

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
Q9ULL4	PLXB3_HUMAN	Homo sapiens	Plexin-B3	26.147272	S1716	NaN	39531497	MCHAAQETPLLLHFFMAPVMARWP PFGLCLLLLLSPPLPLTGAHRFSA PNTTLNHLALAPGRGTYLVGAVNRL FQLSPELQLEAVAVTGPVIDSPDCVP FRDPAECPQAQLTDNANQLLVSSR AQELVACQVQRQVCETRRLLGDVAE VLYQAEDPGDGGQFVAANTPGVATVG LVVPLPGRDLLLVARGLAGKLSAGVP PLAIRQLAGSQPFSSEGLGRLVVGDF SDYNNSYVGAFADARSAYFVFRRRG ARAQAEYRSYVARVCLGDTNLYSYV EVPLACQGGGLIQAFLAPGTLGTVF AAGPRGTQAALCAFPMVELGASME QARRLCYTAGGRGPGSAAEATVEYG VTSRCVTLPLDSPESYPCGDEHTPSP IAGRQPLEVQPLLKLGQPVSAVAALQ ADGHMIAFLGDTQGGQLYKVFHLHGSQ GQVYHSQQVGGPPGSAISPDLDDSS GSHLYVLTAVQVDRIPVAACPQFPD CASCLQAQDPLCGWCVLQGRCTRK GQCGRAGQLNQWLWSYEEDSHCL HIQSLLPGHHPRQEQGQVTLVSRPL PILDADEYFHCAFAGDYDSLAVHVEGP HVACVTPPQDQVPLNPPGTDHVTVP LALMFEDVTVAAATNFSFYDCSAVQA LEAAAPCRACVGSIWRCWCPQSS HCVYGEHCPEGERTIYSAQEVDIQV RGPACQPVEGLAGPHLVPVWGES HLALRVRNLQHFRGLPASFHWCLE LPGELRGLPATLEETAGDSGLIHCQA HQFYPSMSQRELVPYIYVTOGEAQR LDNTHALYVILYDCAMGHPDCSHCQ AANRSLGCLWCADGQPACRYGPLCP PGAVELLCAPSIDAVEPLTGPPEGG LALTILGSLNLRGAFADVQYAVSVASR PCNPEPSLYRTSARIVCVTSPAPNGT TGPVVRVAIKSQPPGISSQHFTYQDPV LLSLSRWGPQAGGTQLTIRGQHLQ TGGNTSAFVGGQPCPILEPVCPEAIV CRTRPQAAPGEAAVLVVFVGHQAQRTL LASPFRTANPOLVAAEPSASFRRGG GRLIRVRGTGLDVVQRPLLSVWLEA DAEVQASRAQPDPQPRRSCGAPAA DPQACIQGGGLLQCSTVCSVNSSS LLCRSPAVPDRAHPQRVFFTLDNV QVDFASASGGQFLYQPNRPLAPLS REGPARPYRLKPGHVLVDEGEGLNL GISKEEVRVHIGRGECLVKTLLRTHL YCEPPAHAPQPANGSGLPQFVVQM GNVQLALGPVQYEAEPPLSAFPVEA QAGVGMGAAVLIAAVLLTLMYRHK SKQALRDYQKVLVQLESLETGVGDQ CRKEFTDLMTMTDLSLDLEGGGIP FLDYRTYAERAFPPGHGGCPLQPKP EGPGEDGHCATVRQGLTQLSNLLNS KLFLLTLIHTLEEQPSFSQRDRCHVA SLLSLALHGKLEYLTDIMRTLLGDLA AHYVHRNPKMLRRRTEVMVEKLLT NWLISICLYAFLREVAGEPLYMLFRAI QYQVDKGPVDAVTGKAKRTLNDLRSRL LREDVEFQPLTMLVVGPGAGGAAG SSEMQRVPARVLDTDITITQVKEKVL DQVYKGTTPFSQRPSVHALDLEWRSG LAGHLTLDSEDLTSTQNHWKRLN TLQHYKVPDGTAVGLVPLHRGSTIS QSLAQRCPGENIPTLEDGEEGGVC LWHLVKATEEPEGAKVRCSSLRERE PARAKAIPEIYLTRLLSMKGTLOKQFV DDTFQAILSVMNRPIAVKYFLDLLDE LAEKHGIEDPGTLHIWKTNSLLLRF WVNALKNPQLIFDVRVSDNVDAILA VIAQTFIDSCCTSEHKVGRDPSVKNL LYAREIPRYKOMVERYADIRQSSPA SYQEMNSALAEKSGNYTSAPHCLEA	False	False	0.918	1.31	0.815	0.875	False	4.366	1.525

