

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	ex re
A0A0B4LHK4	A0A0B4LHK4_DROME	Drosophila melanogaster	NaN	30.60235	T2754;S2757;T2927	NaN	33925313;40245499	MDKAATVDRSTSSFTFLENLTKAMIR RFRYSVDVYLLHLVHDDIPESDPPSC PHEGEVREDEDETEEEESDSESEG EEEEEEEEEIDVLQDNDADDEEIDD EDEEDAPEVSSFLLDANNKRSSNI SALLEAAANEKAPVLRHATHAIDETK QALTKMRCASSPRDKNGFSRSLVAA CTDNDVNTVKRLLCKGNVNLNDAA ASTDDGESLLSMACSGYYELAQVL LAMSAAQVEDKQKSTPLMEAAS AGHLDIVKLLLNHNADVNAHCATG NTPLMFACAGGQVDVVKVLLKHGA NVEEQNENGHTPLMEASAGHVEV AKVLEHGAGINTHSNEFKESALTL ACYKGHLDMVRFLQAGADQEHKT DEMHTALMEASMDGHVEVARLLD SGAQVNMPDTSFESPLTAAACGGHV ELATLLIERGANIEEVNDEGYTPLME AAREGHEEMVALLSKGANINATTE ETQETALTLACCGGFMEVAFLIKE GANLELGASTPLMEASQEGHTDLVS FLLKKKANVHAETQTGDTALHACE NGHTDAAGVLLSYGAELEHESEGG TPLMKACRAGHLCTVKFLIQGANV NKQTTSNDHTALSLACAGGHQSVV ELLKNNADPFHKLKDNSTMLIEAS KGGHTRVVELLFRYPNISPTENAASA NVTQAAPTSNQPGPNQMRQKIMKO QLQHQLQLNAPPGLHELSEARAS NQHFHQQQFSSAGNGSSNIVAMG TGFDFDAGELQLTATAGMSAGAGTS TTGSETGMEEYGEVGGIDLTLGAQ QQEGLIAKSRLFHLQQQQQQQQQ QQQQQQQQQQQQQQQQQQQPPA AGQHQLVPCKHFDLMEHINSLOP PQKAPPAPPVLFHTVCQPVMQQQ QQQLQPGQLKMLPNRNRALKT AEVVEFIDCPVDQQPGEQVRTQPL GEDGKTPQFACAGEDPRLORRRGF MPELKKGELPPESSSSDPNELALKG ADNNQPVPALDNSACAQIPARNSG GAITHSSEVLQSTAISDRPKVKATNK NNRQAAAAAAAAAAAAAAAAAAQ HAQQVLPNPMVSIYNNLHLQLQH PHLQFQQQLLHHQRVAGLDNAAA AAAAAASSANMAYSISPASPLPSPTG SGNYVDQQLQQQSMVALQRKTAM DDFRGMLETAVNGPRGRKDALNT POLNFFKDGWHMVGHNFFGDQP KSPTEPPEMEETMSSPTEADRLG SEPRAEMKNLATLCSAAAAAAVAA VNKDQVEISSDLESECEDDAEGGAG ADCEENTLPEPIELAAALREDGIIVE EEEDDEEEDDDEEQDTNSGEVDK LNYDDEDAEVDNDGEVDYIDEDEG GGEGEEEDDADDEFFLDEPDS QGTGNNNNNKSGASSLPLKQRKM ATRENLILNSQTVCFPPPELSNSEL VHVLQISNLKAAANSNAALNSVLQ QQLAAASAAAAHAKASVVHQKQH GEGDQCEDDGSASASELYSGLEHF ANDGEMEDIFQELASSLNPPELAEF SLNQMKGRFAGNWAQSSGKWTG QEQLVGVVRSPLINPGDVPQDAQR QANLVLLDYPMQQNIQLEQRLLDAE EMHLQQHQQTPLSLLPFTDEQQQ LHHQALSNASDFQQHQQLALENDP ELKQQLQNSNARIKAVAAHQQQ PPTNFVYNVESGDKNAPPVQLLQ PPHMAHQAAQQQGVGEPLTEQQQ QQLHAEQAHLFQHRITGGQRPPTQS ELEQVAQELLQRSGQVPAGAPVVG VQAIPLKQKHFNLHPPPCPTCVQH QVATQTHPASVVVPQAVGYTQFAL QASQQQMQLNELSIWPMATPTPA PSSGVSTKSMGGIAKKAIDKQSRK ERRCVVROTQAGIQENTKHLQPV ATAQQQLVQNLAVATTVSLDKTIE IDSETESNHDALTALACAGGHEELV ELLIRGANIEHRKKGFTPLILAAAT	NaN	NaN	NaN	NaN	NaN	NaN	NaN		

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