

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	extrac region
Q8C170	MYO9A_MOUSE	Mus musculus	Unconventional myosin-IXa	29.185005	NaN	S755;S1243;T1245;S1259;S1300;S1318;S1950;S2293;S2296;S2458	22645316	MNVSDGGRRRFEDNEHTLRIYPGTI SEGTYICPIPARKNSTAAEVIDSLINR LHLDKTKCYVLAEVKEFGGEEWILN PTDCPVQRMMLWPRMALENRLSGE DYRFLLRKKNLDGSIHYGLSQSWLR VTEERRRMMERGFLLPQQQKDFDD LCSLPDLNEKTLLENLRNRFKHEKI YTYVGSILIAINPFKFLPIYNPKYVKM YDNHQLGKLEPHIYAVADVAYHAML QRKKNQCIVISGESGSGKTQSTNFLI HHLTALSQKGFASGVEQIILGAGPVL EAFGNAKTAHNNNSSRFQKFIQVNY QETGTVLGAYVEKYLLKESRLVYQE HNERNYHVFFYLLAGASEEERLAFH LKQPEEYHFLNQITKKPLRQSWDDY CYDSEPCFTVEGEDLRHDFERLQL AMEMVGFPLKTRRQIFSLLSAILHLG NISYKKKTYRDDSIDICNPEVLPVSE LLEVKEEMLFALVTRKTVTVGEKLI LPYKLAEAVTVRNSMAKSLYALFD WIVFRINHALLNSKDLEQDTKTLSIG VLDIFGFEDYENNSFEQFCINFANE RLQHYFNQHFLEQEEYRTEGISW HNIDYDNTCCINLISKKPTGLLHLL DEESNFPQATNQTLDDKFKHQHEE NSYIEFPAVMEPAFIKHAYGKVKYG VKDFREKNTDHMRPDIVALLRSSRN AFVSGMTGIDPVAVFRWAVLRAFFR AVVAFREAGKRHIQRKSGHDDTTPC AILKSMDSFSFLQHPVHQRSLEILQR CKEEKYSITRKNPRTPLSDLOGMNT LNEKNQHDTFDIAWNVRTGIRQSRL PASNTSLLDKDGIFAHSAKLLERA HGILTRNKNFRSKPVLPHKHLLEVNS LKHLTRLTLQDRITKSLHLHKKKKP PSISAQFQASLSKLMETLGQAEPYFV KCIRSNAEKPLRFSDALVLRQLRYT GMLETVIRIQSGYSKYSFQDFVSH FHVLLPQHIIIPSKFNIQDFFRKININS DNYQVGMTMVFLEHEROHLQDLL HQEVLRRIVLLQRWFRVLLSRQOFL HLRQASIIQRFWRNYLNQKQVRNA AVEKDAFIMASASLLQASWRAHLE RQRYLELRAAAVIIQQRWRELYRCR HKAATCIQSRWRGVRQRKQYKEQR NKIILLQSIYRGFRARQRCNALKEEK LREAKLEHGLVHVKACGPLEIQGSD PSEWEDRSFDNRVKAIEECKYVIES NRISRESSMDFSKESPDKQGERGRR QSGTDLQEDVIVRQRPKSLEDLHQK KVGRAKRESRRMRELEQAIFSLLELL KVRSLLGGMSPSEERRWSTELMPEG LQSPHGTDPSESSQGSLELLTCDEN QKSKPESLILDEGELKISSPNTFTNP KSQDNALSASSETSTLAGKASSD SEHLKNGTAKEKLVCSSEPITCKPQL RDSFVSSSLPTFFYIPHQEALKTSSH LDTSIQRNKLPEREAILKTTLTQDIN REARKCQFSGDQMTPLNTDSSCTVL KKLEKLNIEKEKQKQLOQQNEKE MMEQIRQOTDILEKERKAFKTEIQS RTEASVLAPSFYQPRQKVERPCSLYI QNTPSKGEAGVLGSPSAVTKRDAAL ATKDSPSIHLPPKDRPVTLFFEKKGS PCQSRTVKELPKTERTGTQHDAAAYK LSNNRSTERDHFKSTHFYSHRSSDDP SREGSSRAIFFTPKDNITPLVHSGNP QAHKQDESAWKPKLAGPGQOQETSQ RFSSVDEQAKLHKAMSQGEITKLAV RQKASDLDIRPQAKMRFWAKGKQ GEKKTTRVKPASQSEISSFFPGPDVT PAHPFDELTYHPTPLSPPELPGSC RKEFKENKESPKAKRKRGVKISSVA LDSMHWQNDVQIIASADLKSMD EFLKMKMNDLDNEDSKKDTLVDVV FKKALKEFRQNFSSYSALAMDDG KSIRYKDYALFEQILEKTMRLQQRD WNEPVRVWVNTFKVFLDEYMNFE KTLNSTAPKVLKTERKKRRKEDLV EEHNGHFKATQYSIPTCYEYCSLI	None	None	None	None	None	None	None		

