

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane
O15031	PLXB2_HUMAN	Homo sapiens	Plexin-B2	18.148296	S718;S846;T1486	S1236;S1244;S1570	22661428;33465208;34019948;35289036;37217939;38665916	MALQLWALTLGLLGGASLRPRKL DFFRSEKELNHLAVDEASGVVYLGA VNALYQLDAKLEQEQVATGPAALDN KKCTPPIEASQCHEAEMTDNPNQLL LLDPPKRRLVECGSLFKGICALRALS NISLRLFYEDGSGEKSFVANSDEGV ATVGLVSTGPGGDRVLFVKGKNGP HDNGIIVSTRLLDRTDSREAFEAYTD HATYKAGYLSTNTQQFVAAFEDGPY VFFVFNQDQKHPARNRLLARMCR EDPNYYSYLEMDLQCRDPDIHAAAF GTCLAASVAAPGSGRVLVAVFSRDS RSSGGPGAGLCLFPLDKVHAKMEA NRNACYGTREARDIFYKPFHGDIO CGGHAPGSSKSPCGSEHLPYPLGS RDGLRGTAVLQRGGLNLTAVTVAEE NNHTVAFGLTSDGRILKVLTPDGTGS SEYDSILVEINKRVKRDVLSGDLGS LYAMTQDKVFRFPVQECLESYPTCTQ CRDSQDPYCGWCVVVEGRCTRKAEC PRAEEASHWLWRSRKSQVAVTSAQP QNMSSRAQGEVQLTVSPLPALSEED ELLCLFGESPPHARVEGEAVICNSP SSIPVTPPGQDHVAVTIQLLLRRGNI FLTSYQYFPYDCRQAMSLEENLPCIS CVSNRWTCQWDLRYHECREASPNP EDGIVRAHMEDSCQFLGPSPLVIP MNHETDVNFQKNDLTVKGSLLHV GSDLKFMPEPVTMQESGTFARFTRPK LSHDANETLPLHLYVKSYGKNIDSKL HVTLYNCSEFRSDCLCRAANPDYR CAWCGGQSRVCVYEAALCNTTSECPPP VITRIQPETGPLGGGIRITILGSLNGV QAGDIQRISVAGRNCSEFQPERYSVST RIVCVIEAAETPFTGGVEVDVFGKLG RSPPNVQFTFQQPKPLSVEPQQGPQ AGGTTLTIHGTHLDTGSQEDVRVTL NGVPCVKTKFQAQLQCVTGPQATRG QMLLEVSYGSPVNPNGIFFTYREN PVLRAFEPFRSASGGRSINVTGQGF SLIQRFAMVVIAEPLQSWQPPREAES LQPMTVVGTDYVFHNDTKVVFVLSA VPEEPEAYNLTVLIEMDGHALLRT EAGAFEYVPDPTFENFTGGVKKQVN KLIHARGTNLNKAMTLQEAFAEAVGA ERCTMKTLETETDLYCEPPEVQPPPK RRQKRDTHNLPEFIVKFGSREWVL GRVEYDTRVSDVPLSLILPLVIVPMV VVIASVVCYWRKSQAEREYEKIKS QLEGLEESVRDRCKEFTDLMIEME DQTNVHEAGIPVLDYKTYTDRVFF LPSKDGDKDVMITGKLDIPEPRRPVV EQALYQFSNLLNSKSFILNFIHTLEN QREFSARAKVYFASLLTVALHGKLEY YTDIMHTLFLELLEQYVAKNPKLM LRRSETVVERMLSNWMSICLYQYLK DSAGEPLYLKFKAIKHQVEKGPVDA VQKKAKYTLNDTGLLGDVVEYAPLT VSVIVQDEGVDAIPVKVLCNDTISQV KEIIDQVYRGQPCSCWPRPDSVLE WRPGSTAQILSDLTDSQREGRWKR VNTLMHYNVRDGTLLSKVGVSSQ PEDSQDLPGERHALLEENRVWH LVRPTDEVDEGSKRGSVKEKERTK AITEIYLRLLSVKGTLLQFVDFNFQ SVLAPGHAVPPAVKYFFDFLDEQAE KHNIQDEDTIHIWKTNSLPLRFWVN ILKNPHFIFDVHVHEVVDASLSVIAQ TFMDACTRTEHKLSRDSPSNKLLYA KEISTYKMMVEDYKGRQMVQVSD QDMNTHLAEISRAHTDSLNTLVALH QLYQYTKYYDEIINALEEDPAAQKM QLAFRLQIAAALENKVTDL	False	True	1.623	1.812	1.539	1.355	0.985	4.718