

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence
P21333	FLNA_HUMAN	Homo sapiens	Filamin-A	24.826216	S972;S1055;S1367;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	30444036;29351928;34019948;33214551;23301498;28510447;33465208;16408927;18369606;32119511;34229054;30397120;34725712;26853435	MSSSHSRAGQSAAGAAPGGGVDR DAEMPATEKDLAEDAPWKKIQQNTF TRWCNEHLKCVSKRIANLQTDLSDG LRLIALLEVLVSQKKMHRKHNQRPTF RQMQLENVVALEFLDRESIKLVSID SKAIVDGNLKLILGLIWLTLILHYSISM PMWDEEEDEEAKKQTPKQRLLGWI QNKLPQLPITNFSRDWQSGRALGAL VDSCAPGLCPDWDSWDASKPVTNA REAMQQADDWLGIPQVITPEEIVDP NVDEHSVMTYLSQFPKAKLKPGAPL RPKLNPKKARAYGPGIEPTGNMVKK RAEFTVETRSAGQGEVLVYVEDPAG HQEEAKVTANNDKNRTFSVWYVPE VTGTHKVTVLFAGQHIAKSPFEVYVD KSQGDASKVTAQGPGLPSGNIANK TTYFEIFTAGAGTGEVEVVIQDPMGQ KGTVEPQLEARGDSTYRCSYQPTME GVHTVHVTFAGVPIPRSPYTVTVGQA CNPSACRAVGRGLQPKGVRVKETAD FKVYTKGAGSGELKVTVKGPKEER VKQKDLGDGVYGFYYPMPVPGTYIV TITWGGQNIGRSPFEVKVGTCEGNQ KVRAWGPGLEGGVVGKSADFFVEAI GDDVGTLGFSVEGPSQAKIECDDKG DGSCDVRYPQEAAGEYAVHVLCSN EDIRLSPFMADIRDAPQDFHPDRVK ARGPGLEKTGVAVNKPAEFTVDAKH GPKAPLRVQVQDNEGCPVEALVKD NGNGTYSCSYVPRKPVKHTAMVSW GGVSIPNSPFRVNVGAGSHPNKVKV YGPGVAKTGLKAHEPTYFTVDCAEA GQGDSVIGIKCAPGVVGPAAEADIDFD IIRNDNDFTVKYTPRAGSYTIMVL FADQATPTSPIRVKVEPSHDASKVKA EGPGLSRTGVELGKPTHFTVNAKAA GKGLDVQFSGLTGDAVRDVIDIHD HHDNTYTVKYTPVQQGPVGVNVTYG GDPKSPFSVAVSPSLDLSKIKVSGL GEKVDVGKDQFTVKSAGGQGG VASKIVGPSGAAPCKVEPGLGADN SVVRFLPREEGPYEVEVYDGVVPG SPFPLEAVAPT KPSKVKAFGPGQLGG SAGSPARFTIDTKGAGTGGLGLTVEG PCEAQLECLDNGDGTCSVSYVPTPE GDYINILFADTHIPGSPFKAHVVPC FDASKVKCSGPGLERATAGEVGFQ VDCSSAGSAELTIEICSEAGLPAEYVI QDHGDGTHITTYIPLCPGAYTVTIKY GGQVPVNFPSKLQVEPAVDTSGVQC YGPGIEGQGVFREATTEFSVDARALT QTGGPHVKARVANPSGNLTETYVQD RGDGMVYVEYTPYEGLHSVDVTYD GSPVPSSPFQVPVTEGCDPSRVRVH GPGIQSGTTNPKNFVETRGAGTG GLGLAVEGPEAKMSCMDNKDGSC SVEYIPYEAGTYSLVNVTYGGHQVPGS PFKVPVHDVTDASKVKCSGPGLSPG MVRANLPQSFQVDTSKAGVAPLQVK VQGPKGLVEPVDVVDNADGTQTVNY VPSREGPYSISVLYGDEEVPRSPFKV KVLPTHASKVKASGPGLNNTGTPA

SLPVEFTIDAKDAGEGLLAVQITDPE
GKPKKTHIQDNHDGTYTVAYVPDVT
GRYTILIKYGGDEIPFSPYRVRAVPTG
DASKCTVTVSIGGHGLGAGIGPTIQI
GEETVITVDTKAAGKGKVTCTVCTPD
GSEVDVDVVENEDGTFDIFYTAPQP
GKYVICVRFGEHVPNSPFQVTALA
GDQPSVQPPLRSQQLAPQYTYAQQG
QQTWAPERPLVGVNGLDVTSLRPF
LVIPFTIKKGEITGEVRMPSGKVAQP
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TAYGPGLTHGVNKPATFTVNTKDA
GEGGLSLAIEGPSKAEISCTDNQDGT
CSVSYLPVLPGDYSILVKYNEQHVPG
SPFTARVTGDDSMRMSHLKVGSA
DIPINISETDLSLLTATVPPSGREEP
CLLKRLRNGHVGISFVPKETGEHLV
HVKKNGQHVASSPIPVVISQSEIGDA
SRVRVSGQGLHEGHTFEPAEFIIDTR
DAGYGGLSLSIEGPSKVDINTEDLED
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SVANVGSHCDLSLKIPEISIQDMTAQ
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FVDSLTKATCAPQHAGPGPADAS
KVVAKGLGLSKAYVGQKSSFTVDCS
KAGNNMLLVGVHGPRTPCEEILVKH
VGSRLYSVSYLLKDKGEYTLVVKWG
DEHIPGSPYRVVVP