

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
Q9VUH6	Q9VUH6_DROME	Drosophila melanogaster	NaN	30.404062	NaN	NaN	33925313;28604694	MEAVPRLHMLWFALKSSPEGTSFA ALKKYIAEFYHEDPEAYSKEVHALET LRNQAMHTTKDGPVMKRYYCOLH ALQNRFPQLADRGIPTFKWKDLYHS AVHEVTDLRFERAAVLFNIAALHTQ SGASVTRGDVDGMKMACTHFQAAA WAYGELRERYANVNGGDFMTPEL LVFQQQVCFQAQEQECILEKSLIDNRK PHIVAKVTAQIVVYGAALAALLTGG DDGPVAQVIDSSVYKLVKYYVRFKI NYLTCILYLYQGQHSEKROMGERV TLYQASWDKLEEARKEKGLPDQRE INESLSFTADVVEAKRKNAKNEFEI YHEAVPELSTIAAVQGANLVNGIGFQ VSDEEHAGPDIFARLVPMKAHEASS LYSEEKAKLLRKYGALLEEKDTQLES YMSSLTLDNLNINEEQANKLPQGIV DRCAALNANKTAISDLVEAMSQLAE ITADVETNLGEISSMLEAEAKAERE QSATGVQRTPNAHITELSRFPQKYSE AHARAGESNNTLRKAMSLHVNNLK ILARPLPEIQQLPKLSSELNTEIFR DVKLILNKVNEMKAQRAQFHADLRI AINEDDITGKVIHGGQEGQLALFAT ELGKHDKITELLDQNMVAQGNILQA LTENYAKAAPVLKTLQDVKQREHF YSSLAASYDVYEDLLAKSAGLEFYK KLAGNVQKLLTRFRSARDVQSEERQ QRMQSVKAATTPVVSPIAETTPVPA VSSTPKLRDYLKAKAAMADASNPA VPTVRPVPVGSNPTQAACSYATAPP NEPPPPYSLTQQQYFDP5AAGYTNP MYQQQQHIAPPAYKAQASPNSQTL HGALQOMNLQGSQDNNQAGMAY NYGYPGSPVPLAYAPPGTVPASSAS QGLNIQPLYVATSGNPVSVSNPSE LPSTLQAPFVNPMSNPYQTAAGYS GQAYQOVNAQAQQVYTPAPSGSST GQSAQQPLGYAPSQGPQQAGGY QSOTFQQQVQAYQQPLSGYAQQLT PQQQTGYQSQAQPLQAPSYAQNQ QSTGQAQQQTGYPTPQQHLAGY AQSQQQATGYPQSQTSQQQTGYSQ SQTQQQPLAYQQQPSGYPQQQQQS LAPQQPSLYPSQAVQASQPIPGQQA TPPNAGQPLPYQQYTDPNAAAPAPA PGVSSVSPVPVPTPAPTSSQAQVPT SPHPSATYTSYSNHPGYFNPQTGK YEYSSGYQDTSLLKGSQASQSYQF SQSGKQSVGTTDSEIASRSNTATG FDSPIVSHTKVNMMAAKDSTSIAIEGN ESSNYSTPYGYLGSVNPQQQPTPAP PSNSTASIYMQSGASSTAETQTTSSG VPYASSAALTKVEPKPEALPPKVTSN VDLLSDLDIDCSVAVPPMPLPQPVLQ PQVATPTPPASQVSVVVKVESVAEH AAPATAEIPVAATEGTAQTPVTIPSGP KCASLDNLSNCSLDLSSLENFDWDS VSVTHSVSEKQTKASATANGHSSSF AFQSETFTDEKTTKYFQKEVESYEKL LENLHVKMLNGKTQLGAKWQELQQ KLDKEAAAANKRSTTIKLFPEKNRSL DCLPYDHARVKLDKQTDYINAAYM KNLSAGCPNFIVAQTQPNTINDFW SMIWEKSRVTVCLHTPNELFDPYW PQALDQPTHYDDYTVTCLKVQQLSH CSEYQLKLSMHGADAVLDLSSLQK QWTKGAPAQLLGAENALETNRQR CKAANAPQSPLIMNCLTGSERSELV AIGVCAIATQNKQPIILLNTIDVVSRI CAQRQNSLRDSAILEQSMQIVLCNA HNVLNKRGITSYQMKMAPQVTAK EQQENKDPNLDELWKLK	None	None	None	None	None	None	None		