	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	X2JG50	X2JG50_DROME	Drosophila melanogaster	NaN	28.06426	T1318	NaN	40245499	MEWHEVELDGSRTIAFPERIVPGFG REPSAHLDAAEYLGGIIRDGQWGWV TWRYGSDATLLVCSMSTGDYLSWH CFWSESDDLGPRKSIRCVEELFPGE HERPAMLAICLESWNSGDQRPIDCP LSTQVLIYAIRNSQVLRRFDLHGITC SALTFLDKRIYGLTRLRRFKGCLAVA TEEGTVLLVDLNSDSLQASTQRRSL CSPSSKDEPSDGNLYFVSSEESKRQ LSSKLTHCRSKGAHLAVRMDVASIGI SCLMGISMAPGYAAGLEDGRILIYDL INFDVTTDLNSPVKRKGVNRAVKRM CLIMPPDDPKPCFYICALYQNIDVLQ MMLHSVCYRGSYRDRETHTIRFKDY RSRTVRNRQILDGGICSVIGCATAST FSFAGDNGTLLIVISWHSSADKKNK LVLFDINQWYKDEMPTSVHKNEVP NYMSGYILSGLQTGLALDLRSTTILH FVSLQRYDEHFYPNSLTFDCSLLTPT GKRYYAQDGVQHRFLNALRCDRATL FLRPQIYHEDIVRLRLLPQFCELNPN ATFSKIAMYELILSVALEHNCGALLN DCARSWMDGSFLCNMIDNTQLSLS TLTNWILKRAGQIKTRCSELCHGIFD YGGYPLDQRERREFQVLSGQLRELV RLQSYIVEQGRRRLTSSILDDCRANE RALKTVLEYQRVLLWFIDHGLLPEG QHMDNLVPGEQAFVRLQHEYSEKR AQGKILYIDSLGKRASFPEPYPPDSL HAYIHLMLSPDIELCHKHALILYLLM DLNQQLVGRFQIAFQLDKDLATSLR CFWYLDHGDYERGVEELYKEPAPAK NLKSWQMRLLIDKLLAEGAVKAAKK VVSRPPGPLSSALHMKVLLANENIT EAFQIARLDDDEDGQPLLERFFRHCI EIRRFKVLAELYLREPEERLLYSLLR QCRSRQTDCVQLIMLLQKSKFIEAVS FMDEVAAERERDESSNTILPAYSAT MGPVTQNIAGTYLRIRDTLEPYQKTG PLEPFSCQLVKQNASGQLGGIFQSS AVSAHWATQCESPPKMTPVSIQSKI GYTNVPFLRHAQYGHSELPLPRRIVK PVPHQVVEKRQRELEDQRTNLQDQ RQLGTERPNKRPCLMVERMVEDVK DYVRSIREKSSNQMEQEEVKQNEAT NLLQPPNFLQARQSTTIRQSSSSPQP IPPILKGSGAVDAVKRAPPVATFTALA GPKRFRFVPPIPLRTDKSDKSTEMGS EGAAEGEEETDEIIVEIESRSEPRSAC SYESDEEDEFLSPLVSANVSLVDPVP SRNSPHYFAPPAGPQPRNSLLHGGN GSGSKIGTATGSESSSGFGSFSTVQP AQTSSHSQFVPTVCSSKMGETQSQV FSSGSCGIKISERTTICGEMESTDLG AELTAAPSAQWSLPSARPAIQGHHQ MMDTTLGMSTYDVASLEQQDTQDV ENEEELKLGDTKSLEEQQNPQDEQ KPEQEQDQDEDQAQEPLATGGQLA FLSNSEGTAQEPLSSPIYSLSSEDSN VSSAGIRNPMLPTLHTDDPMYSIVVE SPGSITTSRSVTHTPTSFLPSDTNVS QTSSPQAPHGEDGDGTPISLYRANS LETVDDLDTTKGSLEEEEEYDDDDC VIALDGTEVRGYVARPQQSAASSSAE LFAFKDECQEEAAGVPSPFLSLGATV NSDSDVADTIVLDSDEETAKEKDTQ PEQRKDWPMEEETPSNESVATVEFS EQKQPRADMDIGMEVDAVPDVLEV LEVPEMEPLPVLSDVDIEMAVDEVP NVLEVLEVPELEPLPAGQATQSSGL GEIPEEDVDAEAEEQVVVKVEHVAD EQPKEGDKTESKEASEEETQHNPEP LLPEEEDSRHSLKLIFSGDEDEEEQ DVPTRAIHTLRPRRSFTEHQDSPRTL RPRRVSQEHRDSPTPVAGRTMSLRS	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	None

								TDAPTLSPASNPPVSTPKRRGLQHKY LLEVIDEHSPSDLSLPRTRSRTRLSV DSEATSSRPGTPTMTKARGKRATSQ APPTASPSVRRSLRGHSEPPAALSAQ LVRKPKTARAGVRSRKTSSGVQSPV AVSPTPIDAPIDVPDSTAPEEEQPRLR RTARRRISELSDQSANGTGDLRSEA SSSRTGSKSNSAASTQNRELRPRLR RTSKSEH								