

UniprotKB ID	Entry name	organism	full name	oglcnaсscore	oglcnaс sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
P54296	MYOM2_HUMAN	Homo sapiens	Myomesin-2	27.26403	S39;T40	NaN	31492838	MSLVTVPFYQKRHRHFQSYRNQIQT RYLLDEYASKKRASTQASSQKSLSQRS SSSQRASSQTSLLGGTICRVCARKVST QEDEEQENRNSRYQSLVAAYGEAKRQ RFLSELAHLEEDVHLARSQARDKLD KYAIQQMMEDEKLAWERHTFEERISR APEILVRLRSHTVWERMSVKLCFTV QGFPTPVQWYKDGSILCQAEPGK YRIESNYGVHTEINRADFDDTATYS AVATNAHGQVSTNAAVVRRFRGD EEPFRS VGLPIGLPLSSMIPYTHFDV QFLEKFGVTFRREGETVTLKCTMLV TPDLKRVQOPRAEWYRVDVLLKESK WTKMF GGEGQASLSFSHLHKDDEG LYTLRIVSRGGVSDHS AFLFVRDADP LVTGAPGAPMDLQCHDANRDYVIVT WKPPNTTTESPVGMGYFVDRCEVGT NNWVQCNDAPVKICKYKPVTLFEGGR SYIFRVR A RVNSAGISRPSRVSDAVAA LDPLDLRRLQAVHLEGKEIAIYQDD LEGDAQVPGPPTGVHASEISRNYYVVL SWEPPTRGKDPLMYFIEKS VVGSG SWQRVNAQTA VRSPRYAVF DLM E G KS YF RVR VLSA NRG LSE PSE IT S PI Q AQDVTVVPSA PGRV LASRN TKT SVV VQWDRPKHEEDLLGYYVDCCVAGT NLWEPCN H KPIGYNR FV VHGLTGE QYIFRKAVNA VGMSEN S QESDVIK VQAALT VPSH PYG IT LLNC DGH SMT LGW KVPK FSGG SPIL GYY LD KREV H HKNWHEVNSSPSKPTILTVDGLTEG SLYEFKIAAVNLAGIGE P S D PSE HF K CEAWTMPEPGPAYDLT C E V RDT S L VMLW KAPV YSGSSP VSGYF VDFREE DAGEWITVNQTTTAS RYL KVSDL LQ Q GKTYF RVR A V N A N G V G K P S D T S E P VLVEARPGTKEISAGV D E Q G N I Y L G F DCQEMTDASQFTWCKSYEEIS DDER FKIETVGDHS KLYLKNPD KEDLG T Y S VS VSDT DGVSSSFVLDPEELER L R M A LSNEIKNPTIPLKSELAYEIFDKGRVR FWLQAEHLSPDAS YRFIINDREVSDS EIHIRIKCDKATG I M V M D R F S I E N E GTYTVQIH DGKA KSQSSLV LIGDAFK TVL EAE F Q R K E F L R K Q G P H F A E Y L HWDV TEE C V RL V C K V A N T K K E T V F KWLKD DVLY E T E T L P N L E R G I C I E L L I PKLSK D H G E Y K A T L K D D R Q D V S I L E I A G K V Y D D M I L A M S R V C K S A S P LKVLC T P E G I R L Q C F M K Y F T D E M K V NWCHK DAKIS S E H M R I G G S E E M A WLOICE PTE KDKG K YT F E I F D G K D N HORS L D L S G Q A F D E A F Q Q F K A A AFAEKNRGRLIGGLPDVVTIMEGKTL NLTCTVFGNPDPPEVIWFKNQDIQL SEHFSVKVEQAKYVSMTIKGVTSED SGKYSINIKNKYGG EKIDVTVSVYKH GEKIPDMAPPQAKPKLIPASASAAG Q	True	False	3.816	3.513	4.725	2.647	2.57	2.788	2.554