

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membra
Q5VU43	MYOME_HUMAN	Homo sapiens	Myomegalin	18.633598	S1777;S1778	T704;S252;S252	30379171;38665916;28411811;23301498;34105348;29351928	MSNGYRTLSQHLNDLKKENFSLKLRIFLEERMQQKYAESREIDYKRNIE LKVEVESLKRQLDQKKQHLDKTWA DVENLNSQNEAELRRQFEERQOET EHVYELLENKIQLLQEEESRLAKNEA ARMAALVEAEKECNLESEKLGKVT KNWEDVPGDQVKPDQYTEALAQRD KRIEELNQSAAQERLVEQLSREKQ QLLHLLLEPTSMVEVQPMTEELLKQO KLNSHETTTTQQSVSDSHLAEQLKEI QQTTEATNKILQEKLNEMSYELKCAQ ESSQKQDGTIQNLKETLKSRETERE ELYQVIEGONDTMAKLREMLHQSQ LGQLHSSEGTSPAQQVALLDLQSA LFCSQLEIQKLRVVRQKERQLADA KQCVQFVEAAHSESEQKEASWKH NQELRKALQQLQEEELQNKSQLRA WEAKEYNEIRTQEONIQLNHSLSH KEQLLQEFRELLQYRDNSDKTLEAN EMLLEKLRQRHDKAVALERAIDEK FSALEEKEKELRQLRLAVRERDHD LERLRDVLSSNEATMQSMESLRAK GLEVEQLSTTCQNQLWLKEEMETK FSRWQKEQESIIQQLQTLSDHRNKE VEDLSATLLCKLPGQSEIAEELCQR LQQRKERMQLDQLSDRNKQVLEHEM EIQGLLQSVSTREQESQAAAEKLVQ ALMERNSELQALROYLGGRDSLMS QAPISNQAEVTPTRGLGKQTDQGS MQIPSRDDSTSLTAKEDVSIPRSTLG DLDTVAGLEKELSNAAKELELMAKK ERESQMELSALQSMMAVQEEELQV QAADMESLTRNIQIKEDLIKDLQMQ LVDPEIPAMERLTQEVLLREKVAS VESQGEISGNRRQQLLLMLEGLVD ERSRLNEALQAERQLYSSLVKFHAH PESSERDRTLQVELEGAQVLRSRLE EVLGRSLERLNRLETLAAGGAAAGD DTEDTSTEFSDSIEEEAAHSHQQL VKVALEKSLATVETQNPFSFPPSPM GGDSNRCLQEEMHLRAEFHQHLE EKRAEEELKELKAQIEEAGFSSVSH IRNTMLSCLENAELKEQMGEMS DGWEIEEDKEKGEVMVETVTK EGL SESSLQAEFRKLGKLNNAHNIINLL KEQLVLSKKEGNSKLTPELLVHLTST IERINTELVGSPGKHQHQEEGNVTV RPFPRPQSLDLGATFTVDAHQLDNQ SQPRDPGQSAFSLPGSTOHLRSOL SQCKQRYQDLQEKLLSEATVFAQA NELEKYRVMLTGESLVKQDSKQIQV DLQDLGYETCGRSENAEREETTSP ECEEHNSLKEMVLMGLCSEQGRR GSTLASSSERKPLENOLGKQEEFRV YGKSENILVLRDKDKDLKALQANAN KVIQNLKSRVRSLSVTSDYSSSLERP RKLRAVGTLEGSSPHSVPEDEGWL SDGTGAFYSPGLQAKKDLES LIQRVS QLEAQLPKNGLEEKLAEEELRSASWP GKYSLSIQDQARELSYLROKIREGRG ICYLITRHKADTVKSFEDLLRSNDID YYLQGSFREQLAQSOLTERLTSKLS TKDHKSEKDQAGLEPLALRLSRELQ EKEKVIEWLQAKLDARSLTPSSSHAL SDSHRSPSSTSFSDLEACSDMDI VSEYTHYEEKKASPSHSDSIHSSH SAVLSSKPSSTSASOGAKAENSNSPI SLPTPQNTPKEANQAHSGFFHFSIP KLASLPQAPLPSAPSSFLPFSPTGPLL LGCCETPVVSLAEAQELQMLQKQL GESASTVPPASTATLLSNDLEADSS YLNSAQPHSPPRGTIELGRILEPGYL GSSGKWDVMRPOKGSVSDLSSGS SVYQLNSKPTGADLLEHLGEIRNL RQRLEESICINDRLREQLHRLTSTA RGRGSTSNFYSQGLSIPQLCNENR VLREDNRRLQAQLSHVSRHSQETE SLREALLSSRSHLQELEKELEHQV ERQQLLEDLREKQEVVLFHFRERLS LQENDSRLQHKLVLLQQQCEKQO	None	None	None	None	None	None	None	

LFESLQSELQIYEALYGNSKKGLKAY
SLDACHQIPLSSDLSHLVAEVRALRG
QLEQSIQGNCLRLQLQQLESAG
KASLSPSSINQNFPASTDPGNKQLL
QDSAVSPPVRDVG MN SPALVFPSSA
SSTPGSETPHINRANGLGLDTS PVMK
TPPKLEGDATDGSFANKHGRHVIGH
IDDYSALRQQAEGKLLVKKIVSLVRS
ACSFPGLEAQGTEVLGSKGIHELRS
TSALHHALEESALLTMFWRAALPS
THIPVLPKVGESTERELLELRTKVS
KQERLLQSTTEHLKNANQQKESME
QFIVSQLTRTHDVLK KARTNLEVKSL
RALPCTPAL