

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	ext rec
Q9W4M7	Q9W4M7_DROME	Drosophila melanogaster	NaN	30.60235	T33;S37;T42;S323;S1474	NaN	33925313;40245499	MNNEQTSSSDTPADRVASGGAAA KLPTTIPDTPIVSIAAGTMSSESTTTTTV TKTTPTFPFQELMTMMSDHVAKA DAQLDEACRNQGAKDEDSQGAAPV AANHVATSGSSSRGNPKKSSSPSN SHSSGNHAATADAAKGSAAEAAAAGD TSFSQVFAMLKDSPAELSRPNRRV LQYGATAKGTQDDQNVGKROKKK KTKYDTWEDSDFNDLDDASLKKLLE EAYWYRNPGRKNKSERFLQMLKK AEYDEEISYRAIKSCLTINPSALTSSA ATGSSGGSSSAGHNSSYNSTNHRHS TDPGQRHKQGGSLQDLVEAAHRSE LATTSAAAAAATAAATORFNCDYQ LSGRSNRRQQQQQQHQNQATSSA SASKKIKNLNVSGRQREGGSLPSSV NFEPASSAMEAKQNKQAQPSSTA AGGSFSGSVGNKHHHRSSTGSCSSL ITQSRDTEANNQFDLMDDDATGVG ASAVVGASGDQDDNMLEQLDPONP SMKFLIDALNDTPLEARYTGAGKKF LIDRLHFSVLELSARRKLQQAQY LAALTGFGLGLEEKRKVEAGYVS LNDNYTACSSVYGGGAGSPAAVEGS KPSTSSAVSGSNCGASSDALSSD LRPAKIGRMVPAAAAATAAPMGGKT TTRQLDENGNALGDGFGGSAASGSS GASGASAAASSNGNGNANQFTALI TPTVGSVPSTVAHRQNSVSTLLST GTNTTTTAMAAAAVAASYSQLQAP VGAAGTVSGIGIGMQPPTKQKTKK KSQQRNTTTVDVESVAGYRGNDPV EQLVKYIENDVNGGNSAAGORKKE RKKQNKLKKNSLEELRTCSKMEV DDLKRSATTEMRRHKKGTNNASS GGSSSTASGSSNSGKHNSASVADIN KNCNKEQQQSTPTVQVRNSNPNP TQQRKGERRSWGTEELQYLDGHQEI SAAWSELETVGQKELPLALPALARM SELDALNTVSETAEFHVVTKKKKP KKORAVTMDDAAVAAAATVGGNLQ RMQITKSASSNIMSORMHYTTPYN SNNGGGSVNYKQQQQSQYQEHY QAPQGQHSHHHHHHHHHHHHS GSAVSNQVDSSRRKSTSSMPPEKS DSSDLDSVHSLPIQTGKKSLGGGN NKQRGAPSASQRQAKQNNAAPIS YADIARNKQEALNNATASDTELELG DKMQIKSGGKSRPDPFPELPGAVT AVAASGGAANQATVVSSQNTPPSSS SSISYSQSLNATPPSSSDAESTNSP ELLAQVQIPAYSMITPTLTASMISSVS SSVASTSSTSCPPALQKSKSVEHDT SYSCNSSNLDQQYPALEKTVKRHST NNVSVAAASTSASASSLYNFAAA AKQQLTENTHSAVPPAAVTTTSTAV AASAPAPTTVTVAAVTVPCYSSSST HGSTQTSTSTASSAIAALPSGKAKAK PKELSPSSSCSKKPTKPSQDVPISLS ISTTPRATTSTTTTQKTTAATQTEG AKKLIGIHLKPSSSCIAKGAGAVLE ATAGRRAVIILNDDREAGRSNNEFIF GDFNEDELKLFDDNLDDEEEGQHK QSSNKKQTEGESDVTQDDTEDVD QDLDKLECLGRRPEKKQERQDIS ASSDQHLNDSGAASDAVNSSASLD MLSISAEAAQSSPNAGATATSSSVAS PINSSTPSGASSASASTSTSSSVSIS SSSGNGAACLASVSGMLGGVANQ SGDSGYAAANTSIKEHVNTFLSKAS SSEETLPSPNISMQOLETCNDIEAAA IAAAARAAAARSTSCSRNSQEQDA LQPQVKTKATPNPEAKMVLVVFVTY NNNNDDDDDEEDDESLELQELFSM ADLKADAATEDIAMQPPPPSCPAMM TNTELIVDYIAKTWNAIANSKYVTTY NEQEQQEET	False	False	1.641	2.578	False	False	False	False	