

Fig.S2. Multiple amino acid sequences alignment^a of transmembrane helices^b (TMH)6, 7 and 8 of Cu-ATPases encoded in the genomes of PAFDs and PPFMs. The motifs involved in Cu binding and translocation shared among them are in bold. Full names of strains can be seen in Fig. 1

MloCh	IFAIVSAVSVLIIA CPC ALG	489
Rfr1Ch	AHALLAAVAVLIIA CPC ALG	485
RtrCh	AHALLAAVAVLIIA CPC ALG	483
Rle2p111	ANGLLAAVAVLIIA CPC ALG	491
Retpe	ADALLAAVAVLIIA CPC ALG	490
Mno3p2	AHALVAAVAVLIIA CPC ALG	438
Rle1Ch	AHGLVAAVAVLIIA CPC ALG	389
SfGR1	AHGLVAAVAVLIIA CPC ALG	391
SfrNGR1Mpb	AHALVSAVAVLIIA CPC ALG	391
Sme1Mpa	THGLVAAVAVLIIA CPC ALG	355
MeAM2Ch	TFALLAAVAVLIIA CPC ALG	448
Mor2Ch	TFALLAAVAVLIIA CPC ALG	462
MeAM3Ch	TFALLAAVAVLIIA CPC ALG	455
MeAM5Mp	TFALLAAVAVLIIA CPC ALG	455
MeAM6Mp	TYALLAAVAVLIIA CPC ALG	459
Mno1Ch	TYGLLAAVAVLIIA CPC ALG	473
AcfeACH663	SIALVAAVAVLVVA CPC AMG	470
AcfeACH207	SVALVTAVAVLVVA CPC AMG	467
MeAM1Ch	GHALVAGISVLIIA CPC AMG	481
MexTK1Ch	GHALVAEISVLIIA CPC AMG	481
Mor1Ch	GPALVNAVAVLIIA CPC AMG	458
Mra1Ch	GPALVNAVAVLIIA CPC AMG	458
Rfr2Ch	TFALVNAVAVLIIA CPC AMG	476
Mno2p2	TFALVNAVAVLIIA CPC AMG	483
Rle3p111	TFALVNAVAVLIIA CPC AMG	475
Sme2Mpa	TFALVNAVAVLIIA CPC AMG	475
Sme3Mpb	SFALVNAVAVLIIA CPC AMG	476
SfrNGR2Mpb	SFALVNAVAVLIIA CPC AMG	480
SfrNGR3Mpb	TFALVNGVAVLIIA CPC AMG	475
SfGR2	TFALVNSVAVLIIA CPC AMG	475
	TMH6 CXC	

MloCh	NLFFAFL YNVLGVP VAAAGVLYPLTGMLLSPLMAAA MSLSS SVSVIANALRLRTLKL----	839
Rfr1Ch	NLAFAFG YNALGVP LAAGVLYPVFSLLLSPMIAAA MSLSS SVSVIANALRLRLAK----	834
RtrCh	NLAFAFG YNALGVP LAAGVLYPIFGLLLSPMIAAA MSLSS SVSVIGNALRLRLAK-----	832
Rle2p111	NLGFAFG YNALGVP VAAAGMLYPIFGLLLSPMIAAA MSLSS SVSVISNALRLRFAKL----	841
Retpe	NLGFAFG YNALGVP VAAAGVLYPIFGLLLSPMIAAA MSLSS SVSVIANALRLRFAKS----	840
Mno3p2	NLFFAFI YNAAGVP VAAAGILYPSFGILLSPVIAAA MALSS SVSVIGNSLRLRSVRL----	788
Rle1Ch	NLFFAFI YNAAGIP VAAAGVLYPAFGLLLSPIIAAA MALSS SVSVIGNSLRLRRSPLD---	740
SfGR1	NLFFAFI YNAAGVP VAAAGVLYPAFGLLLSPIIAA LAMALSS SVSVIGNALRLRSAQI----	741
SfrNGR1Mpb	NLFFAFI YNAAGVP VAAAGVLYPAFGLLLSPIIAAA MALSS SVSVIGNSLRLRSTQP----	741
Sme1Mpa	NLFFAFI YNAAGVP VAAAGVLYPAFGLLLSPIIAAA MALSS SVSVIGNSLRLRSTRI----	705
MeAM2Ch	NLFFAFI YNTAGVP VAAAGVLYPFLGILLSPVIAAA MALSS SVSVIGNALRLRGVGLDPSR	802
Mor2Ch	NLFFAFV YNAAGVP VAAAGVLYPFLGILLSPVIAAA MALSS SVSVIGNALRLRATDLDPAP	816
MeAM3Ch	NLFFAFV YNAAGVP MAAGVLYPFLGILLSPVIAAA MALSS SVSVIGNALRLRATRLG---	806
MeAM5Mp	NLFFAFI YNAAGVP VAAAGILY PFLGILLSPVIAAA MALSS SVSVIGNALRLRAARLG---	806
MeAM6Mp	NLFFAFI YNAAGVP VAAAGVLPFLGILLSPVIAAA MALSS SVSVIANALRLRAVRL----	809
Mno1Ch	NLFFAFI YNAAGVP VAAAGVLYPVLGILLSPVIAAA MALSS SVSVIGNALRLRSLDI----	823
AcfeACH663	NLFWAFF YNILLIP VAAAGVAVPI-GIHLNPMVAGV AMGLSS VFVLSNSLRLKRLKAYVPT	820
AcfeACH207	NLFWAFF YNILLIP IAAGVAAPI-GIHLNPMVAGV AMGLSS VFVLGNSLRLKRLKAYIPL	817
MeAM1Ch	NLFWAFAY YNAALIP VAAAGGLAVFGGPQLSPVLAAG AMALSS VFVVGNALRLKRAGGTA--	832
MexTK1Ch	NLFWAFAY YNAALIP VAAAGGLAVFGGPQLSPVLAAG AMALSS VFVVGNALRLKRAGGTA--	832
Mor1Ch	NLFWAFAY YNAALIP VAAAGVLPFGGPALSPVLAAG AMAFSS VFVLGNALRLRRAGGRPAA	813
Mra1Ch	NLFWAFAY YNAALIP VAAAGVLPFGGPALSPVLAAG AMAFSS VFVLGNALRLRRAGGRPAA	813

Rfr2Ch	NLFWAFAY NTALVP VAAAGALYPFTDILLSPVFAAGAM MALSS VFVLGNALRLRRFKLAD-- 833
Mno2p2	NLFWAFAY NTALIP VAAAGVLFPAFGILLSPVFAAGAM MALSS VFVLGNALRLRRFKVAH-- 835
Rle3pl11	NLFWAFV YNASLVP VAAAGLLYPVNGTLLSPVFAAGAM MAMSS VFVLGNALRLRRIEA--- 824
Sme2Mpa	NLFWAFAY YNVSLVP VAAAGVLYPLNGTLLSPILAAAA MAMSS VFVLGNALRLRSVNPA--- 826
Sme3Mpb	NLFWAFAY YNVSLIP VAAAGVLYPVTGILLSPIFAAAA MAMSS VFVLGNALRLKSVNPA--- 827
SfrNGR2Mpb	NLFWAFAY YNTVLVP VAAAGALFPAYGLLLSPMIAAGAM MALSS VFVLGNALRLKRFRAPMKF 834
SfrNGR3Mpb	NLFWAFAY YNVVLIP VAAAGALYPGYGMLLSPVFAAGAM MALSS VFVVGNALRLKRFRGLERQ 829
SfGR2	NLFWAFAY YNVVLIP VAAAGALYPGYGVLLSPVFAAAA MALSS VFVVGNALRLKRFRGLERQ 829
	YN (X₄) P TMH7 M (X₃) S TMH8

^aThe multiple sequence alignment was performed with Clustal Omega version 1.2.4. at MBL-EBI ([Clustal Omega < Multiple Sequence Alignment < EMBL-EBI](#))

^bThe TMH (black lines) were predicted with [TOPCONS: Consensus prediction of membrane protein topology and signal peptides](#).