

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q62261-2	SPTB2_MOUSE	Mus musculus	Isoform 2 of Spectrin beta chain, non-erythrocytic 1	34.295697	NaN	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	MELQRTSSISGPLSPAYTGQVPYNYN QLEGRFKQLQDEREAVQKKTFTKW VNSHLARVSCRITDLYTDLRDGRMLI KLLEVLSEGERLPKPTKGRMRIHCLE NVDKALQFLKEQRVHLENMGSHDI VDGNHRLTLGLIWTIILRFQIQDISVE TEDNKEKKSAKDALLLWCQMKTAG YPNVNIHNFTTSWRDGMFAFNALIH KHRPDLIDFDKLLKKSNAHYNLQNAF NLAEQHLGLTKLLDPEDISVDHPDE KSIITYVVYYHYFSKMKALAVEGKRI GKVLDNAIETEKMIEKYESLASDLE WIEQTHILNNRKFNANSLVGVQQQLQ AFNTYRTVEKPPKFTEKGNLEVLLFT IQSKMRANNQKVMPREGKLISDIN KAWERLEKAEHERELALRNELIRQE KLEQLARRFDRKAAMRETWLSNQ RLVSQDNFGFDLPAVEAATKKHEAI ETDIAAYEERVQAVVAVARELEAENY HDIKRITARKDNVIRLWEYLLELLRA RRQRLEMNGLQKIFQEMLYIMDW MDEMKVLLLSQDYGKHLGVEDLL QKHALVEADIAIQAERVRGVNASAQ KFATDGEYKPCDPQVIRDRVAHME FCYQELCQLAAERRARLEESRRLWK FFWEMAE EEGWIREKEKILSSDDYG KDLTSVMRLLSKHRAFEDEMSGRS GHFEQAIKEGEDMIAEEHFGSEKIR ERIIYIREQWANLEQLSAIRKKRLEE ASLLHQFQADADDIDAWMLDILKIV SSNDVGHDEYSTQSLVKKHKDVAEE ITNYRPTIDTLHEQASALPQAHAESP DVKGRLAGIEERCKEMAELTRLRKQ ALQDTLALYKMFSEADACELWIDEK EQWLNMMQIPEKLEDLEVIQHRFES LEPEMNNQASRVAVVNQIARQLMH NGHPSEKEIRAQQDKLNTRWSQFR ELVDRKKDALLSALSIGNYHLECNE TKSWIREKTKVIESTQDLGNDLAGV MALQRKLTGMRDLVAIEAKLSDLQ KEAEKLESEHPDQAQAILSRLAEISD VWEEMKTTLKNREASLGEASKLQQ FLRDLDDFQSWLSRTQTAIASEDMP NTLTEAEKLLTQHENIKNEIDNYEE DYQKMRDMGEMVTQGQTDAYMF LRQRLQALDTGWNELHKMWENRQ NLLSQSHAYQQFLRDTKQAEAFLN QEYVLAHTEMPTTLEGAEEAIKKQE DFMTTMDANEKINAVVETGRRVLS DGNINSDRIQEKVDSIDDRHRKNRE AASELLMRLKDNRDLQKFLQDCQE LSLWINEKMLTAQDMSYDEARNLH SKWLKHQAFMAELASNKEWLDKIE KEGMQLISEKPETEAVVKEKLTGLH

KMWEVLESTTQTKAQRFLDANKAE  
LFTQSCADLDKWLHGLESQIQSDDY  
GKDLTSVNILLKKQMLENQMEVR  
KKEIEELQSQAQALSQEGKSTDEVD  
SKRLTVQTKFMELLEPLSERKHNL  
ASKEIHQFNRDVEDEILWVGERMPL  
ATSTDHGHNLQTVQLLIKKNQTLQK  
EIQGHQPRIDDIFERSQNIITDSSSLN  
AEAIRQLADLKQLWGLLIEETEKR  
HRRLEEAHKAQQYYFDAEAEAWM  
SEQELYMMSEEKAKDEQSAVSMK  
KHQILEQAVEDYAETVHQLSKTSRA  
LVADSHPESEISMRSQSKVDKLYAG  
LKDLAEERRGKLDERHRLFQLNREV  
DDLEQWIAEREVVAGSHELGDYE  
HVTMLQERFREFARDTGNIGQERV  
DTVNNMADELINSGHSDAATIAEWK  
DGLNEAWADLLELIDTRTQILAASYE  
LHKFYHDAKEIFGRIQDKHKKLPEEL  
GRDQNTVETLQRMHTTFFEHDIQAL  
GTQVRQLQEDAARLQAAYAGDKAD  
DIQKRENEVLEAWKSLLDACEGRRV  
RLVDTGDKFRFFSMVRDLMLWMED  
VIRQIEAQEKPRDVSSVELLMNNHQ  
GIKAEIDARNSFTACIELGKSLLAR  
KHYASEEIKEKLLQLTEKRKEMIDK  
WEDRWEWLRLILEVHQFSRDASVA  
EAWLLGQEPYLSSREIGQSVDEVEK  
LIKREAFEKSAATWDERFSALERLT  
TLELLEVRRQEEEEERKRRPPSPDP  
NTKVSEEAESQQWDTSKGDQVSON  
GLPAEQGSPRVSYRSQTYQNYKNFN  
SRRTASDHSWSGM