	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	X2JDD7	X2JDD7_DROME	Drosophila melanogaster	NaN	28.06426	S1156	NaN	40245499	MRALGGITLLLAVAICQGYETYQRSS FRSSSSSSYGGGQTVPQLNSFASAH FNEVRELANQLKQKFNVLSQGSTNF AYTSPWSASILDLSGKSTLQLDQLSS EISRQLVQDMREGITNYHTIAQPNFF EAKAAELLERYSGAESASLQQTVGL GPYQPVDLSGFDEVKNYAYPAEVKVI DGKTYVVHRNCTEATKLSDYGSSGQ LNSGFLGHQQTSLPLSSTTTTITRKK TIHDWVRENMEPSVVGYNSVVKLD GQLRNSALNQMVPLSPGSNVVIHRF NKTITTNPDGTSSVGGSEWQQRWQ DGKLVYDHQQPFGQSTIPRDEQWKR EERERLFWYLTTPQRLDDWQQQQE ERLLGVVQRYQVSLPVLKEFHRREL ARYEALLGQYQSRVQDTSSWQRQER GRLDWLIHQNGFTVQDIERWQNEN ARKLAEAARQHGISQNQLQQFQREE LQRLYVHFNQVNESLAPQVPSVPQT TYNYQSSSSLTEDNTKEQQRLEELIR QHNATIAALQNSIKTDQQRLKNLSIK YQGDMQSQTQWLRGEVARIGDLIKE QNEQVSKITAWQSSERSRLENILLQ HRGSVEEVQQRINMDRNYLQNLAT KYQVSVEELEKWQKEELERLQVRGQ QQLEEHIKDWQISVSSNLRDIATQN KLTIDEFQNYIINDRSHLEEMARLYK VKVEEIEQWIKSELKKFQSEGLLKGV EQELIQWQQKERERLQAIVQQNSLT VEQLEVRIKNDQDHFFKLADKYKIN VEDIQDWLKKELLRLQSEGLVKAET LKEWQQQERAQISLLVQQNKYSLDE FERKMLADRARLQELSNTYNVKVSE IEQWIKSEGDRLQHEGQLRMESQL NNWQKIERQRLLDLINKNNLSIEEIE SKISKDQTHLYSLAQQHQVRVEEIEQ WIRQQIQKLQDQGLIEMQKLKNWQ LEWRGNLTNMVQDRDFTVEEFHK WLLKDREQLQSLAMQHNVQIEEIEQ FVKKEEQRFIGMGLLKPSEKLTNWQ EVERLHLKNLAQQQYKSTEQLEARL RQDRELLERLARQYSVQVEEIESWM KQELARMRDEGQLQIDNLTSWQLA ERERLEALIKQNKQWSAEELRAELE KDREHMQTMAFQYHTSVEEIEKWL QSEIERLKQQGKLNIEQLTAWQRTE QQRILSLLQQHSNITLEQFQAKVHN DRRFLMNLAEQHHVHIEEVDNYVK QVIEDLRKNGQFEIEQLQTWQRVER DYIKSLISEYKNSLSTAEYEEKLLADR AHLKHLADQYRINVEQIEEWMIAEL KRLRGSTEETLKSLSAWQVSELERL QNLVKQQNHLTFVEFEMELNQERD RLQKLANQYSVNVVEIEEWLRQQLI NLRTTGQAKVENLSKWQVEEQQRLI EMLLKKQQEMPYEQVERELTQDHA RLQSLSQTHHVDIDHVDHWLREEL RRLQSSGLVQIEQQTQWQQKISNGF NNWLEQQRNGASYQDFVDFLKRDK QRMDGIATDYHVTVEQVEKWVQKE AARLSLIGVIERPENNLKYEDISNIW VGDQTDSWKNELVTRLRSVTRQRPF TRQEFESYLIRNKPIFEQIARQYHVTI EDIHLWLDQSAKNEGLVTTEWQAK ERLHIDNLINQQLRKQQRWTIEELE LRLNNDQKHLQDAVAQYHVTVEEL KVWYKDELNRLLEQRRIDRGSGISW QNIESQRIYLAIVNNPGISRQALENR LFRDVHVRASQYQITVEELRQFILSQ LRRFSDMGLIVDNGRQANNWHDQE RKRLREVVKGVVITEQELLDFISQDT SFQTQLAQSYQVGLEQLAPVQRIFIG NLAREQLLEQRRLNHLTTWQQRER DRLYEFIGNQNMTQTELKTWQIQDS KLLAEFAKRYEISVQQLSDWQKKEL	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	None

								ARINQLARYYGMSQSDLQQFREGEL RQLAYINHRQLLSAAEAQKWEKRH QWTLSRLQSRYGKFGQELVAWRRT LYLLSQGLIDLPADSGSNGGYVVDAG STNATAVYKPIFSKDRGDQPPHTYDE SFVEGDEPGLEGETARPRPPNPAPIV STPKPPLPYSRGGPSGGFEYRRQDYT FNVPVGSASASASGGPTGSSASASAS LGKWNRASGDEPLQQEVDLGQQQQ IEELGWNEKLEDLGQQTQVEDTDW NQQAEDLGQQQQVQVEDDLHFDQT QGHSSSSNSRSQPLQQATKVEVEAT SEPSFWEKLKEKLG								