

TgFtsH1 (1) -----MSSRRGGSPARRSSRRCSASRRAGRHRSDSGAGECRPGTDGRSLSTSSDFLNSSSSPGSYSDRVQGGIGDPEVFPVFPFANGPKFSSDRRS

AtFtsH1 (1) -----MASNSLLRSSNFFLGSIISSPTPKTRRKPSPF

Yta12p (1) MLLLSWSRIATKVVRPVRFRSYGLTHIKSLHTQYRLNRLQENKSGNKNEDNEDAKLNKEIPTDEVEAIRKQVEKYEIQTKNNTIPANWKEQKRKI

TgFtsH1 (93) STSPSLNRKATFTRVLAALDSADALRPPAPASTYTYARDPASDTFR**VTGLSSLVLALAPPPVPPFFIT**PNMPTQSNRALPPPSGPTDAAGSPRRGSP

PfFtsH1 (1) -----MSKYDNQSFLS

BpFtsH (1) -----MAK**NLMLLVLAVVLMIFQNF**S---

AtFtsH1 (35) PFSFVSRACYQITRSS-----QDENSPNGKPNSPFSS**VALAAILLSSISSPLALAV**VEDEPASEVSVIESQAVKPSPTSPPLFIQNEILKAPSPKS---

Yta12p (101) DESIRRLLEDAVLKQESNRIQERKEKEEENGESKAKSNRTEQGYFEGNNSRNIPPPPPPPPKPLNDPSPVSKVNV**NLFIQIGLTFLLFLDLLL**---

TgFtsH1 (193) TPRARGEQHRMHHYDSGHVSSSHVSNESHSPQRIRSNPVLPEKTOGDAPTYPNQGEKAGGGRMRAA**LILLIGVCIGLAWMPVSVLTF**RLLSLHSDGADG

PfFtsH1 (13) TGSDKYGEQENSVLHDEEYIINENKKRNERDKFRYYEN-----FFNRRRSKWN**YFIIFFLVGLGFAWPFPMITIT**TYR---LFYKDNFN

BpFtsH (24) ANNINNRKIDYSTFLSDVNDQDREVHIS--GREMNIIRKDN-----GRYITYIPISDPKLLDNLVKNVKIIGAAPBEQ-----SFFT**ATFI**

AtFtsH1 (126) S**DLPEGSQWR**SEPLNAVKKGV**ERVRF**SKDGSVQLTAVDN-----RRASVIVPN-DPDLIDILAMNGVDISVSEGESSG-----NDLFT**VIGN**

Yta12p (198) NSLEEQSEITWQDREKLLAKGYVAKLIVNKMVKVMLNDNGKNQADNYGRNFYFTIGSIDSEHKLQKAQDELDDKDFRIPVLVQEGNWAK**AMFO**

TgFtsH1 (293) VDDIDSTDYEGVDDDGIIPDGSYGNHMMHNTDSSSGSNVTNSEALVPPQPTFPPLTF**NDLAGL**TEAKTELOEVVQFLRDPSPKFERL**CARL**PKGVLLVGP

PfFtsH1 (100) NTNRYRTNNSSTSLKSYGNEKNKSDNN-----GKVPMDQSPN-KVSPHFKPIREETIAGIDESKLELLEVVDLKNREKHEMGARMPKGVLLVGP

BpFtsH (105) **SWFPM**LLLI**GVWV**FFMRQMQVGGCK-----GAMSFGSKAR-MLPEDQVKITFSDVAGCDEAKEEVOELVEYLKEPSRFQKLGKIPK**GHLM**VGP

AtFtsH1 (210) **LIFP**LL**AFGLFL**FRRAQGGPGGGGG-----LGCMPDFGRSKSK-FQEVETPGVSVADVAGADQAKLEQEVVDPLKNEKDYTA**CAK**IPK**CCLLV**VGP

Yta12p (298) **LLPTV**ML**AGL**ILWLRSAQAAGSG-----GIFGLSRSKAKFNTETDVKIKK**KDVAGC**DEAKEE**IMEFV**SLKEPSR**EKMGAK**IP**CAI**LSGP

TgFtsH1 (393) PG**GKT**ALARAVAE**CA**VPYFYASGSEFVELYVCGARRV**RG**FSYARNHSP**CI**FL**DE**LD**DAV**GR**RO**ASAGP**GAG**NR**EH**DOT**NO**LL**VE**MDG**FN**QASRI

PfFtsH1 (191) PG**S****GKT**MLARAVAE**CA**NPVPIYITSGPFI**EL**YVCGAKRIR**Q**FAHARSVA**PS**IV**FD**DE**DAI**CGKRSSG**SVN**GAGQ**RE**HDOT**NO**LL**VE**MDG**FN**QASRI

BpFtsH (194) PG**G****KT**LLAKATA**EA**CV**PF**FTISGSD**F**EM**FG**VGASRVR**DM**EHRSK**VAP**CI**IF**DE**DAV**GR**RO**AG--LGGG**H**DER**EQ**TL**NO**LL**VE**MDG**FN**QASRI

AtFtsH1 (304) PG**G****KT**LLARAVAE**CA**VP**PF**SCAAS**EF**VELYVCGASRVR**DL**FEKAKSK**AP**CI**IF**DE**DAV**GR**RO**AG--MGGG**N**DER**EQ**TL**NO**LL**VE**MDG**FN**QASRI

Yta12p (390) PG**G****KT**LLAKATA**EA**CV**PF**YFVSGSE**F**EM**FG**VG**AR**VR**DL**FEK**TARE**NA**PS**IV**FD**DE**DAI**CKAR**Q**KN-FSG**AN**DER**ENT**TL**NO**LL**VE**MDG**FN**QASRI

TgFtsH1 (493) VVLAATNR**VD**LLD**SALL**RG**RF**DR**I**VH**SL**PDVAARE**IL**L**Q**K**Y**LQ**RV**VELPTESHEGT**V**SG**F**ST**LV**NAGDERANA**Q**GGSPAP**L**AS**PH**S**R**SS**SD**K**R**E**E**K

PfFtsH1 (291) MVIGATNR**VD**LLD**SALL**RG**RF**DR**I**VY**PL**PD**IN**GR**K**II**LE**I**Y**IK**K**IK**S**

BpFtsH (292) ILIAATNR**VD**LLD**SALL**RG**RF**DR**Q**I**F**VAL**PD**IR**GR**K**II**Q**V**H**M**K**K**V

AtFtsH1 (402) IVLAATNR**VD**LLD**SALL**RG**RF**DR**Q**TV**DR**PDVAG**RV**IL**Q**V**S**RG**K**

Yta12p (489) VVLAGATNR**VD**LLD**SALL**RG**RF**DR**I**HIN**DK**PE**LE**GR**K**AI**F**AV**H**L**H**L

TgFtsH1 (593) DRSSGRFPRSEEGKKEVEPE**TY**RQ**RP**Q**S**GREKA**AF**SD**NT**AIGDKEG**SE**DE**SAE**HE**KK**PGLTQ**V**H**K**D**L**A**K**O**L**AK**IT**PG**F**SG**A**EL**EN**LV**NEA**AL**I**A**RA**

PfFtsH1 (340) -----DLKLE**DE**IK-----L**AR**IT**PG**SG**A**EL**EN**LV**NEA**AL**I**A**RA**

BpFtsH (339) -----PLGN**VD**PMI-----L**AR**CT**PG**SG**A**EL**EN**LV**NEA**AL**I**A**RA**

AtFtsH1 (449) -----ALG**KD**VD**FD**K-----V**AR**RT**PG**SG**A**EL**EN**LV**NEA**AL**I**A**RA**

Yta12p (536) -----KLAGE**IF**DL**KN**R-----L**AR**IT**PG**SG**A**EL**EN**LV**NEA**AL**I**A**RA**

TgFtsH1 (693) DKEIVTLQ**EL**Q**EA**RDKV**MG**FA**R**K**TR**MSAY**Q**RL**TA**Y**HEAGH**AI**IA**F**Y**LQ**PA**Y**DP**I**H**K**AI**IV**S**R**G**S-AL**GF**VE**Q**V**PL**ED**RY**GH**G**---VA**Q**LE**AR**L**CV**M

PfFtsH1 (376) NKS**L**VT**IN**EL**Y**EA**R**D**K**VM**SG**PER**KS**LR**Q**SD**H**OR**RI**TA**Y**HEAGHAI**IV**AY**FL**Q**PK**TD**PI**H**K**AI**IV**S**R**GN-AL**CY**VE**Q**IP**V**DD**R**HN---Y**F**KS**Q**ME**A**K**L**AV**CM**

BpFtsH (376) NR**D**V**MM**S**DF**ES**A**K**DK**IT**Y**CS**ERR**SM**VT**E**K**Q**ES**TA**Y**HEAGHVI**LV**GR**LV**P-E**H**DP**A**K**V**II**PR**GR-AL**GV**TF**FL**PK**D**V**LS**---IN**K**N**K**LE**S**Q**I**ST**LY**

AtFtsH1 (486) EL**K**E**IS**DK**E**IS**D**AL**ER**II**AG**PE**K**NA**V**SE**E**KK**LV**AY**HEAGH**AL**V**GA**L**MP-E**Y**DP**V**AK**IS**II**PR**GO-AG**GL**TF**F**AP**SE**ER**LE**SG**LY**SR**Y**EN**Q**MA**VAL**

Yta12p (575) DED**AV**KL**N**H**F**Q**A**TER**I**IG**V**ER**K**SK**LL**SP**E**E**K**V**V**AY**HEAGH**AV**CE**W**Y**L**K**-Y**AD**PL**L**K**V**SI**IP**RG**Q**AL**CY**A**YL**PC**D**IF**L**L**T**---EQ**L**K**R**DM**T**MS**L**

TgFtsH1 (789) G**GR**VA**ER**L**I**FG**RD**AL**SN**G**AS**SD**I**ET**AT**RM**AV**VM**TE**W**G**MS**E**K**I**CP**LS**Y**K**V**H**GR**S**-----RR**AF**T**S**ET**AN**LV**EE**EV**K**OL**VI**TA**ER**KA**E**KL**LR**R**IR**K**Q**

PfFtsH1 (472) G**GR**TA**EE**IV**F**G**K**SET**SG**AS**SD**IS**R**ATE**IA**Y**K**M**TE**W**G**MS**E**K**I**CP**LN**Y**K**K**R**M**GD**G**YS**-----SN**RL**S**AG**TV**SS**TE**V**EV**K**SL**VE**K**G**SL**SE**II**LR**R**IR**K**KE**

BpFtsH (471) G**GR**LA**EE**IL**I**Y**GN**V**NS**IG**AN**DI**K**VA**IN**L**AR**N**MT**Q**NG**F**S**K**K**IC**EL**L**M**SE**E**GE**IF**L**GR**TV**T**K**SK**H**MS**DE**T**AR**LD**EV**KL**LV**E**K**N**Y**RA**K**II**LE**EN**DI

AtFtsH1 (584) G**GR**VA**EE**IV**FG**DEN**V**TT**GA**SN**DF**M**Q**VS**RV**AR**MT**ER**FG**F**S**K**K**IQ**V**AV**GG**PG**NP**FM**Q**Q**MS**S**Q**K**DY**SM**AT**AD**IV**DA**EV**RL**VE**K**AY**K**R**ATE**IT**TT**IDI**

Yta12p (670) G**GR**V**SE**EL**HF**--PS**VT**SG**AS**DF**FK**V**TS**MA**TAM**V**TE**W**G**MS**E**K**I**CP**LN**Y**K**R**DD**S-----DL**T**K**PF**SD**ET**GD**LD**SE**V**Y**IR**IV**Q**EC**H**DR**CT**KL**L**KE**KA**ED

TgFtsH1 (881) I**RE**VAL**Q**L**E**KE**T**LS**G**EE**ISE**ILD**P**--SG**S**Y**RT**K**VE**RL**TR**M**Q**Q**E**Q**P**-----S**FL**Q**RL**V**V**Q**L**K**R**G**F**W**L**F**LP**R**D**Q**TE**FA**AVE**AD**K**Q**L**KT**Q**EE**TE**K**K**NG**S**

PfFtsH1 (566) LD**N**L**AF**AD**LD**KE**T**LS**G**EE**IK**NI**ID**P**N**NS**K**Y**SG**K**VE**ML**K**ND**TK**NE**KK**S**NS**V**S**K**N**K**ST**IS**ED**Y**DK**N**Q**N**N**VE**Q**NY**Q**SH**D**TL**V**K**NE**EN**L**N**M**K**ND**ID**DN**NT

BpFtsH (571) L**H**AM**K**D**AL**IK**Y**ET**INS**R**Q**LD**LM**K---R**K**S**I**Q**SS**NI**CT**DD**DN**

AtFtsH1 (684) L**H**K**L**A**Q**L**L**KE**T**IV**D**CE**EF**MS**L**FI---D**G**Q**A**E**LY**IS

Yta12p (761) V**E**KA**IQ**VL**L**KE**T**IT**RE**DM**IDL**L**G**---K**R**PF**ER**ND**AF**D**K**Y**L**ND**Y**ET**E**-----K**IR**KE**E**E**K**NE**K**R**NE**PK**P**ST**N**-----

TgFtsH1 (974) T**NE**AP**K**TK**G**D**DD**DES**GN**S**R**RE**M**Q**E**AA**T**RA**E**PH**R**ND**Q**DR**DR**H**G**DE**H**PF**AD**V**NE**IS**A**K**Q**P**Q**IS**G**AT**R**T**G**H**E**D**H**S**E**ST**H**L**R**CS**R**GN**V**A**E**G**Q**H**C**S**D**L

PfFtsH1 (666) R**D**G**V**NS**D**S**F**V**K**RE**V**T**D**Q**IN**G**EL**SE**MD**NE**K**EN**K**LD**G**E**EL**N**K**I**I**D**ND**N**K**M**G**D**M**K**NI**KE**V**IK**M**K**K**Q**S**K**G**Y**K**Y**K**N**V**L**K**S**V**SE**H**KE**L**K**T**Q**K**KA

TgFtsH1 (1074) S**VE**A**Q**VP**EP**FF**V**PK**R**H**SH**Q**VE**ET**GR**E**H**FS**RY**A**EV**K**S**L**PS**N**PM**V**PR**G**K**L**D**SE**AA**S**D**G**E**A**K**IR**L**R**D**G**E**A**GL**PH**G**D**L**V**Q**D**W**HT**RT**PR**S**V**Q**R**HE**A**FT**L**E**D**D**FR

PfFtsH1 (766) D**EN**K**IV**AD**N**NE**K**S**NN**SL**D**K**N**NT**Q**S**I**DE**K**G**Y**K**NN**N**N**N**N**N**M**V**K**N**I**N**EL**F**E**EN**F**PE**Y**K**Y**D**N**EN**ND**F**V**K**T**EN**Y**DF**N**F**EV**DI**S**H**I**K**N**V**D**EM**K**FN**I**F**E**

TgFtsH1 (1174) K**KG**NS**S**ER**D**V**FS**R**G**IR**RG**VE**V**Q**S**AS**LV**S**Q**Q**CC**ES**G**T**K**NC**ANS**Q**ARE**HS**RR**T**K**R**V**Q**Q**W**L**TP**W**GL**GL**ST**I**TR**DE**

PfFtsH1 (866) H**N**L**N**KL**FL**DF**DI**FK**S**D-----

FIG. S1. Alignment of TgFtsH1 with the PfFtsH1 (PFL1925w), a chloroplast FtsH-*Arabidopsis* FtsH1 (Q39102), a mitochondria FtsH-*Saccharomyces cerevisiae* Yta12p (NP_013807), and a bacterial FtsH-*Baizongia pistaciae* (Q89AF2) is shown above. Black shading marks residues identical in all sequences, while dark and light gray shading mark residues identical or similar in at least 3 sequences, respectively. Conserved residues in Walker A (GTK- bold and blue), Walker B (DE- bold and pink), SRH (RXXR- bold and green), Zn binding (HEAGH- bold and yellow) are highlighted. Transmembrane domains predicted by either TMHMM or TMpred and are shown in red, bold and italics. Arrows indicate the C-termini of

the FtsH deletion mutants (354, 694 and 925). The strain specific amino acid changes from the ME49 are at location 1008, 1024, 1194 and 1222.