	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	Q8CJH3	PLXB1_MOUSE	Mus musculus	Plexin-B1	37.975063	S540	NaN	33300544;40885482	MSVLGPVLLQVFWAGCVVTLRSPLP AAFTANGTHLQHLARDPTTGTLYVG ATNFLFQLSPGLQLEAVVSTGPVND SRDCLPPVIPDECPQAQPTNNPNQL LLVSPEALVVCGSVHQGICELRSLGQ IRQLLLRPERPGDTQYVAANDPAVST VGLVAQGLVGEPLLFVGRGYTSRGV GGGIPPITTRALRPPDPQAAFSYEETA KLAVGRLSEYSHHFVSAFVRGASAY FLFLRRDLKAPSRAFRAYVSRVCLQD QHYYSYVELPLACQGGRYGLIQAAAV ATSKEVARGDVLFAAFSSVAPPTVD WPLSASTGASGTSVLCAFPLDEVDQ LANYTRDACYTREGRAENGTKVADI AYDVLSDCAQLPVDTPDAFPCGSDH TPSPMVSCVPLEATPILELPGVQLTA VAVTMEDGHTIAFLGDSQGQLHRVY LGPGRSAAPYSKQSIQPGSPVNRDLT FDGTFEHLYVATQTTLVKVPVAPCA QHLDCDSCLAHRDPYCGWCVLLGR CSRRSECSRDQGPEQWLWSFQPEL GCLRVVAVSPANISREERREVFLSVP GLPSLWPGESYFCYFGDQQSPALLT SSGVMCPSPDPSEAPVLQRGADHIS VNVELRFGAVVIASTSLSFYDCVAVT ASSPSAPCRACVSSRWGCNWCVWQ QLCTHKASCDAGPMVASQQSPLLPL IPPARDELTPFPPTVPQTTVTPTPNSF PIEPRAPSTASDVLPGAKPSRLSLWG PWAGPGPILSPTSTESPLHEKPLPPD PPTIPGTTVPAPTGLGPSTTPEDLLAS YPFPSDAAAVSPAEPGPEALPSMVAL DQPPGTVPDTTFPGAPGSMKPVLDW LTKGGGELPEADEWMGGDTPAFST STLLSGDGDSAEHEGPPAPLILLSSL DYQYDTPGLWELGEVNQRVSSCPCV ETVQGSLLIPVHVEREVQLRGRNLW LFQDGPRSSECVLELGSREVAVEAQ VECAPPPDVWCHIKCQQHQFSYEAL KPELQVGLFLRWAGGLRVDSADGL HVVLYDCSVGHGDCSRCQTAMPQY DCVWCEGERPRCVAREACNEAETV ATQCPAPLIHSVDPLTGPIDGGTRVTI RGSNLGQHVQDVLDMVRVAGVPCA VDAGEYDVSSSLVCITGASGEEVTGT VAVEVPGRGHGVSEFSFAYQDPKVH SIFPARGPRAGGTRLTLHGSKLLTGR LEDIRVVVGDQPCHLLLEQQSEQLH CETGPYPVPAELPVTVLFGATERRLQ HGQFKYTSDPNVTSVGPSKSFFSGG REIWVRGQDLDVVQRPRIRVTVVPR QHGQGLAQKQHVVPEKFEEPCLVN SSHLLMCRTPALPGPPWDSGVQVEF ILDNMVFDFAALSPTPFSYEADPTLR SLNPEDPSTPFRHKPGSVFSVEGEN LDLAMSKEEVVAMIGDGPCVVKTLT RNHLYCEPPVEQPLPHPHALREAPD ALPEFTVQMGNLRFSLGHVQYDGES PVAFPVAAQVGLGVGTSLLALGVIIIV LIYRRKSKQALRDYKKVQIQLENLES SVRDRCKKEFTDLMTEMTDLTSDLL GSGIPFLDYKVYAERVFFPGYRESPL HRDLGVPDSRRPTVEQGLGQLSNLL NSKLFLTKFIHTLESQRTFSARDRAY VASLLTVALHGKLEYFTDILRTLLSD LVAQYVAKNPKLMLRRTETVVEKLL TNWMSICLYTFVRDSVGEPLYMLFR GIKHQVDKGPVDSVTGKAKYTLNDN RLLREDVEYRPLTLNALLAVGPGAG EAQCVPVKVLDCDTISQAKEKMLDQ LYKGVPLAQRPDSCTLDVEWRSGVA GHLILSDEDVTSELQGLWRRLNTLQ HYKVPDGATVALVPCLTKHILRENQ DYVPGERTPMLEDVDEGGIRPWHLV KPSDEPEPPRPRRGSLRGGERERAK AIPEIYLTRLLSMKGTLQKFVDDLFQ VILSTSRPVPLAVKYFFDLLDEQAQQ	False	True	1.403	1.819	1.199	1.078	0.847	4.719	1.982

									HGISDQDTIHIWKTNSLPLRFWINII KNPQFVFDVQTSDNMDAVLLVIAQT FMDACTLADHKLGRDSPINKLLYAR DIPRYKQMVERYYADIRQTVPASDQE MNSVLAELSRNCSADLGARVALHEL YKYINKYYDQIITALEEDGTAQKMQL GYRLQQIAAAVENKVTDL										