	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	extr regi
0	Q24107	Q24107_DROME	Drosophila melanogaster	NaN	28.06426	T970;T977;T1010;T1012;T1013;T1495;S1969;S2108	NaN	40245499	MENATTTTAKHYKTAGKQYKTNKV NNTRRATAAAAAAATTTVTTAATPTK KRTYRETATATTVTQRSTNKANIAAA IALAAATEATASASASATATATDATLT ASKAAATAAATTDAASGNSNSSSKP STSTRDKLGEVPLPTVDSNHIISNNN NNNNNNNTSNNNNNNHHSDNSIS ENNYEFKSRDKASLSDSKMTLQQM AAVSSNQEPVAPNVANTMSNSSIIN SQQTTVNATPATDEAPLGDRSNISRY LHKKFKRLASTTEVDSWSATNGGGA LQASGDAVRTTSLSSNSSLSPPPTTP LANGHHLMTQQQSHQQVQQQQQQ QTPPPSVAIHEFSANFVNSNHVNAI GHEESIISNSGYKAAGRTRTPLANSN SNTNSTSNSNSNHAANATLSPASFA QHQQLTQPTTVSPGIPGGAAAPNPA CEKSGRYVCQYCNLICAKPSVLEKHI RAHTNERPYPCDTCGIAFKTKSNLY KHCRSRSHAARARGLEVPADADDGL SDQDAELSNSSSELPSRAGSPYEEPI NSPTPSPSTLSAAKSAYIQQPPLPTY MQQLPLGSPAAGTLPPTTADNHHSA TAQHRQSIDYKPYKPKFHNASMYSC SSKELQQQQQQLQIQQQQQQHQLA QQKLSIQLPLVQQPSLAHPTLSPSTQ MKMKHHINSHQIQLQLQQQQSLLA QQSLLAAMPPGGVYYLGQPSYYNQD TAAAIHQHALAIQQFQIHLAQQQQQ QQQQHPPLVKATPPMQQPPSLPPQQ LVRANSQISSVATAPATPTPAANLST FASSSGGKQVNVAKVQEHISKLISQ NEAIVENKEILLQKKYPKQLSRSRSF NNANSNNASQHGSNASALHANNS HNNTNAQMPERETKVNLAQAIFQK QQHQLQQQQQQQITQQQQQQLEQQ NYYTYIQQQQECQQQQLEPPNGVVK RNAYKPGVVMTTPVKQQQQLPPPPS PLPMQTMQYRQDPATPVTKIEQPTT AVPVMPLNLSAKPKPTLVTVPVSSLS TSSLAPTPTTSTNPTSSSKTAPPPAQ VNNSIIKNLLLNARGLAVPIGEGDDA VYSCPICASEFRSADDLKLHNSTYCQ DASSSAPMSPASSPFRSNSISLSLPE LKSHMANSKNPLSLAKLAWSQLKT KRSSLVLSRLSAAQTPARTSTVTAPT VTASAPAPAVATVTAPSSAPAPQIEAL RFVDAPLPSPGPLLGKTPLVDYAQQS TPRKAQDSVVITKMHEDRQFVIEAQ PAKRIKTSDLVVASSSQQPTSFNFSF NNQNSSNSVPELQSSKEERLRRFTS SGGSMIPISECPDLDNSPKMIRTPLL SGGSFQDVSVKVNNETGSSSKERKL MALVSGSGLLGVSSGPQHFQFPPIN SITAFNPLTLPPMSGGDKTTPVTPIP HVPGMPGPGSLTPQMPLLPPPPQQL QLPIPSSRGRSPNRKQPSPLLLGGGS GELKALSPFGGVQNVPSEFSRQPPT PAQRQALQWNSKETPKKAPFNFLR MADNVKTTEPEVRHFNLENVISGKQ QELPLTPLHVDTPNGNAPEETSPVA SASASAKSKFLRPTSLPLKPGTFTPK RHHGITPTANTLPLISPETPRPSKSC VQLYLNGHAYTYLGLKCSTKMFYCT VNCPQPSYVAGMHKLSMYSVWQVC EENQPHPLGFKLKQVMALYDSRQR MLGNGSSTAMAGSGKLSYNLVASQ QIVSSPSTSSTSSAFYQGPLKTPPTVT IAALSEANVAAKANEEAQAKKLETSP SGQPLVGGYESHEDYTYIRGRGRGR YVCSECGIRCKKPSMLKKHIRTHTD VRPFTCSHCNFSFKTKGNLTKHMQ SKTHFKKCIELGINPGPMPPDSEFLD VDMDFDQQSSTSAGGRTSSMAGES DSDDYSDNESESSDTDESKSRQKEH EAARGLLSLSMTPPIPQSVSPYPQLQ DTPLPAASPANSIGSSGSQPKRLVCS FTSPKPPFDYQKQEQYYSNPEESKP KRSVANEESAPMDLTKPRGSILLISP SPVSVPAHDLPKSQAQQMHDVIFGT	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	Non

									SGNESGFMKTLISVSDKVRISAEME EQAKHEAEGEDVQLQTYIKEHALHQ AKIKQSQFSRSYLINTLYTAASPVMS SSSTLFTANSRPVMSVNEVPSIEVHE VKTPEAIESPRSAPEQAPVILAQIAQE ENEEPNIAEPHNANLPAAVQQPDVN EFTGVLGNPTAPPTSSVTATSVSTTT AAPVAPSSTANSTQPAQRTVIVGEDG FKSSTPTSKIGDLQHVSYGRGVPPAP IAGDARPTCTMCSKTFQRQHQLTLH MNIHYMERKFKCEPCSISFRTQGHL QKHERSEAHKNKVMMTSTFGVPTT SNPRPFECTDCKIAFRIHGHLAKHLR SKTHVQKLECLQKLPFGTYAEIERAG ISLTEIDTSDCENSLISLKLLAQKLQE KDPGKLSSYTTPSGMMQLAQDAAGP VSQDSASEDGFSAAIASAIASLDNDS AGNTPKRASSMSEDETVANGLNHS LKRRLPGSFSSTGEESDNPPESSGE KRARSGQELPLPVAVPVAASAAASN								