

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	pl m			
Q8BTM8	FLNA_MOUSE	Mus musculus	Filamin-A	41.669571	NaN	S11;S16;S20;S968;S1055;S1084;T1089;S1301;S1338;S1459;S1533;S1630;S1734;T1750;S1835;S1967;S2053;S2128;S2152;S2158;S2163;S2180;S2284;S2327;S2329;T2336;S2338;S2370;S2414;S2510;S2523;S2526;T2599	21540332;37453647;22645316;36288343;29187734	MSSSHSRCGQSAAVASPGGSIDSRD AEMPATEKDLAEDAPWKKIQNTFT RWCNEHLKCVSKRIANLQTDLS DGL RLIALLEVLVLSQKKMHRKHNRPTFR QMQLENVVALEFLDRESIKLVSDS KAIVDGNLKLILGLIWLTLILHYSIMP MWDEEEDEEAKKQTPKORLLGWIQ NKLPLPITNFSRDWQSGRALGALV DSCAPGLCPDWDSWDASKPVNNAR EAMQQADDWLGIPQVITPEEIVDPN VDEHSVMTYLSQFPKALKKPGAPLR PKLNPKKARAYGPGIEPTGNMVKKR AEFTVETRSAGQGEVLVYVEDPAGH QEEAKVTANNDKNRTFSVWVYVPEV TGTHKVTVLFAGQHIAKSPFEVYVDK SQGDASKVTAQGPGLPSGNIANKT TYFEIFTAGAGMGEVEVVIQDPTGQK GTVEPQLEARGDSTYRCSYQPTMEG VHTVHTVTFAGVPIPRSPYTVTVGQAC NPAACRAIGRGLQPKGVRVKETADF KVYTKGAGSGELKVTVKGPKEERV KQKDLGDGVYGFYYPTIPGTYVTI TWGGQNIGRSPFEVKVGTCEGNQK VRAWGPLEGGIVGKSADVVVEAIG DDVGTGFSVEGSPQAKIECDDKGD GSCDVRVYWPQEAAGEYAVHVLNCE DIRLSPFMADIREAPQDFHPDRVKA RGPGLKTVAVNKPAAEFTVDAKHA GKAPLRVQVDNEGCSVEATVKDN GNGTYSYVPRKPVKHTAMVSWG GVSI PNSPFRVNVGAGSHPNKVYVY GPGVAKTGLKAHEPTYFTVDCTEAG QGDVSIKICAPGVVGPTEADIDFDII RNDNDTFTVKYTPCGAGSYTIMVLF ADQATPTSPIRVKVEPSHDASKVKA GPGLNRTGVELGKPTHFTVNAKTAG KGKLDVQFSGLAKGDVARDVDIHDH HDNTYTVKYPVQGGPVGVNVTYGG DHIPKSPFSVGVSPSLDLSKIKVSGL GDKVDVKGKQDEFTVSKSGAGGQGG VASKIVSPSAAVPCVPEPGLGADNS VRFVPREEGPYEVEVTYDGVVPPGS PFPLEAVAPTKPSKVKAFGPGLOGG NAGSPARFTIDTKGAGTGGLGLTVE GPCEAQLCLDNGDGTCSVSYVPTPE PGDYNINILFADTHIPGSPFKAHVAP CFDASKVKCSGGLERATAGEVGGQF QVDCSSAGSAELTIEICSEAGLPAEV YIQDHGDGTHITTYIPLCPGAYTVTIK YGGQVPNFPKLVQVEPAVDTSVGVQ CYGPGIEGQGVFREATTFFSVDARAL TQTGGPHVKARVANPSGNLTDITYVQ DCGDGTYKVEYTPYEEGVHSDVITY DGSVPVSSPFQVPVTEGCDPSRVRV HCGPIQSGTTNKNKFTVETRGAGT GGLGLAVEGPSEAKMSCMDNKDGS CSVEYIPYEAGTYSLNVTYGGHQVPG SPFKVPVHDVTDASKVKCSGPGLS GMVRANLQSFQVDTSKAGVAPLQV KVQGPKGLVEPVDVVDNADGTQTV NYVPSREGSYSISVLYGEEVPRSPF KVKVLPHTDASKVKASGPGLNNTTGV PASLPVEFTIDAKDAGEGLLAVQITD PEGPKKTHIQDNDHGTYYAVVPD VPGRYTILIKYGGDEIPFSPYRVRAVP TGDASKCTVTVSIGGHLGAGIGPTI QIGEETVITVDTKAAGKGVCTVCTVCT PDGSEVDVVDVENEEDGTDFIDYFAP QPGKYVICVRFGEHVPNSPFQVTA LAGDQPTVQTPRSQQLAPQYNYPO GSQQTWPERPMVGVNGLDVTSLRP FDLVIPFTIKKGEITGEVRMPGSKVA QPSITDNKDGTVTVRYSPEAGLHE MDIRYDNMHIPGSPQLQFYVDVNCG HITAYGPLTHGVVKNPATFTVNTK DAGEGGLSLAIEGPSKAEISCTDNQD GTCVSYLPLVPGDYSILVKYNDQHI PGSPFTARVTDGDDSMRMSHLKVG AADIPINISETDLSLLTATVVPPSGRE EPCLLKRLRNGHVGISFVPKETGEH	None	None	None	None	None	None	None	None	None	None	None

LVHVKNKGQHVASSPIPVVISQSEIG
DASRVRVSGQLHEGHTFEPAEFIID
TRDAGYGGLSLSIEGPKVDINTEDL
EDGTCRVTYCPTTEPGNYIINIKFADQ
HVPGSPFVSVKVTGEGRVKESITRRRR
APSVANIGSHCDLSLKIPEISIQDMT
AQVTSPSGKTHEAEIVEGENHTYCIR
FVPAEMGMHTVSVKYKGQHVPGSP
FQFTVGPLGEGGAHKVRAGGGLER
AEVGVPAEFGIWTREAGAGGLAIAVE
GPSKAEISFEDRKDGGCGVAYVVQE
PGDYEVSVKFNEEHIPDSPFVVPVAS
PSGDARRLTVSSLOESGLKVNQPAS
FAVSLNGAKGAIDAKVHSPSGALEE
CYVTEIDQDKYAVRFIPRENGIYLIDV
KFNGTHIPGSPFKIRVGEPCGGDP
GLVSAYGAGLEGGVTGSPAEIFVNTS
NAGAGALSVTIDGPSKVKMDCQEC
EGYRVTYTPMAPGSYLISIKYGGPYHI
GGSPFKAKVTGPRLVSNHSLHETSS
VFVDSLTKVATVPQHATSGPGPADV
SKVVAKGLGLSKAYVQGKSNFTVDC
SKAGNNMLLVGVHGPRTPCEILVK
HMGSRLYSVSYLLKDKGEYTLVVKW
GDEHIPGSPYRIMVP