

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P16546-2	SPTN1_MOUSE	Mus musculus	Isoform 2 of 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	MDPSGVKVLETAEDIQERRQQVLDLRYHRFKELSTLRRQKLEDSYRFQFFQRDAEELEKWIQEKLVASDENYKDP TNLQGKQLQKHQAFEAEVQANS GAIVKLDEGTGNLMISEGHFAS ETIRTRML ELHRQWEL LLEKMKREKGIKLLQAQK LVQYLRECEDVMDWINDKEA IVTSE ELGQDLEHVEVLQKK FEEFQTDLAA HEERVNEVSQFAAKLIQ EQHPPEELI KTKQDEVNAAWQRLKGLAL QRQGLFGAAEVQRFNRD VDETIQWIKKEQLMASDDFGRDLASVQALLRKHEG LERDLAALEDKVKALCAEADRLQOS HPLSASQIQVKREELITNWEQIRTLA AERHARLDDSYRLQRF LADFRDLTS WVT EMKALINADELANDVAGAEALL DRHQEHKGEIDAHE DSFKSADESG QALLAASHYASDEVREKLSILSEERT ALLELWELRRQQYEQCM DLQLFYR DTEQVDNWM SKQEAFLNEDLGDS LDSVEALLKKHEDFEKSL SAQEEKIT ALDEFATKLIQ NNHYAMEDVATR RD ALLSRRNALHERAM HRRRAQLADSF HLQO FFRDSDELKSWVNEK MKTAT DEAYKDPSNLQ GKVQKHQAFEALS ANQSRIDALEKAGQK LIDVNHYAKE EVAARMNE VISLWKKLLEATEL KGI KLREANQQQFNR NVEDIELWLYE VEGH LASDDYGKDLTNVQ NLQKKH ALLEADVA AHQDRIDGITIQA RQFQD AGHFDAENIK KKQEALVARYEAL KE PMVARKQKLADSL RLQQLFRDVEDE ETWIREKEPIAAS TNRGKDLIGVQNL LKKHQALQAEIAG HEPRIKAVTQKG NAMVEEGHF AAEDVKAKLSEL NQK WEALKAKASQ RRQDLEDSLQAQ QY FADANEAESW MREKEPIVGST DYGK DEDSAEALL KKHEALMSDLS AYGSS IQALREQA QSCRQVAPMDD ETGKE LVLALYD YQEKSPREVT MKKGDILTL LNSTNKDWWK VEVNDRQGFV PAAY VKKLDPAQ SASRENLL EEQGSIALR QGQIDNQYQ SLLLELGEK RKGMLEKS CKKFMLFRE ANELQQWITE KEAALT NEEVGAD LEQVEVLQK KFDDFQKD LKANESRL KDINKVAED LESEGLMA EEVQAVQQ QEVYGAMPR DEADSKT ASPWKSAR LMVHTVATF NSIKELNE RWRSLQQL AEERSQLL GSAHEVQRF HRDADETK EWIEEKNQ ALNTDNYG HDLASVQ ALQRKHEG FERDLAAL GD KVNSLGETA QRLIQSH PESAEDLKE KCTELNQ AWTSLGK RADQRKAK LG DSHDLQR FLSDFRDL MSWINGIR GL VSSDELAK DVTGAEAL LERHQEHRT

EIDARAGTFQAFEQFGQQLLAHGHY
ASPEIKEKLDILDQERTDLEKAWVQR
RMMLDHCLELQLFHRDCEQAENW
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LIAVDHYAKGDIANRRNEVLDRWRR
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SKHQKHQAFEELHANADRIRGVID
MGNSLIERGACAGSEDAVKARLAAL
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KEKRDTINGRFQKIKSMATSRRAKL
SESHRLHQFFRDMDEESWIKEKK
LLVSSDYGRDLTGQNLRKKHKRL
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GIANITALKDQLLAAKHIQSKAIEAR
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KSFRVASNPYTWFTMEALEETWRN
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MQHNLEQQIQARNTTGVTEEALKEF
SMMFKHFDKDKSRLNHQEFKSCL
RSLGYDLPVVEEGEPDPEFEAILDTV
DPNRDGHVSLQEYMAFMISRETN
VKSSEIE SAFRALSSEGKPYVTKEE
LYQNL TREQADYCVSHMKPYVDGK
GRELPTAFDYVEFTRSLFVN