

UniprotKB ID	Entry name	organism	full name	oglcnaScore	oglcna sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane
Q99104	MYO5A_MOUSE	Mus musculus	Unconventional myosin-Va	27.478975	NaN	S600;T1032;S1450;S1650;T1758	29187734;33300544	MAASELYTKFARVWIPDPPEEVKWSA ELLKDYKPGDKVLLHLEEGKDLLEY RLDPKTGELPHLRNPDILVGENDLT ALSYLHEPAVLHNLRVRFIDSKLIYT YCGIVLVAINPYEQLPYIGEDHINAYS GQNMGMMDPHIFAVAEAEAYKQMAR DERNQSIIVSGESGAGKTVSAKYAM RYFATVSGSASEANVEEKVLASNPI MESIGNAKTTRNDNSSRFKYIEIGF DKRYRIIGANMRTYLLKSRVVFQAE EERNYHIFYQLCASAKLPEFKMLRL GNADSFHYTKQGGSPMIEGVDADK EMAHTROACTLLGISESYQMGIIFRIL AGILHLGNVGFASRDSDSCTIPPKHE PLTIFCDLMGVDEEMCHWLCHRK LATATETYIKPISKLOATNARDALAK HIYAKLFNWIVDHNQALHSVAVKQH SFIGVLDIYGFETFEINSFEQFCINYA NEKLQQQFNMHVFKLEQEEYMKE QIPWTLIDFYDNQPCINLIESKLGILD LLDEECKMPKGTDDTWAQKLYNTH LNKCALFEKPRMSNKAFIKHFADK VEYQCEGFLEKNKDTVFEEQIKVLK SSKFKMLPELFDDEKAIPTSATSS GRTPLTRVPVKPTKGRPGQTAKEHK KTVGHQFRNSLHLLMETLNATTPHY VRCIKPNDFKFPFTFDEKRAVQQLR ACGVLETIRISAAGFSPRWTYQEFFS RYRVLMKQKQDLVLDGDRKQTKNVLE KLILDKDYQFGKTKIFFRAGQVAYL EKLADKLRACAIRIQTIRGWLLRK RYLCMQRAAITVQRYVRYGQARCYA KFLRRTKAATTIQYWRMYVRRRY KIRRAATIVIQSYLRGYLTRNRYRKIL REYKAVIQRVWGLRTHYKRTM KAIVYLQCCFRMMAKRELKLLKIE ARSVRYKKLHIGMENKIMQLQRKV DEQNKDYKCLEMEKLTNLEGVYNS TEKLRNDVERLQLESEEAKVATGRV LSLQEEIAKLRKDLQTRSEKKSIEE RADKYKQETDQVSNLKEENTLLKQ EKETLNHRIVEQAKEMTETMERKLV EETKQLELDLNDERLRYQNLNNEFS RLEERYDDLKEEMTLMLNVPKPGH KRTDSTHSSNESEYTFSSFAETEDI APRTEEPIEKVPLDMSLFLKQKRV TELEQEKQLMQDELDRKEEQVFRS KAKEEERPOIRGALEYESLKRQELE SENKKNELNELRKALSEKSAPEV TAPGAPAYRVLMELQTSVSEELDVR KEEVLLRSQVLSQKEAIQPKDDKNT MTDSTILLEQVQKMKDKEIAQAYIG LKETNRLLESQSQKRSHEAEAE LRGEIQSLKEENNRQQQLLAQNQL PPEARIEASLQHEITRLTNENLYFEE LYADDPKQYQSYRISLYKRMIDLME QLEKQDKTVRKLKQKVFACKIGE LEVQGMENISPGQIHDEPIRPNIPRK EKDFQGMLEYKREDEQKLVKNLILE LKPRGVAVNLIPLPAYILFMCVRHA DYLNDQKVRSLTSTINSIKKVLK RGDDFETVSWFLSNTCRFLHCLKQY SGEEGFMKHNTSRQNEHCLTNFDL AEYRQVLSDLAIQYQQLVVRLENIL QPMIVSGMLEHETIQGVSGVKPTGL RKRTSSIADEGTYTLDSILRQLNSFH SVMCQHGMPELIKQVVKOMFYIV GAILNLLLRKDMCSWSKGMQIRY NVSQLEEWLRDKNLMNSGAKETLE PLIQAAQLLQVKKKTDDEAEICSM CNALTQAQIVKVLNLYTPVNEFEERV SVSFIRTIQMRRLDRKDSPLLMDA KHIFPVTFPNPSSLALETIQIPASLG LGFARV	True	True	4.732	2.29	2.62	4.394	5.0	2.373