

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
O00468	AGRIN_HUMAN	Homo sapiens	Agrin	10.921994	T1285;S1852	S674;S676	29237092;33214551;34725712;35289036;34019948	MAGRSHPGPLRPLLPLLVAACVLP GAGGTCPERALERREEEANVVLGT VEEILNVDPVQHTYSCKVRVWRYLK GKDLVARESLLDGGNKVVISGFGDP LICDNQVSTGDTRIFFVNPAPPYLWP AHKNELMLNSSLMRITLRNLEEF CVEDKPGTHFTFPVPTPPDACRGML CGFGAVCEPNAEGPGRASCVCCKSP CPSVAPVCGSDASTYSNECELQRA QCSQORRIRLLSRGPCGSRDPCSNV TCSFGSTCARSADGLTASCLCPATCR GAPEGTVCGSDGADYPGECQLLRA CARQENVFKKFDGPCDPCQALPDP SRSCRVNPRTRRPEMLLRPESCPAR QAPVCGDDGVTYENDCVMGRSGAA RGLLLQKVRSGQCQGRDQCPEPCRF NAVCLSRGRPRCSCDRVTCDGAYR PVCAQDGRTYSDCWRRQQAECRQQ RAIPSKHQGPCDQAPSPCLGVQCAF GATCAVKNQQAACECLQACSSLYDP VCGSDGVTYGSACELEATACTLGREI QVARKGPCDRCGQCRFGALCEAETG RCVCPSECVLAQPVCGSDGHTYPS ECMLHVHACTHQISLHVASAGPCET CGDAVCAFGAVCSAGQCVCPRCEHP PPGPVCGSDGVTYGSACELREAACL QQTQIEEARAGPCEQAECGSGGSGS GEDGDCEQELCRQRGGIWDSESD GPCVDFSCQSVPGSPVCGSDGVTY STECCLKKARCESQRGLYVAAQGAC RGPTFAPLPPVAPLHCAQTPYGCCQ DNITAARGVGLAGCPSACQCNPHGS YGGTCDPATGQCSCRPGVGLRCDR CEPGFWNFRGIVTDGRSGCTPCSCD PQGAVRDDCEQMTGLCCKPGVAG PKCGQCPDGRALGPAGCEADASAPA TCAEMRCEFGARCVEESGSAHCVC PMLTCPEANATKVCSDGVTYGNEC QLKTIACRQGLQISIQSLGPCQEAVA PSTHPTSASVTVTTPGLLLSQALPAP PGALPLAPSSTAHSQTTPPSSRPRT TASVPRTTVWPVLTVPPTAPSPAPSL VASAFGESGSDGSSDEELSGDQEA SGGGSGGLEPLEGSSVATPGPPVER ASCYNSALGCCSDGKTPSLDAEGSN CPATKVFQGVLELEGVEGQELFYTP EMADPKSELFGETARSIESTLDDLFR NSDVKKDFRSVRLRDLGPGKSVRAI VDVHFDPTTAFRAPDVARALLRQIQV

SRRRSLGVRRLQEHVRFMDFDWF
PAFITGATSGAIAAGATARATTASRLP
SSAVTPRAPHPSHTSQPVAKTTAAPT
TRRPPTTAPSRVPGRRPPAQPPPKP
CDSQPCFHGGTCQDWALGGGFTCS
CPAGRGGAVCEKVLGAPVPAFEGRS
FLAFPTLRAYHTLRLLALEFRALEPQG
LLLYNGNARGKDFLALALLDGRVQL
RFDTGSGPAVLTSAVPVEPGQWHRL
ELSRHWRRGTLSDGETPVLGESPS
GTDGLNLDLDFVGGVPEDQAAVAL
ERTFVGAGLRGCIRLLDVNNQRLEL
GIGPGAATRGSVGECDHPCLPNP
CHGGAPCQNLEAGRFHCQCPPGRV
GPTCADEKSPCQPNPCHGAAPCRVL
PEGGAQCECPLGREGTFCQTASGQD
GSGPFLADFNGFSHLELRGLHTFAR
DLGEKMALEVVFLARGPSGLLLYNG
QKTDGKGFVSLALRDRRLEFRYDL
GKGAAVIRSREPVTLGAWTRVSLER
NGRKALRVGDGPRVLGESPKSRKV
PHTVLNLKEPLYVGGAPDFSKLARA
AAVSSGFDGAIQLVSLGGRQLTPEH
VLRQVDVTSFAGHPCTRASGHPCLN
GASCVPREAAVCLCPGGFSGPHCE
KGLVEKSAGDVTLAFDGRTFVEYL
NAVTESELANEIPVPETLDSGALHSE
KALQSNHFELSLRTEATQGLVLWSG
KATERADYVALAIVDGHQLSYNLGS
QPVLRSTVPVNTNRWLRVVAHRE
QREGSLQVGNEAPVTGSSPLGATQL
DTDGALWLGGLPELPVGPALPKAYG
TGFVGCLRDVVVGRHPLHLLLEDAVT
KPELRPCPTP