

| UniprotKB ID | Entry name  | organism     | full name                                | oglcnacscore | oglcnac sites | phosphorylation sites   | PMIDS                               | sequence   | intracellular | extracellular | cytosol | nucleus | mitochondrion | endoplasmic reticulum | golgi apparatus |
|--------------|-------------|--------------|--|--------------|---------------|---|-------------------------------------|--|---------------|---------------|---------|---------|---------------|-----------------------|-----------------|
| P16546       | SPTN1_MOUSE | Mus musculus | Spectrin alpha chain, non-erythrocytic 1 | 37.526017    | NaN           | S587;S924;S982;S999;S1029;S1031;S1041;T1176;S1190;S1207;S1217;S1291;S1306;S1323;S1338;S1550;S1557;S1578;S1615;S1647;T2020;T2066 | 22645316;36064721;33300544;36288343 | MDPSGKVKLETAEDIQERRQOVLDRYHRFKELSTRRQKLEDSYRFQFFQ RDAEELEKWIQEKLVASDENYKDP TNLQGKLVKQHQAFEAQVANSQAV KLDEGTGNLMISEGHFASFTIRTRML ELHRQWELWELKMKREKIGKLLQAKL LVQYLRECEVMDWINDKEAIVTSE ELGQDLEHVEVLQKKFEEFOTDLAA HEERVNEVSQFAAKLIQEQHPPEELI KTKQDEVNAAWQRLKGLALQRQGG LFGAAEVQRFNRDVDETIQWIKKE QLMASDDFGRDLASVQALLRKHEG LERDLAALEDKVKALCAEADRLQQS HPLSASQIQVKREELITNWEQIRTLA AERHARLDDSYRLQRFLADFRDLTS WVTEMKALINADELANDVAGAEALL DRHQEHKGEIDAHEDSFKSADESG QALLAASHYASDEVREKLSILSEERT ALLELWELRRQQYEQCMDLQLFYR DTEQVDNWMMSKQEAFLNEDLGDS LDSVEALLKHEDFEKLSSAQEEKIT ALDEFATKLIQNNHYAMEDVATRRD ALLSRRNALHERAMHRRALQADSF HLOQFFRDSDELKSWVNEKMKMTAT DEAYKDPNLSQKQVQKHQAFEAELS ANQSRIDALEKAGQKLDVNVHYAKE EVAARMNEVISLWKKLEATELKG IKLREANQQQFNRNVEDIELWLYE VEGHLASDDYKDLTINVQNLQKKH ALLEADVAHQDRIDGITQARQFQD AGHFDAENIKKQAEALVARYEALKE PMVARKQKLADSLRLQLFRDVEDE ETWIREKEPIAASTNRGKDLIGVQNL LKKHQALQAEIAGHEPRIKAVTQKG NAMVEEGHFAAEDVKAKLSELNQK WEALKAKASQRRQDLEDSLQAOQY FADANEAESWMREKEPIVGSSTDYGK DEDSAEALLKKHEALMSDSLAYSQSS IQALREQAQSCRQVAPMDDDETGKE LVLALYDYQEKSPREVTMKKGDILT LNSTNKDWWKVEVNDRQGFVPAAY VKKLDPAQSASRENLEEQSIALR QGQIDNQTRITKEAGSVSLRMKQVE ELYQSLELGEKRGMLEKSKKFM LFRANELQQWITEKEAALTNEEVG ADLEQVEVLQKKFDDFKDLKANES RLKDINKVAEDLESEGLMAEEVQAV QQQEVYGAMPREADSKTASPWKS ARLMVHTVATFNSIKELNERWRSLO QLAEERSQLLSAHEVQRFHRDADE TKEWIEKNQALNTDNYGHDLASV QALQRKHGFERDLAALGDKVNSL GETAQRLLIQSHPESAEDLKEKCTEL NQAWTSLGKRADQRKAKLGDSDHL QRFLSDFRDLMSWINGIRGLVSSDE LAKDVTGAEALLERHQHRTEIDAR AGTFQAFQFGQQLLAHGHYASPEI KEKLDILDQERTDLEKAWVQRRMM LDHCLLEQLFHRDCEQAENWMAAR EAFLNTEDKGDSLDSVEALIKKHED FDKAINVQEEKIAALQAFADQLIAVD HYAKGDIANRRNEVLDRWRRKKAQ MIEKRSLGESQTLQOFSRDVDEIE AWISEKLQASDESYKDPNTIQSKH QKHQAFEAELHANADRIRGVIDMG NSLIERGACAGSEDAVKARLAALAD QWQFLVQKSAEKSQKLEANKQON FNTGIKDFDFWLSEVALLASEDYG KDLASVNNLLKHKHQLLEADISAHED RLKDLNSQADSLMTSSAFDTSQVKE KRDTINGRFQKIKSMATSRRAKLSSES HRLHQFFRDMDEESWIKEKLLV SSEDYGRDLTGTVQNLRRKHKRLEAE LAAHEPAIQGVLDTGKLSDDNTIG QEEIQORLAQFVEHWKELKQLAAR GORLEESLEYQQFVANVEEEEAWIN EKMTLVASEDYGDTLAAIQGLLKKH EAFETDFTVHKDRVNDVCTNGQDLI KKNHHHEENISSKMKGLNGKVSDDL EKAAAQRKAKLDENSAFLQFNWKA | None          | None          | None    | None    | None          | None                  |                 |

DVVESWIGEKENSLKTDYGRDLSS  
VQTLTKQETFDAGLQAFQEGIANI  
TALKDQLLAAKHIQSKAIEARHASLM  
KRWTQLLANSATRKKKLEAQSHFR  
KVEDLFLTFAKKASAFNSWFENAE  
DLTDPVRCNSLEEIKALREAHDAFR  
SSLSSAQADFNQLAELDRQIKSFRVA  
SNPYTWFTMEALEETWRNLQKIIKE  
RELELQKEQRRQEENDKLRQEFQAQ  
HANAFHQWIQETRYLLDGSCMVE  
ESGTLESQLEATKRKHQEIRAMRSQ  
LKKIEDLGAAMEEALILDNKYTEHST  
VGLAQQWDQLDQLGMRMQHNLEQ  
QIQARNITGVTEEALKEFSMMFKHF  
DKDKSGRLNHQEFKSCRLSLGYDLP  
MVEEGEPDPEFEAILDTVDPNRDGH  
VSLQEYMAFMISRETVKSSSEIES  
AFRALSSEGKPYVTKEELYQNLTRE  
QADYCVSHMKPYVDGKRELPTAFD  
YVEFTRSLFVN