

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q7Z406	MYH14_HUMAN	Homo sapiens	Myosin-14	14.903721	S35;T51	S60;T1194;S1969;S1980;S1983;S1989	26853435;30397120;29351928;34019948;34725712;35008409	MAAVTMSVPGRKAPPRPGVPVEAAQ PFLFTPRGPSAGGGPGSGTSPQVEW TARRLVWVPSSELHGFEAAALRDEGE EEAEVELAESGRRLRLPRDQIQRMN PPKFSKAEDMAELTCLNEASVLHNL RERYYSGLIYTYSGLFCVVINPYKQLP IYTEAIVEMYRGKKRHEVPPHVYAVT EGAYRSMQLQDREDQSILCTGESGAG KTENTKKVIQYLAHVASSPKGRKEP GVPGELERQLLQANPILEAFGNAKT VKNDNSSRFGKFIRINFDVAGYIVGA NIETYLLEKSRAIRQAKDECSFHIFY QLLGGAGEQLKADLLEPCSHYRFL TNGPSSSPGQERELFQETLESRLVL GFSHEEIIISMLRMVSAVLQFGNIALK RERNTDQATMPDNTAAQKLCRLLG LGVTDGFRALLTPRIKVGGRDYVQKAQ TKEQADFALEALAKATYERLFRWL LRLNRLDRSPRQASFLGILDIAFG EIFQLNSFEQLCINYTNKQLQFLN HTMFVLEQEEYQREGIPWTFDFGL DLQPCIDLIERPANPPGLLALLDEEC WFPKATDKSFVEKVAQEQGGHPKF QRPRHLRDQADFSVLHYAGKVDYKA NEWLMKNMDPLNDNVAALLHQST DRLTAEIWKDVEGIVGLEQVSSLGD GPPGGRPRRGMFRTVGGQLYKESLSR LMATLSNTNPSFVRCIVPNHEKRAG KLEPRLVLDQLRCNGVLEGIRICRQG FPNRILFQEFQRQYEILTPNAIPKGF MDGKQACEKMIQALELDPNLYRVG QSKIFFRAGVLAQLEEEERDLKVTDII VSFQAAARGYLARRAFQKROQQQSA LRVMQRNCAAYLKLRLHWQWWRLF TKVKPLLQVTRQDEVLQARAQELQK VQELQQQSAREVGELQGRVAQLEEE RARLAEQLRAEAEELCAEAEETRGR AARKQELELVVSELEARVGEES RQMOTTEKKRLQQHIQLEAHLEAEE GARQKLQLEKVTTEAKMKKFEEDLL LLEDQNSKLSKERKLEDRLEAFSS QAAEEEEKVKSLNKLRLKYEATIAD MEDRLRKEEKGRQELEKLRRLDG ESSELQEQMVEQQQRAEELRAQLG RKEEELQAALARAEDEGGARAQLLK SLREAQAALAEAQEDLESERVARTK AEKQRRDLGEELEALRGELEDTLDS TNAQQELRSKREQEVTELKKTLEEE TRIHEAAVQELRQRHGQALGELAEQ LEQARRGKGAWKTRLALEAEVSEL RAELSSLQATARQEGEQRRRRLQL QEVQGRAGDGERARAEAAEKLQRA QAELENVSGALNEAESKTIRLSKELS STEAQLHDAQELLQEETRAKLALGS

RVRAMEAEAAGLREQLEEEAAARER
AGRELQTAQAQLSEWRRRQEEAG
ALEAGEEARRRAAREAEALTQRLAE
KTETVDRLERGRRRLQQLDDATM
DLEQQRQLVSTLEKKQRKFDQLLAE
EKA AVLRAVEERERAEAEGREREAR
ALS LTRALEEEQEAREELERQNRAL
RAELEALLSSKDDVGVKSVHELERAC
RVAEQ AANDLRAQVTELEDELTAEE
DAKLRLEVTVQALKTQHERDLQGRD
EAGEERRRQLAKQLRDAEVERDEER
KQRTLAVAARKKLEGELEELKAQMA
SAGQGKEEAVKQLRKMQAQMKEK
WREVEETRTRSEEIFSQNRESEKRL
KGLEAEVLRQLQEELAASDRARRAQ
QDRDEMADEVANGNLSKAAILEEK
QLEGR LGQLEEELEEEQSNSELLND
RYRKL LLQVESLTTELSAERSFSAKA
ESGRQQLERQIQELRGR LG EEDAGA
RARHKMTIAALESKLAQAEQLEQE
TRERILSGKLVRRAEKRLKEVV LQVE
EERRVADQLRDQLEKGNLRVKQLK
RQLEEAEEEEASRAQAGRRRLQRELE
DVTESAESMNREVTTLRNRLRRGPL
TFTTRTVRQVFRLEEGVASDEEAE
AQP GSGPSPEPEGSPPAHPQ