	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
0	Q9QYF3	MYO5A_RAT	Rattus norvegicus	Unconventional myosin-Va	28.175057	NaN	S600;T1032;S1425;S1625;T1733	18683930	MAASELYTKFARVWIPDPEEVWKSA ELLKDYKPGDKVLLLHLEEGKDLEY RLDPKTSELPHLRNPDILVGENDLTA LSYLHEPAVLHNLRVRFIDSKLIYTY CGIVLVAINPYEQLPIYGEDIINAYSG QNMGDMDPHIFAVAEEAYKQMARD ERNQSIIVSGESGAGKTVSAKYAMRY FATVSGSASEANVEEKVLASNPIME SIGNAKTTRNDNSSRFGKYIEIGFDK RYRIIGANMRTYLLEKSRVVFQAEEE RNYHIFYQLCASAKLPEFKMLRLGN ADSFHYTKQGGSPMIEGVDDAKEM AHTRQACTLLGISESYQMGIFRILAGI LHLGNVGFASRDSDSCTIPPKHEPLI IFCDLMGVDYEEMCHWLCHRKLAT ATETYIKPISKLQATNARDALAKHIYA KLFNWIVGHVNQALHSAVKQHSFIG VLDIYGFETFEINSFEQFCINYANEK LQQQFNMHVFKLEQEEYMKEQIPW TLIDFYDNQPCINLIESKLGILDLLDE ECKMPKGTDDTWAQKLYNTHLNKC ALFEKPRMSNKAFIIKHFADKVEYQ CEGFLEKNKDTVFEEQIKVLKSSKFK MLPELFQDDEKAISPTSATSSGRTPL TRVPVKPTKGRPGQTAKEHKKTVGL QFRNSLHLLMETLNATTPHYVRCIK PNDFKFPFTFDEKRAVQQLRACGVL ETIRISAAGFPSRWTYQEFFSRYRVL MKQKDVLGDRKQTCQNVLEKLILDK DKYQFGKTKIFFRAGQVAYLEKLRAD KLRAACIRIQKTIRGWLLRKRYLCMQ RAAITVQRYVRGYQARCYAKFLRRTK AATTIQKYWRMYVVRRKYKIRRAATI VLQSYLRGYLARNRYRKILREHKAVII QKRVRGWLARTHYKRTMKAIIYLQC CFRRMMAKRELKKLKIEARSVERYK KLHIGMENKIMQLQRKVDEQNKDY KCLMEKLTNLEGVYNSETEKLRNDV ERLQLSEEEAKVATGRVLSLQEEIAK LRKDLEQTRSEKKSIEERADKYKQET EQLVSNLKEENTLLKQEKETLNHL MVEQAKEMTETMERKLVEETKQLE LDLNDERLRYQNLLNEFSRLEERYD DLKEEMTLMLNVPKPGHKRTDSTH SSNESEYTFSSEFAETEDIAPRTEEP TEKKVPLDMSLFLKLQKRVTELGQE KQLMQDELDRKEEQVLRSKAKGGE RPQIRGAELGYESLKRQELESENKKL KNELNELRKALSEKSAPEVNAPGAP AYRVLMEQLTAVSEELDVRKEEVLIL RSQLVSQKEAIQPKDDKNTMTDSTI LLEDVQKMKDKGEIAQAYIGLKETN RLLESQLQSQKRSHENEAEALRGEI QSLKEENNRQQQLLAQNLQLPPEA RIEASLQHEITRLTNENLDLMEQLE KQDKTVRKLKKQLKVFAKKIGELEV GQMENISPGQIIDEPIRPVNIPRKGK DFQGMLEYKREDEQKLVKNLILELK PRGVAVNLISGLPAYILFMCVRHADY LDDDQKVRSLLTSTINSIKKVLKKRG DDFETVSFWLSNTCRFLHCLKQYSG EEGFMKHNTSRQNEHCLTNFDLAE YRQVLSDLAIQIYQQLVRVLENILQP MIVSGMLEHETIQGVSGVKPTGLRK RTSSIADEGTYTLDSILRQLNSFHSV MCQHGMDPELIKQVVKQMFYIVGAI TLNNLLLRKDMCSWSKGMQIRYNV SQLEEWLRDKNLMNSGAKETLEPLI QAAQLLQVKKKTDDDAEAICSMCNA LTTAQIVKVLNLYTPVNEFEERVSVS FIRTIQVRLRDRKDSPQLLMDAKHIF PVTFPFNPSSLALETIQIPASLGLGFI ARV	None	None	None	None	None	None	None	None	None