

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	46.353237	NaN	T11;S628;T754;S1114;S1714;T1939;S1943	37507081;37453647;29187734;34887587;36064721;24788674;21540332;36288343;39627609;39927985;22645316	MAQQAADKYLVDKFNFINPLAQAD WAAKKLVVWPPSSKNGFEPASLKEEV GEEAIVELVENGKVKVKNKDDIQKM NPPKFSKVEDMAELTCLNEASVLHN LKERYYSGLIYTSGLFCVINPYKNL PIYSEIIVEMYKGGKRHEMPPHIYAI TDTAYRSMMDQREDQSILCTGESGA GKTENTKKVIOYLAHVASSHKSCKD QGELERQLLQANPILEAFGNAKTVK NDNSSRFGKFRINFVNGYIVGANI ETYLLEKSRAIRQAKEERTFHIFYLL SGAGEHLKTDLLLEPYNKYRFLSNG HVTIPGQDDKDMFQETMEAMRIMG IPEDEQMGLLRVISGVLQLGNIAFKK ERNTDQASMPDNTAAQKVSHELLGI NVTDFTRGILTPRIKVGDRYVQKAQT KEQADFAIEALAKATYERMFRLVVL RINKALDKTKRQGASFIGILDIAGFEI FDLNSFEQLCINYTNEKLQQLFNHT MFILEQEEYQREGIEWNFIDFGLDL QPCIDLIEKPAGPPGILALLDEECWF PKATDKSFVEKVVQEQGTHPKFQKP KQLKDKADFCIIHYAGKVVDYKADEW LMKNMDPLNDNIATLLHQSSDKFV SELWKDVDRIIGLDQVAGMSETALP GAFKTRKGMFRITVGQLYKEQLAKL MATLRNTNPNFVRCIIPNHEKKAGK LDPHLVLDQLRCNGVLEGIKRCROG FPNRVVFQEFRQRYEILTNSIPKGF MDGKQACVLMIKALELDSNLYRIGQ SKVFFRAGVLAHLEEEERDLKITDVII GFQACCRGYLARKAFARQQQLTA MKVLRNCAAYLRLRNWQWWRFL TKVKPLLSIRHEDELLAKEAELTKV REKHLAAENRLTEMETMQSQLMAE KLQEQEQLQAETELCAEAELRRL TAKKQEEIEICHDLARVEEEERC QYLQAEKKMQQNIQEELEEQLEEE SARQKLQLEKVTTEAKLKKLEEDQII MEDQNCCLAKEKKLLEDRVAEFTT NLMEEEEKSKSLAKLKNKHEAMITD LEERLRREKQROLEKTRRKLKGD STDLSQIAELQAIAELKMLAKKE EELQAALARVEEAAQKNMALKKIR ELETQISELQEDLESERASRNKAEK QKRDGEELEALKTELEDTLSTAA QQELRSKREQEVSKLKTLEDAKT HEAQIQEMRQKHSQAVEELADQLE QTKRVKATLEKAKQTLNERGELAN EVKALLQKGDSEHKRKKVEAQLQE LQVKFSEGERVRETELADKVTKLQVE LDSVTGLLSQSDSKSKLTKDFSAL SQLQDTQELLQEEENRQKLSLSTKLC QMEDEKNSFRELEEEEAARNLE KQIATLHAQVTDKMKKMGDVGCL ETAEEAKRRLQKDLGLSQRLEEKV AAYDKLEKTRLQQLDLDLLVLDL HQRSVSNLEKKQKFFDQLLAEKKT ISAKYAEERDRAEAEAREKETKALS ARALEEAMEQKAELELNLKQFRTE MEDLMSKDDVGVKSVHELEKSKRA LEQQVEEMKTQLELEDELAQATEA KLRLVNLQAMKAQFERDLQGRDE QSEKKKQLVROVREMAELEDER KQSMAMAARKKLEMDLKDLEAHI DTANKNREEAIKQLRKLQAQMKDC MRELDLTRASREEILAQAKENEKLL KSMEAEMLQLEELAAERAKRQAQ QERDELADEIANSNGKALALEEKR RLEARIAQLEEELEEQGNTLINDR LKKANLQIDQINTDLNLSHAQKN ENARQQLERQNKELKAKQEMESA VSKYKASIAALEAKIAQLEEQLDNE TKERQAASKQVRRTEKLLKDVLLQV EDERRNAEQKQADKASTRLKQK RQLEEAEEEAQRANASRRKLORELE DATEADAMNREVSSLKNKLRGD LPFVTRRVRKGTGDCSDEEVDGK ADGADAKAAE	True	True	4.535	4.309	False	False	5.0	5.