

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
O15020	SPTN2_HUMAN	Homo sapiens	Spectrin beta chain, non-erythrocytic 2	3.021871	NaN	S6;S31;S959;S1073;S2171;S2199;T2354;S2359	30379171;34019948	MSSTLSPTDFDSLEIQGOYSDINNR WDLPDSWDNDNDSSSARLFERSRIKA LADEREAVQKKFTFTKWNHSHLARVT CRVGDLYSDLRDGRNLLRLEVLVSG EILPKPTKGRMRIHCLENVDKALQF LKEQKVHLENMGSHDIVDGNHRLT LGLVWTHILRFQIQDISVETEDNKEK KSAKDALLLWCQMKTAGYPNVNVH NFTTSWRDGLAFNAIVHKHRPDLID FESLKKCNAHYNLQNAFNLAEKELG LTKLLDPEDVNVDPDEKSIITYVAT YYHYFSKMKALAVEGKRIGKVLDA MEAERLVEKYESLASELLQWIEQTIV TLNDRQLANSLSGVQNQLQSFNSYR TVEKPPKFTEKGNLEVLLFTIQSKLR ANNQKVYTPREGRLISDINKAWERL EKAEHEREALRTELIRQEKLEQLAA RFDRKAAMRETWLSNQRLVSQDN FGLELAAVEAAVRKHEAIETDIVAYS GRVQAVDAVAEELAAERYHDIKRIAA RQHNVARLWDFLRQMVAAARRERLL LNLELQKVFQDLLYLMDWMEEMK GRLQSQDLGRHLAGVEDLLQLHELVE EADIAVQAERVRAVSASALRFCNPG KEYRPCDPQLVSERVAKLEQSYEAL CELAARRARLEESRRLWRFLWEVVG EAEAWVREQQHLLASADTGRDLTG ALRLLNKHTALRGEMSGRLGPKLKT LEQQQQLVAEGHPGASQASARAAEL QAQWERLEALAEERAQRLAQAASLY QFQADANDMEAWLVDALRLVSSPE LGHDEFSTQALARQHRALEEEIRSH RPTLDALREQAAALPPTLSRTPEVQS RVPTLERHYEELQARAGERARALEA ALALYTMLSEAGACGLWVEEKEQW LNGLALPERLEDLEVVQQRFFETLEP EMNTLAAQITAVNDIAEQLLKANPP GKDRIVNTQEQLNHRWQQFRRLAD GKKAALTSALSIGNYHLECTETQAW MREKTKVIESTQGLGNDLAGVLALQ RKLASTERDLEAIAARVGETREANA LAAGHPAQAVAINARLREVQTGWED LRATMRRREESLGEARRLQDFLRSL DDFQAWLGRTQTAVASEEGPATLPE AEALLAQHAALRGEVERAQSEYSRL RALGEEVTRDQADPQCLFLRQRLEA LGTGWEELGRMWESRQGRLAQAH GFQGFRLDARQAEGVLSSQEYVLSH TEMPGTLQAADAAIKKLEDFMSTMD ANGERIHGLLEAGRQLVSEGNIHAD

KIREKADSIERRHKKNQDAAQQFLG  
RLRDNREQQHFLQDCHELKLWIDE  
KMLTAQDVSYDEARNLHTKWQKHQ  
AFMAELAANKDWLDKVDKEGRELT  
LEKPELKALVSEKLRDLHRRWDELE  
TTTQAKARSLFDANRAELFAQSCCA  
LESWLESQAQLHSSDDYGKDLTSVN  
ILLKKQQMLEWEMAVREKEVEAIQA  
QAKALAQEDQGAGEVERTSRAVEEK  
FRALCQPMRERCRRLQASREQHQF  
HRDVEDEILWVTERLPMASMEHG  
KDLPSVQLLMKKNQTLQKEIQGHEP  
RIADLRERQRALGAAAAGPELAELQE  
MWKRLGHELELRGKRLDALRAQQ  
FYRDAAEAEAWMGEQELHMMGQE  
KAKDELSAQAEVKKHQVLEQALADY  
AQTIHQLAASSQDMIDHEHPESTRIS  
IRQAQVDKLYAGLKELAGERRERLQ  
EHLRLCQLRREDDLEQWIQEREVV  
AASHELGDYEHVTMLRDKFREFS  
RDTSTIGQERVDSANANGLIAGG  
HAARATVAEWKDSLNEAWADLLEL  
LDTRGQVLAAYELQRFLHGARQAL  
ARVQHKQQQLPDGTGRDLNAAEAL  
QRRHCAYEHDIQALSPQVQQVQDD  
GHRLQKAYAGDKAEIIGRHMQAVA  
EAWAQLQGSSAARRQLLLDTTDKFR  
FFKAVRELMLWMDEVNLQMDAQE  
RPRDVSSADLVIKNQGGIKAEIARA  
DRFSSCIDMGKELLARSHYAAEEISE  
KLSQLQARRQETAEKWQEKMDWLQ  
LVLEVLVFGRDAGMAEAWLCSQEPL  
VRSaelGCTVDEVESLIKREAFQKS  
AVAWEEERFCaleklTaleEREKERK  
RKREEEERRKQPPAPEPTASVPPGD  
LVGGQTASDTTWDTGTQPRPPPSTQA  
PSVNGVCTDGEPSQPLLGQQRLEHS  
SFPEGPGPGSGDEANGPRGERQTRT  
RGPAPSAMPQSRSTESAHAATLPPR  
GPEPSAQEQMEGMLCRKQEMEAFG  
KKAANRSWQNVYCVLRGSLGFYK  
DAKAASAGVPYHGEVPSLARAQGS  
VAFDYRKRKHVFKLGLQDGKEYLFQ  
AKDEAE MSSWLRVVNAAIATASSAS  
GEPEEPVVPSTTRGMTRAMTMPPVS  
PVGAEGPVVLRSKDGREREREKRFS  
FFKKNK