

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	pl m
Q80X90	FLNB_MOUSE	Mus musculus	Filamin-B	37.887727	S2103	T216;T519;S730;S886;S932;S983;S1028;T1307;S1316;S1433;S1505;S1602;S2083;S2113;S2369;S2465;S2478;S2481;S2492	34887587;22645316;24788674;25153642;34418053;37507081;37453647	MPVTEKDLAEDAPWKKIQQNTFTR WCNEHLKCVNKRIGNLQTDLSDFGL RLIALLEVLQSKRMHHKHYQRPTFR QMKLENVVALEFLDHEISIKLVSDS KAIVDGNLKLILGLVWVTLILHYSISM PVWEDEGDDDAKQTPKQRLLGWI QNKIPYLPITNFNQNWQDGKALGAL VDSAPGLCPDWESWDPRKPDVNA REAMQQADDWLGVPQVITPEEIIHP DVDEHSVMTYLSQFPKAKLKPAPL KPKLNPKKARAYGRGIEPTGNMVKQ PAKFTVDTISAGQGDVMVFVEDPEG NKEEARVTPDSKKNKTYSVYLPKV TGLHKVIVLFAQQHISKSPFEVNVDK AQQDASKVTAAGPGLTTGNIANKP TYFDIYTAGAGVGDIGIEVEDPQGN SVELLVEDRGNQVYRCVYKPVQGP HVVKVSFAGDAIPKSPFGVQIGEACN PNACRASGRGLQPKGVRIRRETADFK VDTKAAGSGELGVTVKGPKGLEELV KQKGFLDGVYSFEYYPSTPGKYSVAV TWGGHHIPKSPFEVQVPEAGMOK VRAWGPGHLGGIVGRSADFVVESIG SEVGTGLFAIEGPSQAKIEYDDQNDG SCDVKYWPKEPGEYAVHIMCDDEDI KDSPYMAFIHPATGDYNDLVQAYG PGLKSGCTINNPAEFIVDPKDAGSA PLKILAQDGEQPIDIQMKSMDGT YACSYTPLKAIKHTIAVWGGVNIPH SPYRVNIGQGSHPQKVKVFGPGVER SGLKANEPHTFTVDCTEAGEGDVSV GIKCDARVLSDDDEEDVDFDIHNAN DTFTVKYVPPAPGRYTIKVLFAEQEIP ASPFVRKVDPSHDASKVKAEGPGLS KAGVENKPTHTFTVHTKGAGKAPLN VQFSSPLPGEAVKDLDIIDNYDYSHT VKYPTQQGNMQVLVYGGDPIPKS PFTVGVAAPLDLSKIKINGLENRVEV GKDQEFADITNGAGGQGLDVTLS PSRKVVCLVAPVAGRECSTAKFIPR EEGLFAVDVTDGHPVPGSPYTVEA SLPPDPTKVKAHGPGLEGGVKGPA EFTIDTKGAGTGGGLTVEGPCAKI ECSNDGDGTCVSYLPTKPGYFVNI LFEVHIPGSPFKADIEMPFDPKVV ASGPGLEHGKVGEPGILCVDCSEAG PGTLGLEAVSDSGAKAEVSIQNNKD GTYAVTYVPLTAGMYTLTMKYGGEL VPHFPAWVKVEPAIDTSGIKAFPGI EGKDFREATDFTVDSRPLTQVGG DHIKAQITNPSGASTEFCVKDNADG TYQVEYTPFEKGFHVVEVTVDDVIP NSPFKVAVTEGCQPSRVHAQPGPK EAFNKSNTVFTVTRGAGIGGLGIV EGPSESKINCRDNKDGSCSAEYIPFA PGDYDVNITYGGVHIPGSPFRVPSKD VVDPSKVIAAGPLSSCVRACIPQSF TVDSSKAGLAPLEVRVLGPRGLVEPV NVVDNGDGTHTVYTPSQEGPYIVS VKYADEEIPRSPFKVLPYDASKV TASGPGLSAYGVPASLPVEFAIDARD AGEGLLAVQITDQEGKQORATVHDN KDGTYAVTYIPDKTGRYMIGVYGGD NIPLSPYRIRATQTDASKCLATGPGI APT VKTGEEVGFVDAKTAGKGV CVILTPDGTAEADVIENEDGTYDIF YTAAPGTYVIYVRFGGVDIPNSPFT VMATDGEVTAMEEAPVNACPPGFR FWVTEAYVPVSDMNLGFKFPDLV IPFAVRKGEITGVHMPSGKATPEI VDNKDGTVTVRYAPTEVGLHEMHIK YRGSHIPESPLQFYVNYPNPNSGSVAY GPGLVYGVANKATATFTIVTEDAGEG GLDLAIEGPSKAEISCIDNKDGTCTV TYLPTLPGDYSILVYNDKHIPGSPFT AKITDDNRRCSQVKGSAADFLLDIS ETDLSTLTASIKAPSGRDEPCLLKR PNNHIGISFIPREVGHELVSIKKNGN HVANSPVSIMVVQSEIGDARRAKVY GQGLSEGRTFEMSDFIVDTRDAGY	False	False	3.954	3.151	2.308	1.766	1.443	3.1

GISLAVEGPSKVDIQTEDLEDGTCKV  
SYFPTVPGVYIVSTKFADEHVPGSPF  
TVKISGEGRVRESITRTRAPAVATV  
GSICDLNLKIPAINSSDMSAHVTSPS  
GHVTEAEIVPMGKNSHCVRFVPQE  
MCGVHTVSVKYRGOHVTGSPFQFTV  
GPLGEGGAHKVRAGGPGLEGEAGI  
PAEFSIWTREAGAGGLSIAVEGPSKA  
EITFDDHKNGSCGVSYIAQEPGNYE  
VSIKFNDEHIPDSPYLVPVIAPSDDAR  
CLTVLSLQESGLKVNQPASF AIRLNG  
AKGKIDAKVHSPSGAVEECHVSELE  
PDKYAVRFIPHENGIHTIDVKFNESH  
VVGSPFKVRVGEPEGQAGNPALVSAY  
GAGLETGTTGIQSEFFINTTQAGPGT  
LSVTIEGPSKVKMDCQEIPEGYKVM  
YTPMAPGNYLIGVKYGGPNHISRSPF  
KAKVTGQRLVSPGSANETSSILVESV  
TRSTETCYSAIPKSSSDASKVTSKG  
AGLSKAFVGOQSSFLVDCSKAGSNM  
LLIGVHGPTTPCEEVSMKHVKGQQY  
NVTYVVKERGDYVLAVKWGEEHIPG  
SPFHVTVP