

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P16546	SPTN1_MOUSE	Mus musculus	Spectrin alpha chain, non-erythrocytic 1	21.100048	NaN	S587;S924;S982;S999;S1029;S1031;S1041;T1176;S1190;S1207;S1217;S1291;S1306;S1323;S1338;S1550;S1557;S1578;S1615;S1647;T2020;T2066	22645316;33300544;36064721;36288343	MDPSGVKVLETAEDIQERRQQVLDR YHRFKELSTLRRQKLEDSYRFQFFQ RDAEELEKWIQEKLVASDENYKDP TNLQGKQKQHQAFEAEVQANS GAIV KLDETGNLMISEGHFASETIRTRLM ELHRQWELLEKMKREKGIKLLQAQK LVQYLRECEDVMDWINDKEAIVTSE ELGQDLEHVEVLQKKFEEFQTDLAA HEERVNEVSQFAAKLIQEQHPPEELI KTKQDEVNAAWQRLKGLALQRQGG LFGAAEVQRFNRDVDEITIGWIKKE QLMASDDFGRDLASVQALLRKHEG LERDLAALEDKVKALCAEADRLQQS HPLSASQIQVKREELITNWEQIRTLA AERHARLDDSYRLQRFADFRDLTS WVTEMKALINADELANDVAGAEALL DRHQEHKGEIDAHEDSFKSADESG QALLAASHYASDEVREKLSILSEERT ALLELWELRRQQYEQCMDLQLFYR DTEQVDNWMSKQEAFLNEDLGDS LDSVEALLKKHEDFEKSLSAQEEKIT ALDEFATKLIQNNHYAMEDVATRDR ALLSRRNALHERAMHRRALQADSF HLQOFFRDSDELKSWVNEKMKAT DEAYKDPSNLQKQVQKHQAFEELS ANQSRIDALEKAGQKLIDVNHYAKE EVAARMNEVISLWKKLLEATELKI KLREANQQQFNRNVEDIELWLYE VEGHLASDDYGKDLTNVQNLQKKH ALLEADVAHQDRIDGITIARQFQD AGHFDAENIKKKQEALVARYEALKE PMVARKQKLADSLRLQQLFRDVEDE ETWIREKEPIAASNTRGKDLIGVQNL LKKHQALQAEIAGHEPRIKAVTQKG NAMVEEGHFAAEDVKAKLSELNOK WEALKAKASQRRQDLEDSLQAQY FADANEAESWMREKEPIVGSTDYGK DEDSAEALLKKHEALMSDLSAYGSS IQALREQAQSCRQVAPMDDDETGKE LVLALYDYQEKSPREVTMKGKDILT LNSTNKDWWKVEVNDRQGFVPAAY VKKLDPAQSASRENLLQGSIALR QGQIDNQTRITKEAGSVSLRMKQVE ELYQSLELGEKRKGMLEKSCCKFM LFREANELQQWITEKEAALTNEEVG ADLEQVEVLQKKFDDFQKDLKANES RLKDINKVAEDLESEGLMAEEVQAV QQQEVYGAMPREADSKTASPWKS ARLMVHTVATFNSIKELNERWRSLQ QLAEERSQLLGSAAHEVQRFHRDADE TKEWIEKNQALNTDNYGHDLASV QALQRKHGFERDLAALGDKVNSL GETAQRLIQSHPESAEDLKEKCTEL NQAWTSLGKRADQRKAKLGDSDHL QRFLSDFRDLMSWINGIRGLVSSDE

LAKDVTGAEALLERHQEHRTEIDAR
AGTFQAFEQFGQQLLAHGHYASPEI
KEKLDILDQERTDLEKAWVQRRMM
LDHCLELQLFHRDCEQAENWMAAR
EAFLNTEDKGDSDLDSVEALIKKHED
FDKAINVQEEKIAALQAFADQLIAVD
HYAKGDIANRRNEVLDRWRRLKAQ
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AWISEKLQTASDESYKDPTNIQSKH
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NSLIERGACAGSEDAVKARLAALAD
QWQFLVQKSAEKSQKLKEANKQQN
FNTGIKDFDFWLSEVEALLASEDYG
KDLASVNNLLKKHQLEADISAHED
RLKDLNSQADSLMTSSAFDTSQVKE
KRDTINGRFQKIKSMATSRRAKLSES
HRLHQFFRDMDEESWIKEKLLV
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VQTLTKQETFDAGLQAFQQEGIANI
TALKDQLLAAKHIQSKAIEARHASLM
KRWTQLLANSATRKKLLEAQSHFR
KVEDLFLTFAKKASAFNSWFENAE
DLTDPVRCNSLEEIKALREAHDAFR
SSLSSAQADFNQLAELDRQIKSFRVA
SNPYTWFTMEALEETWRNLQKIKE
RELELQKEQRRQEENDKLRQFAQ
HANAFHQWIQETRTYLLDGSCMVE
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MVEEGEPDPEFEAILDTVDPNRDGH
VSLQEYMAFMISRETEENVKSSEEIES
AFRALSSSEKPYVTKEELYQNLTRE
QADYCVSHMKPYVDGKGRELPTAFD
YVEFTRSLFVN