

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q13813	SPTN1_HUMAN	Homo sapiens	Spectrin alpha chain, non-erythrocytic 1	15.887716	S1550	S587;S924;S982;S999;S1029;S1031;S1041;T1176;S1190;S1207;S1217;S1291;S1306;S1323;S1338;S1550;S1557;S1578;S1615;S1647;T2020	30379171;22121020;34019948;26853435;35008409;33214551;34725712;35138101;35083852;30620550	MDPSGVKVLTAEDIQERROQVLDLRYHRFKELSTLRRQKLEDSYRFQFFQRDAEELEKWIQEKLQIASDENYKDP TNLQGKQKHQAFEAEVQANS GAIV KLDETGNLMISEGHFASSETIRTRLM ELHRQWELLEKMKREKGIKLLQAQK LVQYLRECEDVMDWINDKEAIVTSE ELGQDLEHVEVLQKKFEEFQTDMA AHEERVNEVNQFAAKLIQEQHP EEEE LIKTKQDEVNAAWQRLKGLALQRQG KLFGAAEVQRFNRDVDETISWIKEK EQLMASDDFGRDLASVQALLRKHE GLERDLAALEDKVKALCAEADRLQQ SHPLSATQIQVKREELITNWEQIRTL AAERHARLND SYRLQRF LADFRDLT SWVTEMKALINADELASDVAGAEAL LDRHQEHKGEIDAHEDSFKSADESG QALLAAGHYASDEVREKLTVLSEER AALLELWELRRQQYEQCMDLQLFY RDTEQVDNWMSKQEAFLNEDLGD SLDSVEALLKKHEDFEKSLSAQE EKI TALDEFATKLIQNNHYAMEDVATRR DALLSRRNALHERAMRRRAQLADS FHLQQFFRDSDELKSWVNEKMKTA TDEAYKDPSNLQGKVQKHQAFEAEAL SANQSRIDALEKAGQKLIDVNHYAK DEVAARMNEVISLWKKLLEATELKG IKLREANQQQQFN RNVEDIELWLYE VEGHLASDDYGKDLTNVQN LQKKH ALLEADVAHQDRIDGITIQARQFQD AGHFDAENIKKKQEALVARYEALKE PMVARKQKLADSLRLQQLFRDVEDE ETWIREKEPIAASN RGKDLIGVQNL LKKHQALQAEIAGHEPRIKAVTQKG NAMVEEGHF AAEDVKAKLHEL NQK WEALKAKASQRRQDLED SLQAQQY FADANEAESWMREKEPIV GSTDYGK DEDSAEALLKKHEALMSDLSAYGSS IQALREQAQSCRQVAPT DDETGKE LVLALYDYQEKSPREVTM KKG DILT LNSTNKDWWKVEVNDRQGFVPAAY VKKLDPAQSASREN LLEE QGSIALR QE QIDNQT RITKEAGSVSLRMKQVE ELYHS LLELGEKRKGMLEKSCCKFM LFREANELQQWINEKEAALTSEEVG ADLEQVEVLQKKFDDFQKDLKANES RLKDINKVAEDLESEGLMAEEVQAV QQQEVYGMMPRDETDSKTAS PWKS ARLMVHTVATFNSIKELNERWRS LQ QLAEERSQLL GSAHEVQRFHRDADE TKEWIEEKQALNTDNYGHD LASV QALQRKHG EFERDLAALGDKVNSL GETAERLIQSHPE SAEDLQEKCTEL NQAWSSLGKRADQRKAKLGD SHDL QRFLSDFRDLMSWINGIRGLVSSDE

LAKDVTGAEALLERHQEHRTIDAR
AGTFQAFEQFGQQLLAHGHYASPEI
KQKLDILDQERADLEKAWVQRRMM
LDQCLELQLFHRDCEQAENWMAAR
EAFLNTEDKGDSLDSVEALIKKHED
FDKAINVQEEKIAALQAFADQLIAAG
HYAKGDISSRRNEVLDRWRRLKAQ
MIEKRSLGESQTLQQFSRDVDEIE
AWISEKLQTASDESYKDPTNIQSKH
QKHQAFEELHANADRIRGVIDMG
NSLIERGACAGSEDAVKARLAALAD
QWQFLVQKSAEKSQKLKEANKQQN
FNTGIKDFDFWLSEVEALLASEDYG
KDLASVNNLLKKHQLEADISAHED
RLKDLNSQADSLMTSSAFDTSQVKD
KRDTINGRFQIKSMAASRAKLNE
SHRLHQFFRDMDEESWIKEKLL
VGSEYGRDLTGVQNLRKKHXRLEA
ELAAHEPAIQGLDTGKKLSDDNITIG
KEEIQORLAQFVEHWKELQLAAR
GORLEESLEYQQFVANVEEEEAWIN
EKMTLVASEDYGDTLAAIQGLLKKH
EAFETDFTVHKDRVNDVCTNGQDLI
KKNNHHEENISSKMKGLNGKVSDL
EKAAAQRKAKLDENSAFLQFNWKA
DVVESWIGEKENSLKTDYGRDLSS
VQTLTKQETFDAGLQAFQQEGIANI
TALKDQLLAAKHVQSKAIEARHASL
MKRWSQLLANSAARKKKLLEAQSH
FRKVEDLFLTFAKKASAFNSWFENA
EEDLTDPVRCNSLEEIKALREAHDA
FRSSLSSAQADFNQLAELDRQIKSFR
VASNPYTWFTMEALEETWRNLQKII
KERELELQKEQRRQEENDKLRQEF
QHANAQHWIQETRTRYLLDGSCMV
EESGTLESQLEATKRKHQEIAMRS
QLKKIEDLGAAMEEALILDNKYTEH
STVGLAQWDQLDQLGMRMQHNL
EQIQARNTTGVTEEALKEFSMMFK
HFDKDKSGRLNHQEFKSLRSLGY
DLPVVEEGEPDPEFAILDVDPNR
DGHVSLQEYMAFMISRETVKSSE
EIESAFRALSSGKPYVTKEELYQNL
TREQADYCVSHMKPYVDGKGRLEPT
AFDYVEFTRSLFVN