

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
G3UW82	MYH2_MOUSE	Mus musculus	Myosin-2	29.125745	NaN	T64;T69;T389;T419;S625;S1095;S1099;S1165;S1240;T1244;S1246;T1258;S1264;T1289;S1291;S1295;S1306;S1309;T1467;T1470;S1477;T1495;S1498;T1504;S1517;T1520;S1557;S1577;S1603;S1606;S1717;S1729;T1733;T1739;S1742	39927985	MSSDAEMAVFGEAAPYLKSEKERIEAQNRPFDKATSVFVAEPKESFVKGTIQSKDAGKVTVKTEAGATLTVKEDQIFPMNPPKYDKIEDMAMMTHLHEP AVLNLKERYAAWMIYTYSGLFCVT VNPYKWLVPVYNPEVVAAYRGKKRQE APPHIFISDNAYQFMLTDRENQSIL ITGESGAGKTVNTRKRVIQYFATIAVT GDKKKEEATSGKMQGTLEDQIISAN PLLEAFGNAKTVRNDNSSRFKGFIRI HFGTTGKLASADIEITYLLEKSRVTFQ LKAERSYHIFYQITSNKKPELIEMLLI TTNPYDYPFVVSQGEISVASIDDOEEL MATDS AIDILGFTNDEKVSIIKLTGA VMHYGNMKFKQKQREEQAEPDGTE VADKAAYLQGLNSADLLKALCYPRV KVGNEYVTKGQTVQVTVNAV GALAK AMYEKMFWMVTRINQQLDTKQPR QYFIGVLDIAGFEIFDFNSLEQLCINF TNEKLQFFNHMHFVLEQEEYKKE GIEWTFIDFGMDLAACIELIEKPMGI FSILEEECMFPKATDTSFNKLYEQ HLGKSANFQKPKVVKGAEAHFSLI HYAGTVDYNITGWLDKNKDP LNETV VGLYQKSSVKT LAYLFSGAQTAEAEA SSGGAAKKGAKKKGSSFTV SALFR ENLNKMLMNLNRSTHPHFVRCIIPNE TKTGAMEHELVLHQLRCNGVLEGI RICRKGFP SRIYADFQKRYKVLNAS AIPEGQYIDSKKASEKLLGSIDIDHTQ YKFGHTKVF FKAAGLLGLEEMRDDK LAQLITRTQAMCRGFLARVEYQKMV ERRESIFCIQYNIRAFMNVKHWPW MKLFFKIKPLLSAETEKEMATMKE EFQKTDDLAKSEAKRKELEEKMVS LLKEKNLQ LQVQAAEAEG LADAEER CDQLIKTKIQLEAKIKEVTERAEDEE EINAELTAKKRKLEDECSELKDDIDD LELTLAKVEKEKHATENKVKNLTEE MAGLDETI AKLTKEKKALQEAHQQT LDDLQAEEDKVNLT LKAKIKLEQQV DDLEGSLEQEKKLRMDLERAKRKE GDLKLAQESIMDIENEKQQLDERLK KKEFEMS NLQSKIEDEQAIGIQLQKK IKELQARIEE EEEIEAERASRAKAEK QRS DLSRELEIEISERLEEAGGATSAQ IEMNKKREAEFQKMRRL EEA TLQ HEATAATLRKKHADSVAELGEQIDN LQRVKQKLEKEKSEMMEIDDLAS NVETVSKAKGNLEKMCRTLEDQVS ELKSKEEEQORLINDLTTQRGRLQT ESGEFSRQLDEKALVSQLSRGKQA FTQIEELKRQLEEEVKAKNALAHA LQSSRHDCDLLREQYEEEQESKAEL QRALSKANSEVAQWRTKYETDAIQR TEELEAAKKLAQRLQAAEEHVAV NAKCASLEKTQRLQNEVEDLMLD VERTNAACAALDKQRNFDKILAEW KQKYETHAELEASQKEARSLGTEL FKMKNAYEESLDQLET LKRENKNL QQEISDLTEQIAEGGKRIHELEKIKK QVEQEKCELQAALEAAEASLEHEEG KILRIQLELNQVNSEIDRKIAEKDEEI DQLKRNHRRVVE MSQSTLDAEIRSR NDAIRIKKMEGDLNEMEIQLNHSN RMAAEALRNRYRNTQGILKDTQLHLD DALRGQEDLKEQLAMVERRANLLQ AEIEELRATLEQTERSRIAEQELLD ASERVQLLHTQNTSLINTKKKLETDI SQIQGEMEDIVQEARNAEKAKKAIT DAAMMAEELKKEQDTS AHLERMKK NMEQTVKDLQLRLDEAEQLALKGG KKQIQKLEARVRELEGEVESEQKRN AEAVKGLRKHERRVKELTYQTEEDR KNILRLQDLVDKLQAKVKS YKRQAE EAAEQSNTNLSKFRKIQHELEEAEE RADIAESQVNKL RLVKSREVHTKIISE E	False	False	2.737	1.312	False	False	4.0	False	False