

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion
P21333	FLNA_HUMAN	Homo sapiens	Filamin-A	20.314592	S11;S972;S1055;S1367;S1476;T1557;T1558;S2617	S11;S968;S1055;S1081;S1084;T1089;S1301;S1338;S1459;S1533;S1630;S1734;S1835;S1967;S2053;S2128;S2152;S2158;S2163;S2180;S2284;S2327;S2329;T2336;S2338;S2370;S2414;S2510;S2523;S2526;T2599	35083852;23301498;34019948;34725712;37217939;30444036;18369606;35254053;28510447;33465208;29351928;16408927;35138101;30397120;34229054;35132862;33214551;26853435;38253038;32119511;35008409;38665916	MSSSHSRAGQSAAGAAPGGVDTR DAEMPATEFKDLAEDAPWKIQNTF TRWCNEHLKCVSKRIANLQTDLSDG LRLIALLEVLVLSQKKMHRKHNRPTF RQMQLENVVALEFLDRESIKLVSID SKAIVDGNLKLILGLIWLILHYSISM PMWDEEEDDEAKKQTPKQRLLGWI QNKLPQLPITNFSRDWQSGRALGAL VDSCAPGLCPDWDSWDASKPVTNA REAMQQADDWLGIPQVITPEIVDP NVDEHSVMTYLSQFPKAKLKPGAPL RPKLNPKKARAYGPGIEPTGNMVKK RAEFTVETRSAGQGEVLVYVEDPAG HQEEAKVTANNDKNRTFSVWVYVPE VTGTHKVTVLFAGQHIAKSPFEVYVD KSQGDASKVTAQGGPLEPSGNIANK TTYFEIFTAGAGTGEVEVVIQDPMGQ KGTVEPQLEARGDSTYRCSYOPTME GVHTVHVTFAGVPIPRSPYTVTVGQA CNPSACRAVGRGLQPKGVRVKETAD FKVYTKGAGSGELKVTVKGPKGEER VKQKDLGDGVYGFYYPMPVPGTYIV TITWGGQNIGRSPFEVKVGTCEGNQ KVRAWGPLEGGVVGKSAFVVEAI GDDVGTLGFSVEGPSQAKIECDDKG DGSCDVRVYWPQEAAGEYAVHVLNS EDIRLSPFMADIRDAPODFHPDRVK ARGPGLKTVAVNKAPEFTVDAKH GGKAPLRVQVDNEGCPVEALVKD NNGTYSCSYVPRKPKHTAMVSW GGVSIPIPSFRVNVGAGSHPNKVKV YGPVAKTGLKAHEPTYFTVDCAEA GQGDSVIGIKCAPGVVGAEDIDFD IIRNDNDTFTVKYTPRGAGSYTIMVL FADQATPTSPIRVKVEPSHDASKVKA EGPGLSRTGVELGKPTHFTVNAKAA GKGKLDVQFSGLTKGDAVRDVID HHNDNTYTKYTPVQGGPVGVNVTYG GDPPIKSPFSVAVSPSLDLSKIKVSGL GEKVDVGKQDEFTVKSAGGQGGK VASKIVGPSGAAPCKVEPGLGADN SVRFLPREEGPYEVEVTDGVPVPG SPFPLEAVPTKPSKVKAFGPGLOGG SAGSPARFTIDTKGAGTGGGLLTVEG PCEAQLCELDNGDGTCSVSYVPTPE GDYNINILFADTHIPGSPFKAHVVP FDASKVKCSGPLERATAGEVQGFQ VDCSSAGSAELTIEICSEAGLPAEVI QDHGDGTHITTYIPLCPGAYTVTIKY GGQVPNPFPSKQVPAVDTSGVQC YGPGEQGVFREATTEFSDARALT QTGGPHVKARVANPSGNLTETVYVD RGDGMKYVEYTPYEEGLHSDVTDYD GSPVPSPFQVPVTEGCDPSRVRVH GPGIQSGTTNKNKFTVETRCAGTG GLGLAVEGPSEAKMSCMDNKGSC SVEYIPYAGTYSLNVTYGGHQVPGS PFKVPVHDVTDASKVKCSGGLSPG MVRANLPQSFQVDTSKAGVAPLQVK VQPKGLVEPVDVVDNADGTQTVNY VPSREGPYSISVLYGDEEVPSPFKV KVLPTHDAKVKASGGLNITGVP SLPVEFTIDAKDAGEGLLAVQITDPE GKPKKTHIQDNHDGTYTVAYVPDVT GRYTILIKYGGDEIPFSPYRVRVPTG DASKCTVTVIGGHGLGAGIGPTIQI GEETVITVDTKAAGKGVCTVCTPD GSEVDVDVVENEDGTFDIFYTAPQP KYYVICRFRGGEHVPNSPFQVTA GDQPSVQPPLRSQQLAPQYTYAQQG QQTWAPERPLVGVNGLDVTSLRPF LVIPFTIKKGEITGEVRMPGKVAQP TITDNKDGTVTVRYAPSEAGLHEMD IRYDNMHIPGSPLQFYVDYVNCGHV TAYGPLTHGVVNPATFTVNTKDA GEGGLSLAIEGPKAEISCTDNQDGT CSVSYLPVLPGDYSILVKYNEQHVP SPFTRVTDGDSMRMSHLKVGSAA DIPINISSETLSLLTATVPPSGREEP CLLKRLRNGHVGISFVPKETGEHLV	None	None	None	None	None

HVKKNGQHVASSIPVVISQSEIGDA
SRVRVSGQLHEGHTFEPAEFIIDTR
DAGYGGLSLSIEGPKVDINTEDELD
GTCRVTYCPTTEPGNYIINIKFADQHV
PGSPFSVKVTGEGRVKESITRRRRAP
SVANVGSHCDLSLKIPEISIQDMTAQ
VTSPSGKTHEAEIVEGENHTYCIRFV
PAEMGHTVSVKYKQHVPGSPFQF
TVGPLGEGGAHKVRAGGPGLERAEA
GVPAEFSIWTREAGAGGLAIAVEGPS
KAEISFEDRKDGS CGVAYVVQEPGD
YEVSVKFNEEHIPDSPFVVPVSPSG
DARRLTVSSLQESGLKVNQPASFAV
SLNGAKGAIDAKVHSPSGALEECYV
TEIDQDKYAVRFIPRENGVYLIDVKF
NGTHIPGSPFKIRVGE PGHGGDPGL
VSAYGAGLEGGVTGNPAEFVVNTSN
AGAGALSVTIDGPSKVKMDCQECPE
GYRVTYTPMAPGSLISIKYGGPYHIG
GSPFKAKVTGPRLVSNHSLHETSSV
FVDSLTKATCAPQH GAPGPGPADAS
KVVAKGLGLSKAYVGQKSSFTVDCS
KAGNNMLLVGVHGPRTPC E EILVKH
VGSRLYSVSYLLKDKGEYTLVVKWG
DEHIPGSPYRVVVP