

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
O00468	AGRIN_HUMAN	Homo sapiens	Agrin	9.459382	T1285	S674;S676	29237092;34019948;33214551	MAGRSHPGPLRPLLPLLVAAACVLP GAGGTCPERALERREEEANVVLGT VEEILNVDPVQHTYSCKVRVWRYLK GKDLVARESLLDGGNKVVISGFGDP LICDNQVSTGDTRIFFVNPAPPYLWP AHKNELMLNSSLMRITLRNLEEEVF CVEDKPGTHFTFPVPTPPDACRGML CGFGAVCEPNAEGPGRASCVCKKSP CPSVAPVCGSDASTYSNECELQRA QCSQORRIRLLSRGPCGSRDPCSNV TCSFGSTCARSADGLTASCLCPATCR GAPEGTVCGSDGADYPGECQLLRA CARQENVFKKFDGPCDPCQGALPDP SRSCRVNPRTRRPEMLLRPESCPAR QAPVCGDDGVTYENDCVMGRSGAA RGLLLQKVRSGQCQGRDQCPEPCRF NAVCLSRGRPRCSDRVTCDGAYR PVCAQDGRTYSDCWRRQQAECRQQ RAIPSKHQGPCDQAPSPCLGVQCAF GATCAVKNQQAACECLQACSSLYDP VCGSDGVTYGSACELEATACTLGREI QVARKGPCDRCGQCRFGALCEAETG RCVCPSECVLAQPVCGSDGHTYPS ECMLHVHACTHQISLHVASAGPCET CGDAVCAFGAVCSAGQCVCPRCEHP PPGPVCGSDGVTYGSACELREAACL QQTQIEEARAGPCEQAECGSGGSGS GEDGDCEQELCRQRGGIWDSESD GPCVDFSCQSVPGSPVCGSDGVTY STECCLKKARCESQRGLYVAAQGAC RGPTFAPLPPVAPLHCAQTPYGCCQ DNITAARGVGLAGCPSACQCNPFGS YGGTCDPATGQCSCRPGVGLRCRDR CEPGFWNFRGIVTDGRSGCTPCSCD PQGAVRDDCEQMTGLCCKPGVAG PKCGQCPDGRALGPAGCEADASAPA TCAEMRCEFGARCVESGSAHCVC PMLTCPEANATKVCSDGVTYGNEC QLKTIACRQGLQISIQSLGPCQEAVA PSTHPTSASVTVTTPGLLLSQALPAP PGALPLAPSSTAHSQTTPPSSRPRT TASVPRTTVWPVLTVPPTAPSPAPSL VASAFGESGSDGSSDEELSGDQEA SGGGSGGLEPLEGSSVATPGPPVER ASCYNSALGCCSDGKTPSLDAEGSN CPATKVFQGVLELEGVEGQELFYTP EMADPKSELFGETARSIESTLDDLFR NSDVKKDFRSVRLRDLGPGKSVRAI VDVHFDPPTAFRAPDVARALLRQIQV

SRRRSLGVRPLQEHVRFMDFDWF
PAFITGATSGAIAAGATARATTASRLP
SSAVTPRAPHPSHTSQPVAKTTAAPT
TRRPPTTAPSRVPGRRPPAPQPPKP
CDSQPCFHGGTCQDWALGGGFTCS
CPAGRGGAVCEKVLGAPVPAFEGRS
FLAFPTLRAYHTLRALALEFRALEPQG
LLLYNGNARGKDFLALALLDGRVQL
RFDTGSGPAVLTSAVPVEPGQWHRL
ELSRHWRRGTLSDGETPVLGESPS
GTDGLNLDTLDFVGGVPEDQAAVAL
ERTFVGAGLRGCIRLLDVNNQRLEL
GIGPGAATRGSVGECDHPCLPNP
CHGGAPCQNLEAGRFHCQCPPGRV
GPTCADEKSPCQPNPCHGAAPCRVL
PEGGAQCECPLGREGTFCQTASGQD
GSGPFLADFNFGSHLELRGLHTFAR
DLGEKMALEVVFLLARGPSGLLLYNG
QKTDGKGFVSLALRDRRLEFRYDL
GKGAAVIRSREPVTLGAWTRVSLER
NGRKALRVGDGPRVLGESPKSRKV
PHTVLNLKEPLYVGGAPDFSKLARA
AAVSSGFDGAIQLVSLGGRQLTPEH
VLRQVDVTSFAGHPCTRASGHPCLN
GASCVPREAAVCLCPGGFSGPHCE
KGLVEKSAGVDVTLAFDGRTFVEYL
NAVTESELANEIPVPETLDSGALHSE
KALQSNHFELSLRTEATQGLVLWSG
KATERADYVALAIVDGHQLSYNLGS
QPVVLRSTVPVNTNRWLRVVAHRE
QREGSLQVGNEAPVTGSSPLGATQL
DTDGALWLGGLPELPVGPALPKAYG
TGFVGCLRDRVVVGRHPLHLLLEDAVT
KPELRPCPTP