	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	D3ZPX4	PLXA3_RAT	Rattus norvegicus	Plexin-A3	23.439218	NaN	S1597	38843836	MHTVCLLPLLFFTIGGCLGSSRPFRT FVVTDTTLTHLAVHRVTGEVFVGAV NRVFKLASNLTELRAHVTGPIEDNA RCYPPPSMRVCSHRLVPVDNVNKLL LIDYAARRLVACGSIWQGICQFLRLD DLFKLGEPHHRKEHYLSGAQEPDS MAGVIVEQGQGPSKLFVGTAVDGKS EYFPTLSSRKLIDDEDSGDMFSLVYQ DEFVSSQIKIPSDTLSLYPAFDIYYIYG FVSASFVYFLTLQLDTQQTLLDTAGE KFFTSKIVRMCAGDSEFYSYVEFPIG CSWRGVEYRLVQSAHLAKPGLLLAQ ALGVPADEDVLFTIFSQGQKNRANP PRQTILCLFTLSSINAHIRRRIQSCYR GEGTLALPWLLNKELPCINTPMQIN GNFCGLVLNQPLGGLHVIEGLPLLA DSTDGMASVAAYTYHQHSVVFIGTR SGNLKKVRVDGSQDAQLYETVSVVQ GTPILRDLLFSPDHRHIYLLSEKQVS QLPVETCEQYLSCAACLGSGDPHCG WCVLQHRCCREGACPGASAPHGFA EELNKCIQVRVRPNNVSVTSSGVQL TVAMRNVPDLSLGVSCSFEEVTESE AILLPSGELRCPSPSLQELQTLTRGH GATHTVRLQLLSMETGVRFAGVDFV FYNCSALQSCMSCVGSPYPCHWCK YRHVCTSHPHECSFQEGRVHSPEG CPEILPRGDLLIPVGVMQPLTLRAKN LPQPQSGQKNYECVVRVQGRQHRV PAVRFNSSSVQCQNASYFYEGDEFG DTELDFSVVWDGDFPIDKPPSFRAL LYKCWAQRPSCGLCLKADPRFNCG WCISEHRCQLRVHCPAPKSNWMHP SQKGARCSHPRITQIHPLTGPKEGGT RVTIVGENLGLTSREVGLRVAGVRC NSIPTEYVSAERIVCEMEESLVPSPP PGPAELCVGDCSADFRTQSQQLYSF VTPTLDRVSPTRGPASGGTRLTISGT SLDAGSRVTVIIRDGECQFVRRDAEA IVCISPISTLGPSQAPIILAIDHANISST GVIYTYTQDPTVTHLEPTWSIINGSTS ITVSGTHLLTVQEPRVRAKYRGIETT NTCQVINDTAMLCKAPGIFLGHPQP RAQGEHPDEFGFLLDHVQAARSLN RSSFTYYPDPSFEPLGPSGVLDVKPG SHVVLKGKNLIPAAAGSSRLNYTVLI GGQPCALTVSDTQLLCDSPSQTGRQ PVMVLVGGLEFWLGTLHITADRALT LPAMVGLAAGGGLLLLAITVVLVAYK RKTQDADRTLKRLQLQMDNLESRV ALECKEAFAELQTDINELTNHMDGV QIPFLDYRTYAVRVLFPGIEAHPVLK ELDTPPNVEKALRLFGQLLHSRAFL LTFIHTLEAQSSFSMRDRGTVASLT MVALQSRLDYATGLLKQLLADLIEK NLESKNHPKLLLRRTESVAEKMLTN WFTFLLHKFLKECAGEPLFLLYCAIK QQMEKGPIDAITGEARYSLSEDKLIR QQIDYKTLTLHCVCPESEGSAQVPVK VLNCDSITQAKDKLLDTVYKGIPYSQ RPKAEDMDLEWRQGRMARIILQDE DITTKIECDWKRINSLAHYQVTDGSL VALVPKQVSAYNMANSFTFTRSLSR YESLLRAASSPDSLRSRAPMLTPDQ EAGTKLWHLVKNHDHADHREGDR GSKMVSEIYLTRLLATKGTLQKFVDD LFETVFSTAHRGSALPLAIKYMFDFL DEQADQRQISDPDVRHTWKSNCLPL RFWVNVIKNPQFVFDIHKNSITDAC LSVVAQTFMDSCSTSEHRLGKDSPS NKLLYAKDIPNYKSWVERYYRDIAK MASISDQDMDAYLVEQSRLHANDF NVLSALSELYFYVTKYRQEILTSLDR	False	False	0.945	1.33	0.683	0.683	0.188	4.345	2.341

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