Gli/Gem and its regulation of cell shape and calcium channel activity. J Cell Sci. 2005 May 1;118(Pt 9):1929-34.

**References to 14-3-3 binding to Gli/Gem**

1. Drewes G, Kuster B, Bouwmeester T, Acker Angrand PO, Segura I, Völkel P, Ghidelli S, Terry R, Brajenovic M, Vintersten K, Klein R, Superti-Furga G, Crawford JR. transgenic mouse proteomics identifies novel proteins and modulates cell shape remodeling by regulated nuclear transport. Traffic. 2007 Sep;8(9):1164-78. Béguin P, Mahalakshmi RN, Nagashima K, Cher DH, Takahashi A, Yamada Y, Seino Y, Hunziker W. Nuclear localization of endogenous RGK like protein KIR induced T cell protein; AltName: Full=GTP-binding protein KIR

**Human GIT1**

1 121 DGEATILL DMWENKGENE LWLHDMCQVG DAYLIVYSIT DRASEKASE LIQLRRARQP
2 181 TEDIPILIVG NKSDDLVCRES VSVSEGRACA VVFDCFKIERT SAAQHNVKF LGEFQVGRVR
3 241 LRRSDKNEE RRLAYQKERE SMPRKARRWF GKVXAKNNK MAFKLKSGC HLDVSL

**Notes**

Human - Phosphorylation of serine 289 in conjunction with serine 23 results in bidentate 14-3-3 binding, leading to increased Gli protein half-life (Ward et al 2004).

**References to 14-3-3 binding to Gli/Gem**

1. Drewes G, Kuster B, Bouwmeester T, Acker Angrand PO, Segura I, Völkel P, Ghidelli S, Terry R, Brajenovic M, Vintersten K, Klein R, Superti-Furga G, Crawford JR. transgenic mouse proteomics identifies novel proteins and modulates cell shape remodeling by regulated nuclear transport. Traffic. 2007 Sep;8(9):1164-78. Béguin P, Mahalakshmi RN, Nagashima K, Cher DH, Takahashi A, Yamada Y, Seino Y, Hunziker W. 14-3-3 and calmodulin control subcellular distribution of Gli/Gem and its regulation of cell shape and calcium channel activity. J Cell Sci. 2005 May 1;118(Pt 9):1929-34.

**Human GIT1**

1 121 DGEATILL DMWENKGENE LWLHDMCQVG DAYLIVYSIT DRASEKASE LIQLRRARQP
2 181 TEDIPILIVG NKSDDLVCRES VSVSEGRACA VVFDCFKIERT SAAQHNVKF LGEFQVGRVR
3 241 LRRSDKNEE RRLAYQKERE SMPRKARRWF GKVXAKNNK MAFKLKSGC HLDVSL

**Notes**

Human - Phosphorylation of serine 289 in conjunction with serine 23 results in bidentate 14-3-3 binding, leading to increased Gli protein half-life (Ward et al 2004).

**References to 14-3-3 binding to Gli/Gem**

1. Drewes G, Kuster B, Bouwmeester T, Acker Angrand PO, Segura I, Völkel P, Ghidelli S, Terry R, Brajenovic M, Vintersten K, Klein R, Superti-Furga G, Crawford JR. transgenic mouse proteomics identifies novel proteins and modulates cell shape remodeling by regulated nuclear transport. Traffic. 2007 Sep;8(9):1164-78. Béguin P, Mahalakshmi RN, Nagashima K, Cher DH, Takahashi A, Yamada Y, Seino Y, Hunziker W. Nuclear localization of endogenous RGK like protein KIR induced T cell protein; AltName: Full=GTP-binding protein KIR

© The Author(s) 2010. This article is distributed under the terms of the Creative Commons Attribution-NonCommercial License (http://creativecommons.org/licenses/by-nc/2.5/) which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.
which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.

© 2010 The Author(s)

Notes

Similar PKA-phosphorylated sites in Gli1, Gli2 and Gli3 (see other entries).

References to 14-3-3 binding to Gli2

Asaoka Y, Kanai F, Ichimura T, Tateishi K, Tanaka Y, Ohta M, Seto M, Tada M, Ijichi H, Ikenoue T, Kawabe T, Isobe T, Yaffe MB, Omata M. Identification of a suppressive mechanism for hedgehog signaling through a novel interaction of Gli with 14-3-3. J Biol Chem. 2009 Dec [Epub ahead of print]

Human Gli1 family zinc finger 2 (Tax helper protein) transcription factor (SwissProt = P10070)

1 MEAQSHTSE TEKCTSTRDS VEVKASSTTS NEDESPQGTYR HERRNATIM

Notes

Similar PKA-phosphorylated sites in Gli1, Gli2 and Gli3 (see other entries). In the form of Gli2 studied by Asaoka et al (2009 prepublication date), the 14-3-3 binding site (Ser970 in the reference sequence above) is at Ser975.

References to 14-3-3 binding to Gli2

Asaoka Y, Kanai F, Ichimura T, Tateishi K, Tanaka Y, Ohta M, Seto M, Tada M, Ijichi H, Ikenoue T, Kawabe T, Isobe T, Yaffe MB, Omata M. Identification of a suppressive mechanism for hedgehog signaling through a novel interaction of Gli with 14-3-3. J Biol Chem. 2009 Dec [Epub ahead of print]

Human Gli2

Notes

Similar PKA-phosphorylated sites in Gli1, Gli2 and Gli3 (see other entries). In the form of Gli2 studied by Asaoka et al (2009 prepublication date), the 14-3-3 binding site (Ser970 in the reference sequence above) is at Ser975.

References to 14-3-3 binding to Gli2

Asaoka Y, Kanai F, Ichimura T, Tateishi K, Tanaka Y, Ohta M, Seto M, Tada M, Ijichi H, Ikenoue T, Kawabe T, Isobe T, Yaffe MB, Omata M. Identification of a suppressive mechanism for hedgehog signaling through a novel interaction of Gli with 14-3-3. J Biol Chem. 2009 Dec [Epub ahead of print]
Similar PKA-phosphorylated sites in Gli1, Gli2 and Gli3 (see other entries). Phosphorylated 14-3-3-binding site is Ser106.

**Human**

| Protein | RecName: Full=Platelet glycoprotein Ib alpha chain; Short=Glycoprotein Ibalpha; AltName: Full=Antigen CD42b; Short=GP-Ib alpha; Short=GPIb-alpha; Short=GPIb; Flags: Precursor; Contains: RecName: Full=Glycocalicin; Flags: Precursor |
|---------|--------------------------------------------------------------------------------------------------------|
| GPIb    | NIP7359.                                                                                     |

**References to 14-3-3 binding to Gli3**

Asaoka Y, Kanai F, Ichimura T, Tateishi K, Tanaka Y, Ohta M, Seto M, Tada M, Ijichi H, Ikenoue T, Kawabe T, Isobe T, Yaffe MB, Omata M. Identification of a suppressive mechanism for hedgehog signaling through activation of integrin \(\alpha I I b {\beta 3}\). J Biol Chem. 2009 Dec 7. [Epub ahead of print].

**References to 14-3-3 binding to Gremlin 1**

Human **Gremlin 1** 14-3-3-binding sites not defined precisely

Gremlin 1 14-3-3-binding sites not defined precisely

**Human GRIN2C** (NMDAR2C) NMDA receptor subunit 2C (Swissprot = Q14957).

| EnGeneID | RecName: Full=Human GRIN2C protein antagonist gremlin 1 is overexpressed in human cancers and interacts with YWHAH protein. Flags:graded |
|----------|---------------------------------------------------------------------------------------------------|
| 481      | Family of protein antagonists gremlin 1 is overexpressed in human cancers and interacts with YWHAH protein. |

**Notes**

Underlined is the signal sequence, papers quote residue numbers that do not include this.

From references in Bialkowski et al (2003) (to Proc Natl Acad Sci U S A. 1987 August; 84(16): 5615–5619. PMCID: PMC298913). Truncation of the last 19 aa prevents 14-3-3 binding although there is no obvious 14-3-3 consensus.

**Mangin et al (2009)** S609 is phosphorylated in resting platelets (phosphospecific antibody) and so is the 580-590 peptide S580A reduces co-ip of 14-3-3 zeta although S587A also weakens the interaction but to a lesser extent. Dephosphorylation of these sites appears after adherence to a VWF matrix.

**Inhibitors of PKA and PKG have no effect on S609 phosphorylation** Forskolin does not induce incorporation of 32P in S609 of GPIb. Inhibitors of PKA and PKG have no effect on S609 phosphorylation.

**Notes**

Underlined is the signal sequence, papers quote residue numbers that do not include this.

From references in Bialkowski et al (2003) (to Proc Natl Acad Sci U S A. 1987 August; 84(16): 5615–5619. PMCID: PMC298913). Truncation of the last 19 aa prevents 14-3-3 binding although there is no obvious 14-3-3 consensus.

**Mangin et al (2009)** S609 is phosphorylated in resting platelets (phosphospecific antibody) and so is the 580-590 peptide S580A reduces co-ip of 14-3-3 zeta although S587A also weakens the interaction but to a lesser extent. Dephosphorylation of these sites appears after adherence to a VWF matrix.

**Inhibitors of PKA and PKG have no effect on S609 phosphorylation** Forskolin does not induce incorporation of 32P in the 580-590 peptide S580A and S609 are 19 residues apart.

“GPlb/VWF signaling leads to the mobilization of intracellular Ca2+, platelet shape change, and activation of integrin (alpha)IIb(3eta).” Filamin binds 570-580

Human platelets were tested for 14-3-3 expression and all isoforms found except sigma.

CHO cells were tested and they found all isoforms except sigma. S587A/S590A double mutant abolished co-ip of endogenous 14-3-3 in CHO cells as did deletion of Ser605-610.

RLP5p570,Gpi5, TDP, RYSGHSL117.

In Yuan et al (2009) the R557Gp561 sequence is reported to bind to 14-3-3 (with pSER575 in the proteome).
References to 14 (WARGSRPRHA(s1084)LPSSVA).

Chen and Roche (2009) demonstrate that PKB/Akt directly phosphorylates NR2C on serine 1096.

Notes

© 2010 The Author(s)
which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.

© 2010 The Author(s)

Ellis JJ, Valencia TG, Zeng H, Roberts LD, Deaton RA, Grant SR. CaM kinase I directs the phosphorylation of 14-3-3 beta in vascular smooth muscle cells: activation of class II histone deacetylase repression. Mol Cell Biochem. 2003 Jan;242(1-2):153-61.

References to 14-3-3-binding (see entry for HDAC9)

Human HDAC9 Histone deacetylase 9 (SwissProt = Q9UKV0)

1) MRSNISDDV KSEVFVQGLEP IFSLDRLTDL RMMFPFVDPW VREKQLQQEQL LIIQQQQQIQ
2) QULALTPEF QHEHITQG AQGCSPHELQ LAIKQOELL EQREKLEQQR QGQEVQHRHP
121) EQOPPLRGK DRGRRAVAS TEVQOKLQRFL LSLSKADKT TQPKNSHVR RSHPKMLYTA
181) HHTDSLQSSP LSLTPTSPYSK YTLPGQDAK DDPLNRTQK EPNKLVRL PKQVAERKSS
241) PLLRKGDNV VSTSPKRME FTESSSSSS PSGSPSSPNN PGTPGTSVE TSVLPPTPHA
301) EVMQVQRIL IHEKNNMLLS LITSPSLPNL TLGAPFVSQ LNASKLQKR QKCGQTLRQ
361) GVPLPGQVVG SIAPASSSHPP VTLRKEPNEQ SHQALQLHL LKQEMQQLR LGAGVVPPLH
421) QSPLATKERI SGGHRFPLHK HPRPLNRTQ KALQRSTAQL QLVIQIQQO QFEQKYYQDO
481) QIHMQKKLS SIEQLQKPGS HLHEAEELQ GQDMQKDERA FSPGNSTGRS SACCVDDMDL
541) QYVAGKVEKKE FPDOSDAAQ ESMEEQGEEA FMQQQPLLEQ HATRSLVQA PLAAVCGMVL
601) EKHLRVSRTH SSPAASVLPF PANDRFLQPG SAGIATAYDL MLHKQCVCGC STHFEHEAGR
661) IQSTKLRLE TOLLNKEI QKQASLEIKI QHUFHSHHL YLSTNPDELG KLDRPFLILD
721) DSQKFCSSFL CGGLGDVDST IWNELHSSGA ARMAVGCVE LQIAVSGKELL KNFAVVRPP
781) GHAEDBASMT GCFFNSVAVI TAYKYLQDNL ISKIVLWDD VHIGHTQFAQ YPADSILYI
841) SLRYDENGNF FPFGJAGPNPG GTGLCGEYNI NAMTSQGLD GDQMVYELA FRTIKVRKVA
901) EFNPDMVLS AGFADAEHGT FPLLQHYVTA KCFGHLTQNL TMLADGVRVL ALEGGHDALT
961) CSADAYNN ALLGNELEL AEIDLQGQPNN BMNADVQIQI TEEQDSIKRQ <gi>19865267|sp|Q9UKV0.2| Human HDAC9_HUMAN RecName: Full=Histone deacetylase 9; AltName: Full=MEF2-interacting transcription repressor MTR MRSNISDDV KSEVFVQGLEP IFSLDRLTDL RMMFPFVDPW VREKQLQQEQL LIIQQQQQIQ</gi>

Notes: Specifically, phosphorylation of HDAC5 serines 259 and 498 causes HDAC5 to bind to 14-3-3 and dissociate from ME2.

Histone deacetylase, HDAC5 RKTAPSS"EP, RTQCS"SSP

Histone deacetylase, HDAC7 RKTVPs"EP, RTQPs"EP, RAQSp"SSP

14-3-3-binding sites on HDAC4 Ser246, Ser467 and Ser632 (Paroun et al 2007).

"The binding of HDAC7 to 14-3-3 pSEP is more dependent on the serine residues Ser-178, Ser-344, and Ser-479, since the replacement of these residues by alanine reduced 14-3-3 binding to HDAC7. Interestingly, all three 14-3-3-binding sites within each HDAC7 are not equivalent. Ser178 in the 14-3-3-binding site is the most critical for 14-3-3 binding in both HDAC4 and HDAC7 (47). Indeed, the inactivation of this site had a stronger effect than that of the two others (Fig. 5, C and D). Sequence comparison revealed that among the three sites, the NH2-terminal domain presented the best homology to the consensus-binding motif. Nevertheless, other sites also contributed to the binding of 14-3-3 by HDAC7 since the binding of HDAC7 by 14-3-3 was completely abolished only when all three motifs were inactivated. Similar results have also been observed for HDAC4 (47). Taken together, these results suggest that these three serines are the primary regulatory sites for nuclear export of class II HDACs. It is also interesting to note that class II HDACs are the only molecules identified so far that contain more than two 14-3-3-binding sites."

Kao et al 2001

References to HDAC4, HDAC3, HDAC5, and HDAC7

Backs J, Song K, Bezprozvannaya S, Chang S, Olson EN. CaM kinase II selectively signals to histone deacetylase 4 during cardiomyocyte hypertrophy. J Clin Invest. 2006 Jul;116(7):1853-64.

Chang S, Bezprozvannaya S, Li S, Olson EN. An expression screen reveals modulators of class II histone deacetylase phosphorylation. Proc Natl Acad Sci U S A. 2005 Jun 7;102(23):8120-5.

Deng X, Ewton DZ, Mercer SE, Friedman E. Mirk/dyrk1B decreases the nuclear accumulation of class II histone deacetylases during skeletal muscle differentiation. J Biol Chem. 2005 Feb 11;280(6):4894-905.

Dequidt F, Martin M, Von Blume J, Vertommen D, Leconte E, Mari N, Heinen MF, Bachmann M, Twizere JC, Huang MC, Rider MH, Pwina-Worms H, Seufferlein T, Kettmann R. New role for hPar1 kinases EMK and C-TAK1 in regulating localization and activity of class II histone deacetylases. Mol Cell Biochem. 2006 Oct;26(19):1086-102.

Ellis JJ, Valencia TG, Zeng H, Roberts LD, Deaton RA, Grant SR. CaM kinase I directs the phosphorylation of 14-3-3 beta in vascular smooth muscle cells: activation of class II histone deacetylase repression. Mol Cell Biochem. 2003 Jan;242(1-2):153-61.
which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.

© 2010 The Author(s)

Human HJURP

Mol Cell Biol. 2001 Sep;21(17):5992-6005.

McGee SL, van Denderen BJ, Howlett KF, Mollica J, Schertzer JD, Kemp BE, Hargreaves M. AMP-activated protein kinase regulates GLUT4 transcription by phosphorylating histone deacetylase 5. Diabetes. 2008 Apr;57(4):860-7.

McKinsey TA, Zhang CL, Olson EN. Activation of the myocyte enhancer factor-2 transcription factor by calcium/calmodulin-dependent protein kinase-stimulated binding of 14-3-3 to histone deacetylase 5. Proc Natl Acad Sci U S A. 2000 Dec 19;97(26):14400-5.

McKinsey TA, Zhang CL, Olson EN. Identification of a signal-responsive nuclear export sequence in class II histone deacetylases. Mol Cell Biol. 2001 Sep;21(18):6312-21.

Miska EA, Langley E, Wolf D, Karlsson C, Pines J, Kouzarides T. Differential localization of HDAC4 orchestrates muscle differentiation. Nucleic Acids Res. 2001 Aug 15;29(16):3439-47.

Nishino TG, Miyazaki M, Hoshino H, Miwa Y, Horinouchi S, Yoshida M. 14-3-3 regulates the nuclear import of class Ia histone deacetylases. Biochem Biophys Res Commun. 2008 Dec 19;377(3):852-6.

Paroni G, Cernotta N, Dello Russo C, Gallinari P, Pallaoro M, Fazi C, Talamo F, Orsatti L, Steinkühler C, Brancolini C. HDAC4 recruits HDAC4a nuclear import. Mol Cell Biol. 2008 Feb;18(2):655-67.

Paroni G, Fontanini A, Cernotta N, Fazi C, Gupta MP, Yang XJ, Fasino D, Brancolini C. Dephosphorylation and caspase processing generate distinct nuclear pools of histone deacetylase 4. Mol Cell Biol. 2007 Oct;27(19):6718-32.

Wang AH, Grégoire S, Ziza E, Xiao L, Li CS, Li H, Wright KL, Ting JP, Yang XJ. Identification of the ankyrin repeat proteins ANKRA and RFXANK as novel partners of class Ia histone deacetylases. J Biol Chem. 2005 Aug 12;280(28):29117-27.

Wang AH, Kruhlak MJ, Wu J, Bertos NR, Posner BI, Bazett-Jones DP, Yang XJ. Regulation of histone deacetylase 4 by binding of 14-3-3 proteins. Mol Cell Biol. 2000 Sep;20(18):6904-12.

Wang AH, Yang XJ. Histone deacetylase 4 possesses intrinsic nuclear import and export signals. Mol Cell Biol. 2001 Sep 12;21(17):5992-6005.

Zhang CL, McKinsey TA, Olson EN. The transcriptional corepressor MTR is a signal-responsive inhibitor of myogenesis. Proc Natl Acad Sci U S A. 2001 Jun 19;98(13):7354-9. (HDAC9)

Zhang T, Kohlihaa M, Barks J, Mishra S, Phillips W, Dybkova N, Chang S, Ling H, Berz DS, Maier LS, Olson EN, Brown JH. CaMKIIdelta isoforms differentially affect calcium handling but similarly regulate HDAC/MEF2 transcriptional responses. J Biol Chem. 2007 Nov 30;282(48):35078-87.

Zhao X, Ito A, Kane CD, Liao TS, Bolger TA, Lemrow SM, Means AR, Yao TP. The modular nature of histone deacetylase 3 high affinity consensus motifs. Winter et al (2008)
which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.

© 2010 The Author(s)

~20% of the efficiency of wtHSF1. Our experiments indicate that serines 303 and 307 are required for efficient Ser303Ala/Ser307Ala mutant. However, the HSF1 Wild localization of HSF1, implicating a role for ERK/14 acutely by stress, during recovery from h complex, however, depending on extracellular conditions, in that HSF1 ERK activation results in the recruitment of the phosphoserine alternatively spliced isoforms have been described. 

Notes
"Centromeric protein that plays a central role in the incorporation and maintenance of histone H3-like variant

CENP at centromeres. Acts as a specific component for CENP and is required for the incorporation of newly synthesized CENP molecules into nucleosomes at replicated centromeres. Directly binds Holliday junctions" Interacts with 14-3-3 family members in a phosphorylation-dependent manner. Interacts with MSH5 and NBN. Directly binds Holliday junctions.

14-3-3/FAKTS interaction was markedly enhanced by the expression of activated Akt/PKB, suggesting a phosphorylation dependent event. Ser479 as the predominant residue that mediates the association (RRLS479LP).

References to 14-3-3 binding to JURP (FAKTS)

Luhn P, Wang H, Marcus AI, Fu H. Identification of FAKTS as a novel 14-3-3 family member expressing gene 1 protei

Human HSF1 Heat-shock transcription factor (Swissprot = Q00613)

SITES NOT DEFINED

PRECISELY, NOT INCLUDED IN WEBLOGO ANALYSIS

Notes
HSF1 a heat shock transcription factor. Transcription of heat-shock genes is regulated in a phosphorylation-dependent manner. Interacts with MSH5 and NBN. Directly binds Holliday junctions.

References to 14-3-3 binding to HSF1

Wild-type HSF1 binds to 14-3-3 (epiQ00613) - GST with markedly greater avidity than the double Ser303Ala/Ser307Ala mutant. However, the HSF1 mutant was observed to bind in repeated experiments, at least ~20% of the efficiency of wildHSF1. Our experiments indicate that series 303 and 307 are required for efficient HSF1 binding to 14-3-3 (epiQ00613). They also suggest the possibility that 14-3-3 (epiQ00613) can bind for efficient HSF1 binding to the unphosphorylated Ser-303/307 region or to another as-yet uncharacterized site in HSF1.
Wang X, Grammatikakis N, Siganou A, Stevenson MA, Calderwood SK. Interactions between extracellular signal-regulated protein kinase 1, 14-3-3epsilon, and heat shock factor 1 during stress. J Biol Chem. 2004 Nov 19;279(47):49460-9.

Wang X, Grammatikakis N, Siganou A, Calderwood SK. Regulation of molecular chaperone gene transcription involves the phosphorylation, 14-3-3 epsilon binding, and concomitant sequestration of heat shock factor 1. Mol Cell Biol. 2003 Sep;23(17):6013-26.

Calderwood SK. Regulatory interfaces between the stress protein response and other gene expression programs in the cell. Methods. 2005 Feb;35(2):139-48.

**Human HspB6** (Swissprot = P08069)

1. **Human IGF1R** Insulin-like growth factor 1 receptor (Swissprot = P08069)

References to 14-3-3 binding to HSP20

Drezza CM, Brophy CM, Komalavilas P, Furnish EJ, Joshi L, Pallero MA, Murphy-Ullrich JE, von Rechenberg B, Ho YS, Richardson B, Xu N, Zhen Y, Peltier JM, Panitch A. Transducible heat shock protein 20 (HSP20) as a partner of heat shock factor 1 during stress. J Biol Chem. 2005 Feb 18;280(9):8919-27.

Calderwood SK. Regulatory interfaces between the stress protein response and other gene expression programs in the cell. Methods. 2005 Feb;35(2):139-48.
Notes
Spence et al (2003) report PMA-stimulated phosphorylation and 14-3-3 binding to VPLDPSASSSp(242)LP (=Ser1313 in P80069).

References to 14-3-3 binding to IGF1 receptor
Craparo A, Freund R, Gustafson TA. 14-3-3 (epsilon) interacts with the insulin-like growth factor I receptor and insulin receptor substrate 1 in a phosphoserine-dependent manner. J Biol Chem. 1997 Apr 25:272(17):11663-9.

Spence SL, Dey BR, Terry C, Albert P, Nissey P, Furlanetto RW. Interaction of 14-3-3 proteins with the insulin-like growth factor I receptor (IGFIR): evidence for a role of 14-3-3 proteins in IGFIR signaling. Biochem Biophys Res Commun. 2003 Dec 26;312(4):1060-6.

Furlanetto RW, Dey BR, Lopaczynski W, Nissey SP. 14-3-3eta interacts with the insulin-like growth factor receptor but not the insulin receptor. Biochem J. 1997 Nov 1;327( Pt 3):765-71.

Human IL-9R (α-Chain of interleukin 9 receptor)

Notes
KARPsWiptFc.com

References to 14-3-3 binding to a chain of interleukin 9 receptor (IL-9R)
Silva D, Gu M, Zhu YX, Chen J, Tsai S, Du X, Yang YC. 14-3-3zetaeta interacts with the alpha-chain of human interleukin 9 receptor. Biochem J. 2000 Feb 1;341 Pt 3:747-51.

Human ING1 (p33ING1b) Inhibitor of growth protein 1 (Swissprot = Q9UK53)

Notes

References to 14-3-3 binding to a chain of interleukin 9 receptor (IL-9R)
Gong W, Russell M, Suzuki K, Riabowol K. Subcellular targeting of p33ING1b by phosphorylation. FEBS Lett. 2006.

The REASPADLP motif, which has homology to the ING1/ING2 region, is involved in targeting of p33ING1b by phosphorylation (Gong et al 2006). N.B. This site has a proline at +1.

References to 14-3-3 binding to p33ING1b
Gong W, Russell M, Suzuki K, Riabowol K. Subcellular targeting of p33ING1b by phosphorylation-dependent 14-3-3 binding regulates p21WAIP1. Mol Cell Biol. 2006 Apr;26(8):2947-54.

Human IRS1 Insulin receptor substrate 1 (Swissprot = P35568)

Notes

References to 14-3-3 binding to p33ING1b
Gong W, Russell M, Suzuki K, Riabowol K. Subcellular targeting of p33ING1b by phosphorylation-dependent 14-3-3 binding regulates p21WAIP1. Mol Cell Biol. 2006 Apr;26(8):2947-54.

The human IRS1 (also known as IRS-1, insulin receptor substrate 1) protein is a key mediator of insulin signaling. IRS1 is a scaffold protein that links insulin receptor activation to downstream signaling pathways.

Human IRS1 is involved in insulin receptor binding and signaling.

In 2006, Gong et al reported that p33ING1b targets IRS1 by phosphorylation-dependent 14-3-3 binding. This binding is regulated by p21WAIP1, a protein that negatively regulates IRS1 activity.

The REASPADLP motif in p33ING1b is involved in targeting IRS1 by phosphorylation (Gong et al 2006). This site has a proline at +1.

Human IRS1 has two NLS and one NLS-like region, suggesting that it may be targeted to the nucleus in a phosphorylation-dependent manner.

The data from these studies suggest that phosphorylation-dependent targeting of IRS1 by 14-3-3 binding is a mechanism for regulating IRS1 activity in response to insulin signaling.

© 2010 The Author(s)

The author(s) has/have paid for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial License (http://creativecommons.org/licenses/by-nc/2.5/) which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.
The following phosphopeptides bound to 14-3-3 and displaced them from IRS-1 in in vitro competition assays: DEFPRPSK[pS]Q5SSC [pS] corresponds to Ser-270 in human IRS-1), HPPLNSR[pS]IPMPAS (Ser-374 in human IRS-1), MPMS3KSV[pY]APQ[QH] (Ser-641 in human IRS-1) (Ogihara et al. 1997). Of these sites, only Ser270 and Ser374 have been demonstrated to be phosphorylated in vivo in several studies (http://www.phosphosite.org/). Sequence alignment indicates that IRS-1 contains at least five putative 14-3-3 binding sites. Three of them are within the amino-terminal portion of the molecule that is important for the interaction of IRS-1 with the insulin receptor and PKB and might contribute to its subcellular localization (Xiang et al. 2002).

**References to 14-3-3-binding to IRS1**

Oriente F, Andreozzi F, Romano C, Pervolos G, Perfetti A, Fiory F, Miele C, Beguinot F, Formisano P. Protein kinase C alpha regulates insulin action and degradation by interacting with insulin receptor substrate-1 and 14-3-3 epsilon. J Biol Chem. 2005 Dec 9;280(49):40642-9.

Xiang X, Yuan M, Song Y, Ruderman N, Wen R, Luo Z. 14-3-3 facilitates insulin-stimulated intracellular trafficking of insulin receptor substrate 1. Mol Endocrinol. 2002 Mar;16(3):552-62.

Craparo A, Freund R, Gustafson TA. 14-3-3 (epsilon) interacts with the insulin-like growth factor I receptor and insulin receptor substrate 1 in a phosphoserine-phosphoinositol manner. J Biol Chem. 1997 Apr 25;272(17):11663-9.

Ogihara T, Iobe T, Ichimura T, Taoka M, Funaki M, Sakoda H, Onishi Y, Inukai K, Anai M, Fukushima Y, Kikuchi M, Yazaki Y, Oka Y, Asano T. 14-3-3 protein binds to insulin receptor substrate 1, one of the binding sites of which is pS978 a known PKA phosphorylation site (S1011 here). J Biol Chem. 1997 Oct 2;272(40):24612-7.

Kosaki A, Yamada S, Suga J, Otaka A, Kuzuya H, Deakin et al (2009) used a different version because residue numbers don’t match although sequence alignment indicates that IRS-1 contains at least five putative 14-3-3 binding sites. Three of them are within the amino-terminal portion of the molecule that is important for the interaction of IRS-1 with the insulin receptor and PKB and might contribute to its subcellular localization (Xiang et al. 2002).

**Human ITGA4 (CD49D) Integrin alpha4 (Swissprot = P13612)**

50 HPPLNHSR[pS]IPMPAS (Ser270 in human IRS3) and decreases insulin receptor substrate 1, one of the binding sites of which is pS978 a known PKA phosphorylation site (S1011 here). J Biol Chem. 1997 Oct 2;272(40):24612-7.

Kosaki A, Yamada S, Suga J, Otaka A, Kuzuya H, Deakin et al (2009) used a different version because residue numbers don’t match although sequence alignment indicates that IRS-1 contains at least five putative 14-3-3 binding sites. Three of them are within the amino-terminal portion of the molecule that is important for the interaction of IRS-1 with the insulin receptor and PKB and might contribute to its subcellular localization (Xiang et al. 2002).

**Notes**

Deakin et al (2009) used a different version because residue numbers don’t match although sequence around 14-3-3 binding motif is the same. Y991 (2004 here)

ROQQKL – 14-3-3 binding motif with pS978 in paper (S1011 here) 3

ENRRD – paxillin binding region with S988 a known PKA phosphorylation site (S1021 here) 4.

S978A decreases metabolic labeling of integrin alpha 4 with 32P-orthophosphate

FRET analysis found an interaction between 14-3-3 zeta and integrin cd4"The interaction between cd4 integrin and 14-3-3ζ is enhanced by the direct association between 14-3-3ζ and paxillin, resulting in the formation of a ternary complex that stabilizes the recruitment of each component. The ternary complex focuses Cd42 activity at
lanellipodial leading edge."

“Here, we show that MSP-mediated PI3K pathway activation induces Ron serine phosphorylation at residue 1394 as well as α6β4 phosphorylation in the connecting line generating 14-3-3 binding sites on both molecules. Thus, dimeric 14-3-3 proteins mediate the MSP-dependent formation of a Ron/α6β4 complex that in turn induces disassembly of HDs and α6β4 relocation at lamellipodia. Further, α3β1 integrin activation and keratinocyte spreading/migration on laminin-5 takes place. All these findings suggest a role for Ron and 14-3-3 in epidermal reepithelization processes”. (Santoro et al 2003)

References to 14-3-3 binding to integrin alpha4

Deakn NO, Bass MD, Warwood S, Schoolerem J, Mostafavi-Pour Z, Knight D, Ballestrem C, Humphries MJ. An integrin-alpha4-14-3-3-ζeta-paxillin ternary complex mediates localised Cdc42 activity and accelerates cell migration. J Cell Sci. 2009 May 15;122(Pt 10):1654-64.

Santoro MM, Gaudino G, Marchisio PC. The MSP receptor regulates alpha4beta4 and alpha3beta1 integrins via 14-3-3 proteins in keratinocyte migration. Dev Cell. 2003 Aug;5(2):257-71.

Human ITGB1 Integrin beta 1 subunit (fibronectin receptor) (Swissprot = P05556)

1 MNLQF PKWGL LISS DCVFAPQDG AMNCGC WCTN STFLQG MPTSA RCDLEAL KKKPCDDIPR SMSGKD RGEK NGVSRG SLQV YVEKQVYK ECVVYKSL YCVNGVNGT NRGK CNISI 2 121 RQLSSEQPT FTFLKFRARED YIDLYLMDS LYSMKDLLE NVSKSDLM MEMRITDS 211 RIG SFSVKE TVMPYI STTP AKLNPRCTSE QCNTSFSY KVLSSLTNKGE FVNL KVRF 221 ISNLD SLYMDMSKDLLE NVSKSDLM MEMRITDS 311 CHERNMTMY SHYDPYSIA LVQKSLRHNV IQTIFAYT EYFKVKLNL LIKPSA VOTL 361 SANSSVQL IDAYNSLS SVELENGKL ECVYISKYG CVNGVNGT G NRGK CNISI 411 GDEQVF EISI TSNCKFKKDS KDSKIRLGFP TEEV VILQQ EICSCSEQ Efp2 ECHPGC 461 NGTTEGACAR CNEVRGVRHC ECSTDEVNSE DMDAYKRCRN SSEECSNGNE CVCQCV CVC R 511 KRNDBIYSGS KFCEDNFCP DNSQCLLIGCQCNRCG VCNPSYTNGAC DCSLDSTSE 561 ASNQHC INGR GICEVGCVC TDFKPDGQ TC EMQCTLCGLVC AEKHECVCQCR APKNGEKF DT 611 CSGSCVPTQX SVQPSDQPVH CKERKDVDC FYTPSVYHKLHN 661 72 PCPEG TPDII PIVAGVAVGI VLGLA IIIWLWWMLHHRR EFAFKEEK MNAKWD G 718 PIYKAS NVPNK 781 Include RecName: Full=Cell surface adhesion glycoprotein 1; AltName: Full=Integrin beta 3; AltName: Full=Fibronectin receptor subunit beta; AltName: Full=Integrin VLA-4 subunit beta; CD antigen: CD29; Flags: Precursor

Human ITGB3 Integrin beta 3 subunit (fibronectin receptor) (Swissprot = P05107)

I MLGLRPPLLA LVGLLLAVC LGQECTFKV SACRCIESG PGCTWQKLN PTGPGDPSI 61 RCDTPQQLM RGCAAADDNQ PTLAETQED HNCGQKQLSP PTVYLRLP QAAE FWTPR 111 RAKGYIDLY YLMDSLYSM DDLRNKVLKG DDLRNALRI TRESGIRPGF PVDKTVLPFF 161 NTHFDPKR LP CNPKKEQCP PFAF RHLV WLN TNNSQFQTE VQGQLISNL DAPEGGDLM 211 MVQACPEEI GWRNTVL R PTDGGFHPA GDGRKAILT PNRCHL NLYR SNFEDF 261 YSVPQVLK HAENIQPIF AVTRSMWTVTE KLEITEPKP AVGELSEDS MVLQIKKNAY 311 SNKLSPFVLH NLALPFLKY TVDSFCNONG THRNRPGDC DGQVQINPVT FQPVYATEC 361 I QEQSVIRGA LGDFTIVDVQ LVQPCCECR DSRQSRLSH KGFLEG CIGC RDTDYGNK 411 EECQTGORSS QLELESSCRKD NSSICISSLG DCVCQCLICH TSDVPGLY QYYCQDCTL 461 CERYQVNGQF PGRGFCCGC FCRCRGPFEG SACQCCRTFE GCVPNFRVEC SGGRCRVCN 511 CECHSOSQFL QCQSCOPCFS PSCQYSICAE CLKEFEGFGK MNSACQPGL QSLNPFVKOR 561 TKCERDSEQ MVATLBEQDG CDMDRLYV DLEBCVAGPN IAAVGTGATVA GIVLGLL 611 Include RecName: Full=integrin beta-1; AltName: Full=Integrin VLA-4 subunit; CD antigen: CD29; Flags: Precursor

MNLQFPKFWGL LISSDCVFAPQDGAMNCWCWCTNSTFLQGMPTSACRDDEALKKKCPDDPIPRSMSGKDRGENGVSRGSVLQVYVEKQVYECCVYKSLWYCNGVNGTNGRKCNISI

© 2010 The Author(s)

The author(s) has paid for this article to be freely available under the terms of the Creative Commons Non-Commercial License (http://creativecommons.org/licenses/by-nc/2.5/) which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.
ITGB2 the integrin beta 2 subunit. Can combine with multiple partners resulting in different integrins. For example, beta 2 combines with the alpha L chain to form the integrin LFA-1, and combines with the alpha M chain to form the integrin Mac-1. Participates in cell adhesion as well as cell-surface mediated signaling. Defects are the cause of leukocyte adhesion deficiency type I (LAD1).

From Fagerholm et al. (2002) pp. 775 and 778.

Endogenous 14-3-3 proteins bind while filamin cannot bind so phosphorylation acts as a switch. Phosphorylation of T758 may lead to detachment of talin from the integrin tail.

Notes

ITGB2 the integrin beta 2 subunit. Can combine with multiple partners resulting in different integrins. For example, beta 2 combines with the alpha L chain to form the integrin LFA-1, and combines with the alpha M chain to form the integrin Mac-1. Participates in cell adhesion as well as cell-surface mediated signaling. Defects are the cause of leukocyte adhesion deficiency type I (LAD1).

References to ITGB2

From Fagerholm et al. (2002) pp. 775 and 778.

Endogenous 14-3-3 proteins bind while filamin cannot bind so phosphorylation acts as a switch. Phosphorylation of T758 may lead to detachment of talin from the integrin tail.

Notes

ITGB2 the integrin beta 2 subunit. Can combine with multiple partners resulting in different integrins. For example, beta 2 combines with the alpha L chain to form the integrin LFA-1, and combines with the alpha M chain to form the integrin Mac-1. Participates in cell adhesion as well as cell-surface mediated signaling. Defects are the cause of leukocyte adhesion deficiency type I (LAD1).

Integrin beta 1 (fibronectin receptor) 780 NP1Y.................................KSAVTTVV NP_002202

Integrin beta 3 (platelet glycoprotein Ila) 770 NPLYKEA.............................TSTF7N MP_000203

Integrin beta-7 775 NP1Y..............................................GISTSFK A37057

References to 14-3-3 binding to integrin beta2

Fagerholm S, Morrice N, Gahmberg CG, Cohen P. Phosphorylation of the cytoplasmic domain of the integrin CD18 chain by protein kinase C isoforms in leukocytes. J Biol Chem. 2002 Jan 18;277(3):1728

Takala H, Nurminen E, Nurmi SM, Aatonen M, Strandin T, Takatalo M, Kienna T, Gahmberg CG, Yläne J. Fagerholm SC. Beta2 integrin phosphorylation on Thr758 acts as a molecular switch to regulate 14-3-3 binding. J Biol Chem. 2002 Jan 18;277(3):1728

From Takala et al. (2008) pp. 785.

Phorbol ester treatment (PDBu) of T cells leads to T758 phosphorylation, seen with a phosphospecific antibody. Peptide affinity columns corresponding to phospho-T758 and non-phospho-T758 were used to pull down proteins from T cell lysates. 14-3-3 proteins bind while filamin showed preference for the non-phosphorylated column. When T758 is phosphorylated, 14-3-3 bnd while filamin bind not so phosphorylation acts as a switch. Phosphorylation of T758 may lead to detachment of talin from the integrin tail.

Notes

ITGB2 the integrin beta 2 subunit. Can combine with multiple partners resulting in different integrins. For example, beta 2 combines with the alpha L chain to form the integrin LFA-1, and combines with the alpha M chain to form the integrin Mac-1. Participates in cell adhesion as well as cell-surface mediated signaling. Defects are the cause of leukocyte adhesion deficiency type I (LAD1).

Integrin beta 1 (fibronectin receptor) 780 NP1Y.................................KSAVTTVV NP_002202

Integrin beta 3 (platelet glycoprotein Ila) 770 NPLYKEA.............................TSTF7N MP_000203

Integrin beta-7 775 NP1Y..............................................GISTSFK A37057

References to 14-3-3 binding to integrin beta2

Fagerholm S, Morrice N, Gahmberg CG, Cohen P. Phosphorylation of the cytoplasmic domain of the integrin CD18 chain by protein kinase C isoforms in leukocytes. J Biol Chem. 2002 Jan 18;277(3):1728

Takala H, Nurminen E, Nurmi SM, Aatonen M, Strandin T, Takatalo M, Kienna T, Gahmberg CG, Yläne J. Fagerholm SC. Beta2 integrin phosphorylation on Thr758 acts as a molecular switch to regulate 14-3-3 and filament binding. Blood. 2008 Sep 1;112(5):1853-62.

Takala H, Nurminen E, Nurmi SM, Aatonen M, Strandin T, Takatalo M, Kienna T, Gahmberg CG, Yläne J. Fagerholm SC. Beta2 integrin phosphorylation on Thr758 acts as a molecular switch to regulate 14-3-3 and filament binding. Blood. 2008 Sep 1;112(5):1853-62.

From Takala et al. (2008) pp. 785.

Phorbol ester treatment (PDBu) of T cells leads to T758 phosphorylation, seen with a phosphospecific antibody. Peptide affinity columns corresponding to phospho-T758 and non-phospho-T758 were used to pull down proteins from T cell lysates. 14-3-3 proteins bind while filamin showed preference for the non-phosphorylated column. When T758 is phosphorylated, 14-3-3 bnd while filamin bind not so phosphorylation acts as a switch. Phosphorylation of T758 may lead to detachment of talin from the integrin tail.

Notes

ITGB2 the integrin beta 2 subunit. Can combine with multiple partners resulting in different integrins. For example, beta 2 combines with the alpha L chain to form the integrin LFA-1, and combines with the alpha M chain to form the integrin Mac-1. Participates in cell adhesion as well as cell-surface mediated signaling. Defects are the cause of leukocyte adhesion deficiency type I (LAD1).

Integrin beta 1 (fibronectin receptor) 780 NP1Y.................................KSAVTTVV NP_002202

Integrin beta 3 (platelet glycoprotein Ila) 770 NPLYKEA.............................TSTF7N MP_000203

Integrin beta-7 775 NP1Y..............................................GISTSFK A37057

References to 14-3-3 binding to integrin beta2

Fagerholm S, Morrice N, Gahmberg CG, Cohen P. Phosphorylation of the cytoplasmic domain of the integrin CD18 chain by protein kinase C isoforms in leukocytes. J Biol Chem. 2002 Jan 18;277(3):1728-38.

Takala H, Nurminen E, Nurmi SM, Aatonen M, Strandin T, Takatalo M, Kienna T, Gahmberg CG, Yläne J. Fagerholm SC. Beta2 integrin phosphorylation on Thr758 acts as a molecular switch to regulate 14-3-3 and filament binding. Blood. 2008 Sep 1;112(5):1853-62.

Takala H, Nurminen E, Nurmi SM, Aatonen M, Strandin T, Takatalo M, Kienna T, Gahmberg CG, Yläne J. Fagerholm SC. Beta2 integrin phosphorylation on Thr758 acts as a molecular switch to regulate 14-3-3 and filament binding. Blood. 2008 Sep 1;112(5):1853-62.

The focus of the paper below was not on integrin beta2 but on c-Kit.
Deletion of the ANKRD15 gene at 9p24.23 causes parent-of-origin-dependent inheritance of familial cerebral palsy. The Kank family of proteins, Kank1–Kank4, are characterized by their unique structure, coiled-coil motif, in the N-terminal region, and ankyrin-repeats in the C-terminal region, with an additional motif, the KN motif, at the N-terminus. Kank is a KANK potential tumour suppressor for renal cell carcinoma and an Akt substrate located downstream of PI3K and a 14-3-3-binding protein. The interaction between Kank and 14-3-3 is regulated by insulin and EGF and is mediated through phosphorylation of Kank by Akt. Q14678 is the KANK-1 (long isoform), whereas Kakinuma et al. (2008) must have lost the KANK-N form, which lacks the 158 amino acids, because they report the phosphorylated residue to be Ser167 (NCVCYRRKRSYAGNASQLEQL). (Variants described in Wang Y, Onishi Y, Kakinuma N, Roy BC, Aoyagi T, Kiyama R. Alternative splicing of the human Kank gene produces two types of Kank protein. Biochem Biophys Res Commun. 2005 May 20;330(4):1247–53.)

References to 14-3-3 binding to KANK1
Kakinuma N, Zhu Y, Wang Y, Roy BC, Kiyama R. Kank protein interacts with and regulates RDK1 and TASK-1 binding to KANK1 and TASK-3-dependent formation of actin stress fibers and cell migration via 14–3–3 in PI3K-Akt signaling. J Cell Biol. 181(3):537–49
Kakinuma N, Zhu Y, Wang Y, Roy BC, Kiyama R. (2008) Kank regulates RhoA-dependent formation of actin stress fibers and cell migration via 14-3-3 in PI3K-Akt signaling. J Cell Biol. 181(3):537-49.
References to 14-3-3 binding to KIF1C
Zuzaarte M, Heusser K, Renigunta V, Schlichthölter G, Rinné S, Wissmeyer E, Daut J, Schwappach B, Preiss-Müller R. The kinesin-14 family of K+ channels TASK-1 and TASK-3: role of N- and C-terminal sorting signals and interaction with 14-3-3 proteins. J Physiol. 2009 Mar 1;587(Pt 5):929-52.

Human KIF1C (Kinesin-like protein KIF1C) (Swissprot = O43896)

1 MAGASKVAVK VQETQAPRT SQADCAVSMQGNTSINQP SQADKAPST TFDISYWSHT 61 STEPDQAQV QQVDIQGEEL MLLHAFEGY QFICAFAYQGG ASKTMMQR ETTEQQQGGVF 121 QELDFISIS QNENGVLQSY GVEVSVMILY CERPVRILNP KGRSGLRVPL HPGQYQD 181 LSKLATVY DIADLDMCOC KARTVAATNET SSRSRAOH FDTICLQLDSEK 241 VSIISLVIDLA GSERADSSG RGRMLKEGAN INKSLTLTGG VIGALMDQG KRRKSDFIY 301 KDSVLTLIK ELNNGSNRT AIMAASPAI NYETETLSTL YARDTQRGC NAINEPADPN 361 RLKILQEOV ARLRELLMAQ GSLASALELG KTERGSUGKA LPATSSSPPAP VSPSSSPFTHN 421 GELEPOSTPN TEQOGKPEVA MRLPQETEK IAIBLNTWKE KLRATELNM KERRALMNG 481 VAVREDGGTV GVFSKPTTH VNLEDNPLDM SECLLYHHD VGTQVQDVDM DIKLQTFIRQ 541 EQHCFLFRISP QQDGEDVVTG EPCFAGETYV NGKLTEPVL LKSNIRMVG KHNNVFHRNP 601 EQALARERLE VPPPFGPQFE VFDNWFAQKE LEOQGGIDK MERTKLQOL ENQREVKEE 661 ADLLELQQRQL YADDSOSGDD DRKSCSEWW LISSLREQLP PFTQTVIKRL CGPSGSKRKR 721 PASSPPQPV RROQMLNQ WRADMLKQW AKVEICYVEA LAOBDWRAE IEOAALMKN 781 ENLGGNSRTA MIAALSPA ATQVREDGGTV 841 VAVREDGGTV GVFSKPTTH VNLEDNPLDM SECLLYHHD VGTQVQDVDM DIKLQTFIRQ 901 EQHCFLFRISP QQDGEDVVTG EPCFAGETYV NGKLTEPVL LKSNIRMVG KHNNVFHRNP 961 EQALARERLE VPPPFGPQFE VFDNWFAQKE LEOQGGIDK MERTKLQOL ENQREVKEE 1021 PSPRRSHPPR RNSLDOGGRS MAGGAGQAPPQ HQMPQPKXNS YOOQQVQAPA RQPPGYFPPP 1081 YTTPPPMRRO EQPSLANDKEEAV

Notes
RRKPs$$^\text{V-Conn}$$

References to 14-3-3 binding to KIF1C

Domer C, Ullrich A, Haring HU. The kinesin-like motor protein KIF1C occurs in intact cells as a 14-3-3 family. J Biol Chem. 1999 Nov 19;274(47):33654-60.

Human KIF1C (Swissprot = O98186)

1 MAMMVFPREE KLSSQDEIVLGM TKAVIGQLET LRGREARRAALL PLVAPAAEAE GAPQEQRICL 61 LRSLREIAEL GLGEAQVIL LSHHLGAVES EQKQLRAQVR RLQVQNQWR EELAQTQQLK 121 QRSEQAVAA WELKELHLMF QIQLKLDDDA SPMEEGD GDTXDDLPFEM EDEQPSASPF 181 QQGGDVSQQHS GEYFIPALKRT LHNLVYQAS QEGRYAVPLC QMQUELDER SQNSNDFVDA 241 TMNHLAVY RQGNEQGKQTLH ETLGQKMRP VAAALNQILV WQDRQGVYKE 301 AEPJLRCA IREKVQGKFLH PDVAKQNLQ LQCCAQPQKEV YYYYVARRY LEIYATLRGP 361 DDPHNATKLN NLASCLLYQKV KQDSTQLYT EILITRAHEK FGSSNGNK wrink 421 SKDRKRDSAP YGEEQSWYKA CVKDSPTVNT TLRSGLGAR YQSKLEA AlTEDCAINRR 481 QQLDPAQTR VVLEDDOSG MRRSRSRDARR MAGGSAPPGS SLDDLGVQPT EMWDGSGS 541 RSRSGPSBCD DALTRESHGGN VQKQQGQPGP EPPNMRKKA $$\beta$$FNFKNGG EEEFTPGQGSG 601 LQDQRTLSSSL SMDSLRSSRLVG

Notes
RRQRS$$^{3972\text{AP}}$$

References to 14-3-3 binding to KIF1C

Domer C, Ullrich A, Haring HU. The kinesin-like motor protein KIF1C occurs in intact cells as a dimer of the proteins with 14-3-3 in the accessory proteins. J Biol Chem. 1999 Nov 19;274(47):33654-60.
KLC2 is a microtubule-associated factor that may play a role in organelle transport. The light chain may function in coupling of cargo to the heavy chain or in the modulation of its ATPase activity. Subsequent analyses showed that 14-3-3 directly binds to kinesin heterodimers through interaction with KLC2 and that this interaction is dependent on the phosphorylation of KLC2. Studies on the interaction between 14-3-3 and KLC2 variants expressed in cultured cells with mass spectrometric analysis proved that Ser575 (RASp575) in mouse KLC2 (686058) is the site of phosphorylation in KLC2 that is responsible for the in vivo interaction with the 14-3-3 protein (Ser582 in human KLC2 Q91086).

References to 14-3-3 binding to kinesin light chain 2

Ichimura T, Wakamiya-Tsunoda A, Itagaki C, Taoka M, Hayano T, Natsume T, Isebo T. 1998 Apr;17(7):1892-9. Proc Natl Acad Sci U S A. 2002 Apr 30;99(8):5517-22. Pozuelo Rubio M, Geraghty KM, Wong BH, Wood NT, Campbell DG, Morrice N, Mackintosh C. 14-3-3-affinity purification of over 200 human phosphoproteins reveals new links to regulation of cellular metabolism, proliferation and trafficking. Biochem J. 2004 Apr 15;379(Pt 2):395-408.

Notes
KLC2 is a microtubule-associated factor that may play a role in organelle transport. The light chain may function in coupling of cargo to the heavy chain or in the modulation of its ATPase activity. Subsequent analyses showed that 14-3-3 directly binds to kinesin heterodimers through interaction with KLC2 and that this interaction is dependent on the phosphorylation of KLC2. Studies on the interaction between 14-3-3 and KLC2 variants expressed in cultured cells with mass spectrometric analysis proved that Ser575 (RASp575) in mouse KLC2 (686058) is the site of phosphorylation in KLC2 that is responsible for the in vivo interaction with the 14-3-3 protein (Ser582 in human KLC2 Q91086).

**Human KRT18** Keratin 18 (Swissprot = P05783)

| Amino Acid Sequence | Description |
|---------------------|-------------|
| IATRQDRAQYDELARSKRK | Keratin, type I cytoskeletal |
| ETNDTKVLRH | Keratin, type I cytoskeletal |

**Human KSR1** (kinase suppressor of Ras) (Swissprot = Q8IVT5)

| Amino Acid Sequence | Description |
|---------------------|-------------|
| MDRAALRAAA MKEKKGQGQ GLAESAGGAA AASRALQCGG QQLKLDISI GSLGLATKQD | Keratin, type I cytoskeletal |
| VQETKLLGQGQ | Keratin, type I cytoskeletal |

**References to 14-3-3 binding to keratin 18**

Sivaramakrishnan S, Schleifer C, Kim Y, Blumenfeld M, Dong J, Gustin DM. 1995 Aug;160(3):708-14. Keratin is a soluble cofactor produced by keratinocytes and cultured fibroblasts. J Biol Chem. 1996 Apr;271(15):8655-62. Liao J, Omary MB. 1998 Apr 1;17(7):1892-9. Human KSR1 (kinase suppressor of Ras) (Swissprot = Q8IVT5)

| Amino Acid Sequence | Description |
|---------------------|-------------|
| MDRAALRAAA MKEKKGQGQ GLAESAGGAA AASRALQCGG QQLKLDISI GSLGLATKQD | Keratin, type I cytoskeletal |
| VQETKLLGQGQ | Keratin, type I cytoskeletal |

Notes
Shear stress activates PKC {zeta}, which then phosphorylates K18pSer33 and promotes the interaction of 14-3-3 with KIFs (Ser33 = Ser34 in P05783). Shear stress activates PKC {zeta}, which then phosphorylates K18pSer33 and promotes the interaction of 14-3-3 with KIFs (Ser33 = Ser34 in P05783).
which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.

The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial Licence (http://creativecommons.org/licenses/by-nc/2.5/)

© 2010 The Author(s)

References to 14

GKEDFLSVSD IIDYFRKM

Here, we identify 14 constitutive and ras

isoform 2; AltName: Full=SH2 domain

protein kinase binding, and KSR overexpression. Mol Cell. 2001 Nov;8(5):983-7

Müller J, Ory S, Zhou M, Conrads TP, Veenstra TD, Morrison DK. Protein phosphatase 2A positively regulates Ras

functional interaction of 14 KSR a serine/threonine kinase of the Raf family with no demonstrated kinase activity.

Jiménez F, Nebreda AR, Alba E, Lozano J. The

Rivas LG, Ruiz EJ, Ranea JA, Sánchez

as SLP76 at serine 376.

ASVDNQLN AQLAAGNPGY

SPTSNGGRS RAYMPPRSRS

RDDLY

Agkata SVGP

Here, we identify 14-3-3 binding and zeta proteins as SLP-76 binding partners. This interaction was induced by
tory 14-3-3 proteins with the ERK1/2 scaffold KSR1 occurs in an isoform-specific manner. J Biol Chem. 2008 Jun 20;283(25):17450-62.

Notes

Two 14-3-3 binding sites are RSKpSHE (=S309 in Q81VT5) and RTEpSVP (= Ser404 in Q81VT5) KSR a serine/threonine kinase of the Raf family with no demonstrated kinase activity. KSR, 14-3-3 and Raf form an oligomeric complex and that KSR positively regulates the Ras signaling pathway in vertebrate organisms.

References to 14-3-3 binding to KSR

Xing H, Xiong KD, Muslin AJ. The protein kinase KSR interacts with 14-3-3 protein and Raf. Curr Biol. 1997 May 17(5):294-300

Jagemann LR, Pérez-Rivas LG, Ruiz EJ, Ranea JA, Sánchez-Jiménez F, Nebreda AR, Alba E, Lozano J. The functional interaction of 14-3-3 proteins with the ERK1/2 scaffold KSR1 occurs in an isoform-specific manner. J Biol Chem. 2008 Jun 20;283(25):17450-62.

Müller J, Ory S, Copeland T, Piwnica-Worms H, Morrison DK. C-TAK1 regulates Ras signaling by dephosphorylating the MAPK scaffold, KSR1. Mol Cell. 2001 Nov;13(16):1356-64.

Cacace AM, Michaud NR, Therrien M, Mathes K, Copeland T, Rubin GM, Nat Medical KC. Identification of constitutive and ras-inducible phosphorylation sites of KSR: implications for 14-3-3 binding, mitogen-activated protein kinase binding, and KSR overexpression. Mol Cell. 1999 Jan;19(1):229-40.

Human LCP2(SLP-76) (Lymphocyte cytotoxic protein 2, aka SLP-76) (Swissprot = Q13094)

Human LSR Isoform 2 of lipolysis-stimulated liprotein receptor (Swissprot = Q86X29)
Human MAP3K3 (MEKK3) Protein kinase of the STE11 family (Swissprot = Q99759)

1 MDEQALNSI MNDIVALQMN RRHRMPGTY MEKMRKDGHN RSQSDVRKFE HNGERRIIAF 61 3RPFYVEDV HKVTTVPQQP LDDLHYNNEL SILLKhQDQL DRAIDLDRS SSMSRRIL 121 1L5Q5HUNNS SRAGDRVTV RIKASQQAGD INTIQYQFRP RSRHLVESQQ NQGRPSEPP 181 YVIPQERQHIA RQGSSTYINS EGEFIPETSE QCMLDPLSHA ENLSGQSCC LDGRDASPSF 241 4KRSMRQAS PPFDNQYESD RETQLYDRKV KGTYPVRVH VSVHVDKYS DRGFRPRR 301 3HQLNFTSLGE NSMLAVQYLD PGRRLRSAD LSANELQSEN VPTRSPPSAPI 361 466 WRRK2LQOQ GAPGRVLQCV DTVGTRLEAS RKQQFDPSDF ETSKEVSALE CEIQLKLNQ 421 524 HERIVQYYGCL RSRMTGGGLGK QKDGAVQY VGSSVFYMKVLTSTPM LPQCLEMOMY 481 623 HSNIVHRDLI KGANIRLDA GNVKLDQGFA SRKLTQMCS GCTMGRSTVT PGVMSPEVIS 541 616 M3GEGYRRKAD WSLGCTVVE LTKFPPWAEY EAMAIKFI KQTFNTPLP5 HIHEGGRDFL 601 656 0RRFVBARQ RSAEELLTHH FAQMLY>
>gi|160332306|sp|Q99759.2|M3K3_HUMAN RecName: Full=Mitogen-activated protein kinase kinase kinase 3; AltName: Full= MAPK-activated kinase kinase kinase 3; Short=MEK 3; Short= MEK3

Notes

MEKK3 is a protein kinase of the STE11 family. Phosphorylation and activated by MLK3 and TAK1. Phosphorylates and activates MEK5.

Endogenous MEKK3 was phosphorylated on Ser526 in response to osmotic stress. In addition, phosphorylation of Ser526 was required for MKK6 phosphorylation in vitro, whereas dephosphorylation of Ser526 was mediated by protein phosphatase 2A and sensitive to okadaic acid (Mati et al. 2008).

We identified two phosphorylated amino acids at Ser166 and Ser337 which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.
The N-terminal of ASK1-interacting protein (AIP1) (Ras GTPase-activating protein) containing the C2 and GAP domains constitutively binds to ASK1 and facilitates the release of 14-3-3 proteins from ASK1. Oncogene. 2008 Feb 11;29(7):1297-305.

Liu, Guoyong Yin, James Surapisitchat, Bradford C. Berk, and Wang Min (2001) Laminar flow inhibits TNF–alpha-induced ASK1 activation by preventing dissociation of ASK1 from its inhibitor 14-3-3. J Clin Invest. 2001 Apr;107(7):917-23.

Zhang R, He X, Liu W, Lu M, Hsieh CC, Papaconstantinou J. Thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredoxin or thioredox
We show that ASK2 specifically interacts with 14-3-3 proteins through phosphorylated S964. Although a 14-3-3-binding defect to mutant of ASK1 (S967A) has no effect on the ASK2/14-3-3 interaction, both overexpression of the analogous ASK2 (S964A) mutant and knockdown of ASK2 dramatically reduced the amount of ASK1 complexed with 14-3-3. These data suggest a dominant role of ASK2 in 14-3-3 control of ASK1 function. Indeed, ASK2 S964A-induced dissociation of 14-3-3 from ASK1 correlated with enhanced phosphorylation of ASK1 at T838 and increased c-Jun N-terminal kinase phosphorylation, the two biological readouts of ASK1 activation. Our results suggest a model in which upstream signals couple ASK2 S964 phosphorylation to the ASK1 signalosome through dual engagement of 14-3-3.3. (Cockrell et al 2009 prepublication date).

References to 14-3-3 binding to ASK2

Cockrell LM, Puckett MC, Goldman EH, Khuri FR, Fu H. Dual engagement of 14-3-3 to ASK2 mediates cell growth and survival. Previous data show that BMK1 can be activated by steady laminar flow and is atheroprotective by preventing endothelial cells from undergoing apoptosis. References to 14-3-3 proteins through phosphorylated S964 (Berk et al 2000). Mutation of serine 486 (Big mitogen activated protein kinase 1 (BMK1)/ERK5) prevents the interaction with 14-3-3 proteins through phosphorylated S964 (Berk et al 2000). These data suggest a dominant role of ASK2 specifically interacts with 14-3-3 proteins through phosphorylated S964. Although a 14-3-3-binding defect to mutant of ASK1 (S967A) has no effect on the ASK2/14-3-3 interaction, both overexpression of the analogous ASK2 (S964A) mutant and knockdown of ASK2 dramatically reduced the amount of ASK1 complexed with 14-3-3. These data suggest a dominant role of ASK2 in 14-3-3 control of ASK1 function. Indeed, ASK2 S964A-induced dissociation of 14-3-3 from ASK1 correlated with enhanced phosphorylation of ASK1 at T838 and increased c-Jun N-terminal kinase phosphorylation, the two biological readouts of ASK1 activation. Our results suggest a model in which upstream signals couple ASK2 S964 phosphorylation to the ASK1 signalosome through dual engagement of 14-3-3.3.
Six isoforms of human tau generated by alternate splicing, of which tau3 (P10636) is the shortest. This is the sequence sent by Nikolai B. Gusev. He says “We were working with the shortest isoform of human tau protein (P10636-3), fetal brain isoform. The sites that were mutated and/or phosphorylated by cAMP-dependent protein kinase and that seem to be important for interaction with 14-3-3, might be involved in the pathology of this protein isoform. The shortest isoform is sending you the primary structure of this isoform with phosphorylation sites marked in red as an attachment.”

MABFQFEQEVDMHACTYGLQGDKQQQQYTMHQQEDQDDTDALGKAEGIOTGSPLEDLEQAGTFTQKQVSTEPQSEQGKQANA TRIPKTPPA PKTEDGSSPGPKGDSRGSPSGPSTGPSRSRTLPT TPETPKMVVRVTPPKSPSS AKSLQQTAPVMPDLKVKG KISTENLHK PQGGQKVQV YPKVPSKTV SKCQG LNIHHRGGQKVKEVEKLSGPGKEDS DKLKVRPSKQSKLG SNIITHVPGGGKNKIRLKHITFKRPRENAK AKTDHGAEIYVKPVPSGDSTPRHLNSVTSSTGDSIMVDPQLATLADVEASLAKQGL

Notes

Six isoforms of human tau generated by alternate splicing, of which tau3 (P10636-3) is the shortest. This is the sequence sent by Nikolai B. Gusev. He says “We were working with the shortest isoform of human tau protein (P10636-3), fetal brain isoform. The sites that were mutated and/or phosphorylated by cAMP-dependent protein kinase and that seem to be important for interaction with 14-3-3, might be involved in the pathology of this protein isoform. The shortest isoform is sending you the primary structure of this isoform with phosphorylation sites marked in red as an attachment.”

MABFQFEQEVDMHACTYGLQGDKQQQQYTMHQQEDQDDTDALGKAEGIOTGSPLEDLEQAGTFTQKQVSTEPQSEQGKQANA TRIPKTPPA PKTEDGSSPGPKGDSRGSPSGPSTGPSRSRTLPT TPETPKMVVRVTPPKSPSS AKSLQQTAPVMPDLKVKG KISTENLHK PQGGQKVQV YPKVPSKTV SKCQG LNIHHRGGQKVKEVEKLSGPGKEDS DKLKVRPSKQSKLG SNIITHVPGGGKNKIRLKHITFKRPRENAK AKTDHGAEIYVKPVPSGDSTPRHLNSVTSSTGDSIMVDPQLATLADVEASLAKQGL

References to 14-3-3 binding to Tau
Chun I, Kwon T, Lee EJ, Kim CH, Han YS, Hong SK, Hyun S, Kang SS. 14-3-3 Protein mediates phosphorylation of microtubule-associated protein tau by serine- and glucocorticoid-induced protein kinase 1. Mol Cells. 2004 Dec 31;18(3):360-8
Sadik G, Tanaka T, Kato K, Yanagi K, Kudo T, Takeda M. Phosphorylation of tau at Ser214 mediates its interaction with 14-3-3, but 14-3-3 or 14-3-3(tau analog) that can only bind to phosphorylated Ser214. J Neurochem. 2009 Jan;108(1):33-43
Sluchanko NN, Seit-Nebi AS, Gusev NB. Phosphorylation of more than one site is required for tight interaction of human tau protein with 14-3-3(tau analog). Mol Cells. 2004 Dec 20;18(3):360-8
Sluchanko NN, Seit-Nebi AS, Gusev NB. Phosphorylation of more than one site is required for tight interaction of human tau protein with 14-3-3(tau analog). Mol Cells. 2004 Dec 20;18(3):360-8

Human MARK2 (aka Par-1b/EMK) (Swissprot = Q7KZ17)

1  MSSARTPLPT LNERQDQTPT LGHDSKPS KSNRMRGNS ATSADEQPHI GNRYLLKTIG
2  LKNFAPKRLA RHILTGKEVA VKIDKQTQNL SSSLKQLFRE HRMVKLMV NIVKRLEVEY
3  D121 TKTDLKVE YASQGVSVDY LWNSRMRKE EARAARFQXQ SAVQYCHQF IVHRDNLKEN
4  L181 LIADDDNMK IADISPQFNEP TGQONLFQVE PQFPPYAQER DLKQVSQGD
5  241 YTLVSSGLPF DQNLKKEVL RLRVLYKRPY FMYSTDCECN KKLFLLINPS KRQTELQIMK
6  321 DWNNVHGED DELFQVYEL PFDYKDPRT ELMVSQYETE IQEODQLOVR YNEVATYLL
7  361 LGYKSELEG DITLKLFRPS ADLTSNASPS PSHKQVQSY AMIPQRFSFD QAAGAPITPS
8  421 YNQYKQPGN NAENKRRSEED RXASVRASPSL RKLEKTPPT STNGLSTST
9  481 NRSNREGL RASLQSTAS QNGDSLTMPO RSTASASA AAQVAPRQQ QKMSASASYH
10 511 NKAAGLPETE SNECVPRRP STAQRPVPSV SAIHNISASSG APOTRNPFRQ VSSRSHFAG
11 601 QLVRQDQPQN LPYQVTPASS GSHGSRQRGA SGGISFSKTE FKVPRNLSTR FARNNLNEPE
12 651 SOKRVETLPF HVGQGQGNKD KEKEFRFKEP RGLRFTWSMK TSSMNPÆMME REIRKLVDLA
13 721 NOSQLEFL MLNMCNMGPT HDSFQPQEME EVCKLPRSL SNGVPRISG TSMAPFNANAS

© 2010 The Author(s)
The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial Licence (http://creativecommons.org/licenses/by-nc/2.5/) which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.
Notes

Phosphorylation of human Par1b is mediated by PKCs at Ser400 (not sure but think it is RSVsANP) and Thr595 (SR595/SRF140Q). Thr595 is conserved in all 4 mammalian Par-1 kinases as well as the fly ortholog. 2 arms of the PKC pathway regulate interactions between Par-1b and 14-3-3 proteins: one involving aPKC and the other nPKC/PKD.

References to 14-3-3 binding to Mdm2

Lin J, Hou KK, Pwnica-Worms H, Shaw AS. The polarity protein Par1b/EMK/MARK2 regulates T cell receptor-induced mitrobule-organizing center polarization. J Immunol. 2009 Jul 15;183(2):1215-21.

Watkins JL, Lewandowski KT, Meek SE, Storz P, Toker A, Piwnica-Worms H. Phosphorylation of the Par-1 kinase polarity by protein kinase D regulates 14-3-3 binding and membrane association. Proc Natl Acad Sci U S A. 2008 Nov 25;105(47):18738-83.

Human Mdm2

Human Mdm4 (Swissprot = O15151)

Notes

Serine 367 (S367) abolishes binding of Mdmx to 14-3-3. Transfection assays indicated that the S367A mutation, in cooperation with Mdm2, enhances the ability of Mdmx to repress the transcriptional activity of p53 (Swissprot = O15151).

© 2010 The Author(s)

The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial Licence (http://creativecommons.org/licenses/by-nc/2.5/) which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.
which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.
structural features. Plays a critical role in the differentiation of various cell types including neural crest-derived melanocytes, mast cells, osteoclasts and optic cup-derived retinal pigment epithelium. Two isoforms are known: the M-isofom is expressed exclusively in melanocytes, while the A-isofom has a much broader range of expression. Mutations in MITF can lead to Waardenburg syndrome. Ten alternatively spliced isoforms have been described, which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.

C-TAK1 increased MITF/14-3-3 complex formation and thus promoted cytoplastic localization of MITF. C-TAK1 interaction was disrupted by RANKL/CSF-1 treatment. 14-3-3-binding site is Ser173 (PGLTISN|CPANLPN) (Bronisz et al 2006, supplementary, which is equivalent to Ser280 in the canonical OT5030).

MITF is highly related to the HLH-Zip transcription factor TFE3 that was identified as 14-3-3 binding partner by mass spectrometry analysis (Jin et al Curr Biol. 2006 Dec 24;16(14):1436-50). TFE3 has a site similar to 143 in MITF, which is a potential 14-3-3-binding site in TFE3 (PAITVSN|CPAELPN).

References to 14-3-3 binding to MITF
Bronisz A, Sharma SM, Hu R, Godlewski J, Tzivion G, Mansky KC, Ostrowski MC. Microphthalmia-associated transcription factor interactions with 14-3-3 module differentiate of committed myeloid precursors. Mol Cell Biol. 2006 Sep;17(9):3897-906.

Human MITF
Myeloid leukemia factor 1 isofom 1 (Swissprot = P58340)

| Human MITF | Myeloid leukemia factor 1 isofom 1 | (Swissprot = P58340) |
|------------|-----------------------------------|---------------------|
| 1 MFRMLNSSF EPDFPFESEI AHIENRQMI RSFGPPEGFR LLISIDRGKR AHNRRGHNGD |
| 61 EDLSITIDVS SFQFHEMQVS RMRNYKQLE RNQFDQSDWP NGNCFSSSY MSTIKIDGEP |
| 121 PVQQGSTQ TRAAPFGEIKET TAAMRDSQSG LEMAIGHHE LHRAMAIVIKK KNKTVSEQE |
| 181 NQFETINMMA DHAFDEHEQ SEVLYKPVQ PHNLGNTMRWS VHHENPSGSEQ IRRKREPKQPS |
| 241 PEAIHORRSPN VLDGLKHIQG SSVKSNNK |

Notes
MRQoM(Gs534)SFEFGDRL = 14-3-3 binding site on MITF! (protein kinase unknown, tagetted by NRP1 ?)(pseudokinase in WNK branch of kinase)

88KLERNFQGQSLDP = NES human (Yoneda-Kato and Kato 2008) Alav50 to Gin125 = Interaction with CSN3/COPS3 (Yoneda-Kato and Kato 2008)

Klinken et al (2002) Studies the MOUSE form of MITF! 88ELQRNFGQLSM100 = NES DIFFERENT ISOFORM?

References to 14-3-3 binding to MITF
Winteringher LN, Endersby R, Kobelke S, McCulloch RK, Williams JH, Stillitano J, Cornwall SM, Ingley E, Tiao JY, Lalonde JP, Tsai S, Tilbrook PA, Klinken SP, Winteringham LN, Endersby R

References to MITF mRNA
(1999) MFRMLNSSFE DDPFPESEI AHIENRQMI RSFGPPEGFR LLISIDRGKR AHNRRGHNGD |

Human MLK3
(Swissprot = Q16584)

| Human MLK3 | (Swissprot = Q16584) |
|------------|---------------------|
| 1 MEPLKSLFLK SPLGWSNGSS GGGGGGGGG RPEPSKKQAAY AANPWFATLDF YEPSQSDQEL |
| 61 ALRKGDRPVE LSRDAAISGDD EGNWAOQVYG QVGFPSNYV SRGCGPPCPC VAQFQRLKRE |
| 121 EYIGQOGFKG VIRGVQRGWE LAVYAAQRDFP DEDISVTARS VRQEARLAMF LARHPITALK |
| 181 AMVCPRPL LVCAYAAGPP LKALAGGRVW FPPHLYNVAVP QAIBOMQIMV VQIHYN |
| 241 DLGSNNILL QPIEUSHDEMEK KTLKITEQGL AREWHTKQMT SAAGYTYAWM FVWIKATSTF |
| 301 KGDSWSGV LGWELGTVQ YFGRIDCLAV AGYVAVNLH LPISTCPET FAPLMADCA |
| 361 QDHPHRDFPSA SILQOLEAEQ AVQLREMPPR SFHSMQEGKW REIQOLDFL RAREKELLSS |
| 421 EELITRAEARQ RSQAQELRKR REHLIAQWML EYFERVETLL LQVDQRRPHR VRARRGTFTK |
| 481 RSLIDRQEGE RIPSPDPEFP PTPVQASQEL DBRRNHFVQY PGDSTTPFRPA RAIQKREPAE |
| 541 QAGWPGQSPR RLDSRENSHER RACWNGPSW PKPEGAQERQ SRSRMDEATW YLDSDISSPQ |
| 601 GSPGTLPPALN NNPFRSLPSEP EERKFPVPAE RGSSSGPPKTL QRALGRTLA LLASILIGDR |
| 661 LQPPQGPGTRE TEGSTTPFT PTPACFQET PPSPLICFTSL KTPDSPPTPA PSLDLLLGTPV |
| 721 DQPSASKPRF EEPFRVGTYS PPFGTRSRAP GTPGTRSPRS LGLSIPRSR PRSLRDRPSW |
| 781 FSQAGRPSP LFSPQAPAPR AWTIGFDOS PWDPSPAPMP FPQGQCPQRA QTMOKVQAAP |

Notes
SITES NOT KNOWN.
SITES NOT IN WEBLOGO.

© 2010 The Author(s)
The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution-Non-Commercial-Licence (http://creativecommons.org/licenses/by-nc/2.5/) which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.
Human MST1R (Ron) Tyroside kinase receptor for MSP (macrophage-stimulating protein receptor) (Swissprot = Q04912)

1 MELLPLPQS FLLLLLPKFA PAAGEDQNCP RTPYAASDRDF KDVYVQVPSF AGGLVQAMTVT
61 YEGDORNEAS FVAIRNBLQVG LPGDLKSVQS LATGPAAGDP CTQACAAACRG PHGGPDGTD
121 KVLVDLPAL ALVSCGSSLQ GRCLFLHLPET QGTAHLAAAP ACLFASSHNR PDDPCDCVAS
181 PLGTRTVVTE QOQAQYYIVA SDLAADVAGS FSPRVSISIR LDKASSAAGF GVMALVSPLK
241 HLVLSISIEY VHSFTGAFVY FLTVQVAPST DDPSHALMTRL ARLSATEPEL GDYRELVLLOC
301 RPL3FILERHRAS AREDEQQPYVPY TVQVHASYAVG AQUTATELSD IQEVVLQGVPV VTQDGQGVPV
361 GPNSVQVCA ILDLLOTTLE GVERCEPSY HPLGRLGDFO PQSGSPFCNP FGLEALSNT
421 SCRHPFVLS SSFSRVDLFN GLLGPQVTQA LVVTNRDNLTV VAMHTMDGR ILQVELVRLS
481 NYYLVSNFSL GDSSQPVQVR DSLRDLHSL FQDSQFVPQF PRFGPCHGFL TLRGCMLRAW
541 HFMCCGWGNC MCGQKRCPCF SQQDHCPCFK LTFEPHFRQP GSQSLTRLIC GSFPYLHPSG
601 LVPEEQGTVT VQSQSCPRLP KGSKSLRPFV RPKEEPVEFEE ELEPQTGAQ VQTVSSQVLTVT
661 NMFPFQHRVF DOTSVLRFPS FMEPLEVIAQ PLFGRAGHST LCTELQGSLQ VTSRGAELNV
721 GTECLLARVS EGQCLATTPG ATQVSVGPLL QLVQGAAQVQP SWTVQYREDP VVLFSISNPCG
781 YSINTHICST QRALTSAWHL LSHFDJAGRY ERSQERLQPE QCLLRFELTV VRDPOQNVAG
841 NLSARGGAA GTAFLGFPFLR PQHPSQANL VPLFKTVEAE FKEYILOGAV ADCVYVINTV
901 GQSCQCHQPFR GMDCVPRPFL RPQGSDQGAP LQVCVQGDECH ILERVQVKVRR HDQVQPLLG
961 ILLPLLLLVA ATAALVTFSV WRRKQLVLP NLNDLQSLTD QATGTAPLTL LYSGDSYRG
1021 LALPAIDGDL STTCTVHASF SDDSEDESCVP LRLKSEQULR DLSSDAEVL KDLVPHERV
1081 VTRSDHRVIG GHGFVYYVHE YDQDACNRQR QAISLRKDIRM EQYMFAPLH EGLMRMLNGH
1141 PNVLAILIGL LFPFGQFLVLW LPMCHGDLL QFIRSPQRNP TVKLISFQFG QAVKROMYELA
1201 PRNALSMLRQ LERNCMLQRLAG LFDGFLQRA RQDLRPEYV RPQGHTVEP VIEQLEKMAELQ
1261 TYRPTKTSDV WSFSSVWMLV LTRGAPFHRH IDPFDLTHLF AGRQELRPQF YCPSOLYQVM
1321 QCQWEADPAV RPTFVRWGLVE VQVSVALLAG DLHQVLQAPAT MNLGPTSHR MNVRFQEQQF
1381 SPMGVHRRPF RLPFPRPT

Notes

RPL (pS1394)EP

Human NCOR1 (Transcriptional corepressor of SMRT, which also binds 14-3-3, and also binds to SRTM, which also binds 14-3-3) and MST1R (Ron) formation of a 14-3-3/MST1R/NCOR1 complex.

Could not find papers characterizing an interaction between MLK3 and 14-3-3. Papers do however mention phosphorylation of 14-3-3 affecting Bax localization. MLK3 is a TKI kinase of the MLK family. Has an amino-terminal SH3 domain followed by the kinase domain, two leucine zipper domains, a cdc42/Rac1 binding (CRIB) domain and several other domains/motifs at the carboxy-terminal region. Phosphorylates IkappaB and activates SEIK1 and MKK7. Zhong QG. Akt inhibits MLK3/JNK3 signaling by inactivating Rac1: a protective mechanism against ischemic brain injury. J Neurochem. 2006 Sep;98(6):1886-98

Human NCOR1 (Transcriptional corepressor) was determined to be (Swissprot = Q04912)
which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.

© 2010 The Author(s)

with the loss of vitamin D responsiveness in aggressive androgen programming including that for myo

Phosphorylation of Ser2345 and Ser2348 (by IKKalpha) creates a functional 14 notes

VTTSGSVSSRGHSFADPASNLGLEDIIRKALMGFSDDKVEDHGUVMSQMPVGFANTSVSTEGRE

© 2001 IACAPSVAQRN IERWRAPELSE QYETLSDSDD 2001

Notes Phosphorylation of Ser2345 and Ser2348 (by IKKalpha) creates a functional 14-3-3-binding domain (SRK(pS2348)KSPIPGQ) (Fernández-Majada et al. 2007) N creates a protein that regulates the activity of some independent prostate cancer cells. Its gene tends

TQFPYNPLTMRMLSSTPPTPIACAPSVAQRN IERWRAPELSE QYETLSDSDD 2001

Notes Phosphorylation of Ser2345 and Ser2348 (by IKKalpha) creates a functional 14-3-3-binding domain (SRK(pS2348)KSPIPGQ) (Fernández-Majada et al. 2007) N creates a protein that regulates the activity of some independent prostate cancer cells. Its gene tends

TQFPYNPLTMRMLSSTPPTPIACAPSVAQRN IERWRAPELSE QYETLSDSDD 2001

Notes Phosphorylation of Ser2345 and Ser2348 (by IKKalpha) creates a functional 14-3-3-binding domain (SRK(pS2348)KSPIPGQ) (Fernández-Majada et al. 2007) N creates a protein that regulates the activity of some independent prostate cancer cells. Its gene tends
to be overexpressed in multiple-myeloma cell lines.

References to 14-3-3 binding to N-CoR
Fernández-Majada V, Pujadas J, Vilardell F, Capella G, Mayo MW, Bigan A, Espinosa L. Ablation of cytoplasmic localization of N-CoR in colorectal Cancer. Cell Cycle. 2007 Jul 15;6(14):1748-52.

Human Nedd1 (Swissport = Q9GZM8)

MDGEDI-lfsSLKETAEYWKKLSWYKGFQPQEEDELVEF QGEEREREAEQ LEALVQLAAEQ
61 NRQRDLQKVLEKEALKLEKLQKVQVSVELOD LSQTAKEIQLKLYVRELQ
121 ANDDLERAK ATMVL5SVEQL LQRINAIERN AFLESELRDL ESSLVSQVRKL KEDARLQRO
181 LAVRKEQVET TRKASPGET LTDEERDSAV QASLSLPFQ P VGRQGTETFP KPAIRIENGQF
241 TSPIFACARI ALALIVDGEL RFGALESKL AICRNFNDQK ASRKSISGNSVCGLVGL NGS
301 TFKSRSFGHTS FPDKQGVDF SAPPPLGRG SSRSQAGPOM LPLS V

Notes
"14-3-3e binds to CDK5/p35 phosphorylated NUDEL and this binding maintains NUDEL phosphorylation. Similar to LIS1, deficiency of 14-3-3 results in mislocalization of NUDEL and LIS1, consistent with reduction of cytoplasmic dynein function. We produced substitution mutants for each of the CDK5 sites of NUDEL: S198A, S242A, T245A. Mutation of two other phosphorylation sites (Ser242, Thr245) located outside of the binding interaction with 14-3-3e had no effect on the interaction of LIS1 and NUDEL in yeast or as recombinant proteins. Mutation of two other phosphorylation sites (Ser242, Thr245) located outside of the binding region had only mild effects on interaction." (Toyo-oka et al 2003)

References to 14-3-3 binding to Nedd1
Toyo-oka K, Shionoya A, Gambello MJ, Cardoso C, Levantér R, Ward HL, Ayala R, Tsai LH, Dobyns W, Ledbetter D, Hirotsune S, Toyo-oka et al 2003)

Human Nedd4L (Swissport = Q7Z5N3)

1 MATGELGEVY GLSEDGEGSR ILRJVVGGS1 DALKDIDPG1 SDVPLYKSLVD VADRENAL
61 VQTRKTIKTL NPKWNEEEFP RVNSHNLRLF FENVDELNL ADDLQLQVFPL FSLHPLTEPFD
121 NPPVTLKPY TKLIRRPSHS RKVGFRKLMK AWYMPAKQQGQ DQESIQGQDKH EMWMGVXVSN
181 DSAQSGQIKP PFPFLPFGNRE EVKNDLGRGTV YVHNHNNRQQ TWRSPDMLVS NEDSDNRQ
241 NQEAABRRFRR SRRHISDDLE PEPSGEGDPVF EPWFTISIEVE NIADGDLSLQ LPPFSPASGS
301 RTFSQDLSE LSRRLIQTDPD NGQEPSLIS1 QREISSPLCRS CLTDVAEQLQ HGLPPSAPAA
361 SFLNLQNLG FFPGEWEIRHL GDTFYDIHHN SKITQMEDR LQNPITAIGP VVYQRSFQKR
421 YDFFRKDDLK PADIWNNRFR LLHRNIFEE RYSIMVSRK PDVLRKIRLEW EKEFEGKDL
481 LGGVARWFNL LSKEMWNPY FLQFESTADNN YTLQINPNSG LCNEDLSHYF TAFQGRAVGL
541 VCHQKSLALG FIPFRYMKML QGQITLNDME SVDSVEYNQV RLW16ENDP RDMLDFCDA
601 NNHAAAEHAGQ KFQKPGKLQV QKQPPLSPK QVPPPPLKFGA KPLRIFDKLR MDDKEMD
721 NNPHQGVQVQDL KPNSIEIMVT NRENKRYIDL VQRQFVNPQR QXQMKAQPLEF FETLPPIDL
781 NFGQOTQVDL KNPNSIEIMVT NRENKRYIDL VQRQFVNPQR QXQMKAQPLEF FETLPPIDL
841 KIDFNEENE LMCCLGDV VDNDQSHSRR NQYGCNHVPHI QWQRVAKLVM DAERKRLIRQ
901 FVTGSTSRPM NGAEFLGSN QGFLITQIQQM GSPKFLRPRA TCNRNNLPLF YETLFEDER
961 LIMAVANAEG FQG

Notes
NEDD4L E3 ubiquitin-protein ligase which accepts ubiquitin from an E2 ubiquitin-conjugating enzyme in the formation of a thoreiste and then directly transfers the ubiquitin to targeted substrates. Inhibits TGF-beta signaling by triggering SMAD2 and TGF-β1 ubiquitination and proteasome-dependent degradation. Promotes ubiquitination and internalization of various plasma membrane channels such as ENaC, Nav1.2, Nav1.3, and KCNQ1. Also regulates ISO-3 binding to N-CoR. It is involved in the regulation of various pathways including apoptosis, cell proliferation, and differentiation. SCNS8A, SCNS9A, SCNS1A, SCNS2A, SCNS3A, SCNS5A, SCNSA, SCNS9A, SCNS10A and CLCN5. Interacts with SMAD2, SMAD3, SMAD6 and SMAD7. The phosphorlated form interacts with 14-3-3 proteins. Interacts with Epstein-Barr virus LMP2A. Interacts with NDFIP1 in vitro. 8 isoforms of the human protein are produced by alternative splicing.

References to 14-3-3 binding to Nedd4.2
Liang X, Butterworth MB, Peters KW, Walker WH, Frizzell RA. An obligatory heterodimer of 14-3-3bta and 14-3-3ep is required for aldosterone regulation of the epithelial sodium channel J Biol Chem. 2008 Oct
which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.

The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial Licence (http://creativecommons.org/licenses/by-nc/2.5/)

© 2010 The Author(s)

Oxygen species (ROS) which participate in a variety of biological processes including host defense, hormone

NOXA1 is an activator of NOX1, a superoxide-producing NADPH oxidase in the production of reactive oxygen species (ROS) which participate in a variety of biological processes including host defense, hormone
biosynthesis, oxygen sensing and signal transduction. May also activate CYBB
phox and NOX3. NOX1, NOX1A, NOX1C, RAC1 and CYBA forms a functional complex that supports ROS production.
Interaction with 14-3-3 prevents the interaction of NOX1A with NOX1 and RAC1 and its targeting to
membranes, hence reducing its ability to activate NOX1. Belongs to the NCF2/NOX1A family. Three isoforms
are produced by alternative splicing. Ser172) and Ser461) of NOX1A as
phosphorylation sites for protein kinase A (PKA). A consequence of this phosphorylation was the
enhancement of NOX1A complex formation with 14-3-3 proteins. 14-3-3 binding induce the dissociation of
NOX1A from the NOx1 complex at the plasma membrane, suggesting a mechanism for the inhibitory effect on
Nox1 activity. GST-NOX1A deletion mutants were amplified by PCR using pGEX4T-3-NOx1A as a template, and
the following oligonucleotides as primers. The sequence (AA10841) and phosphorylated 14-3-3-binding sites
were confirmed in an email from the authors.

References to 14-3-3 binding to human NOX1
Kim JS, Diebold BA, Babior BM, Knaus UG, Bokoch GM. Regulation of Nox1 activity via protein kinase A
mediated phosphorylation of NoxA1 and 14-3-3 binding. J Biol Chem. 2007 Nov 30;282(48):34787-800

Human NRIP1 (RIP140) Receptor interacting protein of 140 kDa (Swissprot = P48552)

| Amino Acid | Protein Name                  |
|------------|-------------------------------|
| 1-146       | Full-Receptor interacting protein 1; AltName: Full=Nuclear factor RIP140; AltName:           |
| 1141-121    | GEVYGLLGSV                     |
| 1081-1140   | SRETQDKDIW                     |
| 781-800     | FLGMAPAVQR                     |
| 721-780     | NK                            |
| 661-720     | KPIGMIDRLN                     |
| 541-660     | ESPSTNRTTP                     |
| 481-540     | KEDQDTSKNS                     |
| 421-480     | NPSFTDDSSG                     |
| 361-420     | GYKNSLERNN                     |
| 301-360     | MARLQENGQK                     |
| 241-300     | QAVAMYDRKAPAKVYKPS             |
| 181-240     | ASSHLKTLLK                     |
| 121-180     | DSVPKGKQDS                     |
| 61-120      | CMTHEELEGSD                     |

Notes

KRRKL(pS102)DIVN pSer102 PKC, 14-3-3 (species?) and DHTRF(pS1003)YPGMV pSer1003 PKC, 14-3-3
(species?) Ser1003 S=Ser1001 in P48552.
RIP140 modulates transcriptional activation by steroid receptors such as NR3C1, NR3C2 and ESR1. Also
modulates transcriptional repression by nuclear hormone receptors. Interacts with the ligand binding domain
(LBD) of NR2C1 in the absence of ligand. Interacts with RAR and RXR homodimers and RAR/RXR heterodimers
in the presence of ligand. Interacts with HDAC1 and HDAC3 via its N-terminal domain. Found in a
complex with both NR3C1 and YWHAE.

References to 14-3-3 binding to NRIP1 (RIP140)

Gupta P, Ho PC, Huq MD, Khan AA, Tsai NP, Wei LN. PKC epsilon stimulated amino genination of RIP140
for its nuclear-cytoplasmic export in adipocyte differentiation. PLoS ONE. 2008 Jul 16;3(7):e2658.
Zilliauc J, Holter E, Waku H, Tazawa H, Treuter E, Gustafsson JA. Regulation of glucocorticoid receptor activity
by 14-3-3-dependent intracellular relocalization of the coressor RIP140. Mol Endocrinol. 2001 Apr;15(4):501-11.

Human PACS2 phosphofurin acidic cluster sorting protein 2 (Swissprot = Q86VP3)

| Amino Acid | Protein Name                  |
|------------|-------------------------------|
| 1-152      | MAERGRGLLP                     |
| 5-152      | GAPGALTFPMV                     |
| 10-152     | GMGFSCEVFR                     |
| 15-30      | LSLLKSLFLKMLQKRGK               |
| 31-46      | VYKRTTTELEPSFKPKQPSQFQKPSQPSQPV |
| 47-62      | SQYQVNGVQG                     |
| 63-77      | ESSSFGXTQ                     |
| 78-92      | EASDQQVQQQ                     |
| 93-107     | DQDQDDVQG                     |
| 108-122    | KPPQKQRSITV                   |
| 123-138    | RTTMTTRQCN                     |
| 139-154    | FKVQVKVXLR                     |
| 155-170    | SVPSSDVSIS                    |
| 171-185    | YEAEHDDYLS                  |
| 186-200    | DSVEALMSQ                     |
| 201-215    | EYKQGKYYLQ                    |
| 216-230    | RLLGHPPQKPS                    |
| 231-245    | VAVQSTAV                     |
| 246-260    | DHLQKVPQK                     |
| 261-275    | VQKTCVQGSQ                 |
| 276-290    | MTPHHLQKPVQK                  |
| 291-305    | SQVQKVQGQ                |
| 306-320    | HSKQVQGQQ                 |
| 321-335    | LKVSKVQGQQ                |
| 336-350    | KPVQKQPSQQ              |
| 351-365    | SQVQKQPSQQ              |
| 366-380    | KPVQKQPSQQ              |
| 381-395    | SQVQKQPSQQ              |
| 396-410    | KPVQKQPSQQ              |

© 2010 The Author(s)

The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution-No-Commercial Licence (http://creativecommons.org/licenses/by-nc/2.5/) which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.
which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.

© 2010 The Author(s)

Phospho metabolism.

Phosducin may participate in the regulation of visual phototransduction or in the integration of photoreceptor

**Notes**

*PKB/Akt*-phosphorylated Ser437 binds 14-3-3 with high affinity

**References to 14-3-3 binding to PACS2**

Aslan JE, You H, Williamson DM, Endig J, Youker RT, Thomas L, Shu H, Du Y, Milewski RL, Brush MH, Possemato A, Sprott K, Fu H, Greiss KD, Runckel DN, Vogel A, Thomas G. Akt and 14-3-3 control a PACS-2 homeostatic switch that integrates membrane traffic with TRAIL-induced apoptosis. Mol Cell. 2009 May 14;34(4):497-509

**Human PCTK1**

**PCTAIRE**

1 MDRMKKIRQ LSLMRLRGGG IDKNGAPEQ IGLDESGGG GSDGPEAPTR AAPGELSA 1
2 GPLSAPEIV HEDLMMGSD ESDQASTSS DEVQPSVVR MRHHPPKRS TIDENKLRL
121 PADIRLPQY LEKTLKMSF FDRLPLSSLA VLSELSEIGFG KLETYKLLG LETGAYTVY
241 EYLDKLQKY LDDCNGIN IMHVKLFLQL LRLGACYR QVLRDQFLQ NLLINERGL
310 KLADEQGLA KSPIKTPYSN EVTVLWYRP DILLGSTDTS QIDMDQGVC IFYEMATGRP
361 LHPGSTDVEQ LFHIFIRLGT PEEOTPGIL SNEEFTKYN PYKREAILHS HAPRLDSDG
421 DLLTLQILPEE GRANREAEDA MHFFLSSLG EIRKHLFDTO SFALKEIQLE QEASKLASSS
481 MDPGSPRAAP VDTEF

**Notes**

- PKB/Akt-phosphorylated Ser437 binds 14-3-3 with high affinity

**References to 14-3-3 binding to PCTK1**

Graeser R, Gannon J, Poon RY, Dubois T, Aitken A, Hunt T. Characterization of brain PCTAIRE protein kinase 1 from mouse brain. Eur J Biochem. 1998 Oct 1;257(1):112-20.

**Human PDC**

Phosducin (Swissprot = P20941)

1 MEEAKQSLE EDFEQQATH PTGPVQDNRK KFKLQSDSD SSPPSKKEIL RQMSQQSRN 1
6 GDOKSERVRS RGMQQYELI HEEKDEDNL KRYRQTRMCQD MQRSLQSPFR YGFYLYTLEG
121 KQFLTEIEKE LKTTTVHPI YEDIGKSCDA LNSLSTTLAA EYFPYFKCR KASNTAOGDR
181 SSLDVLPTLL YTVGKELSS PISUAVEQAE EFFAODGDEV SNEYGLFFER EVKLYELHKT
241 DVEV

**Notes**

Phosducin may participate in the regulation of visual phototransduction or in the integration of photoreceptor metabolism.

phospho-Pd is found to interact with 14-3-3 in material from dark-adapted retina, and this interaction is markedly
diminished by light, which dephosphorylates Pd. Phosphorylation by Ca(2+)/calmodulin-dependent kinase II at Ser-54 and Ser-73 led to binding of the phosphoserine-binding protein 14-3-3 (Thulin et al 2001).

**References to 14-3-3 binding to phosducin**

Nakano K, Chen J, Tarr GE, Yoshida T, Flynn JM, Bitensky MW. Rethinking the role of phosducin: light-regulated binding of phosducin to 14-3-3 in rod inner segments. Proc Natl Acad Sci U S A. 2001 Apr 10;98(8):4693-8. Epub 2001 Apr 3

Thulin CD, Savage JR, McLaughlin JN, Truscott SM, Old WM, Ahn KA, Hamm HE, Bitensky MW, Willardson BM. Modulation of the G protein regulator phosducin by 14-3-3 protein binding. J Biol Chem. 2001 Jun 29;276(26):23805-15.

**Human PDE3A**

**Phosphodiesterase 3A (Swissprot = Q14432)**

| Entry | Species | Accession | Name | Description |
|-------|---------|-----------|------|-------------|
| PDE3A | Human | sp|O60825.2| F262_HUMAN RecName: Full=Fructose-2,6-bisphosphatase 2 (Swissprot = O60259) |

Ser248 was selectively phosphorylated in response to PMA and dephosphorylated in cells treated with aphidicolin and mimoseine. Phosphorylation of Ser248 therefore correlated with 14-3-3 binding to PDE3A (Pozuelo Rubio et al 2001).

Platelet activation also led to a PKC-dependent association between PDE3A and 14-3-3 proteins. In contrast, cAMP-consuming agents such as PGE(1) and forskolin mediated phosphorylation and activation of PDE3A regulatory subunit (Swisprot = O60259). Epub 2009 Mar 4.

**References to 14-3-3 binding to PDE3A**

PDE3A hydrolyzes both cyclic AMP (cAMP) and is inhibited by cyclic GMP (cGMP).

**Notes**

- PDE3A binds to 14-3-3 proteins. In contrast, cAMP-consuming agents such as PGE(1) and forskolin-induced phosphorylation of Ser(312) and increased PDE3A protein binding.

- Independent association between PDE3A and 14-3-3 proteins. In contrast, cAMP-consuming agents such as PGE(1) and forskolin-induced phosphorylation of Ser(312) and increased PDE3A protein binding.

- The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial Licence (http://creativecommons.org/licenses/by-nc/2.5/)

- © 2010 The Author(s)
Human PKP2 (Swissprot = Q9UBF8) phosphatidylinositol 4-kinase III beta; Short=PKP2; AltName: Full=NPK2; AltName: Full=QUB8

References to 14-3-3 binding to PKP2

Zhu B, Zhai J, Zhu H, Kyprianou N. Prohibitin regulates TGF-beta induced apoptosis as a downstream target of Smad-dependent and -independent signaling. Prostate. 2009 Sep 1. [Epub ahead of print]

| Human PKP2 | Plakophilin 2 (Swissprot = Q99959) |
|------------|-----------------------------------|
| 1 MGGTVEFAP LKPTSEPTSG PFQGNGSLL SVITEGEVG SVIDEVEQAV ACQCEVLEKVK 61 LHGLVAVGS RGTPLEVLNG DGSSIEIRL DDPPAIRE EDEMSGAAVS GTAAGARRR 121 QNANQKSWL LRLEPSKFLD ISAITYLNYN SKEPPGQAIY GNLRFCFPRN DVDFYPLQLL 181 NMYTHMDGQV DAIGKTPVHV RCRQINSFSL QCALLLGLAS SMDHISTQRM SAGTHLKLRI 241 LEDLSHAPR KRELPSLA PPQDLGSPKR THQGRKSQAT ASILSSQNKL RTAIGPKVYEN 301 LEAEODIYAQ LGSRNNTYLP AGSQSVQL LFQ |

Notes

PKB-dependent binding of 14-3-3s to phospho-Ser483 of cardiac PKF-2 mediates the stimulation of glycolysis by growth factor.

References to 14-3-3 binding to cardiac PKF-2

Pozuelo Rubio M, Peggie M, Wong BH, Morrice N, MacKintosh C. 14-3-3s regulate fructose-2,6-bisphosphate levels by binding to PKB-phosphorylated cardiac protein kinase/phosphatase. EMBO J. 2003 Jul 22;12(14):3514-22.
which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.

The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial Licence (http://creativecommons.org/licenses/by-nc/2.5/)

© 2010 The Author(s)

References to 14-3-3 binding to plakaphilia

Müller J, Ritt DA, Copeland TD, Morrison DK. Functional analysis of C-TAK1 substrate binding and identification of PKP2 as a new C-TAK1 substrate. EMBO J. 2003 Sep 1;22(17):4431-42.

Human PMCA1, 3 and 4 (Plasma membrane Ca2+-ATPases)

NOT IN WEBLOGO.

NOT IN WEBLOGO.

NOT IN WEBLOGO.
Selective Targeting at Cell

Hollande F, Joubert D.A 2008 Apr 15;411(2):319

Durgan J, Cameron AJ, Saurin AT, Durgan J, Cameron AJ, Saurin AT, Hanrahan S, Totty N, Messing RO, Parker PJ. The identification and characterization of protein kinase C epsilon (PKC\(\epsilon\)) isoforms in the control of cytokinesis. Mol Biol Cell. 2008 Oct;19(21):5866-75.

Saurin AT, Durgan J, Cameron AJ, Faisal A, Marber MS, Parker PJ. The regulated assembly of a PKC\(\epsilon\) interaction module controls the completion of cytokinesis. Nat Cell Biol. 2008 Aug;10(8):891-9. doi:10.1038/ncb1742

References to 14

Koga Y, Ikebe M. A novel regulatory mechanism of myosin light chain phosphorylation via binding of 14-3-3 to myosin phosphatase 1. Mol Biol Cell. 2008 Mar;19(3):1061-72.

Human PRKCE (PKCE) Protein kinase C epsilon (Swissprot = Q02156)

| Accession | Description |
|-----------|-------------|
| Q02156    | Protein kinase C epsilon (PKCE) |

Notes

Phosphorines 346 (RSK\(\beta\)) and 368 (RKL\(\gamma\)S-FD) interacting with 14-3-3. These sites are unique for PKC\(\epsilon\) and are conserved through evolution. The actions of 348 (RSK\(\beta\)) and 368 (RKL\(\gamma\)S-FD) are crucial for the exit from cytokinesis, as shown by PKC\(\epsilon\) mutants S346A/S368A or R343A, which prevent the ability of PKC\(\epsilon\) to recover cytokinesis defects after PKC\(\epsilon\) knockout or knockdown.

References to 14-3-3 binding to PKC epsilon

Saurin AT, Durgan J, Cameron AJ, Faisal A, Marber MS, Parker PJ. The identification and characterization of protein kinase C epsilon (PKC\(\epsilon\)) isoforms in the control of cytokinesis. Mol Biol Cell. 2008 Oct;19(21):5866-75.

Durgan J, Cameron AJ, Saurin AT, Hanrahan S, Totty N, Messing RO, Parker PJ. The identification and characterization of protein kinase C epsilon (PKC\(\epsilon\)) isoforms in the control of cytokinesis. Mol Biol Cell. 2008 Oct;19(21):5866-75.

Saurin AT, Durgan J, Cameron AJ, Faisal A, Marber MS, Parker PJ. The regulated assembly of a PKC\(\epsilon\) interaction module controls the completion of cytokinesis. Nat Cell Biol. 2008 Aug;10(8):891-9. doi:10.1038/ncb1742

References to 14-3-3 binding to PKC epsilon

Saurin AT, Durgan J, Cameron AJ, Faisal A, Marber MS, Parker PJ. The identification and characterization of protein kinase C epsilon (PKC\(\epsilon\)) isoforms in the control of cytokinesis. Mol Biol Cell. 2008 Oct;19(21):5866-75.

Durgan J, Cameron AJ, Saurin AT, Hanrahan S, Totty N, Messing RO, Parker PJ. The identification and characterization of protein kinase C epsilon (PKC\(\epsilon\)) isoforms in the control of cytokinesis. Mol Biol Cell. 2008 Oct;19(21):5866-75.

Saurin AT, Durgan J, Cameron AJ, Faisal A, Marber MS, Parker PJ. The regulated assembly of a PKC\(\epsilon\) interaction module controls the completion of cytokinesis. Nat Cell Biol. 2008 Aug;10(8):891-9. doi:10.1038/ncb1742

Notes

Phosphorines 346 (RSK\(\beta\)) and 368 (RKL\(\gamma\)S-FD) interacting with 14-3-3. These sites are unique for PKC\(\epsilon\) and are conserved through evolution. The actions of 348 (RSK\(\beta\)) and 368 (RKL\(\gamma\)S-FD) are crucial for the exit from cytokinesis, as shown by PKC\(\epsilon\) mutants S346A/S368A or R343A, which prevent the ability of PKC\(\epsilon\) to recover cytokinesis defects after PKC\(\epsilon\) knockout or knockdown.

References to 14-3-3 binding to PKC epsilon

Saurin AT, Durgan J, Cameron AJ, Faisal A, Marber MS, Parker PJ. The identification and characterization of protein kinase C epsilon (PKC\(\epsilon\)) isoforms in the control of cytokinesis. Mol Biol Cell. 2008 Oct;19(21):5866-75.

Durgan J, Cameron AJ, Saurin AT, Hanrahan S, Totty N, Messing RO, Parker PJ. The identification and characterization of protein kinase C epsilon (PKC\(\epsilon\)) isoforms in the control of cytokinesis. Mol Biol Cell. 2008 Oct;19(21):5866-75.

Saurin AT, Durgan J, Cameron AJ, Faisal A, Marber MS, Parker PJ. The regulated assembly of a PKC\(\epsilon\) interaction module controls the completion of cytokinesis. Nat Cell Biol. 2008 Aug;10(8):891-9. doi:10.1038/ncb1742

References to 14-3-3 binding to PKC epsilon

Saurin AT, Durgan J, Cameron AJ, Faisal A, Marber MS, Parker PJ. The identification and characterization of protein kinase C epsilon (PKC\(\epsilon\)) isoforms in the control of cytokinesis. Mol Biol Cell. 2008 Oct;19(21):5866-75.

Durgan J, Cameron AJ, Saurin AT, Hanrahan S, Totty N, Messing RO, Parker PJ. The identification and characterization of protein kinase C epsilon (PKC\(\epsilon\)) isoforms in the control of cytokinesis. Mol Biol Cell. 2008 Oct;19(21):5866-75.

Saurin AT, Durgan J, Cameron AJ, Faisal A, Marber MS, Parker PJ. The regulated assembly of a PKC\(\epsilon\) interaction module controls the completion of cytokinesis. Nat Cell Biol. 2008 Aug;10(8):891-9. doi:10.1038/ncb1742

Notes

Phosphorines 346 (RSK\(\beta\)) and 368 (RKL\(\gamma\)S-FD) interacting with 14-3-3. These sites are unique for PKC\(\epsilon\) and are conserved through evolution. The actions of 348 (RSK\(\beta\)) and 368 (RKL\(\gamma\)S-FD) are crucial for the exit from cytokinesis, as shown by PKC\(\epsilon\) mutants S346A/S368A or R343A, which prevent the ability of PKC\(\epsilon\) to recover cytokinesis defects after PKC\(\epsilon\) knockout or knockdown.

References to 14-3-3 binding to PKC epsilon

Saurin AT, Durgan J, Cameron AJ, Faisal A, Marber MS, Parker PJ. The identification and characterization of protein kinase C epsilon (PKC\(\epsilon\)) isoforms in the control of cytokinesis. Mol Biol Cell. 2008 Oct;19(21):5866-75.

Durgan J, Cameron AJ, Saurin AT, Hanrahan S, Totty N, Messing RO, Parker PJ. The identification and characterization of protein kinase C epsilon (PKC\(\epsilon\)) isoforms in the control of cytokinesis. Mol Biol Cell. 2008 Oct;19(21):5866-75.

Saurin AT, Durgan J, Cameron AJ, Faisal A, Marber MS, Parker PJ. The regulated assembly of a PKC\(\epsilon\) interaction module controls the completion of cytokinesis. Nat Cell Biol. 2008 Aug;10(8):891-9. doi:10.1038/ncb1742

References to 14-3-3 binding to PKC epsilon

Saurin AT, Durgan J, Cameron AJ, Faisal A, Marber MS, Parker PJ. The identification and characterization of protein kinase C epsilon (PKC\(\epsilon\)) isoforms in the control of cytokinesis. Mol Biol Cell. 2008 Oct;19(21):5866-75.

Durgan J, Cameron AJ, Saurin AT, Hanrahan S, Totty N, Messing RO, Parker PJ. The identification and characterization of protein kinase C epsilon (PKC\(\epsilon\)) isoforms in the control of cytokinesis. Mol Biol Cell. 2008 Oct;19(21):5866-75.
which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited. The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial Licence (http://creativecommons.org/licenses/by-nc/2.5/)

© 2010 The Author(s)

481 SPHFSETDQTF PLLPQKEPT FPASKPLDVYE IHIKNQKDQA LSLLPKQRDS GRKPRQPF
541 ENNKEYAKVS GVMHNNILVL VDFPQHNVCF CEFSSEAKEP PSLQENQAEK ALANFATSS
601 KCRQLGGDL LYPDACFTPHS FH

>gi|130321|sp|P16471.1|PRLR_HUMAN RecName: Full=Prolactin receptor; AltName: Full=Protein tyrosine phosphatase H1 (PTPH1) (Swissprot – P26045)

1 MTSLRALKG RINNIRTEL PFEKTRESVI CHSIFLDGVY QTQKTVKDQT QVULLMVHN
6 GLQOODDSSVD LPSNLAEIAK IRQLKGQFPP CTLLHFVRVF IPDPNTLQOE
121 QTHRLYFLQL MIDEKICRLT CPNSAVALV SYAVQSFHGD YNSIHHPGY LSDSHITPIDQ
181 NEDFLTVKES LHEQSHSLQG 5EAESCYINI ARTLDFYQGE LSQGRDLNLN DLMIAGASG
241 VAYRYKICT SFYPWNWLL ISFPRKRFPI HQRQKQAESR EHIVAFMNLM YRSCMNLWKS
301 CVEHHEFFTP KELLQPFKN LSQHTMGRS NTKSVNNYQ CKKVVGMMP NAPMRSSLV
361 EHELEKSLPS RSPPTIPWNR SPRLBEIKR PHRSSADNL NEMYITETE DVFYTYKGS
421 APQDSSDEVS QNRSFQPHEL SNNAPQYQL TQKSSSSVSP NNASSPGCP DGVQQDLDD
481 FHRVTKGGST EDAASYQYCK DNMDSGLYVL IRITPDEIXK FGKFLNKGDD QRMLPLYVSR1
541 NITPADDTCL PKLNEQDGIV LINGNOSHEI TQDQVMTK ASRESHERSEL ALVIRRARA
601 SFADAFKSRDE LNLQFPEFIA FMCPEGGDTL EGSAALQKLK LEGSTQVLIP EQLYKPQKL
661 HCSAGIRATG VSITLMTAMC IERTLMPFY LDVIRKRMQ DVQMTSTQSY YKFKEAIYR
721 IVEEGLQVQMS

>gi|229462761|sp|P26045.2|PTN3_HUMAN RecName: Full=Tyrosine-protein phosphatase non type 3 (aka Protein-tyrosine phosphatase H1 (PTPH1)) (Swissprot – P26045)

1 MTSRLRALKG RINNIRTEL PFEKTRESVIC SIHFLDGVY QTQKTVKQDT QVULLMVHN
6 GLQOODDSSVD LPSNLAEIAK IRQLKGQFPP CTLLHFVRVF IPDPNTLQOE
121 QTHRLYFLQL MIDEKICRLT CPNSAVALV SYAVQSFHGD YNSIHHPGY LSDSHITPIDQ
181 NEDFLTVKES LHEQSHSLQG 5EAESCYINI ARTLDFYQGE LSQGRDLNLN DLMIAGASG
241 VAYRYKICT SFYPWNWLL ISFPRKRFPI HQRQKQAESR EHIVAFMNLM YRSCMNLWKS
301 CVEHHEFFTP KELLQPFKN LSQHTMGRS NTKSVNNYQ CKKVVGMMP NAPMRSSLV
361 EHELEKSLPS RSPPTIPWNR SPRLBEIKR PHRSSADNL NEMYITETE DVFYTYKGS
421 APQDSSDEVS QNRSFQPHEL SNNAPQYQL TQKSSSSVSP NNASSPGCP DGVQQDLDD
481 FHRVTKGGST EDAASYQYCK DNMDSGLYVL IRITPDEIXK FGKFLNKGDD QRMLPLYVSR1
541 NITPADDTCL PKLNEQDGIV LINGNOSHEI TQDQVMTK ASRESHERSEL ALVIRRARA
601 SFADAFKSRDE LNLQFPEFIA FMCPEGGDTL EGSAALQKLK LEGSTQVLIP EQLYKPQKL
661 HCSAGIRATG VSITLMTAMC IERTLMPFY LDVIRKRMQ DVQMTSTQSY YKFKEAIYR
721 IVEEGLQVQMS

Notes
Motif (KCSPt™WP) in the long form of the human PrlR is conserved among a wide variety of species.

References to 14-3-3 binding to prolactin receptor

Olayioye MA, Guthridge MA, Stomski FC, Lopez AF, Visvader JE, Lindeman GJ. Threonine phosphorylation of the human prolactin receptor mediates a novel interaction with 14-3-3 proteins. J Biol Chem 2003 Aug 29;278(35):32929-35.

Fiol DF, Samnari E, Sacchi R, Kultz D. A novel tilapia prolactin receptor is functionally distinct from its paralog. J Exp Biol. 2009 Jul;212(Pt 13):2007-15. (two fish prolactin receptors of which only isoform 1 contains the 14-3-3 binding site)

Human PTPN3 Tyrosine-protein phosphatase non type 3 (aka Protein-tyrosine phosphatase H1 (PTPH1)) (Swissprot – P26045)

3 853 EDASQYCKD NMDGDSVLIR IRITPDEIXK FGKFLNKGDD QRMLPLYVSR1
359 15. (two fish prolactin receptors of which only isoform 1 contains the 14-3-3 binding sites, both of which are distinct from the consensus binding motif)

1 MTSLRALKG RINNIRTEL PFEKTRESVIC SIHFLDGVY QTQKTVKQDT QVULLMVHN
6 GLQOODDSSVD LPSNLAEIAK IRQLKGQFPP CTLLHFVRVF IPDPNTLQOE
121 QTHRLYFLQL MIDEKICRLT CPNSAVALV SYAVQSFHGD YNSIHHPGY LSDSHITPIDQ
181 NEDFLTVKES LHEQSHSLQG 5EAESCYINI ARTLDFYQGE LSQGRDLNLN DLMIAGASG
241 VAYRYKICT SFYPWNWLL ISFPRKRFPI HQRQKQAESR EHIVAFMNLM YRSCMNLWKS
301 CVEHHEFFTP KELLQPFKN LSQHTMGRS NTKSVNNYQ CKKVVGMMP NAPMRSSLV
361 EHELEKSLPS RSPPTIPWNR SPRLBEIKR PHRSSADNL NEMYITETE DVFYTYKGS
421 APQDSSDEVS QNRSFQPHEL SNNAPQYQL TQKSSSSVSP NNASSPGCP DGVQQDLDD
481 FHRVTKGGST EDAASYQYCK DNMDSGLYVL IRITPDEIXK FGKFLNKGDD QRMLPLYVSR1
541 NITPADDTCL PKLNEQDGIV LINGNOSHEI TQDQVMTK ASRESHERSEL ALVIRRARA
601 SFADAFKSRDE LNLQFPEFIA FMCPEGGDTL EGSAALQKLK LEGSTQVLIP EQLYKPQKL
661 HCSAGIRATG VSITLMTAMC IERTLMPFY LDVIRKRMQ DVQMTSTQSY YKFKEAIYR
721 IVEEGLQVQMS

Human Raf1 (CRAF) (Swissprot – P00409)

1 MEHTIQGAWKT ISNGGFGKDA VDFSGSSCISP TIVQCOFGYQR RASDDGKDLT PKSTSNTIRV
6 FLPNQKVTRTV NVRNNSMLHD CILMKALKVR LQPECCAVFR LLHEHKGRKA RLWNTADA
121 LIGRELQFD LDHVFPLTHN FAKRTFKLIA FCDICQRFELL NGFCRQTGCG KHKNCSTKV
181 PTMCVDMSNI ROLLTFGT IDGSSVAPLP SITLRRNAMES YVSRQVVRSLQ RSYTHAPTFT
241 NTSSPSSESGS LSqgrstFt FNWNYSTCL PVDSRMIEDA IR3HSSEAS SAILSSSPNPNL

The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial Licence (http://creativecommons.org/licenses/by-nc/2.5/) which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.
which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.

© 2010 The Author(s)

Human Raptor Regulatory-associated protein of mTOR (Swissprot = Q8N122)

1 MESEMQLQPSL LGLGEDEAD LTLDNLPLAF MKRRHCEKIE GSKSLAQLSW MRDMRKTSVS
2 ALIVCVLNNQV DPQVYFTTC CARLEWDF LQMDQRALE TISANILQKVN ENWQFBRAYK
3 GILQERDVEF KLCTSLRPR AEKERVYLF NGHOVRPFVT NGEWVQPMX YTVWPLIOSY
4 EFLQGVRDSS IFVYDCNAG LIVKSKQFQA LQREQELEVA AINPNHLQMQ MPLSPSMKNC
5 IQLACEATE LLMPIDFLPA DLFTSCINTT KIALRWFMC QVCYSLSVPG TLLDKIKPG
6 NRQDRLTPFL ELNWINFATT PDIANMVLPR LFQKFLQFRQ LDVLASLLRN LAERHMSY
7 NCTVPSRPL PTYMMWAXQ AKDLVDIC 1QLQPTIIEEG TARPSPFPA EQLTAPQVWL
8 TMVQENHRNP EQLPVLIFQ LSQVLRPFR DLGRLFDLG MAVALSALV GIPFVYKLL
9 QSASARELP LVFINAVILA VDSSCADQLV KONGHYFLS VLADPYMPAR HRTMATAFLA
10 VIYNVSHTQ EACLQNLDA ICLELQNDPH PLRRQWAIC LIRWIGQFDS ARWCGVIRDASA
11 HEKILSLLSD PIELPVECAAV FALGTFVONS AERTHDSTTI DHMVAMDLQP LSQSMPSVR
12 KEUVNLSSH VQQVESNPC QTALQFIREE NYALPSSKT GEGSLTQPRD SPTCPRLRSP
13 STQGNYRAN TARSILNQSL WLSLEEGG AVAFPSPNL TSSSASTG SPENERHILS
14 FEITIDKRMA SYSSLNSLI GVSNSVSVTQ IWRLVHLLAA DPYFSEDVCA MKVLINSIAYK
15 ATVNRQVPR LRDSLSQTXA PASPNTKVRH IQAGQPSSPA SSTSSSTLTN DVAQKVPVRSD
16 LPFSGPFGTT PAGQQTFRHS QFRPFTRMF DKGEPQATDD ADADGREGHK LASITQVOTG
17 DWSARYFAQP VRNPYVYDFH LEQIRKEREN RPLRRSMVRRQ AQOQVIGKTR TRQODQIFP
18 KNPQFVFHFQ VHFPFTCPI AAdRDCIFED WEGKEKLDVF HNGPNPRTY TAMEYLNQOD
19 KSRLEWATGG ARVWMNKAFA DLEKPNMVT WTPQGDMWQ VTEGQIGLMS
20 SDGVRVIRN DIDTDREMKWQ IPTAGDSCTV SLSCHSRSRL VIAGDLGDSQ RYDVRDMPMS
21 DRAWVYVNC RWAQDSKQ KPEQDSTMQ PALPSEWNQL WQIVGSDL
22 HIPQADLIAC GSNQHTQAY NSSGELLINII KYGDMFQROW VGAISCLAFH PFWHLAVGVS
23 NYDYSYVSYV EKRVR

Notes to References

1. Freed E, Symons M, Macdonald SG, McCormick F, Ruggieri R. Binding of 14-3-3 proteins to the protein kinase Raf and effects on its activation. Science. 1994 Sep 16;265(5179):1713-6.
2. Irre K, Gotoh Y, Yashar BM, Errede B, Nekhoroshkova E, Sibilski C, Metz R, Albert S, Rajalingam K, Hekman M, Rapp UR. Recognition of phosphoserine. Cell. 1996 Mar 22;84(6):889-96.
3. Fischer A, Baljuls A, Reinders J, Nekhoroshkova E, Sibilski C, Metz R, Albert S, Rajalingam K, Hekman M, Rapp UR. Recognition of phosphoserine. Cell. 1996 Mar 22;84(6):889-96.
4. Michaud NR, Fabian JR, Mathes KD, Morrisson DK. 14-3-3 proteins. J Biol Chem. 2008 Jan 30;283(40):27239-46.
5. Feng E, Symons M, Macdonald SG, McCormick F, Ruggieri R. Binding of 14-3-3 proteins to the protein kinase Raf and effects on its activation. Science. 1994 Sep 16;265(5179):1713-6.
6. Frey P, Zhou M, Conrads TP, Veenstra TD, Morrison DK. Protein phosphatase 2A positively regulates Raf and effects on its activation. Science. 1994 Sep 16;265(5179):1713-6.
7. Fujii T, Ueda H, Nishida E, Matsui T, Matsumoto K. Raf and effects on its activation. Science. 1994 Sep 16;265(5179):1713-6.
8. Freed E, Symons M, Macdonald SG, McCormick F, Ruggieri R. Binding of 14-3-3 proteins to the protein kinase Raf and effects on its activation. Science. 1994 Sep 16;265(5179):1713-6.
9. Michaud NR, Fabian JR, Mathes KD, Morrisson DK. 14-3-3 proteins. J Biol Chem. 2008 Jan 30;283(40):27239-46.
10. Fujii T, Ueda H, Nishida E, Matsui T, Matsumoto K. Raf and effects on its activation. Science. 1994 Sep 16;265(5179):1713-6.
11. Michaud NR, Fabian JR, Mathes KD, Morrisson DK. 14-3-3 proteins. J Biol Chem. 2008 Jan 30;283(40):27239-46.
References to 14-3-3 binding to Raptor

Gwinn DM, Shackelford DB, Egan DF, Mihaylova MM, Mery A, Vasquez DS, Turk BE, Shaw RJ. AMPK phosphorylation of raptor mediates a metabolic checkpoint. Mol Cell. 2008 Apr 25;30(2):214-26.

Human RGS3

Finlin BS, Andres DA. Phosphorylation sequestration of beta2AR in adrenal medulla prevents endocytosis and reverses the functions of Rem2 and its interaction with 14-3-3 proteins. Arch Biochem Biophys. 1999 Aug 15;368(2):401-13.

Béguin P, Mahalakshmi RN, Nagashima K, Cher DH, Kuwamura N, Okuda, K., Guo, N. and Andres, D. Regulator of G protein signaling 3 binds to Rem2 in a phophorylation-dependent manner. Mol Cell. 2008 Apr 25;30(2):214-26.

Notes

Raptor is a regulatory component of the TORC1 complex (with mTOR) by which cells coordinate growth and maintenance of cell size with different environmental conditions. AMPK directly phosphorylates the mTOR binding partner raptor on two conserved serine residues, which phosphorylates induces 14-3-3 binding to raptor.

Human Rem2

Ras (RAD and GEM)-like GTP binding 2 (Swissprot = Q81KY8-1)

**Note**

Fig 1 in Béguin et al (2005) shows that the 14-3-3 binding sites are conserved in Rem2 and Gem, but that a truncated form of Rem2 studied by Finlin and Andres (1999) lacks the first 14-3-3 binding to Rem2. Biochem J. 1999 Nov 1;341(Pt 3):712. Erratum in: Biochem J. 2005 Nov 1;391(Pt 3):712. (Rat Rem2 AF084464).

Béguin P, Mahalakshmi RN, Nagashima K, Cher DH, Boda H, Yamada Y, Seino Y, Hunziker W. Nuclear sequestration of beta-subunits by Rad and Rem is controlled by 14-3-3 protein Rem2. Biochem J. 1999 Nov 1;341(Pt 3):712. (Rat Rem2 AF084464).

**References to 14-3-3 binding to Rem2**

Béguin P, Mahalakshmi RN, Nagashima K, Cher DH, Boda H, Yamada Y, Seino Y, Hunziker W. Nuclear sequestration of beta-subunits by Rad and Rem is controlled by 14-3-3 protein Rem2. Biochem J. 1999 Nov 1;341(Pt 3):712. (Rat Rem2 AF084464).

Finlin BS, Andres DA. Phosphorylation-dependent association of the Ras GTPase-binding Rem with 14-3-3 proteins. Biochem J. 1999 Nov 1;341(Pt 3):712. (Rat Rem2 AF084464).

References to 14-3-3 binding to Raptor

Gwinn DM, Shackelford DB, Egan DF, Mihaylova MM, Mery A, Vasquez DS, Turk BE, Shaw RJ. AMPK phosphorylation of raptor mediates a metabolic checkpoint. Mol Cell. 2008 Apr 25;30(2):214-26.

**Human RGS3 Regulator of G-protein signaling 3 (Swissprot = P90796)**

1 MPFVIALWEV EMGROSEQQEI ETLILARSHS DSTTPLNFLS HSRFPECTCT LTTLSAGAQD 61 SLPFGRRLYS GPRWRCCEV HVSVLNLST SGCLSLSLPI FPGNWEHLSP DFLARPRDEW 121 TQTSPARKR THAKVQAQG LRLSIDAQRD VLLHIEGIC LGLISQXQTCG DPYVKSLIP 181 EDSLRQQKRT QTVFQCDFDA HEHHFPFQQ ELEDDQKRLVL TVWNNARASQR SQGILGCNSSF 242 QGQVLPFTPM RLHLHNGTQG KHEEQLTHKL VARRRLRP DPLRNPMPGG DTENKXLLKI 301 TIPRGKDGFD PTICCDQVR FVQGDSSGA ERAQLQDLD VLQMNRPVR HKVCVCAHE 361 IRSCPDSEIL LVWRRMVQPK PGFDGGLVR ALSKCHTDLQ SFQFNNKRCNG THQVARFEPQ 421 RHSCVLVCS SDGLLLOGGW RTEVEAKRGK QHTPLSLRSA TAPTDPNYIT LAPLNPQSGL 481 LFQVIPQDTI FEESQSSPSKQ KSTTLRLGRK RMAKTVQTKMN GHNSQNCPCV VPFRHATSSHI 541 GITYVTLAPKF LFVFPVQQLCQLFNPARTLL LSEELLVEV RNKEAENPFLT AYSSOLLTPK

**Notes**

Raptor is a regulatory component of the TORC1 complex (with mTOR) by which cells coordinate growth and maintenance of cell size with different environmental conditions. AMPK directly phosphorylates the mTOR binding partner raptor on two conserved serine residues, which phosphorylation induces 14-3-3 binding to raptor.
which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.

© 2010 The Author(s)

RGS3 is a GTPase activating protein that downregulates G-protein signaling 3. Short=RGS3

RGS3 interacts with Rictor (AAS79796) and modulates their activity. J. Biol. Chem. 275, 28167

References to RGS3 here (isoform 3). Ser264 in isoform 1 is equivalent to Ser943 in isoform 3 (shown here).

In a confirmation of the Niu et al (2002) study, Ward et al (2005) report that Ser264 is the key serine for the GTPase-

mediated interactions. The S(264)A mutation resulted in the loss of RGS3 binding to Rictor (Benzing et al 2000). The S(264)A mutation resulted in the loss of RGS3 binding to Rictor (Benzing et al 2000). The S(264)A mutation resulted in the loss of RGS3 binding to Rictor (Benzing et al 2000). The S(264)A mutation resulted in the loss of RGS3 binding to Rictor (Benzing et al 2000). The S(264)A mutation resulted in the loss of RGS3 binding to Rictor (Benzing et al 2000). The S(264)A mutation resulted in the loss of RGS3 binding to Rictor (Benzing et al 2000). The S(264)A mutation resulted in the loss of RGS3 binding to Rictor (Benzing et al 2000). The S(264)A mutation resulted in the loss of RGS3 binding to Rictor (Benzing et al 2000). The S(264)A mutation resulted in the loss of RGS3 binding to Rictor (Benzing et al 2000). The S(264)A mutation resulted in the loss of RGS3 binding to Rictor (Benzing et al 2000). The S(264)A mutation resulted in the loss of RGS3 binding to Rictor (Benzing et al 2000). The S(264)A mutation resulted in the loss of RGS3 binding to Rictor (Benzing et al 2000). The S(264)A mutation resulted in the loss of RGS3 binding to Rictor (Benzing et al 2000). The S(264)A mutation resulted in the loss of RGS3 binding to Rictor (Benzing et al 2000). The S(264)A mutation resulted in the loss of RGS3 binding to Rictor (Benzing et al 2000). The S(264)A mutation resulted in the loss of RGS3 binding to Rictor (Benzing et al 2000). The S(264)A mutation resulted in the loss of RGS3 binding to Rictor (Benzing et al 2000). The S(264)A mutation resulted in the loss of RGS3 binding to Rictor (Benzing et al 2000). The S(264)A mutation resulted in the loss of RGS3 binding to Rictor (Benzing et al 2000).
Notes

Thr135 RIRT(pT)EPVD (numbering for full-length human rictor)

References to 14

Thr1135 RIRTL(pT)EPSVD (numbering for full-length human rictor)
Human RIMS2 Regulating synaptic membrane exocytosis protein 2 (Rab3-interacting molecule 2) (RIM2)

Swissprot = Q9UQ26)

References to 14-3-3 binding (see RIMS2)

Human RIMS2 regulating synaptic membrane exocytosis protein 2 (Rab3-interacting molecule 2) (RIM2)

© 2010 The Author(s)
phosphorylated by PKA, and 14-3-3 binding was tested by mutagenesis and with truncation mutants. They also say that the serine-413 phosphorylation site of RIM1 is conserved in RIM2a.

The S287A (RSTR(pS287)EP), but not the S379A (RYR(pS379)DP) mutation reduced the RIM1–14-3-3 interaction, and RSTR(pS287)QTP mutation further reduced the 14-3-3 binding. These findings indicate that 14-3-3 interacts with RIN1 through two phosphorylated serines, Ser241 and Ser287 (Sun et al 2003). Defects in RIM51 may be a cause of cone-rod dystrophy type 7 (CORD7) [MIM:630649].

Rim2 is encoded by a different gene from RIM1, and permits a potential consensus site for 14-3-3 binding, RYR3534DP, and another site that has similarities to complementary with the proteins of mild. SP3S238VS. Binding to 14-3-3 was strongly reduced by the S335A mutation, whereas no change was observed for the S238A mutation (Sun et al 2003). The Ser335 in Sun et al (2003) is equivalent to Ser366 in Q9UQ26.

Human RIN1

Ras and Rab interactor 1 (RAS effector/interference protein 1) (Swissprot = Q13671)

Alternative Name: Full=Sid 1669

>gi|21362884|sp|Q9Y3C5.1|RNF11_HUMAN

Human RNF11

RING finger protein 11 (Swissprot = Q9Y3C5)

>gi|21362884|sp|Q9Y3C5.1|RNF11_HUMAN

References to 14-3-3 binding to RIN1 and RIM2

Kaeser PS, Kwon HB, Blundell J, Chevaleyre V, Morishita W, Malenka RC, Powell CM, Castillo PE, Südhof TC. RIM1 and RNF11 phosphorylation at serine-413 by protein kinase A are not required for presynaptic long-term plasticity or learning. Proc Natl Acad Sci U S A. 2008 Sep 23;105(38):14680-5.

Simsek-Duran F, Linden DJ, Lonart G., Tall GG, Barbieri MA, Stahl PD, Horazdovsky BF. Ras and Rab interactor 1 (RAS effector/interference protein complement

AltName: Full=Sid 1669

Human RNF11

RING finger protein 11 (Swissprot = Q9Y3C5)

>gi|21362884|sp|Q9Y3C5.1|RNF11_HUMAN

References to 14-3-3 binding to RNF11

© 2010 The Author(s)
RFN1. In addition, T135E RFN1, which does not bind 14-3-3 and is not phosphorylated by AKT, causes a greater enhancement of transforming growth factor-beta signaling than wild-type RFN1.

References to 14-3-3 binding to RFN1

Conner MK, Azmi PB, Subramaniam V, Li H, Seth A. Molecular characterization of ring finger protein 11. Mol Cancer Res. 2005 Aug;3(8):453-61.

Azmi P, Seth A. RFN1 is a multifunctional modulator of growth factor receptor signalling and transcriptional regulation. Eur J Cancer. 2005 Nov;41(16):2549-60

Human RFH3A Rabphilin3 (Swissprot – Q9Y2J0)

1 MTYDFVESNSS RNRHMFSDKP LQSNDREQLQ AGWSVHPGQQ PDQRKRQKEEL TDEEEEIINR
2 61 TATARHAGME MQERIGLVDERNELHRHKNLHACGDOVRCTCQCLQMLGSGACVTDIUEDDCKC
3 121 NVTCTGVEKVN NNTLRSHVLC KICIEIQKEV NWKNAWFFKG FPQFVLPQPFMP PIKKTQPQOP
4 181 VSEPAAPEQP APEEPKPPARA PARGDSSDR GKPUQTPGDAP ASAPGRYNGP PVRRRASAEAR
5 241 MSSSSRSREDDS WSDDSGPSR RNSPAPRLRRA NFGVPSARPAP PQGVPFPOTGPGS
6 301 RFGPGPAQGR FPQKPEFAFS DTGTAPAPRA ERTGGVGVF VAPGEAREME HPSGFPYSQAS
7 361 AAAAAQPAARR QPPPPPREEE EANSYDSD RPPSPEAPQR AGPQKPEDPQGPDGRDGGDIIDII
8 421 PMGNGNADLP YVKLHLPPGA SKNSNLRTX RLTNPRPIWN ELTVLTGHGD EMQGRKLAKG
9 481 SVECDKEFGH NEFIFETGFS LLKLPQKNRF NICNLERVI MKRAGTGTG ARGMALLEYNE
10 541 QVERQVDEEE RGKILVLMSMY STQOGGLLVIG IIRCWHLAM AMNCGYDPSFKL WLLKLPDMGK
11 601 KAKHNQTIK KTLNPEFNEE FFPDIKHDSS AKSLKDSIVYN DDIGYKNSD YGCGQLGISGA
12 661 KDEPLHKWYE CLMNKDKKIE RHQOLQENNI VSDS

Notes

-Ser234 and Ser274 in Rabphilin3 are residues whose phosphorylation and dephosphorylation have been demonstrated to be dynamically regulated during high K+ induction. (Sun et al 2003) (species?) corresponds to induced membrane depolarization. Neither site is phosphorylated by AKT, causes a disruption of the interaction. (Sun et al 2003) (species?) corresponds to Ser274 pinpointed by Sun et al (2003) (species?) binds to Rabphilin3.

References to 14-3-3 binding to Rabphilin3

Sun L, Bittner MA, Holz RW. Rim, a component of the presynaptic active zone and modulator of exocytosis, binds to Ser272 in Q9Y2J0. The Ser274 pin position is demonstrated to be dynamically regulated during high K+

Human SASH1 Sterile alpha motif and SH3 domain containing 1 (Swissprot – O94885)

1 MEDALGAAGPF PEPEPEPEPE PEPAPEPEPE PPFGAGTSSA FSMLWTDMVG ILDLGSLNID
2 61 DNSLQADYYQ NTCDSCVCR MLIEKEKQR QOLEVESKFPA SPTSSLQEQS IEESSLFOSA
3 121 VSTTEVERKN PLHNKSSSED SVVKGDKWKKK NKFQFQWNPFR KQQGIMRTQ KEGDVGGYAS
4 181 EITMSDEERI QLLMMWKKEM ITIEEALRAL KEAYEAQHRS AALDAPDWD GYPTFTGDOSS
5 241 NCNSREQSSD TEETESVFRK LHLLVNRSTR VLRKLIRVE MVKPESTEGGE EHVFENSPVL
6 301 DERGALISVG HXKLFIPFDGS PEKPFPEDSS LTIPTSFPSSS LTDWGARLKL VRTKSGKERS
7 361 ILLYLQSDM VETTSDPPQ KQQVSRILTE GMKRGKLSL SHGRTSGCPP POLTRNLSLHV
8 421 GNSNMDPGCR EGDFVYKEVI KSQAPTSAGA KELYQKGYKSV MRKMKSGSY KSVDSSQGDL
9 481 DOMPQSSPSQP QPDPEHLKDP KLAKGSSVES LRSSLQSGQS MSGQVTSTTD SSTSNRESVR
10 541 SEGIDDEEEPF YRPPGCGRAR VHTFTDPSY DSTDPLKLKKK DIISIDIEKPG MGTWMLLNN
11 601 KVGTTFKFIY DVLSEELDEK KRPFRARRQG FPQFKPSVDE LLDRINLKEN MTFLPLNGYE
12 661 DLDTKFLEE EDLSELMDRK PERRAVILTA VELLQYQYSD SDQQSQQEKL LDQSVLDQGSLC
13 721 SPSROSCYES SENLENGKR KASLSSAKES TESPLSFSFR NQLGNYFPTL MKGSDLDAKQ
14 781 QSEEQLGGG LQPDTDSKCD FPPVGTGLNKN RLSPLVSRIC SCETLEPQFT VDTWPRSHS
15 841 DDLQVEQPE VPDVPQETVE PDQIEWQVEPE PDIPEQPSADN KTASSTAKP PLEQSDAVDN ALLLGSQSKRF
16 901 SEQPKLTTKK LEGSSAIASGR LSFPQCLFPR YNDADQFPGK HGCLARPLEG HRGRKFEOF
17 961 HPLGTKEQGD DAVGQPMQPI PQSPPVPAK KERERLNCAL HPVPVMPGSA LPSPDAPCLP
18 1021 VRRKSGSAEPT SPSDDCAPFA PRLPLSQAGQP SPSSTRPPPW LFPSLENTCAL QEHGVLKGP
19 1081 LTRKNSVCRG VDELTLTENK LHAEGIDLTE EYPSDKHGRQ GIEALYQVR AEQUIQQERD
20 1141 VAAINMQIIR QKLRQQHMR PSAQGGLTRIC RKPVPSGCIS SVDWSLISG LMPDYGTLST
21 1201 AGFSTLQVQP SLHSTCQLQA SITESEHHFK LLSAAFLFK QFSTFEM

Notes

-Containing protein 1; AltName: Full=Proline-glutamate repeat-containing protein

References to 14-3-3 containing protein

Name: Human SASH1 RecName: Full=Rabphilin-3A; AltName: Full=Exophilin-1

© The Author(s) for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial license (http://creativecommons.org/licenses/by-nc-2.5/)

which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.
Human Skp2

S-phase kinase associated protein-2 (Swissprot = Q13309)

- Human Skp2 protein in glomerular mesangial cells. J Biol Chem. 2001 Jul 27;276(29):27479-85.
- Human Skp2:Shc scaffolds integrate phosphoserine and phosphotyrosine signaling. J Biol Chem. 2009 May 29;284(22):12971-82.

NOT IN WEBLOGO.
References to 14

Lehoux S, Abe Ji, Florian JA, Berk BC. RSK phosphorylated S703 on the C terminus of NHE1 mediates Skp2 interaction with the TAK1 kinase and impairs APC/C-directed Skp2 destruction. Nat Cell Biol. 2009 Apr;11(4):397-406.

Gao D, Inuzuka H, Tseng A, Chin RY, Toker A, Wei W. Phosphorylation by Akt1 promotes cytoplasmic localization of Skp2 and impairs APC/C-directed Skp2 destruction. Nat Cell Biol. 2009 Apr;11(4):397-406.

Ecker K, Hengst L. Skp2: caught in the Akt. Nat Cell Biol. 2009 Apr;11(4):420-32.

References to 14

Gao D, Inuzuka H, Tseng A, Chin RY, Toker A, Wei W. Phosphorylation by Akt1 promotes cytoplasmic localization of Skp2 and impairs APC/C-directed Skp2 destruction. Nat Cell Biol. 2009 Apr;11(4):397-406.

References to 14

Gao D, Inuzuka H, Tseng A, Chin RY, Toker A, Wei W. Phosphorylation by Akt1 promotes cytoplasmic localization of Skp2 and impairs APC/C-directed Skp2 destruction. Nat Cell Biol. 2009 Apr;11(4):397-406.

References to 14

Gao D, Inuzuka H, Tseng A, Chin RY, Toker A, Wei W. Phosphorylation by Akt1 promotes cytoplasmic localization of Skp2 and impairs APC/C-directed Skp2 destruction. Nat Cell Biol. 2009 Apr;11(4):397-406.

References to 14

Gao D, Inuzuka H, Tseng A, Chin RY, Toker A, Wei W. Phosphorylation by Akt1 promotes cytoplasmic localization of Skp2 and impairs APC/C-directed Skp2 destruction. Nat Cell Biol. 2009 Apr;11(4):397-406.

References to 14

Gao D, Inuzuka H, Tseng A, Chin RY, Toker A, Wei W. Phosphorylation by Akt1 promotes cytoplasmic localization of Skp2 and impairs APC/C-directed Skp2 destruction. Nat Cell Biol. 2009 Apr;11(4):397-406.

References to 14

Gao D, Inuzuka H, Tseng A, Chin RY, Toker A, Wei W. Phosphorylation by Akt1 promotes cytoplasmic localization of Skp2 and impairs APC/C-directed Skp2 destruction. Nat Cell Biol. 2009 Apr;11(4):397-406.

References to 14

Gao D, Inuzuka H, Tseng A, Chin RY, Toker A, Wei W. Phosphorylation by Akt1 promotes cytoplasmic localization of Skp2 and impairs APC/C-directed Skp2 destruction. Nat Cell Biol. 2009 Apr;11(4):397-406.

References to 14

Gao D, Inuzuka H, Tseng A, Chin RY, Toker A, Wei W. Phosphorylation by Akt1 promotes cytoplasmic localization of Skp2 and impairs APC/C-directed Skp2 destruction. Nat Cell Biol. 2009 Apr;11(4):397-406.
**Human SSH1L** mediates cell cycle and cell death in neurons. J Biol Chem. 2009 Jul 10. [Epub ahead of print]

Jang SW, Liu X, Fu H, Rees H, Yepes M, Levey A, Ye K.

In phosphorylation site for PKB/Akt. )

Akt reported to phosphorylate SRPK2 on T492. (This motif (HDRSRtVSAS) is not a conventional RxRxx(pS/T)

Notes

AE

KEDAEKENIEKDWDVDQELANIDPTWIESPKTNGHIENGPFSLEQQLDDEDDDEEDCPNPEEYNLDEPN

IHTDIKPENILMCVDDAYVRRMAAEATEWQKAGAPPPSGSAVSTAPQQKPIGKISKNKKKKLKKKQKRQA

VKIGDLFNGRYHVIRKLGWGHFSTVWLCWDMQGKRFVAMKVKSAQHYETALDEIKLLKCVRESDPSDP

MSVNSEKSSSSERPEPQQKA PLVPPPPP HPPPPPLDP TPEPEPEEEL GDSEDEQEDDP

61 ADYCGGYP RPVIKDGLFNG VRHIKLPWG HTSWLCLWMD QGSRFVFAM VKCQAQHTY

121 TALEDEIKLKL CVRESDEPSD NKMVQQLID DFKISOSGMGI HVCMVEFVLG HHLKHWIKS

181 NYQGLPVRVC KSIIRQWLGD LLDYHSKCKI IHTDIKPIEM LMCVDAYVRR MAEAAETWQ

241 KAGAPPSSG AVSTAQQPQRP 1GKISKRKK KLKKQRQQA ELEKLREQ1 ELEEAERRR

301 KDEDDVDQEL IIEENITSAA KAGAPPPSGS NYQGLPVRCV

361 KDEDDVDQEL IIEENITSAA KAGAPPPSGS NYQGLPVRCV

421 AESDYTYSSQ YEQFPNGELPN GRHIKPEQSF PEFSSTLSFG SLEPVCAGSV SGLESPPLTEQ

481 EESSPSHDRE SEYVSGAASS LPDKARTRAAD LLVNPDLPDR RADKIRKIA LDGACWVHKH

541 FTIDQGVRQ RSIEVILVAG YSPADINWST ACMAFEALAT DYLFEPEHSQG DSYDRDEHHIA

661 HLIELLOSIP RHFALSOYS KEPFRNRGEL RHITKLFWS LPDVFELKYS WPHEDAAQPT

Notes

In all species examined, the putative 14-3-3 motif (amino acids residues 39–45 within Smn) is conserved. Stanin and 14-3-3 co-immunoprecipitation was demonstrated, but no experiments reported to determine whether Ser45 is phosphorylated or responsible for binding to 14-3-3 proteins. Because Ser695 is both a CK2 substrate and corresponds to a mode 3 motif. Deletion of the six terminal amino acid residues resulted in the complete abolishment of the interaction between purified recombinant 14-3-3 and SLITRK1. A motif in the carboxyl terminus of the intracellular domain of SLITRK1 (SHSLpSD-COOH) meets criteria for the mode 3 motif. This tail is different in the other gene products (SLITRKs 2 to 6). The tail is conserved in the mouse sequence (Q810C1).

References to 14-3-3 binding to SLITRK1

Kajiwara Y, Buxbaum JD, Grice DE. SLITRK1 Binds 14-3-3 proteins. J Neurosci. 2005 Aug 18;25(16):3755–63.

Notes

The phosphatase Slingshot 1 (SSH1L) has been identified as a binding partner for SLITRK1. The interaction of SSH1L and SLITRK1 is specific and requires the presence of the COOH terminus of the intracellular domain of SLITRK1 (SHSLpSD) and Regulates Neurite Outgrowth in a Phosphorylation-Dependent Manner. Biol Psychiatry. 2009 Jul 27. [Epub ahead of print]

Human SRPK2 (SwissProt = P78362)

Serine/arginine-rich protein-specific kinase 2 (Swiss-Prot = P78362)

Notes

Akt phosphorylated SRPK2 with 14-3-3zeta and modulates mitogen-activated protein kinase signaling. Brain Res Mol Brain Res. 2005 Aug 18;138(2):256–63.

References to 14-3-3 binding to SRPK2

Davidson CE, Reece BF, Billingsley ML, Yun JK. The protein stannin binds 14-3-3-zeta and modulates mitogen-activated protein kinase signaling. Brain Res Mol Brain Res. 2005 Aug 18;138(2):256–63.

Human SSH1L

The phosphatase Slingshot 1-1ike, which dephosphorylates colfin. (isoform 1, Swissprot = Q8WYI5)
1 MALVTLQRFSP TPSAASSASS SNELEAGSEE DRDKNLKLS SFSVVMKGA LLFGQSGFGQ
61 QRSILQPHHKK AGDLQLHQVL MINLRCRED IKLAVRLESA WADVRYMV MVYVSQGRDQE
121 ENILQLGVDS SKESSCSTIG MVLRLWDTX ILDGDGGPS VSTAGRMHPF VQVMDQAWMS
181 ALQLVKACEE VARRNHPPG QVALIMATY ESSCIISSQQC INEMANMQQL ESTRPDPSAL
241 PVKGRTEKER TERLIAKRK SIMMGQQLN VTSRKEHRL EKQMNQQIEE NTLFEQLIK
301 LILQQMDKPS FILDLHLYGS EWSNLASNEQ QSSRGVVISL TVRQEINFFP GLFAHNYIRV
361 YDEETDLLLA HNWEAYHF INKARRHNSCL VHHCKMSVRS ASTIVAYMKE EFQWGLEYAE
421 NYYVQKRSRT IPNQFAGNQL SEYEGILDAS QKRRKLNWQ QTSSDQLQSV DDAGPGDFIL
481 PEFPTDGFE PQLFFLDAAAQ PGLGFGPFLC FRRLSDPLRP SPEDETGLSV HLEDFEREAL
541 LEEAPAFQ PEAPQAPPSQ SPILCEKV KXKPFQSKQG QSLKSLVQTE EREQLGGGGR
601 WQLQFTLQDO NLNSLGENSN NSRCSPCHGN EADITQINQF KVPVSSKPSA DCMTYPAGSD
661 PEASRERCED PNAPAICTQF APLFHTISP VAVHLASSRV PEKASPGST PFPPPFLPPAGS
721 RRADTSGPQA GAALLEPPELV LPSRETPKPY LPSSLLKNS HKDNPSTPSR VVIKERSSPK
781 KDMKARDL LLFSNEEKP TTTSYLHMQG ESIILQOQAG LVKRRKTEKL RLSAVPDAE
841 EPPSPSPAPAH LEAEIPSEPS OPAHALHEAM LVMDPGSQAD EKSAEAPPS EGGKQKSPPP
901 FYYRDLHTSS FSKDPLRTIC YTTGSSSSN NLTRSSS3 SDH2VQVPSK VQRLQKRTET
961 KRLALAVTS SLPKSHLLA KGLSLTSTFE DLSEADSP TDASQDTSLG ESIFLHEPGE
1021 TRPDPAASTD QSGPKAPENL PSSWMSKS>

References to Human TBC1D1

Human TBC1D1 (SwissProt=Q86T10)

1 MEIPITFTARK HLLNESVSD PFGQLVGLSL HVLSTTMPL PFWVAEVRLL SQSTREKPVF
61 TQKVLRCLSP SGLCEREPQ RSQGQPDYIP SYLCFTCERC VPLKTHNSSD EYSEASCLYIKE
121 DAVRNSICY FVKAODQTYKV PEISSQARRG GKIARQEEHL CSPSFDTDFS RFKKEFLVCGF
181 TVAHTKAPPAL AILEDICIEF KHVHSSGRSE SPFRNPPHA PAQSGEQFPVR MKRSFQGQPG
241 LRLSAFPKEL QDGGLSSGF SSEESRDEI NLSHIGNQV QPTDEERNT MTHQGIVQMSE
301 YLISPDKTKI AKERNFKEIS FCQSGIRHVD HFGICRECSS GGGSFHVFVC VPQCTNEALV
361 DEINMKTIL FIYVAAQHTA SLQICTLGC PQLQSLKICSE RQENSNKSK KLETQKHLLT
421 DLMTQNGATIR EVQKVLRRPN ERQENELIS FLRCLEEQK KHIHEIEMV QTSOQMAANII
481 GSEQSSLAPSGRLFEMNLKRRS LKLSTLESES LSKRRNGAQ LQEHSLISDSL SSLSLSSTLSN
541 TSKEPSVVEK EALPISESSF KLQGSSDSE ESDHSLRE PFLSPQQAPRR RANAEISLSHF
601 ESCSSISGFC FIESSQPSQK RMRHYSVTR ETNPDKFRR SKANUQNSD QTPFKNPS
661 WQRFQPTLRA TPQCADCCSS RYDRESGSE LPPRSLEPVP CEGDPFPFG EEREKSTRSAL
721 RELVQKAIQ LQILLLNEME QWNLQASEND LLNRKLDY IETEPCLEV TTWVNEKLSMT
781 PGRSFKIGPD EMMHSAQGV VGPHRHERGI KTCPLEFHLK QHPFQEQKQ GPVYKLKYQK
841 LTSQNNHAIL DLRKGFPTTHP YTFSAQLGAQ LGSLINIKAY SLLQQFVCQG QGLSSFVAILG
901 DMLHMEKBAK WMKFMLSYQD ILQRMOLPLQ SKULDFY KFYRQTVYK CHXPFK
961 GIPSIAYPA LMFTAWAFQP GFLVPFLQFT FCQOEUTPK VLASSGLHR PLQHINEGD
1021 DIVTDIFKST CIRCILQYGGK EKQVFEMDI AKQLQAYEVE Y QVVFEMDI AKQLQAYEVE YQVF
1081 DLKLETNSNL KRLQDLLEQ LQVANGRIE LQSSFDQSMR LEATIKELLS SESLKQMLM TLEERLALS
1141 QRVTVEELRRS QTPQFPTSDG>

Notes

14-3-3 proteins associate with SSH1L at serines 937 and 978, thereby sequestering SSH1L in the cytoplasm and preventing phosphorylation of the phosphatase to F-actin–rich membrane protrusions (Nagata-Ohashi et al 2004). PKD1 and PKD2 directly phosphorylate SSH1L at these residues, thereby controlling SSH1L localization and thus cofilin dephosphorylation and activation at membrane protrusions and migration of breast cancer cells ( Petersburg et al 2009).

14-3-3 also binds to the C-terminal region of the related slingshot protein (Eiseler et al 2009)

References to 14-3-3 binding to SSH1L

Petersburg P, Heering J, Link G, Pfenninger M, Kahl S. Protein kinase D regulates cofilin phosphorylation by direct phosphorylation of the cytoplasmic phosphatase slingshot 1 like. Cancer Res. 2009 Jul 15;69(14):5634-46.

Eiseler T, Döppler H, Yan YK, Kitatani K, Mizuno K, Storz P. Protein kinase D1 regulates cofilin phosphatase slingshot 1 like. Cancer Res. 2009 Jul 15;69(14):5634-46.

Human TBC1D1

1 MEIPITFTARK HLLNESVSD PFGQLVGLSL HVLSTTMPL PFWVAEVRLL SQSTREKPVF
61 TQKVLRCLSP SGLCEREPQ RSQGQPDYIP SYLCFTCERC VPLKTHNSSD EYSEASCLYIKE
121 DAVRNSICY FVKAODQTYKV PEISSQARRG GKIARQEEHL CSPSFDTDFS RFKKEFLVCGF
181 TVAHTKAPPAL AILEDICIEF KHVHSSGRSE SPFRNPPHA PAQSGEQFPVR MKRSFQGQPG
241 LRLSAFPKEL QDGGLSSGF SSEESRDEI NLSHIGNQV QPTDEERNT MTHQGIVQMSE
301 YLISPDKTKI AKERNFKEIS FCQSGIRHVD HFGICRECSS GGGSFHVFVC VPQCTNEALV
361 DEINMKTIL FIYVAAQHTA SLQICTLGC PQLQSLKICSE RQENSNKSK KLETQKHLLT
421 DLMTQNGATIR EVQKVLRRPN ERQENELIS FLRCLEEQK KHIHEIEMV QTSOQMAANII
481 GSEQSSLAPSGRLFEMNLKRRS LKLSTLESES LSKRRNGAQ LQEHSLISDSL SSLSLSSTLSN
541 TSKEPSVVEK EALPISESSF KLQGSSDSE ESDHSLRE PFLSPQQAPRR RANAEISLSHF
601 ESCSSISGFC FIESSQPSQK RMRHYSVTR ETNPDKFRR SKANUQNSD QTPFKNPS
661 WQRFQPTLRA TPQCADCCSS RYDRESGSE LPPRSLEPVP CEGDPFPFG EEREKSTRSAL
721 RELVQKAIQ LQILLLNEME QWNLQASEND LLNRKLDY IETEPCLEV TTWVNEKLSMT
781 PGRSFKIGPD EMMHSAQGV VGPHRHERGI KTCPLEFHLK QHPFQEQKQ GPVYKLKYQK
841 LTSQNNHAIL DLRKGFPTTHP YTFSAQLGAQ LGSLINIKAY SLLQQFVCQG QGLSSFVAILG
901 DMLHMEKBAK WMKFMLSYQD ILQRMOLPLQ SKULDFY KFYRQTVYK CHXPFK
961 GIPSIAYPA LMFTAWAFQP GFLVPFLQFT FCQOEUTPK VLASSGLHR PLQHINEGD
1021 DIVTDIFKST CIRCILQYGGK EKQVFEMDI AKQLQAYEVE Y QVVFEMDI AKQLQAYEVE YQVF
1081 DLKLETNSNL KRLQDLLEQ LQVANGRIE LQSSFDQSMR LEATIKELLS SESLKQMLM TLEERLALS
1141 QRVTVEELRRS QTPQFPTSDG>
which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited. The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial Licence (http://creativecommons.org/licenses/by-nc/2.5/) © 2010 The Author(s)

Notes

TBC1D1 (related to AS160/TBC1D4) is a putative GTPase activating protein for Rab family protein(s). May play a role in cell cycle and differentiation of various tissues.

When AMPK (AMP-activated protein kinase) is activated in HEK (human embryonic kidney)-293 cells, 14-3-3s bind primarily to pSer237 (where pSer is phosphorylated serine) in TBC1D1, whereas 14-3-3s bind primarily to pSer237 (where pSer is phosphorylated serine) in cells stimulated with IGF-1 (insulin-like growth factor 1), EGF (epidermal growth factor) and PMA; and both pSer237 and pThr596 contribute to 14-3-3 binding in mouse skeletal muscle. Am J. Physiol. Endocrinol Metab 2009 Jun 16.

References to 14-3-3 binding to TBC1D1

Chen S, Murphy J, Toth R, Campbell DG, Morrice NA, Mackintosh C. Complementary regulation of TBC1D1 and AS160 by growth factors, insulin and AMPK activators. Biochem J. 2008 Jan 15;409(2):449-59

Pehmøller C, Treebak JT, Birk JB, Chen S, Mackintosh C, Hardie DG, Richter EA, Wojtaszewski JF. Genetic disruption of AMPK signaling abolishes bovine osteoclast activity. PLoS ONE 2009;4(11):e769662, in L6 cells.

Human TBC1D1 (AS160), RabGAP TBC1D4 (AS160) (Swissprot # +603343 (longer variant))

1 MEEPSCQDEE PPFPHEPPEPP GVAQASPSGQK PSDKRFLWY VGSCLDHRT TLMPLWNMA 61 EIRRSQKPEE AGGCCAPAAR EVILVLSAPF LRCVPAAPAG AAGSTPSAT QPNAPVFITE 121 HKHQHRSFPI HSSHLDITYFA YLIQAKQDPDF EQGMACHFVR ATDPSQPVOD ISSIRQLSKA 181 AMKEDAPKSK NDEAFADYNQ KFEVFILDCKV TVHKHAFAS LIDOCMDRFS LEHQQKLQIK 241 GQEPGDQDPGE DLADLEVUPP GSPQDCLPEE AGDTDHTHL PAGASQAPALT SRSVCPFERI 301 LEDGSGFDEQQ EFSRCSCSSVT QGVRVHKGSS QKSQPRRHA EASHPVSPDS SEKRTMFLQO 361 VGRFEINLIS PDTKVNGEF VKNDISCSQ GIKVHUDHF QICREPSEPG SQICYIVFQVC 421 ASESSLDVEVM LTLQKAPSTFA AALQASATQKI KLCEACPMHS LHLCRERIEG LYPFRAKFLVI 481 QRHSLSDLNQ EQADIFERQV MRPKVSQDEE NELVYHURLQ LCEAQRKTVH HIGEVPSTIS 541 TTTNPENTAP SRGFYDLILKK HAKRQGSTN LNFISPQAN RMRQLGSGD SFRKNLSAS 601 EKDYSGPSGD PGTPAFSPSMS AMQPFFRRRA DSDSPQPRRA HBFSHPFSSS KRKLNLQDDRG 661 AQOCVRSSLR QSSSECCSML SVSRMYSKE NSSSSLPSLTH TSFASPFSTA FPLKSFYQON 721 SGRSLQVENQ EIRQOTDASES SEDEGKRTKS TSCNSSELSVG GQSTVFPRTS WQRFQIFLRV 781 ASPMNKSFSA MQQQQDLDRN ELLPLGSFLSP TMEELPLVLFW LGSEDEPEKT EREKSSKELTS 841 HKLMRRKQHQ ILLLMMKDNQ QKLLEAERDL QKLEAKDENQ QKLLEAKDENQ 901 RAKIRCMD ED TMELLGKVP KMNERRGKWP LALQYLRHRL LPNQFQPDPS YSKELKLQGLT 961 AQOCQVLSDL GRTFPTHPYF SVLQGPLGSQ LLNLKAKYS LDKEVGQCSQ IFVAGVQLLL 1021 HSMQEAETF LMKLFMDQF DFQMKIPMS QLQMQLYQR DLYHDYRNLH MHLENEISFP 1081 STHIAAPPWFT LFASQFSLGS VARFDOIFLQ QTQEFVQKA LSSLSSQZET IMECESFENI 1141 VEFQVNMKLNO MMTEQEMKI VQFQMDIKSV QLQALYVEV-q VHLQDEVQDQ VQVQDESSY 1201 KLERANQQKLQMOELEL QVAHTIQAL ESNLNLTR ETKMKLRTS LEQEMAYKQ 1261 TVQELRKLPLP ADALVNCDDL LLRLNCNPNN KAKIKNPK

The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial License (http://creativecommons.org/licenses/by-nc/2.5/) which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.
Notes
This is a RabGAP implicated in insulin-stimulated regulation of GLUT4 trafficking and uptake of glucose from blood into tissues.

References to 14-3-3 binding to TBC1D4 (AS160)
Geraghty KM, Chen S, Hartill JE, Ibrahim AF, Toth R, Morrice NA, Vandermoere F, Moorhead GB, Hardie DG, MacKintosh C. Regulation of multisite phosphorylation and 14-3-3 binding of AS160 in response to IGF-1, EGF, PMA and AICAR. Biochem J. 2007 Oct 15;407(2):231-41.

Ramm G, Larance M, Guilhaus M, James DE. A role for 14-3-3 in insulin-stimulated GLUT4 translocation through its interaction with the RabGAP AS160. J Biol Chem. 2006 Sep 29;281(39):28174-80.

Human TGM2 tissue transglutaminase (Swissprot = P07101)

Human Tyrosine 3-hydroxylase is an enzyme involved in the conversion of tyrosine to dopamine. (Swissprot = P07101)

References to 14-3-3 binding to TGM2
Mishra S, Murphy LJ. Phosphorylation of transglutaminase 2 by PKA at Ser216 creates 14-3-3 binding sites on tyrosine hydroxylase are RRAVPpEp (Ser70 in P07101) and LIEADEA (= Ser70 in P07101) binding sites. In summary, we provide convincing evidence that phosphorylation of TG2 by PKA creates binding site(s) for 14-3-3 both in vitro and in vivo. This is a phosphoSer-Pro site, not conventional for PKA or 14-3-3.

References to 14-3-3 binding to TGase
Mishra S, Murphy LJ. Phosphorylation of transglutaminase 2 by PKA at Ser216 creates 14-3-3 binding sites. Biochem Biophys Res Commun. 2006 Sep 8;347(4):1166-70.

© The Author(s)
Moreover, we show that phosphorylation at three of these motifs (containing Ser60, Ser172 and Ser231) are phosphorylated in cells using mass spectrometry. (2004).

Human Tiam 1 was reported to bind directly in a phosphorylation-dependent manner with tyrosine hydroxylase and negatively charged membranes. (1998). Ichimura T, Isobe T, Yamauchi T, Fujisawa H. Brain 14-3-3 proteins: evidence for a phosphorylin dependent association. J Neurochem. 2001, May;77(3):1077-82.

Halskau O Jr, Ying M, Baumann A, Kleppe R, Larrea DR, Almáa B, Haavik J, and Martinez. Three-way interaction between 14-3-3 proteins, the N-terminal region of tyrosine hydroxylase and negatively charged membranes. J Biol Chem. 2009 Sep 28. [Epub ahead of print]
required for the degradation of Tiam1. (Woodcock et al 2009)∗ Tiam1 is a GEF for Rac. Note that phosphorylation at Ser60 was not shown directly, but mutation of this residue had functional effect. Not yet clear how three phosphorylated sites might contribute to 14-3-3 binding of Tiam1.

References to 14-3-3 binding to Tiam1

Pozuelo Rubio M, Geraghty KM, Wong BH, Wood NT, Campbell DG, Morrice N, Mackintosh C. 14-3-3-affinity purification of over 200 human phosphoproteins reveals new links to regulation of cellular metabolism, proliferation and trafficking. Biochem J. 2004 Apr 15:357(Pt 2):395-408.

Woodcock SA, Jones RC, Edmondson RD, Malliri A. A Modified Tandem Affinity Purification Technique Identifies That 14-3-3 Proteins Interact with Tiam1, An Interaction Which Controls Tiam1 Stability. J Proteome Res. 2009 Nov 9. [Epub ahead of print]

Human TPS3 p53 (Swissprot = P06437)

1 MEAQAQLLE EUPLQGERTS FLWKLLEFEN VHLSLPSEQM DDIDMFPDDI SQEFPTEDGPP 61 DEAPRAMPEAA PRVAPAAPAP TAAAPAPAPS WLPSSSVPQ KTVQGSGFVR LGFLHSSTAK 121 SVTCTTSYPAL KMKFCQLAKT CPQVLDWSTD PPPGTRVAM AITYQGQGTM EVVRCPHKE 181 RCDSDGGFL PQHILKREGVN LREYTELDRMN TFHRSSVYPP EEPFVGSDCT TTHYNMCGN 241 SCMGGMKRSP ILTITILLEDS SDLGNGRHSP EVRYCACPSP DRRFEEENLR KFEGPEHPEL 301 FGSTKRALPN NTSSQQPPPK KEDLQEEYTL QISRGFERMF FRELEANEEL KDAQAGKEPG 361 GSRASHKL SSKGQKSTSR KKLMMFKP EQG DSD

Notes

References to 14-3-3 binding to TPS3 (p53)

Rajagopalan S, Jaulten AM, Wells M, Veprintsev DB, Fersht AR. 14-3-3 activation of DNA binding of p53 by enhancing its association to tetrampers. Nucleic Acids Res. 2008 Oct 26;36(18):5983-91.

Waterman MJ, Stavridi ES, Waterman MJ, Halazonetis TD. ATM-dependent activation of p53 involves dephosphorylation and association with 14-3-3 proteins. Nat Genet. 1998 Jun;19(2):175-8.

Lee MK, Sabapathy K. Phosphorylation at carboxyterminal S373 and S375 residues and 14-3-3 mouse p53 function. Neoplasia. 2007 Sep;9(9):690-8.

Huang WG, Cheng AL, Chen ZC, Peng F, Zhang PF, Li MY, Li F, Li JL, Li C, Yi H, Xi HY, Yi B, Xiao ZQ. Targeted proteomic analysis of 14-3-3 sigma in nasopharyngeal carcinoma. Int J Biochem Cell Biol. 2009 Oct 11. [Epub ahead of print]

Rajagopalan S, Sade RS, Townsley FM, Fersht AR. Mechanistic differences in the transcriptional activation of p53 by 14-3-3 isoforms. Nucleic Acids Res. 2009 Nov 20. [Epub ahead of print]

Human TP52L1 Tumour protein D53 (also known as PrLZ and hD53) (Swissprot = Q16890)

1 MEAQAQLIE ELQPLQTQED AVASADPSM LBEKEKEKL AELVQLEDI TTLIRVLQSL 61 EHLRLVEIKQ LOMNLNELM QNFSKWHD QTTAYKAKHT ETLSHAGQKA TAASSVFVOTA 121 ISKKFGDMYS SIRHLSMPA MNNSPTFFKS EERVETTVTS LKTVGGTPN NGSFEEVLS 181 STAHASASAQL AQGSSRTKEE EQGC

Notes

References to 14-3-3 binding to TP52L1 (D53)

D52 (TP52L1)-like proteins are coiled-coil motif-bearing proteins first identified through their expression in human breast carcinoma, which have been worked on to represent signalng intermediates and regulators of vesicle trafficking. The canonical sequence is P53527-1 (different from that shown). Boutros et al (2003) and Boutros and Li MY (2004). However, the sequence alignment shows various forms is given in Wang et al (2009). 14-3-3 binding are not required for mouse p53 function. Neoplasia. 2007 Sep;9(9):690-8. Also, defined by mutagenesis in a yeast 2-hybrid assay by Boutros et al (2003). Some other splice variants lack the proposed 14-3-3 binding site. Wang et al (2009) worked with the longest isoform that they referred to as Genbank GQ499328 = Prostate-specific PrLZ-247 (247 is the longest isoform).

References to 14-3-3 binding to TP52L2 (also known as PrLZ and hD53)

Boutros R, Bailey AM, Wilson SH and Byrne JA. Alternative splicing as a mechanism for regulating 14-3-3 binding: interactions between hD53 (TP52L1) and 14-3-3 proteins. J. Mol. Biol. 332(2003), 675–687.

Boutros R and Byrne JA. D53 (TP52L1) is a cell cycle-regulated protein maximally expressed at the G2-M transition in breast cancer cells. Exp. Cell Res. 310 (2005), 152–165.

Wang R, He H, Su X, Xu J, Marshall FF, Zhou H, Chung LW, Fu H, He D. Transcription variants of the prostate-specific PrLZ gene and their interaction with 14-3-3 proteins. Biochem Biophys Res Commun. 2009 Sep 1. [Epub ahead of print]

Human TPH2 Neuronal tryptophan hydroxylase (TPH2) an enzyme that is rate-limiting in the biosynthesis of serotonin (Swissprot = Q81WU9)

1 MOPDAMMFPS KYWARRQGFL DSAVPEEQHL LGSSSTLKPN SKGKDNGKSN KSSKRRAEAE 61 SGKTVAVFSL KNEVGGVLKRA LRFQKHEVN MVHNESRSKR RGGSEIVFY DCECGDTRFF 121 ELIQFLKQF TITPNHPLPN ITTWEELLED VTWFPKRIKKE LDMSHNVLM YGSDLDNHP 181 GQFKQNYFQ RQYFPVDVAG YQKYPPIPVR EYTEEETKWT GUVFRELKSL YPTHACREYL 241 KNFPLNLYGE YRSENQVLQ EDVMFLOKER SGTVRGVPA LSGRFDLFLAG LARFVFCQTC 301 YIRHGSDPLY TPEPOTCHEL LGHVFPLAPD KFAQFOSQEG ISAGLSDASE DapkLATCYFF 361 TIEGFLCRQE QLAIRAGAY LSSGELGHA LSRACVKAEP DKPTTQLEQC LTITYFPQYEYF

© 2010 The Author(s)

The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial Licence (http://creativecommons.org/licenses/by-nc/2.5/) which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.
Catalyzes the biotin-dependent monoxygenation of 5-hydroxytryptophan (5HT), which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited. The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial Licence (http://creativecommons.org/licenses/by-nc/2.5/). © 2010 The Author(s)

References to 14-3-3 binding to tryptophan hydroxylase

Winge I, McKinney JA, Ying M, D’Santos CS, Kleppe R, Knappskog PM, Haavik J. Activation and stabilization of human tryptophan hydroxylase 2 by phosphorylation and 14-3-3 binding. Biochem J. 2008 Feb 15;410(1):195-204

Furukawa Y, Ikuta N, Omata S, Yamauchi T, Isobe T, Ichimura T. Demonstration of the phosphorylation-dependent interaction of tryptophan hydroxylase with the 14-3-3 protein. Biochem Biophys Res Commun. 1993 Jul 15;194(1):144-9.

Human TSC2 Tuberin (Swissprot = P49815)

1 MAKFTSKDG LKERFKILLG LGTFFPNPRO AEGKQTEFII TAEIELRELM ECLGNLRVLM
2 61 IQGQCEVAT KEFFEREAHE LAWKAQVQDL PERTLEARHA VALLAATIQ QGERQLVRAM
3 121 ALFVKVYDK PSNEDNRELR EIVFKALTDONG RTHITYLERL ADFVLPQMDW GLSEPLFLV
4 181 VNVLKFNSCY LDEYAVIQVC MIIICLVRAT SQGVDIEVSIL LDLIYUVTNC LPAESLPIF
5 241 VTCLRTINVK ELCECPWKL RMNLGLTHLG SAIYNCHML EDRAYMEDAP LLLGAVFVFG
6 301 MAHNGWRHL QLYQGSDSTF PSQYQAMAC RNVSSYIEVL SITIRAIHKT KELQVDWAT
7 361 LINIERTLQLQ QTQLTDGPEL RTIVHDLLT VEELCQDRNF HGOSQERYEL VERCADQPR
8 421 VSESFPSEVC DQCLCNCSLM LSGPCTLRLE RGAPEGFSRT DLHAIVVPL VASLYNLY
9 481 EULLEINSVY SQLHSPDEK DHQVRKLAQ TLLVDALCHE THFNSLIDD LIKVMARLSL
10 541 PPELBERDK AAYASASLED KTVALLGLV LQTKTLTLP HAFRTYVEML WSIQLYHLYK
11 601 SYTPILIASIE KLRGNTPSVF SDNINMPQLE LGNMLAERMA FKBRHATLY KLSDLAPDST
12 661 GPELSPTPGG GPAGAPGAV FLSVPVLLEL RPMQVLQGQ VVSDWFYDLYL GLQTELRLYK
13 721 VLIFSTPSCV DQCLCNCSLM LSGPCTLRLE RGAPEGFSRT DLHAIVVPL VASLYNLY
14 781 DRTKQREMY CLEQGGHHLR ACQVCVALS CISEMVPDIII KALKLPVLK THIATASAMA
15 841 VPLELLFSTL LRPRLHHRNF AEQGTASVFA ISLPTFNPK FNQ1YVCLAH HVIAMFYIRC
16 901 YLSPLPRDVP FITGQDNCSLM LSGPCTLRLE RGAPEGFSRT DLHAIVVPL VASLYNLY
17 961 FPVKEFKESS AAAFRCRSL VSENVHRSR QSMTLQASL GDNSENADVAQ ADDSILNHL
18 1021 ELTELCCDM ARYFVSNTFA VPKRSVPGF VLLALGFRKTV LGVQILTVNT VSVQGTWTKSL
19 1081 ELDSQGELS QPCESSSSPG PVHRQTEKAP KLELSAQVQV SQGRADVRVS MSQGHLRLVR
20 1141 ALDVPAPQSL GATSSPGFTT APAAKERAS AQRTVPVPQR TLNAAALVVL TLQWABILVR
21 1201 RPOTPHRMH 1LENGNLPS SVDMNPMLQP LGNMLAERMA FKBRHATLY KLSDLAPDST
22 1261 AKPPPLPSRN 1LENGNLPS SVDMNPMLQP LGNMLAERMA FKBRHATLY KLSDLAPDST
23 1321 FFVLATDONG RTHITYLERL ADFVLPQMDW GLSEPLFLV
24 1381 VSESFPSEVC DQCLCNCSLM LSGPCTLRLE RGAPEGFSRT DLHAIVVPL VASLYNLY
25 1441 PPEGPSASSR RSPCSLAPRO YLSIDPASOR RGRQVERDAL KSRPAASNA VPKGPNSYPFV
26 1501 FLQYHSPPF GDESNFPII FNEQSFQFSR VQDLQDIPQY DTHKAVLYV GEGQSMELA
27 1561 ILSNHSGHPF YLTEFPLKDY KYGVLQDDVC EDQGQFTYCN HIQDIDADVH
28 1621 IATIMPTKDV DRKCRRHKK LLDNSKSYVI TDQQKQFKNI FNGYKQFFNVI VIVTFLYDEC
29 1681 NLLVSQRCRD MVELGDSVFSA KIVSQRNLFP VQAMAOAHAP MQAVQHRSQ RSAPFIPWSK
30 1741 IARLRHIKL RLECRSEAAY NPSFLPHEV PHSKPAFQT PAEPTFAGV YQQKLRILLSV

© 2010 The Author(s)
Human UBP8: Deubiquitinating enzyme (Swissprot = P40818)

| Accession | Description |
|-----------|-------------|
| P40818    | Deubiquitinating enzyme |

**Notes**

Two 14-3-3 binding sites are RSTpS\(^{1081}\)LN and KSLpS\(^{1210}\)IV (\(\sim\)Ser1254 in P49815) (Liu et al 2002) whereas Ser1210 SWLpS\(^{1081}\)LENPLPFS\(\sim\) is not and RSTpS\(^{1081}\)LN is reported by Li et al (2002).

Tuberin and Hamartin (TSC1) form a tumor suppressor heterodimer that inhibits the mTOR nutrient signaling. Functions as a Rheb GTPase activating protein (GAP). Four alternatively spliced isoforms have been described.

TSC2 mutants that do not bind 14-3-3 are inactive in hypoxia to mTORC1. TSC2, but not TSC1, associates with 14-3-3 in vivo.

Controversy about whether Akt/PKB phosphorylation leads to 14-3-3 binding. Sites marked are based on available information, but not 100% certain.

**References to 14-3-3 binding to TSC2**

Hengstschläger M, Rosner M, Fountoulakis M, Luebc G. Tuberous sclerosis genes regulate cellular 14-3-3 protein levels. Biochem Biophys Res Commun. 2003 Jun 3;303(1):1-5.

Li Y, Inoki K, Yeung R, Guan KL. Regulation of TSC2 by 14\(^{3}\)p38. Biochem Biophys Res Commun. 2003 Apr 18;298(2):375-8.

Shumway SD, Li Y, Xiong Y. 14\(^{3}\)p38 associates with 14\(^{3}\)p38 as a Rheb GTPase activating protein (GAP). Four alternatively spliced isoforms have been described.

Tuberin and Hamartin (TSC1) form a tumor suppressor heterodimer that inhibits the mTOR nutrient signaling. Functions as a Rheb GTPase activating protein (GAP). Four alternatively spliced isoforms have been described.

TSC2 mutants that do not bind 14-3-3 are inactive in hypoxia to mTORC1. TSC2, but not TSC1, associates with 14-3-3 in vivo.

Controversy about whether Akt/PKB phosphorylation leads to 14-3-3 binding. Sites marked are based on available information, but not 100% certain.
The 14-3-3 binding of UBPY was inhibited by the mutation 14-3-3 binding motif RSY(S680)SP, by phosphatase treatment, and by competition with the Ser(680)-phosphorylated RSY(S680)SP peptide. Metabolic labeling with [32P]orthophosphate and immunoblotting using antibody against the phosphorylated 14-3-3 binding motif showed that Ser(680) is a major phosphorylation site in UBPY. Ser680 in the form of phosphorylated by Mizuno et al. (2007) in P40818.

References to 14-3-3 binding to UBPY
Mizuno E, Kitamura N, Komada M. 14-3-3-dependent inhibition of the deubiquitinating activity of UBPy and its cancellation in the M phase. Exp Cell Res. 2007 Oct 1;313(16):3624-34.

Human WWTR1 (TAZ) WW domain-containing transcription regulator protein 1; FullName=Transcriptional coactivator for TEAD/TEF transcription factors (Swissprot=Q92ZV5)

Delta-LightChain

<11> 1. MNHAPASPPPL PFPQGQVHIV TDQQDLTDLEAE LPNSVNFKPS SSRWKKLLRF SFFKEDDGS 61 HRSQSTDDSS GGHPGRALLGGAVQRHSSQPASLQGTTGAAGGSSPAQQAHRLQQSYDVTDLFPLPQEMTFTQAR YFNLHIEKTQWTDQPKAMQLPNHNLHAPAVSSTPFQSVMSAVQPNLVMNHHQQOAMPSLQSQNNHP TQNFPAIGMSMNPATQQQQQKLRGLRIQMEREMRRQMEQELDRQEAALCRLQPEAEATLPAQAVNV FFPTFMPDRKSTINNWSDPFLNCGYHRSEQDSTDGLSGCYSVPTTFPEFLDNDEMTQENVQGQTMNH1 NPPQFTPPDFDLCPGTNVDGLTI3SLEDLPLNPVNLSEKNLVPL3F

Notes

This protein is related to YAP1 (YAP65), TAZ plays a role in the migration, invasion, and tumorigenesis of breast cancer cells and thus presents a novel target for the detection and treatment of breast cancer. 14-3-3 binding requires TAZ phosphorylation on a single serine residue (Ser89), resulting in the inhibition of TAZ transcriptional co-activation through 14-3-3-mediated nuclear export. TAZ may link events at the plasma membrane and cytoskeleton to nuclear transcription in a manner that can be regulated by 14-3-3.

Human WWTR1 (TAZ) WW domain-containing transcription regulator protein 1; AltName=Transcriptional coactivator with PDZ-binding motif PNDZASPPPLPFPQGQVHIVTDQQDLTDLEAE LPNSVNFKPSSSWRKKLLRF SFFKEDDGS 61 HRSQSTDDSS GGHPGRALLGGAVQRHSSQPASLQGTTGAAGGSSPAQQAHRLQQSYDVTDLFPLPQEMTFTQAR YFNLHIEKTQWTDQPKAMQLPNHNLHAPAVSSTPFQSVMSAVQPNLVMNHHQQOAMPSLQSQNNHP TQNFPAIGMSMNPATQQQQQKLRGLRIQMEREMRRQMEQELDRQEAALCRLQPEAEATLPAQAVNV FFPTFMPDRKSTINNWSDPFLNCGYHRSEQDSTDGLSGCYSVPTTFPEFLDNDEMTQENVQGQTMNH1 NPPQFTPPDFDLCPGTNVDGLTI3SLEDLPLNPVNLSEKNLVPL3F

Notes

This protein is related to YAP1 (YAP65), TAZ plays a role in the migration, invasion, and tumorigenesis of breast cancer cells and thus presents a novel target for the detection and treatment of breast cancer. 14-3-3 binding requires TAZ phosphorylation on a single serine residue (Ser89), resulting in the inhibition of TAZ transcriptional co-activation through 14-3-3-mediated nuclear export. TAZ may link events at the plasma membrane and cytoskeleton to nuclear transcription in a manner that can be regulated by 14-3-3.

Human WWTR1 (TAZ) WW domain-containing transcription regulator protein 1; AltName=Transcriptional coactivator with PDZ-binding motif PNDZASPPPLPFPQGQVHIVTDQQDLTDLEAE LPNSVNFKPSSSWRKKLLRF SFFKEDDGS 61 HRSQSTDDSS GGHPGRALLGGAVQRHSSQPASLQGTTGAAGGSSPAQQAHRLQQSYDVTDLFPLPQEMTFTQAR YFNLHIEKTQWTDQPKAMQLPNHNLHAPAVSSTPFQSVMSAVQPNLVMNHHQQOAMPSLQSQNNHP TQNFPAIGMSMNPATQQQQQKLRGLRIQMEREMRRQMEQELDRQEAALCRLQPEAEATLPAQAVNV FFPTFMPDRKSTINNWSDPFLNCGYHRSEQDSTDGLSGCYSVPTTFPEFLDNDEMTQENVQGQTMNH1 NPPQFTPPDFDLCPGTNVDGLTI3SLEDLPLNPVNLSEKNLVPL3F

Notes

This protein is related to YAP1 (YAP65), TAZ plays a role in the migration, invasion, and tumorigenesis of breast cancer cells and thus presents a novel target for the detection and treatment of breast cancer. 14-3-3 binding requires TAZ phosphorylation on a single serine residue (Ser89), resulting in the inhibition of TAZ transcriptional co-activation through 14-3-3-mediated nuclear export. TAZ may link events at the plasma membrane and cytoskeleton to nuclear transcription in a manner that can be regulated by 14-3-3.
References to 14-3-3 binding to human YAP65 and Drosophila Yorkie

Vassilev A, Kaneko KJ, Shu H, Zhao Y, DePamphilis ML. TEAD/TEF transcription factors utilize the activation domain of YAP65, a Src/Yes-associated protein localized in the cytoplasm. Genes Dev. 2001 May 15;15(10):1229-41.

Badouel C, Gardano L, Amin N, Garg A, Rosenfeld R, Le Bihan T, McNeill H. The FERM-domain protein Expanded regulates Hippo pathway activity via direct interactions with the transcriptional activator Yorkie. Dev Cell. 2009 Mar;16(3):411-20.

Wang K, Degenry C, Xu M, Yang XJ. YAP, TAZ, and Yorkie: a conserved family of signal-responsive transcriptional coregulators in animal development and human disease. Biochem Cell Biol. 2009 Feb;87(1):77-91.

Zhao B, Wei X, Li W, Udan RS, Yang Q, Kim J, Xie J, Ikenoue T, Yu J, Li L, Zheng P, Ye K, Chinnaiyan A, Halder G, Lai ZC, Guan KL. Inactivation of YAP oncoprotein by the Hippo pathway is involved in cell contact inhibition and tissue growth control. Genes Dev. 2007 Nov 1;21(21):2747-61.

Basu S, Totty NF, Irwin MS, Sudol M, Downward J. Akt phosphorylates the Yes-associated protein, YAP, to induce interaction with 14-3-3 and attenuation of p73-mediated apoptosis. Mol Cell. 2003 Jan;11(1):11-23.

Vassilev A, Kaneko KJ, Shu H, Zhao Y, DePamphilis ML. TEAD/TEF transcription factors utilize the activation domain of YAP65, a Src/Yes-associated protein localized in the cytoplasm. Genes Dev. 2001 May 15;15(10):1229-41.

Kanai F, Marignani PA, Sarbassova D, Yagi R, Hall RA, Donowitz M, Hisaminato A, Fujiwara T, Ito Y, Cantley LC, Yaffe MB, TAZ: a novel transcriptional co-activator regulated by 14-3-3 and PDZ domain proteins. EMBO J. 2000 Dec 15;19(24):6778-88.

Zhao B, Li L, Tumaneng K, Wang CY, Guan KL. Inactivation of YAP oncoprotein by the Hippo pathway is involved in cell contact inhibition and tissue growth control. Genes Dev. 2007 Nov 1;21(21):2747-61.

References to 14-3-3 binding to Mi2

Wandel M, Kleine-Kohlbrecher D, Herold S, Hock A, Berns K, Park J, Hemmings B, Eilers M. Akt and 14-3-3 proteins. EMBO J. 2000 Dec 15;19(24):6778-88.

Li L, Tumaneng K, Zhao B, Wei X, Li W, Udan RS, Yang Q, Kim J, Xie J, Ikenoue T, Yu J, Li L, Zheng P, Ye K, Chinnaiyan A, Halder G, Lai ZC, Guan KL. Inactivation of YAP oncoprotein by the Hippo pathway is involved in cell contact inhibition and tissue growth control. Genes Dev. 2007 Nov 1;21(21):2747-61.

Basu S, Totty NF, Irwin MS, Sudol M, Downward J. Akt phosphorylates the Yes-associated protein, YAP, to induce interaction with 14-3-3 and attenuation of p73-mediated apoptosis. Mol Cell. 2003 Jan;11(1):11-23.

Vassilev A, Kaneko KJ, Shu H, Zhao Y, DePamphilis ML. TEAD/TEF transcription factors utilize the activation domain of YAP65, a Src/Yes-associated protein localized in the cytoplasm. Genes Dev. 2001 May 15;15(10):1229-41.

Kanai F, Marignani PA, Sarbassova D, Yagi R, Hall RA, Donowitz M, Hisaminato A, Fujiwara T, Ito Y, Cantley LC, Yaffe MB, TAZ: a novel transcriptional co-activator regulated by 14-3-3 and PDZ domain proteins. EMBO J. 2000 Dec 15;19(24):6778-88.

Zhao B, Li L, Tumaneng K, Wang CY, Guan KL. Inactivation of YAP oncoprotein by the Hippo pathway is involved in cell contact inhibition and tissue growth control. Genes Dev. 2007 Nov 1;21(21):2747-61.

References to 14-3-3 binding to Mi2

Wandel M, Kleine-Kohlbrecher D, Herold S, Hock A, Berns K, Park J, Hemmings B, Eilers M. Akt and 14-3-3 proteins. EMBO J. 2000 Dec 15;19(24):6778-88.

Li L, Tumaneng K, Zhao B, Wei X, Li W, Udan RS, Yang Q, Kim J, Xie J, Ikenoue T, Yu J, Li L, Zheng P, Ye K, Chinnaiyan A, Halder G, Lai ZC, Guan KL. Inactivation of YAP oncoprotein by the Hippo pathway is involved in cell contact inhibition and tissue growth control. Genes Dev. 2007 Nov 1;21(21):2747-61.

Basu S, Totty NF, Irwin MS, Sudol M, Downward J. Akt phosphorylates the Yes-associated protein, YAP, to induce interaction with 14-3-3 and attenuation of p73-mediated apoptosis. Mol Cell. 2003 Jan;11(1):11-23.

Vassilev A, Kaneko KJ, Shu H, Zhao Y, DePamphilis ML. TEAD/TEF transcription factors utilize the activation domain of YAP65, a Src/Yes-associated protein localized in the cytoplasm. Genes Dev. 2001 May 15;15(10):1229-41.

Kanai F, Marignani PA, Sarbassova D, Yagi R, Hall RA, Donowitz M, Hisaminato A, Fujiwara T, Ito Y, Cantley LC, Yaffe MB, TAZ: a novel transcriptional co-activator regulated by 14-3-3 and PDZ domain proteins. EMBO J. 2000 Dec 15;19(24):6778-88.

Zhao B, Li L, Tumaneng K, Wang CY, Guan KL. Inactivation of YAP oncoprotein by the Hippo pathway is involved in cell contact inhibition and tissue growth control. Genes Dev. 2007 Nov 1;21(21):2747-61.

References to 14-3-3 binding to Mi2

Wandel M, Kleine-Kohlbrecher D, Herold S, Hock A, Berns K, Park J, Hemmings B, Eilers M. Akt and 14-3-3 proteins. EMBO J. 2000 Dec 15;19(24):6778-88.

Li L, Tumaneng K, Zhao B, Wei X, Li W, Udan RS, Yang Q, Kim J, Xie J, Ikenoue T, Yu J, Li L, Zheng P, Ye K, Chinnaiyan A, Halder G, Lai ZC, Guan KL. Inactivation of YAP oncoprotein by the Hippo pathway is involved in cell contact inhibition and tissue growth control. Genes Dev. 2007 Nov 1;21(21):2747-61.
A zinc finger protein that plays an important role in the assembly of the RNA polymerase III initiation factor TFIIIB. Regulates mRNA levels by targeting transcripts containing AREs (AU-rich elements) into the decay pathway. Phosphorylation by Akt apparently generates 14-3-3 binding sites and inhibits BRF1 from promoting mRNA stability. Containment of PBF by PKR at both S92 and S203. Mutation leads to complete loss of PKB regulation of BRF1 and constitutive mRNA decay. Cell compartment fractionation experiments support a model in which binding to 14-3-3 sequesters BRF1 through relocalization and prevents it from executing its mRNA decay activity, as well as from posttranslational degradation, thereby maintaining high BRF1 protein levels that are required to reinitate decay upon dissolution of the stabilizing signal.

References to 14-3-3 binding to BRF1
Schmidlin M, Lu M, Leuenberger SA, Stoecklin G, Mallau M, Gross B, Gherzi R, Hess D, Hemmings BA, Moroni C. The ARE-dependent mRNA-stabilizing activity of BRF1 is regulated by protein kinase B. EMBO J. 2004 Dec 8;23(24):4760-9.

Benjamin D, Schmidlin M, Min L, Gross B, Moroni C. BRF1 Protein Turnover and mRNA Decay Activity Are Regulated by Protein Kinase B at the Same Phosphorylation Sites. Mol Cell Biol. 2006 December; 26(24): 9497–9507.

### Human ZNF395 (Huntington disease gene regulatory region-binding protein 2, HDBP2) (Papillomavirus-binding factor, PBF) (Swissprot = Q9H8N7)

- **RING finger** = Cys199 to Pro240
- **Zn finger** = Cys160 to Cys179
- **MAGE domain** = Ala41 to Ser120

Note: Inscription of the PBF amino acid sequence revealed two motifs from amino acids 444 to 453 (the sequence SRDSRFSF), and from amino acids 393 to 439 (the sequence LRKQISRKL), that resembled "mode 1", although neither motif was perfect. Individual mutations of the potential binding serine at position 391 (the potential binding site S391A/PBFmt4) or the serine at position −2 to the potential binding serine (S394A; PBFmt5) did not significantly affect the ability of this protein to interact with HA.

**BRF1**
- **Protein Turnover and mRNA Decay Activity Are Regulated by Protein Kinase B at the Same Phosphorylation Sites.** Mol Cell Biol. 2006 December; 26(24): 9497–9507.

| Notes |
| --- |
| SRDSRFSRFSF(pS92)EGGERLPL |
|
A zinc finger protein that plays an important role in the assembly of the RNA polymerase III initiation factor TFIIIB. Regulates mRNA levels by targeting transcripts containing AREs (AU-rich elements) into the decay pathway. Phosphorylation by Akt apparently generates 14-3-3 binding sites and inhibits BRF1 from promoting mRNA stability. Containment of PBF by PKR at both S92 and S203. Mutation leads to complete loss of PKB regulation of BRF1 and constitutive mRNA decay. Cell compartment fractionation experiments support a model in which binding to 14-3-3 sequesters BRF1 through relocalization and prevents it from executing its mRNA decay activity, as well as from posttranslational degradation, thereby maintaining high BRF1 protein levels that are required to reinitate decay upon dissolution of the stabilizing signal.

### References to 14-3-3 binding to BRF1
Schmidlin M, Lu M, Leuenberger SA, Stoecklin G, Mallau M, Gross B, Gherzi R, Hess D, Hemmings BA, Moroni C. The ARE-dependent mRNA-stabilizing activity of BRF1 is regulated by protein kinase B. EMBO J. 2004 Dec 8;23(24):4760-9.

Benjamin D, Schmidlin M, Min L, Gross B, Moroni C. BRF1 Protein Turnover and mRNA Decay Activity Are Regulated by Protein Kinase B at the Same Phosphorylation Sites. Mol Cell Biol. 2006 December; 26(24): 9497–9507.

### Human ZNF395 (Huntington disease gene regulatory region-binding protein 2, HDBP2) (Papillomavirus-binding factor, PBF) (Swissprot = Q9H8N7)

- **RING finger** = Cys199 to Pro240
- **Zn finger** = Cys160 to Cys179
- **MAGE domain** = Ala41 to Ser120

Note: Inspection of the PBF amino acid sequence revealed two motifs from amino acids 444 to 453 (the sequence SRDSRFSF), and from amino acids 393 to 439 (the sequence LRKQISRKL), that resembled "mode 1", although neither motif was perfect. Individual mutations of the potential binding serine at position 391 (the potential binding site S391A/PBFmt4) or the serine at position −2 to the potential binding serine (S394A; PBFmt5) did not significantly affect the ability of this protein to interact with HA.

**BRF1**
- **Protein Turnover and mRNA Decay Activity Are Regulated by Protein Kinase B at the Same Phosphorylation Sites.** Mol Cell Biol. 2006 December; 26(24): 9497–9507.

| Notes |
| --- |
| SRDSRFSRFSF(pS92)EGGERLPL |
| which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited. |
### Mouse AKR13b CAI52035 (mouse)

Ankyrin repeat domain 13b

| Amino Acid Sequence | Notes |
|---------------------|-------|
| 1 RTGLGWRE KTEMVNGYEA KVVQGVSNVE ITRRTTEHLSS EQQHKSVRGC KPTLQSLPGI | 14-3-3-binding sites not defined, therefore NO WEBLOGO ANALYSIS |
| 61 AEQHGPQPQG TLTIQTLSQA NPFAITAEK FHPNFEGLNR AGMRPEELTT KTNQFVFPLG | |
| 121 MODQUGGFPSC GCTGVSTCPCC YISPVWSLPLS WLSHATHFLPS SGSSRCACL LASSQRLKSR | |
| 181 FTTSTSPAS GTSMAAMQG CPCEAVAPA RA | |

Notes

Ankyrin repeat domain 13b CAI52035 (mouse)

### References to 14-3-3 binding to AKR13b

Wanna W, Rexroad CE 3rd, Yao J. Identification of a Functional Splice Variant of 14-3-3E in Rainbow Trout.

Mar Biotechnol (NY). 2009 Jul 10. CAI52035 (mouse)

### Mouse CCT-α

Phosphorylcholine transferase A (Swissprot = P49586)

| Amino Acid Sequence | Notes |
|---------------------|-------|
| 1 MDAQSSAKV SRRKRayKEG PAGNEEITI PESQKVCQAV QRNPAPFSSDE IEVDPKYSFV | |
| 61 KTQMBACRG TPCERPVRVY AGDIFDPLHS GHRAMLQAK NLFPMTLYV GVSDELTNN | |
| 121 FKQGTVMMEN KRYDAVGQCR YVDEFRVMAP WTIDSFPLAE HRDEIVHDO IYPSASGSDD | |
| 181 VYKHKQIAGM FAPFTQEGI STDTSIRIAT ROYDYVARN LQSTQKETE NVSYFSNKEK | |
| 241 HLQERVKDVK KKVQVEEKS KEVFQVKEV SIDIQLQWE KSRFQFL EMFPGPGLK | |
| 301 HMLKEKGRM LQAIKSPQSP SSPPHTERSP SSPFRFPSSG KTSSPSSPSAS LSCRACLVTCD | |
| 361 IDEEDE | |

Notes

In addition to Ser288 (in yellow), a second 14-3-3-binding site is proposed to exist within residues 32 to 343. 14-3-3 binding to CCT-α in response to Ca2+ signals is associated with nuclear import of the enzyme.

### References to 14-3-3 binding to CCT-α

Agassandian M, Chen BB, Schuster CC, Houtman JC, Mallampalli RK. 14-3 binding to CCT-α for calcium-activated nuclear import in lung epithelia. FEBS J. 2005 May 1;118(Pt 9):1923

### Mouse Ed3

mRNA Enhancer of mRNA-decaping protein 3

| Amino Acid Sequence | Notes |
|---------------------|-------|
| 1 MAMDRISIV SINCDSG1GV YQVRSVSAVQQ VSQTITSLTRP FHHNVKCLVP EVTFRAGGTV | |
| 61 ELKLTGIPG GDNOQGVDDL QTEGSGVQG YMDSISQGNT GKVVKPPASS SAAPOSIPKR | |
| 121 TDFQSQVPAD SIQPQQQCSKS YVDRMSICL QRSKSRARP RNH DSSRSSFRPN QAFTPRSKQL | |
| 181 G13QVW4KOE CEQCCQTDS GPDDPQENC ALDKRAAKNG DTDTP licking | |
| 241 PARYRINDE LESEPQYVRR ITPHVHVSKE CTDFSGLSPV SYELYLKLKL SVLAEKGLT | |
| 301 LERRLMGV CAQSMALTLL GCNPRLPNKQ VHQQRTVATL CGPHVQGAA QISCRGLHANL | |
| 361 DQVQVIPFNP VMKLEMSTIN ELSLFGTKQ QVSSRLDLP ASPFDVLINC LDCPENAFLR | |
| 421 DQPYWKAVAA WANNQRAPVL SIDPPVHEVE QSIDAKWLA LGPLPLNLEG AGRVYLCDIG | |
| 481 IFQVQPQVEQG INYHSPFCCK VFIPHLSHA | |

Notes

Ser161 is phosphorylated in response to insulin.

### References to 14-3-3 binding to Ed3

Larance M, Rowland AF, Hoehn K, Humphreys DT, Preiss T, Guillaume M, James DE. Global phosphoproteomics identifies a major role for akt and 14-3-3 in regulating Ed3. Mol Cell Proteomics. 2010 Jan 5. [Epub ahead of print]

### Mouse GEM (Swissprot = P53041)

| Amino Acid Sequence | Notes |
|---------------------|-------|
| 1 MTINNVTRQQ GTVQMOPQQQR WAGPAADHL MVQDKHPCN LRNHRSTAFP EHCRRKGSDD | |
| 61 STGEDSIVSES GNTYVRUVLQ GEQGQVSSTKL ANIFQVHGS MDSCQCELGY DTERTVLYVD | |
| 121 GESATILLDD MWEKKGNEW HLODMQVGDY AYLIVYSTD RASFEKASL RIQLRRARQRT | |
| 181 EDPPILQVRN KSDLVRCVE SVESEGRACAV VFTDCKFIEASS AAQVQNNKEL FEGIVQVQLR | |
| 241 RDSKEEKN RLAQYKREES IFPRAARRGWQ KVIAKNKNN AKFLKSKCH DLSVL | |

### Mouse G30R kinase Like protein 1 (Swissprot = Q8K2D3)

| Amino Acid Sequence | Notes |
|---------------------|-------|
| 1 MTLNNTRQGQ TGVQMOPQQQR WAGPAADHL MVQDKHPCN LRNHRSTAFP EHCRRKGSDD | |
| 61 STGEDSIVSES GNTYVRUVLQ GEQGQVSSTKL ANIFQVHGS MDSCQCELGY DTERTVLYVD | |
| 121 GESATILLDD MWEKKGNEW HLODMQVGDY AYLIVYSTD RASFEKASL RIQLRRARQRT | |
| 181 EDPPILQVRN KSDLVRCVE SVESEGRACAV VFTDCKFIEASS AAQVQNNKEL FEGIVQVQLR | |
| 241 RDSKEEKN RLAQYKREES IFPRAARRGWQ KVIAKNKNN AKFLKSKCH DLSVL | |

Notes

Member of RGM small GTP-binding protein family, which includes Kir/Gem, Rad, Rem and Rem2.

Mouse - Phosphorylation on S22 and S288 (QORWysS7IP and KLKSKeS7CH) is required for binding of 14-3-3, which also retains Kir/Gem in the cytosol, whereas phosphorylation on S286 prevents the association and/or favors the dissociation of 14-3-3 via an unknown mechanism (Mahalakshmi et al 2007).

Human - Phosphorylation of serine 289 in conjunction with serine 23 results in bidentate 14-3-3 binding, leading to increased Gem protein half-life (Ward et al 2004). (Ser23 in human GEM corresponds to Ser22 in mouse GEM)

### References to 14-3-3 binding to GEM

Mahalakshmi RN, Nagashima K, Ng MY, Inagaki N, Hunziker W, Bégüin P. Nuclear transport of Kir/Gem requires specific signals and importin alpha5 and is regulated by calmodulin and predicted serine phosphorylations. Traffic. 2007 Sep;8(9):1164-78.

Bégüin P, Mahalakshmi RN, Nagashima K, Cher DH, Takahashi A, Yamada Y, Seino Y, Hunziker W. 14-3-3 and calmodulin control subcellular distribution of Kir/Gem and its regulation of cell shape and calcium channel activity. J Cell Sci. 2005 May 1;118(Pt 9):1923-34.

Ward Y, Spinelli B, Quon MJ, Chen H, Ikeda SR, Kelly K. Phosphorylation of critical serine residues in Gem separates cytoskeletal reorganization from down-regulation of calcium channel activity. Mol Cell Biol. 2004 Jan;24(2):651-61.

### Mouse Grib10 (Growth factor receptor-bound protein 10 (GRB10 adapter protein) (Swissprot = Q60760)

14-3-3-binding sites not defined, therefore NO WEBLOGO ANALYSIS

The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial Licence (http://creativecommons.org/licenses/by-nc/2.5/) which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.
which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.

The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial Licence (http://creativecommons.org/licenses/by-nc/2.5/)

© 2010 The Author(s)

References to 14 beta accelerated the return of the K(+) current to the resting state after the activation mediated by calcineurin in anesthetics, such as isoflurane. Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.

Outward rectifying potassium channel. Produces rapidly activating outward rectifier K(+) currents. May function as background potassium channel that sets the resting membrane potential. Inhibited by KCNK18 (TRESK)

Notes
“The 14-3-3-Grb10 interaction requires phosphorylation of Grb10, and only the phosphorylated form of 14-3-3 co-immunoprecipitates with endogenous 14-3-3. We could identify a putative phosphorylation site in Grb10, which is located in a classical 14-3-3 binding motif, RSVSE. Mutation of this site in Grb10 diminished binding to 14-3-3. Thus, Grb10 exists in two different states of phosphorylation and complexes with the interaction of 14-3-3 with serine 428.” (Urschel et al 2005) (RSVpS33–37EN = Ser455 in Swissprot Q60760)

“Mutagenesis of serine 428 to alanine, an Akt phosphorylation site known to complex with the interaction of 14-3-3 (21), also prevented the Grb10 anti-apoptotic activity.” (Kebeche et al 2007) used the isoform Mouse Grb10(deltu).

References to 14-3-3 binding to Grb10
Urschel S, Bassermann F, Bai RY, Münch S, Peschel C, Duyster J. Phosphorylation of grb10 regulates its isoform

Urschel S, Bai RY, Münch S, Peschel C, Duyster J. Phosphorylation of grb10 regulates its isoform

Mouse KCNK18 (TRESK) Potassium channel subfamily K member 18 (SwissProt =Q6VV64)

“Mutagenesis of serine 428 to alanine, an Akt phosphorylation site known to complex with the interaction of 14-3-3 (21), also prevented the Grb10 anti-apoptotic activity.” (Kebeche et al 2007) used the isoform Mouse Grb10(deltu).

References to 14-3-3 binding to Grb10
Urschel S, Bassermann F, Bai RY, Münch S, Peschel C, Duyster J. Phosphorylation of grb10 regulates its isoform

Mouse KCNK18 (TRESK) Outward rectifying potassium channel. Produces rapidly activating outward rectifier K(+) currents. May function as background potassium channel that sets the resting membrane potential. Inhibited by arachidonic acid and other naturally occurring unsaturated free fatty acids. Channel activity is enhanced by volatile ed free fatty acids. Channel activity is enhanced by volatile.

Notes
“SITE(S) NOT DEFINED. NOT IN WEBLOG.”

The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial Licence (http://creativecommons.org/licenses/by-nc/2.5/).
Insulin stimulated 14-3-3 binding to lipin-1alpha in 3T3-L1 adipocytes, and a serine-rich region (residues 218 to 260) was implicated in binding to 14-3-3, but precise site(s) were not defined (Pétery et al 2009).

References to 14-3-3 binding to lipin-1alpha

Pétery M, Harris TE, Fujita N, Reue K. Insulin-stimulated interaction with 14-3-3 promotes cytoplasmic localization of lipin-1 in adipocytes. J Biol Chem. 2009 Dec 2. [Epub ahead of print]

Myo1c (Swissprot = Q9W71T)

Differential 14-phosphorylation

Yip MF, Ramm G, Larance M, Hoehn KL, Wagner MC, Guilhaus M, James DE. CaMKII Myo1c undergoes insulin stimulation of the myosin motor Myo1c is required for insulin binding and reduced calmodulin binding. Ser701= Ser736 in Q9WT17.

References to 14-3-3 binding to Myo1c

Yip MF, Ramg L, Larance M, Hoehn KL, Wagner MC, Guilhaus M, James DE. CaMKII-mediated phosphorylation of the myosin motor Myo1c is required for insulin-stimulated GLUT4 translocation in adipocytes. Cell Metab. 2008 Nov;9(5):384-98.

Dubus F, Vandermoege F, Gernez A, Murphy J, Toth R, Chen S, Geraghty KM, Morrice NA, Mackintosh C. Differential 14-3-3-affinity capture reveals new downstream targets of PI 3-kinase signaling. Mol Cell Proteomics. 2009 Aug 1.

Myo1c undergoes insulin-dependent phosphorylation at S701 (EVRQR(qS701))LAKKKQAAA. Phosphorylation was accompanied by enhanced 14-3-3 binding and reduced calmodulin binding. Ser701 = Ser736 in Q9W71T.

References to 14-3-3 binding to Myo1c

Yip MF, Ramg L, Larance M, Hoehn KL, Wagner MC, Guilhaus M, James DE. CaMKII-mediated phosphorylation of the myosin motor Myo1c is required for insulin-stimulated GLUT4 translocation in adipocytes. Cell Metab. 2008 Nov;9(5):384-98.

Dubus F, Vandermoege F, Gernez A, Murphy J, Toth R, Chen S, Geraghty KM, Morrice NA, Mackintosh C. Differential 14-3-3-affinity capture reveals new downstream targets of PI 3-kinase signaling. Mol Cell Proteomics. 2009 Aug 1.

Myoe1c

Myoe1c undergoes insulin-dependent phosphorylation at S701 (EVRQR(qS701))LAKKKQAAA. Phosphorylation was accompanied by enhanced 14-3-3 binding and reduced calmodulin binding. Ser701 = Ser736 in Q9W71T.

References to 14-3-3 binding to Myoe1c

Yip MF, Ramg L, Larance M, Hoehn KL, Wagner MC, Guilhaus M, James DE. CaMKII-mediated phosphorylation of the myosin motor Myoe1c is required for insulin-stimulated GLUT4 translocation in adipocytes. Cell Metab. 2008 Nov;9(5):384-98.

Dubus F, Vandermoege F, Gernez A, Murphy J, Toth R, Chen S, Geraghty KM, Morrice NA, Mackintosh C. Differential 14-3-3-affinity capture reveals new downstream targets of PI 3-kinase signaling. Mol Cell Proteomics. 2009 Aug 1.
References to 14-3-3 binding to mouse myosin

Faul C, Dhume A, Schecter AD, Mundel P. Protein kinase A, Ca2+/calmodulin-dependent kinase II, and calcineurin regulate the intracellular trafficking of myopodin between the Z-disc and the nucleus of cardiac myocytes. Mol Cell Biol. 2007 Dec;27(23):8215-27.

References to 14-3-3 binding to mouse wee1

Honda R, Ohba Y, Yasuda H. 14-3-3 binding to mouse wee1 because in the reference sequence the matching sites for RSLA(pS225)VP and RSVP(r642) are possible. 

References to 14-3-3 binding to mouse IFN

Faul C, Dhume A, Schecter AD, Mundel P. Protein kinase A, Ca2+/calmodulin-dependent kinase II, and calcineurin regulate the intracellular trafficking of myopodin between the Z-disc and the nucleus of cardiac myocytes. Mol Cell Biol. 2007 Dec;27(23):8215-27.

Notes

S225 and T272 mediate the phosphorylation-dependent binding of myopodin to 14-3-3 (The authors must have been working on a shorter protein because in the reference sequence the matching sites for RSLA(pS225)VP and RSVP(r642) are possible. 

S225 and T272 mediate the phosphorylation-dependent binding of myopodin to 14-3-3

References to 14-3-3 binding to mouse IFN

Faul C, Dhume A, Schecter AD, Mundel P. Protein kinase A, Ca2+/calmodulin-dependent kinase II, and calcineurin regulate the intracellular trafficking of myopodin between the Z-disc and the nucleus of cardiac myocytes. Mol Cell Biol. 2007 Dec;27(23):8215-27.

Notes

S225 and T272 mediate the phosphorylation-dependent binding of myopodin to 14-3-3 (The authors must have been working on a shorter protein because in the reference sequence the matching sites for RSLA(pS225)VP and RSVP(r642) are possible. 

References to 14-3-3 binding to mouse IFN

Faul C, Dhume A, Schecter AD, Mundel P. Protein kinase A, Ca2+/calmodulin-dependent kinase II, and calcineurin regulate the intracellular trafficking of myopodin between the Z-disc and the nucleus of cardiac myocytes. Mol Cell Biol. 2007 Dec;27(23):8215-27.

Notes

S225 and T272 mediate the phosphorylation-dependent binding of myopodin to 14-3-3 (The authors must have been working on a shorter protein because in the reference sequence the matching sites for RSLA(pS225)VP and RSVP(r642) are possible. 

References to 14-3-3 binding to mouse IFN

Faul C, Dhume A, Schecter AD, Mundel P. Protein kinase A, Ca2+/calmodulin-dependent kinase II, and calcineurin regulate the intracellular trafficking of myopodin between the Z-disc and the nucleus of cardiac myocytes. Mol Cell Biol. 2007 Dec;27(23):8215-27.

Notes

S225 and T272 mediate the phosphorylation-dependent binding of myopodin to 14-3-3 (The authors must have been working on a shorter protein because in the reference sequence the matching sites for RSLA(pS225)VP and RSVP(r642) are possible. 

References to 14-3-3 binding to mouse IFN

Faul C, Dhume A, Schecter AD, Mundel P. Protein kinase A, Ca2+/calmodulin-dependent kinase II, and calcineurin regulate the intracellular trafficking of myopodin between the Z-disc and the nucleus of cardiac myocytes. Mol Cell Biol. 2007 Dec;27(23):8215-27.

Notes

S225 and T272 mediate the phosphorylation-dependent binding of myopodin to 14-3-3 (The authors must have been working on a shorter protein because in the reference sequence the matching sites for RSLA(pS225)VP and RSVP(r642) are possible. 

References to 14-3-3 binding to mouse IFN

Faul C, Dhume A, Schecter AD, Mundel P. Protein kinase A, Ca2+/calmodulin-dependent kinase II, and calcineurin regulate the intracellular trafficking of myopodin between the Z-disc and the nucleus of cardiac myocytes. Mol Cell Biol. 2007 Dec;27(23):8215-27.
Rat ATP1A1 (Na+, K+-ATPase a1-subunit) (Swissprot = P05023)

| Accession | Description |
|-----------|-------------|
| 1 MGQOD8     | Bradykinin receptor-like protein 1A |
| 61 RLGSRRTT | Membrane protein 1A |
| 181 AAVLNASD | Integral component of ER membrane |
| 241 BEYRIH  | Integral component of ER membrane |
| 310 EPRK    | Integral component of ER membrane |
| 421 FPRH    | Integral component of ER membrane |

Notes

No experimental data, though suggested site is EPRK (RNG[pS]F) in silico analysis. Rat ATP1A1 is a member of the 

References to 14-3-3 binding to rat ATP1A1

Katoh M, Kadotani M. Identification and characterization of rat ATP1A1 gene in silico. Int J Mol Med. 2005 Feb;15(2):359-63.

SITES NOT IN WEBLOGO.
which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.

© 2010 The Author(s)

Rich domain from Crk

Briknarová K, Nasertorabi F, Havert ML, Eggleston E, Hoyt DW, Li C, Olson AJ, Vuori K, Ely KR. The serine protein p130(Cas) and the 14-3-3 protein p130Cas (Swissprot = P06685) translates KKGKK.

Human P06685

1 MGKGVQDRKY EPAAVSEQD GKGKGGKDR DDELKKEVS MDDKSHLSD LHHRYGTDLS

Notes

Cannot find the phosphorylated Ser 18 studied by Efendiev et al (2005) in the rat (P05023) or human protein (P06685), appears to be KGGKK.

References to 14-3-3 binding to Na+, K+-ATPase α1-subunit

Efendiev R, Chen Z, Krmar RT, Uhles S, Katz AI, Pedemonte CH, Bertorello AM. The 14-3-3 protein (Swissprot = P06685), appears to be KKGKK.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

García-Guzman M, Dolfi F, Russo M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.

References to 14-3-3 binding to p130Cas

Guzman M, Dolfi F, Russello M, Vuori K. Cell adhesion regulates the interaction between the docking and activation of phosphoinositide 3-kinase during endocytosis. J Biol Chem. 2005 Apr 22;280(16):16272-7.
Rat CaMKII

1. MERSPAVCCQPDPREELVERVAASIWAHEEAEDEGEPESNVDVPPPFAARRASAVGIPSSAR
2. 61. TPVPVRSLSPAKFQLERPAQGSCLAEQVQPYSTGAPAHSNPRAWPRRPTISHVHAISDE
3. 121. DCCVQLGNQRLQSEGERGAYGVRLYNNERRDRHYLMVNLSSKEKLLQXYGFPFRPPFGROQ
4. 241. VRLQGFPQKQLVPEVQKIEAIILKLYHNYYVKEVLKIELNYVHIDERYLULFILRQGPMVE
5. 241. 241. VPCDKPQFPEEQAQLRILDVLFDIDNRLKSLNLPRQRTVDLNLTDVYTRAQLYLRIDILQLVQKL
6. 581. LGDGGHVKIADFGVSNQGSEDADGQLSGTATGPFAPMAREDIDSTQGSSQFKALDVWAGVTLFCFYVQGS
7. 1081. CFPIIDEYIALHRKINEAVGFEEPEEVESEELKDLILKMDNPETRIVGSDIKLHPWTKHEEPLPSE
8. 1281. EHECSVSVVTVEEKNVSNKLPSWTVTIVKLMSRKFSQFNPFQPQAREERSMSAPGNLLKECGEGG
9. 1561. KSPFQGVDWVEDAS

Notes

Rat CaMKII

References to 14-3-3 binding to CaMKII

Davare MA, Sanyothi T, Guire ES, Nygaard SC, Soderling TR. Inhibition of calcium/calmodulin-dependent protein kinase subunit alpha 4-3-3-3 binding to CaMKII14. J Biol Chem. 2004 Dec 10;279(50):52191-9.

Rat Crhbr4

Nicotinic acetylcholine receptor α 4 subunit (AChRα4) (Swissprot = P09483)

References to 14-3-3 binding to CaMKII

MANSHTQAFPPPLLLLLLLLLLOGLGLPASHHETRRAAEERLRLRLGSYWNKRSVPVANISDVVLFVRLGST
1. 61. SDVVLVRFLGTAIALDVIDKEWMTMVHMRQKVHDKYENVYTISRIPSEL1
2. 121. WRPOLYVLYNADDGFPATLTHARKHLYDRGWQTPPTAIYKSSCSDSTFTFDQQNCMTM
3. 181. FSNGTWYDKACTLDMNSHRQDLDFWESGEGDVEQAOGTYNTRRKEECARIIYDPIOTAFA1
4. 241. 241. IRRLVLLTVTCLLDPVYFLYSGEVKETVLCISVULLTVFLLLITIIIPSPLT1
5. 301. PTSLVPIPLGEYLPTNFIVTSLSIFTVFVNVHHRSPRTTHMAWVRPPFLIDVPRLLF
6. 361. MKRSVVKDNRCRLLISMKEMANPRAFWEYPVPGEPLISDINCQGSLQAPTFCNPTDTAV
7. 421. ETQPTCRRSPFLEVPOLKSTEPVEASSCPSPCSSCPKPASSGAPMLIKARLKVQHVPSSQ
8. 481. EAAEDGICRSKSIQCVCSQOAGALASDASKPTSSSLPLARKQPFLOPQVSDAQSPCKTCCKE
9. 541. DSVPSVPVTVIGAGTQPKAPQHLPSSALTIEVQGQAYKIALREKTZDOEVEKWYRAM
10. 601. 601. VIIDFRLMWIFMIIVGLVTTLGFLPWLAC

Notes

Rat Crhbr4

References to 14-3-3 binding to nicotinic acetylcholine receptor α 4 subunit

Jeanlos EM, Lin L, Treuil MW, DeCoster MA, Anand R. The chaperone protein 14-3-3eta interacts with Huntingtin-associated protein 1 (HAP1a) and Huntingtin-associated protein 1 isoform 1A only. J Biol Chem. 2001 Jul 27;276(28):28281-9.

Rat Huntingtin-associated protein 1 (isoform 1A only)

References to 14-3-3 binding to HAP1A

Rong J, Li S, Sheng G, Wu M, Coblitz B, Li M, Fu H, Li XJ. (2007) 14-3-3 protein interacts with Huntingtin-associated protein 1 and regulates its trafficking. J Biol Chem. 2008, 284, 4748-4756.

Rat Myl2

Rat myosin light chain kinase 2 (MLCK) (Swissprot = P20689)

References to 14-3-3 binding to MLCK

MATENGAVEL GTSSLSTDHP PDTAAAGDSPASEKPSPLDPEKGDLPNTKPKDPGDPPK
1. 61. KNOPPSLKEKTEAPGPSEQSGPAASSNSQSPGSEGODQPGAPEERPGGPGAVLPQQTAT
2. 121. ADASIQKDLAQAPGSGQESGAAKGGKRAEECAREGRGSPAFFHSPECPIAIICSXKELT
3. 181. AMKLSETTEELIFAVSETQBOPQFPADIEGGTNLADKEKAAQACQARQVQDSTQ
4. 241. 241. RZhQPEVEASQVNLCKLTETEKCQPLCDOQPPAPQPFHVPVQPTQNVONQVPS
5. 301. SKEALQGGKFGAVTCTTERTSGLKALKVIQKCKPMKEMVLLEHVMNQLNHNLQGLY
6. 361. SAEITSEHIIPLMEYIIEGELERIIVDQRQCLQCGDPIDMFVVRQCDGDLMPHMVRVLH
7. 421. LKPEINLCVNTTGHLLKRITGDGLARYNPNKEKLYRNFGPETLEPSVENYQDSQIKDRTDMW
8. 481. SLGQVTYMLGSLPFLLGGDTELTNLYLWAHWDFUDEEFNAVSEDENDSAVSNLTKQDS
9. 541. ARMARQCLAARCKNRKDSQILKLVVYMRLKPFNAYSSAARKKQGKQI
10. 601. 601. SSQALMQGV

Notes

Rat Myl2

References to 14-3-3 binding to Myosin light chain kinase 2 (Myl2) (Swissprot = P20689)

© 2010 The Author(s)

The author(s) has paid for this article to be freely available for re-use under the terms of the Creative Commons Attribution Non-Commercial Licence (http://creativecommons.org/licenses/by-nc/2.5/) which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.
skeletal/cardiac muscle; Short=MLCK2
MATENGAVLGTLQSLDSHTDPPGATDAQDSGASEPKESSLPTDEKDLGTPNKTDDKGAPDPKKNPFDPSLKLK
TPEADPGEPKGGGASASNPAGNKEQGGGEGGGPPGPAEGTPPQVPTATADASQKLDDATQPSSQGNES
GEAKAGKRAAEEREGRAPSFLALHPSSPACA155CERKLRFLESEITELFAGVEGPSETPFQDFQAPPADK
EGTCCGSPRRPFRQAAGQVFQDQGQGTSGFQRPAPNRRAGQVCLATKEDECFQGDAPPF
FFHRIVELVIGNVSEFMSKKGKEGKFVAGVCTEETSGILKAAKVIIKQTPGKEMVVLILIEVNNQ
LNHRNQLIQYASTIESHEI111MIEYGELFER111IDVDELQVTEDMTFMVRQI1GFILHMHRVVLHLD
LKENIIVCMTVNLHVDEVILARNYPFEKLNQFPEFLEPSFEPVNYQISQKTDMSVLGSYTVLILL
SGLSFLPLGDDETLMLNVLSANYFDETEFVEASDEADKDEVSNLITKDQSMARSMAEQLAHLFWNLNALEE
AKRCKRMRKLQILYKMRKWKNNFIIYVAASANFPRKSSGSGAIALM

Notes
FLHSP(pS16)CPA in rabbit MLCK phosphorylated by MAPKAP-K2 binds to a 14-3-3 (≈ Ser168 in rat MLCK P206)

References to 14-3-3 binding to MLCK
Haydon CE, Watt PW, Morrice N, Knebel A, Gaestel M, Cohen P. Identification of a phosphorylation site on skeletal muscle myosin light chain kinase that becomes phosphorylated during muscle contraction. Arch Biochem Biophys. 2002 Jan 15;397(2):224-31.

Rat Numb1(Nur77) Nuclear receptor subfamily 4 group A member 1 (Swissprot = P22829)
1 MPCIQAOYQT PATSQSPGRDH LTQGDLAFLK SPLDTMLASP ETAPATAPLTF
61 YTGKFNTFL1 QLPGATACPS ASASTSSSSSA SATPSASAFIPKFEDQVYYG PGTL20GPLD
121 ETLSSGRSD GYSPCPSAPSP PTNPNQPSQ SLWDSGSGNP SQPQETYGLR WTEWQLPKAS
181 GPPPPPTFTSF PSIIITPSQPS LQSSLKLFAP AFATQHLGQK ESYVSPAF GLAPTEDNPC
241 TSIGLDAPVT STKARSGSS GSEGRCAVGC DNASCQHYG RTCECGKFFK RTVQKSYAK
301 ICLANKCDVF DRRRRRRRNCF CFRCQLCAVK MVKVEVRTDS LKGRGRLFP KFKQPDICAP
361 TNLTLLSLIRA HDSSGNTMKT LDIKSQFQEL LRPPFKEAD AVQQFEDLLS GSLOVIRKWA
421 ESKIFSPTPS PQGDQDSLLESAFELFILLR LAYRSPGKEGLK LCSGGLVLHR LQCAFGFDMDINLAFS
481 WIDNILAPSR SLSLGVDVP AFACLSALVL ITRDKHQLOP VRVEELQNS ASLCKEHMA
541 VAGDQPACSR LSRLLGKLE LRTLCTQGLI RIFCGLKED LPPPIVDFK MDTLFLS

Notes
VRTDSLKGRRGRLP(s350)KPKQ (conserved in human and mouse sequences)

References to 14-3-3 binding to Numb
Wingate AD, Campbell DG, Peggie M, Arthur JS. Nur77 is phosphorylated in cells by RSK in response to

Full=NUR77
Full=Nerve growth factor group A member 1; AltName: Full=

Rat Nr4a1(Nur77) Nuclear receptor subfamily 4 group A member 1; AltName: Full=

Nuclear receptor subfamily 4 group A member 1 (Swissprot = P22829)
1 MPCIQAOYQT PATSQSPGRDH LTQGDLAFLK SPLDTMLASP ETAPATAPLTF
61 YTGKFNTFL1 QLPGATACPS ASASTSSSSSA SATPSASAFIPKFEDQVYYG PGTL20GPLD
121 ETLSSGRSD GYSPCPSAPSP PTNPNQPSQ SLWDSGSGNP SQPQETYGLR WTEWQLPKAS
181 GPPPPPTFTSF PSIIITPSQPS LQSSLKLFAP AFATQHLGQK ESYVSPAF GLAPTEDNPC
241 TSIGLDAPVT STKARSGSS GSEGRCAVGC DNASCQHYG RTCECGKFFK RTVQKSYAK
301 ICLANKCDVF DRRRRRRRNCF CFRCQLCAVK MVKVEVRTDS LKGRGRLFP KFKQPDICAP
361 TNLTLLSLIRA HDSSGNTMKT LDIKSQFQEL LRPPFKEAD AVQQFEDLLS GSLOVIRKWA
421 ESKIFSPTPS PQGDQDSLLESAFELFILLR LAYRSPGKEGLK LCSGGLVLHR LQCAFGFDMDINLAFS
481 WIDNILAPSR SLSLGVDVP AFACLSALVL ITRDKHQLOP VRVEELQNS ASLCKEHMA
541 VAGDQPACSR LSRLLGKLE LRTLCTQGLI RIFCGLKED LPPPIVDFK MDTLFLS

Notes
VRTDSLKGRRGRLP(s350)KPKQ (conserved in human and mouse sequences)

References to 14-3-3 binding to Numb
Wingate AD, Campbell DG, Peggie M, Arthur JS. Nur77 is phosphorylated in cells by RSK in response to

Full=NUR77
Full=Nerve growth factor group A member 1; AltName: Full=

Rat Nr4a1(Nur77) Nuclear receptor subfamily 4 group A member 1; AltName: Full=

Nuclear receptor subfamily 4 group A member 1 (Swissprot = P22829)
1 MPCIQAOYQT PATSQSPGRDH LTQGDLAFLK SPLDTMLASP ETAPATAPLTF
61 YTGKFNTFL1 QLPGATACPS ASASTSSSSSA SATPSASAFIPKFEDQVYYG PGTL20GPLD
121 ETLSSGRSD GYSPCPSAPSP PTNPNQPSQ SLWDSGSGNP SQPQETYGLR WTEWQLPKAS
181 GPPPPPTFTSF PSIIITPSQPS LQSSLKLFAP AFATQHLGQK ESYVSPAF GLAPTEDNPC
241 TSIGLDAPVT STKARSGSS GSEGRCAVGC DNASCQHYG RTCECGKFFK RTVQKSYAK
301 ICLANKCDVF DRRRRRRRNCF CFRCQLCAVK MVKVEVRTDS LKGRGRLFP KFKQPDICAP
361 TNLTLLSLIRA HDSSGNTMKT LDIKSQFQEL LRPPFKEAD AVQQFEDLLS GSLOVIRKWA
421 ESKIFSPTPS PQGDQDSLLESAFELFILLR LAYRSPGKEGLK LCSGGLVLHR LQCAFGFDMDINLAFS
481 WIDNILAPSR SLSLGVDVP AFACLSALVL ITRDKHQLOP VRVEELQNS ASLCKEHMA
541 VAGDQPACSR LSRLLGKLE LRTLCTQGLI RIFCGLKED LPPPIVDFK MDTLFLS

Notes
VRTDSLKGRRGRLP(s350)KPKQ (conserved in human and mouse sequences)

References to 14-3-3 binding to Numb
Wingate AD, Campbell DG, Peggie M, Arthur JS. Nur77 is phosphorylated in cells by RSK in response to

Full=NUR77
Full=Nerve growth factor group A member 1; AltName: Full=

Rat Nr4a1(Nur77) Nuclear receptor subfamily 4 group A member 1; AltName: Full=

Nuclear receptor subfamily 4 group A member 1 (Swissprot = P22829)
1 MPCIQAOYQT PATSQSPGRDH LTQGDLAFLK SPLDTMLASP ETAPATAPLTF
61 YTGKFNTFL1 QLPGATACPS ASASTSSSSSA SATPSASAFIPKFEDQVYYG PGTL20GPLD
121 ETLSSGRSD GYSPCPSAPSP PTNPNQPSQ SLWDSGSGNP SQPQETYGLR WTEWQLPKAS
181 GPPPPPTFTSF PSIIITPSQPS LQSSLKLFAP AFATQHLGQK ESYVSPAF GLAPTEDNPC
241 TSIGLDAPVT STKARSGSS GSEGRCAVGC DNASCQHYG RTCECGKFFK RTVQKSYAK
301 ICLANKCDVF DRRRRRRRNCF CFRCQLCAVK MVKVEVRTDS LKGRGRLFP KFKQPDICAP
361 TNLTLLSLIRA HDSSGNTMKT LDIKSQFQEL LRPPFKEAD AVQQFEDLLS GSLOVIRKWA
421 ESKIFSPTPS PQGDQDSLLESAFELFILLR LAYRSPGKEGLK LCSGGLVLHR LQCAFGFDMDINLAFS
481 WIDNILAPSR SLSLGVDVP AFACLSALVL ITRDKHQLOP VRVEELQNS ASLCKEHMA
541 VAGDQPACSR LSRLLGKLE LRTLCTQGLI RIFCGLKED LPPPIVDFK MDTLFLS

Notes
VRTDSLKGRRGRLP(s350)KPKQ (conserved in human and mouse sequences)
Rat TESK1 human testicular protein kinase 1 (a TKL kinase of the LISK family). Phosphorylated and activated by Erk1 and also by two other CaM-Ks (CaM-II and CaM-KIV). Recruitment of 14-3-3 proteins was maximal under basal conditions and decreased significantly upon mitogen stimulation. 14-3-3beta binding negatively regulates RSK activity to maintain signal specificity and that association/dissociation of the 14-3-3beta-RSK1 complex is likely to be important for mitogen-mediated RSK1 activation.

References to 14-3-3 binding to RPS6KA1

Cavet ME, Lehous S, Berk BC. 14-3-3beta is a p90 ribosomal S6 kinase (RSK) isoform 1-binding protein that negatively regulates RSK activity. J Biol Chem. 2003 Aug 29;278(35):31876-83.
Notes
TESS1.a TKL kinase of the LIS family. Its testicular germ cell-specific expression and developmental pattern of expression in the mouse suggests that this kinase plays an important role at and after the meiotic phase of spermatogenesis. 14-3-3-beta interacts with TESS1 through the C-terminal region of TESS1 and in a manner dependent on the phosphorylation of Ser439 within an RXXXP motif. Binding of 14-3-3-beta inhibited the kinase activity of TESS1.

References to 14-3-3 binding to TESS1
Toshima JY, Toshima J, Watanabe T, Mizuno K. Binding of 14-3-3-beta regulates the kinase activity and subcellular localization of testicular protein kinase 1. J Biol Chem. 2001 Nov 16;276(46):43471-8

B. Non-mammalian animal proteins reported to interact directly with 14-3-3

Acynonyx jubatus DAF-16 (Dog hookworm DAF-16; a forkhead transcription factor) (Swissprot = P39875)

B. Non-mammalian animal proteins reported to interact directly with 14-3-3

Caenorhabditis elegans DAF-16 (Dauer formation protein 16) Forkhead box protein O (AAC47803.1 GI:2623943)

References to 14-3-3 binding to dog hookworm DAF16
Kiss JE, Gao X, Krepp JM, Hawdon JM. Interaction of hookworm 14-3-3beta with dog hookworm DAF16 [Caenorhabditis elegans DAF - (Dog hookworm DAF16; a forkhead transcription factor) (Swissprot = gi|2623943|gb|AAC47803.1| DAF-16/FoxO3) - 16 when co-expressed in HEK 293T cells, and was recognized by an antibody against human 14-3-3-beta isoform. Reciprocal co-immunoprecipitation using anti-epitope tag antibodies indicated that Ac-DAF-16 (14-3-3) interacts with Ac-DAF-16 when co-expressed in serum-stimulated HEK 293T cells. This interaction requires intact Akt phosphorylation sites. Parasit Vectors. 2009 Apr 24;2(1):21.

References to 14-3-3 binding to dog hookworm DAF16
Kiss JE, Gao X, Krepp JM, Hawdon JM. Interaction of hookworm 14-3-3 with the forkhead transcription factor DAF-16 requires intact Akt phosphorylation sites. Parasit Vectors. 2009 Apr 24;2(1):21.

References to 14-3-3 binding to dog hookworm DAF16
Kiss JE, Gao X, Krepp JM, Hawdon JM. Interaction of hookworm 14-3-3 with the forkhead transcription factor DAF-16 requires intact Akt phosphorylation sites. Parasit Vectors. 2009 Apr 24;2(1):21.

References to 14-3-3 binding to dog hookworm DAF16
Kiss JE, Gao X, Krepp JM, Hawdon JM. Interaction of hookworm 14-3-3 with the forkhead transcription factor DAF-16 requires intact Akt phosphorylation sites. Parasit Vectors. 2009 Apr 24;2(1):21.

References to 14-3-3 binding to dog hookworm DAF16
Kiss JE, Gao X, Krepp JM, Hawdon JM. Interaction of hookworm 14-3-3 with the forkhead transcription factor DAF-16 requires intact Akt phosphorylation sites. Parasit Vectors. 2009 Apr 24;2(1):21.
Potential 14-3-3 binding to human ARCK is acts as a suppressor of Dictyostelium development. Dev Biol. 2003 Nov 15;263(2):308–667.

References to 14-3-3 binding to human ARCK-1

Aubry L, Lee S, Ravelan K, Firtel RA. The novel ankyrin-repeat containing kinase ARCK-1 acts as an effector of the Spalten signaling pathway during Dictyostelium development. Dev Biol. 2003 Nov;263(2):308–667.
References to 14-3-3 binding to Drosophila FOXO

Nielson MD, Luo X, Biteau B, Syverson K, Jasper H. 14-3-3 Epsilon antagonizes FoxO to control growth, apoptosis and drosophila aging. Cell. 2008 Oct;135(3):686-99.

Drosophila Yki (Yorkie)
Drosophila transcriptional activator related to Yap (Swissprot = Q9IB67)
1  MLGMQGQHRH KALQRRLVSL ASEMIIEELL DHLVSSEILTNMMHINMAY RDASYQNVNL
61  LNLILPRGRPF APSACNLMAH STNQELLAQG VEKEALQERQ FITKSVKHGG FLPPQVQESTL
121  SRFQGRQCRE YREXFT DQGD GTVPVVLQCSY NITYTQACQA YRMSCHPRGR ALLJL
181  TPDLDYRCGG EVDLASLLEKL FSSLGQYQVDC RNCLNASSMQ SLSQAFASLP VSALSCDCV
241  ASLHSLGDLA VYGTDGKLQV LEQVFATDLN AHCPLQONKPK KMMFITCQARC ETERGQVRD
301  DGRQGSGSFQ CEQSAGRED 1KVR1LPTQDS MICAAYACLG TVSLNTRKG SWFQVQDLVS
361  FSHQSHDTHV ADMLVKVNLN IKEREHGAPF TETFHCRKEMS YVSTCLRLDL YLLFPGSPS
421  LPK

Notes
Yorkie phosphorylation at Ser168, which is critical for 14-3-3 binding. Two other sites are also phosphorylated (SHSRANsA(DST) and VHKKQRsY(DVI) (Badouel et al. 2009). Ser145 in Q0E8X1 is equivalent to the reported phosphorylated Ser168 14-3-3-binding site.

References to 14-3-3 binding to Yorkie
Badouel C, Gardano L, Amin N, Garg A, Rosenfeld R, Le Bihan T, McNeil H. The FERM-domain protein Expanded regulates Hippo pathway activity via direct interactions with the transcriptional activator Yorkie. Dev Cell. 2009 Mar;16(3):411-20.

Ren F, Zhang L, Jiang J. Hippo signaling regulates Yorkie nuclear localization and activity through 14-3-3-binding. Dev Biol. 2009 Nov 6. [Epub ahead of print]

Xenopus casp2
Caspase-2 from Xenopus laevis (Swissprot = Q9IB67)
1  MLGMQGQHRH KALQRRLVSL ASEMIIEELL DHLVSSEILTNMMHINMAY RDASYQNVNL
61  LNLILPRGRPF APSACNLMAH STNQELLAQG VEKEALQERQ FITKSVKHGG FLPPQVQESTL
121  SRFQGRQCRE YREXFT DQGD GTVPVVLQCSY NITYTQACQA YRMSCHPRGR ALLJL
181  TPDLDYRCGG EVDLASLLEKL FSSLGQYQVDC RNCLNASSMQ SLSQAFASLP VSALSCDCV
241  ASLHSLGDLA VYGTDGKLQV LEQVFATDLN AHCPLQONKPK KMMFITCQARC ETERGQVRD
301  DGRQGSGSFQ CEQSAGRED 1KVR1LPTQDS MICAAYACLG TVSLNTRKG SWFQVQDLVS
361  FSHQSHDTHV ADMLVKVNLN IKEREHGAPF TETFHCRKEMS YVSTCLRLDL YLLFPGSPS
421  LPK

Notes
Ser135 to Ala mutation prevents 14-3-3 binding.

References to 14-3-3 binding to Caspase-2
Nutt LK, Buchakjian MR, Gan E, Darbandi R, Yoon SY, Wu JQ, Miyamoto YJ, Gibbon JA, Andersen JL, Freel CD, Tang W, He C, Kurokawa M, Wang Y, Margolis SS, Fissore RA, Kornbluth S.

Xenopus wee1
Xenopus Wee1 (Swissprot = P47817 for Xenopus laevis Wee1)
1  MRTAMSCCGG LVQRPFLSSS DEEELDNSG1 NEPQGKGSPV SWRTWNNCF PIPFPQRNE
61  L5PQTLPSLS SDYSPDSVSG AECGPTPLHY STWRKLKCL TDPTTPKSLTY KTLPSGPGVR
121  HCQCRQLLRF VAGTAELDDL FSLVINIPFT PESYRTQHPP MNQKRERKE DDCTRQDRKM
181  YAEKHPAENV QSRRFVLREAT MNGMRRKETF LEIERKGAGR FGSFVCKVRD LDCGFAYAIR
241  SRFQGRQCRE YREXFT DQGD GTVPVVLQCSY NITYTQACQA YRMSCHPRGR ALLJL
301  DNNKEQGCQVL EQELQKILLO SMLQKLYKH SGLVMHIDKP SNIFICQKRT ELQQESDGE
361  D3LSQGSVLY KIGDGLHVTS 1INPQVQEDR SRFLALEIQ EDYSQFPLKD IFALGLTLAL
421  AAGAAPPLEPCN EDSWHHHRK NLPHQFQLL PVLFALLKLL VHDPVMPRSS AALASKNSVL
481  RVCQGYKAAQL QRQLNVEKF PK TLAMERELKA AKLAQTSGKD ECSDLPPFGS FSCRGKRKLV
541  GAKWTRSLF TCQGY

Notes
Ser135 to Ala mutation prevents 14-3-3 binding.

References to 14-3-3 binding to Wee1
Nutt LK, Buchakjian MR, Gan E, Darbandi R, Yoon SY, Wu JQ, Miyamoto YJ, Gibbon JA, Andersen JL, Frebel CD, Tang W, He C, Kurokawa M, Wang Y, Margolis SS, Fissore RA, Kornbluth S.

Fungal proteins reported to interact directly with 14-3-3

Saccharomyces cerevisiae Acm1 (APC/C-CDH1 modulator 1) (yeast) Anaphase-promoting complex (APC) inhibitor (YPL267W)
Sacharomyces cerevisiae Fin1 Filament protein FIN1 (Filaments in between nuclei protein 1) (Swissprot = Q03898)

1 MNKSHNRSL RDIIGNTRN NIPSDKDNVF VRLSMLSPRT TSQKEFLKPP MRISPNTKDG
121 KIBH6QTVRL RMSPECMCC LGVSKEQOGL RPQFNKRNSN VKIYQDSHIT NIIFFPTSTKR
181 LTFSNENKIG DGDDLTRIA RPFGNLMSPE RTOQQQQQHI LPSDAKSNND LCSNTELKD
181 PFENDLRPR LAKNLKVLPE KEEEDDONG IESLTSKNTY SGNLASHNLH IAKQSAQKSV
241 KFPKLNIVT ETELAEKIK DQILQRAQ RRRISLPLNL ELSQTFPLPQ

>gi|41017084|sp|Q03898.1|FIN1 YEAST RecName: Full=Filament protein FIN1; AltName=Filaments in between nuclei protein 1
MNKSNRSLRDIIGNTRNIPSDKDNVFVRLSMLSPRTTSQKEFLKPPMRISPNTKDG
RMSPECMLCGLVSKQETQDLPQFRQKSNKNVQKIYQDSHITNIIFFPTSTKR

Notes
"Our results suggest that both sequences around residue 58 and the C-terminal part of Fin1p are required for association with Bmh2p (van Hemert et al. 2003)." 14-3-3-binding site(s) not defined precisely

References to 14-3-3 binding to Saccharomyces cerevisiae FIN1
van Hemert MJ, Deelder AM, Molenaar C, Steensma HY, van Heusden GP. Self-association of the spindle pole body-related intermediate filament protein Fin1p and its phosphorylation-dependent interaction with 14-3-3 proteins in yeast. J Biol Chem. 2003 Apr 25;278(17):15049-55.

Mayordomo I, Sanz P. The Saccharomyces cerevisiae 14-3-3 protein Bmh2p is required for regulation of the phosphorylation status of Fin1, a novel intermediate filament protein. Biochem J. 2002 Jul 15;365(Pt 1):51-6.

Sacharomyces cerevisiae Msn2 Zinc finger protein MSN2 (Multicopy suppressor of SNF1 protein 2) (Swissprot = P33748)

1 MTVDHPFNSE DILPFIESSS SIQYVENNFP NNINNDIVP Y SDLIKNTVLD SADLNDQIN
61 ETSNLGLPFL LFSDPSLPVTT ETIPSTDNSM LHLKADSNKN RDAERTNIEO EIKSTNNHAS
121 SANGYVTLH SPYPPMDLY WNNMFPQEPS PSSVPQNPFT NSIPNTSAGN TNLPSVTSGN
181 NETLISPRQA QHTSKNDNL RLPANGANL FDPINNPNNL EKLRMQNLNS TGSYNSNSN
241 SANSNSGNL SNNFSLNLD SMLDDVYSS LILNNDDDDL NLSRFRFSDV ITQFQPSMTN
301 SRMSHSLED LWHHPKINPS NNHRTNLLT NTTSTNSSAP NTTTMMNAD SNIAGKNPKN
361 DATDIELTQL ILEYNYNNFP NDLTGTSTGK NKGAPPSFAD ANMTKIFPS QLQQQLNNVR
421 SAPFSSSNL NDSSGFQRQ ATEELQEDG DVLPPDDELS YNLKQFQED PHNMLPSN
481 LSSQQFQIPK SMILSDNASV IAKVATGGTS NDNPFLTEEG EQNASNTSPF DLTISQNMMA
541 PLSFASSSST SLATNYHVR FPPQGHXTMN SKIGSSLLRR KSAPVLMTG PTQLNNQNS
601 SSVSPNSTG ONAVKRPERS YRRKSMTPSR GSSVIEERLK ELEKFPFCH ICPSKPSKRE
661 HLKRHVRVSH SNERPFACH CDDKFRSRDA LNQIKTHK HGDI

>gi|4626252|sp|P33748.1|MSN2 YEAST RecName: Full=Zinc finger protein MSN2; AltName=Full=Multicopy suppressor of SNF1 protein 2
MTVDHPFNSE DILPFIESSS SIQYVENNFP NNINNDIVP Y SDLIKNTVLD SADLNDQIN
61 ETSNLGLPFL LFSDPSLPVTT ETIPSTDNSM LHLKADSNKN RDAERTNIEO EIKSTNNHAS

Notes
TOR inhibits expression of carbon-source-regulated genes by stimulating the binding of the transcriptional activators MSN2 and MSN4 to the cytoplasmic 14-3-3 protein BMH2. 14-3-3-binding site(s) not defined.

References to 14-3-3 binding to Saccharomyces cerevisiae Msn2 and Msn4
Beck T, Hall MN. The TOR signalling pathway controls nuclear localization of nutrient-regulated transcription factors. Nature. 1999 Dec 9;402(6762):689-92.
Bruckmann A, Steensma HY, Teixeira De Mattos MJ, Van Heusden GP. Regulation of transcription by Saccharomyces cerevisiae 14-3-3 proteins. Biochem J. 2004 Sep 15;382( Pt 3):867-75
Santhanam A, Hartley A, Döbel K, Broach JR, Garrett S. P2A phosphatase activity is required for Stress and Tor kinase regulation of yeast stress response factor Msn2p. Eukaryot Cell. 2004 Oct;3(5):1261-71.

Sacharomyces cerevisiae Ptk1 Yeast phosphatidylinositol 4-kinase

1 MRASSRKR FFDDDELLKK EQLKLLKNS EFLTNHCWEL LKCHSENIGI HYLQCLKLAT
61 FPHOELQFY PQLVQLVLT MTESEAELDD LLRLRAENFH FALSFLWQQL ALTTLDSTPD
121 ASLYQSVAP NVSNQPEQNPQ TNSSQGNM KHERNAFAL VLSMHNQGAF APLQFQEVYT
181 PLVQEGGQR QAFVFKPYML AMKRTMFMK QLMKNTLLINK SRKSKRVSNN SSTRTIPIDL
241 IDPITKEDAA SSRFRKSEVQ KLLDKFIDDI GQNVQVEEIS SSIKLPRKPKF KYLDSQYHR
301 TYYDGKINNID GSISNTTAKAL DGGNQDIYSP KHGNEDINNI GHNEDETGRR TEDAADGIS
361 FLATPTHSMQD UNQTPSSA SBSALPTKPH YNQDPLQLS PQQAKSSSSSA NLSQSSLQDL
421 SQGSLTSSK TFMLKNRYFCES TQFAIAFELMT SQLARQVTKE ALPLSMALF PLNDFLFAP
481 VDIPILLPPN KQKKGKLHVL ITAEEQAVNL SAEQVPPPLL IEYRELDFDF DFPSETNERL
541 LKKSQNONQV LIFLDNMNKR KENNERNRES KTSLTNNTSS VYGQSFNSNN ASRNEGOLST
601 SRSOGASTAH VRTENVKEDD LMDNMVWV NRTDDEAYRN ALDQVSAANV PFLPDSQDR
661 SPELNPQSNL DELVLEINGN SKNHIQGQDQA LAMQVRSAV MLAQKSFLPQ QLSETESQKIR
721 AQIPSMTKVE QAQFKYGDHE ALHGMEGRRK LEDLMTGSL OTYGDLWAVA TKEKERRKTS
781 EYEFQENWDL CSVIAKGLED LQIEAQAYOM IQAMANINWV EKDVQVWKRM KIIFLTSSNTG
841 LVETITNNMNS VHSAILLKTKT MIEAALDLGD KGIAISLNDH PFLRQFPNGF FYKRQAONDF
901 ASSLAAYSVI CILLYQQEKRH NHNNIDMNEG HVSHEWQGFM LNSPSGVGP FPAAEFLTYE
961 YIEFQCGVQG EAPKFGVFELT KSSPKALYQ ADQIVSMSQE WQDONMNQFC DAEQTVSFLQ
1021 QRQFQDLLEE KEVDVQENF LGKSLGSII TQITYDVQQF TLGIYIS

Notes

390-LNRNTINpðQÞP–399

References to 14-3-3 binding to Ptk1

Demml E, Beck M, Köse C, Schlatt AL, Gloor Y, Hau P, Havliš J, Shevchenko A, Krause E, Kalsidizd E, Walch E, Solimena C, Nucleocytoplasmic shuttling of the Golgi phosphatidylinositol 4-kinase Ptk1 is regulated by 14-3-3 proteins and coordinates Golgi function with cell growth. Mol Biol Cell. 2008 Mar;19(3):1046-61.

Sacharomyces cerevisiae Rtg3 Retrograde regulation protein 3 (SwissProt = P38165)

1 MNNSNIFSEAE NQRDLLDELMN QTKVQITEQDL TSLVSTTIPHH DDDYDRIRGSA YPGAEPFAQQO
61 HEKLYSINETH NSDKUNNNMG SQARNSQSTQ TASTIYEEAE QSYYLDMPRT TRSQSGQRTVP
121 QNSISQGGQ PLSSSSQMYM DSFPDRVMAI PIQEQGQIA ELEPHQFDHQ QTGDONYNLT
181 DLDSLSSS INSMTDNPMT YSSFSYNQPO SLGASPQSTV YSPKRSVPSF SSRAFGFSLS
241 SFPSGINTPO RTPHTSISNN MTEFNGGSPV PKILGLTSKD ELKREKRFNE NAVRRREVL
301 IQRKQKEQROI LVSFFNYRNAI DLOQKGPKNFQ ILGDRTVLR LQYLAELIE QARKHALL
361 KIKELEKKS SVAAGSLFPN NHAASISQNN SENSEERID IRQOGVALM EQLQKAEIN
421 WEFPMLDVPVS NHNAAGHMES HPTNWHQLE KEFLSQLOLE AEEDAKLMGF DENSFPNADYFL
481 LEFSGQ

>gi|1710804|sp|P38165.2|Rtg3_YEAST RecName: Full=Retrograde regulation protein 3 M NNNSNIFSEAE NQRDLLDELMN QTKVQITEQDL TSLVSTTIPHH DDDYDRIRGSA YPGAEPFAQQO

References to 14-3-3 binding to Rtg3

van Heusden GP, Steensma HY. Regulation of transcription by Ptk1 is regulated by 14-3-3 proteins and coordinates Golgi function with cell growth. Mol Biol Cell. 2008 Mar;19(3):1046-61.

Notes

bZIP/HLH transcription factor.

Schizasacharomyces pombe Cdc25 (Genbank: CA9A90849.1)

1 MDSPLSSLLF TNTLGSKRNV LRPAAERLKL MSDNNAQREL DFFPSKXKH ASLTVLDPFGK
61 HDQDRTTNYI NQSNAGEMTN QYQKTRTNEQP YQPKYQTSQG QLSETESQKIR
121 NDALTSEQY RRQPSKQYIS QTQPSRYSIT AIYPSKFRASI ALNHTKSEAT RSLSSSSTFD
181 SYRPVNRVS RSSNPAPFP RLSSPSYISY NKKQRTGSSQ ALTQHTYLAQ RTQCSSNTT
241 SLLSETLDDD TFDPEMQVSE DFTKGTVMA DLFSEQVVE EDAASIQFRP SDFGACNDSN
301 LDLQLEQAPI KPIDMLPKIN KDAIFPLSKVQ RSPSSMAFAM QDAREYDQOE TVLNFRTQOSC
361 FPLNSTRQD KQDLVVCVTQP QSTREKSRF ISSHVLDSLL PCFAVKEQDL KRRQTLNLG
421 LLCREDTDF IKCIIIDCFR EYEYDQISP SAVTEAQDQ IVMAPLQKLK THKVALVQHC
481 ESHAHLRAPEL ALHPFRNTDR MNSHRYFEL YPEBFVILPKG YQSVFYKQK RNQCVNYPY
541 NDASHHMVT CMNKTQINRN TMRTMNQYTF QSJWTSLVF NDSTPAMST SLTLRF

>sp|P06052|MIP1_SCHO M-phase inducer phosphatase O5-Schizosaccharomyces pombe Gm=cdc25 HE=1 SV=2

MDSPLSSLLF TNTLGSKRNV LRPAAERLKL MSDNNAQREL DFFPSKXKH ASLTVLDPFGK

© 2010 The Author(s)

The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial Licence (http://creativecommons.org/licenses/by-nc/2.5/) which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.
References to 14-3-3 binding to Cdc25
Sorelli DA, Marchban AM, Chirnes DA, Dickinson JR, Rogers HJ, Francis D, Grierson CS, Halford NG. The Arabidopsis 14-3-3 protein, GF1omenga, binds to the Schizosaccharomyces pombe Cdc25 phosphatase and rescues checkpoint defects in the rad24-3 mutant. Planta. 2003 Nov;218(1):50-7.

Schizosaccharomyces pombe Mei2P (Meiosis protein 2) P08965
1 MIMETESP8 ITSTPSDDDS FQVMEKTRMH ALPSLLDSP LLSTNHEYPK RSTLLSGPS
61 PRNLQSLAP KSSESNBIDY LDUTQWFPN FYNNENYQP STAPFLIDCA CRVEMKVT
121 TGNLWALSQD OPLSQAQNFV NLSEGPQPN GQSYISSEQQ QVAAQTLKRE SGVTRRSSL
161 NNSDDIFID SHASRYLVT FPRLVPYAT LLELSFKLGD VQDSSTSSLG TDGICVIAYFV
211 DIPQAOODAA AKLSRRQFPPN RLLFYQFCQR SSIQKMNQG ATIQFQDLNDQ RNLSLNMQGG
301 SVLSSIQLQDS ILQTPRLGGPP MKPLRQLSQQ VQICEFYDTR TDFASDALDELD GRIHHNCCLO
361 VADYMDAES VSTSSAASSL SVEPQFGMLM NSQGNNNSMG NSQGNTPTA ASCAVURGIE
421 SYGMSNNFPS FVPLGRTE SPM AGWTSGYDV SSGTPVAPS DSNPFSQNSI RYLVGDNFTPA
481 FPNSRLKQR NSDLNLGINP QSSFSQNSTG VQDFSTDGL GMRSSLVG AASCNPNHTL
541 SFAPIVLTDS KADSDTASS NSFNLNQRY TPTVEKHA SNSVDAQIA SGGITRTTVM
601 IRNIPNFKTO QMLROIYDVT NHRGTDFYIL RDFVNPKNV YGAFANIFIEQ SIIIPTGGKAR
661 VGTQWNVFNS EKIDCIYYAN TQQGDKLLIEK FNSCVCMDE PAPYFKIVFS HSGPHRMEDEP
721 FPAPNARK LRSIIAASAQI GLFPTTPASKC

Specialized Methods
Me2p Phosphorylated by Pat1 Kinase Has a Higher Affinity for Rad24p (S. pombe 14-3-3), and the two sites implicated by mutagenesis are RTEpS and RSLpT.

References to 14-3-3 binding to Mei2P
Sato M, Watanabe Y, Akiyoshi Y, Yamamoto M. 14-3-3 protein interferes with the binding of RNA to the phosphorylated form of fission yeast meiotic regulator Mei2p.Curr Biol. 2002 Jan 22;12(2):141-5.

Ustilago maydis cdc25s
Fungal cdc25s
Mielichthek N, Pérez-Martin J. 14-3-3 regulates the G2/M transition in the basidiospore Ustilago maydis. Fungal Genet Biol. 2008;45(8):1206-15.
Pan S, Snehke PC, Ferl RJ, Gurley WB. Specific interactions with TBP and TFIIB in vitro suggest that 14-3-3 proteins may participate in the regulation of transcription when part of a DNA binding complex. Plant Cell. 1999 Aug;11(8):1591-602.

Plant proteins reported to interact directly with 14-3-3

Arabidopsis AKR2 Ankyrin repeat-containing protein 2 (U70425)
MADQREAPKL LSDKPPKSTE ENKSKQPERA SOSSTSSAMP GLNFAPDFG NMSLINDPS
61 IREMAQRIQ DPAFNLQAEO LIQSPINQAO EGSGPNFDPQ QVYNTQOMQV HNEFTEKMA
121 KNLTLQVDQP QMSPFLDAPF NPETAEHF YAVETGQGDP IFVQVPQKDS
181 NDPEVLKIPG EAMGVQVFG EQtQVGEPE VAEBEPSESV WHSALTSGV VGLAKALAS
241 NOGNNEDDE EGGALHPPCQ 1GELBACQVL IDAGAVSNAN DKNNPFTLHY AAA1GRKESV
301 SLLNANGAV QNLQPEKDP TVDAKMLQQL VEVKLKELEL PA

Specialized Methods
Yeast 2-hybrid screen. 14-3-3 binding site not identified.

References to 14-3-3 binding to AKR2
Yan J, Wang J, Zhang H. (2002) An ankyrin repeat-containing protein plays a role in both disease resistance and antioxidation metabolism. Plant J. 29-193-320.

Arabidopsis APX3 (peroxisomal membrane-bound ascorbate peroxidase) (UNIPROT Q42564)
MAAPIVDASY LKEITKARRE LSRLLANKNC APIMLLRWAH DAGTYDAQSK TGPPGNSRIN
121 NHUEHIGAN GLKIDLRGC LVKRAKUPI HADLYQLAQG VAVEVTGGGP IFVQVPQKDS
181 NCVEPKGPLF DAQGFQFHLR DFPVYMLGD KIVALSGHG TLGARPHERS GDFGTQEP
241 LTDOQSYVE LKGESESSL KLPTDVTLIE DPFBRLVL YKCEKDAFDR FYAEKSSKLS
301 ELFQNSTNSS GAQADSTILL AQASFGVAAA AAVVAPGYF EYIRERMK

Specialized Methods
[sp]Q42564:APX3 ARATH L-ascorbate peroxidase 3, peroxisomal OS=Arabidopsis thaliana GN=APX3 PE=1 SV=1 MAAPIVDASY LKEITKARRE LSRLLANKNC APIMLLRWAH DAGTYDAQSK TGPPGNSRIN

© 2010 The Author(s)
The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial Licence (http://creativecommons.org/licenses/by-nc/2.5/) which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.
117 – 122 is a possible motif for 14-3-3 binding but was not tested

In vitro binding of bacterially expressed proteins found no interaction of ATP1 (14-3-3) and APX3 but they admit that the protein may not be phosphorylated in this system

References to 14-3-3 binding to APX3

Zhang H, Wang J, Nickell U, Allen RD, Goodman HM. Cloning and expression of an Arabidopsis gene encoding a FINNAN protease inhibitor. Plant Mol Bio. 1997 Aug;34(6):967-71.

1. MTSGATSTS AAAAAAAAA AAARPKPSWR ERNRRERRRR RAVAAKYTG LRQQGYDLNLP
2. KHCNNEVLK ALCVEAGWE EDDTYTKRG CKPLFEGIA TSRRVTYFPY QNOMSLSLFAP
3. QVLHGDLDFS 361
4. EFKFENSQVK 301
5. IQRGHYTERK 241
6. KPKHMKRVSS 121
7. FEBS J. 2008 Apr;275(8):1767-75
8. Vener AV, Aro EM. Arabidopsis CaS (CaS). FEBS J. 2008;275(8):1767-75
9. Vainone
10. References to 14-3-3 binding to APX3
11. 541
12. 361
13. 301
14. 241
15. 121
16. 85x78
17. 85x105
18. 85x114
19. 85x123
20. 85x141
21. 85x177
22. 85x186
23. 85x195

References to 14-3-3 binding to Arabidopsis CaS

Gampala SS, Kim TW, Ehrhardt D, Chong K, Burlingame AL, Wang ZY. Essential role for 14-3-3 proteins in brassinosteroid signaling in rice. Proc Natl Acad Sci U S A. 2007 Aug 21;104(34):13839-44.

Arabidopsis CaS: Calcium-sensing receptor (AY341888)

1. MAPMAEMATKS SLAKKLTPS SSKTHTLSLR QVSVSLPTST SISLLLSFS PASPEKAASWS
2. IFTQSSVSSL TEVTERINIQ VQETSQSVFDA TQRVFQVOG ALKPALDTAL PIAQAGEAAE
3. MRLKAPASEF ASKRQAEMQQ SQFSGDSEPVFA NAAKTVDVTVA QTSKASEADIA KFIASTMDT
4. ISSAPTSIVY VAAGAAPLAY LILLPVPSAI SPNPQGYKD LGTPAQTLVOL CKTMYLMVI
5. RSEKDEKEAG IPRFLSNARVS NVKPKGIVNR SKVRAEADIA LKS1YLLKIN
6. KGSNIIILDS YTDASAKIVAK TLKVLKYGNC YIVTDGFSGR RGNGLSRGLT DSNFSPFAQV
7. LSPLRRIPAA KRSFRGTG KFLPSDD
8. Sites of 14-3-3 binding not defined.
9. NO WEBLOGO.
10. tr|Q9FN48|Q9FN48_ARATH Emb|Cab75797.1 OS=Arabidopsis thaliana GN=CaS PE=2
11. Sites of 14-3-3 binding not defined.
12. NO WEBLOGO.

Notes

The phosphorylation level of CaS responded strongly to light intensity. The light-dependent thylakoid protein kinase STN8 is required for CaS phosphorylation (assessed by LC-MS/MS of stn8 knockout plants). The phosphorylation site was mapped to the stroma-exposed Thr380, located in a motif for interaction with 14-3-3 proteins and proteins with forkhead-associated domains, which suggests the involvement of CaS in stress responses and signaling pathways. The knockout Arabidopsis lines revealed a significant role for CaS in plant growth and development.

References to 14-3-3 binding to Arabidopsis CaS

Vainonen JP, Sakuragi Y, Stad S, Tikkanen M, Allahverdiyeva Y, Paakkinen V, Aro E, Sorsa M, Scheller HV, Vener AV, Aro EM. Light regulation of CaS, a novel phosphoprotein in the thylakoid membrane of Arabidopsis thaliana. FEBS Lett. 2008 Apr;578(1):107-11.

Arabidopsis CPDKs (calcium-dependent protein kinase) = – NP 19670.1

1. MNGTVCQPSR NGQVSQSSAA WPRGDQGDHMS ARMNGDIAS EAQSSGLRSLD LSEQVKNKFP
2. DQVETKDRERI ETEKPETLE IGLESSEPKET QETKSETKPE SSKDPAPKPK
3. 121
4. KPKHMRKSS AGLRTSSELQ RTENFKEYL SLGRKQLQQQ GFTTCPFCER TTQGKEAKCS
5. IACRKLITDE DEDVRRREIQ MHLLAHQPN VISIGAYED VADVHLMSCC GCELLGFR3
6. QCIRQYTRER AKEIRIYTVG VIEAKSLQV MNIHRLKNE LIVSVSEKEK LKTSQPGSLM
7. 301
8. 361
9. 301
10. 241
11. 121
12. 85x114
13. 85x123
14. 85x141
15. 85x177
16. 85x186
17. 85x195
18. 85x204
19. 85x213
20. 85x222
21. 85x231
22. 85x240
23. 85x249
24. 85x258
25. 85x267
26. 85x276
27. 85x285
28. 85x294
29. 85x303
30. 85x312
31. 85x321
32. 85x331
33. 85x340
34. 85x349
35. 85x358
36. 85x367
37. 85x376
38. 85x385
39. 85x394
40. 85x403
41. 85x413
42. 85x422
43. 85x431
44. 85x440
45. 85x449
46. 85x458
47. 85x467
48. 85x476
49. 85x485
50. 85x494
51. 85x503
52. 85x512
53. 85x522
54. 85x531
55. 85x540
56. 85x549
57. 85x558
58. 85x567
59. 85x576
60. 85x585
61. 85x594
62. 85x603
63. 85x612
64. 85x621
65. 85x630
66. 85x639
67. 85x648
68. 85x657
69. 85x666
70. 85x675
71. 85x684
72. 85x693
73. 85x702
74. 85x711
75. 85x720
76. 85x729
77. 85x738
78. 85x747
79. 85x756
80. 85x765
81. 85x774
82. 85x783
83. 85x792
84. 85x801
85. 85x810
86. 85x819
87. 85x828
88. 85x837
89. 85x846
90. 85x855
91. 85x864
92. 85x873
93. 85x882
94. 85x891
95. 85x900
96. 85x909
97. 85x918
98. 85x927
99. 85x936
100. 85x945
101. 85x954
102. 85x963
103. 85x972
104. 85x981
105. 85x990
106. 85x1000
Notes

A, Thiel G, Moroni A. The potassium channel KAT1 is activated by plant and animal potassium channel KAT1 by dual modes. Plant Biol (Stuttg). 2008 Mar;10(2):231-241.

References to 14-3-3 binding to CDPK

Cannon L, Harper JF, Palmgren MG. 14-3-3 proteins activate a plant calcium-dependent protein kinase (CDPK). FEBS Lett. 1998 Jul 3;430(3):381-4.

Arabidopsis CONSTANS

Note

Arabidopsis KAT1

References to 14-3-3 binding to Arabidopsis CONSTANS

Mayfield JD, Folta KM, Paul AL, Ferl RJ. The 14-3-3 proteins mu and upsilon influence transition to flowering and early phytochrome response. Plant Physiol. 2002 Dec;145(4):1692-702.

Arabidopsis F2KP

References to 14-3-3 binding to F2KP

Kalina A, Villadsen D, Campbell DG, Meek SE, Harthill JE, Nielsen TH, MacKintosh C. Phosphorylation and 14-3-3 binding to Arabidopsis 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (Swissprot = Q9SP17).

Notes

Arabidopsis 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (Swissprot = Q9SP17)

Sites of 14-3-3 binding not defined. NO WEBLOGO.

Arabidopsis KAT1

Notes

References to 14-3-3 binding to Arabidopsis KAT1

Sottocornola B, Gazzarrini S, Oliviari C, Romani G, Valbusza P, Thiel G, Moroni A, 14-3-3 proteins regulate the potassium channel KAT1 by dual modes. Plant Biol (Stuttg). 2008 Mar;10(2):231-6.

Arabidopsis KCO1

Notes

14-3-3 has been implicated in the regulation of two specific K+ channels, AtTPK1 (KCO1), a vacuolar membrane localized K+ channel [45] and KAT1, a PM inward rectifying K+ channel [46].

References to 14-3-3 binding to Arabidopsis KCO1

Sottocornola B, Visconti S, Orsi S, Gazzarrini S, Giacometti S, Oliviari C, Camoni L, Aducci P, Marra M, Abenavoli A, Thiel G, Moroni A. The potassium channel KAT1 is activated by plant and animal 14-3-3 proteins. J Biol Chem. 2006 Nov 24;281(47):37353-41.
Members of the TPK Channel Family.

TPK1, a Ca(2+) rectifying pot channel/ outward rectifier potassium channel [Arabidopsis thaliana]

Latz A, Becker D, Hekman M, Müller T, Beyhl D, Marten I, Eing C, Fischer A, Dunkel M, Bertl A, Rapp UR,

References to 14

Notes

KCO1 is a calcium-sensing potassium channel whose activity is regulated by the vacuolar membrane localized K+ channel/ outward rectifier potassium channel [Arabidopsis thaliana] (Swissprot = Q8LBL1)

AtTPK1 (AtKCO1) is a transmembrane potassium channel [Arabidopsis thaliana] (Swissprot = Q8LBL1)

References to 14

Notes

Co-localization of wild-type TPK1, but not the TPK1-S42A mutant, indicates that phosphorylation of the 14-3-3 motif of the TPK1 protein represents a prerequisite for interaction.

References to 14-3-3 binding to AtKCO1

Latz A, Becker D, Hekman M, Müller T, Beyhl D, Marten I, Eing C, Fischer A, Dunkel M, Bertl A, Rapp UR, Hedrich R

TPK1, a Ca(2+)-regulated Arabidopsis vacuole two-pore K+ channel is activated by 14-3-3 proteins. Plant J. 2007 Nov;52(3):449

Dunkel M, Latz A, Schumacher K, Müller T, Becker D, Hedrich R. Targeting of Vacuolar Membrane Localized Members of the TPK Channel Family. Mol Plant. 2008 Nov;1(6):938-40

Arabidopsis NIA1 (NRI, Arabidopsis nitrate reductase 1) (Swissprot = P11832)

References to 14

Notes

NIA1 is a nitrate-sensing potassium channel whose activity is regulated by the vacuolar membrane localized K+ channel/ outward rectifier potassium channel (Swissprot = Q8LBL1)

References to 14-3-3 binding to NIA1

Latz A, Becker D, Hekman M, Müller T, Beyhl D, Marten I, Eing C, Fischer A, Dunkel M, Bertl A, Rapp UR

TPK1, a Ca(2+)-regulated Arabidopsis vacuole two-pore K+ channel is activated by 14-3-3 proteins. Plant J. 2007 Nov;52(3):449-59.

The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial Licence (http://creativecommons.org/licenses/by-nc/2.5/) which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.
Arabidopsis NIA2 (NR2, Arabidopsis nitrate reductase 2) (Swissprot = PI1035)

NIA2 proteins

H. Virus

References to 14-3-3 binding to nitrate reductase

Notes

RTApS (1983) TP (Spinach) Arabidopsis NR1 and NR2 isoforms expressed from two gene sequences of 14-3-3 proteins. Plant Physiol. 1998 Nov;118(3):1041

303. Douglas, P. Moorehead G, Hong Y, Morrice N, MacKintosh C. Identification of a nitrate reductase from Spinacea oleracea leaves, and its identification as a calmodulin-domain protein kinase. Planta. 1999 Oct;206(3):435-42.

304. Douglas, P, Morrice N, MacKintosh C. Identification of a regulatory phosphorylation site in the hinge 1 region of 14-3-3 proteins in Spinacea oleracea leaves. FEBS Lett. 1999 Jun 11;453(1):26-30.

305. Douglas, P, Moorhead G, Hong Y, Morrice N, MacKintosh C. A spinach leaf nitrate reductase in an isoform TP (Spinach) Arabidopsis NR1 and NR2 isoforms expressed from two gene sequences of 14-3-3 proteins. J Biol Chem. 2000 Oct 6;275(41):31695-700.

Kaiser WM, Weiner H, Kandlbinder A, Tsai CB, Rockel P, Sonoda M, Planchet E. Modulation of nitrate reductase: some new insights, an unusual case and a potentially important side reaction. J Exp Bot. 2002 Apr;53(370):87-92.
Kanamurak K, Wang R, Su W, Crawford NM. Ser-534 in the hinge 1 region of Arabidopsis nitrate reductase is conditionally required for binding of 14-3-3 proteins and in vitro inhibition. J Biol Chem. 1999 Feb 12;274(7):4160-5.

Lea US, Ten Hoopen F, Provan F, Kaiser WM, Meyer C, Lillo C. Mutation of the regulatory phosphorylation site of tobacco nitrate reductase results in high nitrite excretion and NO emission from leaf and root tissue. Planta. 2004 May;219(1):59-65.

Lillo C, Kazazaa S, Ruiz F, Meyer C. Characterization of Nitrate Reductase from Light- and Dark-Exposed Leaves (Comparison of Different Species and Effects of 14-3-3 Inhibitor Proteins). Plant Physiol. 1997 Aug;114(4):1377-1383.

Lillo C, Lea US, Leydecker MT, Meyer C. Mutation of the regulatory phosphorylation site of tobacco nitrate reductase results in constitutive activation of the enzyme in vivo and nitrate accumulation. Plant J. 2003 Sep;35(5):566-73.

Lillo C, Meyer C, Lea US, Provan F, Olmedal S. Mechanism and importance of post-translational regulation of nitrate reductase. J Exp Bot. 2004 Jun;55(401):1275-82.

MacKintosh C, Meek SE. Regulation of plant NR activity by reversible phosphorylation, 14-3-3 proteins and proteolysis. Cell Mol Life Sci. 2001 Feb;58(2):205-14.

Moorehead G, Douglas P, Morrice N, Scarrabell M, Atken A, MacKintosh C. Phosphorylated nitrate reductase from spinach leaves is inhibited by 14-3-3 proteins and activated by fusccocin.Curr Biol. 1996 Sep 1;6(9):1104-13.

Nakamura K, Shiraishi N, Hosoo S, Sueyoshi K, Sugimoto T, Nannori T, Nakagawa H, Oji Y. A protein kinase activated by darkness phosphorylates nitrate reductase in Komatsuna (Brassica campestris) leaves. Physiol Plant. 2002 Aug;115(4):496-503.

Perdono G, Navarro FI, Medina B, Machin F, Tejera P, Siverio JM. Tobacco Nia2 cDNA functionally complements a Hansenula polymorpha yeast mutant lacking nitrate reductase. A new expression system for the study of plant proteins involved in nitrate assimilation. Plant Mol Biol. 2002 Oct;50(3):405-13.

Pigaglio E, Durand N, Meyer C. A conserved acidic motif in the N-terminal domain of nitrate reductase is necessary for the inactivation of the enzyme in the dark by phosphorylation and 14-3-3 binding. Plant Physiol. 1999 Jan;118(1):219-30.

Shen W, Clark AC, Huber SC. The C-terminal tail of Arabidopsis 14-3-3omega functions as an autoinhibitor and may contain a tenth alpha-helix. Plant J. 2003 May;34(4):473-84.

Shen W, Huber SC. Polycations globally enhance binding of 14-3-3omega to target proteins in spinach leaves. Plant Cell Physiol. 2006 Jun;47(6):764-71.

Sinning MP, Roozem B, Bunney TD, Visser AJ, Mol JN, de Boer AH. Single amino acid variation in barley 14-3-3 proteins leads to functional isoform specificity in the regulation of nitrate reductase. Plant Mol Biol. 2005 Dec;44(6):1001-20.

Tsai CB, Kaiser WM, Kaldenhoff R. Molecular cloning and characterization of nitrate reductase from Ricinus communis L. heterologously expressed in Pichia pastoris. Planta. 2003 Oct;217(6):962-70.

Tucker DE, Allen DJ, Ort DR. Control of nitrate reductase by circadian and diurnal rhythms in tomato. Planta. 2004 Jun;219(2):277-85.

Weiner H, Kaiser WM. Binding to 14-3-3 proteins is not sufficient to inhibit nitrate reductase in spinach leaves. FEBS Lett. 2000 Sep 1;480(2-3):217-20.

**Arabidopsis NUDT7 (in paper = At14g12720)**

Site of 14-3-3 binding not well defined see below

**Notes**

“Mutant plants deprived of AtNUDT7, exhibit growth retardation, spontaneous cell death and increased resistance to pathogen infection.”

Wildtype and V26A mutations had no effect on 14-3-3 binding

V69A, F73A and V168A all had no interaction with 14-3-3 in Y2H assay

14-3-3 beads pulled out NUDT7 from Arabidopsis cell extracts

F73A and V168A have problems dimerizing and instead aggregate NUDT7

**References to 14-3-3 binding to NUDT7**

Olejnık K, Plochocka D, Gryenberg M, Goeh G, Gruszeczki WL, Basińska T, Kraszewska E. Mutational analysis of the AtNUDT7 Nudix hydrolase from Arabidopsis thaliana reveals residues required for plant quaternary structure formation and activity. Acta Biochim Pol. 2009;56(2):291-300.

**Arabidopsis OMT1** caffeic acid 3-hydroxyferulic acid O-methyltransferase

Sequence not defined.

**References to 14-3-3 binding to OMT1**

Zhang H, Wang J, Goodman HM. An Arabidopsis gene encoding a putative 14-3-3-interacting protein, caffeic acid 3-hydroxyferulic acid O-methyltransferase. Biochim Biophys Acta. 1997 Sep 12;1353(3):199-202.

**Arabidopsis PHOT1** (Phototropin receptor kinase from Arabidopsis) (Swissprot = O48963)

Sites of 14-3-3 binding not defined.

Three sites implicated in 14-3-3 binding, but not...
References to 14

Notes

Arabidopsis photosystem I N, full length precursor)

Arabidopsis PMA1 targeted chloroplast precursor protein and the presence of 14

References to 14

Notes

Arabidopsis photosystem I N

2003;133:1453

Kinoshita T, Emi T, Tominaga M, Shimura H, Imagawa Y, Inoue K, Adachi S, Shimokawa K, Kitamoto T, Takio K, Shimazaki T

2008;105:5626

Phototropin is a primary step for signaling. Proc. Natl. Acad. Sci. USA. 2008;105:5626–5631.

Kinoshita T, Emi T, Tominaga M, Shimura H, Imagawa Y, Inoue K, Adachi S, Shimokawa K, Kitamoto T, Takio K, Shimazaki T

Phototropic hypocotyl protein 1; AltName: Full=Root phototropism

Arabidopsis PMA1 targeted chloroplast precursor protein and the presence of 14

References to 14

Notes

Arabidopsis photosystem I N

2003;133:1453

Kinoshita T, Emi T, Tominaga M, Shimura H, Imagawa Y, Inoue K, Adachi S, Shimokawa K, Kitamoto T, Takio K, Shimazaki T

2008;105:5626–5631.

Kinoshita T, Emi T, Tominaga M, Shimura H, Imagawa Y, Inoue K, Adachi S, Shimokawa K, Kitamoto T, Takio K, Shimazaki T

Phototropic hypocotyl protein 1; AltName: Full=Root phototropism

Arabidopsis PMA1 targeted chloroplast precursor protein and the presence of 14

References to 14

Notes

Arabidopsis photosystem I N, full length precursor)
**Notes**

The mode III 14-3-3-binding site (YgtP’TgV-COOH) is found in members of the large family of V-type plasma membrane proton pumps (see sequence alignment in Duby and Boutry 2008). The sequence of PMA1 is given here. Structural studies indicate that a hexameric complex resulting from the assembly of three H+ATPase dimers linked by three 14-3-3 dimers. The complex is stabilised by fuscinquist, which binds to the 14-3-3 and H+ATPase within the central groove of the 14-3-3 dimer.

**References to 14-3-3 binding to plant plasma membrane H+-ATPase**

Alsterfjord M, Sehnke PC, Arkell A, Larsson H, Svennelid F, Rosenquist M, Ferl RJ, Sommarin M, Larsson C. Expression of a constitutively activated plant plasma membrane H+ ATPase. Biochemistry. 1999 Jun 1;38(22):7227-34.

Babakov AV, Chelysheva VV, Klychnikov OI, Zorinyanz SE, Trofimova MS, De Boer AH. Involvement of 14-3-3 proteins in the osmotic regulation of H+ATPase in plant plasma membranes. Planta. 2000 Aug;211(3):446-8.

Baunsgaard L, Fuglsang AT, Jahn T, Korthout HA, de Boer AH, Palmgren MG. The 14-3-3 proteins associated with the plant plasma membrane H+ATPase interact to form a fuscinquist binding and a fuscinquist responsive system. Plant J. 1998 Mar;13(3):661-71.

Block P, Weskamp N, Wolf A, Klebe G. Strategies to search and design stabilizers of protein-protein interactions: a feasibility study. Proteins. 2007 Jul 1;68(1):170-86.

Borch J, Bych K, Roepstorff P, Palmgren MG, Fuglsang AT. Phosphorylation-independent interaction between 14-3-3 protein and the plasma membrane H+-ATPase. Biochim Biophys Acta. 2002 Aug;1587(2):411-5.

Camosi L, Iori V, Marra M, Aducci F. Phosphorylation-dependent interaction between plant plasma membrane H+-ATPase and 14-3-3 proteins. J Biol Chem. 2000 Apr 7;275(14):9919-23.

Camosi L, Marra M, Garufi S, Aducci S. The maize root plasma membrane H+ATPase. J Biol Chem. 2001 Aug 24;276(34):31709-12.

Chelysheva VV, Smolenskaya IN, Trofimova MC, Babakov AV, Chelysheva VV. Role of the 14-3-3 proteins in the regulation of H+ATPase activity in the plasma membrane of suspension-cultured sugar beet cells under cold stress. FEBS Lett. 1999 Jul 30;456(1):226.

Dambly S, Boutry M. The two major plant plasma membrane H+-ATPases display different regulatory properties. J Biol Chem. 2001 Mar 9;276(10):7017-22.

Duby G, Boutry M. The plant plasma membrane proton pump ATPase: a highly regulated P-type ATPase with multiple physiological roles. Pflogers Arch. 2009 Jan;457(3):645-55.

Duby G, Poreba W, Piotrowiak D, Bobik K, Derua E, Waclens E, Boutry M. Activation of plant plasma membrane H+-ATPase by 14-3-3 proteins is negatively controlled by two phosphorylation sites within the H+-ATPase C-terminal region. J Biol Chem. 2009 Feb 13;284(7):4213-21.

Emi T, Kinosita T, Shimagaki K. Specific binding of v1-4-3-3a isoform to the plasma membrane H+-ATPase in response to blue light and fuscinquist in guard cells of broad bean. Plant Physiol. 2001 Feb;125(2):1115-25.

Finn C, Andersen CH, Borch J, Gjetting S, Christenssen AB, de Boer AH, Thorald-Christenssen, Collinge DB. Do 14-3-3 proteins and plasma membrane H+-ATPase interact in the barley epidermis in response to the barley powdery mildew fungus? Plant Mol Biol. 2002 May;49(2):157-47.

Fuglsang AT, Borch J, Bych K, Jahn TP, Roepstorff P, Palmgren MG. The binding site for regulatory 14-3-3 protein in plant plasma membrane H+-ATPase: involvement of a region promoting phosphorylation-independent interaction in addition to the phosphorylation-dependent C-terminal end. Biol Chem. 2003 Oct 24;278(43):42266-72.

Fuglsang AT, Guo Y, Cui TA, Qiu Q, Song C, Christiansen KA, Bych K, Schulz A, Shabalba S, Schumaker KS, Palmgren MG, Zhu JK. Arabidopsis protein kinase PKS5 inhibits the plasma membrane H+-ATPase by preventing interaction with 14-3-3 protein. Plant Cell. 2007 May;19(5):1617-34.

Fuglsang AT, Visconti S, Brunner D, Jahn T, Stenstelle B, Mattei B, Jensen ON, Aducci P, Palmgren MG. Binding of 14-3-3 proteins to the plasma membrane H+ATPase AHA2 involves the three C-terminal residues Tyr(946)-Thr(948)-Thr(950) and requires phosphorylation of Thr(947). J Biol Chem. 1999 Dec 17;274(51):36774-80.

Fullone MR, Visconti S, Marra M, Fogliano V, Aducci P. Fuscinquist effect on the in vitro interaction between plant 14-3-3 proteins and plasma membrane H+-ATPase. J Biol Chem. 1998 Mar 27;273(13):7698-702.

Garufi A, Visconti S, Camoni L, Aducci P. Polyamines as physiological regulators of 14-3-3 interaction with the plant plasma membrane H+-ATPase. Plant Cell Physiol. 2007 Mar;48(3):434-40.

Gévaudant F, Duby G, von Stedingk E, Zhao R, Morosmome P, Boutry M. Expression of a constitutively activated plasma membrane H+-ATPase alters plant development and increases salt tolerance. Plant Physiol. 2007 Aug;144(4):1763-76.

Giacomelli S, Camoni L, Albani C, Visconti S, De Micheli M, Aducci P. Tyrosine phosphorylation inhibits the interaction of 14-3-3 proteins with the plant plasma membrane H+-ATPase. Plant Biol (Stuttg). 2004 Jul;6(4):422-31.

Jahn T, Dietrich J, Andersen B, Leidvik B, Otter C, Briving C, KühbrantW, Palmgren MG. Large scale expression,
purification and 2D crystallization of recombinant plant plasma membrane H+-ATPase. J Mol Biol. 2001 Jun 1;309(2):465-76.

Jahn T, Fuglsang AT, Olsson A, Bründrup IM, Collinge DB, Volkman D, Sommarin M, Palmgren MG, Larsson C. The 14-3-3 protein interacts directly with the C-terminal region of the plant plasma membrane H+-ATPase. Plant Cell. 1997 Oct;9(10):1805-14.

Jahn TP, Schulz A, Tappalanenu I, Palmgren MG. Post-translational modification of plant plasma membrane H+-ATPase as a requirement for functional complementation of a yeast transport mutant. J Biol Chem. 2002 Feb 22;277(8):6353-8.

Jaspert N, Oecking C. Regulatory 14-3-3 proteins bind the atypical motif within the C terminus of the plant plasma membrane H+-ATPase via their typical amphipathic groove. Planta. 2002 Nov;216(1):136-9.

Jelich-Ottmann C, Weller EW, Oecking C. Binding of regulatory 14-3-3 proteins to the C terminus of the plant plasma membrane H+-ATPase involves part of its autoinhibitory region. J Biol Chem. 2001 Oct 26;276(43):39852-7.

Kanczewska J, Marco S, Vandermeeren C, Maudoux O, Rigaud JL, Bourtier M. Activation of the plant plasma membrane H+-ATPase by phosphorylation and binding of 14-3-3 proteins converts a dimer into a hexamer. Proc Natl Acad Sci U S A. 2005 Aug 16;102(33):11675-80.

Kinoshita T, Shimazaki K. Analysis of the phosphorylation level in guard-cell plasma membrane H+-ATPase in response to fusicoccin. Plant Cell Physiol. 2001 Apr;42(4):424-32.

Kinoshita T, Shimazaki K. Biochemical evidence for the requirement of 14-3-3 protein binding in activation of the guard-cell plasma membrane H+-ATPase by blue light. Plant Cell Physiol. 2002 Nov;43(11):1559-65.

Malera M, Bianchetti R. 14-3-3 protein-activated and autoinhibited forms of plasma membrane H+-ATPase. Biochem Biophys Res Commun. 2001 Sep 7;286(5):984-90.

Maudoux O, Batoke H, Oecking C, Gevaert K, Vandekerckhove J, Bourtier M, Morosomme P. A plant plasma membrane H+-ATPase expressed in yeast is activated by phosphorylation at its penultimate residue and binding of 14-3-3 regulatory proteins. J Biol Chem. 2000 Jun 9;275(23):17762-70.

Morandin P, Valera M, Albumi C, Bonza MC, Giacometti S, Ravera G, Murgia I, Soave C, De Micheli M. A novel interaction partner for the C-terminus of Arabidopsis thaliana plasma membrane H+-ATPase (AHAl isoform): site and mechanism of action on H+-ATPase activity differ from those of 14-3-3 proteins. Plant J. 2002 Aug;31(4):487-97.

Oliveri C, Albumi C, Pugliarello MC, De Micheli M. Phenylnasline oxide inhibits the fusicoccin-induced activation of plasma membrane H+-ATPase. Plant Physiol. 2000 Feb;122(2):463-70.

Oliveri C, Meanti C, De Micheli MI, Rasi-Caldogno F. Fusicoccin binding to its plasma membrane receptor and the activation of the plasma membrane H+-ATPase. IV. Fusicoccin induces the association between the plasma membrane H+-ATPase and the fusicoccin receptor. Plant Physiol. 1998 Feb;116(2):529-37.

Olsson A, Svennelid F, Ek B, Sommarin M, Larson C. A phosphothreonine residue at the C-terminal end of the plasma membrane H+-ATPase is protected by fusicoccin-induced 14-3-3 binding. Plant Physiol. 1998 Oct;118(2):551-5.

Ottmann C, Marco S, Jaspert N, Marcon C, Schauer N, Weyand M, Vandermeeren C, Duby G, Bourtier M, Wittinghofer A, Rigaud JL, Oecking C. Structure of a 14-3-3 coordinated hexamer of the plant plasma membrane H+-ATPase by combining X-ray crystallography and electron cryo-microscopy. Mol Cell. 2007 Feb 9;25(3):427-40.

Palmgren MG. PLANT PLASMA MEMBRANE H+-ATPASES: Powerhouses for Nutrient Uptake. Annu Rev Plant Physiol Plant Mol Biol. 2001 Jun;52:817-845.

Pertl H, Hnimy M, Gehwolf R, Kriechbaum R, Strasser D, Michelak W, Richter K, Ferreira F, Obermeyer G. Molecular and physiological characterisation of a 14-3-3 protein from lily pollen grains regulating the activity of the plasma membrane H+-ATPase during pollen grain maturation and tube growth. Planta. 2001 May;213(1):132-41.

Piotrowski M, Morosomme P, Bourtier M, Oecking C. Co- crystallization of the Saccharomyces cerevisiae plasma membrane H+-ATPase by a plant H+-ATPase generates a highly fusicoccin binding site. J Biol Chem. 1998 Nov 6;273(45):30018-23.

Svennelid F, Olsson A, Piotrowski M, Rosenquist M, Ottman C, Larsson C, Oecking C, Sommarin M. Phosphorylation of Thr-948 at the C terminus of the plasma membrane H+-ATPase creates a binding site for the regulatory 14-3-3 protein. Plant Cell. 1999 Dec;11(12):2379-91.

Ueno K, Kinoshita T, Inoue S, Emi T, Shimazaki K. Biochemical characterisation of plasma membrane H+-ATPase activation in guard cell protoplasts of Arabidopsis thaliana in response to blue light. Plant Cell Physiol. 2005 Jun;46(6):955-63.

Viotti C, Luoni L, Morandini P, De Micheli M. Characterization of the interaction between the plasma membrane H+-ATPase of Arabidopsis thaliana and a novel interacter (PPI1). FEBS J. 2005 Nov;272(22):5864-71.

Visconti S, Camoni L, Fullone MR, Lalle M, Marra M, Aducci P. Mutational analysis of the interaction between 14-3-3 proteins and plant plasma membrane H+-ATPase. J Biol Chem. 2003 Mar 7;278(10):8172-8.

Visconti S, Camoni L, Marra M, Aducci P. Role of the 14-3-3 C-terminal region in the interaction with the plasma membrane H+-ATPase. Plant Cell Physiol. 2008 Dec;49(12):1887-97.

Woloszynska J, Kinoshita T, Maudoux O, Bourtier M. Function and regulation of the two major plasma membrane H+-ATPases. Annu Rev Plant Biol. 2003 Apr;54:198-203.

Württele M, Jelich-Ottmann C, Wittinghofer A, Oecking C. Structural view of a fungal toxin acting on a 14-3-3 regulatory complex. EMBO J. 2003 Mar 3;22(5):987-94.

Zhang X, Wang H, Takemiy A, Song CP, Kinoshita T, Shimazaki K. Inhibition of blue light-dependent H+-pumping activity by abscisic acid through hydrogen peroxide-induced depolyphorylation of the plasma membrane H+-ATPase in guard cell protoplasts. Plant Physiol. 2004 Dec;136(4):410-8.
The RPW8 locus from Arabidopsis thaliana Ms-0 includes two functional paralogous genes (RPW8.1 and RPW8.2) and confers broad susceptibility and resistance to the salicylic acid-dependent signaling pathway to the biotrophic fungal pathogens Golovinomyces spp. that cause powdery mildew diseases on multiple plant species. The C-terminal domain of RPW8.2 is required for the interaction of this protein with 14-3-3 (Yang et al. 2009). References to 14-3-3 binding to Arabidopsis RPW8.2

Yang X, Wang W, Coleman M, Orgil U, Feng J, Ma X, Fei R, Turner JG, Xiao S. Arabidopsis 14-3-3 lambda is a positive regulator of RPW8-mediated disease resistance. Plant J. 2009 Jun 16. [Epub ahead of print]

**Arabidopsis SERK1 (uniprot Q94AG2)**

- Sites of 14-3-3 binding not confirmed. NO WEBLOGO.

**Notes**

14-3-3 binding site has not been confirmed, but there is a putative binding site at S394. Just used 266-625 of AtSERK1, (kinase domain) as bait in Y2H of silique tissue.

| Residue | Site Name | Start | End |
|---------|-----------|-------|-----|
| 229      | Binding site Ser229 | 83 | 229 |
| 266      | Binding site to SPS | 266 | 305 |

**Arabidopsis SPS**

ATPS1 (sucrose phosphate synthase 1F) (NM_122035.2)

**Notes**

In dicotyledonous plants there are three SPS gene families: A, B, and C, and five families (A, B, C, and two D subfamilies) of SPS genes in wheat (Triticum aestivum) and other monocotyledonous plants from the family Poaceae (grasses) (Castleden et al. 2004). The 14-3-3-binding site Ser229 is found within the A type SPS sequences. The site of the Arabidopsis version of SPS (SPS1F) is given.
Hordeum vulgare lipoygenase 2 (LoxC) in response to ABA. Plant Cell Physiol. 2007 Aug;48(8):1182-21.

Takahashi Y, Kinoshiba T, Athwal GS, Huber SC. Site-specific regulatory interaction between spinach leaf sucrose-phosphate synthase and 14-3-3 proteins. FEBS Lett. 1998 Sep 11;435(1):110-4.

Moorehead G, Douglas P, Cotelle V, Harthill J, Morrice N, Meek S, Castleden CK, Aitken A, Moorhead PJ, Costa Pereira DD, De Boer AH. Dual role for 14-3-3 proteins and ABF transcription factors in the regulation of sucrose-phosphate synthase isoforms in tobacco. Plant Physiol. 2006 Jul;141(1):11-21.
Medicago truncatula CDS (plastid glutamine synthetase) (Genbank AY225150)

1 MAQILAPSTQ CQAIRITKRP VPATIPSSHWV SSLVMRKQVR XRASKFIRVM AGVSNSRVR Q
2 EDJNLDTPT FDDSIAEY WINSISIDV KRSTKIFPK EPWPSEIFRK WDSSGTQPAP
3 QIIEVQVFQR QAIIPQVRE GIIIQVLCGID YTPGPEIPI KORHKSSAPF SPS
4 WSEYGIQYTEL LTDTVKVMPL WPVVGQYGQPC PGPYCCAGAG CSGFRDGSX HYKACLAYGI
5 NISGNGRMQF SQMYEYQVGP SVJIEAGDHH WASYRILY TERQAGVVLTL DPKFPGWDN
6 GACHTNYST KMSREDQGFE VIKKAILLS LRHKIGEAY GEENRTLG RHETASINTF
7 SWGNAVRCSS IVRGRDTEKN ALFDRESSADR PNNPQDFVUT ALLAERTLVM EPTLEELEAL

References to 14-3-3 binding sites not defined

Klyuchnikov et al (2007) used endogenous protein from barley tonoplast membranes but suggested the sequence above and mentioned RGVS\(^3\)-AP as being putative 14-3-3 binding sites that are conserved in other species with the 544 site being phosphorylated in the Maize equivalent. The catalytic A subunit of the V-ATPase binds directly to 14-3-3 in an overlay and is phosphorylated in vitro with endogenous kinases in the tonoplast membrane purification (where the kinase properties are affected by blue light) but sites of phosphorylation were not identified. Conclusions, “the data show that binding not identified. No WEBLOGO.”

Notes

RKPDSKP at position 234 is suggested as a potential 14-3-3-binding site, but no experimental data on site.

References to 14-3-3 binding to 13-LOX

Holton WL, Roberts MR, Oppedijk BJ, Testerink C, van Zeijl MJ, Wang M. 14-3-3 proteins and a 13-lipoxygenase form associations in a phosphorylation-dependent manner. Biochem Soc Trans. 2000 Dec;28(6):835-850.

Hordeum vulgare vacuolar H(+)-ATPase (V-ATPase) (Genbank Q04002)

1 ELRVGQHDSDL IGEIIILRED SATIQVYRTE AGTVNDPVL RTKPKLSCCL GPGILNFD P
2 IQITQLPTKL QSKVPAKDI QSWPVKNL QGVHITQID LVTFVENTL

Notes

Sites of 14-3-3 binding not defined.

No WEBLOGO.
References to 14-3-3 binding to GS2
Lima I, Seabra A, Mello P, Cullimore J, Carvalho H. Phosphorylation and subsequent interaction with 14-3-3 proteins regulate plastid glutamine synthetase in Medicago truncatula. Planta. 2006 Feb;223(3):558-67.
Finnemann J, Schjoerring JK. Post-translational regulation of cytosolic glutamine synthetase by reversible phosphorylation and 14-3-3 protein interaction. Plant J. 2000 Oct;24(2):171.
Riedel J, Tischer R, Mack G. The chloroplastic glutamine synthetase (GS2) of tobacco is phosphorylated and associated with 14-3-3 proteins inside the chloroplast. Planta. 2001 Jul;213(3):396-401.

Nicotiana tabacum DBP1 (DNA-binding protein phosphatase-1) (GenBank AF520810)

Results

Note: See Site is well conserved among other plant chloroplastic GS proteins.

References to 14-3-3 binding to Tobacco DBP1
Carrasco JL, Castelló MJ, Vera P. 14-3-3 mediates transcriptional regulation by modulating nucleoeroplasmic shuttling of tobacco DNA-binding protein phosphatase-1. J Biol Chem. 2006 Aug 21;281(32):2875-1.
T389A weakened homodimerisation K33R mutation in the ATP binding loop abolishes kinase activity and decreases interaction with activator RSG in response to gibberellins. Nakata M, Igarashi D, Ishida S, Fukazawa J, Takahashi Y. Involvement of 14-related kinase 1 (PNek1) (Uniprot Q8SA64) in the regulation of the transcriptional activator REPRESSION OF SHOOT GROWTH by gibberellins. Plant Cell. 2001 Nov;13(11):2483-97. Ishida S, Yuasa T, Nakata M, Takahashi Y. A tobacco calcium-dependent protein kinase, CDPK1, regulates transcription factor REPRESSION OF SHOOT GROWTH in response to gibberellins. Plant Cell. 2008 Dec;20(12):3273-85. Schoonheim PJ, Veiga H, Pereira Dda C, Friso G, van Wijk KJ, de Boer AH. A comprehensive analysis of the 14-3-3 interactome in barley leaves using a complementary proteomics and two-hybrid approach. Plant Physiol. 2009 May;148(3):968-79. Igarashi D, Ishida S, Fukazawa J, Takahashi Y. 14-3-3 proteins regulate intracellular localization of the bZIP transcriptional activator RSG. Plant Cell. 2004 Jul;16(10):2641-51. Poplar NIMA-related kinase 1 (PNek1) (UniProt Q8A404) is a calcium-dependent protein kinase, regulates transcriptional activity of RhoGAP1 in response to gibberellins. Plant Signal Behav. 2009 May;4(5):372-4.
which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.

References to 14-3-3 binding to Pac1
Cloutier M, Vigneault F, Lachance D, Séguin A. Characterization of a poplar NIMA-related kinase PNek1 and its potential role in meristematic activity. FEBS Lett. 2005 Aug 29;579(21):4659-63.

Rice ACC synthase I (Genbank AC135965 but this gives a human chromosome 3 complete clone)

Notes

References to 14-3-3 binding to rice ACC synthase 1
Yao Y, Du Y, Jiang L, Liu JY. Interaction between ACC synthase 1 and 14-3-3 proteins in rice: a new insight. Biochemistry (Mosc). 2007 Sep;72(9):1003-7.

Rice VP1 (VIVIPAROUS1)

Notes

References to 14-3-3 binding to VP1
Schultz TF, Medina J, Hill A, Quartaro RS. 14-3-3 proteins are part of an abscisic acid-VIVIPAROUS1 (VP1) response complex in the Em promoter and interact with VP1 and EmIP1. Plant Cell. 1998 May;10(5):837-47.

Tomato SPAK (Genbank acc. = AF079103)

Notes

References to 14-3-3 binding to SP
Tomato PRUNING (SP) gene confers accelerated termination of stem units until is eventually terminated by two consecutive inflorescences

Y2H screen with SP as bait, identified 5 SIPs (SP interacting proteins)

SIP2 and SIP74 were ID’d as 14

SIP3 was SP

SIP2 and SIP74 were ID’d as 14

Y2H screen with SP as bait, identified 5 SIPs (SP interacting proteins)

is eventually terminated by two consecutive inflorescences

A recessive mutation in the SELF

By Y2H, 14

SPAK also phosphorylates the SIP4 protein and only phosphorylated SIP4 binds 14

SPAK autophosphorylates a truncated SPAK lacking the kinase domain (SPAK exprd in bacteria)

By Y2H, 14

SPAK forms homodimers in yeast

By Y2H, 14-3-3 isoforms can interact with SPAK and SP and SIP4

In vitro binding results consistent with yeast results

SPAK autophosphorylates a truncated SPAK lacking the kinase domain (SPAK exprd in bacteria)

SPAK also phosphorylates the SIP4 protein and only phosphorylated SIP4 binds 14-3-3

References to 14-3-3 binding to SPAK

Pouel L, Gutfinger T, Hareven D, Ben-Naim O, Ron N, Adir N, Lifschitz E. Tomato SP-interacting proteins define a conserved signaling network that regulates shoot architecture and flowering. Plant Cell. 2001 Dec;13(12):2687-97.

Trichium aestivum GAPN (non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase (Swissprot = Q8LK61)

Notes

References to 14-3-3 binding to GAPN
Cloutier M, Vigneault F, Lachance D, Séguin A. Characterization of a poplar NIMA-related kinase PNek1 and its potential role in meristematic activity. FEBS Lett. 2005 Aug 29;579(21):4659-63.

© 2010 The Author(s)
The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial Licence (http://creativecommons.org/licenses/by-nc/2.5/) which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.
The ARAApsAPA phosphopeptide that competes for 14-3-3 binding increased the activity of specifically the phosphorylated GAPN enzyme almost 3-fold. Suggested to be 1 mol tetrameric GAPN to 2 mol dimeric 14-3-3. Mg2+ disrupts the GAPN-14-3-3 interaction which is unusual, divalent cations normally stabilize it. A computer model putting S404 in one of the pockets implicates S447 as being in the other pocket although there is no experimental evidence for this.

Plant non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase (NP-Ga3PDHase) – sites not well defined

References to 14-3-3 binding to NP-Ga3PDHase
Bustos DM, Bustamante CA, Iglesias AA. Involvement of non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase in response to oxidative stress. J Plant Physiol. 2008 Mar 13;165(4):456-61.

Bustos DM, Iglesias AA. Variable interactions between sucrose non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase from heterotrophic cells of wheat interacts with 14-3-3 binding to WPK4 and NP14 protein kinase OS=Triticum aestivum GN=wpk4 PE=2

Trichicum aestivum WPK4 (Wheat protein kinase) (Swissprot = Q41592)

| T204 | 14-3-3 by Y2H |
| T204 in paper but T205 in this sequence? Is an autophosphorylation site in the activation loop |

Trichicum aestivum WP4 (Wheat protein kinase) (Swissprot = Q41592)

| T204A reduced binding to 14-3-3 by 25% indicating that binding was dependent on the kinase activity |

K75D mutant shows only a modest reduction suggesting additional 14-3-3 binding to WT and in WT, these sites are probably autophosphorylation sites.

S388A and S418A single mutants show mild reduction in 14-3-3 binding by quantitative Y2H reporter assay.

1 to 34 fragment lacking putative residues showed only 10% binding

Overlay assay was done on C-terminal fragment containing the putative binding sites and it was shown that the displayed only a modest reduction suggesting additional 14-3-3 binding site in C-terminus

S388A/S418A double shows only ~25% binding of WT and in WT, these sites are probably autophosphorylation sites.

References to 14-3-3 binding to WPK4
Bustos DM, Iglesias AA. A model for the interaction between plant GAPN and 14-3-3 binding increased the activity of specifically the phosphorylated GAPN enzyme almost 3-fold. Suggested to be 1 mol tetrameric GAPN to 2 mol dimeric 14-3-3. Mg2+ disrupts the GAPN-14-3-3 interaction which is unusual, divalent cations normally stabilize it.

Bustos DM, Iglesias AA. Phosphorylated non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase from heterotrophic cells of wheat interacts with 14-3-3 binding to WPK4 and NP14 protein kinase OS=Triticum aestivum GN=wpk4 PE=2

Zea mays HOX1a Maize homeodomain protein with PHD and leucine zipper (Arabidopsis relative HAT3.1) (Swissprot = P46605)

| Sites of 14-3-3 binding not defined. NO WEBLOGO. |
References to 14-3-3 binding to Plant homeodomain proteins with PHD and leucine zipper

Halbach T, Scheer N, Werr W. Transcriptional activation by the PHD finger is inhibited through an adjacent leucine zipper region of was found to bind to 14-3-3 omega inside Arabidopsis cells.

Zea mays MPK6 A MAP kinase (Uniprot Q6TAR9)

1 MQHQKKKAP SEMDFDTEYG EGSRYKIREVGKGSYYVGVC SAVDTHTGKE VAJKKINDIF
1165
1 EHDSATIRLI REIKLRLLHR PDIEVEIKHI LIPSRREF ERIVYVFMLEB SDLQQVIKAN
121 DDLTPEHYYQ FLUILMLGKL YHITANVEHR DLKPNILAN ADCLKCILDEF GLARVAFNDT
181 PTAIFWTDIV ATWIRAPEL CLSEFFSHYTP AFIDIVISICG PAELTOLKFL FKGGFMYHQL
241 DIITDCGTP SEPHKRXIFP FFNDPFFPPQ FXFNPADPGL CLSERLMAFE
301 PKDRPSEAEE LADPYFNYA SVDREPSAQA VTKLEFEEFR RRVTEDRED LIYREYLEYH
361 PKRMLPESSE LSSGMYPS ADVFHKKQA YLLEEYAKGS TQGTPETQRH SLRFPVVSYS
421 DNRQTTAN IDTLLDKCMLE RENTKYRTHPS ASVASKFPHP VPQDPVARG KAVGVSQYMS
481 PCPAEARPY EQRIARRHPA VAPPNIPS QGSSYPFRQ CTQKSETGAEHSMQDNARQPKP
541 YAANLKPATD DSRSGHW

Notes: Several plant homeodomain proteins have a conserved peptide, with a leucine zipper followed by a PHD domain. The leucine zipper region of was found to bind to 14-3-3 in a yeast two-hybrid assay, but the precise site is not defined. It is suggested that a leucine zipper-like segment in helix alpha 4 of 14-3-3 interacts with the leucine zipper of the homeodomain proteins.

References to 14-3-3 binding to Plant homeodomain proteins with PHD and leucine zipper

Lalle M, Visconti S, Marra M, Camoni L, Velasco R, Aducci P. ZmMPK6, a novel maize MAP kinase that interacts with 14-3-3 proteins. Nucleic Acids Res 2001; 29(22): 467.

Deletion constructs were expressed and 14-3-3 binding was found to be in 337 - 467.

References to 14-3-3 binding to ZmMPK6

Lalle M, Visconti S, Marra M, Camoni L, Velasco R, Aducci P. ZmMPK6, a novel maize MAP kinase that interacts with 14-3-3 proteins. Plant Mol Biol 2000; 35(3):180-184.

Proteins from bacteria and viruses that interact with 14-3-3 inside eukaryotic host cells

Agrobacterium rhizogenes RolB (Swissprot P49408)

1 MAEFDLCALF SLSKVGDVS DDELKHHIQS AQSKERTPLTE PEGQSGMDI EGGRCGPDGI
1 LYLIVDCTPM MRCYFGLPS LSRNPGHTR LNPYQKVIDS LGVCRGLRQ ASQFFQDYDVE
12 ISKRYFAALS VPGFYKRDQ QMELTSTGKR SLTPDLHASN QRLEPFALV RGECGKFMG
13 153308.24 [sp] P49408.1 [RO2C_AGRH] RecName: Full=Cytokinin-beta-glucosidase; AltName: Full=ROL C protein

Notes: Soil-borne Gram-negative bacteria and causal agent of hairy root disease in many dicotyledonous plants. rolB gene derived from pR1724 in A. rhizogenes MAFF301724, named 1724 rolB. Hydrolizes cytokinin glucosides thus liberating free cytokinins. Contributes to the root inducing activity. Interacts directly with 14-3-3 omega inside Arabidopsis cells.

References to 14-3-3 binding to RolB

Morishita H, Okamoto C, Nishihara R, Yamashita I, Machida Y, Tanaka N. Nuclear localization and interaction with 14-3-3 proteins. Plant J 2003; 36(1):145-159.
interaction of RolB with plant 14-3-3 proteins correlates with induction of adventitious roots by the oncogene rolB. Plant J. 2004 Apr;38(2):260-75.

| Pseudomonas aeruginosa ExoS | exoenzyme S of Pseudomonas aeruginosa (NC_002516.2) |
|-----------------------------|-----------------------------------------------------|
| 1 MPHSLQSP SFAVELQGAA GSLRLQIEAR QVATPSEAQQ LARQGDPASQ KLLARLGAA | |
| 61 LVRFPYAMD WLOGLGLSHA RSGPQPSQDA QPAMVSSAVV FQMLQQAL PMLKGLDKA | |
| 121 SELATLPFEG LARQGDLRAS GDLQALGSLT ALAGRFAQQ VSE3RFQAGR LLLRSTGGLA | |
| 181 LQWQSGGTS AQLQVIDASP LREITIQQL HQVMSQAVL RQAVEEVSRS VSAKDALADG | |
| 241 LVRKQGDADE KLYRQGQPQG HSDAVMAVL LYTGIYHADL NRALQRPQGQ DQGQLIDQG | |
| 301 MSAAFKESQG AQVPVETFG TRGDADFNAY EERKVGHDV YLSLSTNPVG ARSFQGTGTS | |
| 361 TPGQGIDQV GSGNYSNEK EILYKETIM RVLLASDEQ GQTVRVLLEA ALGQSHQ | |

Notes

The phosphorlyation-independent interaction between ExoS and 14-3-3 occurs in a completely novel reversed fashion and is dependent on hydrophobic interactions (residues Lue422, Leu423, Leu426, and Leu428) rather than being electrostatically driven, as occurs with mode I–III consensus peptides. Exoenzyme-S, ADP-ribosylation.

References to 14-3-3 binding to ExoS

Fu H, Coburn J, Collier RJ. The eukaryotic host factor that activates exoenzyme S of Pseudomonas aeruginosa is a member of the 14-3-3 protein family. Proc Natl Acad Sci U S A. 1993 Mar 15;90(6):2320-4.

Ottmann C, Yasmn L, Weyand M, Veesenmeyer JL, Diaz MH, Palmer RH, Francis MS, Hauser AR, Hallberg B. Phosphorylation-independent interaction between 14-3-3 and exoenzyme S: from structure to pathogenesis. EMBO J. 2007 Feb 7;26(3):902-9.

Henriksson ML, Francis MS, Peden A, Aili M, Stefansson K, Palmer RH, Francis MS, Hallberg B. A delineation of exoenzyme S residues that mediate the interaction with 14-3-3 and its biological activity. FEBS J. 2006 Feb;273(3):638-46.

Hansen нагрузд та 14-3-3 binding motif on exoenzyme S that is functional in vivo. Eur J Biochem. 2002 Oct;296(20):4921-9.

Zhang L, Wang H, Masters SC, Barbieri JT, Fu H. Residues of 14-3-3 zeta required for activation of exoenzyme S of Pseudomonas aeruginosa. Biochemistry. 1999 Sep 14;38(37):12159-64.

Masters SC, Pederson KJ, Zhang L, Barbieri JT, Fu H. Interaction of 14-3-3 with a nonphosphorylated protein ligand, exoenzyme S of Pseudomonas aeruginosa. Biochemistry. 1999 Apr 20;38(16):5216-21.

Polyomavirus Middle T antigen (Swissprot = P03076)

1 MDRPRLNAR KRELLLELR QAGSDPDSM QAYKYQQLT LHPDKGSSA LMQELNSLOQ
| 61 TFKTEVNLK MNLGQTGVQ RRLHADVWNL STKDFGQD YQRQCMPLT CLNQVKVSSC | |
| 121 SCIQLRRKQ HRELKDKCA CRLVCLGECF LECYMNWGFT PTRGLVNLY FDIASMPIDW | |
| 181 LDDVHSVY KPEKSELR LAAVHTMTM GHAMEASST GQNMISSES GTAPSRLRLR | |
| 241 LFSLQLSPTY SVNRSH YFP TRVLQOIHHP ILLEDEILY LLSTMATYFR TFPFLEIFP | |
| 301 DQQLKPLEE EEEVNYMPED LYLIDLPEQQ VPLQIPPPPT PRAGLSWREG LILRQLQRAH | |

Notes

RSH(pSY)YPPT – phosphorylation identified by solid phase Edman sequencing fater protein extracted from NIH 3T3 cells.

References to 14-3-3 binding to polyomavirus middle T antigen

Chatterjee A, Mullane KP, Pallas DC, Benjamin TL, Roberts TM, Schaffhausen BS. Serine 257 phosphorylation regulates association of polyomavirus middle T antigen with 14-3-3 proteins. J Virol. 1998 Jan;72(1):558-63.
Supplementary Table 2. Reported 14-3-3-binding sites flanked by 20 amino acids on either side, based on the data collated in Supplementary Table 1. A. Mammalian proteins; B. Non-mammalian animal proteins; C. Fungal proteins; D. Plant proteins; E. Bacterial and viral proteins that interact with 14-3-3s inside eukaryotic host cells.

Where two sites have been identified for a given protein, the sequence around the second site is in pink type.

Caveat emptor: The data collected here is likely to include assignments that are incorrect, due to inaccuracies in the original assignments, or our interpretation of authors' intentions for which we apologise. To aid future improvements in the dataset, we ask authors to report any corrections to c.mackintosh@dundee.ac.uk.

| Mammalian proteins reported to interact directly with 14-3-3 | Sequences for WEBLOGO analysis |
|-------------------|--------------------------------|
| **Human AANAT** | Serotonin N-acetyltransferase; aroylalkylamine N-acetyltransferase. (Swissprot = Q16613) |
| **Human Abil** | Abelson murine leukemia viral oncogene homolog 1 (Tyrosine kinase) (Swissprot = P00519) |
| **Human ADAM22** | Disintegrin and metalloproteinase domain-containing protein 22 (Swissprot = Q9P0K1) |
| **Human AKAP13** | AKAP-Lbc, guanine nucleotide exchange factor (GEF) for RhoA (Swissprot = Q12802) |
| **Human AKT1S1 (PRAS40)** | (Swissprot = Q96B37) |
| **Human ARF1 (ARAF)** | (Swissprot = P10398) |
| **Human ARHGGEF2** | GEF-H1 microtubule-localized Rho exchange factor (Swissprot = Q92974) |
| **Human ATXN** | Ataxin 1 (Swissprot = Q13176) |
| **Human BAD** | (Swissprot = Q92934) |
| **Human BAIP2 (also known as IRSp53)** | Brain-specific angiogenesis inhibitor 1-associated protein 2 (Swissprot = Q9LQ88) |
| **Human BCl2L11** | Bcl-2 like protein 11 = BimEL isoform of Bim (Swissprot = O43521) |
| **Human B RafII (BRAF)** | (Swissprot = P15056) |
| **Human Cabin1** | (Calcineurin-binding protein cabin-1) (Q9Y6d0) |
| **Human CBY1** | Chibby = antagonist of β-catenin (ARPP-binding protein) (Swissprot = Q9Y3M2) |
| **Human CD74** | Major histocompatibility complex, class II invariant chain (Swissprot = P04233-1 for canonical long isoform) |
| **Human Cdc25A** | M-phase inducer phosphatase 1 (Swissprot = P50300) |
| **Human Cdc25B** | M-phase inducer phosphatase 2 (Swissprot = P50305) |
| **Human Cdc25C** | M-phase inducer phosphatase 3 (Swissprot = P30307) |
| **Human CDC2L2–CDK11p110** | (Cyclin-depandent Kinase 11) (Swissprot = P21127) |
| **Human CDKN1B (p27Kip1)** | Cyclin-dependent kinase inhibitor 1B (Swissprot = P46527) |
| **Human CENPJ** | (Centromere protein J) CPAP (Centrosomal Protein 4.1-Associated Protein) (Swissprot = Q9HC77) |
| **Human CFL1 (Cofilin 1)** | (Swissprot = P23528) |

© 2010 The Author(s)
| **Human** | **KANK1** | **ITGB2** | **ITGB1** | **IRS1** | **ING1** | **HJURP** | **HI** | **HDAC9** | **HDAC7** | **HJURP** |
|-----------|-----------|-----------|-----------|----------|----------|-----------|--------|-----------|-----------|----------|
| **Human CG322** | (ORC1) | (Swissprot = Q53ET0) | (Swissprot = P32927) | (Swissprot = P35222) | (Swissprot = P13022) | (Swissprot = P17032) | (Swissprot = Q5VWQ8) | (Swissprot = Q9WX9) | (Swissprot = Q9VDK4) | (Swissprot = Q9VDK4) |
| **Human CRTC2** | (MCM4) | (Swissprot = Q53ET0) | (Swissprot = P32927) | (Swissprot = P35222) | (Swissprot = P13022) | (Swissprot = P17032) | (Swissprot = Q5VWQ8) | (Swissprot = Q9WX9) | (Swissprot = Q9VDK4) | (Swissprot = Q9VDK4) |
| **Human DAB2IP** | (Disrupted homolog 2- interacting protein) | (Swissprot = Q53ET0) | (Swissprot = P32927) | (Swissprot = P35222) | (Swissprot = P13022) | (Swissprot = P17032) | (Swissprot = Q5VWQ8) | (Swissprot = Q9WX9) | (Swissprot = Q9VDK4) | (Swissprot = Q9VDK4) |
| **Human DCLK1** | (Disrupted homolog 2- interacting protein) | (Swissprot = Q53ET0) | (Swissprot = P32927) | (Swissprot = P35222) | (Swissprot = P13022) | (Swissprot = P17032) | (Swissprot = Q5VWQ8) | (Swissprot = Q9WX9) | (Swissprot = Q9VDK4) | (Swissprot = Q9VDK4) |
| **Human DCLK2** | (Disrupted homolog 2- interacting protein) | (Swissprot = Q53ET0) | (Swissprot = P32927) | (Swissprot = P35222) | (Swissprot = P13022) | (Swissprot = P17032) | (Swissprot = Q5VWQ8) | (Swissprot = Q9WX9) | (Swissprot = Q9VDK4) | (Swissprot = Q9VDK4) |
| **Human DMP2** | (Disrupted homolog 2- interacting protein) | (Swissprot = Q53ET0) | (Swissprot = P32927) | (Swissprot = P35222) | (Swissprot = P13022) | (Swissprot = P17032) | (Swissprot = Q5VWQ8) | (Swissprot = Q9WX9) | (Swissprot = Q9VDK4) | (Swissprot = Q9VDK4) |
| **Human DMP2L** | (Disrupted homolog 2- interacting protein) | (Swissprot = Q53ET0) | (Swissprot = P32927) | (Swissprot = P35222) | (Swissprot = P13022) | (Swissprot = P17032) | (Swissprot = Q5VWQ8) | (Swissprot = Q9WX9) | (Swissprot = Q9VDK4) | (Swissprot = Q9VDK4) |
| **Human DMP3** | (Disrupted homolog 2- interacting protein) | (Swissprot = Q53ET0) | (Swissprot = P32927) | (Swissprot = P35222) | (Swissprot = P13022) | (Swissprot = P17032) | (Swissprot = Q5VWQ8) | (Swissprot = Q9WX9) | (Swissprot = Q9VDK4) | (Swissprot = Q9VDK4) |
| **Human DMP3L** | (Disrupted homolog 2- interacting protein) | (Swissprot = Q53ET0) | (Swissprot = P32927) | (Swissprot = P35222) | (Swissprot = P13022) | (Swissprot = P17032) | (Swissprot = Q5VWQ8) | (Swissprot = Q9WX9) | (Swissprot = Q9VDK4) | (Swissprot = Q9VDK4) |
| **Human DMP3L** | (Disrupted homolog 2- interacting protein) | (Swissprot = Q53ET0) | (Swissprot = P32927) | (Swissprot = P35222) | (Swissprot = P13022) | (Swissprot = P17032) | (Swissprot = Q5VWQ8) | (Swissprot = Q9WX9) | (Swissprot = Q9VDK4) | (Swissprot = Q9VDK4) |
Human KCNK5  Two-pore-domain potassium channel TASK-1 (Swissprot = Q14649) SVSTGLNLSTPTFRGLMKRRS V--------------
Human KCNK9  Two-pore-domain potassium channel TASK-3 (Swissprot = Q9NPC2) S1SPGLIRLFDHRLMRRKAV V--------------
Human KIF1C (Kinesin-like protein KIF1C) (Swissprot = O43896) KFPGRYPYTTTPPDFREKRAPKALFDEPD GPPRSPPRKK
Human KLH2 (Swissprot = Q9R0B6) KLQKGPQGPGPNIKRRSA LNFLNKGQEEPTPGGGSLS
Human KRT18  Keratin 18 (Swissprot = P05783) RLSGQAPGYPAGRPVSAA VYAGAGGGSRIVSRSTTF
Human KSR1 (kinase suppressor of Ras) (Swissprot = Q8IVT5) PSRRKVPQFLPPTLTSRKS RESQLGRRNIDVSMRFLDS
Human LCP2 (SLP-76) (Lymphocyte cytosolic protein 2; aka SLP-76) (Swissprot = Q15094) FSSMHPGAPFEGGNNSPQSA LLPVFQSGSPKNNPFLAEGR
Human LSR  Isoform 2 of lipolysis-stimulated lipoprotein receptor (Swissprot = Q86X29) QEPKEAQGGRGWAEKRS VAAADLDPFLPTASEGSSP
Human MAP3K3 (MEKK3) Protein kinase of the STE11 family (Swissprot = Q99759) TPYQPRVYPSHHKVDYSQGDP FPRFRPQGQNLPTLPSRSSC
Human MAP3K5 (ASK1, MEKK5) Apoptosis signal-regulating kinase 1 (Swissprot = Q99683) KTQPKRLAISMNELYSI1 LPVPLVDGSTESSEYGVS
Human MAP3K6 (ASK2, MAPKKK6, MEKK6) Apoptosis signal-regulating kinase 2 (Swissprot = Q95382) TFFCPQAPSHPFSPPKRCLE YGTGTSQRVFPEPEAEFPAS
Human MAPK7 (ERK5, BMK1) (Swissprot = Q13164) KRKGAIASNTKAAKALKK LKSRRLDGQ5APLAEEPFPKR
Human MAPT Microtubule-associated protein tau (Swissprot = P10636) RSGYTPSGPQGPGSRGTF LPITPFRERKVARMVPFRR
Human MARK2 (aka Par-1b/EMK) (Swissprot = Q7KZ17 Not FOUND) QVQEKASIGLDKRKFIQ16K RLQKHVLKQGFLK97KL
Human Mdm2 (Swissprot = Q00987) SADLNNSASPSHSKQRVS QAPKQKRFSDOAQGAAPTPS
Human Mdm4 (MdmX) (Swissprot = Q15151) SADLNNSASPSHSKQRVS QAPKQKRFSDOAQGAAPTPS
Human MEFV Pyrin (Swissprot = O15553) PFCGPRALEQOAVRLRNS AGLQGLAGGQEGECRKP
Human MITF Microphthalmia-associated transcription factor (Accession = NP_937820, isoform 2) NOT FOUND NLIDLYGNQGPFILTSMN CAPNLNIKRELTESEARAL
Human MTHF Methylenetetrahydrofolate dehydrogenase 1 (Swissprot = P58340) FSSSIEILARRENMBMRQISF PEPPGRDLS1SGGRGRHNR
Human MST1R (Ron) Tyrosine kinase receptor for MSP (macrophage-stimulating protein receptor) (Swissprot = Q04912) RFEFQCPSPMNPVRNEPRPL EPPRRTT------------------------
Human NCO1 Transcriptional coressporer (Swissprot = Q7376) , related to SMRT, which also binds 14-3-3 SPSGQSVCGRKLSSKGNRKEQDSRQVPSV
Human NEDD4 L3 ubiquitin ligase Nedd4.2 (Swissprot = Q7235N) NSEQQSSLIGQPSRLASLGQ VTDVADYCAQNLIFPAPAGR
Human NFATC4 (NFAT3) Nuclear factor of activated T-cells (Swissprot = Q14934) AIPGTPASPPASFCGKRRY SGSTTPSSASPLSRSG LGE
Human NOX1 activator of NOX1, a superoxide-producing NADPH oxidase (Swissprot = Q86UR1) WPEGSNLGQDLAQGQRGQL LPPQPRFREDVFPRHRWHLK
Human NRIP1 (RIPT40) Receptor interacting protein of 140 kDa (Swissprot = P48552) KIKRIQLSEWNAAKKRL GSTIMLNVKELALAGLVD QKARRGSSCSNMDNRTTYPQVGEPIFPEEHGC
Human PACS2 phosphofurl acid cluster sorting protein 2 (Swissprot = Q86V53) LVIPSTRSEKAGRGRGST LFADQARQQRNERRANSLDNE
Human PCTK1 PCTAIRE protein kinase 1 [Homo sapiens] (Swissprot = Q00536) VRMRNHPKRIKTEDQKNLK LPADLRELPGYELKTLNSF
Human PDC Phosducin (Swissprot = P20941) LSSQDSPIPPKKEILQRGM SPQSNKQDSERKVRM1
Human PDE3A Phosphodiesterase 3A (Swissprot = Q14432) SUDSSDEKDKLAPKRRLP LLPSQRLVRSQVTTTTSAT
Human PFKFB2 cardiac PFK-2,6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2 (Swissprot = O60825) RDQIP2NFRMNOQTFVRMRNFTPLLSSSNTIIRPRNN VWS
Human PI4KB (PI4KIIIbeta) Phosphatidylinositol 4-kinase III beta (Swissprot = Q9UBF8) RSQSDTRASLSSLNNKRTPA NFKVNEDELRLLSSETEIDN
Human PKP2 Plakophilin 2 (Swissprot = Q09959) QTLAKRGGQTVGYNLNTS VSKYTVYNLHVLKNDVFGORS
Human PPP1R12A (Swissprot = Q14974) ITASKRQDKEKTPAVKSA 5FRLSSLSLEKEDRSGK
Human PRKCE (PKCE) Protein kinase Cep5ion (Swissprot = Q02156) GAESQIQASIFFEPDEKPAP TSPDCQK1KENN1RKA
Saccharomyces cerevisiae Pik1

Saccharomyces cerevisiae Acm1

Xenopus wee1

Drosophila Yki

Drosophila FOXO

Dictyostelium AX4

Caenorhabditis elegans DAF

Ancylosoma caninum DAF

Non-mammalian animal proteins reported to interact directly with 14-3-3 proteins

Non-mammalian animal proteins reported to interact directly with 14-3-3 proteins

Ancylosoma caninum DAF-16 (Dog hookworm DAF16; a forkhead transcription factor (Swissprot = B3G3K1)

Caenorhabditis elegans DAF-16 (Dauer formation protein 16) Forkhead box protein O (AAC47803.1 GI:262943)

Dicyostelium AX4 Ankyrin repeat-containing protein tyrosine kinase A (Swissprot = Q54HC6)

Drosophila FOXO Forkhead box transcription factor (Swissprot = Q9V555)

Drosophila Yki (Yorkie) Drosophila transcriptional activator related to Yap (Swissprot = Q0E8X1) NOT FOUND

Xenopus casp2 Capase-2 from Xenopus laevis (Swissprot = Q08186)

Xenopus weel Xenopus Weel (Swissprot = P47817 for Xenopus laevis Weel1)

Fungal proteins reported to interact directly with 14-3-3 proteins

Saccharomyces cerevisiae Acm1 (APC/C-CDH1 modulator 1) Anaphase-promoting complex (APC) inhibitor (YPL267W)

Saccharomyces cerevisiae Pik1 Yeast phosphatidylinositol 4-kinase NON SWISS PROTO
### Schizosaccharomyces pombe Mei2P (Meiosis protein 2) (Swissprot = P08965)

| Sequence |
|----------|
| IGSSYQMSNFGSVPGLRTFESPAWGTSGYYOVSTSFVAP |

### Plant proteins reported to interact directly with 14-3-3

| Organism | Protein Name | Note |
|----------|--------------|------|
| Arabidopsis | BZR1 | Brassinosteroid receptor (Brassinazole-resistant 1) (Swissprot = Q8S307) |
| | F2KP | Arabidopsis 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (Swissprot = Q8SP17) |
| | KCO1 | AtTPK1 Car(2+)-regulated Arabidopsis vacuole two-pore K(+) channel (Swissport = Q8LBI1) |
| | NIA1 | (NR1, Arabidopsis nitrate reductase 1) (Swissprot = P11832) |
| | NIA2 | (NR2, Arabidopsis nitrate reductase 2) (Swissprot = P11035) |
| | PMA1 | Plasma membrane H+-ATPase (Swissprot = P20649) |
| | SPS | ATSPS1F (sucrose phosphate synthase 1F) (NM_122035.2) |
| | TPS5 | Arabidopsis trehalose-phosphate synthase 5 (Swissprot = Q23617) |
| Medicago truncatula | GS2 | (plastid glutamine synthetase) (Genbank AY225150) |
| Nicotiana tabacum | RSG | (Tobacco Repression of shoot growth; bzip transcription factor) (Swissprot = Q9LRC7) |
| Poplar | NIMA-related kinase 1 (PNck1) (Uniprot Q8SA64) |
| Tomato | SPAK | (Genbank acc. = AF079103) |

### Proteins from bacterial and viruses that interact with 14-3-3 inside eukaryotic host cells

| Organism | Protein Name |
|----------|--------------|
| Polyomavirus | middle T antigen |
| | RKLRLPSLSSNPYVMRSHYPPTRVLQQIHPHLILDEE |

© 2010 The Author(s)
The author(s) has paid for this article to be freely available under the terms of the Creative Commons Attribution Non-Commercial Licence (http://creativecommons.org/licenses/by-nc/2.5/) which permits unrestricted non-commercial use, distribution and reproduction in any medium, provided the original work is properly cited.