

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
O15031	PLXB2_HUMAN	Homo sapiens	Plexin-B2	16.596801	S718;S846;T1486	S1236;S1244;S1570	34019948;37217939;22661428;35289036;33465208	MALQLWALTLLGLLGAGASLRPRKL DFFRSEKELNHLAVDEASGVVYLGA VNALYQLDAKLQLEQQVATGPALDN KKCTPPIEASQCHEAEMTDNVNQLL LLDPPRKRLVECGSLFKGICALRALS NISLRLFYEDGSGEKSFVASNDEGV ATVGLVSSTGPGGDRVLFVKGKNGP HDNGIIVSTRLLDRTDSREAFEAYTD HATYKAGYLSTNTQQFVAAFEDGPY VFFVFNQQDKHPARNRTLLARMCR EDPNYYSYLEMDLQCRDPDIHAAAF GTCLAASVAAPGSGRVLYAVFSRDS RSSGGPGAGLCLFPLDKVHAKMEA NRNACYTGTREARDIFYKPFHGDIQ CGGHAPGSSKSFPCGSEHLPYPLGS RDGLRGTAVLQRGGLNLTAVTVAEE NNHTVAFLGTS DGRILKVYLTPDGTS SEYDSILVEINKRVKRDLVLSGDLGS LYAMTQDKVFRFPVQECLSYPTCTQ CRDSQDPYCGWCVVEGRCTRKAEC PRAEEASHWLWSRSKSCVAV TSAQP QNMSRRAQGEVQLTVSPLPALSEED ELLCLFGESP PHPARVEGEAVICNSP SSIPVTPPGQDHVAVTIQLLLRRGNI FLTSYQYPFYDCRQAMSLEENLPCIS CVSNRWTCQWDLRYHECREASPNP EDGIVRAHMEDSCPQLGSPPLVIP MNHETDVNFQGNLDTVKGSSLHV GSDLLKFMEPVTMQESGTF AF RTPK LSHDANETLPLHLYVKSYGKNIDSKL HVTLYNCSFGRSDCSLCRAANPDYR CAWCGGQSRCVYEALCNTTSECPPP VITRIQPETGPLGGGIRITILGSNLGV QAGDIQRISVAGRNC SFQPERYSVST RIVCVIEAAETPFTGGVEVDVFGKLG RSPPNVQFTFQPKPLSVEPQQGPQ AGGTTLTIHGTHLDTGSQEDVRVTL NGVPCKVTKFGAQLQCVTGPQATRG QMLLEVS YGGSPVNP GIFFTYREN PVLRAFEP LRSFASGGRSINVTGQGF SLIQRFAMVIAEPLQSWQPPREAES LQPMTVVGTDYVFHNDTKVVFLSPA VPEEPEAYNLTVLIEMDGH RALLRT EAGAFEYVPDPTFENFTGGVKKQVN KLIHARGTNLNKAMTLQEAEAFVGA ERCTMKTLTETDLYCEPPEVQPPK RRQKRDTTHNLPEFIVKFGSREWVL GRVEYDTRVSDVPLSLILPLVIVPMV VVIASVYCYWRKSQAEREYEKIKS QLEGLEESVRDRCKKEFTDLMIEME DQTNVDVHEAGIPVLDYKTYTDRVFF

										LPSKDGDKDVMITGKLDIPEPRRPVV EQALYQFSNLLNSKSFLINFIHTLEN QREFSARAKVYFASLLTVALHGKLEY YTDIMHTLFLELLEQYVVAKNPKLM LRRSETVVERMLSXWMSICLYQYLK DSAGEPLYKLFKAIKHQVEKGPVDA VQKKAKYTLNDTGLLGDDVEYAPLT VSVIVQDEGVDAIPVKVLNCDTISQV KEKIIDQVYRGQPCSCWPRPDSVVLE WRPGSTAQILSDDLTSQREGRWKR VNTLMHYNVRDGATLILSKVGVSSQQ PEDSQQDLPGERHALLEENRVWH LVRPTDEVDEGKSKRGSVKEKERTK AITEIYLTRLLSVKGTLQQFVDNFFQ SVLAPGHAVPPAVKYFFDFLDEQAE KHNIQDEDTIHIWKTNSLPLRFWVN ILKNPHFIFDVHVHEVVDAASLSVIAQ TFMDACTRTEHKLSRDSPSNKLLYA KEISTYKKMVEDYYKGIRQMVQVSD QDMNTHLAEISRAHTDSLNTLVALH QLYQYTQKYYDEIINALEEDPAAQKM QLAFRLQQIAAALENKVTDL
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