

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extra regio
Q02566	MYH6_MOUSE	Mus musculus	Myosin-6	24.088486	NaN	T379;S417;S1090;S1139;T1261;S1271;T1277;T1284;S1309;T1310;T1311;S1512;T1515	37507081;36288343	MTDAQMADFGAAAOYLKSEKERLEAOTRPFDIRTECFVPPDKEEYVKAKVVSREGGKVTAEENGKTVTIKEDQVMQQNPPKFDKIEDMAMLTFLHEP AVLNLKERYAAWMIYTSGLFCVTVNPKWLPVYNAEVVAAAYRGKKRSE APPHIFISISDNAYQYMLTDRENOQSILITGESGAGKTVNTRKVIQVFASIAAIGDRSKKENPNANKGTLEDQIIQANPALEAFGNAKTVRNDNSSRFGKFRIRHFGATGKLASADIEITYLLEKSRVIFQLKAERNYHIFYQILSNKKPELLDMLLV TNNPYDYAFVVSQGEVSVASIDDSEELATDSAFDVLSTAEKAGVYKLTGAIMHYGNMKFKQKQREEQAEPDGTE DADKSAYLMGLNSADLLKGLCHPRVKVGNYYVTGGQSVQQVYYSIGALAKSVYEKMFNWMVTRINATLETKQPRQYFIGVLDIAGFEIFDFNSFEQLCINF TNEKLQFFNHMHMFVLEQEEYKKEGIEWEFIDFGMDLQACIDLIEKPMGIMSILEEEMFPAKSDMTFKAKLYDNHLGKSNNFQKPRNVKQKQEAHFSLVHYAGTVDYNIMGWLEKNKDPLENTVVGLYQKSSKLMATLFTYASADTGDGSGKGGKGGKSSFTVSAHLHRENLNKLMTNLKTTHPHFVRCIIPNERKAPGVMDNPLVMHQLRCNGVLEGI RICKRGFPNRILYDFRQRYRILNPA AIPEGQFIDSRKGAEKLLGSLDIDHN QYKFGHTKVFVKAGLLGLEEMRDERLSRIITRIQAARGQLMRIEFKKIVE RRDALLVIQWNIRAFMGVKNWPWM KLYFKIKPLLKSAETEKEMANMKEE FGRVKDALEKSEARRKELEEKMVSLLOEKNDLQVQAEQDNLNDAEERCDQLIKNKIQLEAKVKEMTERLEDEEEMNAELTAKKRKLEDECSSELKKDIDDLELTLAKVEKEKHATENKVKNLTEEMAGLDEIIAKLTKEKKALQEAHQALDDLQAEEDKVNTLTKSVKLEQQVDDLEGSLEQEKVVRMDLERAKR KLEGDCLKTQESIMDLENDKLEELK LKKKKEFDISQQNSKIEDEQALALQLQKKLKENQARIEELEELEAERTARAKVEKLRSDLSRELEEISERLEEAGGATSVQIEMNKKREAEFQKMRRDLE EATLQHEATAAALRKKHADSVAELEGEQIDNLRVKQKLEKESEFKLELD DVTSNMEQIHKAKANLEKVSRTLEDQANEYRVKLEEAQRSLNDFTTQRAKLQTEGELARQLEEKALISQLTRGKLSYTOQMEDLKRQLEEEGKAKNALAHALQSSRHDCDLLREQYEEEMEA KAELOQVLSKANSEVAQWRKYETDAIORTEELEAKKLAQRLODAEEAVEAVNAKCSSLEKTKHRLQNEIEDLMVDVERSNAAAAALDKQRNFDKILAEWKQKYEESQSELESSQKEARSLS TELFKLKNAYEESLEHLETFKRENK NLQEEISDLTEQLGEGGKNVHELEKIRKQLEVEKLELQSALEEAASLEHEEGKILRAQLEFNQIKAEIERKLAEKDEEMEQAQRNHLRMVDSLQTSLEDAE TRSRNEALRVKKKMEGDLNEMEIQLSQANRIASEAQHKLKNSQAHLKDTQLQLDDAVHANDDLKENIAIVERRNLLQAELEELRAVVEQTERSRLAEQELIETSERVQLLHSQNTSLINQKKK MESDLTQLQTEVEEAVQECRNAAEKAKKAITDAAMMAEELKKEQDTSAL LERMKNMEQTIKDLQHRLEDAEQIALKGGKKQLQKLEARVRELENELEAEQRNAESVKGMRKSERRIKELTYQTEEDKKNLMRLQDLVDKQLKVKAYKROAEEAEEQANTNLSKFRKVQHELDEAEERADIAESQVNKLRAKSRDIGAKKMHDDEE	False	False	3.724	3.485	2.589	2.495	1.671	2.415	2.249