	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	Q9VUB5	Q9VUB5_DROME	Drosophila melanogaster	NaN	28.06426	S16;T119;T120;S378;S812	NaN	40245499	MPMSSHDSVFVEPAVSSSGGGSTSS INRIGVASGPQPPPPHIVIDGSSLSTQ AQLRIMQRRMSISTRQILSASQSQSI NQSQKYAVRTAAGTGALAAGAASSG SSGQELINPQIYKIVTTDGSTSNVIID ASAAAPPHNSKLLLSNLTVLSKQAPV QGAAGQQQQQLNYLGAKSLPYVSAS PAKTQQQPQKFGSISAFKAQHQQQQ QHPHATLQKVTLGSRVATRLQSYVP ASPSQIMVQPAQPKYVNATATTIGGN AALLKKANQKITVKSVSNMSQQQQQ QQQQQQQQLLQAQQLKTFITQQQQ QQTYKAGAKAKFVKQTTALSIAALPQ QQQQTTYAKQSMVTTSTPAKVTKLN SKYVQQQISLPQGTQLQHKASPNVT GGGYLLQQSQAAVGGTIKFVNSHGT VIQQHPQQQQATKRTHYNSSGSSD NEQHAVANSSLITDDVMIVNGTQMT DELSARILQSMAQKSFSQQQRFHQV PATGSGNMPPPTQIIYSNSTSNGAAA SSPGGNASGNMLLAHYQAAGTKPV SSASFITVTGTPPVTVATTPSVSISSH GFASGSAAISSYMSSATAARRQSVSA PSSRAVSLERKQHHQQLQHDVIGGG RKAPTVIEYYNKHGVNSIVGSSNNLA QSNSMSNLAGPRSNSGSGFATTTPT PATPLHLTPVNVPVHVEAAPPSSPAL VKGSSQPPAQPQQQQQQAHPLGPN QLNANDEELYIEEVRPVPVLTQDLRL QQLHAIMQDHTYASQQQQQQPQQA AGDTTNPGAAQQVQQPQQWSLGGI GVTVSGSQGTPTAVGGYCSYFGQQI ARSQADDDAHSAISSSSRMGLASTDI DPGEETETAPEAEAEDDSVTRCICEL THDDGYMICCDKCSAWQHVDCMGI DRQNIPEEYMCELCQPRAVDKARAR ALQRQKRKEHMLLVATQAANGAAA VAAGTTLSGGLGSGLPMSEELQHRL ASGLNGGFATGTGMSKKSKKTKEN SGSTSTLKKTKKSAVGMGGEKNASG SGTPTGSSGKTSKKSSKRKSKSGGD GSSGGGSSPALTAAEKHAANLRQWI ENYEYAVTNHYSPELRARLHAIQKQ PSLLQSIQNTENKALRQIQQQLSTAG SAEQLEQRAQLIPYAGAKVLISSVDL SPHAPIHELRGKYMLTTQFRTQNPT VNMNTPPPSNYLNSFKAHKTPGQF VFFYQLPGVEAPMQTLRPDGSVPQV AQQPPSYLKGPEVCVDTRTYGNDAR FVRRSCRPNAELQHYFEKGTLHLYIV ALTHIRAQTEITIRHEPHDLTAVEQK KSHAAVIQPTSTRCACDMGSDCLFA LPLAVQQQLQAPPTQPRSSHRNKAA AAAAAAAAANSAAAIQLTMGLGVGA TVAAGASVLPNSRNRSTSSSGESSQ MGLNSPQLGQLNLGFKTSVTATSLT APVPGVHCNNSGGSSSSSNNSCSVS MSSVLHDSGICTSSSSPSVSIPSPTPT QMQSPTLQQHPQQIPQQQLSLLQRS PTQQHQQQILAALPTPMLTPMLSPQ LPKPAQQQAHVVLPQSQQTSLLQQQ QSQQSQEPLAVIAAAAAAQQPMATY FVRQPQQQQQQQSPKPQALVAQQQ HVVGAQQQQHFLQQQQKQQQQQM ADEARMAVSALQTLHAAPTSHIVSPI KVAAVQQQSQPQQQQQNTHQQPH NQQAVQQQSNQLQQQQSQQPNYP QSPQRQQKPQPVQHQPQIVISTGAQ AIPATMPTKLSSPTKSAAPVISNNNIT VSAQSSVVGGKKTPAKHPQQQQQQ QQQPVTPVSAATAPAATPSSSESKED DVSASSTTTPTTRTPAKDKPKQSRED RKLEAILRAIEKMEKQEARGKKDTR QSSGGKRQASNSPASPNKRNSSNSI SEDVETPTSTNSAAAAAQRRNKKKR KVSRSLNNNTNGLGSGGGSNNKRR KSIVVESDGESHALTNSESEDQGQH PQSHHSGSEDQAAGLLLALAHNNS SPNEPFKSPLSQSHSLPATPASVSSA CLLIEAAMGPLQQQPAPASASPSLAE	True	False	1.547	5.0	0.607	False	False	False	False

								FKYPPGGAKTKKSLMSSWFQQAEQ QHASGLDSLVQAAMSEINGEREQLQ RQPQGESLPAPALLKVEQFIHQAEST TAVPAREQLHLPLQNNSSVKKRWLR QAISEETTPVDELQQSQNQSVTATPS PQPVPTVSPLANGFSTPLKKRRLVVV SNGTNVESDETHIDVIGEPKDEAEE NVAMTELKVEIENHHQEQDDDVDIL RSPSPGTHQIVAEDNLVKIEPEDTSA AADDVKIDVEREESQACDKFEEMVK VKREEEEQREKEIKQLQERQEHEQP KVEPAPVEPKLENTVAKAEPKVEPS QEIVSKKEPTKVEPKPGESLLRSTAT VTATPTAATIAATTLLDVSKVAFKTRP PLKLEDEPQKKKPKLESILPAPVATV PPVSVPPIPAASNATTSAVTNTAAAS LTTTTAPSSTKNLTEHDIQERLLSFH AANISYLQSRNKKATAALTSASPSQK SNSSSGGSGTESKKSSKDKDEKRDK EKQLKKSKKEKKKSKDKEKQKAAVN VNSTSQIVDTKKKTTQPSKPDSKSSI APVLVPPSLPVATANGKTKHTAYNN VDQQQQQQMRRRTMSMCITPVTPT PVVTPSPLHGTPPSTKKRQTNFEQE LTKPNSQILSSSILLNSSKGLGLPLAA PTVVSVPTAVQQQQHRKENNHQEA TPASGGPMSLAAAIASGKLNAISRRR ESMCGSRQQQALIAAALKKEKKEKK KSKKKDREKQKHDKQKGKEKEREK DKEKDNKQKTNHIQKPAHPTTVPAN SMPISAPAPVPVLVPTPVTTPKAAPIP VLITQPTPSPIHVTQPLVNNCSTKVA SLPFYNTIYGKLQDPSTPTSSPIPVTN TMPSLAEYLESTKSKTTALSAVKPIGI AAVTPLSSAITPAKVAPSSLEMPPPA TTPLKLYTRTASHDPRLNPMLTVPD PTPMPKRKLSISEYRMRHRPSVDTA PTTPTTPTTPTTPTTPPGSNKDRSFA KPQTINKCSLQSPERFQAAIRERRNS ISAHHPQQNAHHNLNNNKGGISNK SGSSSGNHLQQALGVAGGRLQSKN AIVDPAATTLSTVNSILSTAQKLHMF DDKPKGGHFNAAPTLLEQQQEKMS ERSRCLQRTISCDSRVIERLGTGAAA GALEKVTTASTRRDAV								