

**Supplementary Table 1. Mitochondrial protein import and quality control components - human and yeast homologs<sup>1</sup>**

	Complex <sup>2</sup>	Human (mammalian) <sup>3</sup>	Fungal homolog <sup>3</sup>	Localization <sup>4</sup>	Function <sup>5</sup>		
Cytosolic targeting factors		HSP70	Hsp70	cytosol	ATP-dependent molecular chaperone		
		HSP90	Hsp90	cytosol	ATP-dependent molecular chaperone		
		NAC	NAC	cytosol	Ribosome-binding factor / recruitment of RNCs to mitochondria		
		SYNJ2BP	—	MOM	Putative mRNA binding factor		
TOM and SAM complexes	TOM	TOM40	Tom40	MOM	Channel-forming $\beta$ -barrel	core complex	
		TOM22	Tom22	MOM	Receptor / central organizer		
		TOM5	Tom5	MOM	Complex assembly / stabilization		
		TOM6	Tom6	MOM	Complex assembly / stabilization		
		TOM7	Tom7	MOM	Complex assembly / stabilization		
		TOM20	Tom20	MOM	Receptor (primarily MTSs)		receptors
		TOM70	Tom70	MOM	Receptor (primarily hydrophobic proteins) / chaperone		
	SAM	SAM50	Sam50	MOM	Core subunit for $\beta$ -barrel integration		
		MTX1/3	Sam37	MOM	Accessory subunit for $\beta$ -barrel insertion / mitochondrial trafficking		
		MTX2	Sam35	MOM	Accessory subunit for $\beta$ -barrel insertion / mitochondrial trafficking		
TIM23 complex	TIM23	TIM23	Tim23	MIM	Voltage-regulated protein-conducting channel	core complex	
		TIM17 A/B1/B2	Tim17	MIM	Protein-conducting channel		
		TIM50	Tim50	MIM	MTS receptor / phosphatase		
		TIM44	Tim44	matrix	Peripheral scaffold	TIM23 <sup>MOTOR</sup> / PAM-specific subunits	
		mtHSP70 (Mortalin)	mtHsp70 (Ssc1)	matrix	ATPase motor		
		DNAJC15 / DNAJC19	Tim14 (Pam18)	MIM	J-type protein cochaperone		
		MAGMAS 1/2	Tim16 (Pam 16)	MIM	J-type protein cochaperone		
		GrpEL1/2	Mge1	matrix	mtHsp70 nucleotide exchange	TIM23 <sup>SORT</sup> -specific subunits	
		—	Pam17	MIM	Complex organization		
		TIM21	Tim21	MIM	Sorting of MIM proteins		
ROMO1	Mgr2	MIM	Lateral integration of MIM proteins				
Mitochondrial processing peptidases	MPP	PMPCA	Mas2	matri	Metalloprotease; cleavage of MTSs from matrix-directed precursors		
		PMPCB	Mas1				
	IMP	IMMP1L	Imp1	MIM	Serine protease; cleavage of hydrophobic sorting signals from IMS-directed precursors		
		IMMP2L	Imp2				
		MIP	Oct1	matrix	Metalloproteases; N-terminal processing of imported proteins after MPP cleavage		
	XPNPEP3	Icp55					
	PREP	PreP	matrix	Metalloprotease; digestion of presequences			
Mitochondrial folding complexes	Chaperonin	HSP60	Hsp60	matrix	Forms enclosed barrel structure with central cavity		
		HSP10	Hsp10				
	HSP70	mtHSP70 (Mortalin)	mtHsp70 (Ssc1)	matrix	ATPase-driven chaperone		
		GrpEL1/2	Mge1	matrix	mtHsp70 nucleotide exchange		
		TID1	—	matrix	mtHsp70 J-type cochaperone		
HSP90 paralog	HEP1	Hep1	matrix	mtHsp70 cochaperone			
	TRAP1	—		ATP-dependent molecular chaperone; great functional diversity			
Mitochondrial proteases	m-AAA	AFG3L2	Yta12	MIM	ATP-dependent metalloprotease; catalytic domain faces the matrix		
		SPG7 (Paraplegin)	Yta10				
	i-AAA	YME1L	Yme1	MIM	ATP-dependent metalloprotease; catalytic domain faces the IMS		
	CLPXP	CLPP	—	matrix	ATP-dependent serine protease		
		CLPX	Mcx1				
		LONP	Pim1			matrix	ATP-dependent serine protease
		HTRA2	—			MIM	Serine protease
		PARL	Pcp1			MIM	Serine protease; processing of proteins involved in mitophagy
	OMA1	Oma1	MIM	Stress-activated metalloprotease; processing proteins involved in stress response and dynamics			

<sup>1</sup>Color coding of major functional groups corresponds to that used in Figure 2.

<sup>2</sup>Common names of homo- or hetero-oligomeric assemblies that operate as a functional machinery.

<sup>3</sup>Column entries are blank where no corresponding human/mammalian or fungal homologs are known.

<sup>4</sup>For integral membrane proteins, this column indicates the membrane in which they are embedded. For soluble or peripheral proteins, this column indicates the aqueous compartment in which they reside, respectively.

<sup>5</sup>Functional features emphasize those of human/mammalian proteins and complexes.