

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus
Q61818	RAI1_MOUSE	Mus musculus	Retinoic acid-induced protein 1	48.748264	S1714;T1717	S322;S328;T455;S551;S666;T679;S863;S875;S1047;T1051;S1105;S1332;S1343;S1400	22517741;40885482;28135057;34678516;40997131	MQSFRERCGFHKGQNYPQTSQET SRLENYRQPGQAGLSCDRQLLAKD YYSPOPYTYGEGGTGTPSGTVATAAA DKYHRGSKSLQGRPAFPHYQDSSP YPRYSGEGLQTVGGPQPPPPQ PLPGAVSKYEENLMKKTVPVPPNRQ YEQGQPLPFRTHSLHVPVPPQPP LAYPKLQROKQNDLASEPLFPQGS HFPQHSQSFPSTSYAPTVOGGGG AHSYKSCAPSAQPHDRPMSANAN LAPGQRVONLHAYQPGRLGYEQQQ QALQGRHHTQETLHYQNLAKYQHY GQQGGYCPDPAVRTPEQYYQTF PSSSHSPARSVGRSPSYSTPSPLMP NLENFPYSQQPLSTGAFPTGITDHS HFMPLLNPSPTDAASSVDPQAGNCK PLQKEKLPDNLSDLSLQSLTALTSQ VENISNTVQQLLSKATMPQKKGVK NLVSRTPQEHKSQHCSPGEGSYSAE PAGTLPSEPPSSTPQSTHAEPQDQDY LSGSEDLERSFLYCSQARGSPARV NSNSKAKPESVSTCVTSPPDMSTK SDDSFQSLHSTLPLDSFSKVFAGER DCPRLLSALAQEDLASEILGLQEAI VEKADKAWAEASSLPKDNKPPFSL ENHGACLDTVAKTSWSQGEPELTP EPLQDKGGSTKDFSPGLFEDPSVA FATTDPKKTSSSLSPFGTKPLLGTATP DPTTAADFCDPDTPTASSVDGANPF AWPEENLGDACPRWGLHPGELTKG LEQKAKASDGVGKADAHEASACMG FQEDHAIGKPAALSGDFKQQAEG VKEEVGGLQCPVAKANQWLEES RHCCSSTDFGDLPLPPPPGRKEDLE AEEYSSLCCELLGSPEQRPSLQDPLS PKAPLMCTKEEAEEALDTKAGWVSP CHLSGEPVLLGSPVGAQSKVQSWF ESSLSHMKPGEEGPEMERAPGSSG TSQGLAPKPNKPAVPEGPIAKKEPV PRGKLSRRVHRGLPEAEDSPCRV PALPKDLLLPESCTGPPQQAEGAG APGRGLSEGLPRMCTRLTALSEPQ TPGPPGLTTTPDPKLGKQRAAFK SGKRVGKPSKAASSPSNPAALPVAS DSSPMGSKTKEPDSMPPGKDQRS MVLRSRTKQQVFHAKRRRPSERI PDCRATKLPANNHLPTAYKVSSGP QKEGRMNQRVKVPKPGTGKLSDR PLHTLKRKSAFMAPVPAAKRSLLRS NNGSGDGREERAESSPGLRRMA SPQRRARPRGSGEPVPPPPLEPPAAC MGLSTQSSLPASAVRTKVLPRKGRG LKLEAIVQKITSPGLKKLACRVAGAP PGTSPALPERRPGGSPAGAEGL GGMGQMLPAASGADPLCRNPASRS LKGKLLNSKLLSAADCPKAEAFMS PETLPSLGTARAPKRSRKGRTGLG PSKGPLEKRPCGQPLLLAPHDRAS STQGGGEDNSSGGGKPKTEELGPA SQPPEGRPCQPOTRAQKOPGQASY SYSKRKRLSRGRGKTAHASPCKGRA TRRROQVPLDPAEPEIRLKYISSC KRLRADSRTPAFSPFVVEKRDAYTT ICTVNSPGDEPKPHWKPSSSAASS STSSSLEPAGASLTFPGGVLQQR PSLPLSSTMHLGPVSKALSTSLVC CLCQNPANFKDLGDLCPYYPHCL PKKPKLKEKARLEGTLEASPLER TLKGLECSASTAAAPTATITPTAL GRLSRPDGPADPAKQGPLRTSARGL SRRLQSCYCCDGGDGGEEVAQAD KSRKHECSKEAPTEPGGDTQEHVW HEACAVWTSVGVLVAGKLFGLQEA MKVAVDMPCTSCHEPGATISCSYKG CIHTYHYPCANDTGCTFIEENFTLKC PKHKRLPL	True	False	1.962	5.0	False	False	False