

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
Q9QY40	PLXB3_MOUSE	Mus musculus	Plexin-B3	24.474581	NaN	NaN	33300544	MLTDFLQAPVMAPWSPFSLHLLLF LPLLPLTRVHRFVSPNTSFNHLVLP DQGKLYGAVNHLFQLSPELKMESV AVTGPVIDSPDCVPPFRDLAECPOAQL TDNANQLLLVSSRTQELVACGQVKQ GVCEKRRLDGVTQVLYQAEDPGDGG FVAANTLGVTTVGLVVPLPGRDLLLLV ARGLAGKLSAGVPLTVRQLAGPOP FSSEGLGRLVVGDFSDYNNNSYVGF SDAHSAYFVFRRRGARAQTEYRSYV ARVCLRDVNLYSYVEMPLTCHGQGL IQAAFLTPDTLLGAFSAGTSQAQAAL CAFPLADLDRSMEQARRLCYTTGGQ GPSGMEEAATVEYGVTSRCVTLPPDS PESYPCGDEHTPSPIAGRQPLEAQPL LQLGQISAVAALQTDGHTIAFLGDT QGQLHKVFLNSSHGQVYHSQQVGP PGSAISPDLVDSNGDHLVYVLTAAQ VDRILVAACQPPNCTTCLQARDPLC GWCILQGRCTRRECEGCGRAAQP LWSYEDNHCPYIQSLLPAQHPRQEQ GQIILSVRPLPTLAMDEYFHCFAFGGY NSLAQVEEPHVCTTPPDQMPNP PGSDHVTLLALMFEDVVLTTATFS FYDCSAVQALEVAAPCRACVSSLWR CHWCPQSSHCIYGEHCPEGEKAVYS AQEVDILVRGPEACPQVEGLASPOLV PVGWESHVTLHIQNLHYFQGLPALY HCWLELPGKLOKLPASLEETS LIHCQAQQFYPSMSQWELVPIYVT RGEIQRLDNAGDLHVTLYDCAMGH PDCSHCQAANGSLSCLWCGDQPA CRYGPLCPPGAVEQLCPIPSIDVIEPL TGPPEGGLAITILGSLGQAFNDVRN AVTVAGQPCNPDPSPYRISARIVCVT SPAPNGTAGPVQVAIKSRPPGISTQN FTYQDPVLLSLNPQWGPQAGGTQLT IHGQYLQTGGNISVFGDQPCPIQEP VCPAHCHTMPQTEPGEAVLVVFG HVERKLLTTPFRYANPQLVEAEPV SFRGGRRVIRVGTGLDVVWQPLLS VWLEDEPKVKALGVQAQDANRRS CGAPAADPQACHLESGLQCSTLCS VNSSSLLLCHSPAVPDGALPKRVFFA LDNMQVDFASASGGGFLYQPNPR LAPLSHEGITHPYHLKPGHVLDVEG EGLNLGISKEEVQVHIGDGECLVKTL TLTHLYCEPPPQAPOPTNGSGTLPO FVVQMGNLRLLALGPVQYEAESMMS TFPVEAQLGLMGAAVLIAAVLLTL MYRHKSKKALRDYQKVLVQLENLET GVGDQCRKEFTDLMEMTDLTSDL EASGIPFLDYRTYAERAFFPGHVGCP LQPGLEGLGEEGRSVTVRQGLTQLS NLLNSKLFLLTLIHTLEEQPSFSQRD RCHVASLLSLALHSKLEYLTDIMRTL LGDAAHYVHKNPKMLRRTETMV EKLLTNWLSICLYTFLKEVAGEPLYM LFRAIKYQVDKGPVDAVTGKAKRTL NDSHLLREDVEFQPLTMLALVGPEA DRAAGNSGVHRVPARVLDTDITQV KEKVLDDQYKGTFFSQRPSVHSLDLE WRSLAGHLTLDSEDLTSTVQNH KRLNTLQHYKVPDQATVVLIPQVHN GGTVSOSLQGTGCPGSGENTPMLED GEEGGVRLWHLVKATEAEAGAKVR RSSLRDRERERSRAKAIPIYLTRLLS MKGTLQKFVDDTFQAILS MNRPVPI AVKYLDFDLDELAEKHGIEDPETLHI WKTNSLLRFWVNLKPNQLIFDVQ VSDNEDAILAVIAQTFFIDSCMVSEHK VGRDSPVNKLLYAREIPRYKQMV EKKYADIRQSSPASYQEMNSALAELSG NYSSAPHCLEALRELYNHHIHYDDQI	False	False	0.805	1.274	0.727	0.731	0.188	4.358	2.414

