

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q9Y411	MYO5A_HUMAN	Homo sapiens	Unconventional myosin-Va	5.263779	NaN	S600;T1032;S1452;S1652;T1760	34019948	MAASELYTKFARVWIPDPEEVWKS AELLKDYKPGDKVLLHLEEGKDLE YHLDPKTKELPHLRNPDILVGENDL TALSYLHEPAVLHNLRVRFIDSKLI YTYCGIVLVAINPYEQLPIYGEDIIN AYSGQNMGMMDPHIFAVAEAYKQMA RDERNQSIIVSGESGAGKTVSAKYAM RYFATVSGSASEANVEEKVLASNPI MESIGNAKTTRNDNSSRFGKYIEIGF DKRYRIIGANMRTYLLEKSRVVFQAE EERNYHIFYQLCASAKLPEFKMLRL GNADNFNYTKQGGSPVIEGVDDAKE MAHTRQACTLLGISESHQMGIFRIL AGILHLGNVGFTRDADSDCTIPPKHE PLCIFCELMGVDYEEMCHWLCRHRK LATATETYIKPISKLQATNARDALAK HIYAKLFNWIVDQVNVQALHSQAVKQ HHSFIGVLDIYGFETFEINSFEQFCIN YANEKLQQQFNMHVFKLEQEEYMKE QIPWTLIDFYDNQPCINLIESKLGILD LLDEECKMPKGTDDTWAQKLYNTH LNKCALFEKPRLSNKAFIIQHFADKV EYQCEGFLEKNKDTVFEQIKVLKS SKFKMLPELFDQDEKAIPTSATSSG RTPLTRTPAKPTKGRPGQMAKEHKK TVGHQFRNSLHLLMETLNATTPHYV RCIKPNDFKFPFTFDEKRAVQQLRA CGVLETIRISAAGFPSRWTYQEFFSR YRVLMKQKDVLSDRKQTCNVLEKL ILDKDKYQFGKTKIFFRAGQVAYLEK LRADKLRAACIRIQKTIRGWLLRKKY LRMRKAAITMQRVVRGYQARCYAKF LRRTKAATIIQKYWRMYVRRRYKIR RAATIVLQSYLRGFLARNRYRKILRE HKAVIIQKRVRGWLARTHVKRSMHA IIYLQCCFRMMAKRELKCLKIEARS VERYKKLHIGMENKIMQLQRKVDE QNKDYKCLVEKLTNLEGIYNSETEK LRSDLERLQLSEEEAKVATGRVLSL QEEIAKLRKDLEQTRSEKKCIEEHAD RYKQETEQLVSNLKEENTLLKQEK EALNHRIVQQAEMTETMEKKLVEET KQLELDLNDERLRYQNLNNEFSRLE ERYDDLKEEMTLMVHVPKPGHKRT DSTHSSNESEYIFSSEIAEMEDIPSR TEEPSEKKVPLDMSLFLKLQKRVT ELEQEKQVMQDELDRKEEQVLR SKAKKEEERPQIRGAELEYESLKRQ ELEASENKKLKNELNELRKALSEKSA PEVTA

PGAPAYRVLMEQLTSVSEELDVRKE  
EVLILRSQLVSQKEAIQPKDDKNTMT  
DSTILLEDVQKMKDKGEIAQAYIGLK  
ETNRSSALDYHELNEDGELWLVYEG  
LKQANRLLESQLOSQKRSHENEAEA  
LRGEIQSLKEENNRQQQLLAQNLQL  
PPEARIEASLQHEITRLTNEIDLME  
QLEKQDKTVRKLKQKQKVFACKIGE  
LEVGQMENISPGQIIDEPIRPVNIPRK  
EKDFQGMLEYKKEDEQKLVKNLILE  
LKPRGVAVNLIPGLPAYILFMCVRHA  
DYLNDQKVRSLTSTINSIKKVLKK  
RGDDFETVFWLSNTCRFLHCLKQY  
SGEEGFMKHNTSRQNEHCLTNFDL  
AEYRQVLSDLAIQIYQQLVRVLENIL  
QPMIVSGMLEHETIQGVSGVKPTGL  
RKRTSSIADEGTYTLDLSILRQLNSFH  
SVMCQHGMPELIKQVVKQMFYIIG  
AITLNNLLLRKDMCSWSKGMQIRYN  
VSQLEEWLRDKNLMNSGAKETLEP  
LIQAAQLLQVKKKTDGDAEAIKSMC  
NALTTAQIVKVLNLYTPVNEFEERVS  
VSFIRTIQMRLDRKDSPQLLMDAK  
HIFPVTFFPNPSSLALETIQIPASLGL  
GFISRV