

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q8CJH3	PLXB1_MOUSE	Mus musculus	Plexin-B1	24.474581	NaN	NaN	33300544	MSVLLGPNLLQVFWAGCVVTLRSLPL AAFTANGTHLQHLARDPTTGTLYVVG ATNFLFQLSPGLQLEAVVSTGPNVD SRDCLPPVIPDECPQAQPTNPNQL LLVSPEALVCGSVHGGICELRSLGQ IRQLLRPERPGDTQYVAANDPAVST VGLVAQGLVGEPLLFVGRGYTSRGV GGGIPITRALRPPDPQAAFSYEETA KLAVGRLSEYSHHFVSAFVRGASAY FLFLRRDLKAPSRAPFRAYVSRVCLQD QHYYSYVELPLACQGGRYGLIQAAAV ATSKAVARGDVLFAAFSSVAPPTVD WPLSASTGASGTSVLCAPFLDEVDO LANYTRDACYTREGRAENGTKVADI AYDVLSDCAQLPVDTPDAFPDGSNDH TPSPMVSCVPLEATPILELPGVQLTA VAVTMEDGHTIAFLGDSQGGQLHRVY LGPGRSAAPYSKQSIQPGSPVNRDLT FDGTFEHLYVATQTTLVKVPVAPCA QHLDLDCSCLAHRDPYCGWCVLLGR CSRRECSRDQGPQWLWSFQPEL GCLRVVAVSPANISREERREVFSLVP GLPSLWPGESYFCYFGDQQSPALLT SSGVMCPSPPDPSEAPVLQRGADHIS VNVELRFGAVVIASLTSFYDCVAVT ASSPSAPCRACVSSRWGCNWCVVQ QLCTHKASC DAGPMVASQQSPLLLPL IPPARDELTPFPPTVPQTTVTPNSF PIEPAPSTASDVLPGAKPSRSLWLG PWAGPGPILSPTSTESPLHEKPLPPD PPTIPGTTVPAPTGLGPSTTPEDLLAS YFPFSDAAAVSPAEPGPEALPSMVAL DQPPGTVPDITTFPGAPGSMKPVLDW LTKGGGELPEADEWMGGDTPAFST STLLSGDGDSEHEGPPAPLILLSSL DYQYDTPGLWELGEVNQRVSSCPCV ETVQGSLLIPVHVEREVQLRGRNLW LFQDGRSSECVLELGSREVAVEAQ VECAPPDVWCHEKQHQHFYSYAL KPELVGLFLRWAGGLRVDSDGL HVVLYDCSVGHGDCSRCQTAMPQY DCVWCEGERPRCVAREACNEAETV ATQCPAPLIHSDVPLTGPIDGGTRVTI RGSNLGQHVQDVLDMVRVAGVPCA VDAGEYDVSSSLVCITGASGEEVTGT VAVEVPGRGHGVSEFSFAYQDPKVH SIFPARGPRAGGTRTLHGSKLLTGR LEDIRVVVGDQPCHELLLEQQSEQLH CETGYPVPAELPVTVLFGATERRLO HGQFKYTSDPNVTSGPSKSFSSGG REIWRGQDLVQVPRIRVTVVPR QHGGGLAQKQHVVPKFEPECLVN SSHLLMCRTPALPGPPWDSGVQVEF ILDNMVDFDFAALSPTPFSEADPTLR SLNPEDPSTPFRHKPGSVFSVEGEN LDLAMSKEEVVAMIGDGPVVKTLT RNHLYCEPPVEQLPHPHALREAPD ALPEFTVQMGNLRFSLGHVQYDGES PVAFPVAAQVGLGVGTSLLALGVIII LIYRRKSKQALRDYKQVQIQLLENLES SVRDRCKKEFTDLMTEMTDLTSDLL GSGIPFLDYKVAERVFPPGYRESPL HRDLGVPSRRPTVEQGLGQLSNLL NSKFLTKFIHTLESQRTFSARDRAY VASLLTVALHGKLEYFTDILRLLSD LVAQYVAKNPKMLRRTETVVEKLL TNWMSICLYTFVDRDSVGEPLYMLFR GIKHQVDKGPVDSVTGKAKYTLNDN RLLREDVEYRPLTLNALLAVGPGAG EAQCVPVKVLDLDCDTISQAKEKMLDQ LYKGVPLAQRPDSCSLDVEWRSGVA GHLLSDEDVTSELQGLWRRLNTLQ HYKVPDGATVALVPCLTKHILRENQ DYVPGERTPMLDEVDEGGIRPWHLV	False	True	1.407	1.819	1.191	1.086	0.865	4.719	1.98

