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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.

	Mitochondrial Signal Sequence			MPP cleavage			
	xxxxxxx	ITPAAR	-----RVISG	PAAVRRFHYY	HHLPTGGIQR	VEIAARGLRR	SVQFPALANA
ctMgm1	MSAQLRAAAA	ITPAAR	-----RVISG	PAAVRRFHYY	HHLPTGGIQR	VEIAARGLRR	SVQFPALANA
atMgm1	MSGRILSHR	---LVP---	-----LLRTG	NL-A-RHMHN	AGARTGGLLR	ADGGAALRGR	SW--PVGANA
ciMgm1	MSGRLLSR	---SAL---	-----LSRRS	ALAARRLHHA	GGIQSGGLLR	TQNGYYLRA	RLPSVIRQNW
kmMgm1	-----	-----	-----	-----	-----	-----	-----
scMgm1	---MNASPV	LLILRRQLAT	HPAILYSSPY	IKSPLVHLHS	R-----	-----MSNVH	RS---AHANA
caMgm1	-----	-----	-----MIY	RNGRLLTHG	RHIPLQSF	-----ALLRT	AR---VHTQL
psMgm1	-----	-----	-----	-----	-----	-----	-----
cjMgm1	MSRVGPLRRH	AGPLRCQVGL	NVKMSLTRAY	TRHHRFLSN	-----T--	-----SLLMS	SN---AKQMV
ppMgm1	---MLPRSRH	MVPMMR---	-----RT-	-----FG-	-----V--	-----RLIQH	QI---PKKQI

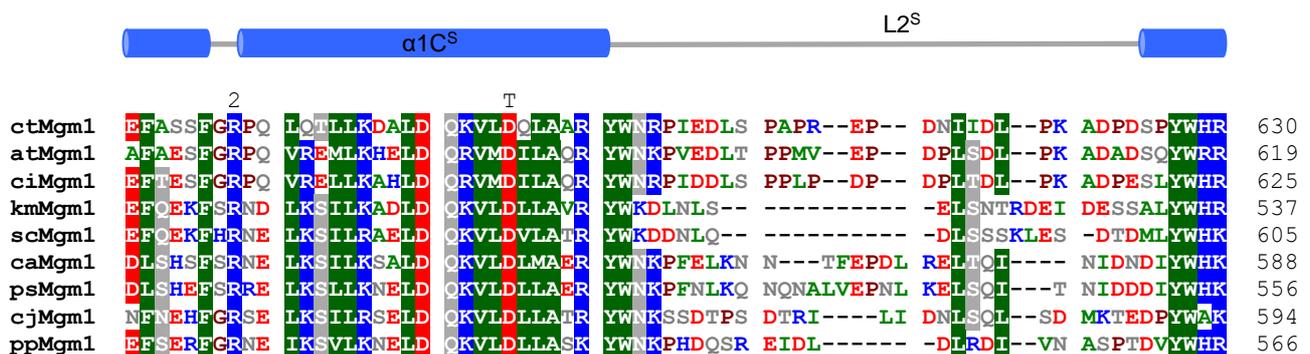
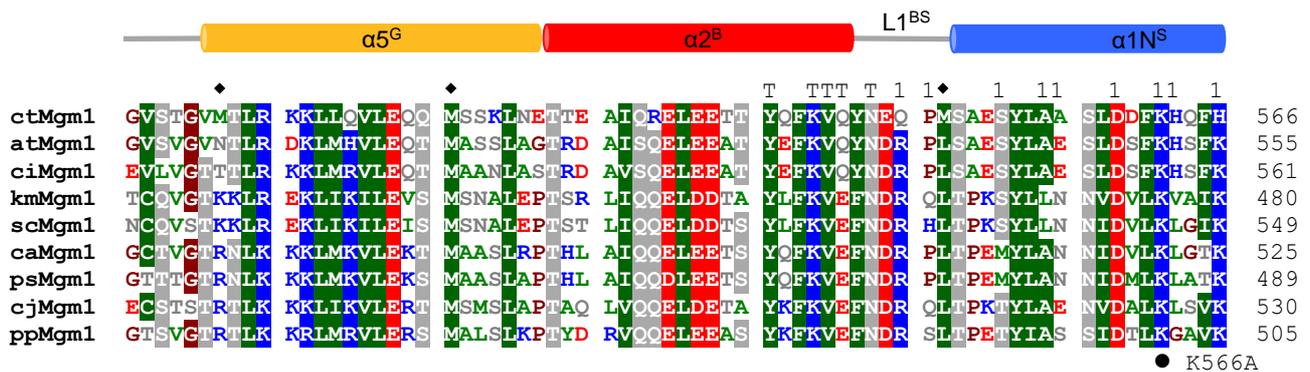
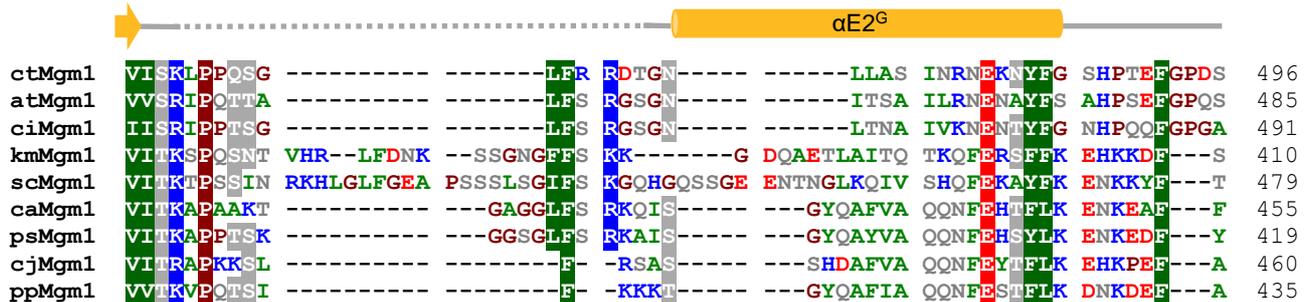
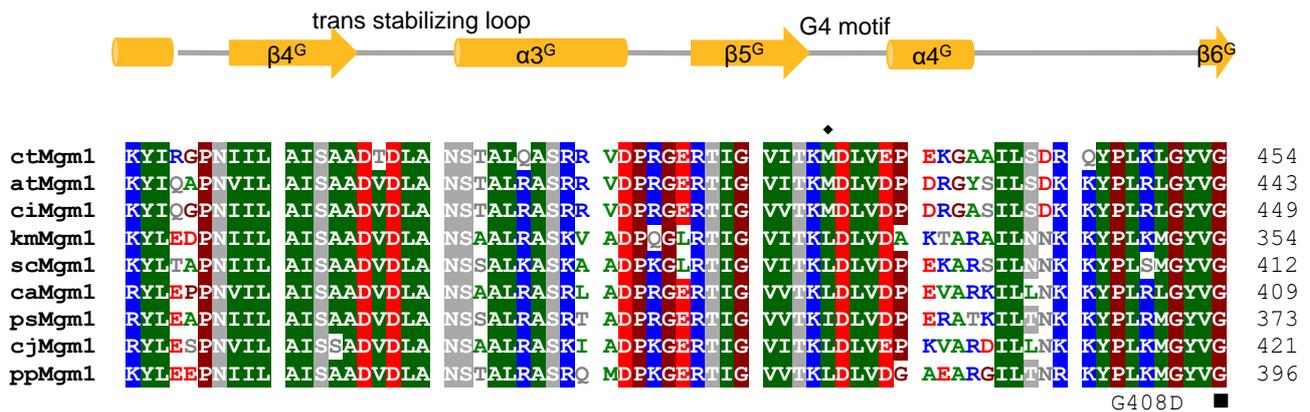
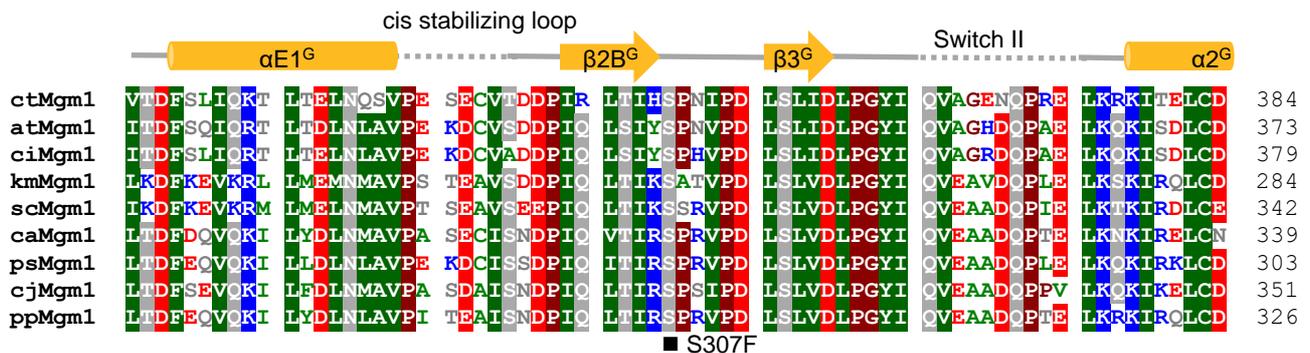
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ctMgm1	YHNAVIVRN	ASFTRLPKL	ALKFIRVPAL	FGMMLGAVG	WVQYQAIKVS	NSAQEFYGNL	KATVADTAFS	131
atMgm1	-IHNVPVRA	ISFSRMLPKL	ALKLVRVPAM	LGGATVAGLA	YFOYQATQAG	NYAMDVLRRA	GETAGGAAST	122
ciMgm1	-IHNVPVART	ISFARIIPKL	AMKLVRVPAM	FGGAMTAGLA	YLOYQASQAG	NYVIDDFKSA	GETAGGIASS	126
kmMgm1	-----	-----M	IGKVIRIPAY	IGGGAAALGS	YVAYKVNQAG	SFTGQQLSKF	KDFTGDMRER	51
scMgm1	-LSFVI--TR	RSI-SHFPKI	ISKIIRLPY	VGGGMAAAGS	YIAYKMEEAS	SFTKDKLDRI	KDLGSEMKKEK	116
caMgm1	-K-YIPTYP	TRN-LGFETI	VTRVVKMPAY	VGGAMAAGGS	YVAYKVEQAS	SFTQDKLSAL	KDISEGFFDK	100
psMgm1	-----	MRH-IGFTKI	LAKTTRIPAY	VGGTLAAGGS	YVAYKVEQAS	TYTQDQLSSI	KDFTQGVFDT	59
cjMgm1	-LPMGLKRS	FSF-SAIIPKI	VAKSVKVPAY	LGGGIAAAGS	YIAYKVEEAS	NYTQDKLGQL	KDLGNSAYDK	120
ppMgm1	-QFGLIKTRP	FSI-YSEFKE	AGRVVKAPAA	VGGGLAAAGS	YVAYKVEQAS	SYTKDQVDR	KDLGGLYDN	98
ctMgm1	VWSSAVDIAE	QTKRGWENTK	NQFEIPEWLD	RIMKGEGLAG	EGSGSGEGGP	NGGPEPPROS	RAGAATVAGA	201
atMgm1	LFSEIQGVAE	QTORGWQKTT	EDIEVPEWLO	KILRMDEAAQ	SGGGSS---	-GGGQPPNES	RVGASTAAGA	188
ciMgm1	AIQGIQGVAE	QTORGWERTT	EGIELPEWAO	KILRLEEHAE	KNGGGSGSDG	AGSGSGPKKS	RIGAAGVAGA	196
kmMgm1	-----	-----	---LGDWLQ	---KDGQSG	DGGNN-----	-----SNNN	GSDTVA----	78
scMgm1	-----	-----	---FNKMF	---GDKSQD	GGHGN-----	-----	-DGTVP----	138
caMgm1	-----	-----	---TGDFFK	---GLGTTD	GS--G---S	NGGQQGGDN	GGGATA-AGA	135
psMgm1	-----	-----	---AGDFEK	---GMGKS	SESG---S	SGSGSPGGS	NDTTTA-VGA	96
cjMgm1	-----	-----	---ASEFTN	---GLEFGS	QGDGS---G	S-GSSGNGGG	GGDSTA-ALG	156
ppMgm1	-----	-----	---ISGFFG	---KFG--G	---N---G	S-EGVPPDN	GSNAAA-LGG	128

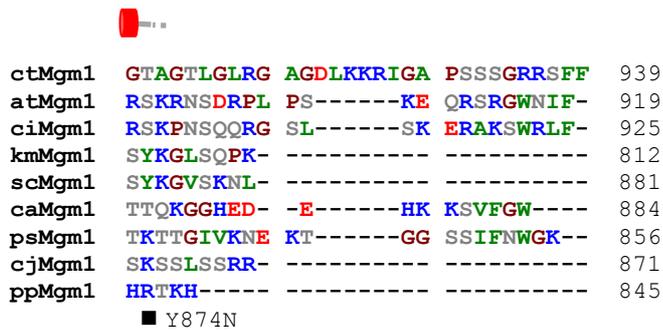
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atMgm1	AAGSVLGYEQ	SDE-----	-----	---EDQ	RLKRDMAEND	QMMILTRKMI	EIRNILLQTVG	234
ciMgm1	TTGSALGYDS	TDD-----	-----	---EVA	EGR--RAVDE	QMMILTRKMI	EIRNMLORIG	240
kmMgm1	-AATLIASMS	DDESDKKT	KEG-E--DDD	EDDEDEDEDE	NDETEDNTQD	EMLNLTROMI	EIRSIILNKVD	144
scMgm1	-TATLIATS	LDDDE-SKRQ	GDP-K--DDD	EDDDDD-EDD	ENDSVDTTQD	EMLNLTROMI	EIRTIILNKVD	202
caMgm1	-AAAAGFTS	DEGEST--TA	ESDLEEDDE	ETLIE-DEDE	EDFENDETDD	HMLNLTROMI	EIRNLLTNIN	201
psMgm1	-TAAALGLTS	EDENESEDE	NDDLAQDEDE	ETLYNDYDD	DDLENETSN	EMLNLTROMI	EIRNLIASID	165
cjMgm1	-TAAATAAKL	DEEEEREK-	---LIEQED	-----D	EEEEEDTTDD	QMMNLTROMI	EIRSILOEID	211
ppMgm1	-TAAAVGFKS	DDDEDEETL-	---YLDEDE	-----DEEE	EEEDSETMDD	EMLNLTROMI	EIRSILOSID	186



ctMgm1	QG-STVTLPS	IVVIGSQSSG	KSSVLEAIVG	HEFLPKGSNM	ITRRPIELIL	VNDPEAKVDY	GEFPDLGLAR	314
atMgm1	QS-NTLTLPS	IVVIGSQSSG	KSSVLEAIVG	HEFLPKGSNM	VTRRPIELIL	VNTPNGQAEY	GEFPALGLGK	303
ciMgm1	QS-NSLTLPS	IVVIGSQSSG	KSSVLEAIVG	HEFLPKGSNM	VTRRPIELIL	INTPNSQAEY	GEFPALGLGK	309
kmMgm1	SSSANLTLPS	IVVIGSQSSG	KSSVLESIVG	KDFLPKGSNM	VTRRPIELIL	VNTPNSQAEY	ADFPALRLYN	214
scMgm1	SSSAHLTLPS	IVVIGSQSSG	KSSVLESIVG	REFLPKGSNM	VTRRPIELIL	VNTPNSQAEY	ADFPALRLYN	272
caMgm1	H--DGIRLPS	IVVIGSQSSG	KSSVLECIIVG	QEFLPKGSNM	VTRRPIELIL	VNTPPEAAANV	AEFPALKMFN	269
psMgm1	H--DGLRLPS	IVVIGSQSSG	KSSVLEAIVG	QEFLPKGSNM	VTRRPIELIL	INTPEAAADV	AEFPALKMHN	233
cjMgm1	RSSETLKLPS	IVVIGSQSSG	KSSVLEAIVG	QEFLPKGSNM	VTRRPIELIL	VNTPNTAAET	ADFPALKMYN	281
ppMgm1	PNDNTLKLPS	IVVIGSQSSG	KSSVLEAVVG	REFLPKGSNM	VTRRPIELIL	VNSPDLAEEV	AEFPALRMNN	256

○ S224A ■ P236L ○ T244A





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 Å² 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.