

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q68FG2	Q68FG2_MOUSE	Mus musculus	Spectrin beta chain	26.09834	NaN	NaN	36064721	MSSTLSPTDFDSLEIQGOYSINNRR WDLPSDWDNDSSSARLFERSRIKA LADEREAVQKKTFTKWVNSHLARVT CRVGDLYSDLRDGRNLLRLELVLSG ETLPKPTKGRMRIHCLENVDKALQF LKEQKVHLENMGSHDIVDGNHRLT LGLVWTIILRFQIDISVETEDNKEK KSAKDALLWCQMKTAGYPNVNVH NFTTSWRDGLAFNAIVHKHRPDLDD FESLKKCAHYNLQNAFNLAEKELG LTKLLDPEDVNVDPDEKSIITYVAT YYHYFSKMKALAVEGKRIGKVLDDHA MEAEHLVEKYESLASELLQWIEQTIV TLNDRQLANSLSGVQNLQSFNSYR TVEKPPKFTTEKGNLEVLLFTIQSKLR ANNQKVYTPREGRLISDINKAWERL EKAETHERELALRTELIRQEKLEQLAA RFDRKAAMRETWLSNQRLVSDQN FGLELAAVEAAVRKHEAIEDIVAYS GRVQAVDAVAEELAAEHYHDIKRIAA RQNNVARLWDFLRQMVARRERLL LNLELQKVFQDLLYMDWMAEMKG RLOSQDLGKHLAGVEDLLQLHELVE ADIAVQAERVRAVSASALRFCDPGKE YRPCDPQLVSERVATLEQSYEALCEL AATRRARLEESRRLWRFLWEVGEAE AWVREQQHLLASADTGRDLTGVLRL LNKHAALRGEMSGRLGPKLTLEQG QQLVAEGHPGANQASTRAAELQAO WERLEALAEERAQQLAQAASLYQFO ADANDMEAWLVDALRLVSSPEVGH DEFSTQALARQHRALEEEIRAHRT LDALREQAAALPPALSHTPEVQGRV PTLEQHYEELQARAGERARALEAAL AFYTMLSEAGACGLWVEEKEQWLN GLALPERLEDLEVQQRFETLEPEM NALAARVAVNDIAEQLLKASPPGK DRIIGTQEQLNQRWQQFRSLADGKK AALTSALSIGNYHLECTETQAWMRE KTKVIESTQGLGNDLAGVLALQRKL AGTERDLEAISARVGELEQANALAA GHPAQAPAINTRLGEVQAGWEDLRA TMRRREESLGEARRLQDFLRSLDDF QAWLGRTOAVASEEGPATLPEAEA LLAQHAALRGEVERAQSEYSRLRTL GEEVTRDQADPQCLFLRQREALGT GWEELGRMWESRQGRLAQAHGFQ GFLRDARQAEGVLSQEYVLSHTEM PGTLQAADAAIKKLEDFMSTMDANG ERIRGELLEAGRQLVSKGNHAEKIQE KADSIEKRHRKNQEAQQLLGRLRD NREQQHFLQDCQELRLWIDEKMLT AQDVSYDEARNLHTKWQKHQAFMA ELAANKDWLDKVDKEGRELTLEKPE LKVVVSEKLEDLHRRWDELETTTQA KARSLFDANRAELFAQSCSALESWL ESLQAQLHSDDYGKDLTSTVNILLKK QQMLEREMAVREKEVEAIQAQAQA LAQEDQSAGEVERTSRAVEEKFRAL CQPMKERCRRLHASREHQHFHRDV EDEILWVTERLPMASLEHGKDLPS VQLLMKKNQTLQKEIQGHEPRIADL KERQRTLGTAAAGPELAELQEMWK RLSHELELRGKRLEALRAQQFYRD AAEAEAWMGEQELHMMGOEKAKD ELSAQAEVKKHQVLEQALADYAQTI KQLAASSQDMIDHEHPSTRLTIRQ AQVDKLYASLKELAGERERRLEHIL RLCQLRRELDDEQWIQEREVVAAS HELGDYEHVTMLRDKFREFSKDT STIGQERVDSANALANGLIAGGHAA RATVAEWKDSLNEAWADLLELDTR GOVLAAAYELQRFLHGARQALARVQ HKQQQLPDGTGRDLNAAEALQRRH CAYEHDIQALSTQVQQVQDDGQRLQ	True	True	4.612	2.265	1.281	1.103	4.162	5.0	1.089

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