

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	ext							
Q7KRY7	SCRIB_DROME	Drosophila melanogaster	Protein lap4	33.882171	NaN	S433;S435;S700;S702;S705;S834;S837;S1031;S1041;S1475;S1477;S1478;T1599	33925313;20146544	MFKCIPFKGCNRQVEFVDKRHCSL POVPEEILRYSRTELEELFLDANHIRD LPKNFRLHRLRKLGLSDNEIGRLPP DIQNFENLVELDVSRNDIPDIPDDIK HLQSLQVADFSSNPPIKLPSPGFSQLK NLTVLGLNDMSLTTLPADFGSLTQL ESLELRENLLKHLPETISQLTKLKRL DLGDNEIEDLPPYLGYPGLHELWL DHNQLORLPELGLLTKLTYLDVSE NRLEELPNEISGLVSLTDLDAQNLL EALPDGIAKLSRLTILKLDQNRQLRQL NDTLGCENMQELILTENFLSELPA SIGQMTKLNLNVDNRNALEYLPLEI GQCANLGVLSLRDNKLLKLPPELGN CTVLHVLDVSGNQLLYLPYSLVNLQ LKAVWLSENQSQPLLTQPDQDAET GEQVLSCYLLPQQEYQPIPPARDLES DSEPFEEERPSRTVVKFSEEAQKEKE TPFVVRQNTPHPKDLKAKAQKLVKVER SRNEEHANLVTLPEENGTKLAETPT ETRTIANNHQQQPHPVQPIVGVNS KQPVVGVVPTTTTIVAPTGVQGS EGASSTANNKAATAAVVAELAATV GGSDEVDDEDEFEFSDRRVGF QVEGEDDDFYKRPPKLRDRDTPHHL KNKRVQHLLDKQASEILANALASQE RNDTTPHSLSGKVTSPIEEEEQLEV EQEQQQQQQHPFDSLSISPISAGKT AEASTDPDNLGVTCLRLEQYEHIE RTAAGLGLSIAGGKGSTPFKGDDDDGI FISRVTEAGPADLAGLVKGDVIVKVN GIVVVDADHYQAVQVLKACGAVLVL VVQREVTRLIGHPVFSEDSVSVQISV ETRPLVADAPPAASISHERYIPAPIEIV PQQQHLQQQQQPIQVQVAPTHSYS GNVFATPTAAQTVQPAVSAAPNGLL LNGREAPLSYIQLHTTLIRDQIGQGL GFISIAGGKSGPPFKDDCDGIFISRITE GGLAYRDGKIMVGDVMAINGNM TEAHHDAVAACLTEPQRFVRLVLRQ EYRGPLEPPTSPRSFAVLNLSLSPSGY LANRPAFNSRSVVEVEQPYKYNTLA TTTTPTKPTVPASISNNNTLPSKKT NGFATAAAATIDSSTGQVPAARRTN SVPMDGDDIGAGSTTSGDSGGEAQP SLRPLTSDDFQAMIPAHFLSGGSQH QVHVARPNEVGSVAVTVNVNKPQP DLPMPAAPTTELGRVTETITKSTFTE TVMTRITDNQLAEPLISEEVLKPNQ GSLGFSIIGGTDHSCVPFGTREPQIF SHIVPGGIASKCGKLRMGDRILKRVNE ADVSKATHQDAVLELLKPGDEIKLTI QHDPLPPGFQEVLLSKAEGERLGM HIKGGNLGQGRGNPADPSEGVFVSK INSVGAARRDGRKLVGMRLLEVNG HSLLGASHQDAVNVLNRNAGNEIQLV VCKGYDKSNLIHSIGQAGGMSTGFN SSASCSSGSRQGSRASETGSELSQS QSVSSLDHEEDERLQDFDVFASQK PDAQQPTGPSVLAAMVHGASSP TPPAATSNITPLPTAAAVASADLTAP DTPATQTVLIIHAEQAHQQQQQTQ LAPLGQEKSTQEKVLEIVRAADAFTT VPPKSPSEHHEQDKIQTITVVISKH TLDTNPTTPTPAAPLSIAGAESANS AGAPSPAVPASTPGSAPVLPVAVVQT QTQTTSTEKDEEEESQLQSTPASRD GAEQQEEVRAKPTPTKVPKSVSDK KRFFESAMEDQHKPTOKTKVFSFL SKDEVEKLRQEEERKIATLRRDKNS RLDAANDNIDKDAQQRTKSNNS SSGDDNDDSDQEEGIARGDSVDNA ALGHFDDAEDMRNPLDEIEAVFRS	None	None	None	None	None	None	None	None	None	None	None	None	None	None	None	No