

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	extracellular region
P13542	MYH8_MOUSE	Mus musculus	Myosin-8	23.627151	NaN	T66;T71;T389;T419;T424;S625;S1091;S1095;S1161;S1236;T1254;S1260;T1285;S1291;S1302;S1305;T1463;T1466;T1491;S1494;T1500;S1513;T1516;S1553;S1573;S1602;S1713;S1725;T1729;S1738	37453647	MSAGSDAEMAIFGEAAPYLKSEKE RIEAQNKPFDAKTSVFVAEPKESVVK SVIQSKDGGKVTVKTESGATLTVKED QVFPMPNPPKYDKIEDMAMMTHLHE PGVLYNLKERYAAWMIYTSGLFCV TVNPKWLPVYNPEVVAAYRGKKRQ EAPPHFISISDNAYQFMLTDRENQSI LITGESGAGKTVNTRKRVIOYFATIAVT GDKKKEESGKMQGTLEDQIISANPL LEAFGNAKTVRNDNSRFGKFIH FGTTGKLASADIETYLLEKSRVTFQL KAERSYHIFYQITSNKKPELIEMLLIT TNPYDYAFVSOGEITVPSIDDEELM ATDSADILDGFSPEEKVSIYKLTGAVM HYGNMKFKQKQREEQAEPDGTEVA DKAAYLQCLNSADLLKALCYPRVKV GNEYVTGGQTVQVYNAV GALAKAV YEKMFLLWVTRINQQLDTKQPROY FIGVLDIAGFEIFDNLSLEQLCINFN EKLOQFFNHHMFVLEQEEYKKEGIE WTFIDFGMDLAACIELIEKPLGIFSIL EEECMFPKATDTSFKNKLYDQHLGK SNNFQPKPPTKGKAEAHFSLVHYAG TVDYNTGWLDKNKDP LNDTVVGLY QKSAMKTLASLFTYASAEADGGAK KGAKKKGSSFTVSALFRENLNKLM TNLRSHTPHFVRCIIPNETKTPGAM EHELVLHQLRCNGVLEGIRICRKGFI PSRILYGFQRYKVLNASAIPEGQFI DSKKASEKLLGSIDIDHTQYKFGHTK VFFKAGLLGLEEMRDEKLAQIITRT QAVCRGYLMRVEYQKMLLRRESIFC IQYNVRAFNMVNHWPWMKLFKIK PLLKSAETEKEMATMKEEFOKTKDE LAKSEAKRKELEEKMVTLLEKNDL QLQVQSEADSLADAERCEQLIKNKI QLEAKIKEVTERAEDEEINAELETAK KRKLEDECSSELKDDIDDLLETLAKVE KEKHATENKVKNLTEEMAGLDENIA KLTKEKKALQEAHQQTLLDQLAEED KVNTLTKAKTKLEQQVDDLEGSLEQ EKCLRMDLERAKRKLKLEGDLKLAQES TMDIENDKQQLDEKLLKKEFEISNLI SKIEDEQAVEIQKKIKELQARIEEL EEEIEAERASRAKAEKQRSDLRELE EISERLEEAGGATSAQVEMNKKRET EFQKLRRDLEATLQHEATAAALRK KHADSVAEALGEQIDNLQRVKQKLEK EKSELKMEIDDLSSNAEAIKAKGN LEKMCRTLEDQVSELKSKEEQQL INELTAQRARLQTEAGEYSRQLEK DALVSQLSRSKQASTQOIEELKQLE EETKAKNALAHALQSSRHDCDLLRE QYEEEQEGKAELQRALSKANSEVAQ WRKYETDAIQRTETELEEAKKLAQ RLQAAEEHVEAVNAKASLEKTKQR LQNEVEDLMIDVERTNAACAALDKK QRNFDKVLSEWRQKYEETQAELESC QKESRTLSTELFKVKNAYEESLDHL ETLRRENKLOQEISDLTEQIAEGG KHIHELEKIKKQVEQEKCEIQAALEE AEASLEHEEGKILRIQLELNQVKSEI DRKIAEKDEEIDQLKRNHVRVVTM QSTLDAEIRSRLDALRVKKMEGDL NEMEIQLNHANRLAAESLRNRYRNT QGILKDTQLHLDALRGQEDLKEQL AIVERRANLLQAEIEELRATLEQTER SRKIAEQELLDASERVQLLHTQNTSL INTKKLENDVSQLQSEVEEVIQESR NAEKAKKAITDAAMMAEELKKEQ DTAHLERMKKNMEQTVKDLQHRL DEAEQLALKGGKKQIQKLEARVREL EGEVENEQKRNAEAVKGLRKHERR VKELTYQTEEDRKNVRLQDLVDKL QAKVSKYKRAEEAEQSNANLAKF RKLQHELEAEERADIAESQVKNLKR VKSREVHTKISAE	False	False	3.313	2.355	1.652	1.355	0.636	1.705	1.275