

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	ext ref
015084	ANR28_HUMAN	Homo sapiens	Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A	34.490536	T1009	S1007;S1011	40914422;37217939;28657654	MAFLKLRDQPSLVQAIFNGDPDEV ALIFKKEEDVNFQDNEKRTPLHAAAY LGD AEIHELLILSGARVNAKDSKWL T PLHRAVASCSEAVQVLLKHSADVN ARDKKNWQTPLHIAAANKAVKCAEAL VPLLSNVNVSDRAGR TALHHA AFSG HGEMV KLLL SRGANINAFDKKDRRA IHWAAYMGHIEVVKLLVSHGAEVTC KDKKSYTPLHAAASSGMISVVKYLLD LGVDMNEPNAYGNTPLHVACYNGQ DVVVNELIDCGAIVNQKNEKGF TPL HF AAASTHGALCELELVGNGADV N MKS KDGK TPLHMTALHGRFSRSQTI IQSGAVIDCEDKNGNTP LHI AARYGH ELLINTLITSGADTAKRGIHGMFPLH LAALSGFSDCCRKLLSSGFDIDTPDD FGRTCLHAAAAGGNLECLNLLLNTG ADFNKKDKFGRSPLHYAAAANCNYQ CLFALVSGSASVNDLDERGCTPLHY AATSDTDGKCLEYLLRNDANPGIRD KQGYNAVHYSAA YGHR LCLQLIASE TPLDVL METSGTDMLS DSDNRATIS PLHLAAYHGH HQALEVLVQSLDLD VRNSSGRTPDLAAFKGHVECDV L INQGASILVKDYILKRTPIHAAATNG HSECLRL LIGNAEPQNAVDIQDNGG QTPLMLSVLNGHTDCVYSLLNKGA NVDADKDKWRTALHRGAVTGHEEC VDALLQHGAKLLRDSRGRTPHILS AACGHIGVLGALLQSAASMDANPAT ADNHGYTALHWACYNGHETCVELL LEQEVFQKTEGNAFSP LHC AVINDN EGAAEMLIDTLGASIVNATDSKGRTP LHAAAFTDHVECLQLLLSHNAQVNS VDSTGKTPLMMAAENGQTNTVEML VSSASAELTLQDNSKNTALHLACSK GHETSALLILEKITDRNLINATNAAL QTP LHVAARNGLT MVVQELLGKGAS VLAVDENGYPALACAPNKDVADCL ALILATMMPVSSSSPLS SLTFNAINR YTNTSKTVSFEALPIMRNEPSSYCSF NNIGGEQEYLYTDVDELNDSSEY	True	False	4.408	4.468	1.111	0.603	0.188	1.134	0.7