

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
G3V6S0	G3V6S0_RAT	Rattus norvegicus	Spectrin beta chain	25.563465	NaN	NaN	34502162	<p>MTTIVATDYDNIEIQQQYSDVNNRW  DVEDDWDNENSSARLFFERSRIKALAD  EREAVQKKTFTKVVNSHLARVSCRI  TDLYTDLRDGRMLIKLLEVLGGERLP  KPTKGRMRIHCLENVDKALQFLKEQ  RVHLENMGSHDIVDGNHRLTLGLI  WTIILRFQIQDISVETEDNKEKKS  DALLWCQMKTAGYPNVNIHNFTTS  WRDGMFALNIHKHRPDLIDFDKLLK  KSNAHYNLQNAFNLAEQHLGLTKL  LDPEDISVDHPDEKSIITYVVTYYHYF  SKMKALAVEGKRIGKVLDAIETEK  MIEKYESLASDLEWIEQTIILNNRK  FANSLVGVQQQLQAFNTYRTVEKPP  KFTEKGNLEVLFTIQSKMRANNQK  VYMPREGKLISDINKAWERLEKAEH  ERELALRNELIRQEKLEQLARRFDR  KAAMRETWLTSENQRLVSDNFGFD  LPAVEAATKKHEAIEDIAAYEERVQ  AVVAVARELEAESYHDIKRITARKDN  VIRLWEYLLELLRARRQRLEMNLGL  QKIFQEMLYIMDWMDEMKVLLLSQ  DYGKHLGVEDLLQKHALVEADIAIQ  AERVGVNASAQKFATDGEYKPCD  PQVIRDRVAHMEFCYQELCQLAER  RARLEESRRLWKFFWEMAEEEGWI  REKEKILSSDDYGKDLTSMVRLLSK  HRAFEDEMSGRSGHFEQAIEGED  MIAEEHFGSEIRERISYIREQWANEQ  LSAIRKKRLEEASLLHQFQADADDID  AWMLDILKIVSSNDVGHDEYSTQSL  VKKHKDVAEISNYRPTIDTLHEQAG  ALPQAHAESPDVKGRLAGIEERYKE  VAELTRLRKQALQDTLALYKMFSEA  DACEWIDEKEQWLNMMQIPEKLE  DLEVIQHRFESLEPEMNNQASRVAV  VNQIARQLMHSQHPSEKEIRAQQDK  LNTRWSQFRELVDKRDALLSALSI  QNYHLECNKTSWIREKTKVIESTQ  DLGNDLAGVMALQRKLTGMERDLV  AIEAKLSDLQKAEKLESEHPDQAAQ  AIIISRLAEISDVWEEMKTTLKNREAS  LGEASKLQQFLRDLDDFQSWLSRTQ  TAIASEDMPNTLTAEKLLTQHENIK  NEIDNYEEDYQKMRDMGEMVTQG  QTDAQYMFRLRQLALDTGWNELH  KMWENRQNLSSQSHAYQQFLRDTK  QAEAFNLNOEYVLAHTEMPPTLEGA  EAAIKKQEDFMTTMDANEKINAVV  ETGRRLVSDGNINSDRIQEKVDSIDD  RHRKNREAASELLMRLKDNRDQLQK  FLQDCQELSLWINEKMLTAQDMSY  DEARNLHSHKWLKHQAFMAELASNK  EWLDKIEKEGMQLISEKPEAVEVVK  EKLTLGLHKMWEVLESTTQTKAQRFL  DANKAELFTQSCADLDKWLHGLES  QIQSDDYGKDLTSMVILLKKQMLE  NQMEVRKKEIEELQSQQAALSQEGK  STDEVDSKRLTVQTKFMELLEPLNE  RKHNLASKEIHQFNRDVEDEILWV  GERMPLATSTDHGHNLQTVQLLIK  NQTLOKEIQGHQPRIDDIFERSQNI  TDSSSLNAEAIQRLADLQKLGWLLI  EETEKRRHRLLEEAKQAQYFDDAE  AEAWMSEELYMMSEKAKDEQSA  VSMLKKHQILEQAVEDYAETVHQLS  KTSRALVADSHPESESRMSRQSKVD  KLYAGLKDLEERRGKLDERHRLFQ  LNREVDDLEQWIAEREVAVAGSHEL  QDYEHVTMLQERFREFARDTGNIG  QERVDTVNHMADDLINSGHSDAATI  AEWKDGLNEAWADLLELIDTRTQIL  AASYELHKFYHDAKEIFGRIQDKHK  KLPEELGRDQNTVETLQRMHTTFF</p>	None	None	None	None	None	None	None	None	

HDIQALGTQVRQLQEDAARLQAAYA  
GDKADDIQKRENEVLEAWKSLLDAC  
EGRRVRLVDTGDKFRFFSMVRDLM  
LWMEDVIRQIEAQEKPRDVSSVELL  
MNNHQGKAEIDARNDSTACIELG  
KALLARKHYASEEIKEKLLQLTEKRK  
EMIDKWEDRWEWLRLILEVHQFSR  
DASVAEAWLLGQEPYLLSSREIGQSV  
DEVEKLIKRRHEAFEKSAATWDERFS  
ALERLTTLELLEVRRQEEEEERKRR  
PPSPEPSAKVSEEAEQQWDTSKGD  
QVSNQGLPAEQGSPRMACTMETSE  
MVNGAAEQRTSSKESPVPSPSTDR  
KAKSALPAQSAATLPARTLETPAAQ  
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HNVCVINNQEMGFYKDAKSAASG  
VPYHSEVPVSLKEAICEVALDYKKKK  
HVFKLRSDGNEYLFQAKDDDEMND  
TWIQAITSAISSDKHDTASTQSTPA  
SSRAQTLPTSVVITITSESSPGKREKD  
KEKDKEKRFSLFGKKK