

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q8IUG5	MY18B_HUMAN	Homo sapiens	Unconventional myosin-XVIIIb	7.026191	S2155	S1216;S1829;S2193;S2296;S2309;S2377	30379171;35254053	MAISSRLALWEQKIREEDKSPPPSSP PPLFSVIPGGFIKQLVRGTEKEAKEA RQRKQLAVASPEREIPESISQPNSKS SSGTRSGSQQISQDDQSSSPGSSDIL GKESEGRSPDPEQMTSINGEKAQE LGSSATPTKKTVPFKRGVRRGDVLL MVAKLDPDSAKPEKTHPHDAPPCKT SPPATDTGKEKKGETSRTPCGSQAS TEILAPKAEKTRTGGLDGPQGTVAL KKGEEGQSIVGKGLGTPKTTELKEAE PQKDRQGTRPQAQGGPGEVVRPGK AEKEGAEPNTVEKGNVSKDVGSEG KHVRPQIPGRKWGGFLGRRSKWDG PQNKDKEGVLLSKAECTGEPQTQ MEKTSQVQGELGDDLRLMGEKAGEL RSTTGKAGESWDKKEKMGQPQGKS GNAGEARSQTEKGCEAPKEVSTMV ESPAAPGKGGWPGSRGQEAEEPCSR AGDGAGALETELEGPSQPALEKDAE RPRIRKENQDGPAPQEEGKGGQSRD SDQAPEDRWYEAKEVWLAQKDGFT LATVLKPDEGTADLPAGRVRLWIDA DKTITEVDEEHVHRANPPELDQVED LASLISVNESSVLNLLQRYKAQLLH TCTGPDILVLPQPRGSPVPSAGKVPKG RRDGLPAHIGSMAQRAYWALLNQR RDQSIVALGWSGAGKTTCCCEQVLEH LVGMAGSVDGRVSVEKIRATFTVLR AFGSVSMHSRSATRFSMVMSLDF NATGRITAAQLQTMLEKSRVARQP EGESNFLVFSQMLAGLDLDRTELN LHQMADSSSFGMGVWSKPEDKQKA AAFAQLQGAMEMLGISESEQRAV WRVLAAYHLGAAGACKVGRKQFM RFEWANYAAEALGCEYEELNTATFK HHLRQIIQQMTFGPSRWGLEDEETS SGLKMTGVDCVEGMASGLYQELFA AVVSLINRSFSSHLSMASIMVVDSD PGFQNPQRHQGKDRAATFEELCHNY AHERLQLLFYQRTFVSTLQRYQEEG VPVQFDLPDPSPGTTAVAVDQNPQS VRLPAGGGAQDARGLFWVLDEEVH VEGSSDSVVLRLCAAFFKKGAGTE GSSALRTCEQLQCEIFHQLGWDPV RYDLTGWLHRAKPNLSALDAPQVLH QSKREELRSLFQARAKLPPVCRAVA GLEGTSQQALQRSRMVRRTFASSLA AVRRKAPCSQIKLQMDALTSMIKRS RLHFIHCLVPNPVVESRSGQESPPPP QPGRDKPGAGGPLALDIPALRVQLA GFHILEALRLHRTGYADHMGLTRFR

RQFQVLDAPLLKKLMSTSEGIDERK
AVEELLETLDLEKKAVAVGHSQVFL
KAGVISRLEKQREKLVQSIVLFQAA
CKGFLSRQEFKKLKIRRLAAQCIQKN
VAVFLAVKDWPWWQLLGSLLQPLLS
ATIGTEQLRAKEEELTLRRKLEKSE
KLRNELRQNTDLESKIADLTSDLA
DERFKGDVACQVLESERAERLQAFR
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SELENMTRNKSLVDEQLYRLOFEKA
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RQSATSSRILSPRINEEAGDTERTQS
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FVRRQKYCHFGDGEVLAVQRKSTER
LEPASSPLASRSTNTSPLSREKLSP
SAALSEFVEGLRRKRAQRGQSTLG
LEDWPTLPYQTTGASTLRRGRAGSD
EGNLSLRVGAKSPLIEGAAGLLRS
TSLKCISSDGVGGTLLPEKSKTQFS
SCESLLESRPSMGRKLSPTTPRDM
LLSPTLRPRRRCLESSVDDAGCPDL
GKEPLVFQNRQFAHLMEEPLGSDPF
SWKLPSLDYERKTKVDFDDFLPAIRK
PQTPTSLAGSAKGGQDGSQRSSIH
ETEEANRSFLSGIKTILKKSPEPKED
PAHLSDS SSSSGSIVSFKSADSIKSRP
GIPRLAGDGGERTSPERREP GTGRK
DDDVASIMKKYLQK