	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	Q9HCM2	PLXA4_HUMAN	Homo sapiens	Plexin-A4	22.903221	T233;T235;S278	NaN	38253038	MKAMPWNWTCLLSHLLMVGMGSS TLLTRQPAPLSQKQRSFVTFRGEPAE GFNHLVVDERTGHIYLGAVNRIYKLS SDLKVLVTHETGPDEDNPKCYPPRIV QTCNEPLTTTNNVNKMLLIDYKENR LIACGSLYQGICKLLRLEDLFKLGEP YHKKEHYLSGVNESGSVFGVIVSYS NLDDKLFIATAVDGKPEYFPTISSRK LTKNSEADGMFAYVFHDEFVASMIK IPSDTFTIIPDFDIYYVYGFSSGNFVYF LTLQPEMVSPPGSTTKEQVYTSKLVR LCKEDTAFNSYVEVPIGCERSGVEYR LLQAAYLSKAGAVLGRTLGVHPDDD LLFTVFSKGQKRKMKSLDESALCIFI LKQINDRIKERLQSCYRGEGTLDLA WLKVKDIPCSSALLTIDDNFCGLDM NAPLGVSDMVRGIPVFTEDRDRMTS VIAYVYKNHSLAFVGTKSGKLKKIRV DGPRGNALQYETVQVVDPGPVLRD MAFSKDHEQLYIMSERQLTRVPVES CGQYQSCGECLGSGDPHCGWCVLH NTCTRKERCERSKEPRRFASEMKQC VRLTVHPNNISVSQYNVLLVLETYN VPELSAGVNCTFEDLSEMDGLVVGN QIQCYSPAAKEVPRIITENGDHHVVQ LQLKSKETGMTFASTSFVFYNCSVH NSCLSCVESPYRCHWCKYRHVCTH DPKTCSFQEGRVKLPEDCPQLLRVD KILVPVEVIKPITLKAKNLPQPQSGQR GYECILNIQGSEQRVPALRFNSSSVQ CQNTSYSYEGMEINNLPVELTVVWN GHFNIDNPAQNKVHLYKCGAMRES CGLCLKADPDFACGWCQGPGQCTL RQHCPAQESQWLELSGAKSKCTNP RITEIIPVTGPREGGTKVTIRGENLGL EFRDIASHVKVAGVECSPLVDGYIPA EQIVCEMGEAKPSQHAGFVEICVAV CRPEFMARSSQLYYFMTLTLSDLKP SRGPMSGGTQVTITGTNLNAGSNVV VMFGKQPCLFHRRSPSYIVCNTTSS DEVLEMKVSVQVDRAKIHQDLVFQY VEDPTIVRIEPEWSIVSGNTPIAVWG THLDLIQNPQIRAKHGGKEHINICEV LNATEMTCQAPALALGPDHQSDLTE RPEEFGFILDNVQSLLILNKTNFTYY PNPVFEAFGPSGILELKPGTPIILKGK NLIPPVAGGNVKLNYTVLVGEKPCTV TVSDVQLLCESPNLIGRHKVMARVG GMEYSPGMVYIAPDSPLSLPAIVSIA VAGGLLIIFIVAVLIAYKRKSRESDLTL KRLQMQMDNLESRVALECKEAFAE LQTDIHELTSDLDGAGIPFLDYRTYT MRVLFPGIEDHPVLRDLEVPGYRQE RVEKGLKLFAQLINNKVFLLSFIRTL ESQRSFSMRDRGNVASLIMTVLQSK LEYATDVLKQLLADLIDKNLESKNH PKLLLRRTESVAEKMLTNWFTFLLY KFLKECAGEPLFSLFCAIKQQMEKG PIDAITGEARYSLSEDKLIRQQIDYKT LVLSCVSPDNANSPEVPVKILNCDTI TQVKEKILDAIFKNVPCSHRPKAAD MDLEWRQGSGARMILQDEDITTKIE NDWKRLNTLAHYQVPDGSVVALVS KQVTAYNAVNNSTVSRTSASKYENM IRYTGSPDSLRSRTPMITPDLESGVK MWHLVKNHEHGDQKEGDRGSKMV SEIYLTRLLATKGTLQKFVDDLFETIF STAHRGSALPLAIKYMFDFLDEQAD KHGIHDPHVRHTWKSNCLPLRFWV NMIKNPQFVFDIHKNSITDACLSVV AQTFMDSCSTSEHRLGKDSPSNKLL YAKDIPSYKNWVERYYSDIGKMPAIS DQDMNAYLAEQSRMHMNEFNTMS ALSEIFSYVGKYSEEILGPLDHDDQC GKQKLAYKLEQVITLMSLDS	None	None	None	None	None	None	None	None	None