

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence | intracellular | extracellular | cytosol | nucleus | mitochondrion | endoplasmic reticulum | golgi apparatus | plasma membrane | extracell region |
|--------------|------------|--------------------------|---|--------------|---------------|---|----------|--|---------------|---------------|---------|---------|---------------|-----------------------|-----------------|-----------------|------------------|
| P47068 | BBC1_YEAST | Saccharomyces cerevisiae | Myosin tail region-interacting protein MT11 | 24.475439 | NaN | S103;S158;S166;S565;S621;S631;S634;T636;S638;S647;T850;S889;T894;T895 | 33229814 | MSEPEVFPFKVVAQFPYKSDYEDDLN FEKDQEIIVTSVEDAEWYFGEYQDS NGDVIEGIFPKSFVAVQGSVEVGKEAE SSPNTGSTEQRTIQEVEEQKDLPEPI SPETKKEITLGGPVPVPAATVPVPAAT VPVPAATAVSAQVQHDSSSGNGERK VPMDSPKPKARLSMFDITEQVPL PKSTHLDLENIPVKKTIVADAPKYVYV PPGIPTNDTSLERKSKLKENEKKIV PEPINRAQVESGRIETENDQLKKDLP QMSLKERIALLEQQRLQAAREEEL LRKKAKLEQEHESAVNKNEPYTET EEAEENEKTEPKPEFTPETEHNEEP QMELLAHKEITKTSREADEGTNDIE KEQFLDEYTKENQKVEESQADEARG ENVAEESIEIGYGHEDREGDNDEEKE EEDSEENRRAALRERMAKLSGASRF GAPVGFNPFMGASGVGNKPSEEPK KKQHKEKEEEEEPEQLQELPRAIPVM PFVDPSSNPFFRKSNLSEKNQPTET KTLDPHATTEHEQKQEHGTHAYHN LAAVDNAHPEYSDHSDDEDTDDHE FEDANDGLRKHSMVEQAFQIGNNE SENVNSGEKIYPQEPPIHRTAEVSH DIENSSQNTTGNVLPVSSPQTRVAR NGSINSLTKSISGENRRKSINEYHDT VSTNSSALTETAQDISMAAPAAPVLS KVSHPEDKVPVPPVPSAPSAPPVPSA PSVPSAPPVPPAPPALSAPSVPVPPV PPVSSAPPALSAPSIPPVPTPPAPPA PPAPLALPKHNEVEEHVKSAPLPPV SEYHPMPNTAPPLPRAPPVPPATFE FDSEPTATHSHTAPSPPHQNVTS TPSMMSTQQRVPTSVLSGAEKESRT LPHVPSLTNRPVDSFHESDTPKV ASIRRSTTHDVGEISNVKIEFNAQE RWWINKSAPPAISNLKLNFLMEIDD HFISKRLHQKVVVRFYFLFENYSQ LRFSLTFNSTSPEKTVTTLQERFSP VETQSARILDEYAQRFNKAVVEKSH SLINSHIGAKNFVSVQIVSEFKDEVIQ IGARTFGATILSYKPEEGIEQLMKSL QKIKPGDILVIRKAKFEAHKKIGKNEI INVMDSAAPYSSVTDYDFTKNKF RVIENHEGKIQNSYKLSHMKSGKL KVFRIVARGYVGVW | None | None | None | None | None | None | None | | |