	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extrace region
0	Q9JMH9	MY18A_MOUSE	Mus musculus	Unconventional myosin-XVIIIa	28.439263	NaN	S35;S52;S72;S74;T79;S83;S98;T99;S102;S103;S140;S145;S157;S160;S164;S234;S983;S1063;S1064;S1066;S1636;S1938;S1966;S1970;S1994;S1998;S2002;S2003;S2016;S2032;S2037;S2039;T2041;S340	39627609	MFNLMKKDKDKDGGRKEKKEKKEK KERMSAAELRSLEEMSMRRGFFNL NRSSKRESKTRLEISNPIPIKVASGSD LHLTDIDSDSNRGSIILDSGHLSTAS SSDDLKGEEGSFRGSVLQRAAKFGS LAKQNSQMIVKRFSFSQRSRDESAS ETSTPSEHSAAPSPQVEVRTLEGQL MQHPGLGIPRPGPRSRVPELVTKRF PADLRLPALVPPPPPALRELELQRRP TGDFGFSLRRTTMLDRAPEGQAYRR VVHFAEPGAGTKDLALGLVPGDRLV EINGQNVENKSRDEIVEMIRQSGDS VRLKVQPIPELSELSRSWLRTGEGH RREPADAKTEEQIAAEEAWYETEKV WLVHRDGFSLASQLKSEELSLPEGK ARVKLDHDGAILDVDEDDIEKANAP SCDRLEDLASLVYLNESSVLHTLRQ RYGASLLHTYAGPSLLVLSTRGAPAV YSEKVMHMFKGCRREDMAPHIYAV AQTAYRAMLMSRQDQSIVLLGSSGS GKTTSFQHLVQYLATIAGTSGTKVFS VEKWQALSTLLEAFGNSPTIMNGSA TRFSQILSLDFDQAGQVASASIQTML LEKLRVARRPASEATFNVFYYLLACG DATLRTELHLNHLAENNVFGIVPLS KPEEKQKAAQQFSKLQAAMKVLAIS PEEQKTCWLILASIYHLGAAGATKEA AEAGRKQFARHEWAQKAAYLLGCSL EELSSAIFKHQLKGGTLQRSTSFRQ GPEESGLGEGTKLSALECLEGMASG LYSELFTLLISLVNRALKSSQHSLCS MMIVDTPGFQNPEWGGSARGASFE ELCHNYAQDRLQRLFHERTFLQELE RYKEDNIELAFDDLEPVADDSVAAV DQASHLVRSLAHADEARGLLWLLEE EALVPGATEDALLDRLFSYYGPQEG DKKGQSPLLRSSKPRHFLLGHSHGT NWVEYNVAGWLNYTKQNPATQNAP RLLQDSQKKIISNLFLGRAGSATVLS GSIAGLEGGSQLALRRATSMRKTFTT GMAAVKKKSLCIQIKLQVDALIDTIK RSKMHFVHCFLPVAEGWPGEPRSA SSRRVSSSSELDLPPGDPCEAGLLQL DVSLLRAQLRGSRLLDAMRMYRQG YPDHMVFSEFRRRFDVLAPHLTKKH GRNYIVVDEKRAVEELLESLDLEKSS CCLGLSRVFFRAGTLARLEEQRDEQ TSRHLTLFQAACRGYLARQHFKKRK IQDLAIRCVQKNIKKNKGVKDWPW WKLFTTVRPLIQVQLSEEQIRNKDEE IQQLRSKLEKVEKERNELRLSSDRLE TRISELTSELTDERNTGESASQLLDA ETAERLRTEKEMKELQTQYDALKKQ MEVMEMEVMEARLIRAAEINGEVD DDDAGGEWRLKYERAVREVDFTKK RLQQELEDKMEVEQQSRRQLERRL GDLQADSDESQRALQQLKKKCQRLT AELQDTKLHLEGQQVRNHELEKKQ RRFDSELSQAHEETQREKLQREKLQ REKDMLLAEAFSLKQQMEEKDLDIA GFTQKVVSLEAELQDISSQESKDEAS LAKVKKQLRDLEAKVKDQEEELDEQ AGSIQMLEQAKLRLEMEMERMRQT HSKEMESRDEEVEEARQSCQKKLK QMEVQLEEEYEDKQKALREKRELES KLSTLSDQVNQRDFESEKRLRKDLK RTKALLADAQIMLDHLKNNAPSKRE IAQLKNQLEESEFTCAAAVKARKAM EVEMEDLHLQIDDIAKAKTALEEQL SRLQREKNEIQNRLEEDQEDMNEL MKKHKAAVAQASRDMAQMNDLQA QIEESNKEKQELQEKLQALQSQVEF LEQSMVDKSLVSRQEAKIRELETRL EFEKTQVKRLENLASRLKETMEKLT EERDQRAAAENREKEQNKRLQRQL RDTKEEMSELARKEAEASRKKHELE MDLESLEAANQSLQADLKLAFKRIG DLQAAIEDEMESDENEDLINSLQDM VTKYQKKKNKLEGDSDVDSELEDRV DGVKSWLSKNKGPSKAPSDDGSLKS	False	False	2.195	2.344	False	False	4.0	False	False

									SSPTSHWKPLAPDPSDDEHDPVDSI SRPRFSHSYLSDSDTEAKLTETSA											