	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
0	Q0E9I8	Q0E9I8_DROME	Drosophila melanogaster	NaN	28.06426	T673	NaN	40245499	MNMPNERLKWLMLFAAVALIACGS QTLAANPPDADQKGPVFLKEPTNRI DFSNSTGAEIECKASGNPMPEIIWIR SDGTAVGDVPGLRQISSDGKLVFPPF RAEDYRQEVHAQVYACLARNQFGSI ISRDVHVRAVVQQFYESEVNNEYVIR GNAAVLKCSIPSFVADFVQVVSWQD EEGQLYGSLGDQQGTDGKYLVLPSG ELHIREVGPEDGYKSYQCRTKHRLT GETRLSATKGRLVITEPISSAVPKVVS LAKFDMKTYSGSSTMALLCPAQGYP VPVFRWYKFIEGTTRKQAVVLNDRV KQVSGTLIIKDAVVEDSGKYLCVVNN SVGGESVETVLTVTAPLSAKIDPPTQ TVDFGRPAVFTCQYTGNPIKTVSWM KDGKAIGHSEPVLRIESVKKEDKGM YQCFVRNDQESAEASAELKLGGRFD PPVIRQAFQEETMEPGPSVFLKCVA GGNPTPEISWELDGKKIANNDRYQV GQYVTVNGDVVSYLNITSVHANDGG LYKCIAKSKVGVAEHSAKLNVYGLPY IRQMEKKAIVAGETLIVTCPVAGYPID SIVWERDNRALPINRKQKVFPNGTLI IENVERNSDQATYTCVAKNQEGYSA RGSLEVQVMVLPQIMPFDFGEDVIN ELDMVSAYCTVNRGDLPVDIAWTKN GGRIYTNDGLIVTRNSQRISVLSIESV RARHAGNYSCVATNSAGETRQSAIL AVNVPPRWILEPTDKAFAQGSDAKV ECKADGFPKPQVTWKKAVGDTPGEY KDLKKSDNIRVEEGTLHVDNIQKTN EGYYLCEAINGIGSGLSAVIMISVQAP PEFTEKLRNQTARRGEPAVLQCEAK GEKPIGILWNMNNMRLDPKNDNRY TIREEILSTGVMSSLSIKRTERSDSAL FTCVATNAFGSDDASINMIVQEVPE MPYALKVLDKSGRSVQLSWAQPYDG NSPLDRYIIEFKRSRASWSEIDRVIVP GHTTEAQVQKLSPATTYNIRIVAENA IGTSQSSEAVTIITAEEAPSGKPQNIK VEPVNQTTMRVTWKPPPRTEWNGE ILGYYVGYKLSNTNSSYVFETINFITE EGKEHNLELQNLRVYTQYSVVIQAF NKIGAGPLSEEEKQFTAEGTPSQPPS DTACTTLTSQTIRVGWVSPPLESANG VIKTYKVVYAPSDEWYDETKRHYKKT ASSDTVLHGLKKYTNYTMQVLATTA GGDGVRSVPIHCQTEPDVPEAPTDV KALVMGNAAILVSWRPPAQPNGIITQ YTVYSKAEGAETETKTQKVPHYQMS FEATELEKNKPYEFWVTASTTIGEG QQSKSIVAMPSDQVPAKIASFDDTFT ATFKEDAKMPCLAVGAPQPEITWKI KGVEFSANDRMRVLPDGSLLIKSVN RQDAGDYSCHAENSIAKDSITHKLIV LAPPQSPHVTLSATTTDALTVKLKPH EGDTAPLHGYTLHYKPEFGEWETSE VSVDSQKHNIEGLLCGSRYQVYATG FNNIGAGEASDILNTRTKGQKPKLPE KPRFIEVSSNSVSLHFKAWKDGGCP MSHFVVESKKRDQIEWNQISNNVK PDNNYVVLDLEPATWYNLRITAHNS AGFTVAEYDFATLTVTGGTIAPSRDL PELSAEDTIRIILSNLNLVVPVVAALL VIIIAIIVICILRSKGNHHKDDVVYNQ TMGPGATLDKRRPDLRDELGYIAPP NRKLPPVPGSNYNTCDRIKRGRGGL RSNHSTWDPRRNPNLYEELKAPPVP MHGNHYGHAHGNAECHYRHPGME DEICPYATFHLLGFREEMDPTKAMN FQTFPHQNGHAGPVPGHAGTMLPP GHPGHVHSRSGSQSMPRANRYQRK NSQGGQSSIYTPAPEYDDPANCAEE DQYRRYTRVNSQGGSLYSGPGPEYD DPANCAPEEDQYGSQYGGPYGQPYD	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	None

								HYGSRGSMGRRSIGSARNPGNGSPE PPPPPPRNHDMSNSSFNDSKESNEI SEAECDRDHGPRGNYGAVKRSPQP KDQRTTEEMRKLIERNETGPKQLQL QQANGAGFTAYDTMAV									