	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	Q9Y1L3	Q9Y1L3_DROME	Drosophila melanogaster	NaN	28.06426	T1293;T1735;S1736	NaN	40245499	MEVIKPMDFSSFSAFCEHLNKSSQI AATTATMIPPTINNGKGIYLEKMERQ GRMELAAKERESQRLQLIPKKWNRR EEYEFLRVLTGYGVDLHVSTPMASS NGSSLSPDWTKFKQMAHLERKSDE TLTDYYKVFVAMCKRQAGLKLSESE RGLEGIIEEIEKEHAKLILDRLEVLAK LREVARNPMLEERLKLCTKNADTPD WWEPGRHDKELITAVLKHGLYRSET FIFNDPNFSFGESEKRFIRELEAQIQ RTIKLEAFNAEKAEKLAAAEKDAATE KAAATEKAAAEKAASVKNEVIDLDD ELMTNESVIKKESPVTPIKEEIKSEES PEKHDTADNLEDKNSDAEESTKIKG KEDFNPETTEKEALDESTNLNKDKS STETLVPEIEDSKPSEDKMEVEELPV AENGEKEGSPEKCSDAEDKKFSEEK PSSPAVPDGKVSEMEADEAAPNTEE NCSGDSESPEKECEDKVVEKVEEEK GENSYEKAEEQKEETEKLEKSSIESE PSEKSETVLEPEVAVPKKSTGDQDIL DLVAGPSDPDDDEVMKEKEKAVEE ECKKQAAELKARFPDLEVIQPATVKQ QKLEKPKLEMCMIRWFKDFALERRI AHIVACVESGNWPVDSKYSAFATCK GATDLSIALHESIPHLSSLERRSTTP DVITITTDQGVTKHLQTSHMQQVAS SASAASTSSGVPQVTQSKPSSSNSLP GLDAKSINAAVAAAVAAAAAGGNAT SLSSLLPGMSLSAATGSSAGGVSGLS VPSAGSGVGKKRKRHIAIDVETERAK LHALLNSSTMAPKDWESEIANMEA LSGSSGRGRGGNSSASSGMQPPPA HQHASLSRQSSGQFSKPAVPAMKTP PPSMGAPMDLSSSLPKMNMTEMLK SASSSGAIDLSEVQDFSMPSKKSSV HAALSSAFPSMGNKSKLDDTLNKL MKKNNCTIEEPVIGKEKKRKKLDEIV LGLSAAKEQKTFPDPSLPSSKKPQIP PSVSVTPANLQSSSNQQSNQKPFTIT VTTVPGKSKSGSSNSGSGTGGSSSA SGGGAGGSGLSALQNMAMGGLSSK DSLNALLAQTMATDPQTFLKQQQK MMQFLPPAQRKAYENMLAEMEQA MKISSKFSTNSPHDVKVNKWLSDM TSPLGDQLSIDYVGGGGASGSGSGN SRRSNRQQGNSQQSSSAAQLQKQQ QQQQQQQQQQQQHSMPGPQNLTG EEPVPVINKQTGKRLGGNKAPQLKR LMQWLTENPNYEVDPKWLEQMQN PMSTPSPRPASMESAYGSSAVKSHG GRPLSNLSSTSSSSHTQQQSSAAQS QAGGNSGSSKKNSRQQTAASAALD QAALQFGSLAGLNPSLLANLPGLGA FDPKNPLAAFDPKNPLLSMSFGGMP GMGNIPGLGNLNNMNLFASLAGM GGLGNLAGMDTQSLAALMAAAGPT LGGLTGASGGAGSGKSQAQSQSSAT SSSSSASKKKQQQQQQQAQNEAAQ LAAAISASTGGSGASGGKNAAASAS QLAAGFPFLFPNPSLLYPPMGLGGL NPYSLGSSGLGSAYDQLAQQYNLLN GATSSASNTSSTQSKSHQSQSKSSQ SRNTTASANSAASLMNAMASMGGG ASTVTTPSTSASGSGRGRQSSSRNQ SQTTPTAADMAQLSSLLMPGADPHL LESLSRMSNMDLAQATRLMSSLGM PPLSGTPSSSGGGNTSTSKRSSQAA NEANVQAKEQQKWLESLARGALPT DLAALQAFSQGKMPSTSGSNTGTST SSSKSSKAAATAAAAQLPQIPGMSSD FPQAFLAEMAAQAMAAAGGSLPLSG PGSLASLAGLTGGSAGGGGSSASGS TSHSSSKRQREQDAFKQQMDYYTKT LGLGSGISLIPTSSAGGSSASSSAAN AAAAAYAAALDAEQQHQQQQKALSK RARGDLHPTKEELAALAAGLPLNLG ASMSSIEKSLRGGSSSSSSSTPAPMT AEQDKVTLTPLNASGGGSGSSSSSA	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	None

								AAAGLAANLPSQTTITIAPPISSGAST SSERSERSESRISLTITNAADAAKLPP PYEEADELIIQPILKKPTAANPGSSHG GSVDDLDTAENTSAANLSGSSSSSA AAAAAAAAEENRRSSNRLKRPRSGN EQGSGSVEGQPPEKRRELRSTRHTR SSADASTLNLSTGSESGAEERNE									