

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extrac region
Q9JMH9-1	MY18A_MOUSE	Mus musculus	Unconventional myosin-XVIIa	25.685855	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	MFNLMKKDKDKDGGKKEKKEKKEK KERMSAAELRSLLEEMSMRRGFFNL NRSSKRESKTRLEISNPIPIKVASGSD LHLTDIDSDSNRGSILDSGHLSTAS SSDDLKGEESFRGSVLQRAAKFGS LAKQNSQMIVKRFSFSQRSRDESAS ETSTPSEHSAAFPQVEVRTLEGQL MQHPGLGIPRPGPRSRVPELVTKRF PADLRLPALVPPPPALRELELQRRP TGDFGFSLRRTTMLDRAPEGQAYRR VVHFAEPGAGTKDLALGLVPGDRLV EINGQNVENKSRDEIVEMIRQSGDS VRLKVQPIPELSELSRSWLRTGEGH RREPADAKTEEQIAAEEAWYETEKV WLVHRDGFSLASOLKSEELSLPEGK ARVKLDHDGAILDVEDDIEKANAP SCDRLEDLASLVYLNESVHLHLRQ RYGASLLHTYAGPSLLVLSTRGAPAV YSEKVMHMFKGCRRREDMAPHIYAV AQTAYRAMLSRQDQSVILLGSSGS GKTTSFQHLVQYLATAGTSGTKVFS VEKWQALSTLLEAFGNSPTIMNGSA TRFSQILSLDFDQAGQVASASIQTML LEKLRVARRPASEATFNVFYLLACG DATLRTELHLNHLAENNVFGIVPLS KPEEKQAAQQFSLQAAAMKVLAIS PEEQKTCWLLIASIYHLGAAGATKEA AEAGRKQFARHEWAQKAAAYLLGCSL EELSSAIFKHQLKGGTLQRSTFRQ GPESGLGEGTKLSALECLEGMASG LYSEFTLLISLVNRALKSSQHSLCS MMIVDTPGFQNPPEWGGARGASFE ELCHNYAQDRLQRLFHERTFLELE RYKEDNIELAFDDLEPVADDSVAAV DQASHLVRS LAHAD EARGLLWLEE EALVPGATEDALLDRLFSYYPQEG DKKGQSPLLRSSKPRHFLGHSHGT NWWVEYNVAGWLNNTKQNPATQNP RLLQDSQKKIISNLFGRAGSATVLS GSIAGLEGGSQLALRRATS MRKTFIT GMAAVKKKSLCIQIKLQVDALIDTIK RSKMHFVHCFLPVAEGWPGEPRSA SSRRVSSSELDPGDPCEAGLLQL DVSLRAQLRGSRLDAMRMYRQG YPDHMFSEFRFRFVFLAPHLTKKH GRNYIVVDEKRAVEELLESLDLEKSS CCLGLSRVFFRAGTLARLEEORDEQ TSRHLLTFQAAACRGYLARQHFKKRK IODLAIRCQKNIKKNKGVDWPW WKLFTTVRPLIQVQLSEEQIRNKDEE IQQLRSKLEKVEKERNELRLSSDRLE TRISELTSELTDERNTGESASQLLDA ETAERLRTEKEMKELQOTQYDALKKQ MEVMEMEVMEARLIRAAEINGEVD DDDAGGEWRLKYERAVREVDFTKK RLQQELEDKMEVEQSSRRQLERRL GDLQADSDESQRALQQLKKKQRLT AELQDTKLHLEGQQVRNHELEKKQ RRFDSELSQAHEETQREKLQREKLQ REKDMLLAEAFSLKQOMEKDLDDIA GFTQKVVSLEAELQDISSQESKDEAS LAKVKKQLRDLEAKVKDQEEELDEQ AGSIQMLEQAKLRLEMEMERMROT HSKEMESRDEEVEEARQSCQKCLK QMEVQLEEEYEDKQKALREKRELES KLSTLSDQVNQRDFESEKRLRKDLK RTKALLADAQIMLDHLKNNAPSKRE IAQLKNQLESEFTCAA AVKARKAM EVEMEDLHLQIDDIKAKTAL EEQL SRLQREKNEIQNRLEEDQEDMNEL MKKHKA AVAQASRDMAQMNLDQA QIEESNKEKQELQEKLQALQSQVEF LEQSMVDKSLVSRQEA KIRELETRL EFEKTQVKRLENLASRLKETMEKLT EERDQRAAENREKEQNKRLRQL RDTKEEMSELARKEAEASRKKHELE MDLESLEAANQSLQADLKLAFKRIG DLQAAIEDEMESDENEDLINSLQDM VTKYQKKKNKLEGSDVDSELEDRV DGVKSWLSKNKGPSKAPSDDGSLSK	False	True	2.911	3.134	1.166	1.282	4.418	1.529	1.114

