	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi appa
0	P02563	MYH6_RAT	Rattus norvegicus	Myosin-6	33.844526	S18;T34;T59;S172;T176;S179;S241;S242;S392;S622;S626;S644;S739;S749;S843;S880;S1038;S1138;S1148;S1159;T1189;S1200;T1275;T1303;S1308;S1336;S1367;S1414;S1436;S1464;S1466;S1470;S1471;S1597;T1600;S1601;T1606;S1638;T1696;T1710;S1711;T1776;S1777;S1837;S1916	T378;S416;S1089;S1138;T1260;S1270;T1276;T1283;S1308;T1309;T1310;S1511;T1514;T1680	26109417;18988896	MTDAQMADFGAARYLRKSEKERLE AQTRPFDIRTECFVPDDKEEYVKAKI VSREGGKVTAETENGKTVTVKEDQV MQQNPPKFDKIEDMAMLTFLHEPA VLYNLKERYAAWMIYTYSGLFCVTV NPYKWLPVYNAEVVAAYRGKKRSEA PPHIFSISDNAYQYMLTDRENQSILIT GESGAGKTVNTKRVIQYFASIAAIGD RSKKDNPNANKGTLEDQIIQANPAL EAFGNAKTVRNDNSSRFGKFIRIHF GATGKLASADIETYLLEKSRVIFQLK AERNYHIFYQILSNKKPELLDMLLVT NNPYDYAFVSQGEVSVASIDDSEELL ATDSAFDVLGFTAEEKAGVYKLTGAI MHYGNMKFKQKQREEQAEPDGTE DADKSAYLMGLNSADLLKGLCHPRV KVGNEYVTKGQSVQQVYYSIGALAK SVYEKMFNWMVTRINATLETKQPR QYFIGVLDIAGFEIFDFNSFEQLCINF TNEKLQQFFNHHMFVLEQEEYKKE GIEWEFIDFGMDLQACIDLIEKPMGI MSILEEECMFPKATDMTFKAKLYDN HLGKSNNFQKPRNVKGKQEAHFSL VHYAGTVDYNILGWLEKNKDPLNET VVGLYQKSSLKLMATLFSTYASADT GDSGKGKGGKKKGSSFQTVSALHRE NLNKLMTNLRTTHPHFVRCIIPNER KAPGVMDNPLVMHQLRCNGVLEGI RICRKGFPNRILYGDFRQRYRILNPA AIPEGQFIDSGKGAEKLLGSLDIDHN QYKFGHTKVFFKAGLLGLLEEMRDE RLSRIITRIQAQARGQLMRIEFKKMV ERRDALLVIQWNIRAFMGVKNWPW MKLYFKIKPLLKSAETEKEMANMKE EFGRVKDALEKSEARRKELEEKMVS LLQEKNDLQLQVQAEQDNLADAEE RCDQLIKNKIQLEAKVKEMTERLED EEEMNAELTAKKRKLEDECSELKKD IDDLELTLAKVEKEKHATENKVKNL TEEMAGLDEIIAKLTKEKKALQEAH QQALDDLQAEEDKVNTLTKSKVKLE QQVDDLEGSLEQEKKVRMDLERAK RKLEGDLKLTQESIMDLENDKLQLE EKLKKKEFDISQQNSKIEDEQALALQ LQKKLKENQARIEELEEELEAERTAR AKVEKLRSDLTRELEEISERLEEAGG ATSVQIEMNKKREAEFQKMRRDLE EATLQHEATAAALRKKHADSVAELG EQIDNLQRVKQKLEKEKSEFKLELD DVTSHMEQIIKAKANLEKVSRTLED QANEYRVKLEEAQRSLNDFTTQRAK LQTENGELARQLEEKEALIWQLTRG KLSYTQQMEDLKRQLEEEGKAKNAL AHALQSARHDCDLLREQYEEEMEA KAELQRVLSKANSEVAQWRTKYETD AIQRTEELEEAKKKLAQRLQDAEEA VEAVNAKCSSLEKTKHRLQNEIEDL MVDVERSNAAAAALDKKQRNFDKIL AEWKQKYEESQSELESSQKEARSLS TELFKLKNAYEESLEHLETFKRENK NLQEEISDLTEQLGEGGKNVHELEK IRKQLEVEKLELQSALEEAEASLEHE EGKILRAQLEFNQIKAEIERKLAEKD EEMEQAKRNHLRVVDSLQTSLDAE TRSRNEALRVKKKMEGDLNEMEIQ LSQANRIASEAQKHLKNAQAHLKDT QLQLDDAVRANDDLKENIAIVERRN TLLQAELEELRAVVEQTERSRKLAE QELIETSERVQLLHSQNTSLINQKKK MDADLSQLQTEVEEAVQECRNAEE KAKKAITDAAMMAEELKKEQDTSAH LERMKKNMEQTIKDLQHRLDEAEQI ALKGGKKQLQKLEARVRELENELEA EQKRNAESVKGMRKSERRIKELTYQ TEEDKKNLVRLQDLVDKLQLKVKAY KRQAEEAEEQANTNLSKFRKVQHEL DEAEERADIAESQVNKLRAKSRDIGA KQKMHDEE	None	None	None	None	None	None	None