

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
E9Q842	E9Q842_MOUSE	Mus musculus	NaN	25.875327	S1529	NaN	30059200	MPAILVASKMKSGLPKPVHSAAPILH VPPARTGPQPCYLKLGSKVEVSKTAY TSQIPLKSQLQEPTGEGLLPKSSS LENGFDTQIYTDWANHYLAKSGHKKR LIKDLQDVTDGVLLAQHHQVVANDK IEDINGCPKNRSQMIENIDACLNFLA AKGINTQGLSAEEIRNGNLKAILGLF FSLSRKQQQQQQQQQPEKQPLSSS PLPPAGSQVAGAPSQCQAGTPQHQQ LATPQAPCQLLQPVSHQQGKTQVE MQSRLPGPTARVAAAGSEAKTRGGS AAANNRRSQSFNNYDKSKPVTSPPP PAPPSNHEKEPLASSASSHPGMSSE VPAPLENSPSPVNCSSSAIPQPSMT SKPWRSKSLSVKHTATSAMLVSKPA GPEAPRPTPEAMKPAAPNNQKSMLE KLKLFNSKGGSKAGEGASRDTSCE RLEILPSFEETELEATANRALSTVG PASSSPKIALKGIAQRTFSRALTNKK SSPKGNEKEKEKQOREKEKEKEKEK GKDLTKRVSVTDRPDLKEETKADLS GVAVTEMPKSSKIASFIPKGGKLNLS TKKEATAPSHSGIPKPGMKNVSAKS PSAPIPPKEGERSRGKLSGLPPQKA QLDSRHSSSSSLASSEGGKGGGTS LNPSISSQTVSGSVGTTQTGNTVS VQLPQPQQYNHPNTATVAPFLYRS QTDTEGNVTAESSAGVSMEPSHYT KSGQPALEELTEDPEARRLRTVKNIA DLRQNLEETMSSLRGTQVTHSTLET TFDTNVTTEISGRSILSLTGRPTPLS WRLGQSSPRLQAGDAPSMGNGYPP RANASRFISAEAGRYVYSAPLRRQLA SRGSSICHVDVSDKADDDVDLEGIS MDAPGYMSDGDVLSKNIRSDDITSG YMTDGGGLGLYTRRLNRLPDGMAVV RETLQRNTSLGLGDADSWDDSSSVS SGISDTIDNLSTDDINTSSISSYANT PASSRRNLDVQTAEKHSQVERNLSL WGGDDIKKSDGGSDSGVKMEPGSK WRRNPSDMSESDKSVSGKKNPVL SQTGSWRRGMTAEVGITMPRTKPSA PTGTLKTPGTGKDDAKVSEKGRSL PKASQVKRSPSDAGRSSGDESKKTL PSSSRTPTVNANSFGFKKQSGSAAG LAMITASGATVTSRSATLGKIPKSSAL VGRPTGRKTSMDGAPNDDGYSLSL SRTNLQYRSLPRPSKNSNRNAGNR CSTSSIDSNMSSKSAGLPVPKLRPS KASLGSSLPGLVNQTDKEKGISSDSE SVASCNSVKVNPATQPVSSSAQATL QPGTKYADVASPTLRLRFGGKPKPI ATAETMKS AVVISNPHATLTQQGNL ESPSGSGVLSGSSSPLYSKNVLDN QSPASSPSSAHSGPSNSLTWGTSS SAVSKDGLGFQSVSLHTSCESIDIS LGGGGLSHNSSPGPVASTKEDSLM PFVRTSSVKTTLSEPLSSPAASPKF CRSTLPRKQSDPHLDRNTLPKKGL RYTPTSQLRTOEDAKEWFRSHSAGG LQDTATNSPFSSGSSVTSPSGTRFNF SQLASPTAVTQMSLSNPTMLRTHSL SNADGQYDPYTDSEFRNSSMSLDEK SRTMSRSGSFRDGFEEVHGSSLSLV SSTSIYSTPEEKQSEIRKLRRELD SQEKVSALTTQLTANAHLVAAFEQS LGNMTIRLQSLTMTAEQKDESELNEL RKTIELLKKQAAAAQAAINGVINTPE LNCKGNLSAQATDLRIRRHSSSDSV SSINSATSHSSVGSNIESDSKKKKRK NWSVQLRSSFKQAFGKKKSPKSASS HSDIEEMTSSSLPSSPKLPHNGSTG STPLLRNAHSNLSISECMDSEAEV MQLRNLDRKEMKLTDIRLEALSSA	None	None	None	None	None	None	None		

HQLDQLREAMNRMQSEIEKLKAEN
DRLKSESGGCSRAPSQVSIASPR
QSLGSLQHSNLNLTSTSLDMLLDDT
GEC SARKEGGRHVKIVVSFQEAMK
WKEDSRPHLFLIGCIGVSGKTKWDV
LDGVVRRFLFKEYIVHVPVSQLGLSS
DSVLGYSIGEIKRSNAETPELLPCG
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GTGKTYLANRLESEYVVLREGRELT
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QCENSENAVDMPLVILDNLHHVSS
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TSSTPNLQLHHNFRWVLCANHTEP
VKGFLGRFLRRKLMETEISGRVRNA
ELVKIINWIPKVWHHLNRFEAHSS
SDVTIGPRLFLSCLPIDVDGSRVWFTD
LWNYSIIPYLLEAVREGLQLYGRRAP
WEDPAKWVMDTYPWAASPQHEW
PPLLQLRPEDVGFYSLPREGSTSK
QVPPSDTEGDPLMNMLMRLQEAAN
YSSPQSYDSDSNSNSHHDDILDSSL
ESTL