

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q9VT00	Q9VT00_DROME	Drosophila melanogaster	NaN	25.496522	NaN	NaN	33925313	MVVSKDNNKRRRKETETPPPPPPVP PAGSSSLAPPSAVAAIESSPEMPKRTK VQAQRKFAQQQSAPSSSSSIAYSAAA AAAGSGSGPSTSGADSNQPPPIELPN KCPKQDFLTFLCFRGTRALPAHLD FLNQGKSKDSEASSTGANNNNNAR KPNNSRASLAGNKKRGRPARGATK KVDVVAPIPDPTKEPSTAEPASDKN NLIAAEAPKIPSRNPTPVLPGAVRKR AEVVTGDNRRGARGRGAGISHDKTT PAALSKDNKRRSNRSTKESKPVID DDNSEDLDEQEADDEDEFFSAHD ATSRNGEEVKADSPVKAEPKTRGRP SAAKAVEPAPEGQTVLKDAPVVKR VRQRESPIFIPSPSSGRMTRQRAFF EPVKVPPHKEEPGAHDPKDEPKKQ PETPPSKTEKEQEPTKQIKEAKEKTN SSIIAKEAKQOLENGDSLHGAVAKG KKSLSNVDFSSDDEQPLAKSIKLLGG AKGASPKKGAAPAPIAARNRKA KKLDKEKEIEKEKQREKEEIEERDKA KEKKDKEKEKEKEKHPVPESKVEEP PSGGKRGKAGKKAEDAPADEEDLA PPSSKKVATNARGSRKSAKSKASED SAELEPQRSQRPSRKTKEAAAIYMG IGHKLQADDEEDLMSFFDIPN VKEMKEMENEIKRNAAGKLNVP STVLSAGKSTRKPSRPKDSPVTAPV EATRNEPSPPEAEKPPPPARRGR PPKQNKVNAGPAHKPRIEGLVKKG SLAKMSEQQAKPKAKSEHSKVDSD EEDFLINEELNETKRKLEKSFSDSD DEPLAIKVPAAVAVKEKELLPPKMASP PPKLVVPSPIVPTPAVSVAPSLAVP SILPTSTGTTQLTMLPLTAKATSSLG SMPMFPSIQASYSPLKTMKPKPPVP TSKILNVPATYALPGSAGAVSFQKT SSYLPQASPHYHSGYVRPPPTPTHQF GGGAPSGSKTPSQSSPLKYQTPPTT YPPPIEAYQCPKINPNFLTPKERSPL PRSTSSFPSPVVKFQPTSGTTATT VGTSSATKSLAPPPPPVSVQVVIQ TSSLNLSMSIAATVNAAMPVASTSA AAAHQTTVATTVTATSTPPAHSNSA ATGGGAGANSPLKDEIGSILAQATL MPSKEESGKIFGIASVSLAQSSGPDN TKCTLGKCGSIHKPVLGPVPTTEGYF GDQLSSKERRKAKVNMTHQIQKW LIECSSNPDEIQDDDDDFDSSLRP QQSTTPPTRDDKELSAFSSSSKNT RGDLGKSESASWAKGPKATPVLV TPPNRRELHEQADSKDCDALDYDKS STPVNLTOKITSNESLAVEKKVNDR KKGESAKAAASKAATQPRSTAATPPT PISSTPTASLTPSKSSPTPPPAVKQK AEKGRNATAGGATALASPPAAPT PANPKRTPVYNQKNAKAAQQQAET KPASNPPSGAGTKRESVYAFGKDD SGSKSGNRRRTDPSPVPAPALVPNA LSERSPTKRAAAAAAATAVQLTSLP TENCKIEGKPSKAPTGRGAKKQQQO APAPPAPPVEASGSDAEGATFYIPL QGAGVGGSGGGIQGVAVKLGREGP DGNQKQVVMQATLVTKAQMDTNSK PLPELNTNELVKTLLHAASNDAAS TTTSLKSLPKASTSAAAGAAAAPGAS SLVRVNSNSSLFSGSAKSRTAAQTSS TAAAVAKKYKDDTPIKMANNTAFPR HDDPTQMVEAPIFRPTEKEFADPIEF IERITPIAARFGICKIIPASFKPECRIS DEMRFAYNQYVHKMLHRWGPSAK ELSAIKKYLATQSIVMNHPPWIGGM EVDLPRLYHTVQELGGLKEVIEKKK WARVAEEMCIPKLAQDRVTKLDDIY CKYLLPYDTLSPAERQKLFDEVEAD	None	None	None	None	None	None	None		

WAKREARARRNADRFVNTESVSNE  
EDDLSSDEEESSEEEIDGVSMECIV  
KGRSMPLSQFYRIARNTMALWFKST  
DPTVNEVEAEFWRHVAVRDSHVCV  
HSGSIDSSGWGYGFPPSPGPKGKGSN  
YARHPWNLKVLTNNSGSLRSLGPV  
MGVTVPTLHVGMLFSACCWYRDPH  
GLSWIEYLHTGASKLWYGIPDDQSA  
NFRAALTSLIPTHCQNKTIVLPCDTV  
MVPPHMLTDRGVSLCRIEQKPGEFI  
VVFPRAYTSSLATGYVVSSEVYFATM  
SWLDLAKDDFRDIHESCEPAMFSLE  
QLLFALGYDQRVNSEALHQMLPML  
NDVCEKESAAREQLRAAGVTSTEKV  
QAEKGQKAKKQQPPYKSIESECDL  
CRANLYISMVRTEDGNIYCLQHALK  
NLNNGNIQAKQCKLIYAYNVDDIQQ  
LIRQLQEKINHKAAVKKK