	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
0	A0A0G2K3H2	A0A0G2K3H2_RAT	Rattus norvegicus	NaN	23.439218	NaN	NaN	38843836	MAERRAFAQKISRTVAAEVRKQISG QYSGSPQLLKNLNIVGNISHHTTVPL TEAVDPVDLEDYLITHPLAVDSGPLR DLVDFPPDDIEVVYSPRDCRTLVSAV PEESEMDPHVRDCIRSYTEDWAIVV RKYHKLGTGFNPNTLDKQKERQKG LPRQVFESDEAPDGNSYPDEQDDLK RRSMSIDDTPRGSWACSIFDLKNSL PDALLPNLLDRTPNEEIDHQNDDQR KSNRHKELFALHPSPDEEEPIERLSV PDVPKEHFGQRLLVKCLSLKFEIEIE PIFASLALYDVKEKKKISENFYFDLN SEQMKGLLRPHVPPAAITTLARSAIF SITYPSQDVFLVIKLEKVLQQGDIGE CAEPYMIFKEADATKNKEKLEKLKS QADQFCQRLGKYRMPFAWTAIHLM NIVSSAGSLERDSTEVEISTGERKGS WSERRNSSLVGRRSLERTASGDDAC NLTSFRPATLTVANFFKQEGDRLSD EDLYKFLADMRRPSSVLRRLRPITAQ LKIDISPAPENPHYCLTPELLQVKLYP DSRVRPTREILEFPARDVYVPNTTYR NLLYIYPQSLNFANRQGSARNITVKV QFMYGEDPSNAMPVIFGKSSCSEFS KEAYTAVVYHNRSPDFHEEVKVKLP ATLTDHHHLLFTFYHVSCQQKQNTP LETPVGYTWIPMLQNGRLKTGQFCL PVSLEKPPQAYSVLSPEVPLPGMKW VDNHKGVFNVEVVAVSSIHTQDPYL DKFFALVNALDEHMFPVRIGDMRI MENNLESELKSSISALNSSQLEPVV RFLHLLLDKLILLVVRPPVIAGQIVNL GQASFEAMASIINRLHKNLEGNHDQ HGRNNLLASYIYYVFRLPNTYPNSPS PGPGGLGGSVHYATMARSAVRPASL NLNRSRSLSNSNPDISGTPTSPDDE VRSIIGSKGLDRSNSWVNTGPKAAP WGSNPSPSAESTQAVDRSCNRMSS HTETSSFLQTLTGRLPTKKLFHEELA LQWVVCSGSVRESALQQAWFFFEL MVKSMVHHLYFNDKLDAPRKSRFP ERFMDDIAALVSTIAGDVVSRFQKDT EMVERLNTSLAFFLNDLLSVMDRG FVFTLIKSCYKQVSAKLYSLPNPSVL VSLRLDFLRIICSHEHYVTLNLPCSL LTPPASPSPSVSSATSQSSGFSTNVQ DQKIANMFELSLPFRQQHYLAGLVL TELALILDPDAEGLFGLHKKVINMV HNLLSSHDSDPRYSDPQIKARVAML YLPLIGIIMETVPQLYDFTETHNQRG RPICIAPDDYDSESGSMISQTVAMAI AGTSVPQLTRPGSFLLTSTSGRQHTV TFSAESSRSLLICLLWVLKNADETVL QKWFTDLSVLQLNRLLDLLYLCVSC FEYKGKKVFERMNSLTFKKSKDMR AKLEEAILGSIGARQEMVRRSRGQL ERSPSGSAFGSQENLRWRKDMTHW RQNTEKLDKSRAEIEHEALIDGNLAT EANLIILDTLEIIVQTVSVTESKESILG GVLKVLLQSMACNQSAVYLQHCFAT QRALVSKFPELLFEEETEQCADLCL RLLRHCSSSISTIRSHASASLYLLMR QNFEIGNNFARVKMQVTMSLSSLV GTSQNFNEEFLRRSLKTILTYAEEDL ELRETTFPDQVQDLVFNLHMILSDT VKMKEHQEDPEMLIDLMYRIAKGYQ TSPDLRLTWLQNMAGKHSERSNHA EAAQCLVHSAALVAEYLSMLEDRKY LPVGCVTFQNISSNVLEESAVSDDVV SPDEEGICSGKYFTESGLVGLLEQAA ASFSMAGMYEAVNEVYKVLIPIHEA NRDAKKLSTIHGKLQEAFSKIVHQST GWERMFGTYFRVGFYGTKFGDLDE QEFVYKEPAITKLAEISHRLEGFYGE RFGEDVLEVIKDSNPVDKCKLDPNK AYIQITYVEPFFDTYEMKDRITYFDK	False	False	1.856	2.781	0.847	0.853	1.267	1.269	1.12

								NYNLRRFMYCTPFTLDGRAHGELH EQFKRKTILTTSHAFPYIKTRVNVTH KEEIILTPIEVAIEDMQKKTQELAFAT HQDPADPKMLQMVLQGSVGTTVNQ GPLEVAQVFLSEIPGDPKLFRHHNK LRLCFKDFTKRCEDALRKNKSLIGP DQKEYQRELERNYHRLKEALQPLIN RKIPQLYKAVLPVTCHRDSFSRMSL RKMEL									