

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extr regi
P16086	SPTN1_RAT	Rattus norvegicus	Spectrin alpha chain, non-erythrocytic 1	36.054081	NaN	S587;S924;S982;S999;S1029;S1031;S1041;T1176;S1190;S1207;S1217;S1291;S1306;S1323;S1338;S1550;S1557;S1578;S1615;S1647;T2020;T2066	18683930;38843836	MDPSGVKVLETAEDIQERRQQLVDR YHRFKELSTLRRQKLEDSYRFQFFQ RDAEELEKWIQEKLVASDENYKDP TNLQGKQKQHQAFEAEVQANSQAIV KLDETGNLMISEGHFASSETIRTRLM ELHRQWELLLEKMRKGIKLLQAQK LVQYLRCEEDVMDWINDKEAIVTSE ELGQDLEHVEVLQKKFEFQTDLAA HEERVNEVNFQAAKLIQEQHPPEEL IKTKQEEVNAAWQRLKGLALQRQGG LFGAAEVQRFNRDVEITIGWIKEKE QLMASDDFGRDLASVQALLRKHEG LERDLAALEDKVKALCAEADRLQOS HPLSANQIQVKREELITNWEQIRTLA AERHARLDDSYRLQRFLADFRDLTS WVTEMKALINADELANDVAGAEALL DRHQEHKGEIDAHEDSFKSADESG QALLAAGHYASDEVREKLSILSEERA ALLELWELRRQQYEQCMDLQLFYR DTEQVDNWMKQEAFLNEDLGDS LDSVEALLKKHEDFEKSLSAQEEKIT ALDEFATKLIQNNHYAMEDVATRRD ALLSRRNALHERAMHRRQLADSF HLQFFRDSDELKSWVNEKMTAT DEAYKDPNSNLQKQKQHQAFEELS ANQSRIDALEKAGQKLDVNNHYAKE EVAARMNEVISLWKKLEATELKGV KLREANQQQFNRRNVEDIELWLVE VEGHLASDDYKDLTINVQNLQKKH ALLEADVAAHQDRIDGITQARQFQD AGHFDAENIKKQKQEALVARYEALKE PMVARKQKLDLADSLRQLFRDVEDE ETWIREKEPIAASTNRGKDLIGVQNL LKKHQALQAEIAGHEPRIKAVTQKG NAMVEEGHFAAEDVKAKLSELNOK WEALKAKASQRRQDLEDSLQAQY FADANEAESWMREKEPIVGSTDYGK DEDSAEALLKKHEALMSDLSAYGSS IQALREQAQSCRQVAPMDDDETGKE LVLALYDYQEKSPREVTMKKGDILTL LNSTNKDWKVEVNDROGFVPAAY VKKLDPASASRENLEEQGSIALR QGQIDNQTRITKEAGSVSLRMKQVE ELYQSLELGEKRRKGMLEKSCCKFM LFREANELQWINEKEAALTSEEVG ADLEQVEVLQKKFDDFQKDLKANES RLKDINKVAEDLESEGLMAEEVQAV QQQEVYGMMPRDEADSKTASPWKS ARLMVHTVATFNSIKELNERWRSLO QLAEERSQLLGSHEVQRFHRRDADE TKEWIEEKNQALNTDNYGHDLASV QALQRKHGFERDLAALGDKVNSL GETAQRLIQSHPESAEDLKEKCTEL NQAWTSLGKRADQKAKLGDSDHDL QRFLSDFRDLMSWINGIRGLVSSDE LAKDVTGAEALLERHQEHRTEIDAR AGTFQAFQFQGLLAHGHYASPEI KEKLDILDQERTDLEKAWVQRRMM LDHCLELQFHRDCEQAENWMAAR EAFLNTEKGDSDLDSVEALIKKHED FDKAINVQEEKIAALQAFADQLIADV HYAKGDIANRRNEVLDWRRLKAO MIEKRSKLGESQTLQQFSRDVDEIE AWISEKLTASDESYKDPNTIQSKH QKHQAFEAEELHANADRIRGVIDMG NSLIERGACAGSEDAVKARLAALAD QWQFLVQKSAEKSQKLKEANKQON FNTGKDFDFWLSEVEALLASEDYG KDLASVNNLLKKHQLEADISAHED RLKDLNSQADSLMTSSAFDTSQVKE KRDTINGRFQKIKSMATSRRAKLSSE HRLHQFFRDMDDDEESWIKKLLV SSEYGRDLTGVQNLRRKHKRLEAE LAAHEPAIQGVLDTGKLLSDDNTIG QEEIQORLAQFVEHWKELQLAAR GQRLEESLEYQFVANVEEEAWIN EKMTLVASEDYGDTLAAIQGLLKKH EAFETDFTVHKDRVNDVCTNGQDLI KKNHHEENISSKMKGLNGKVS DLKAAAQRKAKLDENSAFLQFNWKA	True	True	4.543	2.676	1.814	1.446	0.948	5.0	1.74

DVVEWIGEKENSLKTDDYGRDLSS
VQTLTKQETFDAGLQAFQQEGIANI
TALKDQLLAAKHIQSKAIEARHASLM
KRWTQLLANSATRKKKLEAQSHFR
KVEDLFLTFAKKASAFNSWFENAE
DLTDPVRCNSLEEIKALREAHDAFR
SSLSSAQADFNQLAELDRQIKSFRVA
SNPYTWFTMEALEETWRNLQKIKE
RELELQKEQRRQEENDKLRQEFQ
HANAFHQWIEQTRTYLLDGSCMVE
ESGTLESQLEATKRKHQEIRAMRSQ
LKKIEDLGAAMEEALILDNKYTEHST
VGLAQWQDQLDQLGMRMQHNLEQ
QIQARNTTGVTEEALKEFSMMFKHF
DKDKSGLLNHQEFKSCLRSLGYDLP
MVEEGEPDPEFEAILDTVDPNRDGH
VSLQEYMAFMISRETENVKSSEEIES
AFRALSSEGKPYVTKEELYQNLTRE
QADYCVSHMKPYVDGKRELPTAFD
YVEFTRSLFVN