

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P35580	MYH10_HUMAN	Homo sapiens	Myosin-10	18.038189	S1145;S1750	S1145;S1935;S1937;S1938;S1939;S1952;S1956;T1960;S1975;S214;S214	33214551;20305658;34229054;29351928;34019948;26853435;3062050;23301498	MAQRTGLEDPERYLFVDRAVIYNPA TQADWTAKKLWVWIPSERHGFEEAASI KEERGDEVMVELAENGGKAMVVKD DIQKMNPPKFSKVEDMAELTCLNEA SVLHNLKDRYSSGLIYTYSGLFCVVI NPYKNLPIYSENIEMYRGKKRHEM PPHIYAISESAYRCMLQDREDQSILC TGESGAGKTENTKKVIQYLAHVASS HKGRKDNIPGELEERQLQANPILE SFGNAKTVKNDSSRFGKIFIRINF VTGYIVGANIETYLLEKSRVAVRQAKD ERTFHIFYQLLSGAGEHLKSDLLLEG FNNYRFLSNGYIPIPGQQDKDNFQE TMEAMHIMGFSHEEILSMLKVVSSV LQFGNISFKKERNTDQASMPENTVA QKLCHLLGMNVMEFTRAILTPRIKV GRDYVQKAQTKEQADFAVEALAKAT YERLFRWLVHRINKALDRTKROGAS FIGILDIAGFEIFELNSFEQLCINYTN EKLQQLFNHTMFILEQEEYQREGIE WNFIDFGLDLQPCIDLIERPANPPGV LALLDEECWFPKATDKTFVEKLVQE QGSLSKFKQPRQLKDKADFCIIHYA GKVVDYKADEWLMKNMDPLNDNVA TLLHQSSDRFVAELWKDVDRIVGLD QVTGMTETAFGSAYKTKKGMFRTVG QLYKESLTKLMATLRNTNPNFVRCII PNHEKRAGKLDPHLVLDQLRCNGV LEGIRICRQGFNRIVFQEFQRQYEIL TPNAIPKGFMDGKQACERMIRALEL DPNLYRIGQSKIFFRAGVLAHLEEEER DLKITDIIFFQAVCRGYLARKAFACK QQQLSALKVLQRNCAAYLKLRRHWQ WWRVFTKVKPLLQVTRQEEELQAK DEELLKVKEKQTKVEGELEEMERKH QQLLEKNILAEQLQAETELFAEAAA MRARLAAKKQEEILHDLESRVVEE EEERNQILQNEKKKMQAHIQDLEE QLDEEEGARQKLQLEKVTAEAKIKK MEEEILLLEDQNSKFIKEKLMEDRI AECSSQLAEEEEKAKNLAKIRNKQE VMISDLEERLKKEEKTRQELEKAKR KLDGETTDLQDQIAELQAQIDELKLQ LAKKEEELQGALARGDDETLHKNN NKAQKQKRDLSLEALKTELEDLTL DTTAAQQELRTKREQVAELKKALE EETKNHEAQIDMRQRHATALEELS EQLEQAKRFKANLEKNKQGLETDN KELACEVKVLQQVKAESEHKRKKLD AQVQELHAKVSEGDRLRVELAEKAS KLQNELDNVSTLLEEAEEKGKIFAK DAASLESQLODTQELLQEETRQKLN LSSRIRQLEEEKNSLQEQEEEEEEA RKNLEKQVLALQSQLADTKKKVDDD

LGTIESLEEAKKLLKDAEALSQRLE  
EKALAYDKLEKTKNRLQQELDDLTV  
DLDHQRQVASNLEKKQKKFDQLLA  
EKSISARYAEERDRAEAEAREKETK  
ALSLARALEEAEAKEEFERQNKQL  
RADMEDLMSSKDDVGKNVHELEKS  
KRALEQQVEEMRTQLEEELEDELQAT  
EDAKLRLEVNMQAMKAQFERDLQT  
RDEQNEEKRLIKQVRELEAELED  
ERKQRALAVASKKKMEIDLKDLEAQ  
IEAANKARDEVIKQLRKLQAQMKDY  
QRELEEARASRDEIFAQSKSEKCLK  
SLEAEILQLQEELASSERARRHAEQE  
RDELADEITNSASGKSALLDEKRRLE  
ARIAQLEEEEEEQSNMELLNDRFR  
KTTLQVDTLNAELAAERSAAQKSDN  
ARQQLERQNKELKAKLQELEGAVKS  
KFKATISALEAKIGQLEEQLEQEAKE  
RAAANKLVRRTTEKKLKEIFMQVEDE  
RRHADQYKEQMEKANARMKQLKR  
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ATEANEGLSREVSTLKNRLRRGGPIS  
FSSSRSGRRQLHLEGASLELSDDDT  
ESKTSVDVNETQPPQSE