

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
A0A0B4LGL0	A0A0B4LGL0_DROME	Drosophila melanogaster	NaN	25.496522	NaN	NaN	33925313	MAQPQLLQIKLSRFDAQPWGFRLOQ GTDFAPQLLVQKVNAGSLSEQAGLQ PGDAVVKINDVDVFNLRHKDAQDIV VRSGNNFVITVQRGGSTWRPHVPT GNVPOPNSPYLQTVTKTSLAHKQQD SQHIGCGYNNAARPFNSGGDGGVK SIVNKQYNTPVGIYSDESIAETLSAQA EVLAGGVLGVNFKKNEKEYQGDRSE VLKFLREEETGQSTPAFGNSHYEHD APQQLQPPQQYNOHQHYHQQQ QQQSSSTRHVSAPVNSPKPPSTGG LPTGQNICTECERLITGVFVRIKDKN LHVECFKCATCGTSLKNQGYNFN NKLYCDIHAKQAAINNPPTGTEGYVP VPIKPNTKLSASTISSALNSHGYGGH SNGYSNGNSTPAPAPVNOGYARPFQ AAAPKSPVSYPPQQQQSPRPAPGG QNPYATLPRSNVGGQGGAEVEELQP EFEEDCYEMDIEVALAASRQSQRG SSFVWPPQDDSHLAPTAAPLYIPPP ETQHVVVSNPVQQVPLPPGGATAR LDPQPVVGTSSANGAPQWQSYSAQQL TTASARQLAEQESSDSYTTSTTTTT TTSEEYQRMVAAQVQAYQMGEQSG SEFDYQVDYASTQDSVQDYPGRRS AQECVDSLAVPLSTYKLVDMVREVT PSPVTTPTQTPAPAAPTTRRVVFNDE PEIKELPQLPALETIPEASEAVEDRE GLVIEQRCQILESERKFQPTPEIKIEI APVRQIPPTKIPNPMKKEWINPMIRV LTTAPEVPHLVECPFFRPGDDEFEA EAAAAEAAKTQEVPELPPQVSAAPP ATVSVPEPAPLRESPPRGSRLSQAM VTAPEFELKFAPPADQGIPLPEETEP YMPPIIDTKPYLREDYRPFVPSAL TTAPDRPFEGHFDKDVPIHMIDLPTP KEHLSMCDALCTAPERGYTPLNPN AMHRVDEEQKQELKREFQVLDH EELGIRPEPPQSVEYETRRDQPRK SSAFAAMQAFQPSREPLSNNTVNSA GSVADTPRASIVSALKEETDLEYQKY LKAQQRNOKRLDYFHQKEEELSLG QGQQLTQLRELSNQQNLLSQQQ LQSKLLQLQCVQSQELQQQVQH LTQKSQQPPQANQQQQQQQQRG TQQQHSQVTQRTQQQQQVPPQOV TQQQQEHSLLSQTTLAETQTLQAN AQSQSSASYSSKATACSNSSSTVPPA NTSTAFAPAPAPAPTSIPVVRSAIAVQ SSYCSSQFDVHELIEETAEELEHSEV LFPPPSPLSHLTKQKAVQSLHKA DSIPKYORNWTVLPTQSPIRTPEPQE LRENVPLAFVDAPKAPVSDSSTVH RPIAQVAAPTTVVAPSREREKERRPQ LSVPIVEDRSGPVTMAFQPLDELVR PDQALTPTRPYTPSLTNKPAPIVPFY QTEEKLVFEECSATHARNYNELNAS PPDRTRSPAPGPPNPLNAIRAPRM KEPETKSNILSVGGPRLQTSITTG QSYQGQLLAHSEQSSQASQSYNQ PERITEQRVGNLNIQREQSSQLQ QAQSQTSQTRSQVGNQTIERRRV TEEFERTQSAKTIERTGSQSVSQSK AQSQISQAQTQAQSQSQNQSDTER RSSYKGTGFVASQAKRLSCMEEIESS LTSQSQAISARASALGEGCFNLRSP TFDSKFPPLKPAESIVPGYATVPAAT KMLTAPPFGFLQQQQQQQORSAFS GYQATSSVQSSFASSKATSSLS SSSASASASAVARSSQLTQASAIT TTNNQATTAYRSSNGSITKPNLASR PSIASITAPGSASAPVPSAAPTAT APFKAPIVPKSVIANAVNAAPPAPA VFPDLDLNLNSVDNSPGAGGKS AGAFGATSAPKRGRGILNKAAGPGV RIPLCNSCNVQIRGPFITLGRWCP DHFICVNGNCRRLQDIGFVEEKGD	None	None	None	None	None	None	None		

