

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	extracellular region
P25304	AGRIN_RAT	Rattus norvegicus	Agrin	23.439218	NaN	S569;S571	38843836	MPPLPLEHRPRQEPGASMLVRYFMI PCNICLILLATSTLGFVALLFLSNYKP GIHFTAPPTPPDVCGRMLCGFGAV CEPSVEDPGRASCVCCKNACPATVA PVCGSDASTYSNECELQRAQCQNQQ RRIRLLRQGPCGSRDPCANVTCSEFG STCVPSADGQTASCLCPTTCFGAPD GTVCGSDGVDYPSECQLLSHACASQ EHIFKFKFNGPCDPCQGSMSDLNHC RVNPRTRHPMELLRPENCPAQHTPI CGDDGVTYENDCVMSRIGATRGLLL QKVRSGQCQTRDOCPETCQFNVC LSRRGRPHCSCDRVTCDGSYRPVCA QDGHYNNDCWRQQAECRQQRRAIP PKHOGPCDQTPSPCHGVQCAFVAV CTVKNGKAECECQRVCSGIYDPVCG SDGVTYGSVCELESMACITLGREIQV ARRGPCDPCGQCRFGSLCEVETGRC VCPSECVESAQPVCSDGHTYASEC ELHVHACTHQISLYVASAGHCQTCC EKVCTFGAVCSAGQVCPCREHPPP GPVCGSDGVTYLSACELREAACQQQ VQIEEAHAGPCEPAECGSGGSGSSE DDECEQELCRQRGGIWEDESDGP CVCDFSCQSVPRSPVCGSDGVTYGT ECDLKKARCESQOELYVAAQGACRG PTLAPLLPVAFPHCAQTPYGCCQDN FTAAQGVGLAGCPSTCHCNPHGSYS GTCDPATGQCSCRPGVGGLRCDRCE PGFWNFRGIVTDGHSCTPCSCDPR GAVRDDCEQMTGLCSCRPGVAGPK CGQCPDGGQVLGHLGCEADPMTPTV CVEIHCEFGASCVEKAGFAQCICPTL TCPEANSTKVCSDGVTYGNECQLK AIACRQRDLISTQSLGPCQESVTPGA SPTSASMTTPRHILSKTLPPPHNSLP LSPGSTTHDWPTPLPISPHTTVSIPR STAWPVLTVPTAAASDVTSLSATSI SESGSANGSGDEELSGDEEASGGGS GGLEPPVGSIVVTHGPPIERASCYNS PLGCCSDGKTPSLDSEGSNCPTAKA FQGVLELEGVGQELFYTPEMADPK SELFGETARSIESTLDDLFRNSDVKK DFWVSVRLRELGPVKLVRAIVDVHFD PTTAFQASDVGQALLRQIQVSRPWA LAVRRPLQEHVRFDFDWFPTFFFTG AATGTTAAMATARATTVSRLPASSVT PRVYPSHTSRPVGRTTAPPTTRRPPT TATNMDRPRTPGHQQPSKSCDSQP CLHGGTCQDQDSGKGFCTCSTAGR GGSVCEKVQPPSMPAFKGHSFLAPP TLRAYHTLRLALEFRALETEGLLLYN GNARGKDFLALALLDGRVQFRFDTG SGPAVLTSLVPVEPGRWHRLELSRH WRQGTLSVDGETPVVGESPSGTDGL NLDTNLYVGGIPEEQVAMVLDRTSV GVGLKGCIRMLDINNQQLELSDWQ RAAVQSSGVGECGDHPCLPNPCHG GALCQALEAGMFLCQCPGFRFGPTC ADEKSPQPNPCHGAAPCRVLSGGG AKCECPLGRSGTFCQTVLETAGSRP FLADFNFGFSYLELKGHTFERDLGE KMALEMVFLARGPSGLLYNGQKT DGKGFVSLALHNRHLEFCYDLGK GAAVIRSKPIALGTWVRVFLERNR KGALQVGDGPRVLGEPKSRKVPHT MLNLKEPLYIGGAPDFSKLARGAAV SSGFSGVIQLVSLRGHQLLTQEHVL RAVDVSPFADHPCTQALGNPCLNGG SCVPREATYECLCPGGFSLHCEKG LVEKSVGDLETLAFDGRTYIEYLNVA IESELTNEIPAPETLDSRALFSEKALQ SNHFELSLRTEATQGLVLWIGKAAE	False	True	1.683	2.095	1.799	1.776	1.553	4.671	4.502

