

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus
Q13813	SPTN1_HUMAN	Homo sapiens	Spectrin alpha chain, non-erythrocytic 1	19.160175	S1550	S587;S924;S982;S999;S1029;S1031;S1041;T1176;S1190;S1207;S1217;S1291;S1306;S1323;S1338;S1550;S1557;S1578;S1615;S1647;T2020	34725712;38665916;34019948;33214551;30379171;30620550;35008409;35083852;35138101;26853435;40596516;22121020	MDPSGVKVLETAEDIQERRQOVLDRYHRFKELSLTRRQKLEDSYRFQFFQ RDAEELEKWIQEKLOIASDENYKDP TNLQGLKQKHQAFEAQVQANSGAIV KLDETGNLMISEGHFASSETIRTRLM ELHRQWELLLEKMKREKGGKLLQAQK LVQYLRECEDEVMDWINDKEAIVTSE ELGQDLEHVEVLQKFFFEFQTDMA AHEERVNEVNOFAAKLIQEQHPPEE LIKTKQDEVNAAWQRLKGLALQROG KLFGAAEVQRFNRDVEETISWIKK EQLMASDDFGRDLASVQALLRKHE GLERDLAALEDKVKALCAEADRLQQ SHPLSATQIQVKREELITNWEQIRTL AAERHARLNDYSYRLQRFADFRDLT SWVTEMKALINADELASDVAGAEAL LDRHQEHKGEIDAHEDSFKSADESG QALLAAGHYASDEVREKLTIVLSEER AALLELWELRRQYEQCMDLQLFY RDTEQVDNWMSKQEAFLNEDLGD SLDSVEALLKKHEDFEKLSAQEEDI TALDEFATKLIQNNHYAMEDVATRR DALLSRRNALHERAMRRRAQLADS FHLLQFFRDSDELKSWVNEKMKTA TDEAYKDPNLSQKVKQKHQAFEAEL SANQSRIDALEKAGQKLDIVNHYAK DEVAARMNEVISLWKKLEATELKG IKLREANQQQFNRNVDIELWLVE VEGHLASDDYKDLTNVQNLQKKH ALLEADVAAHQDRIDGITIARQFQD AGHFDAENIKKKQEAALVARYEALKE PMVARKQKLADSLRLQQLFRDVEDE ETWIREKEPIAASTNRGKDLIGVQNL LKKHQALQAEIAGHEPRIKAVTQKG NAMVEEGHFAAEDVKAKLHELNOK WEALKAKASORRQDLEDSLQAQOY FADANEAESWREKEPIVGSTDYGK DEDSAEALLKHEALMSDL SAYGSS IQALREQAQSCRQOQVAPTDDDETGKE LVLALYDYQEKSPREVTMKKGDILT LNSTNKDWVKVEVNDROGFVPAAY VKKLDPAQSASRENLEEQGSIALR QEQIDNQTRITKEAGSVSLRMKQVE ELYHSLELGEKRRKGMLEKSCCKFM LFRANELQQWINEKEAALTSEEVG ADLEQVEVLQKQKFDQKDLKANES RLKDKINVAEDLESEGLMAEEVQAV QQQEVYGMMPRDETDKSTASPWKS ARLMVHTVATFNSIKELNERWRSIQ QLAEERSQLLGSAAHEVQRFHRDADE TKEWIEEKQALNTDNYGHDLASV QALQRKHGFERDLAALGDKVNSL GETAERLIQSHPESAEDLQEKCTEL NQAWSSLGKRADQRKAKLGDSDHDL QRFLSDFRDLMSWINGIRGLVSSDE LAKDVTGAEALLERHQEHRTEIDAR AGTFQAFEQFGQQLLAHGHYASPEI KQKLDILDQERADLEKAWVQRRMM LDQCLELQLFHRDCEQAENWMAAR EAFLNTEDEKGDLSLVEALIKKHED FDKAINVQEEKIAALQAFADQLIAG HYAKGDISRRNEVLDRWRLKAQ MIEKRSKLGESQTLQQFSRDVDEIE AWIEKLQ TASDESYKDP TNIQSKH QKHQAFEAELHANADRIRGVDMG NSLIERGACAGSEDAVKARLAALAD QWQFLVQKSAEKSQKLEANKQON FNTGIKDFDFWLSEVEALLASEDYG KDLASVNNLLKKHQLLEADISAHED RLKDLNSQADSLMTSSAFDTSQVKD KRDTINGRFQKIKSMAASRAKLNE SHRLHQFFRDMDEEESWIKKLL VGSSEYGRDLTGVQNLRKKHKRLEA ELAAHEPAIQGVLDTGKLSDDNTIG KEIQORLAQFVEHWKELQLAAAR GORLEESLEYQQFVANVEEEEAWIN EKMTLVASEDYDGLAAIQGLLKKH EAFETDFTVHKDRVNDVCTNGQDLI KKNNHHEENISSKMKGLNGKVS DL EKAAAQRKAKLDENSAFLQFNWKA	True	False	4.291	1.453	False	False	False

