

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
Q5SX39	MYH4_MOUSE	Mus musculus	Myosin-4	24.557655	NaN	S36;T64;T69;S79;T389;T391;S392;T419;T424;S625;T776;S1092;S1096;S1162;S1237;T1241;S1243;T1255;S1261;T1265;S1278;T1286;S1288;S1292;S1303;S1306;S1413;T1464;T1467;S1474;T1492;S1495;T1501;S1514;T1517;S1542;S1547;S1554;S1574;S1600;S1603;S1714;S1726;T1730;T1736;S1739	36064721;37507081	MSSDAEMAVFGEAAPYLKSEKERIEAQNKPFDAKSSVFFVDKESYVKA TVQSRREGGKVTAKEGGATVTVKDD QVFSMNPYPKYDKIEDMAMMTHLHE PAVLYNLKERYAAWMIYTYSGLFCVTVNPKYKLPVYNPEVVAAYRGKKRQEA APPHFISISDNAYQFMLTDRENOQ SILITGESGAGKTVNTRKRVIQYFATIAVTGDKKKEEATSGKMQGTLEDQIISAN PLEAFGNAKTVRNDNSSRFGKFIHFHGATGKGLASADIEYLLKSRVTFQLKAERSYHIFYQIMSNKKPELIEMLLITTNPYDFAYVSQGEITVPSIDDEELMATTDTAVDILGFSADKVAIKLTGAVMHYGNMKFKQKQREEQAEPDGTEVADKAAYLTSLSNADLLKALCYPRVKVGNEYVTKGQTVQVYNSVGLAKSMYEKMFWMVTRINQQLDTKQPRQYFIGVLDIAGFEIFDFNTLEQLCINFTEKLEKQOFFNHHMFVLEQEEYKKEGIDWEFIDFGMDLACIELIEKPMGIF SILEEFCMFPKATDTSFKNKLYEQH LGKSNNFQKPKPAKGKAEAHFSLVHYAGTVDYNIIGWLDKNKDPLNETVVGlyQKSGLKTALFLFSGGQAAEAEGGGGKGGKGGSSSFQTVSALFRENLNKLMTNLKSSTHPHFVRLIPNETKTPGAMEHELVLHLRCNGVLEGRICRKGFPSTRILYADFKQRYKVLNSAIP EGQFIDSKKASEKLLGSIDIDHTQYKFGHTKVFVFKAGLLGTLEEMRDEKLAQLITRTQAVCRGYLMRVEFKMMERRESIFCIQYNVRAFNMVXHWPMWKLYFKIKPLLSAETEKEMANMKEDFEKAKEDLAKSEAKRKELEEKMVALMQEKNDLQLQVQAEADGLADAEERCDQLIKTKIQLEAKIKELTERAEDEE EINAELTAKKRKLEDECESELKDDIDLELTLAKVEKEKHATENKVNKLNTEEMAGLDENIAKLTKEKKALQEAHQOTLDDLQAEEDKVNTLTKAKTKLEQQVDDLEGSLEQEKKLMDLERAKRKLGDGDLKLAQESTMDIENDKQQLDEKLEKKEFEMS NLQSKIEDEQALGMQLQKKIKELQARIELEEEIEAERASRAKAEKQRSDDL SRELEIEISERLEEAGGATS AQIEMNKKRAEFQKMRDLLEEATLQHEATAAALRKKHADSV AELGEQIDNLQRVKQKLEKEKSELKMEIDDLASNMETVSKAKGNLEKMCRTLEDQLSEVKTKEEEQQLINELSTQKARLH TESGEFSRQLDEKDMVQSLSRGKQAF TQQIEELKRQLEEEESAKNALAHALQ SARHDCDLLREQYEEEQEAKAE LQRAMSKANSEVAQWRKYETDAIQ RTEELEAKKLAQRLQDAEEHVEAVNSKASLEKTKRQLQNEVEDLMIDVERSNAACAALDKQRNFDKVLAEWKQKYEETQAELEASQKESRSLSTELFKVKNAYEESLDQLETLKRENKNLQQEISDLTEQIAEGGKHIHELEKIKKQIDQEKSELQASLEEAASLEHEEGKILRIQLELNQVKSEIDRKAIEKDEEIDQLKRNLH RVVESMQSTLDAEIRSRNDALRIKKMEGDLNEMEIQLNHANRQAAEAIRNLNRTQGMLKDTQLHLDDALRGQDDLKEQLAMVERRANL MQAEIEELRASLEQTERSRRVAEQELLDASERVQLLHTQNTSLINTKKKLETDISIQGEMEDIVQEARNAEKKAKKAITDAAMMAEELKKEQDTS AHLERMKKNMEQTVKDLQHRLEAEQLALKGGKKIQKLEARVRELENEVENEQKR NIEAVKGLRKHERRVKELTYQTEEDRKNVLRQLDVLVDKLTQVKVAYKRQAEAEQSNVNLAKFRKIQHELEEAERADIAESQVNKL RVKSREVHTK VISEE	None	None	None	None	None	None	None	None	