

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	34.295697	T2296;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	36064721;36852467;36288343;30059200;18683930;34678516;19692427	MTTTVATDYDNIIEIQQYSDVNNRW DVDDWDNENSSARLFERSRIKALAD EREAVQKKTFKQWVNSHLARVSCRI TDLYTDLRDRMLIKLLEVLSSGERLP KPTKGRMRIHCLENVDKALQFLKEQ RVHLENMGSHDIVDGNHRLTLGLI WTIILRFQIQDISVETEDNKEKKS DALLLWCQMKTAGYPNVNIHNFTTS WRDGMFALNLIHKHRPDLIDFDKLLK KSNAHYNLQNAFNLAEQHLGLTKL LDPEDISVDHPDEKSIITYVVYYHYF SKMKALAVEGKRIGKVLDAIETEK MIEKYESLASDLEWIEQTIILNNRK FANSLVGVQQQLQAFNTYRTVEKPP KFTEKGNLEVLFTIQSKMRANNQK VYMPREGKLISDINKAWERLEKAEH ERELALRNELIRQEKLEQLARRFDR KAAMRETWLSNQRLVSQDNFGFD LPAVEAATKKHEAIETDIAAYEERVQ AVVAVARELEAENYHDIKRITARKDN VIRLWEYLLELLRARRQRLEMNLGL QKIFQEMLYIMDWMDEMKVLLLSQ DYGKHLGVEDLLQKHALVEADIAIQ AERVRGNASAKFATDGEYKPCD PQVIRDRVAHMEFCYQELCQLAAER RARLEESRRLWKFVWEMAEFEGWI REKEKILSSDDYGKDLTSMRLLSK HRAFEDEMSEGRSGHFEQAIEGED MIAEEHFGSEKIRERIIYIREQWANL EQLSAIRKKRLEEASLLHQFQADAD DIDAWMLDILKIVSSNDVGHDEYST QSLVKKHKDVAEEITNYRPTIDTLHE QASALPQAHAEVDPVKGRLAGIEER CKEMAELTRLRQALQDTLALYKMF SEADACELWIDEKEQWLNMMQIPE KLEDLEVIQHRFESLEPEMNNQASR VAVVNQIARQLMHNGHPSEKEIRAQ QDKLNTRWSQFRELVDKRDALLSA LSIQNYHLECNETKSWIREKTKVIES TQDLGNDLAGVMALQRKLTGMERD LVAIEAKLSDLQKEAEKLESEHPDQA QAILSRLAEISDVVEEMKTTLNRE ASLGEASKLQQFLRDLDLDFQSWLSR TQTAIASEDMPNTLTEAEKLLTQHE NIKNEIDNYEEDYQKMRDMGEMVT QGQTAQYMFLRQRLQALDTGWNE LHKMWENRQNLLSQSHAYQQFLRD TKQAEAFLNQYVLAHTEMPTTLE GAEAAIKKQEDFMTTMDANEEKINA VVETGRRLVSDGNINSDRIQEKVDSI DDRHRKNREAASELLMRLKDNRDL QKFLQDCQELSLWINEKMLTAQDM SYDEARNLHSHKWLKHQAFMAELAS NKEWLDKIEKEGMQLISEKPEEAV VKEKLTGLHKMWVLESTTQTKAQ RLFDANKAELFTQSCADLDKWLHG

LESQIQSDDYGGDLTSVNILLKKQQ  
MLENQMEVRKKEIEELQSQAQALS  
QEGKSTDEVDSKRLTVQTKFMELLE  
PLSERKHNLASKEIHQFNRDVEDE  
ILWVGERMPLATSTDHGHNLQTVQ  
LLIKKNQTLQKEIQGHQPRIDDIFER  
SQNIITDSSSLNAEAIQRRLADLKQL  
WGLLIEETEKRRHRLLEEAKAQYY  
FDAAEAEAWMSEQELYMMSEEKAK  
DEQSAVSMKKHQILEQAVEDYAET  
VHQLSKTSRALVADSHPESERISMR  
QSKVDKLYAGLKD LAEERRGKLDER  
HRLFQLNREVDLEQWIAEREVAG  
SHELGDYEHVTMLQERFREFARD  
TGNIGQERVDTVNNMADELINSGHS  
DAATIAEWKDGLNEAWADLLELIDT  
RTQILAASYELHKFYHDAKEIFGRIQ  
DKHKKLPEELGRDQNTVETLQRMH  
TTFEHDIQALGTQVRQLQEDAARLQ  
AAYAGDKADDIQKRENEVLEAWKSL  
LDACEGRRVRLVDTGDKFRFFSMVR  
DLMLWMEDVIRQIEAQEKPRDVSSV  
ELLMNNHQGIKAEIDARNDSTACI  
ELGKSSLARKHYASEEIKEKLLQLTE  
KRKEMIDKWEDRWEWLRRLILEVHQ  
FSRDASVAEAWLLGQEPYSSREIG  
QSVDEVEKLIKREAFKSAATWDE  
RFSALERLTTLELLEVRQQEEEEERK  
RRPPSPDPNTKVSEEAESQQWDTSK  
GDQVSQNGLPAEQGSPRMAGTMET  
SEMVNGAAEQRTSSKESPVPSPTL  
DRKAKSALPAQSAATLPARTLETPAA  
QMEGFLNRKHEWEAHNKKASSRS  
WHNVYCVINNQEMGFYKDAKSAAS  
GIPYHSEVPVSLKEAICEVALDYKKK  
KHVFKLRLSDGNEYLFQAKDDEEM  
NTWIQAISSAISSDKHDTASTQSTP  
ASSRAQTLPTSVVTITSESPGKREK  
DKEKDKEKRFSLFGKKK