A signal sequence suppressor mutant that stabilizes an assembled

state of the twin arginine translocase

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SUPPORTING INFORMATION

SI APPENDIX

Table S1. Clones isolated from a *tatB* mutant library following screening for suppression of transport defects of inactive signal peptides. The BRE, BRN, BRQ, BRH, BHH, BKH or BKQ clone nomenclature signify substitutions isolated following screening against RE, RN or KQ variants of the AmiA signal peptide RR motif, respectively.

*identical clones

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Table S2. Clones isolated from a *tatAB* mutant library following screening for suppression of the transport defect arising from the TatC F94Q substitution.

Table S3. Strains used and constructed in this study.

Table S4. Plasmids used and constructed in this study

Table S5. Oligonucleotides used in this study

Supplementary References

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Supplementary Figure Legends

Figure S1. Substitutions of the twin arginines in the AmiA signal peptide prevent growth in the presence of SDS. Strain MCDSSAC ∆*tatABC* producing wild type *tatABC* from plasmid pTAT1d and either wild type ('RR') or signal peptide point-substituted AmiA, as indicated, from pSUAmiA. The strain and plasmid combinations were cultured overnight in LB medium supplemented with chloramphenicol and ampicillin (for plasmid selection), after which they were streaked onto LB agar containing the same antibiotics, with and without the addition of 2% SDS and incubated for 16 hr at 37°C.

Figure S2. TatB variants are able to restore Tat transport to a range of defective twin arginine substitutions in the AmiA signal sequence. Growth of MCDSSAC ∆*tatABC* coproducing the indicated TatB variants (with wild type *tatA* and *tatC*) from pTAT101, or the empty plasmid pTH19kr (indicated by '*tat*') alongside signal peptide variants of AmiA, on LB agar supplemented with chloramphenicol and kanamycin, with and without the addition of 2% SDS as indicated. An 8µl aliquot of each strain/plasmid combination following aerobic growth to an OD_{600} of 1.0 was spotted and incubated for 16 hr at 37 $^{\circ}$ C. A. Individual signal peptide substitutions of AmiA (indicated to the left of each panel) were tested against the TatB suppressors F6Y, L9P, L9Q, L10P, F13Y, K30I and I36N. B. The TatB E8K suppressor was tested for the ability to suppress the indicated AmiA signal peptide substitutions.

Figure S3. TatB variants are able to restore Tat transport to a range of defective twin arginine substitutions in the SufI signal sequence. Growth of MCDSSAC ∆*tatABC* coproducing the indicated TatB variants (with wild type *tatA* and *tatC*) from pTAT101, or the empty plasmid pTH19kr (indicated by '*tat*') alongside signal peptide variants of SufI fused to the AmiA mature domain, on LB agar supplemented with chloramphenicol and kanamycin, with and without the addition of 2% SDS as indicated. An 8ul aliquot of each strain/plasmid combination following aerobic growth to an $OD₆₀₀$ of 1.0 was spotted and incubated for 16 hr at 37°C. A. Individual signal peptide substitutions of AmiA (indicated to the left of each panel) were tested against the TatB suppressors F6Y, L9P, L9Q, L10P, F13Y, K30I and I36N. B. The TatB E8K suppressor was tested for the ability to suppress the indicated AmiA signal peptide substitutions

Figure S4. A subset of amino acid substitutions at TatCF94 abolish Tat activity when produced at medium and low copy number. A and C. Growth of DADE coproducing either wild type TatABC (Tat⁺), wild type TatAB alongside F94-substituted TatC or the cognate empty plasmid (Tat) on LB agar containing 2% SDS. A single colony of each strain/plasmid combination was resuspended in 30μ of PBS and an 8μ aliquot was spotted onto LB agar supplemented with appropriate antibiotics, along with 2% SDS as indicated. Plates were incubated for 16 hr at 37°C. B and D. Detection of TatC protein present in membrane fractions of the same strain and plasmid combinations as in A. and C., respectively, by Western immunoblot with anti-TatC antiserum. A total of 5µg membranes was loaded per lane for TatC produced from $pTAT1d$ (B) and $20\mu q$ per lane for membranes produced from strains harboring pTAT101 derivatives (D).

Figure S5. TatB variants cannot supress TatC inactivating substitutions outside of the signal peptide binding site. Growth of DADE (*tatABCD*, *tatE*) coproducing wild type TatA alongside and the indicated substitution in TatB alongside either of TatC P48L, TatC M59K, TatC V145E, TatC D211K or TatC Q215K as indicated, from plasmid pTAT101 on LB agar or LB agar containing 2% SDS. A single colony of each strain/plasmid combination was resuspended in 30μ of PBS and an 8μ aliquot was spotted onto LB agar supplemented with appropriate antibiotics, along with 2% SDS as indicated, and incubated for 16 hr at 37°C.

Figure S6. The suppressive effect of the TatB variants is not additive and mature AmiC is not exported in the presence of the TatB F13Y suppressor. A. Growth of DADE coproducing either wild type TatABC (Tat⁺), wild type TatAB alongside F94-substituted TatC or the cognate empty plasmid (Tat) on LB agar or LB agar containing 2% SDS. B. Growth of MCDSSAC ∆*tatABC* coproducing the indicated TatB variants (with wild type *tatA* and *tatC*) from pTAT101, or the empty plasmid pTH19kr (indicated by ' Δt at') alongside the RN or KK

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signal peptide variants of SufI fused to the AmiA mature domain, as indicated, on LB agar with or without the addition of 2% SDS. C. Strain MC4100 ∆*ami*A ∆*amiC* ∆*tatABC* coproducing either wild-type TatB or TatB F13Y (with wild type *tatA* and *tatC*) from pTAT101 and the AmiA or AmiC mature domains (from pQE70-mAmiA or pQE70-mAmiC, respectively) on LB agar or LB agar containing 2% SDS. In each case a single colony of each strain/plasmid combination was resuspended in 30μ of PBS and an 8μ aliquot was spotted onto LB agar supplemented with appropriate antibiotics, along with 2% SDS where indicated. Plates were incubated for 16 hr at 37°C.

Figure S7. The TatB suppressors support export of his-tagged SufI with its native signal peptide. A. and B. *E. coli* strain DADE producing wild type TatA and TatC and the indicated TatB variants alongside wild-type SufI-his or the indicated signal-peptide variants were fractionated into whole cell (upper panels) and periplasm (lower panels) fractions, then analysed by Western blot with anti-6X His tag® or anti-RNA polymerase β subunit antibodies (cytoplasmic control protein). wc – whole cell.

Figure S8. TatBC and SufIss-GFP-His twin-arginine variants are detectable in whole cell samples. A. and B. Cells producing Suflss-GFP-His with the wild type (RR) or twin-arginine substituted SufI signal peptide, as indicated, alongside TatC and either wild type TatB or the E8K, F13Y or I36N substituted variants, or C. and D. Cells producing SufIss-GFP-His with the wild type Sufl signal peptide along with either wild type TatBC, the TatC F94Q allele along with either wild type TatB or the L9Q, L10P, F13Y or I36N substituted variants, or the TatC E103K allele along with either wild type TatB or the L9Q, L10P, F13Y or I36N substituted variants, as indicated were harvested and resuspended in PBS. A. and C. The fluorescence intensity and OD_{600} of the samples were measured using a plate reader and the Fluorescence/OD600 plotted for each sample. B. and D. 20 μl of each cell suspension was taken, all samples were normalized to the same OD_{600} and then analysed by SDS-PAGE followed by western blot using a TatB-TatC mixed antibody.

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Figure S9. TatBC complexes containing the TatB F13Y suppressor do not co-purify with signal peptide variants of AmiA. C-terminally his-tagged wild type AmiA, twin-arginine substituted AmiA or signal sequence-less AmiA, as indicated was co-produced alongside wild type TatBC or TatBF13Y/TatC and purified using nickel beads from digitonin–treated cell extracts. Aliquots of the load and elution fractions were subject to SDS-PAGE followed by Western blot using either anti-His, anti-TatB and TatC antibodies.

Figure S10. TatB variants are extracted from the membrane with digitonin. Membrane suspensions (containing equivalent amounts of total protein) from strain DADE coproducing either wild type TatABC or wild type TatA and TatC alongside the indicated amino acid variant of TatB were solubilized by addition of 2% digitonin and incubation on ice for 30 min. Samples total membranes and digitonin solubilized material (each containing 10μ g protein) were analysed by SDS-PAGE followed by western blotting with anti-TatA, anti-TatB or anti-TatC antibodies as indicated.

Figure S11. Constitutive oligomerisation of TatA is not promoted by the TatB L9Q, L10P or I36N substitutions. Fluorescence images of TatA-YFP in representative cells of A. strains AyBCE or AyBC $F_{940}E$ (encoding chromosomal TatC F94Q) in the presence (pAmiA) or absence of plasmid-encoded wild type AmiA, as indicated (reproduced from Fig 5A). B. strains AyB_{L9Q}CE (encoding chromosomal TatB L9Q), AyB_{L10P}CE (encoding chromosomal TatB L10P) and AyB_{136N}CE (encoding chromosomal TatB I36N) or the same strains additionally harboring the chromosomally-encoded TatC F94Q substitution. Scale bar: 1 μm. Note that the pictures in panel A are identical to those in Fig 5A and were included here to provide a direct comparison with panel B.

Fig S1

 LB $LB + 2\%$ SDS

B

TatB E8K Sufl
RD Sufl
RE RR RD RE RR RD RE Sufl R_{N} E_0 $\sum_{i=1}^{n}$ $\overline{\mathsf{RR}}$ $\frac{1}{2}$ $rac{1}{\sqrt{1}}$
 RQ $rac{1}{\sqrt{1}}$
 RH $\overline{\text{Suff}}$ $\n **RN**\n$ RQ RH $rac{1}{\sqrt{2}}$ ${\sf RN}$ KQ Sufl
HH Sufl
KH Sufl
KQ HH KH KQ

 LB $LB + 2\%$ SDS

Eags

Fig S4

A

B

Fig S9

Fig S10

 $AyB_{136N}CE$

 $AyB_{L10P}CE$

PC{F94Q}E

