

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	40.411076	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	30379171;33214551;27655845;31492838;32119511;30620550;20068230;30059200;28314751;26853435;33465208;28657654;29351928;29237092;34019948;27114449;30444036;22661428;32574038	MTTIVATDYDNIEIQQQYSDVNNRW DVDDWDNENSSARLFERSRIKALAD EREAVQKKTFTKWNVSHLARVSCR TDLYTDLRDGRMLIKLLEVLVSGERLP KPTKGRMRIHCLENVDKALQFLKEQ RVHLENMGSHDIVDGNHRLTLGLI WTIILRFQIQDISVETEDNKEKSAK DALLWCQMKTAGYPNVNIHNFTTS WRDGMFAFNALIHKHRPDLIDFDKLL KSNAHYNLQNAFNLAEQHLGLTKL LDPEDISVDHPDEKSIITYVVYYHYF SKMKALAVEGKRIGKVLDAIETEK MIEKYESLASDLEWIEQTHILNNRK FANSLVGVQQQLQAFNTYRTVEKPP KFTEKGNLEVLFTIQSKMRANNQK VYMPREGKLISDINKAWERLEKAEH ERELALRNELIRQEKLEQLARRFDR KAAMRETWLTSENQRLVSDNFGFD LPAVEAATKKHEAIEDIAAYEERVQ AVVAVARELEAENYHDIKRITARKDN VIRLWEYLLELLRARRQRLEMNGL QKIFQEMLYIMDWMDEMKVVLVLSQ DYGKHLGVEDLLQKHTLVEADIGIQ AERVGVNASAQKFATDGEYKPCD PQVIRDRVAHMEFCYQELCQLAAER RARLESRRLWKFFWEMAE EEGWI REKEKILSSDDYKDLTSMVRLLSK HRAFEDEM SGRSGHFQAIKEGED MIAEEHFGSEKIREIRIYIREQWANL EQLSAIRKKRLEEASLLHQFQADAD DIDAWMLDILKIVSSSDVGHDEYST QSLVKKHKDVAEEIANYRPTLDLH EQASALPQEAESPVVRGRLSGIEE RYKEVAELTRLRKQALQDTLALYKM FSEADACELWIDEKEQWLNNMQIP EKLEDEVIQHRFESLEPEMNNQAS RVAVVNQIARQLMHS GHPSEKEIKA QQDKLNTRWSQFRELVDKRDALL SALSIGNYHLECNETKSWIRETKVI ESTQDLGNDLAGVMALQRKLTGME RDLVAIEAKLSDLQKEAEKLESEHPD QAQAILSRLAEISDVWEEMKTTLKN REASLGEASKLQQFLRDLDDFQSWL SRTQTAIASEDMPNTL TEAEKLLTQ HENIKNEIDNYEEDYQKMRDMGEM VTQGQTD AQYMLRQRLQALDTGW NELHKMWENRQNLLSQSHAYQQF LRDTKQAEAF LNNQEYVLAHTEMPT TLEGAEAAIKKQEDFMTTMDANEK INAVVETGRRLVSDGNINS DRIQEKV DSIDDRHRKNRETASELLMRLKDNR DLQKFLQDCQELSLWINEKMLTAQ DMSYDEARNLH SKWLKHQAFMAEL ASNKEWLDKIEKEGMQLISEKPETE AVVKEKLTGLHKMWEVLESTTQTKA QRLFDANKAELFTQSCADL DKWLH GLESQIQSDDYKDLTSVNILLKKQQ MLENQMEVRKKEIEELQSQAQALS QEGKSTDEVDSKRLTVQTKFMELLE PLNERKHNLASKEIHQFN RDVEDE ILWVGERMPLATSTDHGHNLQTVQ LLIKKNQTLQKEIQGHQPRIDDIFER SQNIVT DSSSLSAEAI RQLADLQKL

WGLLIEETKRHRRLLEEAHRAQQYY
FDAAEAEAWMSEQELYMMSEEKAK
DEQSAVSMLKKHQILEQAVEDYAET
VHQLSKTSRALVADSHPESERISMR
QSKVDKLYAGLKDLAEEERRGKLDER
HRLFQLNREVDLEQWIAEREVAVAG
SHELGDYEHVTMLQERFREFARD
TGNIGQERVDTVNHLADELINSGHS
DAATIAEWKDGLEAWADLLELIDT
RTQILAASYELHKFYHDAKEIFGRIQ
DKHKKLPEELGRDQNTVETLQRMH
TTFEHDIQALGTQVRQLQEDAAARLQ
AAYAGDKADDIOKRENEVLEAWKSL
LDACESRRVRLVDTGDKFRFFSMVR
DLMLWMEDVIRQIEAQEKPRDVSSV
ELLMNNHQGIKAEIDARNDSTTCI
ELGKSLARKHYASEEIKEKLLQLTE
KRKEMIDKWEDRWELRLILEVHQ
FSRDASVAEAWLLGQEPYLSREIG
QSVDEVEKLIKREAFEKSAATWDE
RFSALERLTTLELLEVRQQEEEEERK
RRPPSPEPSTKVSEEAESQQQWDTSD
KGEQVSNGLPAEQGSPRMAETVD
TSEMVNGATEQRTSSKESPIPSPTS
DRKAKTALPAQSAATLPARTQETPSA
QMEGFLNRKHEWEAHNKKASSRS
WHNVYCVINNQEMGFYKDAKTAAS
GIPYHSEVPVSLKEAVCEVALDYKKK
KHVFKLRLNDGNEYLFQAKDDEEM
NTWIQAISSAISSDKHEVSASTQSTP
ASSRAQTLPTSVVTTSESSPGKREK
DKEKDKEKRFSLFGKKK