

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extrac region
B2RTY4	MYO9A_HUMAN	Homo sapiens	Unconventional myosin-IXa	27.086674	NaN	S755;S1242;S1258;S1299;S1317;S1364;S1948;S2294;S2464	28657654	MNINDGGRRRFEDNEHTLRIYPGAI SEGTIYCPIPARKNSTAAEVIESLINK LHLDKTKCYVLAEVKEFGGEEWILN PTDCPVQRMMLWPRMALENRLSGE DYRFLLRKLNLDGSIHYGSLQSWLR VTEERRRMMERGFPLPQQKDFDD LCSLPDLNEKTLLENLRNRFKHEKI YTYVGSILVINPFFKFLPIYNPKYVKM YDNHQLGKLEPHIYAVADVAYHAML QRKKNQCVISGESGSGKTQSTNFLI HHLTALSQKGFASGVEQIILGAGPVL EAFGNAKTAHNNNSSRFKGFQVNY QETGTVLGAYVEKYLLEKSRLVYQE HNERNYHVFYLLAGASEDESAFH LKQPEEYHYLNQITKKPLRQSWDDY CYDSEPCFTVEGEDLRHDFERLQL AMEMVGFPLPKTRRQIFSLLSAILHLG NICYKKTYYRDDSIDICNPEVLPVSE LLEVKEEMLFEALVTRKTVTVGKELI LPYKLAEAVTVRNSMAKSLYSALFD WIVFRINHALLNSKDLEHNTKLSIG VLDIFGFEDYENNSFEQFCINFANE RLQHYFNQHIFKLEQEEYRTEGISW HNIDYDNTCCINLISKKPTGLLHLL DEESNFPQATNQTLDDKFKHQHED NSYIEFPAMVEPAFIKHAYAGVKYK VKDFREKNTDHMRPDIALLRSSKN AFISGMIGIDPVAVFRWAILRAFFRA MVAFREAGKRNIHRKTHGDDTAPC AILKSMDSFSLQHPVHQRSLEILQR CKEEKYSITRKNPRTPLSDLQGMNA LNEKNQHDTFDIAWNGRTGIROSRL SSGTSLLDKDGIFANSTSSKLLERAH GILTRKNKFKSKPALPKHLLVNSLK HLTRLTLQDRITKSLHLHLKPKPPS ISAQFQASLSKLMETLGAEPYFVKC IRSNAEKPLRFSDVLRQLRYTGM LETVRIQSGYSSKYSFQDFVSHFHV LLPRNIIPSKFNQDFFRKINLNPDN YQVGKTMVFLKEQERHQLDILLHQ EVLRRILLQRWFRVLLCRQHFLHLR QASVIIQRFWRNYLNQKQVRDAVQ KDAFVMASAAALLQASWRAHLERQ RYLELRAAAIVIQKWRDYRRRHM AAICIQARWKAYRESKRYEQQRKKII LLQSTCRGFRARQRFKALKEQRLRE TKPEVGLVNIKGYGSLEIQGSDPSG WEDCSFDNRKAIEECKSVIESNRIS RESSVDCLKESPKNQQERAQSQSGV DLQEDVLRERPRSEDLHQKKVGR AKRESRRMRELEQAIFSELELLKVRSL GGISPEDRRWSTELVPEGLQSPRG TPDSESSQGSLELLSYEESQSKSLES VISDEGLQFPSPKISSPKFDSRDN ALSASNETSSAEHLKDGTMKEMVV CSSESITCKPQLKDSFISNSLPTFFYI PQQDPLKTNSQLDTSIQRNKLLENE DTAGEALTLIDINRETRRYHCSGKDQI VPSLNTESNPVKKLEKLNTEKEE RQKLOQQONEKEMMEQIRQOTDIL EKERKAFKTIKPRIGECLVAPSSYQ SKQRVERPSSLLSNTSNKGELNVL GSLSLKDAALAQKDSHSAHLPPKDR PVTVFFERKGSQSSVTKELSKTDR MGTQLNVACKLSNNRISKREHFRPT QSYSHNSDDLREGNARPIFFTPKD NMSIPLVSKALNSKNPQLHKEDEP AWKPVKLAGPGQRETSQRFSSVDEQ AKLHKTMSQGEITKLAVRQKASDSD IRPQRAKMRFWAGKQGEKKTTRV KPTTQSEVSPLFAGTDVIPAHQFPDE LAAYHPTPPLSPELPGSCRKEFKENK EPSPKAKRRKSVKISNVALDSMHWQ NDSVQIIASVSDLKSMDEFLLKVN DLDNEDSKKDTLVDVVFKKALKEFR QNIFSFYSALAMDDGKSIRYKDYLA LFEQILEKTMRLERQDLSGESPVRV WVNTFKVFLDEYMNFEKTSDCAT KVPKTERKKRRKKTDLVEEHNGHI FKATQYSIPTCEYCSSLIWIMDRAS	True	False	4.648	1.215	1.01	0.693	0.635	2.451	1.105

VCKLCKYACHKKCLKTTAKCSKKY
DPELSSRQFGVELSRLTSEDRTVPLV
VEKLINYIEMHGLYTEGIYRKSGSTN
KIKELRQGLDTDAESVNLDYNIHVI
ASVFKQWLRDLPNPLMTFELYEEFL
RAMGLQERKETIRGVYVIDQLSRT
HLNTLERLIFHLVRIALQEDTNRMS
ANALAIVFAPCILRCPDITDPLQSVQ
DISKTTTCVELIVVEQMKNYKARLKD
ISSLEFAENKAKTRLSLIRRSMGKGR
IRRGNYPGSSPVVRLPSVSDVSEE
TLTSEAAMETDITEQQQAAMQEEER
VLTEQIENLQKEKEELTFEMLVLEPR
ASDDETLESEASIGTADSSENLNME
SEYAISEKSERLALSSLKTAGKSEPS
SKLRKQLKKQDSDLVVDSSVSLC
LSNTASSHGTRKLFQIYKSPFYRAA
SGNEALGMEGPLGQTKFLEDKQFI
SRCTFNPEKQKQKLVKNSPQKTK
ETPEGTVMSGRRKTVDPDCTSNQQL
ALFGNNEFMV