

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
P70206	PLXA1_MOUSE	Mus musculus	Plexin-A1	24.474581	NaN	NaN	33300544	MPLPPLSRRLLLLLLLLLRGVWIAISPPAGLGPQPAFRFTFVASDWGLTHL VVHEQGTGEVYVAVNRIYKLSGNLT LLRAHVTGPEVNEKCYPPPSVQSC PHGLGSTDNVNKLKLLDYAANRLLA CGSASQGICQFLRLDDLFLKLGEPHH RKEHYLSSVREAGSMAGVLIAGPPG QGQAKLFVGTPIDGKSEYFPTLSSRR LMANEEDADMFGFVYQDEFVSSQL KIPSDTLSKFFAFDIYVYFRSEQFV YYLTLQLDLQTLSPDAAGEHFFTSKI VRLCVNDPKFYSYVEFPIGCEQAGVE YRLVQDAYLSRPGQALAKQLGLAED EEVLFVFAQGQKNRVKPPKESALC LFTLRAIKEKIKERIQSCYRGEKLSL PWLLNKELGCSINPLQIDDDFCGQD FNQPLGGTVTIEGTPLFVDKEDGLTA VAAVDYQGRVVFAGTRSGRIRKILV DLANPSGRPALAYESVVAQEGNPILR DLVLSNQRQYLYAMTEKQVTPVPE SCVQYTSCELCGSRDPHCWCVL HSICSRQDACERAEEPQRFASDLLQ CVQLTVQPRNVSVTMSQVPLVLA WNVVDLSAGVNCSEDFTETESILE DGRHCHSPSAREVAPITQGQDQR VVKLYLKSKEGKGFASVDFVFNCSVHQSLACVNGSFPCHWCKYRHW CTNNAADCAFLEGRVNMSEDCPQIL PSTHIYVPVGVKPIITLAARNLPQPQ SGQRGYECLFHIPGSPARVLTALRFNS SSLQCQNSSYSYEGNDVSDLPVNLV VVWNGNFVIDNPQNIQAHLYKCPAL RQSCGLCLKADPRFECGWCAERR CSLRHHCPADSPASWMHAHHGSSR CTDPKILKLSPETGPRQGGTRLTITG ENLGLRFEDVRLGVHVGKVL CSPVE SEYISAEQIVCEIGDASTLRAHDALV EVCVRDCSLHYRALSPKRFTFVPTF YRVSPSRGPLSGGTWIGIEGSHLNA GSDVAVSIGGRPCFSWRNSREIRC LTPPGHTPGSAPIVININRAQLSNPE VKYNYTEDPTILRIDPEWSINSGGTL LTVTGTNLATVREPRIRAKYGGIERE NSCMVYNDTMMVCRAPSIDNPKRSP PELGERPDEIGFIMDNVRTLLVNSS SFLYYPDPVLEPLSPTGELLEKPSPL ILKGRNLLPPAPGNSRLNYTVLIGST PCILTVSETQLLCEAPNLTGQHKVTV RAGGFESPGMLQVYSDSLLTLPVAV GIGGGGGLLLVLVAVLIAYKRKSRD ADRTLKRLQLQMDNLESVALECKE AFAELQTDIHELTSDDLGAIPFLDY RTYAMRVLFPGIEDHPVLKEMEVA NVEKSLTLFGQLLTKKHFLTFIRTL EAQRSFSMRDRGNVASLIMTALQGE MEYATGVLKQLLSDLIEKNLESKNH PKLLLRRTESVAEKMLTNWFTFLY KFLKECAGEPLFMLYCAIKQOMEKG PIDAITGEARYSLSEDKLIRQIDYKT LTLNVCNPEHENAPEVPVKGLNCDT VTQVKEKLLDAVYKGVYSPYQRPKAG DMDLEWRQGRMARILODEDVTTKI DNDWKRLNLAHYQVTDGSSVALV PKQTSAYNISNSSTFTKLSRYESML RTASSPDSLRSRTPMITPDLESGTKL WHLVKNHDHLDQREGDRGSKMVS EYLRLLATKGTQKFDLDFETIFS TAHRGSALPLAIKYMFDLDEQADK HQIHDSVVRHTWKSNCPLRFVWN VIKNPOFVFDIHKNSITDACLSVVAQ TFMDSCTSEHKLKGDSPSNKLLYA KDIPNYKSWVERYYADIAMPASDQ DMSAYLAEQSRHLHSQFNMSALH EIIYSYIAKYKDEILVALEKDEQARRQR	False	True	2.825	3.135	1.142	1.497	1.084	5.0	2.577

