

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellu region
Q9Z1N3	MYO9A_RAT	Rattus norvegicus	Unconventional myosin-IXa	23.439218	NaN	S755;S1243;T1245;S1259;S1300;S1318;S2016;S2380;S2542	38843836	MNVSDDGRRRRFEDNEHTLRIYPGTI SEGTIYCCPIPARKNSTAAEVIDSLINR LHLDKTKCYVLAIEVKEFGGEEWILN PTDCPVQRMMLWPRMALENRLSGE DYRFLLRKKNLDGSIHYGSLQSWLR VTEERRRMMERGFLLPQPQQKDFDD LCSLPDLNEKTLENLNRNRFKHEKI YTYVGSILIAINPFKFLPIYNPKYVKM YDNHQLGKLEPHIYAVADVAYHAML QRKKNQCIVISGESGSGKTQSTNFLI HHLTALSQKGFASGVEQIILGAGPVL EAFGNAKTAHNNNSSRFGKFIQVNY QETGTVLGAYVEKYLLEKSRLVYQE HNERNYHVFFYLLAGASEEERLAFH LKQPEEYHFLNQITKKPLRQSWDDY CYDSEPDCTVEGEDLRHDFERLQL AMEMVGFPLKTRRRQIFSLLSAILHLG NISYKKTYYRDDSIDICNPEVLPVSE LLEVKEEMLFREALVTRKTVTVEKLI LPYKLAEAVTVRNSMAKSLYSALFD WIVFRINHALLNSKDKLEKDTKLSIG VLDIFGFEDYENNSFEQFCINFANE RLQHYFNQHIFKLEQEEYRTEGISW HNIDYIDNTCCINLISKKPTGLLHLL DEESNFPQATNQTLDDKFKHQHEE NSYIEFPVMEPAFIHKHYAGKVKYG VKDFREKNTDHMRPDIVALLRSSRN AFVSGMTGIDPVAVFRWAVLRAFFR AVVAFREAGKRHIQRKSGHDDTTPC TILKSMDSFSLQHPVHQRSLEILQR CKEEKYSITRKNRPTPLSDLQGMNT LNEKNQHDTFDIAWNVRTGIRQSRL PTNNTSLLDKDGIFANSASSKLLERA HGILTRNKNFRSKPVLPHLLEVNS LKHLLRLLQDRITKSLLLHLHKKKKP PSISAQFOVLSKLMETLDQAEPPYFV KCIRSNAEKLPFRSDALVLRQLRYT GMLETVRIRQSGYSSKYSFQDFVSH FHVLLPQHIIIPSKFNIQDFFRKININP DNYQVGKTMVFLKEHERQHLQDLL HQEVLRRILLQRWFRVLLSRQOFL HLRQASVIIQRFWRNYLNQKQVRNA AVEKDAFIMASAAASLLQASWRAHLE RQRYLELRAAAVIIQQRWRELCRRR HRAATCIQSRWRGYRQSKYKEQRN KIILLQSIYRGFRARQRYKALKEERLK ETKLEHGLAQIKTCGPLEIQGSDPSE WEDRSFANRVKAIEECKSVIESNRIS RESSMDFSKESPDKQOERGRSQSG TDLQGDVIVRQRPKSLEDLHQKKVG RAKRESRRMRELEQAIFSLLELLKVR LGGMSPSEERRWSTELMPEGLQSP QGTDPDESSQGSLELLTCDENQKSK PESLILDDGELKISSPSTFTNPKFDS QNNALSASSETSTFSGKGASSDSE HLKNGTAEKLVYSSQPITCKSQLR DSFVSSSLPTFFYIPHQEPLKTSQSL DTSIQRNKLPERETTLKTTLDINR EARKCQFSGQVTPLNPDSSCTVLK LEKLNIEKEKRQKLOQQNEKEMM EQIROQTIDILEKERKAFKTIQSRTE ASLLAPSFYQSRQKVERPSSLHIQNT PSKGEAGVLGSPSALATKDSPSIHL PKDRPVTLFFERKGSQPCSRVKT KTERMGTOHDAACRLSNHNHTERE HFKSTHYSHRSDPSREGSSRPPIF TPKDNVITPLVHSGNPQVHKODEPA WKSCLAGPGQREVARPAHKKKARM ARTRSDFLTRGTFADGEGDTEEDDY DDIIEPLSLDQASHSELGPVSSLGQ ASHSDSEMTSQRFSSVDEQARLHKA MSQGEITKLAGRQKSSDLDIRPORA KMRFWAKGKQGEKKTTRVKPAPQS EVSSLFAGSDVTPVHPFSDDELTOYH PTPPLSPELPGSCRKEFKENKEPSPK AKRKRGVKISSVALDSMHWQNSV QIIASANDLKSMDLFLKMKMNDLDN EDSKKDLVDVVFVKALKEFRQNF SSYSSALAMDDGKSIRYKDYALFEQ ILEKTMRFQORDWNEPVRVWVNT	False	False	2.864	2.531	0.668	False	False	0.956	0.693

FKVFLDEYMNEFKTLDSTAPKVLKT
ERKRRRKETDLVEEHNGHMFKAT
QYSIPTYCEYCSSLIWIMDRASVCKL
CKYACHKKCCLKTTAKCSKKYDPEL
SSRQFGVELSRLTSEDRAVPLVVEKL
INYIEMHGlyTEGIYRKSgstNKIKE
LRQGLDTDAESVNLDDYNIHVIASVF
KQWLRDLPNPLMTPELYEEFLRAM
GLQERKETIRGVYSVIDQLSRTHLST
LERLIFHLVRIALQEDTNRMSANALA
IVFAPCILRCPDTTDPLOQSVQDISKTT
TCVELIVVEQMNKYKARLKDISSEF
AENKAKTRLSLIRRSMPVLIARVFM
SITRSSVSGKGRHRGSHPNPSSPVI
VRLPSMSDVPEETLTSETAMDDTDT
DQQQAAMQQEEKVLTEQIENLQKE
KEELTFEMLVLEPRASDDEALESEA
SIGTADSSENLNMPEERSLALSSL
KAAGKSEPSKFRKQLRKQPDSDLDS
VSSSVSSCLSNITSSHGTRKRFQIYS
KSPFYRAASACEAQGMGEPGLQAKS
LEDRPQFISRGTFNPEKKGKQKKNV
KNSPQKTKETPEGTVSSGRKKTVDV
DCSSTQQLPLFGNNEFMV