

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
Q9VQM0	Q9VQM0_DROME	Drosophila melanogaster	NaN	25.496522	NaN	NaN	33925313	MAKDPATTRIPRLDGVSRPKPSTFG LASSSGSTTNRTTTTTSTTQHIPP TSAPKATQIFRAPGDPAPKPRPASSYA PSSAALRDLGSSLKKSASGERINNAV SLLSKRTTTLVKYFSPKSSASANAV MSSPCDMTSSLPVTPVPGKRGMA NDQLTSSTPMPLLRSETFVCEDEKQ SNRMKLESTRLSTFGRTMDIESPVP NETKVLIRDGTRIMKGPSTDITQIV RPTQKTPLMTFCSLDTTHEMTVCSR NNATHSVNSSGIMGRTMPVIPAKDA TRTISANSSGLGNLTKVVRGVGNIN QTLEAAGNITKTFRAGADLRTTVEKE ANIGKTFEVAANCTQTFTRGVNLTR TMNDKNEEVSRTIDKGRSTTKTIEV GQNLTTTMDAASNLTKSIDRGATLT NRGANLTKSVIEPGDFTKVIHQGAN LTLSDQLPPLLEHISMPGSLDILSSK CSGNVERPSQETDDTLDVTLTSLAP DKTNMKPLNSTLNTERLLDISALQ SPRHIQLNLTQELERGTSPSRVHLQ SGRRSMPQHSLCLSPQSATTTPHG MRMMGOATPQPVHLLSPLLKQAQS ALVLPTRTPDGDITMDGNGALDSTL TSTSVRGRTRYSGFLDLPDITLDCSI ELVDNSFSSSTQLQQLQQLLKKQS SFDLDESLGILTPDQMKDFLDSPHN NLMHNLEMIRMHHPNLLQLRMEQ TPSPEELPLDPIEKSEIVKQVEASQN QVNTSQHSKLSNSFITSVTSVSLDT GYQGDGEMSRPASRGACDHSPSNG PHLGRVSRQPSFPPNPAPLRRQDP MTDSDFFTESDADDVLHRGDRRAQ VIDGQLYGPDMMQPSASVPQMEDS CMESGIFTDVENRCDEEMRQPELE FDVDMDMSPDDSSQTMKGGQGP STQQQNQLAPQQRPPSSCLSSSSA ATTLSQLSNRTSYCSVDGGSARSF CGDEAFAAGRSTTTAAAAAALSV QKTTSPRPHASLSSLCTVENFRGSV SSNSSIASPKSCKSSVTKTSAGKSRV LKSPKSPKSPKSPKLNKAHTPNKWD AVMNKIASNKSLIKTNYNDVKSVS TTRIMTPASGSSPVSGSGSVSRTA SSPRASPSVSAARRSPATPKVPPK MLLAKRPSSSGKVNATPSPPHAT PPTRQPLDKGSGAGSVGGGGGARAV KTPKSPTSPTTPTTPTSPPAKRLQTS VSRGRSYSKSHKSSHTDLSLMCNA SSSRPSNSASGSGSPKLLANTQLRA AKKRDVRNLSISPTDLGPPPKTQTT KGQSTRSKSSATPTPTSIHKRLNG TLASTAAIATPIKGVATKSGATNKLO QSAKTSTASIKSPAIVGVSEESLRSG VDQTELQELNNGSATGCPPTPPMA RDSKRTSIGNELPCETEAKLKRCE QQDPQASTTASPLPMINPQEQEASG QVKEATITANEPNALSPLDEISNSV SSTMLATPRVDIAAQYVLPKPTEN GELDCARLAKFFQDTQFERKEEQRO ILGLSVMVQFMKELDAVACKENKH QCARTKGTLEKTIILLQHTQKDCER LREDLEDKLEWQIQRQEQEKEYLHRT ELKQAEKLEMEVQLRAKLFCELES QLRAKDEESKQAQEAYRMEVSHKL ALKQEHRTAEQKIQLQTRLQQVE TEEQGHREELIRKENIHTARLAEAN QREODLIDRVKSLTKELNLTKANKE HNERDLRDLALSODEISVLRSSQ RRSPTSLPDNASAEINLRTSEADS LRCVLELKQAEISALS KAKADLIHES EERLKLSNRVALLEAQNEMLRTELE AKTEKEKEIQKMEELQKAYKYESIK RTRLTYDKEELQYHLKQSLQLQSA ESKLQDLSTGSHDNLSSHSRCSLG RSGLEIAVTTSSPTSPVMKGMIRND	None	None	None	None	None	None	None		

