

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
D4A885	D4A885_RAT	Rattus norvegicus	NaN	23.439218	NaN	NaN	38843836	MGHAGRFQFQALLWKNWLCRLRHP VLSLAEFFWPCILFMILTVLRFQEP RHRENCYLQARDLPSRGVLPFVQGL LCNTGSRRCRNFESMDHRFRLPR FQTASDDRRKSSLAFLNEIQDLAEEI LETMDKAKNLQKLWLKRSETPGSSY GSSFLTTLNKTEDVISKLESLHQQP HIWDFLRSPLRLHTSSVHLEDSMGA VTHFLQAGLNSLASLGDLDWLP HQ TIPQVSRHVLNVTVSTLRFQQHGA AVNETVYHLSLKNMLWDPQKVQSD LRYQFGFNDLQVQHILNYSAKREEIP THSFLERMVCSILSNTSEDEAQSRS YQADCHPKWSAVKNIHIVSWPKL YGQVFDQWQQGSLRQNL LAGTSHS LAALRDQFKQSESWKVVEALHTAL LILNDSLAVDGPGDNLHLPQIFQDL DKLQHALSELSPWPSLKRPLLDTV LRNVVSDLQFVQEVLSYLSERSARD FIPAGSEGWRLKDVFFQGLNQLLT KNASTFCLNGHLSQEAPLPTWNASL WRSVWGVLCHTPSFNETSILNKLLR AVKGAGRSLQAVIAGHTNRSVSEHG GHFGWQDLGAQLSEVSFACSRVFO FPRAAASAENNVSPGCENQLVSTV VSHILGEVQMSMQMSYWEIISGIIR KTCELARYVNMHGSFQNSLISFSED SPCDTQNMMDWKVVDNYFVFFNNF KKSPTISITRAFNFTHLLVVDKLDI LESGQMNILLSFVEFLEKLLSNPSGS FTPPEFHNLSSFSELVLRNSVSWKN HFKSLKADSAAAAAQAQKLEFDKMV IEKIQRFKNHWMGQESKNTLRFIELI ILEINSELQEFWLNGISQEERANIEIL SRLVNFVADYEKNFFKSFNFSQLF HSNWPRSPARNADFIHLSSETIHSLY ELSFLTQEQVSIALNTIYALQNTSEF FSALSEPQKQELDNLLTHTYINVKFD KDIALFLKTFSSFYQYLHKFLNIQNR EPLITYLTQVSRHILDLIKQFNQNLR RAFLLSEATEALGTIPEVSYCRQLL SIFSLLELEAQLMARGGPAEAVIHA SLTGLKQLFSADEGFRVSLLOQYVAQ FLNGSAETLLANECFLKNATISSVN YSGNEGSSLPPWTQFFSNLSVNGS EISEFTAIHCTLSWIQTWTEIWGSIS QIFKLDQSIFTPLHVGITQLDDDLGN GRDISKDCQGIVPTYHTARLILNLFK NVTQENGFDWDDLQNLRLDLWVT FDNELTAVQSLNLDQVEKSFITMET SLHQLKTFPMKINASREFLYPLFDVF LELSKASDYVDRDELINFLSTNLT DHRAEFASVITELRETILLLRNVSQG RALSSCADIFQRVTELI FESLLPAN TSNKPAILAMLSSVFSSKNTSSSLE GCIAWTDIINRLCICMNSSSLPRHSH SLLGNFKDIGNKMSYVLKILTWMLN KKVPTCPWNESNIHCINIYKIDITDF LNIILATGLEKENVPNVEILLALFND STRQVGMITNLTKELNVAQSNSWK HFKDLLLLRPIEMSDDIPDQFQKIWO HIELGKEMQALLKGIFPSVLGKNSS SDIETMFSVFSTSPKERDINH LGSI YNLANYFAVNLTHNLQNSSEVVPHE ILKAVDLGIQLTRDVFNSLMPAVRFN IPQNSDHAQALKKVTSLMHSLKKAD IDLLVGQLGENSEILMSFFKNLSRSG INSLGINTLVGLLEKFDVSSHSWSVS QLLRLSRLPKDVVDTVLDVYYALPH IVGLLQRITDKNITESLRDVYNFTLL HGIAMFNITKEDFADVAKTLRDTVE LVSDEPTVVPEVLMCLSRWCSNYT TLRLERNPKVEGCNIQRHMSSSFLR	False	False	False	0.796	0.807	0.707	0.724	3.238	0.997

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