	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
0	Q9VH10	Q9VH10_DROME	Drosophila melanogaster	TBC1 domain family member 30	28.06426	T2678;S2790;S2865	NaN	40245499	MRFSLSPPPQKAITSARLTSPTKNSL SSNNTITTPGSNNRSPSSTKTTMLT RNGGGHGTSPTASGSGHAPSATAAA DDEATSDYNQWLHAMKLVARLPGG TPPEFRRKLWLSLADKYLKSKNVDW AQQREKCFCEEWREDDEELGIQIVK DLHRTGSNLCTGPAGSINQAKLKRIL LGYARYNPEVGYCQGFNMLGALILQ VMDKEEEESMKVMIYLVEGVLPTGY FYGSMGGLQADMGVFRELMQTRLP RLAKHLQRLQGPVENAFEPPLTNVF TMQWFLTMFCTCLPMSCVLRVWDL VLIEGSDVLLRTALVLWSLLEERVIS VRSADEFYGKMGSYSSELLNGHLVD SNGLIERVVKLGPIEDLRQLRDKHLY NIAPLRHKQGLQLYYDEEDTHSDEE RLAVATVFGLNWGRRGSVGPAAAGK QQVEQKDRLALDISLLKKQYDRLRE RQKQAHVILTTACSTAARQGSGPASS SQPAVPVNQLLLGRPAIVTNKGKRV GAPLGAIPPARKPSLPAVLHTKPTSE KQLRRGETLLWRDTDPSRRRRDSLT WKEIKADRAAMIREGVDVSSVRTQK LRTRFGKSDSSSYSEDSDGEQESGT GGGGGSSTDTSLCDDDDPKSTEKSP KQKAKLARKLKEQKQLAGSRETSLE RQRPKSWAPSSHEIPFMLMGTDSG DEKEDKSTKEGPITGDQAEDSATES GHYEFDRELHLVSSKMEPLKLPFDP EFTGMTSVSPIPTPREKSEAEEDLLD ERKPFDVSDDGVTNQYFERVNSVER PNRLELTYSLNEEETDTNAIYLEERE KVEGHSGDREYNSLPPFYPRENDDG VQGGGKVPQIRDDNIPGENKDDYKE LLSMTIEENTVYKPPTPTASTLSNAS RKRRDPRRKTLTRSSTIEIEERYQAL ERRISQDQPSGDRQAKYIPSTAALEE RFNTLEKQLSAEKQRKELSEMEAEY PIKSERIPSTADLESRFNSLTKQMSS SESSSKTPIDLKDEDRPSGSSSKNQK DSEKTSKLHKSEEPESNTKETTGET EASDSNDSKIGEKETEQPRIKKLPST AELEDRFNALERKMSVQKSSPSKNK KEPPDEEESKSTKEPEEPEESEKAN EKTSGRQTPIAKKDSKDSDQKKSET KENQSPTKNQDEKVKVKSPKSEEMI EKETSSNPKEDSHESEAATNKKVEG NRELSSEKGDHKIKEKSEEAPGKAG KETAETKNANVKDSSKKGDSQKNE AAKTSVSQTESDLKPSSKENSTSKD AEQEKTPRKSPPSTEELEKRFNALE KQMSTTNLETTKEPDQTKPATKSQS TSAEVKTQKSMKSFDDKIKEVNVAIE KEQSRVEVEVNAEKKRKNVEEAPKN KEGDSQQPEESQHKGKNQRRASEP PSTEDLEKRYETLKRRMSSKNQFSE TVDEALERIQQEVISEAVEEKKPPPS TEDLESRFEALHGDKKNVESKMDE TKHVDVAIEAHIPSPPPPPPPKERPV LAEPVLHQQQALIEELQSKMRGQSP GEENLKPSEINPQRRQKKLLQRPTP MGDETSEAPANTAYYRAANHEQWQ QRMVRRFSDLPSRADLENRLQFLER QLYKKFYKQRCASDSEVASRVKLPP EDQPSTSRQARKQEAEGQLEQRVLA LEKQLSENSLKLLEAMRERHRSADD SGSPRRLSTETIDATGKELVRYTQNI GELEEVDAHKPINISINIKMMVNKD SESKQPKGESKPTTEDLTRRLEQLE QQLLEERAKNGSIPPENEVLEEKPE KLEEKDSCKKQEKNCHNQHVKGDE VEKTEIPADRKIEPASAKETKTLENV EKAQTRAKVVDTEKSVKDQNAVTDE KSVQDQNVVVDKKADRKILDKKDKS PAAGKSEDTKQTSGKKEKSEDIKQA SEAPKAGASKETSTRGKPSETKLEKP TTKESVLKETFPKKENLESEKPKSKE NEATKTETQKSKETPTVAVSPKESKV SSKQMTEKKETIKDSSSKELPEKMVI NSTDVGPMDPNGKTVVLLMDNEHR	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	None

								ASKVRRLTRANTEELEDLFQALEKQ LNDRNLVKSEDGRLIRVDPKPSAEQ VEQTQAISDLTKEIEDFTSAKPEEEN PKEAAKEDKPEPEEPEDFDWGPNTV KHHLKRKTVYLPSTKELESRFRSLER QIKLLEDVEKIDVEQRLNEIERKIKL QYSLSHEKDLNKYLELCEGKGLDDD EPVPVETPTKEAEITTARDRSRSPGR KALATKSPYTSPSRKATIKTPHTSPTR KPIIKSPYTSPSRKSAKSPYTSPSRNR QRSPSPTRSPERKSKKSPYTSPARRK PHPNDLPISDDLEYKYRVLDLVRSKS KENLAKRMNDPNRKPAIHPLEMILS PSPDADAIPTTGELEHRIRVLDEKLK SPAKTRSKSRSRSPTIEDIKRQKMRD EKKPRTPVHNLERIVSSPGRPEPPTA EELEERIRILEQEHKFDFKTQKDYKA FNQKLKDVISPSLSFDEFRAAKSREQ SPRRHGPTTPKSALRRDDFDEGYCG GTHTSTLYRPTSPKVIRFRDEDEDED QFEEAPRPKSRQTSDRMTLADQPSA TRSYASSTEGLDALGSRLMRETSPIT RTGTHTGVPLRTGENINDRLSSIKNS IKSIDTLCEEKPYQKEKCQRYIDSLFT DSLHFASKKSSLEDLSLSRSLSRSES RGRSIHRSGDYAPSIRVTSEHRSLGS ADSRRSPLGNRDTSPLHHRSHRDIS RELSPRRRRLEEEDEERKDRESSRV RRDNLLPNYFADNRSELSSGSSLTG FNHKVDRQLEETCAKYADDRRSACR TPLSHPYESRTTATRHSHTDPVQIPT NPAGSATATDSFPRPVSPYRQPYDPY HRSPGGAGGTPLYQPGKLEIRHTTVT STFYDRFLTEKQIERQTHSRPPSRSP VVSPSVPAKSYVELCSTSGTSSTTAT STSTSSFMSSSYAGPSFSLPSASNFS YLNPGSGSGSGISSISPRASCSDLRS TTSGPTSTSTTSVTTSSYVPYNFTSSF TSRLNDPIITSTTSAVSTSSLTHSTGV YNPMMSFTLREPLASSSLGGSSASP LLPFQFNRTFTSNFDKEQNKQ								