

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q01082	SPTB2_HUMAN	Homo sapiens	Spectrin beta chain, non-erythrocytic 1	44.315397	S265;T1081;T1216;S1311;T1356;S1452;T2068;S2102;S2164;S2218;T2297;S2303;S2304;S2307;S2314;S2316;T2317;S2319;T2320;S2323;S2324;T2328;T2331;S2332;T2337;S2338;S2341	S36;S228;S817;S825;S903;S1057;S1076;S1079;S1237;S1388;S1447;S1557;T1805;S2102;S2128;S2138;T2147;S2148;T2159;S2160;S2161;S2164;S2165;S2169;T2171;S2172;S2184;T2187;T2195;S2314;S2319;T2320;T2328;S2340;S2341;S14	32119511;34725712;35132862;30444036;32574038;22661428;30059200;20068230;35289036;33214551;29237092;30379171;35083852;34019948;35254053;26853435;28314751;37340703;27655845;28657654;35008409;35138101;27114449;33465208;34846842;30620550;31492838;29351928	MTTIVATDYDNIIEIQQQYSDVNNRW DVDDWDNENSSARLFERSRIKALAD EREAVQKKTFTKVVNSHLARVSCRITDLYTDLRDGRMLIKLLEVLVSGERLP KPTKGRMRIHCLENVDKALQFLKEQ RVHLENMGSHDIVDGNHRLTLGLI WTIILRFQIQIDNSVETDNKEKKSADALLWCQMKTAGYPNVNIHNFSTTS WRDGMFANALIHKHRPDLIDFDKLLKSNAHYNLQNAFNLAEQHLGLTKL LDPEDISVDHPDEKSIITYVVYYHYF SKMKALAVEGKRIGKVLDAIETEK MIEKYESLASDLEWIEQTHILNNRK FANSLVGVQQQLQAFNTYRTVEKPP KFTEKGNLEVLVFTIQSKMRANNQK VYMPREGKLISDINKAWERLEKAEH ERELALRNELIRQEKLEQLARRFDR KAAMRETWLSNQRLVSDNFGFD LPAVEAATKKHEAIETDIAAYEERVQ AVVAVARELEAENYHDIKRITARKDN VIRLWEYLLELLRARRQRLEMNGL QKIFQEMLYIMDWMDEMKVVLVLSQ DYGKHLGVEDLLQKHTLVEADIGIQ AERVGVNASAQKFATDGEYKPCD PQVIRDRVAHMEFCYQELCQLAER RARLESRRLWKFFWEMAE EEGWI REKEKILSSDDYKDLTSMRLLSK HRAFEDMSGRSGHFQAIKEGED MIAEEHFGSEKIREIRIYIREQWANL EQLSAIRKKRLEEASLLHQFQADAD DIDAWMLDILKIVSSSDVGHDEYST QSLVKKHKDVAEEIANYRPTLDTLH EQASALPQEAESPVVRGRLSGIEE RYKEVAELTRLRKQALQDTLALYKM FSEADACELWIDEKEQWLNNMQIP EKLEDEVIQHRFESLEPEMNNQAS RVAVVNQIARQLMHS GHPSEKEIKA QDQKLNTRWSQFRELVDKRDALL SALSIGNYHLECNETKSWIRETKVI ESTQDLGNDLAGVMALQRKLTGME RDLVAIEAKLSDLQKEAEKLESEHPD QAQAILSRLAEISDVWEEMKTTLKN REASLGEASKLQQFLRDLDDFQSWL SRTQTAIASEDMPNTLTEAEKLLTQ HENIKNEIDNYEEDYQKMRDMGEM VTQGQTDQYMFRLRQLQALDTGW NELHKMWENRQNLLSQSHAYQQF LRDTKQAEAFNNQYVLAHTEMPT TLEGAEAAIKKQEDFMTTMDANEK INAVVETGRRLVSDGNINS DRIQEKV DSIDDRHRKNRETASELLMRLKDNR DLQKFLQDCQELSLWINEKMLTAQ DMSYDEARNLHSHKWLKHQAFMAEL ASNKEWLDKIEKEGMQLISEKPETE AVVKEKLTGLHKMWEVLESTTQTKA QRLFDANKAELFTQSCADL DKWLH GLESQIQSDDYKDLT SVNILLKKQQ MLENQMEVRKKEIEELQSQAQALS QEGKSTDEVDSKRLTVQTKFELLE PLNERKHNLASKEIHQFN RDVEDE ILWVGERMPLATSTDHGHNLQTVQ LLIKKNQTLQKEIQGHQPRIDDIFER SQNIVTSSSSLSAEAIRQLADLQKL

WGLLIEETKRHRRLEEAHRAQQYY
FDAAEAEAWMSEQELYMMSEEKAK
DEQSAVSMLKKHQILEQAVEDYAET
VHQLSKTSRALVADSHPESERISMR
QSKVDKLYAGLKDLAEEERRGKLDER
HRLFQLNREVDDLEQWIAEREVVAG
SHELGDYEHVTMLQERFREFARD
TGNIGQERVDTVNHLADELINSGHS
DAATIAEWKDGLEAWADLLELIDT
RTQILAASYELHKFYHDAKEIFGRIQ
DKHKKLPEELGRDQNTVETLQRMH
TTFEHDIQALGTQVRQLQEDAAARLQ
AAYAGDKADDIQKRENEVLEAWKSL
LDACESRRVRLVDTGDKFRFFSMVR
DLMLWMEDVIRQIEAQEKPRDVSSV
ELLMNNHQGIKAEIDARNDSTTCI
ELGKSLARKHYASEEIKEKLLQLTE
KRKEMIDKWEDRWELRLILEVHQ
FSRDASVAEAWLLGQEPYLSSREIG
QSVDEVEKLIKREAFEKSAATWDE
RFSALERLTTLELLEVRRQQEEEERK
RRPPSPEPSTKVSEEASQQQWDTSD
KGEQVSQNGLPAEQGSPRMAETVD
TSEMVNGATEQRTSSKESPIPSPTS
DRKAKTALPAQSAATLPARTQETPSA
QMEGFLNRKHEWEAHNKKASSRS
WHNVYCVINNQEMGFYKDAKTAAS
GIPYHSEVPVSLKEAVCEVALDYKKK
KHVFKLRLNDGNEYLFQAKDDEEM
NTWIQAISSAISDDKHEVSASTQSTP
ASSRAQTLPTSVVTTSESSPGKREK
DKEKDKEKRFSLFGKKK