

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi appara
P35580	MYH10_HUMAN	Homo sapiens	Myosin-10	17.942943	S1145;S1750	S1145;S1935;S1937;S1938;S1939;S1952;S1956;T1960;S1975;S214;S214	34725712;38665916;34019948;33214551;34229054;23301498;39990658;30620550;20305658;35008409;37217939;35138101;26853435;29351928;40596516	MAQRTGLEDPERYLFDRAVIYNPA TQADWTAKKLVWIPSERHGFEAASI KEERGDEVMVELAENGGKAMVNKD DIQKMNPPKFSKVEDMAELTCLNEA SVLHNLKDRYYSGLIYYSGLFCVVI NPYKLNPIYSENIIEMRYGKKRHEM PPHIYAISEAYRCMLQDREDQSILC TGESGAGKTENTKKVIQYLAHVASS HKGRKDHNPGELEERQLLANPILE SFGNAKTVKNDNSSRFQKIRINFD VTGYVGANIETYLLEKRAVRQAKD ERTFHIFYQLLSGAGEHLKSDLLEGG FNMYRFLSNGYIPGQQDKDNFQEE TMEAMHIMGFSHEEILSMLKVVSSV LQFGNISFKKERNTDQASMPENTVA QKLCHELLGMNVMETFTRAILTPRIKV GRDYVQKAQTKQADFAVEALAKAT YERLFRWLVRINKALDRTRKQGGAS FIGILDIAGFIEFELNSFEQLCINYN EKLQQLFNHTMFILEQEEYOREGIE WNFIDFGLDLQPCIDLIERPANPPGV LALLDEECWFPKATDKTFVEKLVQE QGSLSKFKPRQLKDKADFCIIHYA GKVDYKADEWLMKNMDPLNDNVA TLLHQSSDRFVAELWKDVRIVGLD QVTGMTETAFGSAYKTKKGMFRITVG QLYKESLTKLMATLRNTNPNFVRCII PNHEKRAGKLDPHLVLDQLRCNGV LEGIRICRQGFPPNRFVQEFQRQYEIL TPNAIPKGFMDGKQACERMIRALEL DPNLYRIGQSKIFFRAGVLAHLEEEER DLKITDIIHFFQAVCRGYLARKAFACK QQQLSALKVLQRNCAAYLKLHWHWO WVRVFTKVKPLLOVTRQEEELQAK DEELLKVKKEKQTKVEGELEEMERKH QQLLEEKNILAEQLQAETELFAEAE MRARLAACKQELEEILHDLESRVEE EEERNQILQNEKKMQAHIQDLEE QLDEEEGARQKLEKVTAEAKIKK MEEEILLLEDQNSKFIEKKLMEDRI AECSSQLAEKAKNLAKIRNKQE VMISDLEERLKKKEKTRQELKAKR KLDGETTDLQDQIAELQAIQDELKIQ LAKKEEELQGALARGDDETLHKNN ALKVVRELAQAIQELQDFESEKASR NKAQKQKRDLSSELEALKTELEDTL DTTAAQQLRTKREQVVAELKKALE EETKNHEAQIQDMRQRHATALEELS EQLEQAKRFKANLEKNKQGLETDN KELACEVKVLQVQKAESEHKKRKLID AQVQELHAKVSEGDRRLRVELAEKAS KLQNELDNVSTLLEAEKKGKIFAK DAASLESQLODTQELLQEEETROKLN LSSRIRQLEEEKNSLQEQEEEEEEA RKNLEKQVLALQSQLADTKKKVDDD LGTIESLEEAKKLLKDAEALSORLE EKALAYDKLEKTKNRLQQELDDLTV DLDHQRQVASNLEKKQKFFDQLLA EEKSISARYAEERDRAEAEAREKETK ALSARALEEAEAKEEFERONKQL RADMEDLMSSKDDVGGKNVHELEKS KRALEQQVEEMRTQLEEELEDELQAT EDAKLRLEVNMQAMKAQFERDLQT RDEQNEEKKRLLIKQVRELAEELED ERKQRALAVASKKMEIDLKDLAQ IEAANKARDEVIKQLRKLQAMKDY QRELEEARASRDEIFAQSKSEKLLK SLEAEILQLQEELASSERARRHAEQE RDELADEITNSASGKSALLDEKRRLE ARIAQLEEELEEEQSNMELLNDRFR KTTLQVDTLNAELAAERSAAQKSDN ARQQLERQNKELKAKLQLELEGAVKS KFKATISALEAKIGLEEQLEQEAKE RAAANKLVRRTEKKLKEIFMQVEDE RRHADQYKEQMEKANARMKQLKR QLEEAEEEAATRANASRRKLQRELDD ATEANEGLSREVSTLKNRLRRGGPIS FSSSRSGRRQLHLEGASLELSDDDT ESKTSVNETQPPQSE	True	True	4.672	4.094	1.505	False	False