	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	ext reg
0	Q960G3	Q960G3_DROME	Drosophila melanogaster	NaN	28.06426	S722;S1216;T1223;T1248;S1255;T1439	NaN	40245499	MEAVPRLHMLWFALKSSPEGTSFA ALKKYIAEFYHEDPEAYSKEVHALET LRNQAMHTTKDGAPVMKRYYCQLH ALQNRFPQLADRGIFTFKWKDLYHS AVHEVTDLRFERAAVLFNIAALHTQ SGASVTRGDVDGMKMACTHFQAAA WAYGELRERYANVNGGGDFMTPEL LVFQQQVCFAQAQECILEKSLIDNRK PHIVAKVTAQIVVYYGAALAALLTGG DDGPVAQVIDSSVYKLWKKYVRFKI NYLTCILYLYQGQHSEEKRQMGERV TLYQASWDKLEEARKESKGLPDQRE INESLSFTADVVEAKRKNAKNENEFI YHEAVPELSTIAAVQGANLVNGIGFQ VSDEEHAGPDIFARLVPMKAHEASS LYSEEKAKLLRKYGALLEEKDTQLES YMSSLTLDNLNINEEQANKLPQGIV DRCAALNANKTAISDLVEAMSQLAE ITADVETNLGEISSMLEAEAKAEREF QSATGVQRTPNAHITELSREFQKYSE AHARAGESNNTLRKAMSLHVNNLK ILARPLPEIQQLMPKLSSELNTTEIFR DVKLILNKVNEMKAQRAQFHADLRI AINEDDITGKVIAHGGQEGLQALFAT ELGKHDKITELLDQNMVAQGNILQA LTENYAKAAPVLKTLQDVKQKREHF YSSLAASYDVYEDLLAKSAKGLEFYK KLAGNVQKLLTRFRSARDVQSEERQ QRMQSVKAATTPVVSKPIAETTPVPA VSSTPKLRDYLKAKAAMADASNPAY VPTVRPVPVGSENPTQAACSYATAPP NEPPPPYSLTQQQYFDPSAAGYTNP MYQQQQQHIAPPAYKAQASPNSQTL HGALGQMNLQGQSQDNNQAGMAY NYGYPSGSVPPLAYAPPGTVPASSAS QGLNIQQPLYVATSGNPVSVSNPSE LPSTLQAPFVVNPMSNPYQTAAGYS GQAYQQVNAQAQQVTYPTAPSGSST GQSAQQPLGYAPSQGPQQQAGGYP QSQTPQQQVGAYQQQPLSGYAQQLT PQQQTGYSQSQAPQLQAPSYAQNQ QSTGQAQQQTPQQQQTGYPQTPQQ HLAGYAQSQQQATGYPQSQTSQQQT TGYSQSQTPQQPLAYQQQPSGYPQQ QQQQSLAPQQPSLYPSQAVQASPQPI PGQQATPPNAGQPLPYPQQYTDPNA TPAPAPGVSSVPSPVPVPTPAPTSSQ AQVPTSPHPSATYSSYSNHPGYSFN PQTGKYEYSSGYQQDTSSLKGSQAS QSYQFSQSGKQQSVGTTDSEIASRS NTATGFDPPIVSHTKVNMAAKDSIS AIEGNESSNYYSTPYGYLGSVNPQQ QPTPAPPSNSNASIYMQSGASSTAET QTTSSGVPYASSAALTKVEPKPEALP PKVTSNVDLLSDLDIDCSVAVPPPML PQPVLQPHVVATPTPPASQVSVPVKV ESVAEHAAPATPEIPVAATEGTAQTP VTIPSGPKCASLDNLSNCSDLSSLEN FDWDSVSVTHSVSEKQTKASATANG HSSSFAFQSETFTDEKTTKYFQKEV ESYEKLLENLHVKMLNGKTQLGAK WQELQQKLDKEAAANKRSTTIAKLF PEKNRSLDCLPYDHARVKLDKQTDD YINAAYMKNLSAGCPNFIVAQTPQP NTINDFWSMIWSEKSRTVVCLHTPN ELFDPYWPQALDQPTHYDDYTVTCL KVQQLSHCSEYQLKLSMHGADAVL DLSLLQLKQWTKGAPAQLLGVAENA LETHRQRCKAANAPQSPLIMNCLTG SERSELVAIGVCAIIATQNKQPILINTI DVWSRICAQRQNSLRDSAILEQSMQ IVLCNAHNVLNKRGIMTSYQMKMA PQVTAKEQQENKDPLNELDALWKL K	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	Nor