

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	extracellular region
F1M3W5	F1M3W5_RAT	Rattus norvegicus	NaN	28.175057	NaN	NaN	18683930	MHLHQVLTGAVNPGDNCYSVGSVGV EVPFTAYGSGCDIVILASDFECVQIIP GAKHGNIQVSCVCECSNQHGRVAASY GNAVCFIFEPLGINSHKRNSQLKCQW LKTGQFFLSSVTFNLAWDPOQDNRL TATDSIQLWAPPGSDILEEEEEVDNK VPPVLNDWKCIWQCKTSVSIHLME WSPDGEYFATAGKDDCLLKVWYPM TGWKSSIIPQDPHEVKKRRRASTQFSF VYLAHPRAVTGFSWRKTSKYMPRGS VCNVLLTSCHDGVCRLWAETLLPED CLLGEQICETTSSVASNLSSAGKHK DRIQHALETIHHLKNLKRGQRRSSV LVTHAELMPDKTATHEVHRHISHHA NALCHFHAASINPATDIPNVLVGTA FNIDDINGGFVHWLNNKEFHFTSS TEIFMHQLRKLSEKQLDHESDDADR EDDERSQEERERGLRMKLDHELSD DRESEAGTGSSEHEDGEREGSPRTH PRPSVSLPPTVLLDRKIETLLEWN KNPDMLFTIHPVDGTFVWVHKYLD EYNPGIFRQVQVFSRIPVAFPSGD ANSLSKNIMMYACVNATKDSYSTTS QPELMSVDSSHGSQPHYTSHSTDW NILAPTVMVMVSKHIDGSLNQWAVTF ADKSAFTTTLTVSHKFRYCGHRFHL NDLACHSVLPLLLTSSHHNALLTPE ADCQWDTDSKLNRLIDPVKHTKGSS KQPLRNAATRTFHDPNAYSELILWR VDPIGPLSYTGGVSELARINSLHTSA FSNVAWLPTLIPSYCLGTYCNSASAC FVASDGKLNRLRYQAVVDARKLLDEL SDPEASKLIGEVFNIVSQQSTARPGC IIELDAITDQCGSNTQLLHVFDQDFII GYKPKHEDMEKKEKETEIFFQPSQG YRPPPFSEKFFLVVIEKDGNNNSILH MWHLHLQSVQACLAKAAEGISSDSL LSVPGQKNMESSETSSSVSMPHS SSIANLQTASKLILSSRLVYSOPLDLP EAVEVIRATPSAGHLSSSIYPVCLAP YLVVTTCSDNKVRFWKCCMETNSP CSSSGENETYHWRRWPLMNDEEK DNSSTVSIVGRPVAVSCSYTGRLAVA YKQPIHHNGFISKEFMSHVCIFECES TGGSEWVLEQTIHLDDLKVGSVLD SRVSVDSNLFVYSKSDAFLSKDRYLI PNIKHLVHLDWVSKEDGSHLTVGV GANIFMYGRLSGIVNDQTNKDGVA VITLPLGGSIKQGVKSRWVLLRSIDL VSSVDGTPSLPVSLSWVRDGILVVG MDCEMHVYAQWKHSVKFGDVEAD SPVEQTIIQDHSFAFKSSMLTRKSIAE GAAIPDDVFCSPVTVQDGGLEFAAH ALSPTLPQYHPTQLLEMDLGKVR AKAILSHLVKCIAGEVAIVRDPDAGE GTRKRLSRTISVSGSTAKDTVTIGKD GTRDYTEIDSIPPLPHALLAADQDT SYRISEDSAKKPQSYEDHIESQPEDQ YSELFQVQEITTDIDDLEPEKRENKS KVINLSQYGPAYFGQEHARVLSHSL MHSSLPGLTRLEQMFLVALADTVAT TSTELDENRDKNYSGRDLDLDECGLR YLLAMRLHTCLLTSPLPLYRVQLLH QCVSTCHFAWAFHSEAEELINMIP AIQRGDPQWSELRAMGIGWVVRNV NLRRCIEKVAKAQFQRNDALDAA LFYLSMKKKAVVWGLFRSQHDEKM TTFFSHNFNEDRWRKAALKNAFSL GKQRFESAAFFLLAGSLKDAIEVCL EKMEDIQLAMVIARLFESEFETSSTY ISILNQKILGCQKDGTFNCKRLHPD PFLRSLAYVWMKDYTRALDTLLEQT PKEDDEQQVIKSCNPVVFYFNYLR THPLLRNRLASPEGTLATLGLKTEK	False	False	1.184	1.095	1.074	0.797	0.422	0.949	0.6

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DFVSERMENGPSESKPVSSSDGGSG  
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