	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membra
0	Q8IUG5	MY18B_HUMAN	Homo sapiens	Unconventional myosin-XVIIIb	19.817031	S2155	S1216;S1829;S2193;S2296;S2309;S2377	30379171;35254053	MAISSRLALWEQKIREEDKSPPPSSP PPLFSVIPGGFIKQLVRGTEKEAKEA RQRKQLAVASPEREIPEISISQPNSKS SSGTRSGSQQISQDDQSSSPGSSDIL GKESEGSRSPDPEQMTSINGEKAQE LGSSATPTKKTVPFKRGVRRGDVLL MVAKLDPDSAKPEKTHPHDAPPCKT SPPATDTGKEKKGETSRTPCGSQAS TEILAPKAEKTRTGGLGDPGQGTVAL KKGEEGQSIVGKGLGTPKTTELKEAE PQGKDRQGTRPQAQGPGEGVRPGK AEKEGAEPTNTVEKGNVSKDVGSEG KHVRPQIPGRKWGGFLGRRSKWDG PQNKKDKEGVLLSKAEKTGEPQTQ MEKTSQVQGELGDDLRMGEKAGEL RSTTGKAGESWDKKEKMGQPQGKS GNAGEARSQTEKGCEAPKEVSTMV ESPAAPGKGGWPGSRGQEAEEPCSR AGDGAGALETELEGPSQPALEKDAE RPRIRKENQDGPAPQEEGKGGQSRD SDQAPEDRWYEAEKVWLAQKDGFT LATVLKPDEGTADLPAGRVRLWIDA DKTITEVDEEHVHRANPPELDQVED LASLISVNESSVLNTLLQRYKAQLLH TCTGPDLIVLQPRGPSVPSAGKVPKG RRDGLPAHIGSMAQRAYWALLNQR RDQSIVALGWSGAGKTTCCEQVLEH LVGMAGSVDGRVSVEKIRATFTVLR AFGSVSMAHSRSATRFSMVMSLDF NATGRITAAQLQTMLLEKSRVARQP EGESNFLVFSQMLAGLDLDLRTELN LHQMADSSSFGMGVWSKPEDKQKA AAAFAQLQGAMEMLGISESEQRAV WRVLAAIYHLGAAGACKVGRKQFM RFEWANYAAEALGCEYEELNTATFK HHLRQIIQQMTFGPSRWGLEDEETS SGLKMTGVDCVEGMASGLYQELFA AVVSLINRSFSSHHLSMASIMVVDS PGFQNPRHQGKDRAATFEELCHNY AHERLQLLFYQRTFVSTLQRYQEEG VPVQFDLPDPSPGTTVAVVDQNPSQ VRLPAGGGAQDARGLFWVLDEEVH VEGSSDSVVLERLCAAFEKKGAGTE GSSALRTCEQPLQCEIFHQLGWDPV RYDLTGWLHRAKPNLSALDAPQVLH QSKREELRSLFQARAKLPPVCRAVA GLEGTSQQALQRSRMVRRTFASSLA AVRRKAPCSQIKLQMDALTSMIKRS RLHFIHCLVPNPVVESRSGQESPPPP QPGRDKPGAGGPLALDIPALRVQLA GFHILEALRLHRTGYADHMGLTRFR RQFQVLDAPLLKKLMSTSEGIDERK AVEELLETLDLEKKAVAVGHSQVFL KAGVISRLEKQREKLVSQSIVLFQAA CKGFLSRQEFKKLKIRRLAAQCIQKN VAVFLAVKDWPWWQLLGSLQPLLS ATIGTEQLRAKEEELTTLRRKLEKSE KLRNELRQNTDLLESKIADLTSDLA DERFKGDVACQVLESERAERLQAFR EVQELKSKHEQVQKKLGDVNKQLE EAQQKIQLNDLERNPTGGADEWQM RFDCAQMENEFLRKRLQQCEERLD SELTARKELEQKLGELQSAYDGAKK MAHQLKRKCHHLTCDLEDTCVLLE NQQSRNHELEKKQKKFDLQLAQAL GESVFEKGLREKVTQENTSVRWELG QLQQQLKQKEQEASQLKQQVEMLQ DHKRELLGSPSLGENCVAGLKERLW KLESSALEQQKIQSQQENTIKQLEQL RQRFELEIERMKQMHQKDREDQEE ELEDVRQSCQKRLHQLEMQLEQEY EEKQMVLHEKQDLEGLIGTLCDQIG HRDFDVEKRLRRDLRRTHALLSDVQ LLLGTMEDGKTSVSKEELEKVHSQL EQSEAKCEEALKTQKVLTADLESMH SELENMTRNKSLVDEQLYRLQFEKA DLLKRIDEDQDDLNELMQKHKDLIA QSAADIGQIQELQLQLEEAKKEKHK LQEQLQVAQMRIEYLEQSTVDRAIVS RQEAVICDLENKTEFQKVQIKRFEVL	None	None	None	None	None	None	None	None

									VIRLRDSLIKMGEELSQAATSESQQR ESSQYYQRRLEELKADMEELVQREA EASRRCMELEKYVEELAAVRQTLQT DLETSIRRIADLQAALEEVASSDSDT ESVQTAVDCGSSGRKEMDNVSILSS QPEGSLQSWLSCTLSLATDTMRTPS RQSATSSRILSPRINEEAGDTERTQS ALALSRARSTNVHSKTSGDKPVSPH FVRRQKYCHFGDGEVLAVQRKSTER LEPASSPLASRSTNTSPLSREKLPSP SAALSEFVEGLRRKRAQRGQGSTLG LEDWPTLPIYQTTGASTLRRGRAGSD EGNLSLRVGAKSPLEIEGAAGGLLRS TSLKCISSDGVGGTTLLPEKSKTQFS SCESLLESRPSMGRKLSSPTTPRDM LLSPTLRPRRRCLESSVDDAGCPDL GKEPLVFQNRQFAHLMEEPLGSDPF SWKLPSLDYERKTKVDFDDFLPAIRK PQTPTSLAGSAKGGQDGSQRSSIHF ETEEANRSFLSGIKTILKKSPEPKED PAHLSDSSSSSGSIVSFKSADSIKSRP GIPRLAGDGGERTSPERREPGTGRK DDDVASIMKKYLQK								