

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
A0A0B4LJ24	A0A0B4LJ24_DROME	Drosophila melanogaster	NaN	25.496522	NaN	NaN	33925313	<p>MQWKKKFFTRLKAATGNSRVRRMLC CGRRKENGRSVPDVTASPGRAPPPG LPANQMPAMGNQQHHGNQQHHG NQQQHHGNQHSNHRGQSGSLNSA AGVKDPVMLQGDFRKVSIGSSEIFR QIEAVENDHDPNTAAALEAVERRGE MIVRVLEPRCMGSKQAVDAAHKLM NKADARHTVQLVEIVKRPQQTGLGYI REGNGADRTDGVFISRIALESAYVNS GCLRVGDEILAVNLVDVTHMSLDDV VIIMSIPRRLLAIRQRRGNRGTGSP GPPTLSRPEQKPPPVVVIKRDLRDED LDETRMPPRPRSSRRRTGDGDEM TESRSRLGLGLNNYSPOSEQLDMYY NTRGGGGGAMGEPNNGWYKPPPPP SSVITEQPTKAHAFAPSHAYQNAQT LESIAEKVHAFYPGQPGGPPVGPSR RMSTGTGNVGLAQHARFPRSGSD QHLPRVEYSYNSLGRHSLLRSSL KPGTTGGAPMQVGVGGTLGRYGRY DQQRAGVSKYGGPPGGAQSLTRRSR PNLDYSSDTEATIGPRPSYYYNRPPI GSMSRGGGAGGGVGAASAAALLA GAADLNKFNLSLPRRPGTRLOGIRS RMGDRLVDENDGNTSAPEFDVRRG RDLRQRITASPSIFTADEYRAWLRRR PSSSAIAEQMRMTRDMFAQPRAQR FSCSAENIHDALRNTESIYSSRNHIL GTGTLDRNMGLTRPISALPVRSMSS QHIGGAGSIRSIRRMRLLELSAG PASPSGSILSTGGHQSPAPTPSATLP RPHRQIDINPAEFKYLKDKPIVDIG GISGMLWIHLLAGRGLRTAPEGAAG TATQGGQTRDLYCVIECDRVHKARTV VRSGDLQFDWDEFELDLVGNKQL DVLVYSWDPQHRHKLKCYRGAISLSSI LRQSPLHQLALKVEPRGTIYIRMRHT DPLALYKRRGLPSLRAGYPTLFGADL ETVVNRESKNAPGSAPVPIVLRRCVE EVERRGLDIIIGLYRLCGSATKRLRL EAFERNRAVELTPEHVPDINVITGV LKDYLRLEPEPLFTRCLFQMTVDAL AVCLPDDPEGNAKMLMSILDCLPRA NRATLVFLLDHLSLVVNSERNKMS AQALATVMGPPLMLHSASAQPGADI DHAQPIAVLKYLLQIWPQQAQHQ MAQHMGAAGAMMGGLVTAGSMS NMAGVASGRRGESTGQRGSKVSAL PADRQQLLLQQAQLMAAGNLLRS STSPYQLGGVSGAIPDPSPLPLGT PSPGSSASTGSGSGSGKSTDTIKRG ASPVSVKQVKIVDQPSSPYSIVMKKP PLQKDAPEVEITPTTQADTESTLGCK ESNGTASRRGNVDFYDTHKTQAKSV VNEESSYSSKYTGSETKKIIPGNSY PSKANASGLSGGEDYKAMRNKSSAT SSSSSQATVLSAGSTATSAPTSSD DSDDLVSYSKSSASTNALLAQSQAMT TSQLMSKYLKREPRVQFTPIKSPESP SPPGSGDGLPKGTQVLTPIGSSSK PGATTGAISKYTTGSVESSINANSQK LSSPSRLCNSKDNSRTGTASSTTPA TSMVSTGRRFLDLSASSSSSETETKT YIGGTTAASGAIITTIYTNNDTKNSGSS SSKSGIGGSGTGLGAVSGASSETRS FGSTLFGSSGLGNGNGSSHNSAS PSPFTTNGNGNHNMTMHLYGTLPK NGTSTGAALFGGSANSSSYHSSASG SGAGTASSSGVSSMTGSTNSYDFYT STSSTVSSSRPFANGGNNYHTLGTY RAQYAATNPFLDAFDEKPGSNGGNA HGEEKLGADKGHRAAVMAFQSSG DSKNGSDEYDDIK</p>	None	None	None	None	None	None	None		