

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi app:
Q62261	SPTB2_MOUSE	Mus musculus	Spectrin beta chain, non-erythrocytic 1	46.085723	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	18683930;19692427;36852467;34678516;36288343;39627609;36064721;30059200;37507081	MTTIVATDYDNIQOQYSDVNNRW DVIDDWDNENSSARLFERSRIKALAD EREAVQKKTFTKWVNSHLARVSCRI TDLYTDLRDGRMLIKLLEVLVSGERLP KPTKGRMRIHCLENVDKALQFLKEQ RVHLENMGSHDIVDGNHRLTLGLI WTIILRFQIQDISVETEDNKEKKS DALLLWCQMKTAGYPNVNIHNFSTS WRDGMFAFNALIHKHRPDLIDFDK KSNAHYNLQNAFNLAEQHLGLTKL LDPEDISVDHPDEKSIITYVVYYHYF SKMKALAVEGKRIGKVLDNAIETEK MIEKYESLASDLEWIEQTIILNNRK FANSLVGVQQQLQAFNTYRTVEKPP KFTEKGNLEVLFTIQSKMRANNOK VYMPREGKLISDINKAWERLEKAEH ERELALRNELIRQEKLEQLARRFDR KAAMRETWLSQRLVSDNFQFDF LPAVEAATKKHEAIEDIAAYEERVQ AVVAVARELEAENYHDIKRITARKDN VIRLWEYLLELLRARRORLEMNLGL QKIFQEMLYIMDWMDEMVKVLLSQ DYGKHLGVEDLLQKHALVEADIAIQ AERVGVNASAQKFATDGEYKPCD PQVIRDRVAHMEFCYQELCQLAAER RARLEESRRLWFFWEMAEIEGWI REKEKILSSDDYGKDLTSMVRLSK HRAFEDEMSGRSGHFEQAIKEGED MIAEEHFGSEKIRERIRIYEQWANL EQLSAIRKKRLEEASLLHQFQADAD DIDAWMLDILKIVSSNDVGHDEYST QSLVKKHKDVAAEITNYRPTIDTLHE QASALPOAHAESPDKVGRLAGIEER CKEMAELTRLRQALQDRTLALYKMF SEADACELWIDEKEQWLNMMQIPE KLEDLEVIQHRFESLEPEMNNQASR VAVVNIARQLMHNHGHPSKEIRAQ QDKLNTRWSQFRELVDKDKDALLSA LSIQNYHLECNETKSWIREKTKVIES TQDLGNDLAGVMALQKRLTGEMERD LVAIEAKLSDLOKEAEKLESEHPDQA QAILSRLEISDVWEEMKTTLNRE ASLGEASKLQFLRDLDDFQSWLSR TQTAIASEDMPNLTAEAKLLTQHE NIKNEIDNYEEDYQKMRDMGEMVT QGQTDAYMFLRQRLQALDTGWNE LHKMWENRQNLSSQSHAYQQFLRD TKQAEAFLNNOEYVLAHEMPTTLE GAEAAIKKQEDFMTTMDANEEKINA VVETGRRVSDGNINSRIQEKVDSI DDRHRKNREAASELLMRLKDNRD QKFLQDCQELSLWINEKMLTAQDM SYDEARNLHSHKWLKHQAFMAELAS NKEWLDKIEKEGMQLISEKPETEAV VKEKLTGLHMKMWEVLESTTQTKAQ RLFDANKAELFTQSCADLDKWLHG LESQIQSDDYGKDLTSVNIILKKQQ MLENQMEVRKKEIEELQSQQAALS QEGKSTDEVDSKRLTVQTKFMELLE PLSERKHNLASKIEIHQFNRDVEDE ILWVGEMPLATSTDHGHNLQTVQ LLIKKNQTLQKEIQGHQPRIDDIFER SQNIITDSSSLNAEAIQRLADLKQL WGLLIEETEKRHRRLLEEAHKAQQYY FDAAEAEAWMSEQELYMMSEKAK DEQSAVSMKKHQILEQAVEDYAEI VHQLSKTSRALVADSHPESERISMR QSKVDKLYAGLKDLEAERGGKLDER HRLFQLNREVDLEQWIAEREVVAG SHELQDYEHVTMLQERFREFARD TGNIGQERVDVNNMADELINSQHS DAATIAEWKDGLEAWADLLELIDT RTQILAASYELHKFYHDAKEIFGRIQ DKHKKLPEELGRDQNTVETLQRMH TTFEHDJQALGTQVRLQEDAAARLQ AAYAGDKADDIQRENEVLEAWKSL LDACEGRRVRLVDTGDKFRFFSMVR DLMLWMEVIRQIEAQEKPRDVSSV ELLMNNHQIKAIEDARNDSTACI ELGKSLARKHYASEIEKLLQLTE	True	True	4.592	5.0	1.562	1.435	1.15

KRKEMIDKWEDRWELRLILEVHQ
FSRDASVAEAWLLGQEPYLSREIG
QSVDEVEKLIKRRHEAFEKSAATWDE
RFSALERLTTLELLEVRROQEEEEERK
RRPPSPDPNTKVSEEAESQQWDTSK
GDQVSNGLPAEQGSPRMAGTMET
SEMVNGAAEQRTSSKESPVPSPPTL
DRKAKSALPAQSAATLPARTLETAA
QMEGFLNRKHEWEAHNKASSRS
WHNVYCVINNOEMGFYKDAKSAAS
GIPYHSEVPVSLKEAICEVALDYKKK
KHFVFLRLSDGNEYLFQAKDDEEM
NTWQAISSAISDDKHDTSASTQSTP
ASSRAQTLPTSVTTITSESPGKREK
DKEKDKERFSLFGKKK