

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
A8JV18	A8JV18_DROME	Drosophila melanogaster	NaN	27.156312	NaN	NaN	28604694	MEDAQEORESSQAEALAKKHPLTPLK ELPEESEEEEEDESSAGALRES SNNSIMGKMKMRVSSILPASLSGWF SPSSKDGNDALSSPANLRQSQPRQS NGRLTTKRKRGRRRRIMLAEVDADAA DDLDDGSDAKGLNYEEVALADNIAE HDLAAEEDQTRRSEYNVFLLRKRAG AVAAAGGDEDEAEDELEDEDEDG DEEDDDEEQENLQSSAAVQTKRRR LELETPVNLPMRRLPLLSSTPAAPL AAATSSSSSQMYKGVSHIAPHRNRH LNLYGSQRQREPAYNFFTGNAAEAG STGDLPHSIRRSNLNIPFGSSTATSY NNSLSSLPNHKRPSLIGKQTHRRDL TMDETGTGPAMSSEHLNHLRISR TNNNTSNNNNNNNNNNNNVIETKT RRSELSAAAGGCGDSQSESDMNEY HDNGEGHDGLRPSHYNSNSNLEFY GNLQSSKSIFNRSNTAAQSHRNST WSLNSLTQRRRFNASIYGSTSALSD SRLLSGSASNSGSASASSSPFYQGRT TFGGNSGNRNLFSRSNLSSSAASSM LGLNSAGSSPAHQLHASMTGGIGYG MKAVDMRPSDGS LAETS VVGGS KKPGTGLSNTTMRILNLLESYSTPLI DAKRMGSSIKEHOSSRQROGTPAT PYLRSTSASRNVSVPNHINELAE LRS NKLLVPTMQQLLERRRLHRTQNS RDVVHSQNV RAGGENNQEKPKPTA PYVAPIDQSANHTQHTNKMRSLSH QTRNKETRAEEEEAPPPLDLQISFP DMASAPKFDLIIKPTVPVSKPSTTD PIQSSKSSNTNLSTTNSKQMPNFLA NPQPAAPIVNFAANGVSAISKPSKR TFTFSEPTPLSNFQENCIPKPKINRK YTFSAPAPLDDL RITNKQSQPTINGT PSSKEWECDTCMVRNKPEINKCVA CETAKPVASAAPVQAPLPPSTAAIDT QSFVGFGRFKKSTTAWECDACML SNKAEASKCIACETPRKTVAPKVNN FSPLITNAKSNEWECVCLVRNKVE VSKCVACESAKPGATMALPATSNIAV ATPSIITDGFGRFKKSATAWECDAC MLSNKAEASKCIACETPRKSSTPIAN SSYPSINNNLPAGSGFDISFTRKAN MWECQTCLVMNKSSDEECIACQTP NSQARNSNSEALISSISSSSASFSG SLSRPSSRSSSGSTSTCGSVCSGSIV SISSTTESAKALS AKKVPKPDAGFQ QLVAAQKTSTWECEACLAKNDMSR KTCICCEQMMPEAFNPAATTANSAA SSVPKFRFGFHVKEVVKPSVETTTT PAPTSAQFSFGQSNQKDVADSK KTEAPKTFMFGVSKVEEPTVVSFGT GIKETTATSSTEATAPTPAAAAPPV QFVFKAPTATTASSLTTTITTSNAP ALGGFSFGAPSSSTVSSSTTSTSAN PAAVKPMFWSGAGSAVSSSTSSSQ PVAKAPTLGFGVSSSTVTTTSTKV FAFTPASGLDPAATSAPAAGAGFSF GSQSKPATTQNTGTFFFGQPTAVAP ATPTNPSVSSIFGAPATSTASTSVSA TTSTSTANAIASSFAPSTPQLFGNW GEKTDLTTFGASSGSGTTTTPSFG WSSNGDAKSN SAAVGSAAVPSSSA STMATPIFGSSSMFGPSSSNNTTST STSLPFGSAATTAATTPAGGNAALT GLFGNVGNSLAGVAPVATTPAATA AAPLTNIFGNPTVAAAAPVFGSGST IPSAGFGAPAAAAPLAAPALPGA FNF GGATAATPAASSAPFVFGSSTNEPLA KPSFNFTGSAASSTAPAPAFNFTANT AATNNPSGGDSHPRIQFGSSQPAA NNQFGGAGGATNNSAGGMPMFNF SPGAPQMOSTPNANALFQFSATSTA	None	None	None	None	None	None	None		

