

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence |
|--------------|-------------|--------------|--------------------------|--------------|---------------|------------------------------|----------|--|
| Q9Y4I1 | MYO5A_HUMAN | Homo sapiens | Unconventional myosin-Va | 6.287639 | 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 SKAKKEEERPQIRGAELEYESLKR QELESENKKLKNELNELRKALSEK SAPEVTA |

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| | | | | | | | PGAPAYRVLMEQLTSVSEELDVRKE EVLILRSQLVSQKEAIQPKDDKNTMT DSTILLEDVQKMKDKGEIAQAYIGLK ETNRSSALDYHELNEDGELWLVYEG LKQANRLLESQLOSQRSHENEAEA LRGEIQSLKEENNRQQQLLAQNLQL PPEARIEASLQHEITRLTNENLDLME QLEKQDKTVRKLKQKLVFAKKIGE LEVGQMENISPGQIIDEPYRPNIPRK EKDFQGMLEYKKEDEQKLVKNLILE LKPRGVAVNLIPGLPAYILFMCVRHA DYLNDDQKVRSLTSTINSIKKVLKK RGDDFETVFWLSNTCRFLHCLKQY SGEEGFMKHNTSRQNEHCLTNFDL AEYRQVLSDLAIQIYQQLVRVLENIL QPMIVSGMLEHETIQVSGVKPTGL RKRTSSIADEGTYTLDLILRQLNSFH SVMCQHGMPELIKQVVKQMFYIIG AITLNLLLRKDMCSWSKGMQIRYN VSQLEEWLRDKNLMNSGAKETLEP LIQAAQLLQVKKKTDDDAEAICSMC NALTTAQIVKVLNLYTPVNEFEERVS VSFIRTIQMRLDRKDSPLLMDAK HIFPVTFFPNPSSLALETIQIPASLGL GFISRV |
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