

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
F1MAS4	F1MAS4_RAT	Rattus norvegicus	NaN	23.439218	NaN	NaN	38843836	MAPSSPRVLSALVLLAAAAALPALGLG AAAWELRVPGGARAFALGPGWYSL DTTRTPRELLDVSREGPAADQLLGL GAGTRGCARLAGRLLPLQVRLVARG APTAPSLVLRARAYGARCGVRVLSRS ARGTELRRAIRSVPLGDALCFPAS GGGAASLTSVLEAITNFPACSCPPVA GTRCRRGPICLRPGGSAGLRRLVCAL GRAAGAVWVELVVEATSGTPSESPS VSPSSLNQSQPRAQVRRRSGAGS STSPQFPLPSYQVSVPENEPAGTAVI ELRAHDPDEGEAGRLSYQMEALFDE RSNGYFLIDATTGAVTTARALDRETK DTHVLKVSVDHGSRRSAAATYLTV TVSDTNDHSPVFEQSEYRERIRENL EVGYEVLTRATDGDAPSNNMRYR LLEGAGGVFEIDARSVVRTRAVVD REEAAEYQLLVEANDQGRNPGPLSA SATVHIVVEDENDNYPQFSEKRYVV QVPEDVAVNTPVLRVQATDRDQGO NAAIHYSIVSGNLKGFYLSLHSLGSL DVINPLDFEAIREYTLRIKAQDGGRP PLINSSGLVSQVLDVNDNAPIFVSS PFQAAVLENVPLGHSVLHIQAVDAD AGENARLQYRLVDTASTILGGSSIDS ENPVSAPDFPFQIHNSGWITVCAE LDRELLEHYSFGVEAVDHGSPPMSS SASVSITVLDVNDNDPVFTQPVYELR LNEDAAGVSSVLTLRARDRDANSVI TYQLTGGNTRNRFALSSQSGGLITL ALPLDYKQERQYVLAVTASDGTRSH TAQVFINVTDANTHRPVFQSSHYTE SVSEDRPVGTSIATISATDEDTGENA RITYVLEDPVPQFRIDPDTGTIYTMTE LDYEDQAAAYTLAITAQDNGIPQKSDT TSLEILILDANDNAPRFLRDFYQGSV FEDAPPSTSVLQVSAATDRDSCPNR LLYTFQGGDDGDGDFYIEPTSGVIRT QRRLDRENVAVYNLWALAVDRGNP NPLSASVEVQVTVDINDNPPVFKEK DELELFVEENSPVGSVVARIRANDP DEGPNQAQIMYQIVEGNVPEVFQLDL LSGDLRALVELDFEVRRDYMLVVQA TSAPLVSRAVHIRLLDQNDNPPPELP DFQILFNHYVTNKSNSFPSPGVIGRIP AHDPLDSDSLNYTFLQGNELSLLLL DPATGELQLSRDLNRRPLEALMEV SVSDGVHVSVALCTLRVTIITDDMLT NSITVRLNMSQERFLSPLLSLVEG VATVLSITKDDIFVFNQNDTDVSSN ILNVTFSALLPGGARGRFFPSEDLQE QIYLNRTLLTTISAQRVLPFDDNICLR EPCENYMKCVSVLRFDSSAPFISSTT VLFRRPHIPITGLRCRCPPGFTGDYCE TEIDLCSNPGANGRCRSREGGYT CECFEDFTGEHCQVNVRSGRCSAG VCKNGGTCVNLIGGFHCVCPPGEY EHPYCEVSTRSFPQSFVTFRGLRQ RFHFTVSLAFATQDRNALLLYNRF NEKHDFIALEIVEEQQLTFSAGETT TTVTPQVPGGVSDGRWHSVLVQYYN KPNIGHLGLPHGPSGEKVAVVTVDD CDAAVAVHFGSYVGNYSCAAQGTQS GSKKSLDTGPLLLGGVNPDPEDFPV HSRQFVGCMRNLSIDGRIVDMAAFI ANNGTRAGCASQRNFCDTLQNG GTCVNRWNTYLCECPLRFGGKNC QAMPHQRFTGESVSWDLITISV PWYLGLMFRTRKEDGVLMEATAGT SSKHLQILNSYIRFEVSHGPSDVAS MQLSKTRVTDGGWHLLIELRSAGE GKDIKYLAIMTLDYGMQSTVQIGN QLPGLKMRITVIGGVSEDKVSVRHG	False	False	1.117	2.817	0.764	1.141	0.905	4.38	1.318

FRGCMQGVVRGETSTNIATLNMND  
ALKVRVKDGCDEDPASSPCPPHS  
HCRDTWDSYSCICDRGYFGKCVDA  
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NPVCGPCHCAVSSQGFDPDCNKTNG  
QCQCKENYKPPAQDACLPCDCFPH  
GSHSRACDMDTGQACKPGVIGRO  
CNRCNPFPAEVTSLGCEVIYNGCPR  
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VGNVVRHCSGEGKWLPELFNCTS  
GFFVDLKAMNEKLSRNETRMDGNR  
SLRLAKALRNATQRNSTLFGNDVRT  
AYQLLARILQHESQQQGFDLAATRE  
ANFHEDVVHTGSSLLAPDTEAAWE  
QIQRSEAGAAQLLRHFEAYFSNVAR  
NVKRTYLRPFHIVTDNMILAVDIFDKL  
NFTGAQVPRFQDVQEEFPRELESSV  
SFPADTFKPEKKEGPMVRLTNRRT  
APLTAQPEPRTERETSFSRQRHPD  
EPGQFAVALVVIYRTLQQLPEHYDP  
DHRSLRLPNRPVINTPVVNAMVYSE  
GTPFPSSLQRPVLVEFSLLETEERSK  
PVCVFWNHSLDIGGTGGWSAKGCE  
LLSRNRTHVTCQCSHSASCAVLMDI  
SRREHGEVLPLKIITYAALSLSLVALL  
VSFVLLSLVRTLRNLSIHKNLIAA  
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VTATWLLGLLAVNSDTLIFHYLFAAF  
SCLQGIFVLLFHCVTHREVRKHLRA  
VLAGKHLHLLDSDATTRATLLTRSLN  
CNNTYSEGPDMLRTGLGESTASLDS  
TTRDEGVQKLSVSSGPARGNHGEPD  
SSFIPRNSKKAHGPDSDSSELSLDE  
HSSSYASSHTSDSEDDGGEAEDKW  
NPAGGPAHSTPKADALANHPAGW  
PEESLAGSDSEELDTEPHLKVETKVS  
VELHRQAQGNHYGDRASDLESGVL  
AKPVAVLSSQPQEQRKGLKNKVYTP  
PPLPEQPLKCRRLREKLADCEQSPTSS  
RTSSLGSGDGVHATDCVITIKTPRE  
PGREHLNGVAMNVCTGSAQADGSD  
SEGSNETSI