

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q62261	SPTB2_MOUSE	Mus musculus	Spectrin beta chain, non-erythrocytic 1	26.601546	S2323	S36;S228;S817;S903;S1057;S1076;S1079;S1237;S1388;S1447;S1557;T1805;S2102;S2127;S2137;T2146;S2147;T2158;S2159;S2160;S2163;S2164;S2168;T2170;S2183;T2186;T2194;S2313;S2318;T2319;T2327;S2339;S2340;S14	30059200;18683930;19692427	MTTIVATDYDNIEIQQQYSDVNNRW DVDDWDNENSSARLFERSRIKALAD EREAVQKKTFTKWVNSHLARVSCRI TDLYTDLRDGRMLIKLLEVLSEGERLP KPTKGRMRIHCLENVDKALQFLKEQ RVHLENMGSHDIVDGNHRLTLGLI WTIILRFQIQDISVETEDNKEKKS DALLLWCQMKTAGYPNVNIHNFTTS WRDGMFALNIHKHRPDLIDFDKLLK KSNAHYNLQNAFNLAEQHLGLTKL LDPEDISVDHPDEKSIITYVVYYHYF SKMKALAVEGKRIGKVLDNAIETEK MIEKYESLASDLEWIEQTHILNNRK FANSLVGVQQQLQAFNTYRTVEKPP KFTEKGNLEVLFTIQSKMRANNQK VYMPREGKLISDINKAWERLEKAEH ERELALRNELIRQEKLEQLARRFDR KAAMRETWLSNQRLVSQDNFGFD LPAVEAATKKHEAIEDIAAYEERVQ AVVAVARELEAENYHDIKRITARKDN VIRLWEYLLELLRARRQRLEMNLGL QKIFQEMLYIMDWMDEMKVLLLSQ DYGKHLGVEDLLQKHALVEADIAIQ AERVRGVNASAQKFATDGEQYKPCD PQVIRDRVAHMEFCYQELCQLAAER RARLEESRRLWKFFWEMAE EEGWI REKEKILSSDDYGKDLTSMRLLSK HRAFEDEMGRSGHFQAIKEGED MIAEEHFGSEKIRERIIYIREQWANL EQLSAIRKKRLEEASLLHQFQADAD DIDAWMLDILKIVSSNDVGHDEYST QSLVKKHKDVAAEITNYRPTIDTLHE QASALPQAHAESPDKGRLAGIEER CKEMAELRLRKQALQDTLALYKMF KLEDLEVIQHRFESLEPEMNNQASR VAVVNQIARQLMHNHGHPSKEIRAQ QDKLNTRWSQFRELVDKRDALLSA LSIQNYHLECNETKSWIREKTKVIES TQDLGNDLAGVMALQRKLTGMERD LVAIEAKLSDLQKEAEKLESEHPDQA QAILSRLAEISDVWEEMKTTLNRE ASLGEASKLQQFLRDLDDFQSWLSR TQTAIASEDMPNTLTAEKLLTQHE NIKNEIDNYEEDYQKMRDMGEMVT QGQTAQYMFRLRQLQALDTGWNE LHKMWENRQNLLSQSHAYQQFLRD TKQAEAFLLNQEYVLAHTEMPTTLE GAEAAIKQEDFMTTMDANEEKINA VVETGRRLVSDGNINSDRIQEKVDSI DDRHRKNREAASELLMRLKDNRD QKFLQDCQELSLWINEKMLTAQDM SYDEARNLHSHKWLKHQAFMAELAS

NKEWLDKIEKEGMQLISEKPETEAV  
VKEKLTGLHKMWEVLESTTQTAKQ  
RLFDANKAELFTQSCADLDKWLHG  
LESQIQSDDYGDLTSVNILLKKQQ  
MLENQMEVRKKEIEELQSQAQALS  
QEGKSTDEVDSKRLTVQTKFMELLE  
PLSERKHNLLASKEIHQFNRDVEDE  
ILWVGERMPLATSTDHGHNLQTVQ  
LLIKKNQTLQKEIQGHQPRIDDIFER  
SQNIITDSSSLNAEAIRQLADLKQL  
WGLLIEETEKRRHRRLEEAHKAQYY  
FDAAEAEAWMSEQELYMMSEEKAK  
DEQSAVSMMLKKHQILEQAVEDYAET  
VHQLSKTSRALVADSHPESEISM  
QSKVDKLYAGLKDLAEERRGKLDER  
HRLFQLNREVDLDLEQWIAEREVVAG  
SHELGDYEHVTMLQERFREFARD  
TGNIGQERVDTVNNMADELINSGHS  
DAATIAEWKDGLEAWADLLELIDT  
RTQILAASYELHKFYHDAKEIFGRIQ  
DKHKKLPEELGRDQNTVETLQRMH  
TTFEHDIQALGTQVRQLQEDAARLQ  
AAYAGDKADDIQRENEVLEAWKSL  
LDACEGRRVRLVDTGDKFRFFSMVR  
DMLWMEDVIRQIEAQEKPRDVSSV  
ELLMNNHQGIKAEIDARNDSTACI  
ELGKSLARKHYASEEIKEKLLQLTE  
KRKEMIDKWEDRWELRLILEVHQ  
FSRDASVAEAWLLGQEPYLSREIG  
QSVDEVEKLIKREHAEFEKSAATWDE  
RFSALERLTTLELLEVRROQEEEEERK  
RRPPSPDPNTKVSEEAESQQWDTSK  
GDQVSNGLPAEQGSPRMAGTMET  
SEMVNGAAEQRTSSKESPVPSPPTL  
DRKAKSALPAQSAATLPARTLETPAA  
QMEGFLNRKHEWEAHNKKASSRS  
WHNVYCVINNQEMGFYKDAKSAAS  
GIPYHSEVPVSLKEAICEVALDYKKK  
KHFVKLRRLSDGNEYLFQAKDDEEM  
NTWIAISSAISSDKHDTASTQSTP  
ASSRAQTLPTSVVTTITSESSPGKREK  
DKEKDKEKRFSLFGKKK