

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	pl m
Q8VDD5	MYH9_MOUSE	Mus musculus	Myosin-9	43.618763	NaN	T11;S628;T754;S1114;S1714;T1939;S1943	21540332;37453647;34887587;24788674;22645316;36288343;36064721;37507081;29187734	MAQQAADKLYVDKNFNPLAQAD WAAKKLVVWPPSSKNGFEPASLKEEV GEEAIVELVENGKKVKVKNKDDIQKM NPPKFSKVEDMAELTCLNEASVLHN LKERYYSGLIYTSGLFCVVINPYKNL PIYSEIIVEMYKGGKRHEMPPHIYAI TDTAYRSMMDREDQSILCTGESGA GKTENTKKVIOYLAHVASSHKSCKD QGELERQLLANPILEAFGNAKTVK NDNSSRFGKFRINFVNGYIVGANI ETYLLEKSRAIRQAKEERTFHIFYYLL SGAGEHLKTDLLLEPYNKYRFLSNG HVTIPGQQDKDMFQETMEAMRIMG IPEDEQMGLLRVISGVLQLGNIAFKK ERNTDQASMPDNTAAQKVSHLLGI NVTDFTRGILTPRIKVGDRYVQKAQT KEQADFAIEALAKATYERMFRLVVL RINKALDKTKRQGASFIGILDIAGFEI FDLNSFEQLCINYTNEKLQQLFNHT MFILEQEEYQREGIEWNFIDFGLDL QPCIDLIEKPAGPPGILALLDEECWF PKATDKSFVEKVVQEQGTHPKFQKP KQLKDKADFCIIHYAGKVVDYKADEW LMKNMDPLNDNIATLLHQSSDKFV SELWKDVDRIIGLDQVAGMSETALP GAFKTRKGMFRITVGQLYKEQLAKL MATLRNTNPNFVRCIIPNHEKKAGK LDPHLVLDQLRCNGVLEGRICRQG FPNRVVFQEFRQRYEILTPNSIPKGF MDGKQACVLMIKALELDSNLYRIGQ SKVFFRAGVLAHLEEEERDLKITTVDII GFQACCRGYLARKAFARQQQLTA MKVLQRNCAAYLRLRNWQWWRFL TKVKPLLSIRHEDELLAKEAELTKV REKHLAAENRLTEMETMQSQLMAE KLQEQEQLQAETELCAEAELRRL TAKKQEEIEICHLEARVEEEERC QYLQAEKKMQQNIQEELEEQLEEE SARQKLQLEKVTTEAKLKKLEEDQII MEDQNCCLAKEKKLEDRVAEFTT NLMEEEEKSKSLAKLKNKHEAMITD LEERLRREKQROELEKTRRKLQGD STDLSQIAELQAIAELKMLAKKE EELQAALARVEEAAQKNMALKKIR ELETQISELQEDLESERASRNKAEK QKRDLGEELEALKTELEDTLSTAA QQELRSKREQEVSKLKTLEDAKT HEAQIQEMRQKHSQAVEELADQLE QTKRVKATLEKAKQTLNERGELAN EVKALLQKGDSEHKRKKVEAQLQE LQVKFSEGERVRETELADKVTKLQVE LDSVTGLLSQSDSKSKLTKDFSAL SQLQDTQELLQEEENRQKLSLSTKLK QMEDEKNSFREQLLEEEEAARNLE KQIATLHAQVTDKMKKMDGVGCL ETAEEAKRRLQKDLGLSQRLEEKV AAYDKLEKTRQLQELDDLLVDLD HQRSVSNLEKKQKKFDQLLAEKKT ISAKYAEERDRAEAEAREKETKALS ARALEEAMEQKAELERLNKQFRTE MEDLMSKDDVGVKSVHELEKSKRA LEQQVEEMKTQLELEDELAQATEA KLRLVNLQAMKAQFERDLQGRDE QSEKKKQLVROVREMAELEDER QORSMAAARKKLEMDLKDLEAHI DTANKNREEAIKQLRKLQAQMKDC MRELDLTRASREEILAQAKENEKLL KSMEAEMLQLEELAAERAKRQAQ QERDELADEIANS SGKALALEEKR RLEARIAQLEEELEEQGNTLINDR LKKANLQIDQINTDLNLSHAQKN ENARQQLERQNKELKAKQEMESA VSKYKASIAALEAKIAQLEEQLDNE TKERQAASKQVRRTEKLLKDVLLQV EDERRNAEQKQADKASTRLKQK RQLEEAEEEAQRANASRRKLQRELE DATETADAMNREVSSLKNKLRGD LPFVVTRRVRKGTGDCSDEEVDGK ADGADAKAAE	True	True	4.737	4.649	2.043	1.992	2.29	5.