	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
	Q9VH97	Q9VH97_DROME	Drosophila melanogaster	NaN	28.06426	T3855	NaN	40245499	MDPDEAQRRREECERKARRGEMDP RLEFTFQLLIDATQLPRHQLMDYIFE GDMLDEINQLFLPNMKNKLLWFYQ ETDDPEPTPVPDPNKPGPSRSGVAS SSSKTPQGGASPSGMPPPKHKKLFL TDGWTCAFTGVCIYIFRVNTSKQLPE EGFQKDLYCGVIDAKNIGLVTSIERIV EFVFMQALAFPSLEGDEEDVSCGLI KGQLLPGLRSFCSALRVCEQVCDHH NVFADGCDMFEKIDAVEEVKDMSK NQEFCAQLEERVNNWTKGILKILGE SEQLRKENDHSGPQDELEYWKKRG AQFSQLLAHLQDKEVQFTLHCLFLA GSRIIKQWKETDRKITFCYNEARDNS KFIQAMETCCHSLYLDDPVSMKESI LSLLQTVRLIYSVSQFYNTSERTSAL MVKITNQMIETCKSYITCRCKETIWS QDRNVIRTKLSNCIKLNHIYHETYYT VREQPFLPNQTPFGFSENFVFGKFD TFCERLSKIISMFNLIDDYNHLFERR LEGLLLGEALEDASNHFEEAKKEVT SRKYDYLDHRNSDFNIDFERFIHKT NSLKDTIATLIEKDFDTVWETPQCIR FLVRFEKVSEKIPLTRMDEKYTRILR YVEKEVDRILKTFRKQRDDPPLARN FPPIAGRIHWCRALSLHITELMDAV MEHVVLSSLPMAKDLDVRYHNVLGI LQEYEDEIVSIWLDQDVSVADACLLQ PLLSLQGDKLFVNLHPTIPLLIREAK MLAKLDIELPIVAATLMSRQQYFITIQ DSLNCLIKMFLSTVRAVKLEVRPLFL PQLVRLTAMLKPGLHTINWTNQNW TEFYERCKQAIESFDVLVARVHDIYS NRILHVLMWMQDVSLQILPADDEIW TVDEFLERSEEACRKAAIELNRKSQ MVSEAVEEVLSLVDRATAAFKEIAG DDVITLFDAATPKGDNSGSGGRKPE DGGGGGGGAAAPSTSGGGGGGQQQ DWSILWSCFENPLSLLSTTESLPKG MQDMVCNAVVEMRRYYSRKVIDVLI KVIRAALDTLRRRFIADENETVFKKP VFALHAQLQIPHVVIKPNLDELQDIL VTAGKNITGIAKGVAQWSSGKDPPV RTAPLNSFAMFSKILSYQPQQVSMT VQPRVGRNHNESTGGGKSRRRKIYC LASEERPQMPHMLKSFYSAIMDNK EVAKAVNQLASCTKNVKPEIQTYIKR WKPYHFLWKNDRTTRQLMEFGLQE FETTLRCLSDLDANLLVEPDMEVFG QCVAVYNEKLKYGLAIEIKSCNHKIG QAMKKKYKKEMDYVYAVINEMDRK LDRPIRDLDDVRMIMETLGKIREQE VDMELRIDPIEEAFNVLTRYEVQVER EQFDLVDNLRATFQNLLAGALQAQV KLLDMQPAFQDDLRTNLDNFKQDKI SYVTEYRTAGPMQAGLTPREASDRLI LFQNRFEGMWRRLQTYQSGEELFG LPQTDYPELGQIRKELNLLQKLYKLY NDVIDRVSSYYDIPWNEVDIEEINNE LMEFQNRCRKLPKGLKEWPAFHAL KKTIDDFNDMCPLLELMANKAMKP RHWQRIMDVTRYIFEFDSEGFSLKN ILEAPLLKHKEDIEDICISAMKEKDIE AKLKQVTNEWSVHELQFMSFNNRG ELLLRGDTTAETIGQLEDSLMVLGSL LSNRYNAPFRKQIQQWVYDLSNSNE ILERWLLVQNMWVYLEAVFVGGDIA KQLPKEAKRFSKIDKSWQKIMQRAH ETPGVVACCVGDDLLKQLLPHLQEQ LEICQKSLSGYLERKRMMFPRFFFV SDPALLEILGQASDSHTIQNHLLNIF DNTKSVKFHDVEYNKMMAIISSEGE MIQLDRAIRAEGSVETWLTQLLVTA QASLHSIIRTAYATINDPNFTLLSFLE KAPAQIGLLGIQMVWTRDAEMALM	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	None

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									AEEVNQKLKISEVTERKIMKAREEFR AVAKRGSILYFLIVEMSNVNAMYQN SLKQFLVIFNHSITKSTKSSVTEERIN IILRYLTYEVYKFTNRSLYERHKQLFT LMLAIKIDYHNGNISHEEFLTFIKGG ASLDLNAVTPKPFRWILDITWLNLVE ISKLETFSTVLQVIELNEKDWRCWY ECEKPENEEIPCGYNAILDGFRKLLL IRSWCPDRTISQAKKYIEESLGPEYS EMQILDLEEMWLESEPRTPFVCLLS IGSDPTTQIGALAKQKSIVLKSVSMG QGQEYHARKMIIESMAIGGWVLLQN VHLSLPFCSEIIDMLVESEHIDDSFR MWVTTEPHNEFPIGLLQMALKFTN EPPQGIRASLKRSYQSFTQDFLDYTS ATQWPPLLYTVAFLHTIVQERRKFGP LGWNIPYEFNQADFAASVQFIQNHL DEMDPKKGVSWQTLVYMIGEVQYG GRVTDDFDKRLLTTFTSVWFCEPLL SNSFEFYKGYKVPGTKSLQGFIDYIN SLPAYDTPEVFGLHSNADITYQINSA KGILDTILSVQPKEGGGGGGETRESI VYQLADDMLRKLPAQYNAYEVRENL TRMGILLPMNIFLRQEIDRMQRVIK RVHTCLCDLKLAIDGTIVMSPALKES LDAMYDARIPETWMKISWESTTLGF WYTELLERNGQFRTWISTDRPKVFW MTGFFNPQGFLTAMRQEVTRAHKG WALDSVVLQNQITRYNKEDITEYPTE GVYVHGLFLEGASLDRRSGKLIESK MKVLYEQMPVIYIYAINTTAGKDPKL YECPIYRKPQRTDLKYVGSIDFETEF NPKHWTLRGVALLCDIK									