

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion
P35579	MYH9_HUMAN	Homo sapiens	Myosin-9	24.491112	S36;T90;S96;S197;S282;S628;T630;S759;T1146;T1208	T11;S628;T754;S1114;S1714;S1943	34229054;23301498;26853435;34725712;40914422;35138101;30397120;37217939;16408927;40596516;38665916;34019948;29351928;32870666;35083852;20305658;33214551;41018975;32119511;35008409;33465208	MAQQAADKYLVDKFNINPLAQADWAAKKLVVWVPSDKSGFEPASLKEEVGEEAIVELVENGKKVKVKNDDIQKMNPPKFSKVEDMAELTCLNEASVLHN LKERYYSGLIYTYSGLFCVVINPYKNLPIYSEEVEMVYKGGKRHEMPPHYAI TDTAYRSMMDREDQSILCTGESGAGKTENTKKVIQYLAYVASSHKSKDDQELERQLLQANPILEAFGNAKTVKNDNSSRFQKFRINFDVNGYIVGANI ETYLLEKSRAIRQAKEERTFHIFYYLLSGAGEHLKTDLLLEPYNKYRFLSNGHVTIPGQQDKDMFQETMEAMRIMGIPEEEEQMLLRVISGVLQGLNIVFKKERNTDQASMPDNTAAQKVSHELLGINVDFTRGILTPRIKVGDRDYVQKAQTKEQADFAEALAKATYERMFWRWLVRINKALDKTKRQGFASFIGILDIAGFEI FDLNSFEQLCINYTNEKLQQLFNHMTFILEQEYYQREGIEWNFIDFGLDL QPCIDLIEKPPAGPPGILALLDEECWF PKATDKSFVEKVMQEQGTHPKFKPK KQLKDKADFCIIHYAGKVVDYKADEWLMKNMDPLNDNIATLLHQSSDKFVSELWKDVRHIGLDQVAGMSETALP GAFKTRKGMFRTVGLYKQLAKLMATLRNTNPNFVRCIIPNHEKKAGKLDPHLVLDQLRCNGVLEGI RCRQGFNPNRVVFEFRQRYEILTPNSIPKGFMDGKQACVLMIKALELDSNLYRIGQSKVFFFRAGVLAHLEEEERDLKITDVII GFQACCRGYLARKAFARQQQLTAMKVLQRNCAAYLKLNRWQWWRLFTKVKPLLQVSRQEEEMMAKEEELVKVREKQLAAENRLTEMETLQSQLMAEKLQEQEQLOAETELCAEAEBELRARLTAKKQEELEIICHDL EARVEEEER CQHLEAEKKKMQNQIQLEEQLEEEESARQKLQLEKVTTEAKLKKLEEEQIILEDQNKCLAKEKKLLEDRIAFTTNLTEEEKSKSLAKLKNKHEAMITDLEERLRREKQRQLEKTRRKL EGDSTDLSQIAELQAQIAELKMQLAKKEEELQAALARVEEAAQKNMALKKIRELESQISELQEDLESESRASRNKAEKQKRD LGEELEALKTELEDTL DSTAAQQLRSLKREQEVNILKKTLEEEAKTHEAQIQEMRQKHSQAVEELAEQLEQTKRVKANLEKAKQTLNERGELAN EVKVLQGGDSEHKRKKVEAQLQE LQVKFNEGERVTELADKVTKLQVE LDNVTGLLSQSDSKSSKLTDFKFSAL ESQEQDTELLQENRQKLSLSTKLKQVEDEKNSFREQLEEEEA KHNL EKQIATLHAQVADMKKKMEDSVGCLETAEEVKRKLQKDLLEGLSORHEEKVAAYDKLEKTKTRLQEQELDDLVDLDHQRQSACNLEKKQKFDQLLAEETISAKYAEERDRAEAEAREKETKALSLARALEEAMEQKAELERLNKQFRT EMEDLMSSKDDVGVKSVHELEKSKRAL EQQQVEEMKTQLEEELEDELQATED AKLRLEVNQAMKAQFERDLQGRDEQSEKKKQLVRQVREMEAELEDERKQRSMAVAARKKLEMDLKDLEAHI DSANKNRDEAIKQLRKLQAQMKDCMRELD DTRASREIILAQAKENEKLLKSMEAE MIQLQEELAAAERAKRQAQ QERDELADEIANSSGKGALALEEKRRLEARIAQLEEELEEEQGNTELINDRLKKANLQIDQINTDLNLRSHAQKN ENARQQLERQNKELKVKLQEMEGT VKSKYKASITALEAKIAQLEEQLDNETKERQAACKQVRRTEKKLKVLLQVDDERRNAEQYKQADKASTRLKQLKRQLEEAEEEAQRANASRRKLQRELE DATETADAMNREVSSLKKNLRRGDLPFVVRPRMARKGAGDGSDEEVDGKADGAEAKPAE	True	True	4.834	5.0	2.011