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SUPPLEMENTARY INFORMATION

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Structure and assembly of the mitochondrial membrane remodelling GTPase Mgm1

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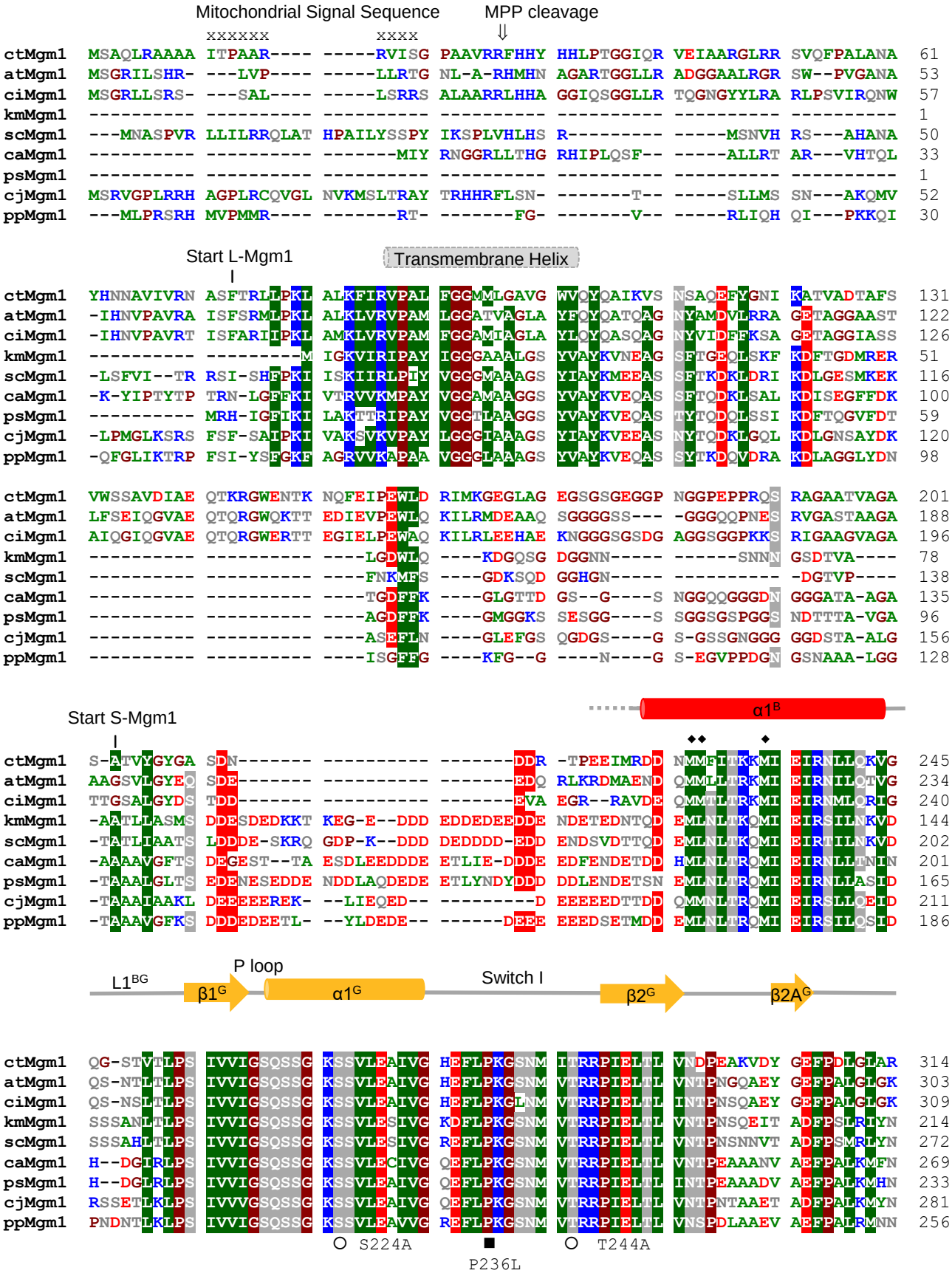
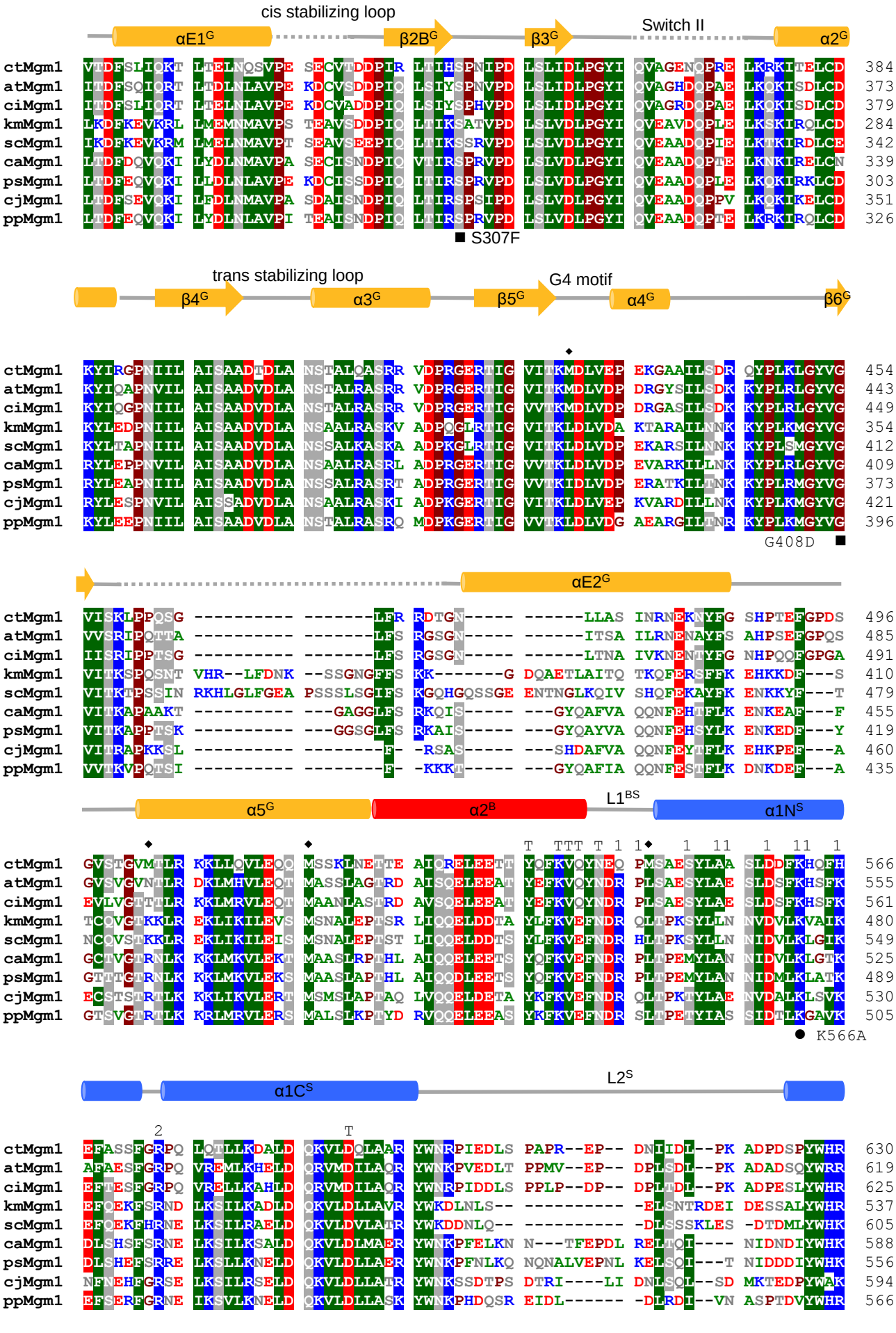
Supplementary Figure 1: Sequence alignment of Mgm1 proteins.

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β3G
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caMgm1 339
psMgm1 303
cjMgm1 351
ppMgm1 326
S307F
trans stabilizing loop
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G4 motif
α4G
β6G
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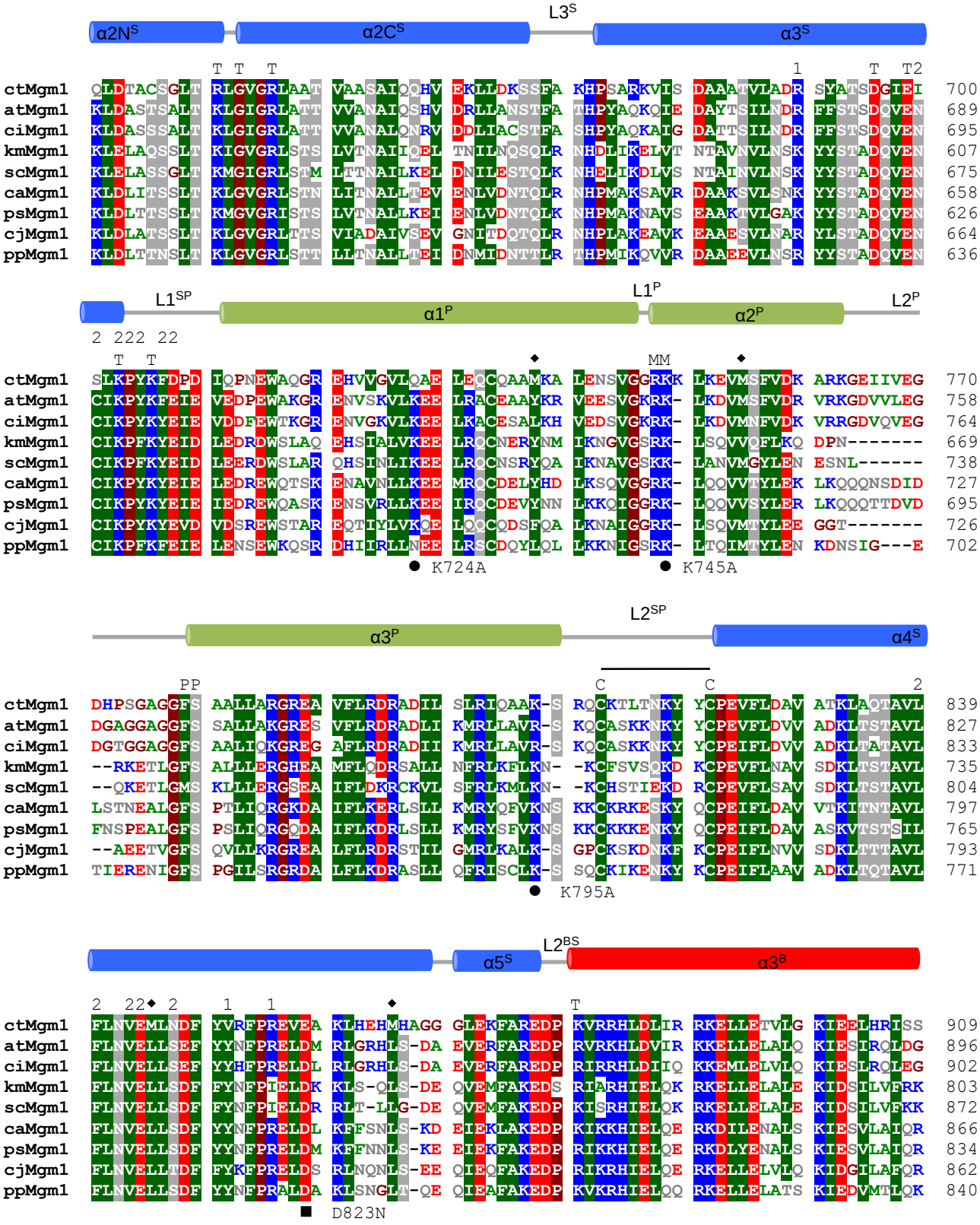
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α4^S
α5^S
L2^BS
α3^B
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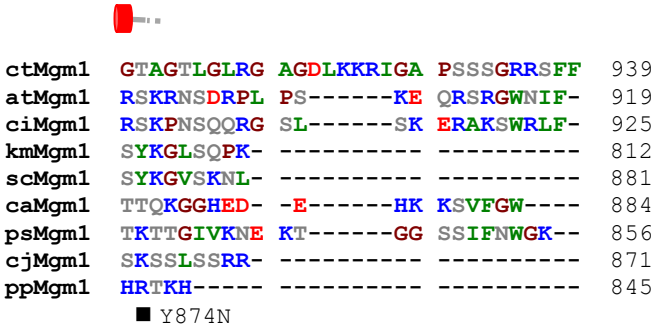

Supplementary Figure 1: Sequence alignment of Mgm1 proteins.
The following sequences were aligned: *Chaetomium thermophilum* (ctMgm1, Uniprot accession number G0SGC7), *Aspergillus terreus* (atMgm1, Q0D0Y9), *Coccidioides immitis* (ciMgm1, J3K1G3), *Kluyveromyces marxianus* (kmMgm1, W0T8X7), *Saccharomyces cerevisiae* (scMgm1, P32266), *Candida tropicalis* (caMgm1, C5M2J4), *Pichia stipites* (psMgm1, A3GGI6), *Pichia jadinii* (cjMgm1, A0A0H5C253), *Komagataella phaffii* / *Pichia pastoris* (ppMgm1, F2QTP9). Amino acids are colour-coded (negative charge D, E: red, positive charge R, K, H: blue, hydrophobic L, I, V, F, Y, W, M, C: gray, P, G: brown) and highlighted if conserved more than 70%. Interface residues with contributions of more than 20 Å^2 are labelled above the alignment (T for tetramer interface, 1,2 for stalk interfaces-1 and 2, respectively). ◆ indicate methionine residues with signal in the anomalous density. The position of temperature-sensitive (■) alleles and nucleotide-binding deficient mutants (○) in *Schizosaccharomyces pombe* Mgm1p according to Wong & Nunnari 2003 and Meussen & Nunnari, 2006 are indicated, as well as membrane-binding deficient mutants in *Saccharomyces cerevisiae* according to Meglei & McQuibban, 2009 (●). L-Mgm1, S-Mgm1 – long and short isoform of Mgm1, MPP – mitochondrial processing peptidase, C-indicates the disulphide bond.