	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	Q3UH93	PLXD1_MOUSE	Mus musculus	Plexin-D1	24.474581	NaN	NaN	33300544	MARRAAGGAPPSARAAAAVPLRPRP HSRGPGLLPLPLLLLLGAARAGALEI QRRFPSPTPTNNFALDGTAGTVYLA AVNRLYQLSSANLSLEAEATVGPVP DSPLCHAPQLPQASCEHPRRLTDNY NKILQLDPGQGLVVACGSIYQGLCQL RRRGNISALAVSFPPAAPTAEPVTVF PSMLNVAANHPNASTVGLVLPPTSG TGGSRLLVGATYTGFGSAFFPRNRS LEDHRFENTPEIAIRSLDARGDLAKL FTFDLNPSDDNILKIKQGAKEQHKL GFVRAFLHPAVPPHSAQPYAYLALN SEARAGDKDSQARSLLARICLPRGA GGDAKKLTESYIQLGLQCAGGAGRG DLYSRLVSVFPAREQFFAVFERPQG APGARNAPAALCAFRFDDVQAAIRA ARTACFVEPAPDVVAVLDSVVQGTG PACESKRNIQLQPEQLDCGAAHLQH PLTILQPLRASPVFRAPGLTAVAVAS ANNYTAVFLGTATGRLLKISLNESM QVVSRRVLTVAYGEPVHHVMQFDP MDPGYLYLMTSHQMARVKVAACEV HSTCGDCVGAADAYCGWCTLETRC TLQQDCTNSSQPHFWTSASEGPSRC PAMTVLPSEIDVHRDYTGMILQISGS LPSLSGMEMACDYGNGVRTVARVP GPAYDHQIAYCNLLPRAQFPSFPAG QDHVTVEMSVRVKGHNIVSANFTIY DCSRIGQVYPHTACTSCLSTQWPCS WCIQLHSCVSNQSQCQDSPNPTSPQ DCPQILPSPLAPVPTGGSQDILVPLTK ATFFHGSSLECSFGLEESFEAVWAN NSLVRCNQVVLHTTQKSQVFPLSLK LKGPPDRFLDSPNPMTVVVYNCAM GSPDCSQCLGREDLGHLCVWNDGC RLRGPLQPLPGTCPAPEIRAIEPLSGP LDGGTLLTIRGRNLGRRLSDVAHGV WIGSVACEPLADRYTVSEEIVCATGP AAGAFSDVVTVNVSKEGRSREQFSY VLPTVHSLEPSMGPKAGGTRITIHGS DLNVGSMLQVLVNDTDPCTDLTRTA TSITCTVPGGTLPSPVPVCVRFESRG CVHGNLTFWYMQNPVITAISPGRSP VSGGRTITVAGERFHMVQNVSMAV HHIGREPTFCKVLNSTLITCPSPGAL SNASAPVDFFINGRAYADEAAEELL DPAEAQRGSRFRLDYLPNPQFSTAK REKWIKHHPGEPLTLVIHKEQDSLG LESHEYHIKIGQVSCDIQIISDRVIHC SVNESLGTAEGQLPITIQVGNFNQTI ATLQLGGSETAIVVSIVICSVLLLLSV VALFVFCTKSRRAERYWQKTLLQME EMESQIREEIRKGFAELQTDMTDLT KELNRSQGIPFLEYKHFVTRTFFPKC SSLYEERYVLPSKTLNSQGGSPPQET HPLLGEWNIPEHCRPSMEEGISLFS SLLNNKHFLIVFVHALEQQKDFAVR DRCSLASLLTIALHGKLEYYTSIMKE LLVDLIDASAAKNPKLMLRRTESVVE KMLTNWMSICMYGCLRETVGEPFF LLLCAIKQQINKGSIDAITGKARYTLN EEWLLRENIEAKPRNLNVSFQGCG MDSLSVRAMDTDTLTQVKEKILEAF CKNVPYSQWPRAEDVDLEWFASST QSYVLRDLDDTSVVEDGRKKLNTLA HYKIPEGASLAMSLTDKKDSTLGRV KDLDTEKYFHLVLPTDELVEPKKSH RQSHRKKVLPEIYLTRLLSTKGTLQK FLDDLFKAILSIREDKPPLAVKYFFDF LEEQAEKRGISDPDTLHIWKTNSLPL RFWVNILKNPQFVFDIEKTDHIDACL SVIAQAFIDACSISDLQLGKDSPTNK LLYAKEIPEYRKTVQRYYKQIQDMTP LSEQEMNAHLAEESRKYQNEFNTN	False	True	1.299	2.218	2.085	1.096	0.798	5.0	1.891

								VAMAEIYKYAKRYRPQIMAALEANPT ARRTQLQHKFEQVVALMENNIYECY SEA										