

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q702N8	XIRP1_HUMAN	Homo sapiens	Xin actin-binding repeat-containing protein 1	12.075716	T1137;S1174	S205;S208;S213;S295;S332	35254053;31637018	MADTQTQVAPTPTMRMATAEDLPL PPPALEDLPLPPPKEFSKHFHQQRQ ASELRRLYRHIHPERLKNLAEVAE DLAEVLGSEEPTEGDVQCMRWIFEN WRLDAIGEHERPAAKEPVLCGDVQA TSRKFEESGFANSTDQEPTRPQPGG GDVRAARWLFETKPLDELTDGQAKEL EATVREPAASGDVQGTRMLFETRPL DRLGSRPSLQEQSPLELRSEIQELKG DVKKTVKLFQTEPLCAIQDAEGAIHE VKAACREEIQSNAVRSARWLFETR LDAINQDPSQVRVIRGISLEEGARPD VSATRWIFETQPLDAIREILVDEKDF QPSPDLIPPGPDVQQQHLFETRAL DTLKGDEEAGAEAPPKEEVVPGDVR STLWLFETKPLDAFRDKVQVGHQR VDPQDGEHLSSDSSALPFSQSAP QRDELKGDVKTFFKNLFETPLDSIG QGEVLAHGSPSREEGTDGSAQAQGI GSPVYAMQDSKGRHALTSVSREQI VGGDVQGYRWMFETQPLDQLGRSP STIDVVRGITRQEVVAGDVGTARWLF ETQPLEMIHQREQQERQKEEGKSQ GDPQPEAPPKGDVQTIRWLFETCPM SELAEKQGSEVTDPTAKAEAQCTW MFKPQPVDRPVGSREQHLQVSQVP AGERQTDHRVFEFTEPLQASGRPCGR RPVRYCSRVEIPSGQVSRQKEVFQAL EAGKKEEQEPRVIAGSIPAGSVHKFT WLFENCMPMGLAAESIQQGNLLEEQ PMSPSGNRMQESQETAAGTLRTL HATPGILHHGGILMEARGPGELCLA KYVLSGTGQGHYPYIRKEELVSGELPR IICQVLRDPDQDQGLLVQEDPTGQL QLKPLRLPTPGSSGNIEDMDPELQ LLACGLGTSVARTGLVMQETEQGLV ALTAYSLQPRLTSKASERSVQLLAS CIDKGDLSGLHSLRWEPPADPSPVP ASEGAQSLHPTESIIHVPLDPSMG MGHLRASGATPCPPQAIGKAVPLAG EAAAPAQLQNTTEKQEDSHSGQKGM AVLGKSEGATTPPGPGAPDLAAM QSLRMATAEAQSLHQQVLNKHKQG PTPTATSNPIQDGLRKAGATQSNIRP GGGSDPRIPAAPRKVSREEQALPRGL PGGWVTIQDGIYTAHPVRTFDPPGG VQLSQREPQSRHRETALSVQAPRPL QGGPGQSTGPGREEPGGCTQMAWG PPGKAMAEVCPGGLQAAETTLKTAP

							LGRHILASGPQAAGASPHPHNAFVP PPPTLPAAVTGPDFPAGAHRAEDSIQ QASEPLKDLLHSHSSPAGQRTPGG SQTTPKLDPTMPPKKKQQLPPKPA HLTQSHPPQRLPKPLPLSPSFSSEVG QREHQRGERDTAIPQPAKVPTTVDQ GHIPLARCPSGHSQPSLQHGLSTTA PRPTKNQATGSNAQSSEPPKLNALN HDPTSPQWGGPSGEPMEGSHQG APESPDSLQRNQKELOGLLNQVQAL EKEAASSVDVQALRRLFEAVPQLGG AAPQAPAAHQKPEASVEQAFGELTR VSTEVAQLKEQTLARLLDIEEAVHKA LSSMSSLQPEASARGHFQGGPKDHS AHKISVTVSSARPSGSGQEVGGQT AVKNQAKVECHTEAQSQVKIRNHTE ARGHTASTAPSTRRQETSREYLCPPR VLPSSRDSPSSPTFISIQSATRKPLET PSFKGNPDVSVKSTQLAQDIGQALL HQKGVQDKTGKKDITQCSVQPEPAP PSASPLPRGWQKSVLELQTPGSSQ HYGAMRTVTEQYEEVDQFGNTVLM SSTTVTEQAEPFRNPGSHLGLHASP LLRQFLHSPAGFSSDLTEAETVQVS CSYSQPAAQ
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