	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	B2RXS4	PLXB2_MOUSE	Mus musculus	Plexin-B2	26.259779	S622	S1240;S1248;S1574	34887587;34418053	MALPLWALTFLGLTGLGLSLRSRKP ESFRSETELNHLAVDEVTGVVYVGA VNALYQLSADLHVQQHVVTGPFMD NKKCTPPIEASQCHEAVLTDNFNQL LLLDPPGKRLVECGSLFKGICALRAM SNISVRLFYEDGSGEKSFVASNDER VATVGLVTSTRPDGERVLFVGKGNG PHDNGIIVSTRLLDRAEGREAFEAYS DHTTFKAGYLSTNTQQFVAAFEDDF YVFFVFNHQDKHPAKNRTLLARMC KDDPSYYSYVEMDLQCQDPSDPQDS AFGTCLAASVATSGAGRALYAVFSRD GRSTGGPGAGLCVFPLDKVREKIEA NRNACYTGAREAGRTIFYKPFHGEIQ CGGHLIGASESFPCGSEHLPYPLGSR DGLVATAVLHRGGLNLTAVTVTAEN DHTVAFLGTSDGRILKVYLAPDGTSA EYGSIPVDINKKIKQDLALSGNLSSL YAMTQDKVFRLPVQECLSYVTCAQC RDSQDPYCGWCVIEGRCTRKSECSR AEETGHWLWSREKSCVAITDAFPQN MSRRAQGEVRLSVSPLPTLTEDDEL LCLFGDSPPHPARVEDDTVICNSPSS IPSTPPGQDHVDVSIQLLLKSGSVFL TSHQYPFYDCREAMSLVENLPCISC ASNRWTCQWDLQYYECREASPNPE EGIIRAHMEDNCPQFLAPDPLVIPM NHETEVTFQGKNLETVKVSSLYVGS ELLNFEETVTMHESDTFSFRTPKLS HDGNETLPLHLYVKSFGKNIDSKLQ VTLYNCSFGRSDCSLCLAADPAYRC VWCRGQNRCVYEALCSNVTSECPPP VITRIQPETGPLGGGILVTIHGSNLGV KADDVKKITVAGQNCAFEPRGYSVS TRIVCAIEASEMPFTGGIEVDVNGKL GHSPPHVQFTYQQPQPLSVEPRQGP QAGGTTLTINGTHLDTGSKEDVRVT LNDVPCEVTKFGAQLQCVTGQQLAP GQVTLEIYYGGSRVPSPGISFTYCEN PMIRAFEPLRSFVSGGRSINVTGQGF SLIQKFAMVVIAEPLRSWRRRRREA GALERVTVEGMEYVFYNDTKVVFLS PAVPEEPEAYNLTVLIRMDGHCAPL RTEAGVFEYVADPTFENFTGGVKKQ VNKLIHARGTNLNKAMTLEEAEAFV GAERCIMKTLTETDLYCEPPEVQPPP KRRQKRDTAHNLPEFIVKFGSREWV LGRVEYDTRASDVPLSLILPLVMVPM VFIIVVSIYCYWRKSQQAEREYEKIKS QLEGLEESVRDRCKKEFTDLMIEME DQTNDVHEAGIPTLDYKTYTDRVFFL PSKDGDKDVMITGKLDIPESRRPIVE QALYQFSNLLNSKSFLINFIHTLENQ REFSARAKVYFASLLTVALHGKLEYY TDIMRTLFLELMEQYVVAKNPKLML RRSETVVERMLSNWMSICLYQYLKD SAGEPLYKLFKAIKHQVEKGPVDAV QKKAKYTLNDTGLLGDDVEYAPLTV SVIVQDEGIDAIPVKVLNCDTISQVKE KIIDQVYRTQPCSCWPKPDSVVLEW RPGSTAQILSDLDLTSQREGRWKRI NTLMHYNVRDGATLILSKVGVSQQP EDSQQDLPGERHALLEEENRVWHL VRPTDEVDEGKSKRGSMKEKERTKA ITEIYLTRLLSVKGTLQQFVDNFFQS VLAPGHAVPPAVKYFFDFLDEQAEK HDIRDEDTIHIWKTNSLPLRFWVNIL KNPHFIFDVHVHEVVDASLSVIAQTF MDACTRTEHKLSRDSPSNKLLYAKE ISTYKKMVEDYYKGIRQMVQVSDQD MNTHLAEISRAHTDSLNTLVALHQL YQYTQKYYDEIINALEEDPAAQKMQL AFRLQQIAAALENKVTDL	None	None	None	None	None	None	None	None	None