

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
A2AQP0	MYH7B_MOUSE	Mus musculus	Myosin-7B	24.036206	T1244	NaN	37507081;34418053	MMDMSELGESACYLRQGYQEMMK VHTVPWDGKKRVVWPDEQDAYVEA EVKTEATGGKVTVETKDQKVLTVRE TEMQPMNPPRFDLLEDMMAMMTHL NEAAVLHNLRQRYARWMIYTSYGLF CVTINPYKWLVPYTAAVVAAYKGRRR SEAPPHIYAVADNAYNDMLRNREN QSMILITGESGAGKTVNTKRVIQYFAI VAALGDGPGKKAQFLATKTGGTLED QHIANPAMEAFGNAKTLRNDNSSR FGKFIRIHFGPTGKLASADIDSYLLEK SRVIFQLPGERGYHVYQILSGKKPE LQDMLLSMNPYDYHFCSSQGVTTV DNMDDGEELIATDHAMDILGFSVDE KCACYKIVGALLHFGNMKFKQKQRE EQAEADGTESADKAAYLMGVSSGDL LKGLLHPRVRVGNVEYVTKGQSVQV VFAVGALAKATYDRLFRWLVSRIHQ TLDTKLPRQFFIGVLDIAGFEIFEFN FEQLCINFTEKLLQFFNQHMVFVLE QEEYKREGIDWVFDLQPCIDL IEKPLGILSILEEEMFPAKASDASRA KLYDNHSGKSPNFQPRPKRKY QAHFEVVHYAGVVPYSIVGWLEKNK DPLNETVVPFQKSNRLLATLYENY AGSCSTPPKSGVKEKRKKAASFOT VSQHKENLNKMLTNLRATQPHFV RCIVPNENKTPGVMDLFLVHLQRC NGVLEGIRICRQGFNRLLYADFRQ RYRILNPSAIPDDTFVDSRKATEKLL GSLDIDHTQYQFGHTKVFQKAGLLGI LEELRDQRLAKVLLQARSRGRML RLEYQRMGLGGRDALFTIQWNIRAFN AVKNWSWMKLFKMKPLLSAQAE EELAALRAELRGLRGALATAEAKRQ ELEETQVSVTQEKNDLALQLQAEQD NLADAEEERCHLLIKSKVQLEAKVKE LSERLEDEEEVNADLAARRRLEDE CTELKKDIDDELTLAKAEKEKQATE NKVKNLTEEMAALDEAVVRLTKEKK ALQEAHQALGDLQAEEDRVSAKAK AKIRLEEQVEDLECSLEQEKLRMD TERAKRKLKLDLKTQETVDTTOD KQLEEKKKKSELSQLNLRVEDE QLVGVQLQKKIKELQARAELEEL EAERAARARVEKQRAEAARELEELS ERLEEAGGASAGQREGCRKREAEALG RLRRELEEAVALRHEATVAALRRKQA DSAAELSEQVDSLQRIROKLEKEKSE LRMEVDDLGAQVETLARGKASAEKL CRTYEDQLSEAKIKVEELQRLADAS TQGRQLQTEGELGRLLLEEKESMIS QLSRGKTSAAQSLLELRRQLEEEESK AKGALAHAVQALRHDCDLLREQHE ESEAQAELOQLLSKANAQVAVQWRS KYEADAIQRTTELEAKKKLALRLQE AEEGVAAANAKSSLEKAKLRLQTE SEDVTLELERATSAAAALDKQRHL ERALEERRRQEEEMQRELEAAQRE ARGLGTFLFRLRHSHEALEALETL KRENKNLQEEISDLTDQVSLSGKSIQ ELEKAKKALEGEKSELQAALEEAEG ALELEETKTLRIQLELSQVKAQVDRK LAEKDEECTNLRNRHQRAVESLQAS LDAETRARNALRLKKMEGDLND LELQGHATROAMEAQAATRLLOAQ LKEEQAGRDEEQRLAAELREQGGAL ERRAALLAAELEELRAALEQGERSR RLAEQELLEATERLNLHSONTGLL NQKKLEVDLAQLSGEVEAAQERR EAEEKAKKAITDAMMAEELKKEQD TSAHLERMKKTLEQTVRELQARLEE AEQAALRGGKKQVQKLEAKVRELEA ELDAEQKKAHAEALKGVRRKHERRVKE LVYQTEEDRKNLARMQDLVDKLOS KVKSQKRFEEAEQASTNLAKYRK AQHELDAAERADMAETQANKLRA RSRDALGPKHKE	False	False	3.264	2.694	2.069	1.192	0.597	1.248	1.205

