

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q9Y623	MYH4_HUMAN	Homo sapiens	Myosin-4	19.994096	NaN	T64;T69;S79;T389;T391;S392;T419;T424;S625;T776;S1092;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	37217939	MSSDSEMAIFGEAAPFLRKSEKERIEAQNKPFDAKTISVFVDPKESYVKAIVQSREGGKVTAKTEAGATVTVKEDQVFSMNPPKYDKIEDMAMMTHLHEPAVLYNLKERYAAWMIYTYSGLFCVTVNPYKWLVPVYNPEVVTAYRGKKRQEA PPHIFISISDNAYQFMLTDRENQSILITGESGAGKTVNTRKVIQYFATIAVITG EKKKEEPASGKMQGTLEDQIISANP LLEAFGNAKTVRNDNSRFKGFIRI HFGATGKLASADIETYLLEKSRVTFQ LKAERSYHIFYQILSNKKPELIEMLLI TTNPYDFAFVSQGEITVPSIDDOEEL MATDSAVDILGFTADEKVAIYKLTGA VMHYGNMKFKQKQREEQAEPDGTGE VADKAAAYLTSLSADLLKSLCYPRVK VGNEFVTKGQTVQOVYNAV GALAKA IYEKMLWMVTRINQQLDTKQPRQY FIGVLDIAGFEIFDNLSLEQLCINFN EKLQQFFNHMHFVLEQEEYKKEGIE WEFIDFGMDLAACIELIEKPMGIFSI LEEECMFPKATDTSFKNKLYEQHLG KSNNFQKPKPAKKGPEAHFSLVHYA GTVDYNIAGWLDKNKDP LNETVVGL YQKSAMKTLAFLFSGAQTAEAEAGGG GKKGGKKGSSFTVSALFRENLNK LMTNLRSTHPHFVRCIIPNETKTPGA MEHELVLHQLRCNGVLEGRICRKG FPSRLYADFQRKYVNLNASEIPEGQ FIDSKKASEKLLGSIEIDHTQYKFGH TKVFFKAGLLGTLEEMRDEKLAQLIT RTQAICRGFLMRVFRKMMERRESI FCIQYNIRAFMNVKHW PPMKLYFKI KPLLKSAETEKEMANMKEEFEKTE ELAKTEAKRKELEEKMVTLMQEKNDLQLQVQAEADALADAEERC DQLIK TKIQLEAKIKEVTERAEDEEEINAELT AKKRKLEDECSLKKDIDDLTLAK VEKEKHATENKVNLT EEMAGLDE TIAKLTKEKKALQEAHQQTLDLQMEEDKVNTLTKAKTKLEQQVDDLEGS LEQEKKLCMDLERAKRKL EGDKLQAEESTMDTENDKQNLNKLKKEFE MSNLQGGKIEDEQALAIQLQKKIKELQ ARIEEL EEEIEAERASRAKAEKQRSD LSRELEIEISERLEEAGGATSAQIEMN KKREAEFQKMRRDLEESTLQHEATA AALRKKHADSV AELGEQIDSLQRVK QKLEKEKSELKMEINDLASNMETVS KAKANFEKMCRTLEDQLSEIKTKEE EQORLINELSAQKARLHTESGEFSR QLDEKDAMVSQLSRGKQAFQTQIEE LKRQLEEEETKAKSTLHALQ SARHDCDLLREQYEEEQEAKAELQRGMSKA NSEVAQWRTKYETDAIQRTEELEEA KKKLAQRLQDAEEHVEAVNSK CASL EKTQRLQNEVEDLMIDVERSNAAC IALDKQRNFDKVLAEWKQYEEETQ AELEASQKESRSLSTELFKVNAYEE SLDHLETLKRENKNLQEQEISDLTEQI AEGGKHIHELEKVKKQLDHEKSELQ TSLEEAASLEHEEGKILRIQLELNQ VKSEIDRKIAEKDEELDQLKR NHLR VVESMQSTLDAEIRSNDALRIKKK MEGDLNEMEIQLNHANRQAAEALR NLRNTQGILKDTQLHLDDAIRGQDD LKEQLAMVERRANLMQAEVEELRA SLERTERGRKMAEQELLDASERVQL LHTQNTSLINTKKKLETDISIQGEM EDIVQEARNAEKAKKAITDAAMMA EELKKEQD TSAHLERMKNMEQTV KDLQLRLDEAEQLALGGKKIQKLEARVRELESEVESEQKHNV EAVKGL RKHERRVKELTYQTEEDRKNILRLQ DLVDKLQTKVKAYKRQAEAEAEQSN VNLAKFRKLQHELEEAERADIAES QVNKLVRKSREVHTKVISEE	False	False	1.557	2.093	2.246	1.648	0.552	1.763	1.518