	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	Q9VRM6	Q9VRM6_DROME	Drosophila melanogaster	NaN	28.06426	T279	NaN	40245499	MSQAAGGSAVGMEQPATGKQLKPP EDLQDNDTNSLEPGEVVTPPHYHPS SPAVKKHLSKELMISKTLRKLPVSVV EQARKENGSGGTPNAQAEDADDSE GLYSESDSSGEDLKNVEDVQKARKE KQEEAAAATLPQAPPTPFLGINPLRF HMRAPCFEFPRMGFMPRMNRGGP RGMRPTFFGRPPAANRMGAPMMG GLPTQGPPPGAYAPQNPPPTGINSNS GRCKRLQSDVIWTALQPPVSFVFNL VSECSNTKHENCRTKAETTDHNSK ESKLPSETKSTEPLIENNRSRELPQH KNYVRGKTSNRSHDRTQNRGRTRE RSKESHGKSTENSKNKDEGRGKGR ERDLFRRKSRERSQDKNLNRAKSM NLSKEKDEVGGEPRNTASGKSQERD QSRGKTKDRSRERDRTRNKTREKSQ ARDQTRSKANDAEHTRAKSRKRSSS RDKRREKSKEKLGDKEKNEDLSKEK LEGKSTEHSEKRNESKVKNKDTNEE NANKKLRERSKDRNHSKERLHERT QNKSEERKPEAKKVRNAIENSKEAP TDRKKDKLLGPLGEKTDERSKDKQI KRSREQSVTKCPKESGKDTLMEHPP QENGLDGSKRSSMPHESFSESAKTR EHASRRKNQTLSPWGSREGTPPMT PPQVQIPQTPIVDIANPKDFDIFADSP PRVNTAVSAPAATIERSTTPPLKSSIP IVPIAKADKLAPLLKASEIHSRIGALL EESDLHLDNLLATKEQLFRRTNEYK ERKEAPKEIKAEYLPNSRHNRSATG RAEVEHHKSQPRHINPFKRESVLSG RKSSSRPSSKERRFQRHDSEVENW DRDLELERNQLNGSQLTGFQPRKSD EYTKFSIKKEKDLTPPPLQTNFTRTTI KIERNATPPRHMEHDVLVRNGAVAT NAPPPAKEQESPDTDDYIDNWEND DSLASMPKNAPPVTPTPAPNANASL NATPLPPVASQFNGDDDDDDSNAL WNAKSTPPPRRKNENLPEGNIHELY DKFMNSIKMSNEHLEPETLDTSKNS SLSNSPAEESSSGTETSSTSSSSSET EDDSSSDDDANESSSNDESATTSGN CNTNQDEAAGKEQLQKKNNVSKDL RKLKSLEDNLARIQMMRENYDAGD EISEELLKMESLFLMQRNAIMDKYR KQELKSNSSEDQQPVDEQGTVQAQ EVVKETSFPVNSIFSANREAIKLTISP LKLTRKSVIFDKDEADLPETSKAEPP KQTLQKPQKEIAIVKPTIVESRSKPKL RSPPPSSGSRRRSRSRSISRSRARRR GSRTKSRTPSPRRRRLPSPRRVSRYA KRIGGGAVGGTRKGRSHSRSLTRSR TRSRSPSRRRRLPPAGHRKRGSISPI PQKLAGPRSPPPSRRRQSLSRDRER EHLSRSRSPLPFKPPSPPMRRSWSK ARSPTRRRSFSRSRSRSISPRSRLSA EEAFANYFEENQGMEAAAYYYNMS LMQQEDQNALGEGYDAYAAYMDSA YNMEQAYAQYSEEYSNTYMDYMVE VASSPQAPGSVLRELPMAPMMPVES LAPIAPLEAMPSMAATASGMPVAVQ KGNVLEIVPSGEDILEAEENIVPDAT DKPVEDTSKPKGKGVNFVDKVLPAY ESDNEDRAVVEMAVKRALRKYHES RSQAAAKLQLIRDELLLLPPPPPPPLT TKPANLEKPVLVQKKPKFRYFHFDP FKCAIVKTYTRTLRSAYRPPFDPKHF AMLMKTGRLPQIPPGFLRHRPPFIPA HVDAVTRGAMLKEFFSKHPPPPLAM PMPVPNGMPYYLSGPPPTSSGAAVS PVPVNVLPQPIPVLDGSGYQGYPQSA TMVPLPVPVPVPVPLPVPLPVSTDTT PSPALETPYFTPPPLPELPPLPELPSQ FTVSSVPTITEIMPVDILQKLGPLPKT	True	False	1.5	4.056	0.908	False	False	False	False

								LDVDDGGGTASPEDISDDLKEVEAK PAEQHVVGVKPQLLVETQ										