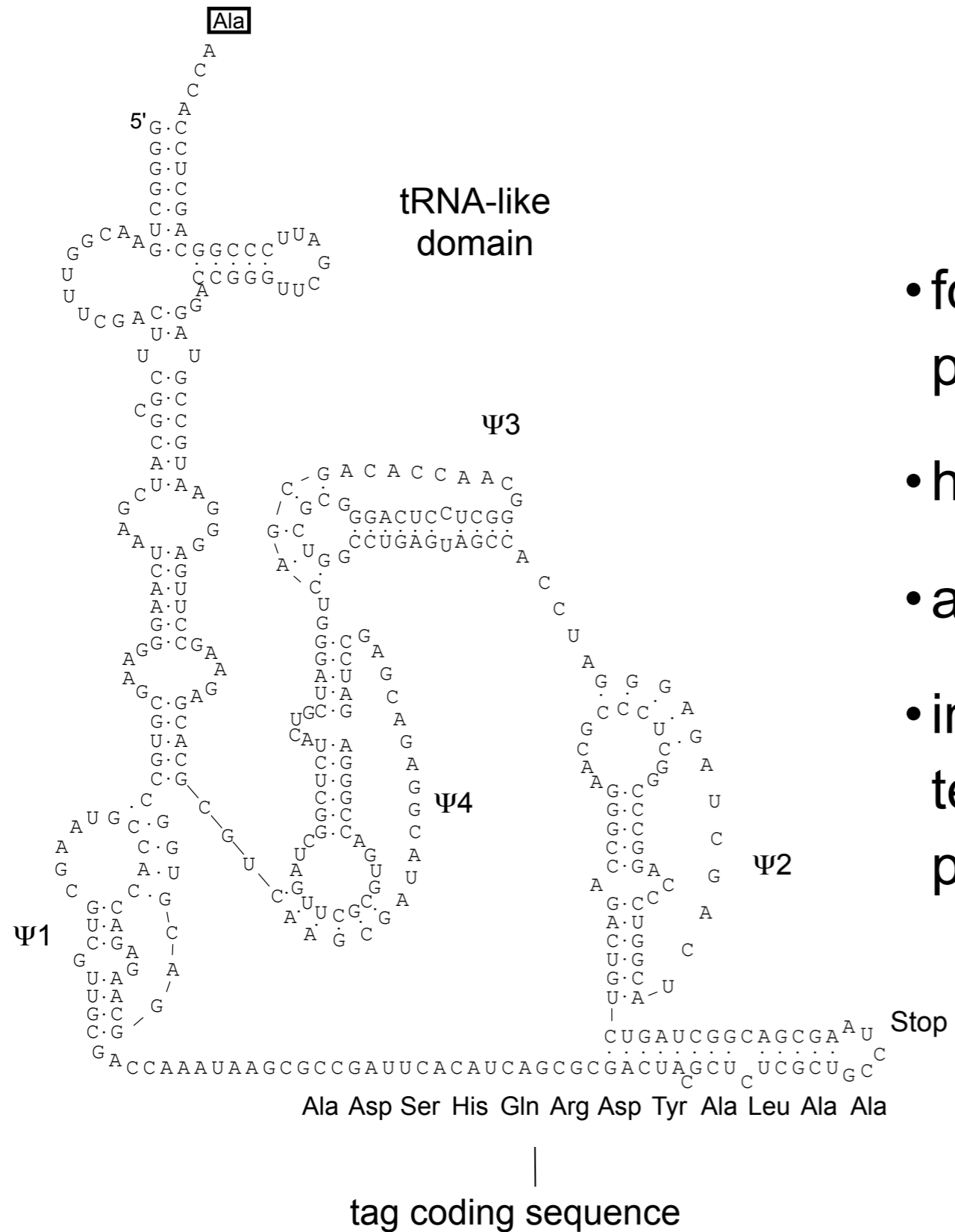


*trans*-translation: SsrA, SmpB,  
EF-Tu, RpsA, and PZA

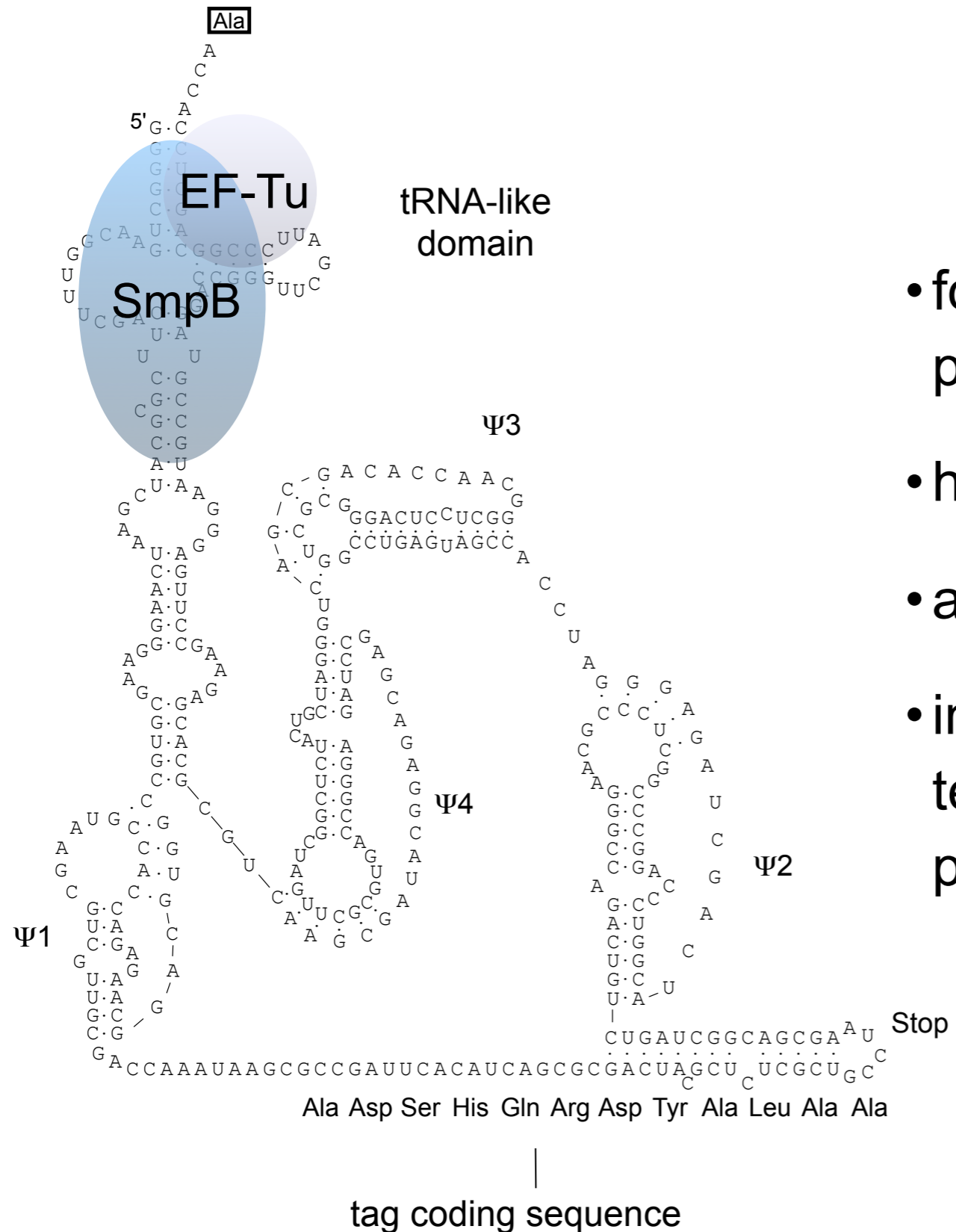
Ken Keiler  
Penn State University

# tmRNA ribonucleoprotein complex



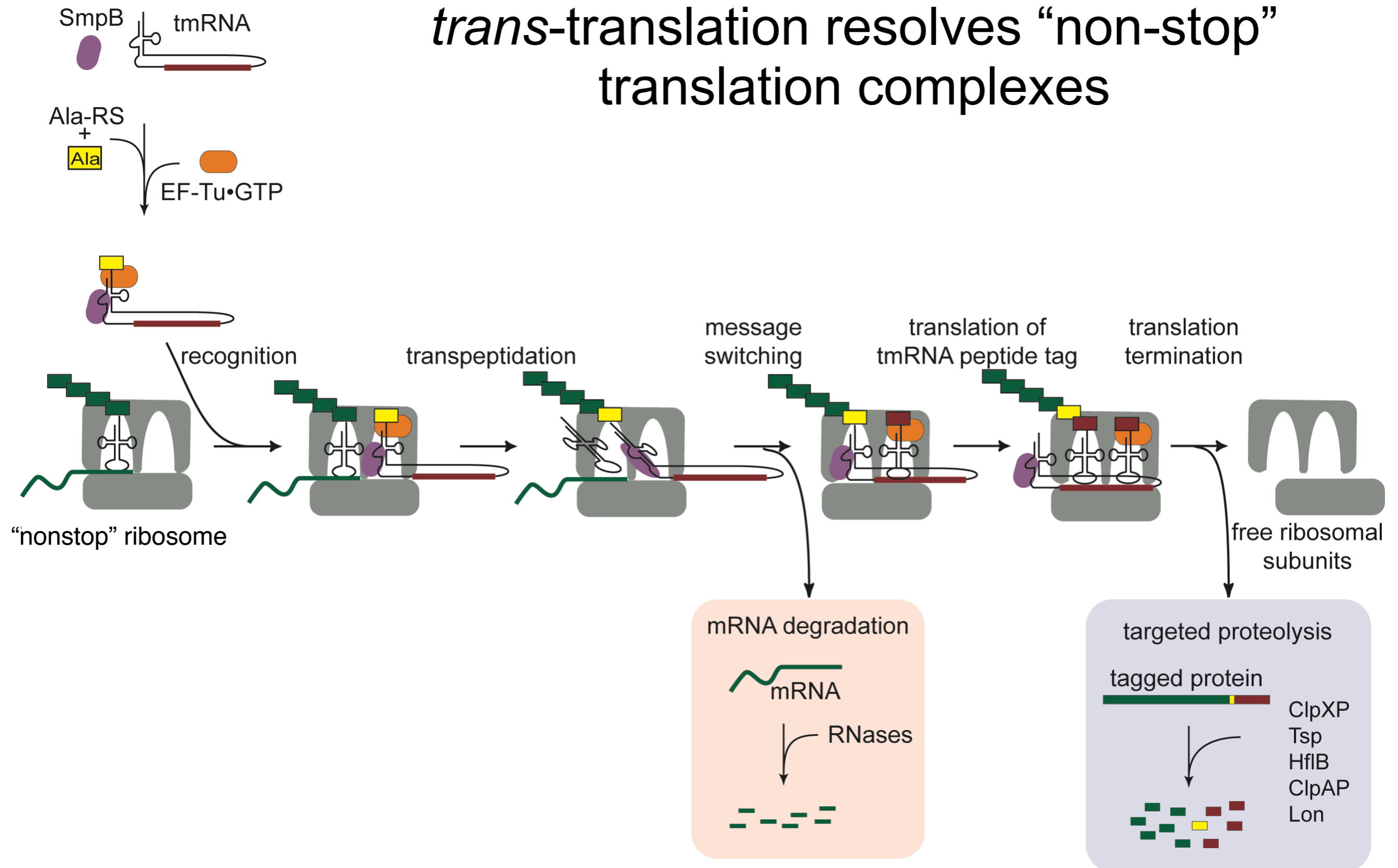
- found in every species of bacteria, some plastids & primitive mitochondria
- highly abundant (~10% rRNA level)
- also called SsrA (Small, stable RNA)
- in *E. coli*, 2-4% of translation initiations terminate by translating tmRNA (5 times per ribosome per cell cycle)

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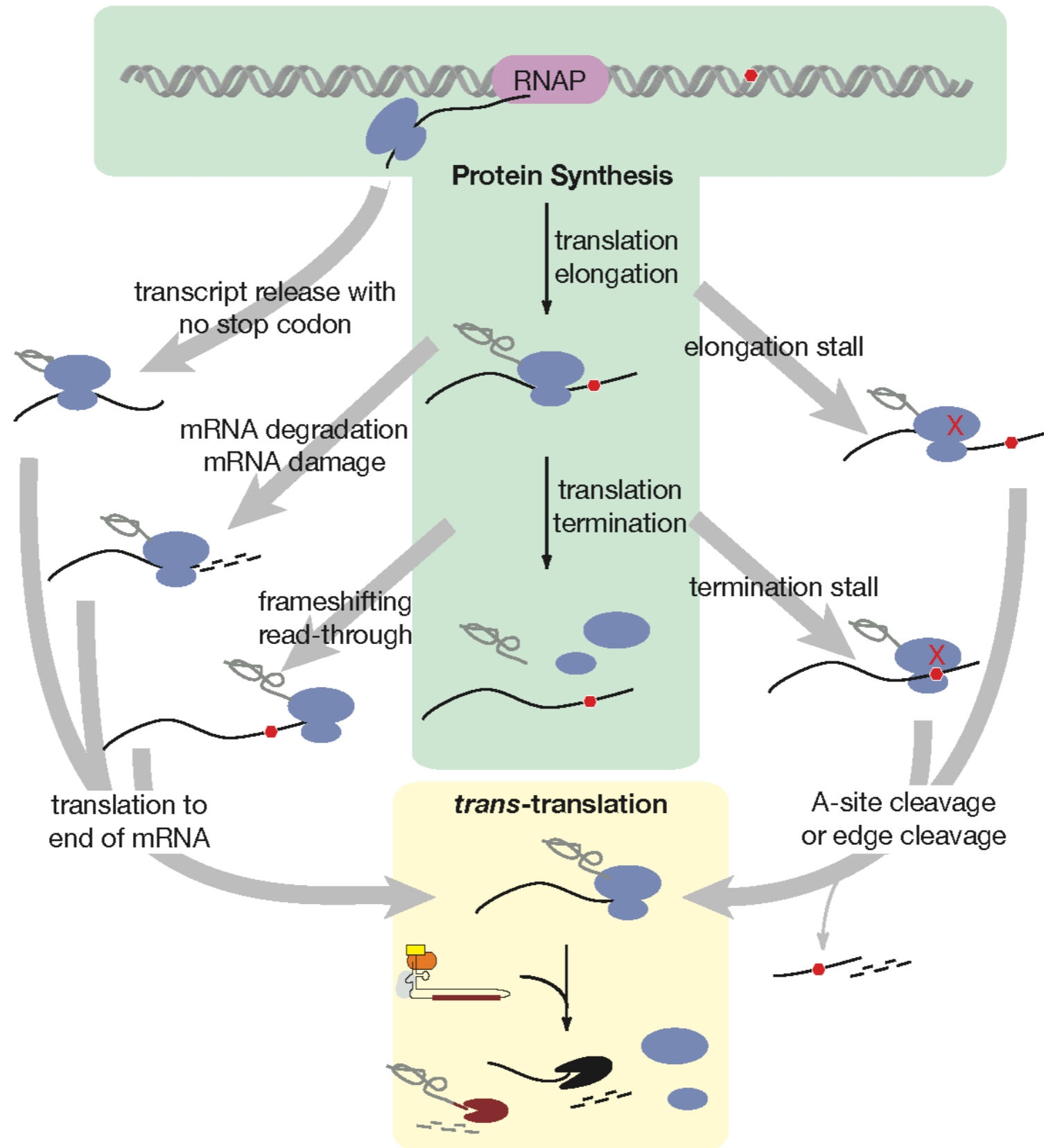


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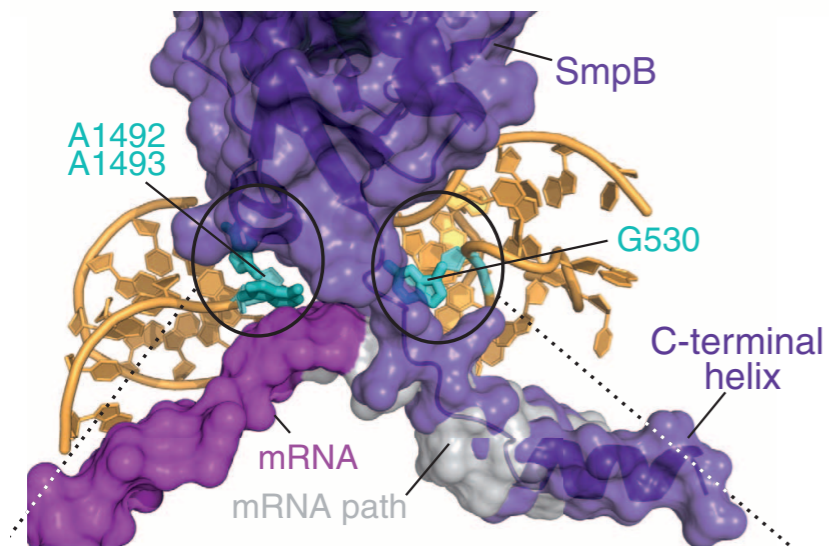
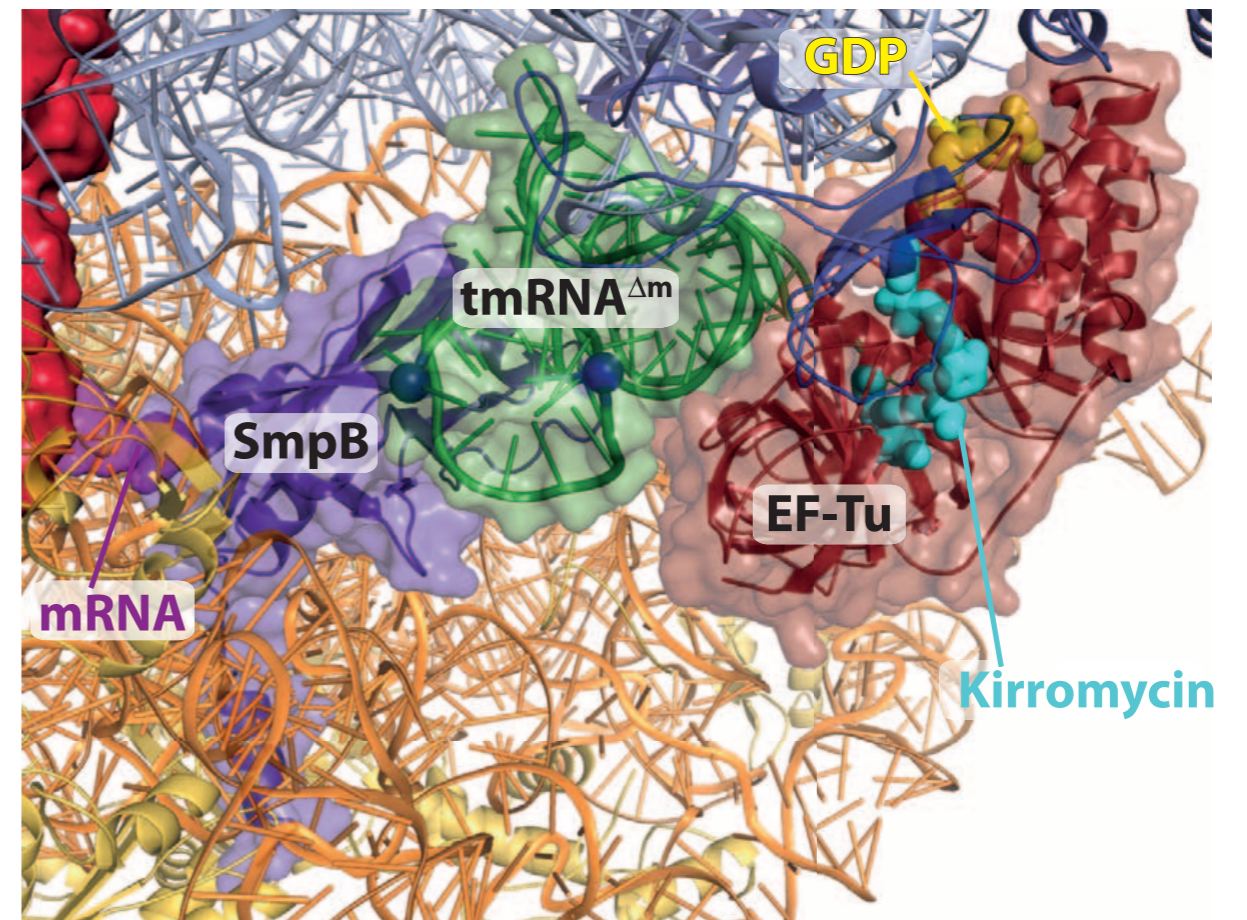
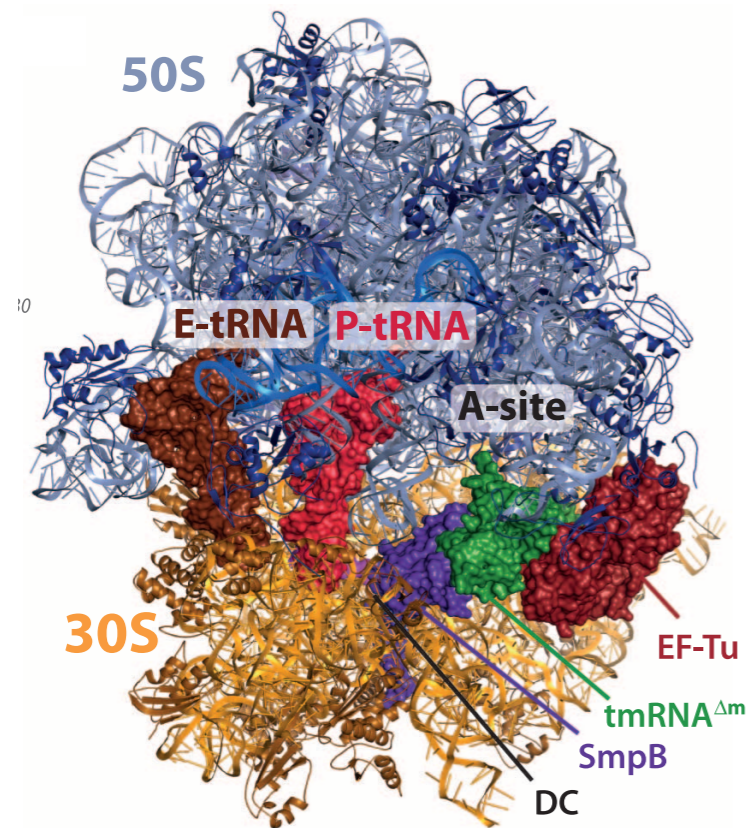
# *trans*-translation resolves “non-stop” translation complexes



# transcription and translation mistakes lead to *trans*-translation



# EF-Tu binds the tRNA-like domain of tmRNA and SmpB mimics the missing mRNA



## Decoding in the Absence of a Codon by tmRNA and SmpB in the Ribosome

Cajetan Neubauer, *et al.*  
*Science* **335**, 1366 (2012);  
DOI: 10.1126/science.1217039

# the RpsA (S1) enigma

- RpsA from *E. coli* and *Thermus thermophilus* binds tmRNA, but not as well as mRNA
- RpsA is not required for *trans*-translation in vitro using *E. coli* or *T. thermophilus* components
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Could PZA act through RpsA and *trans*-translation in MTB?

- RpsA could be important for *trans*-translation in MTB
  - Mycobacterial RpsA has only 4 S1 repeats instead of 6
  - RpsA could be particularly important during latency
- RpsA-POA could inhibit *trans*-translation through a mechanism other than blocking RpsA-tmRNA binding



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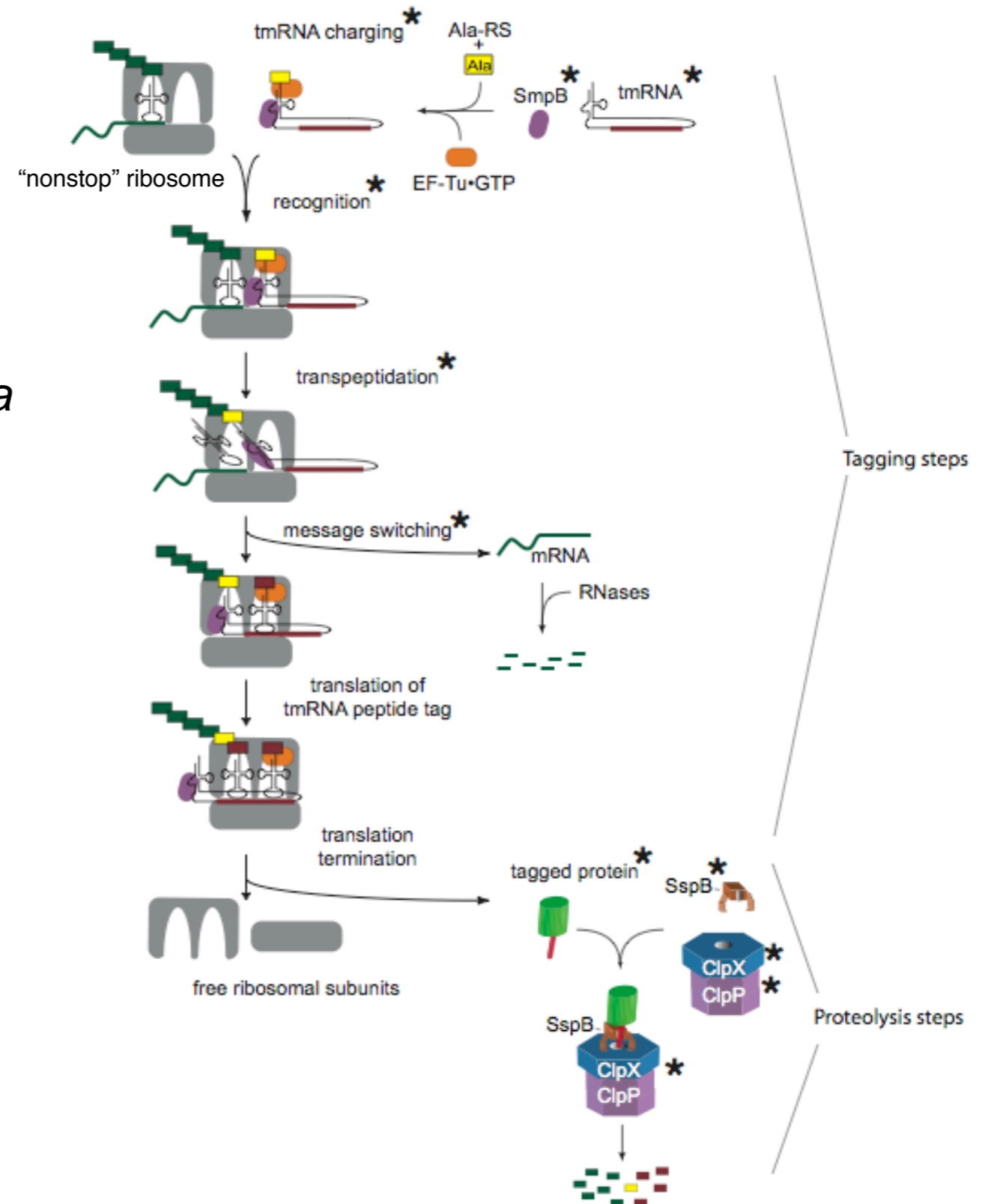
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- need biochemical studies with mycobacterial components

# *trans*-translation is essential in many bacteria

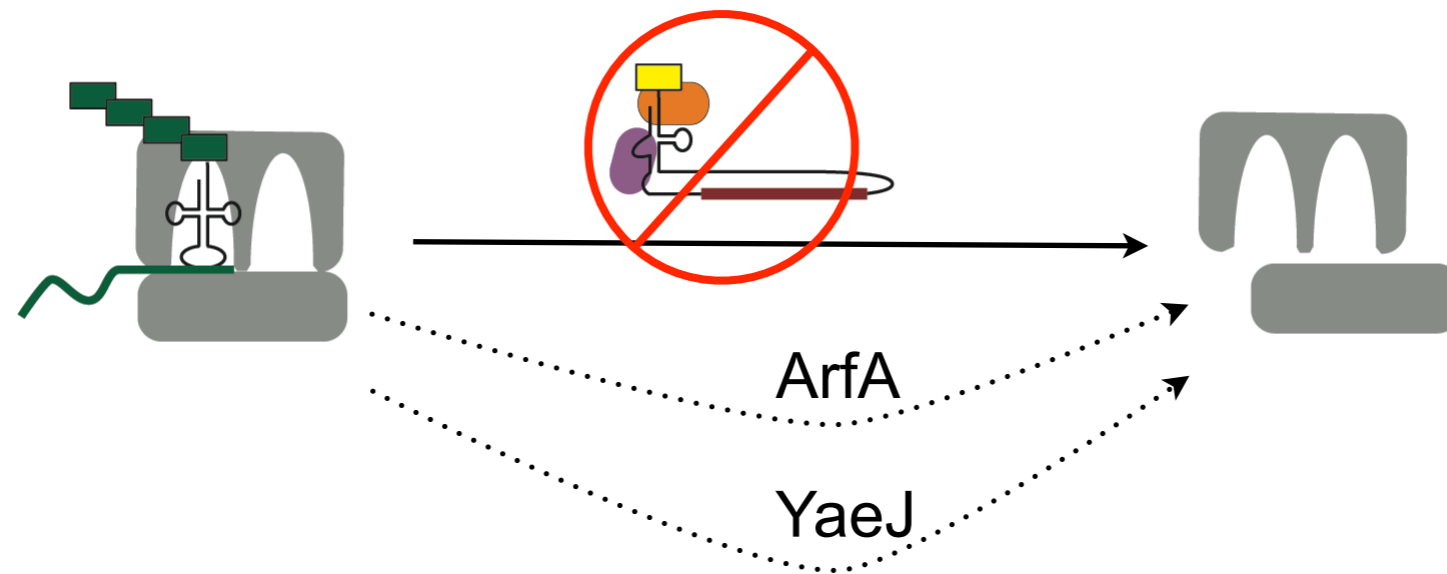
*Neisseria gonorrhoeae*  
*Shigella flexneri*  
*Haemophilus influenzae*  
*Helicobacter pylori*  
*Mycoplasma genitalium* and *M. pneumoniae*  
*Bacillus anthracis*  
*Staphylococcus aureus*  
*Francisella tularensis*

\**Mycobacterium smegmatis*

\**Mycobacterium tuberculosis*



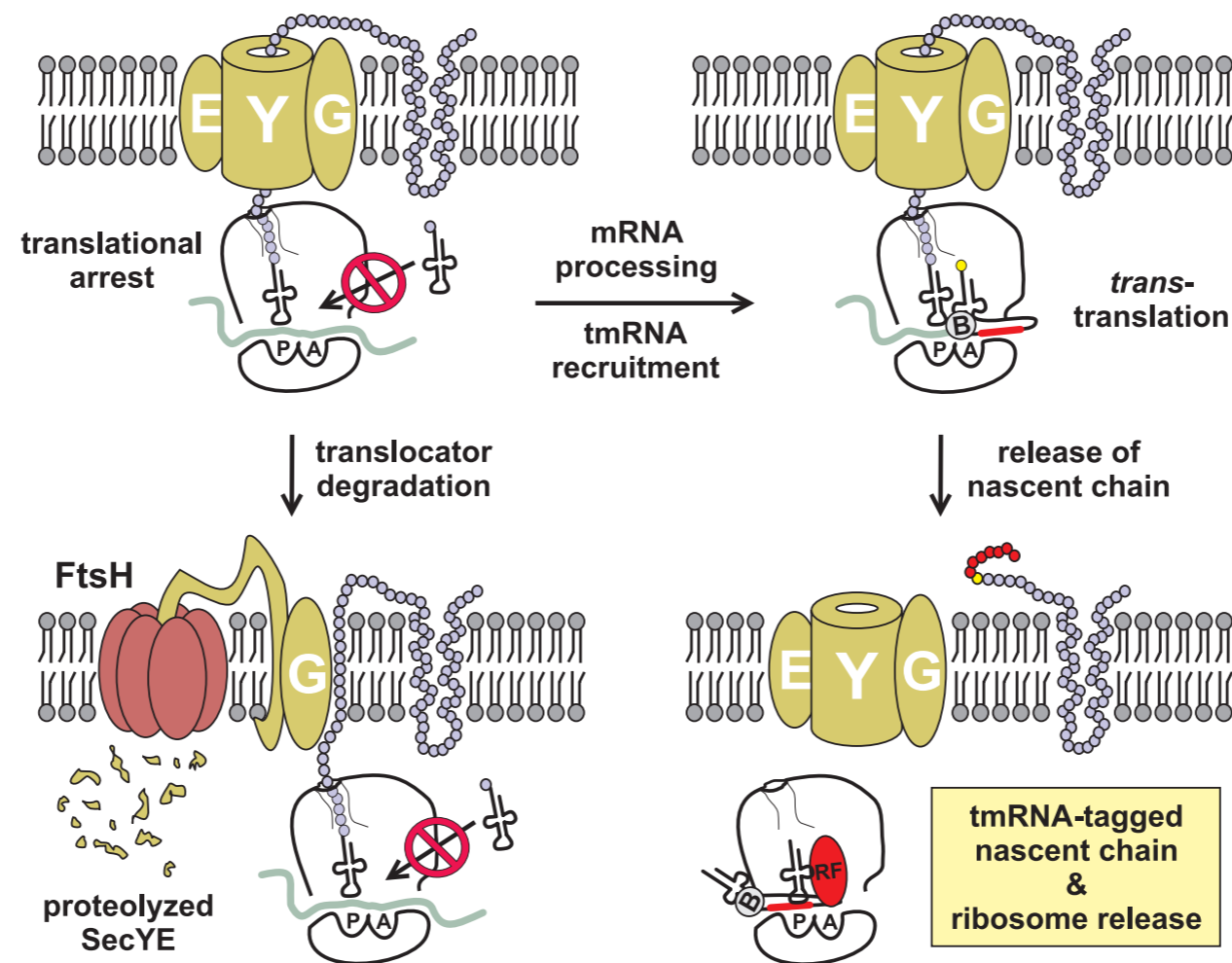
# some species have backup systems for ribosome release



- in all cases studied, deletion of tmRNA and the backup system is lethal
- MTB and *M. smegmatis* do not have obvious homologs of ArfA or YaeJ

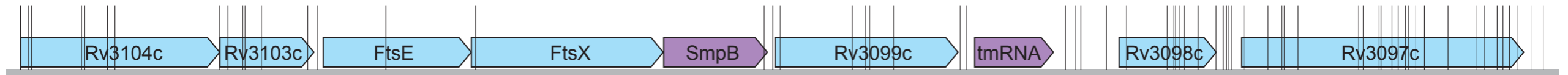
# Why is loss of *trans*-translation detrimental?

1. loss of translation capacity
2. accumulation of incomplete proteins
3. particular problems with membrane proteins



# neither *ssrA* nor *smpB* can be deleted in *Mycobacteria*

## 1. no transposon hits from saturating mutagenesis in MTB



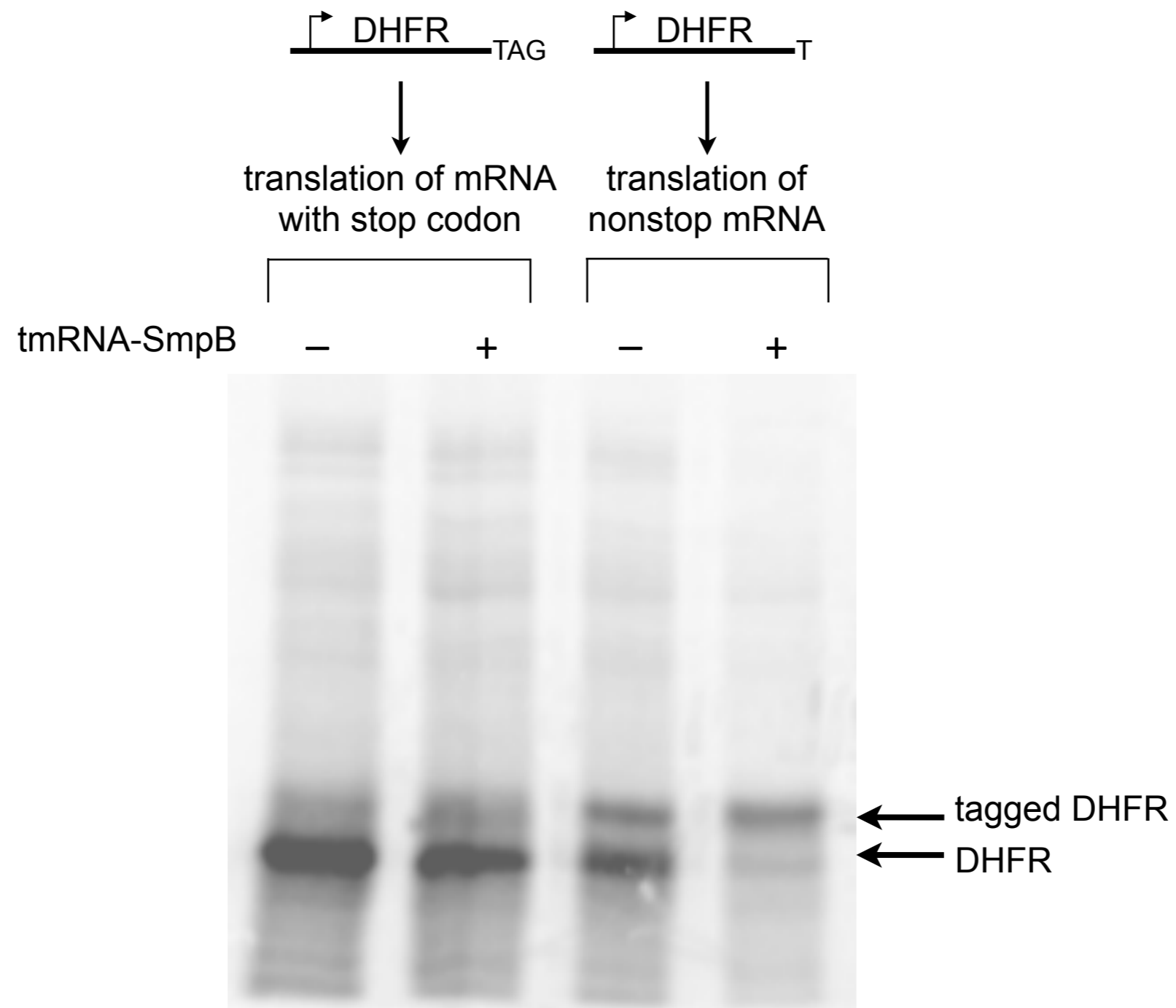
data from Griffin, et al. (2011) *PLOS Path.*

## 2. targeted genetic deletions cannot be isolated in MTB or *M. smegmatis*

- depletion strains are under construction

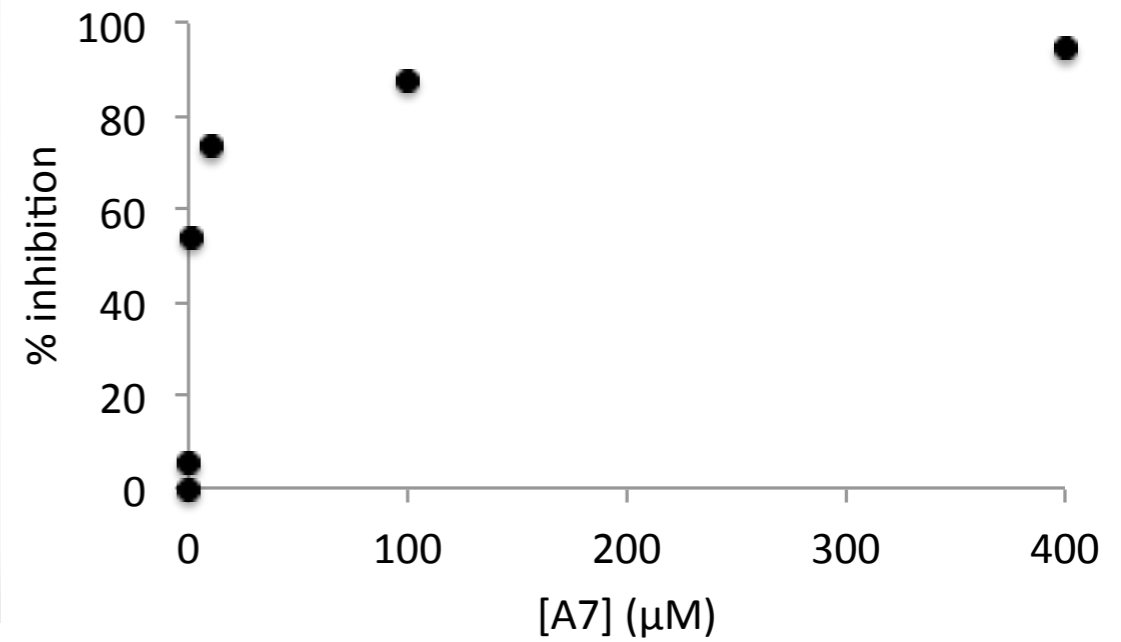
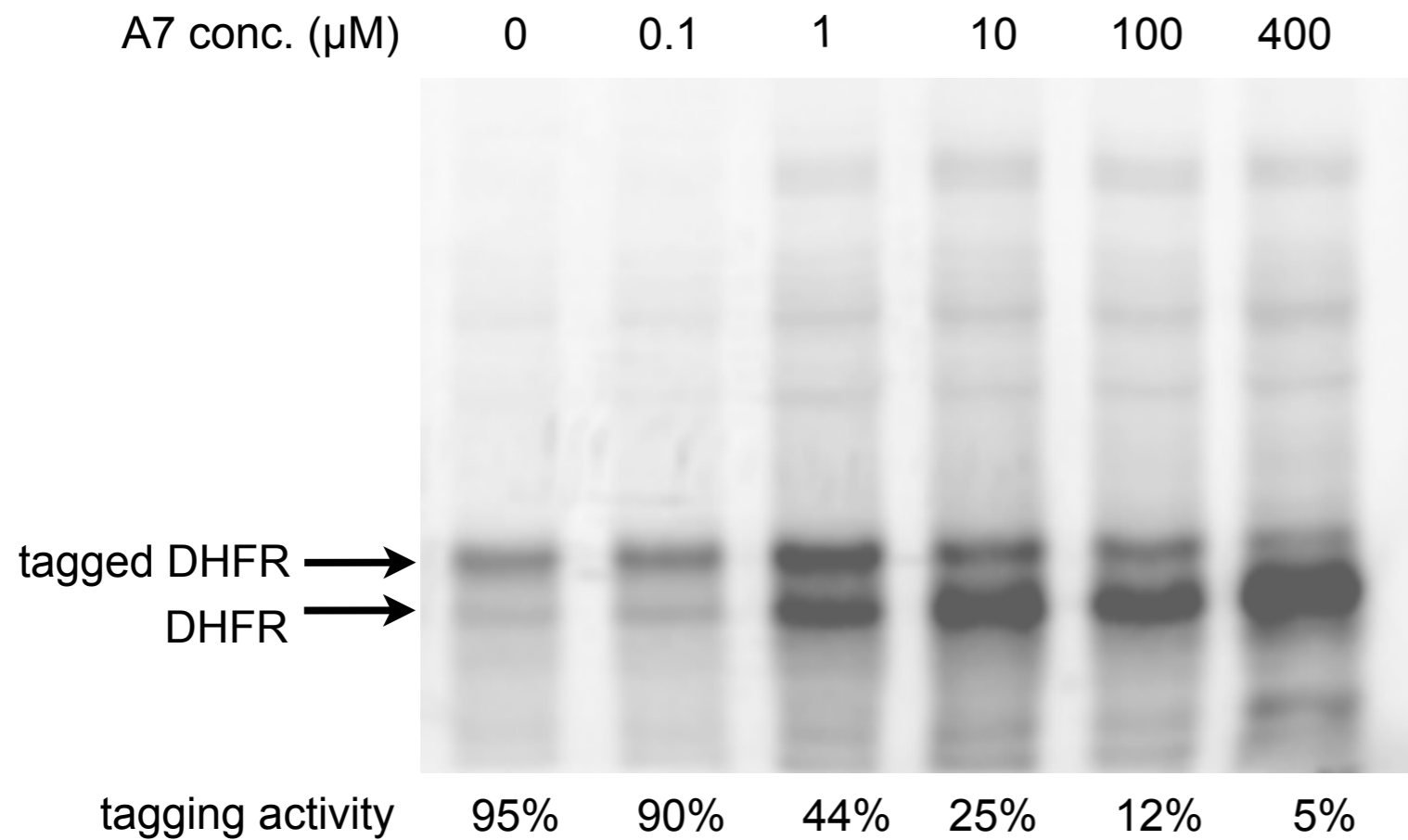
## 3. small molecule inhibitors of *trans*-translation kill MTB and *M. smegmatis*

# in vitro *trans*-translation assay with *E. coli* extracts

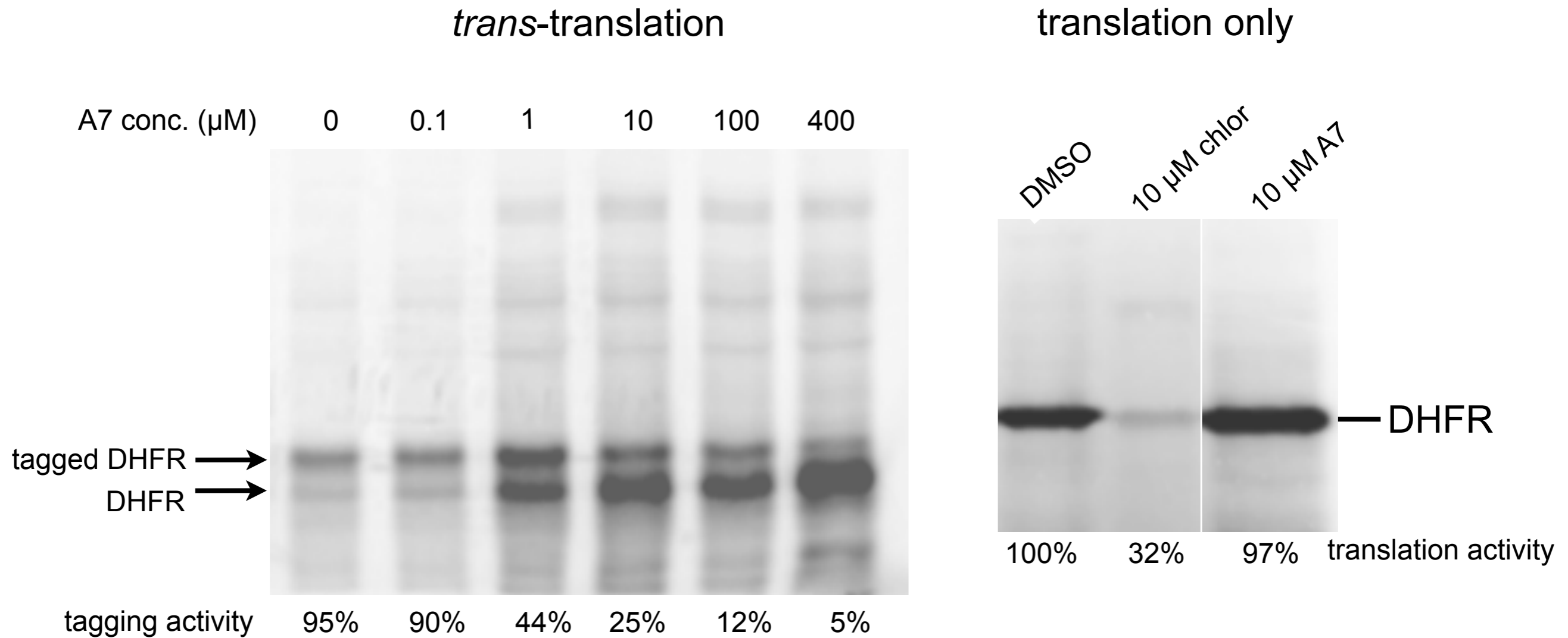


# A7 specifically inhibits *trans*-translation in vitro

## *trans*-translation

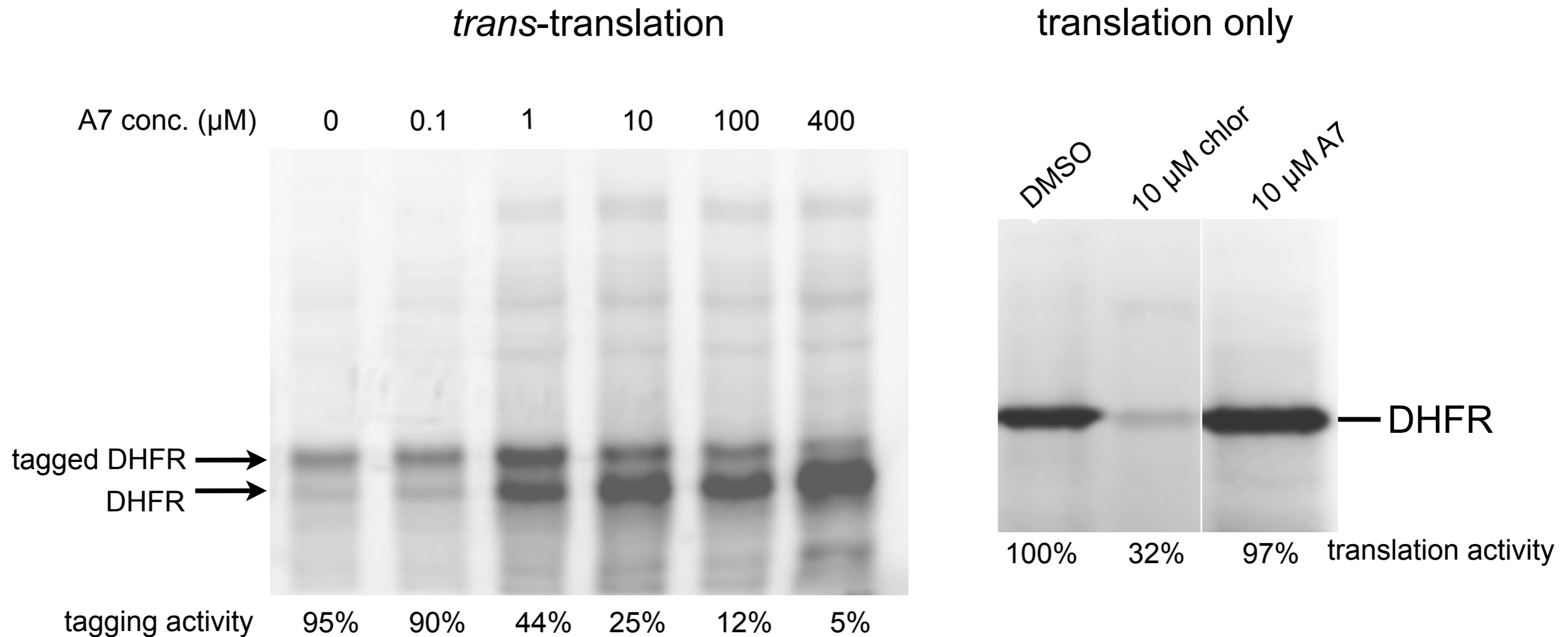


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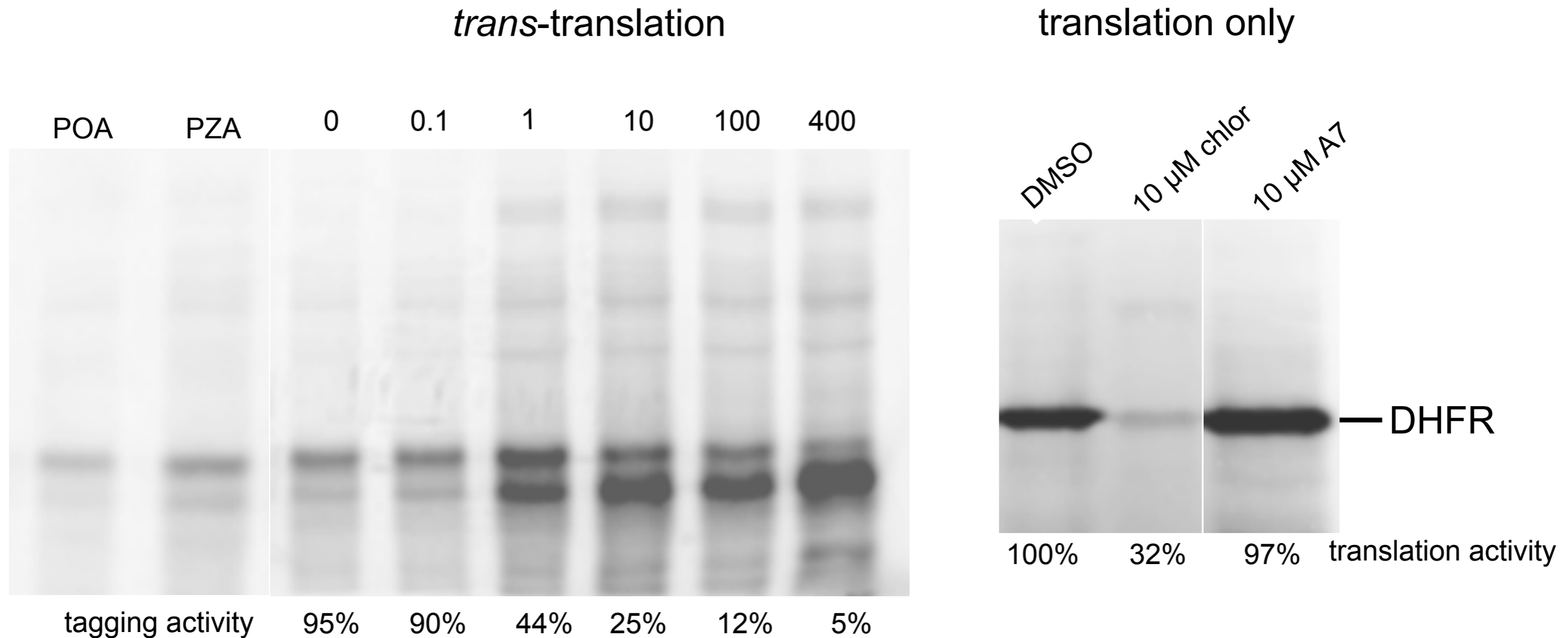
MIC of A7 against *M. tuberculosis H37Rv* = 12 μM (4 mg/ml)

*M. smegmatis* = 1.5 μM

*B. anthracis* = 25 μM

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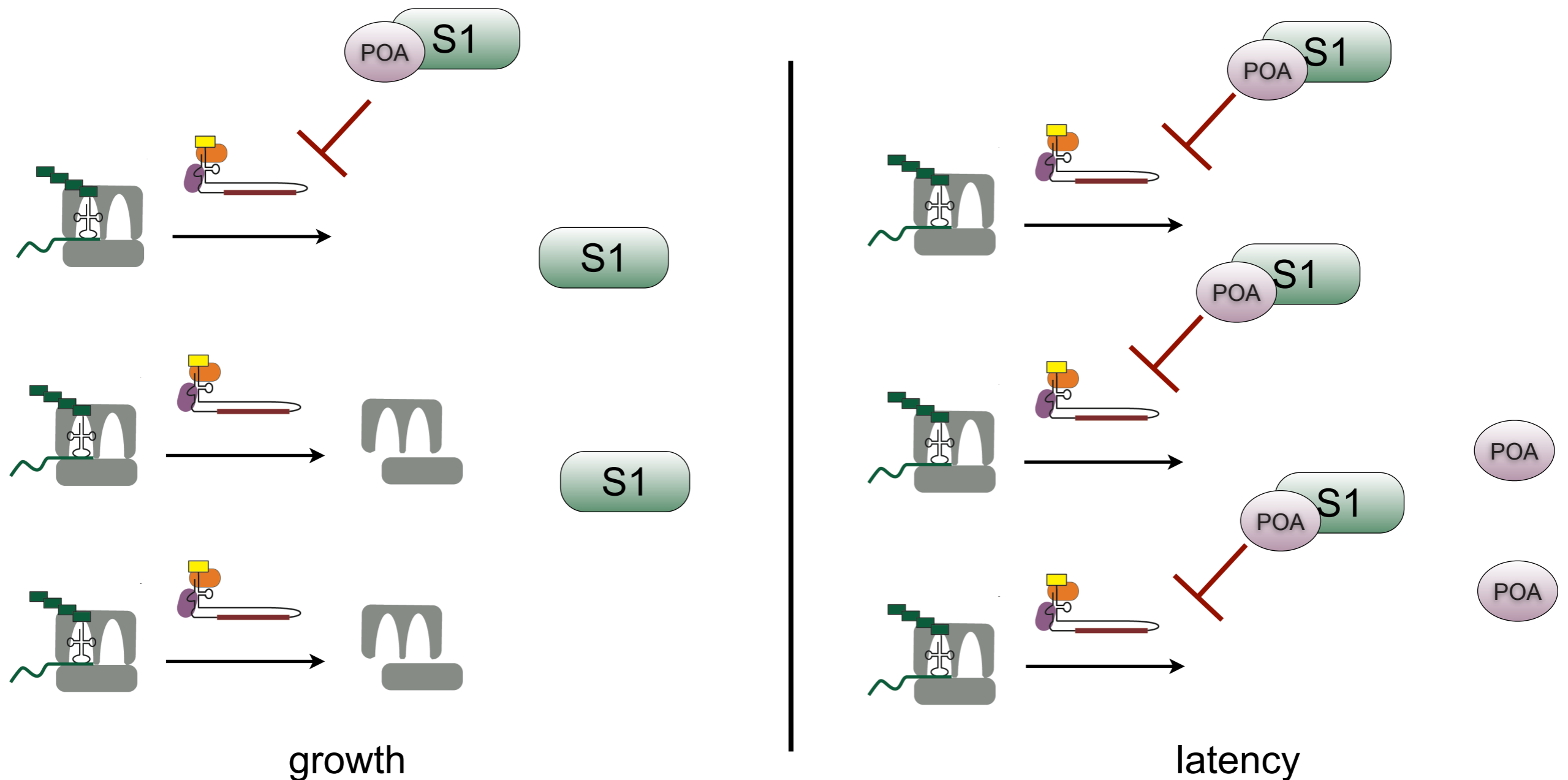
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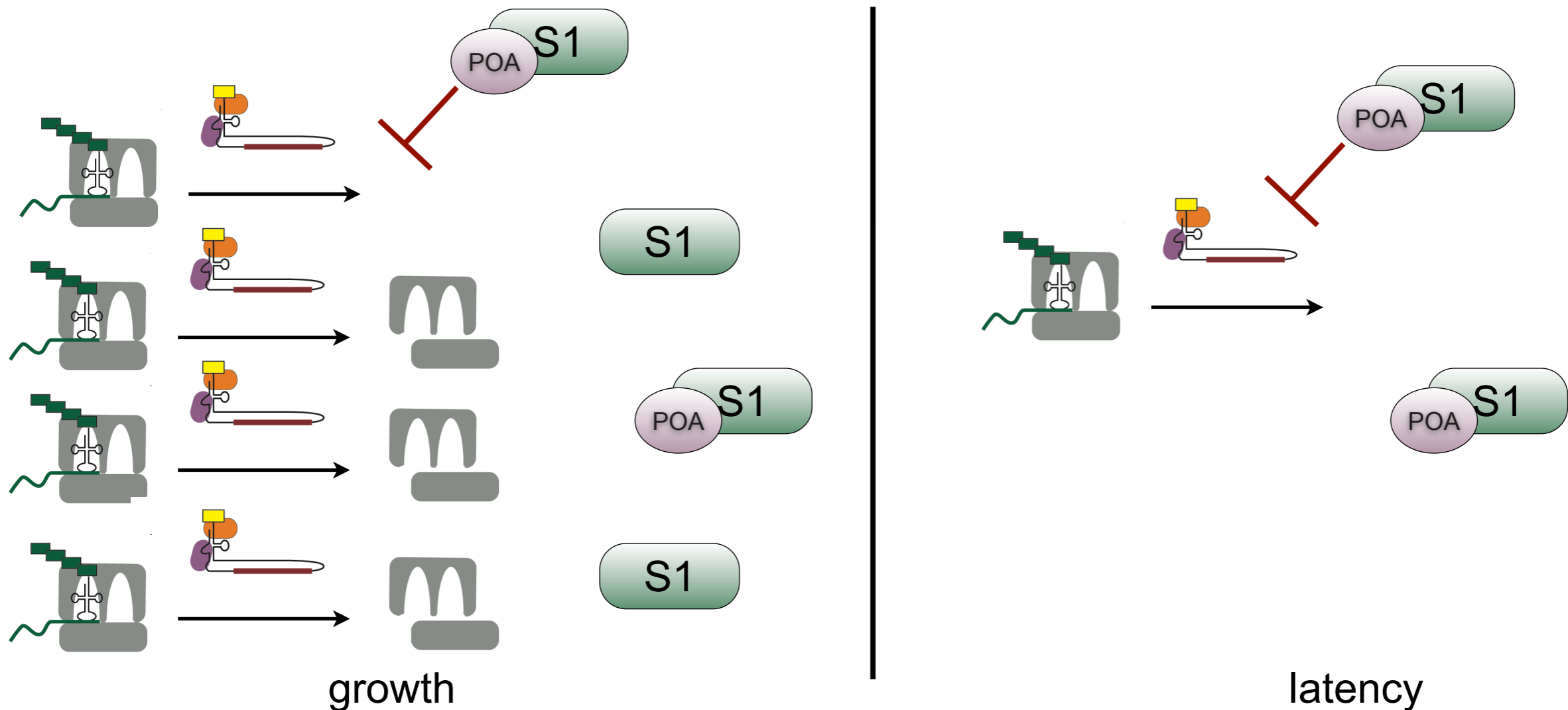
If *trans*-translation is essential and PZA inhibits *trans*-translation through RpsA, why does PZA work so much better on latent cells?

1. metabolism or bioavailability of active form of PZA



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  3. RpsA is required for *trans*-translation only during latency
- if *trans*-translation is the target of PZA, other *trans*-translation inhibitors should be as effective as PZA against latent cells
  - likewise, drugs that act like PZA might inhibit *trans*-translation
    - ➔ test in vitro
    - ➔ test in vivo with reporters for *trans*-translation activity

# conclusions and suggestions

- loss of *trans*-translation in MTB is either lethal or has a major growth defect
  - do other *trans*-translation inhibitors act like PZA on latent cells?
  - do molecules that act like PZA inhibit *trans*-translation?
- RpsA is not required for *trans*-translation in other species
  - test the role of RpsA on *trans*-translation in vitro using MTB components
  - test whether RpsA-POA can interfere with *trans*-translation in vitro using MTB components



**Nitya Ramadoss**  
**John Alumasa**  
Lin Cheng

Jeff Cox (UCSF)  
Paolo Manzanillo  
Lynn Connolly  
Trisha Lundrigan

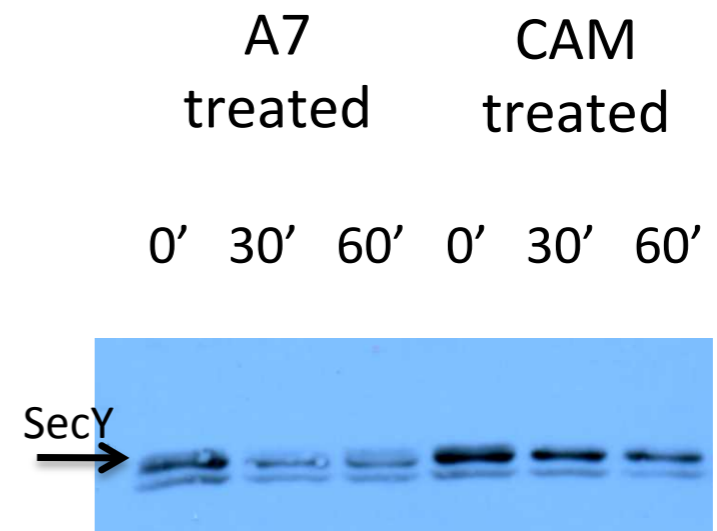
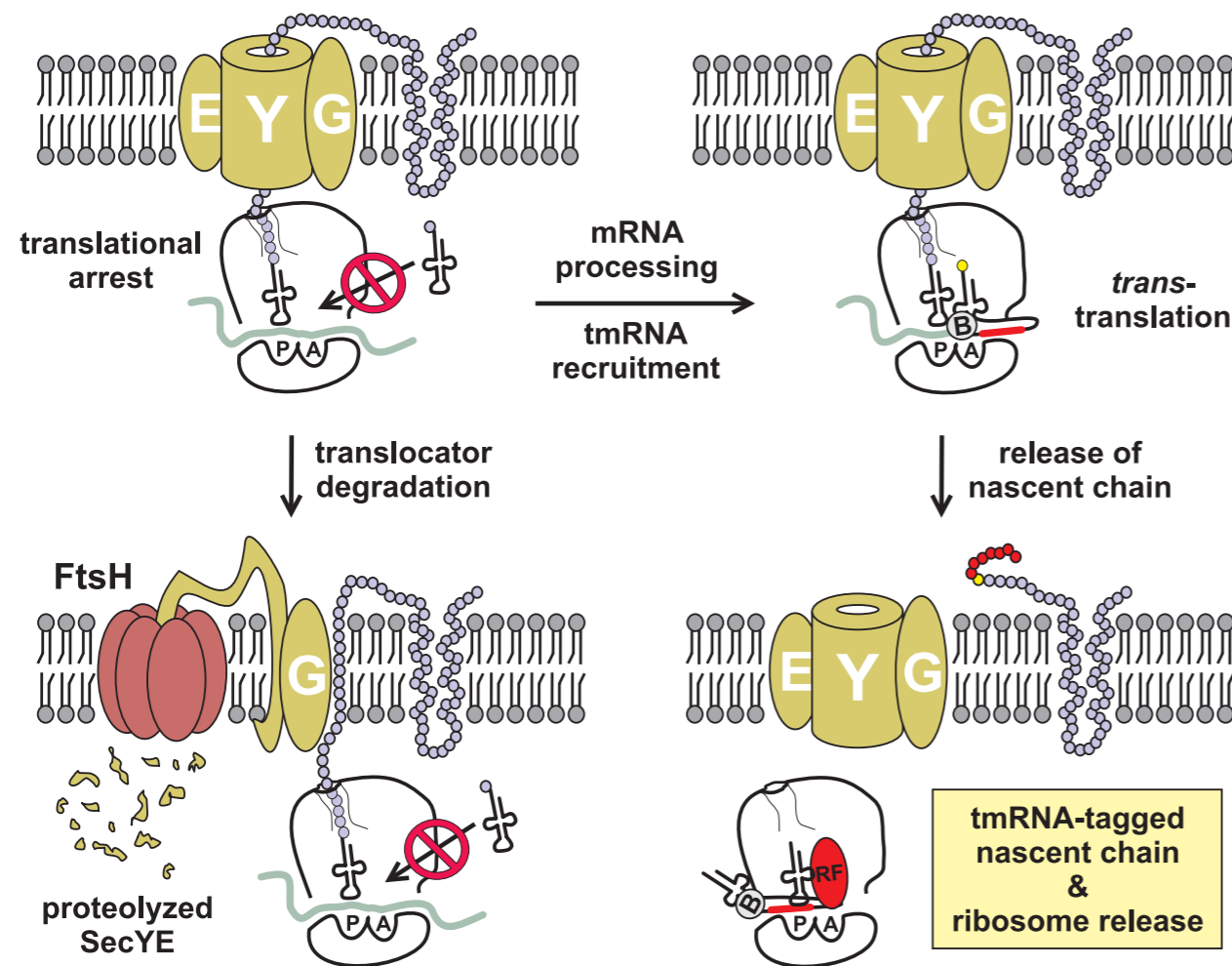
Pete Schultz (GNF)  
Achim Brinker  
Ingo Engels  
Yu Wang

TB Alliance  
Anna Upton  
Takushi Kaneko

NIH/NIGMS

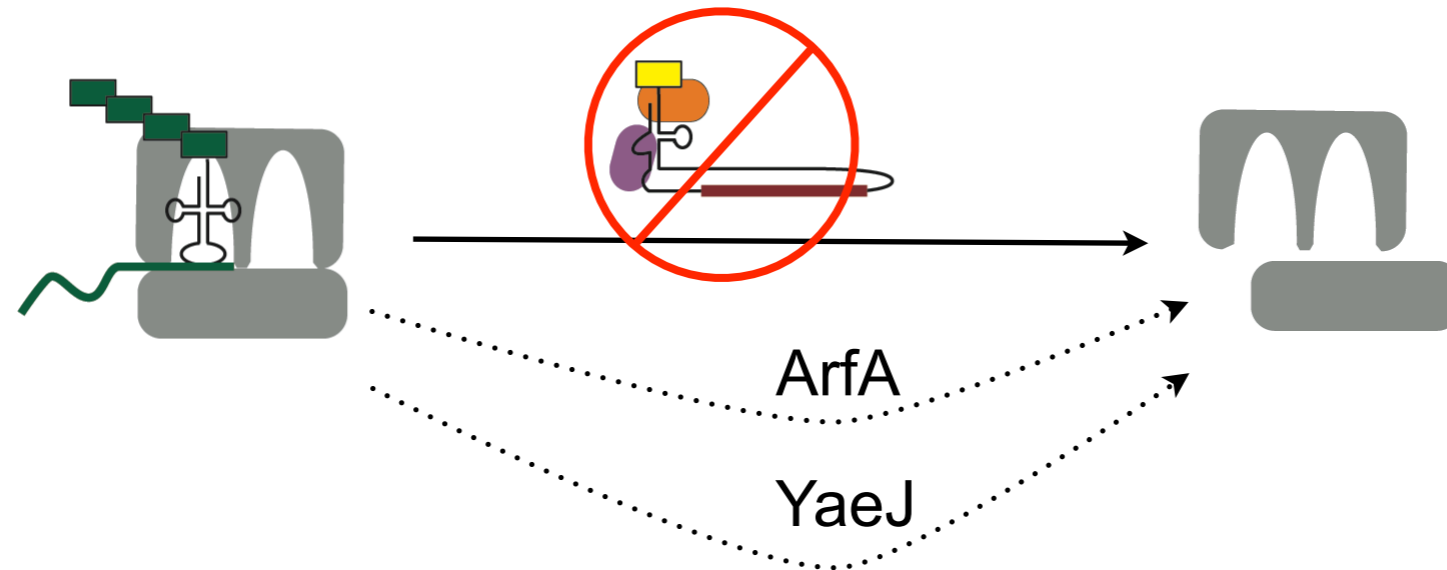


# A7 causes rapid turnover of SecY



Holly Cardoso and Tom Silhavy

when there is a backup system, inactivation of *trans*-translation typically causes defects in resuming proliferation



Proliferation after stationary phase and stasis induced by T/A system toxins: ***E. coli***

Proliferation after macrophage invasion: ***Yersinia pestis*, *Y. pseudotuberculosis*  
*Salmonella enterica*, *S. typhimurium***

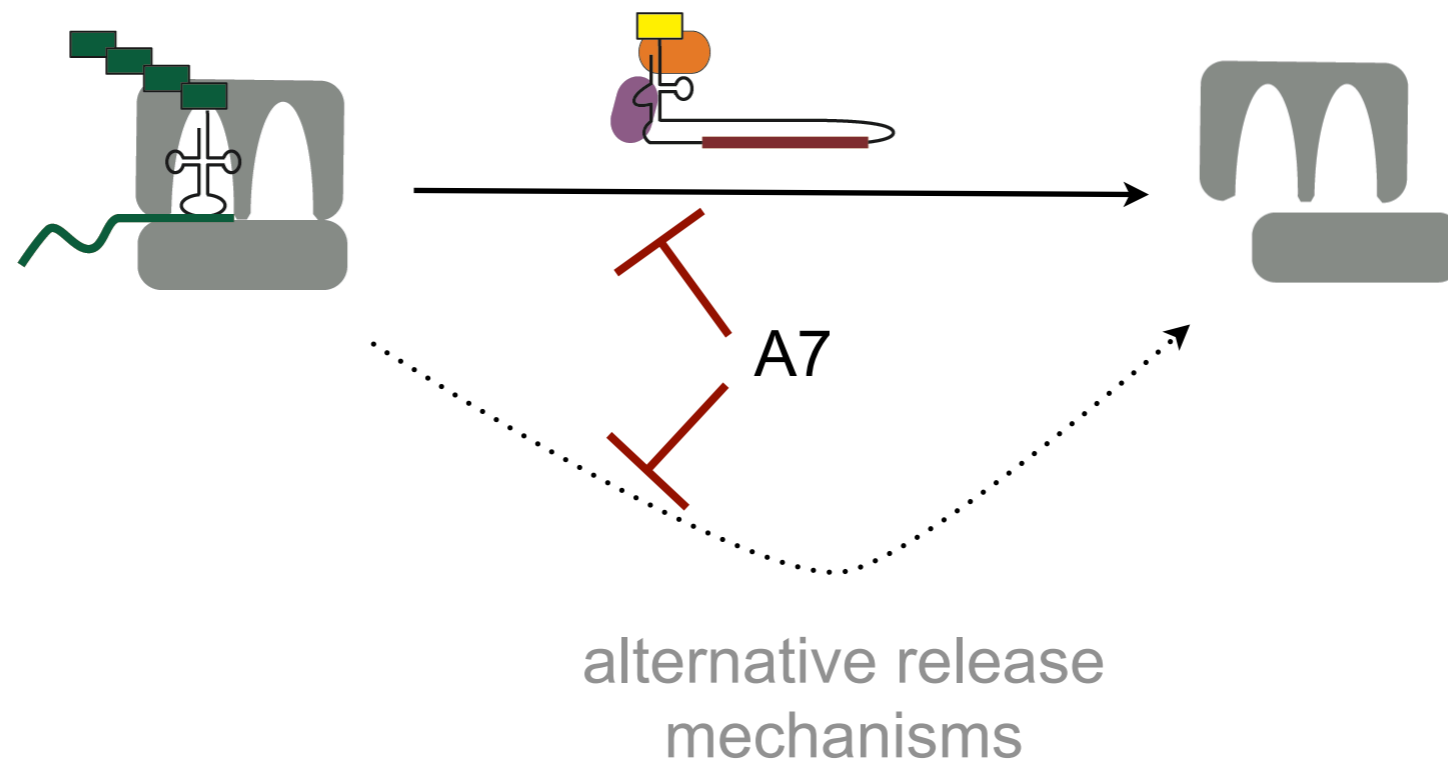
Proliferation after root cell invasion: ***Bradyrhizobium japonicum***

Proliferation after dispersal state: ***Caulobacter crescentus***

Other general phenotypes: increased sensitivity to oxidative stress and antibiotics

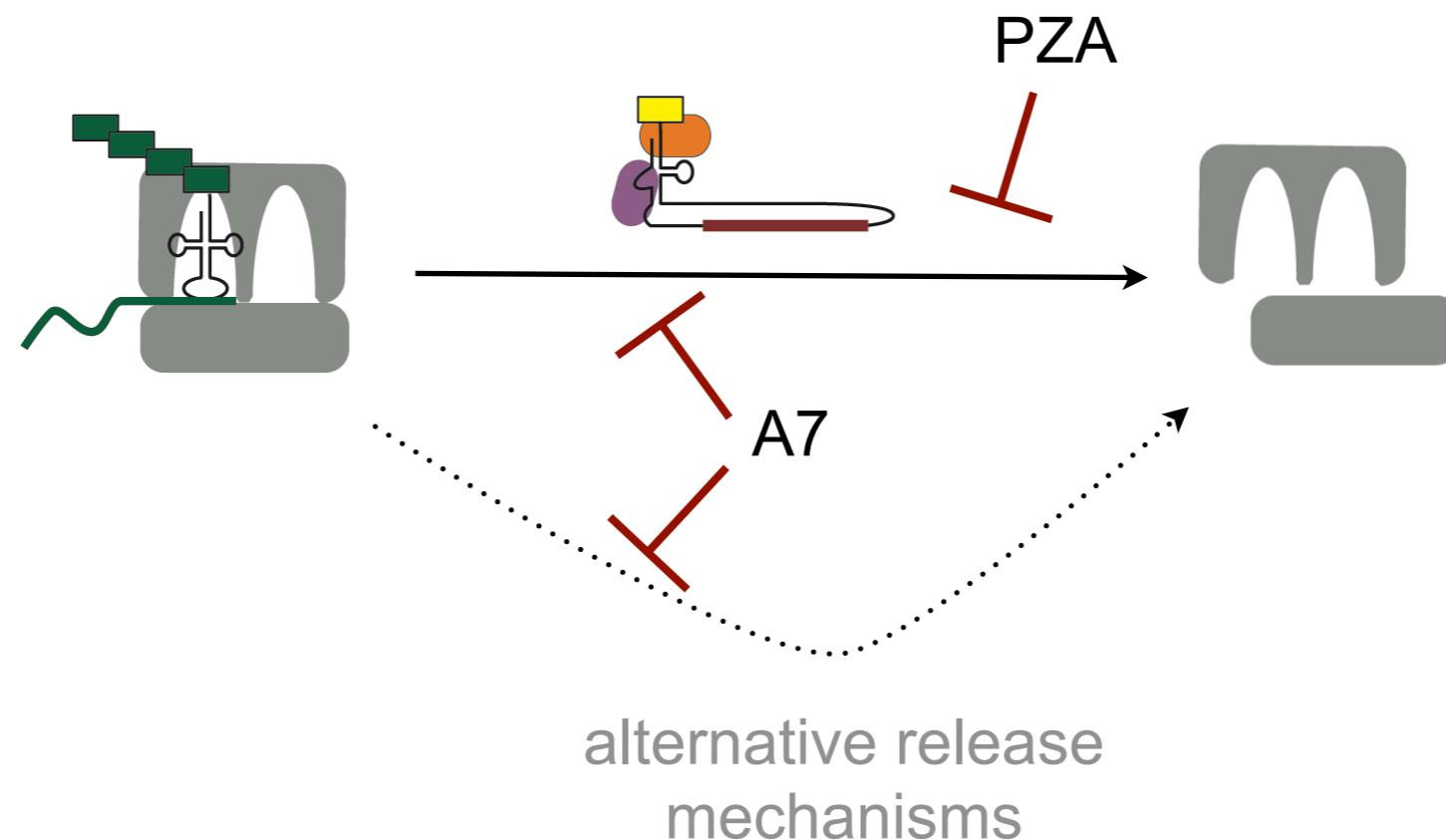
# neither *ssrA* nor *smpB* can be deleted in *Mycobacteria*, but...

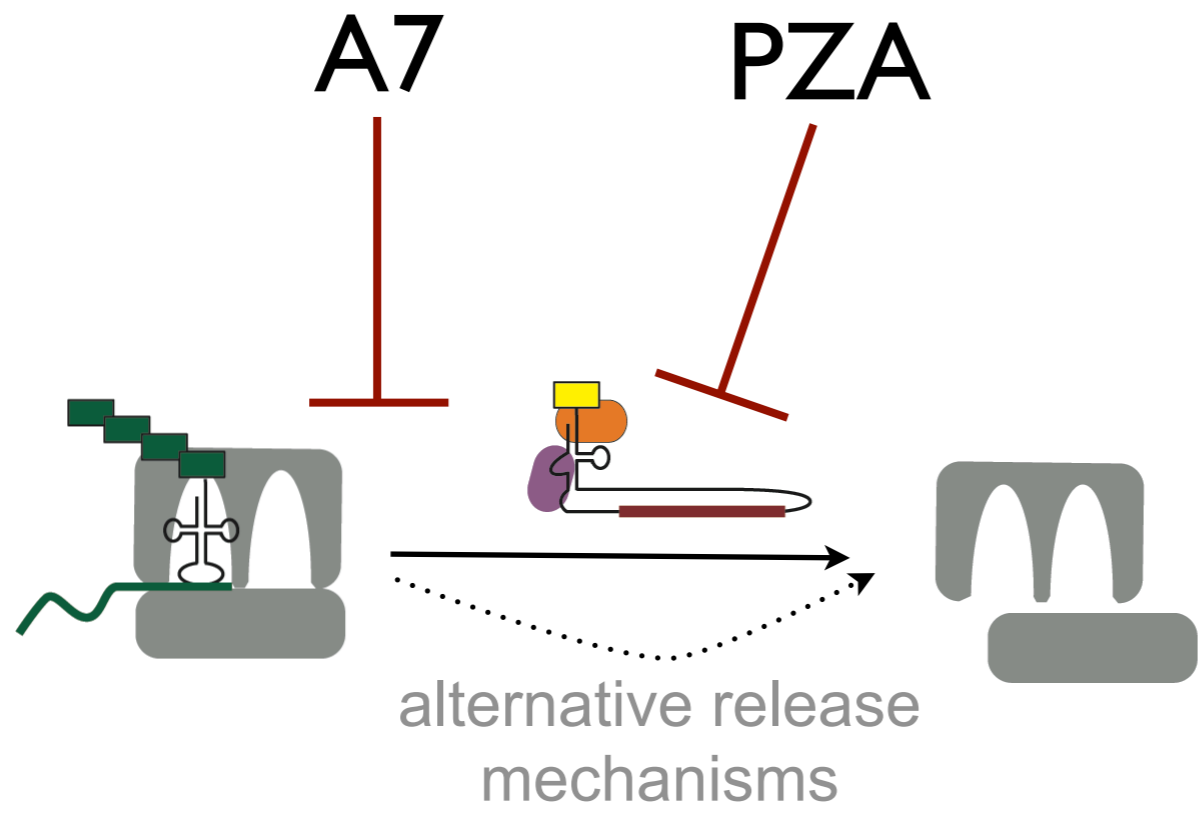
- severe growth defects can prevent recovery of Tn insertion mutants and genetic deletions (depletion strains are required to confirm)
- A7 acts upstream of alternative release mechanisms

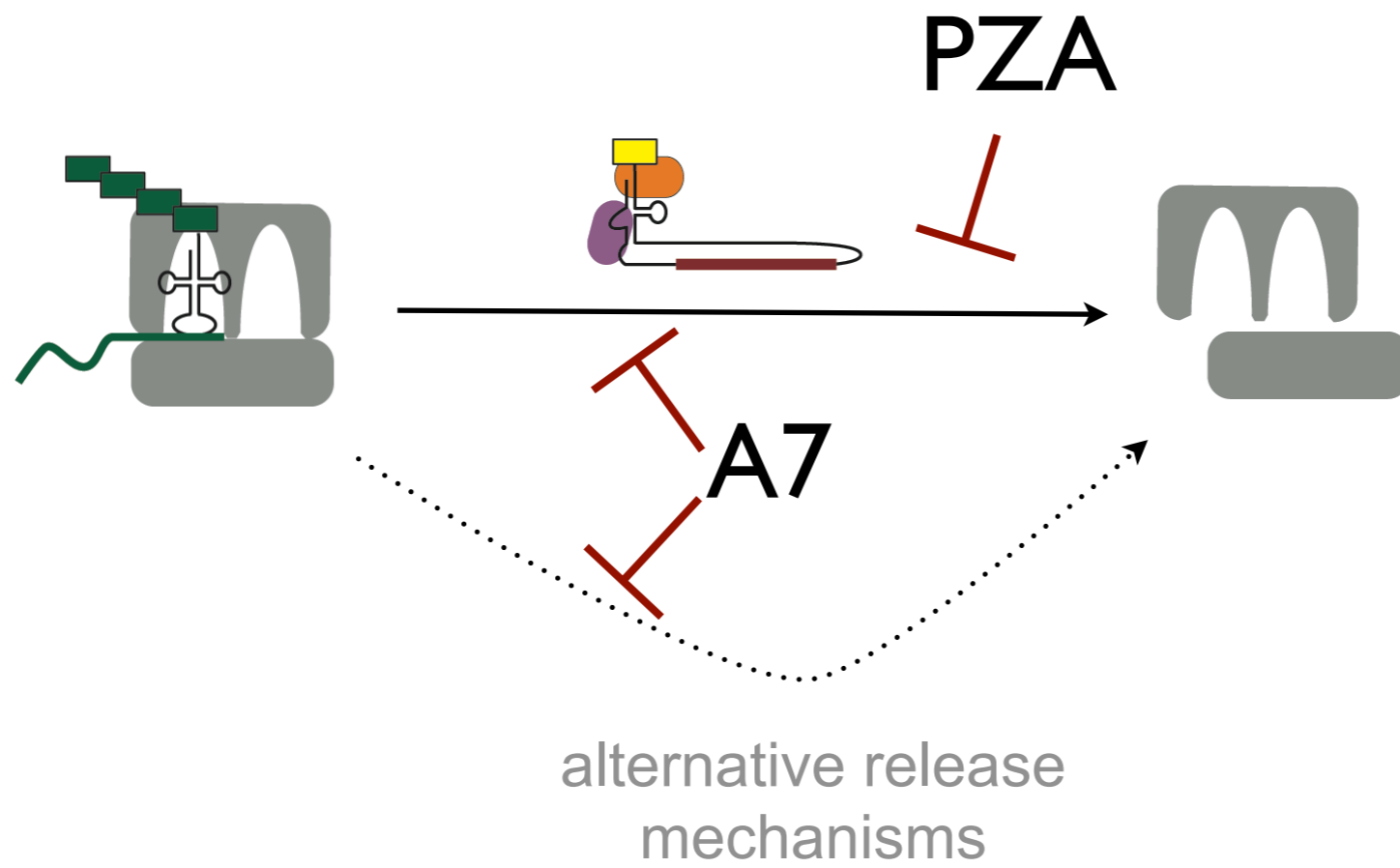


# conclusions and speculations

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- ➔ If MTB has a backup system for *trans*-translation, PZA may still act through *trans*-translation by preventing a return to proliferation.

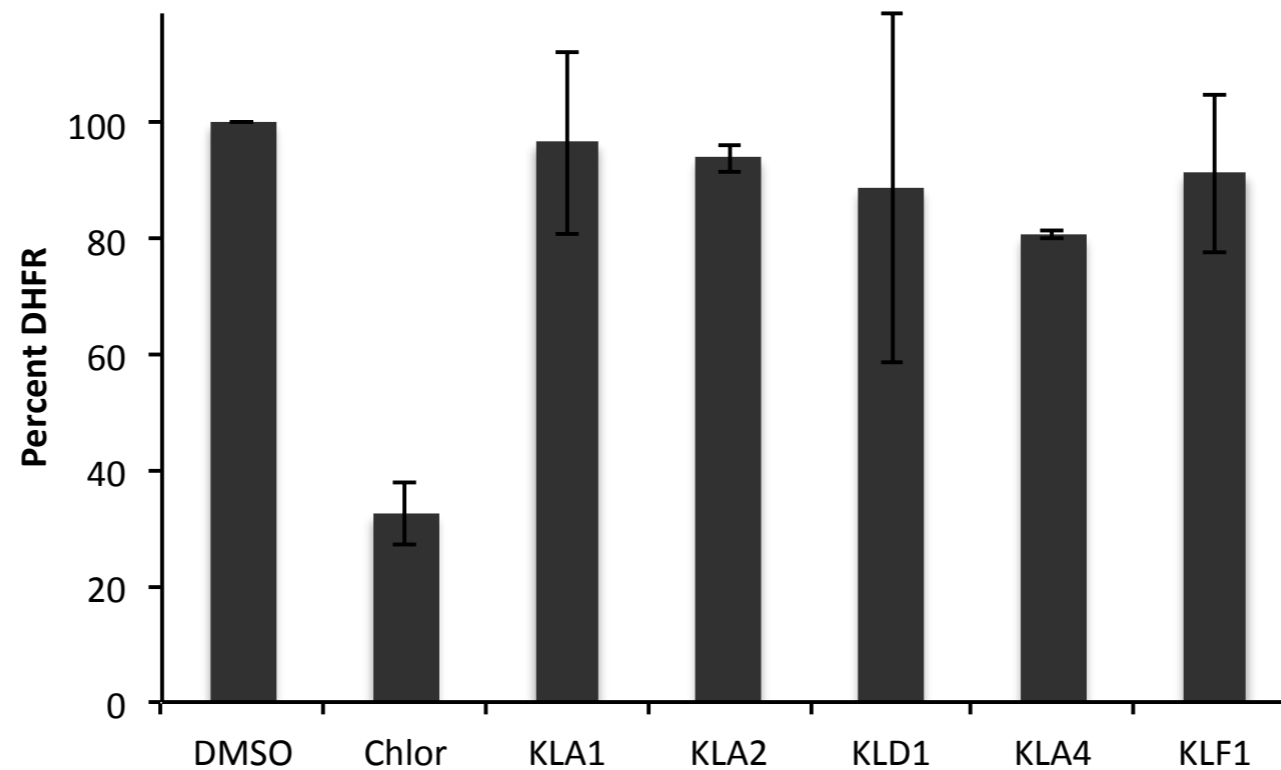
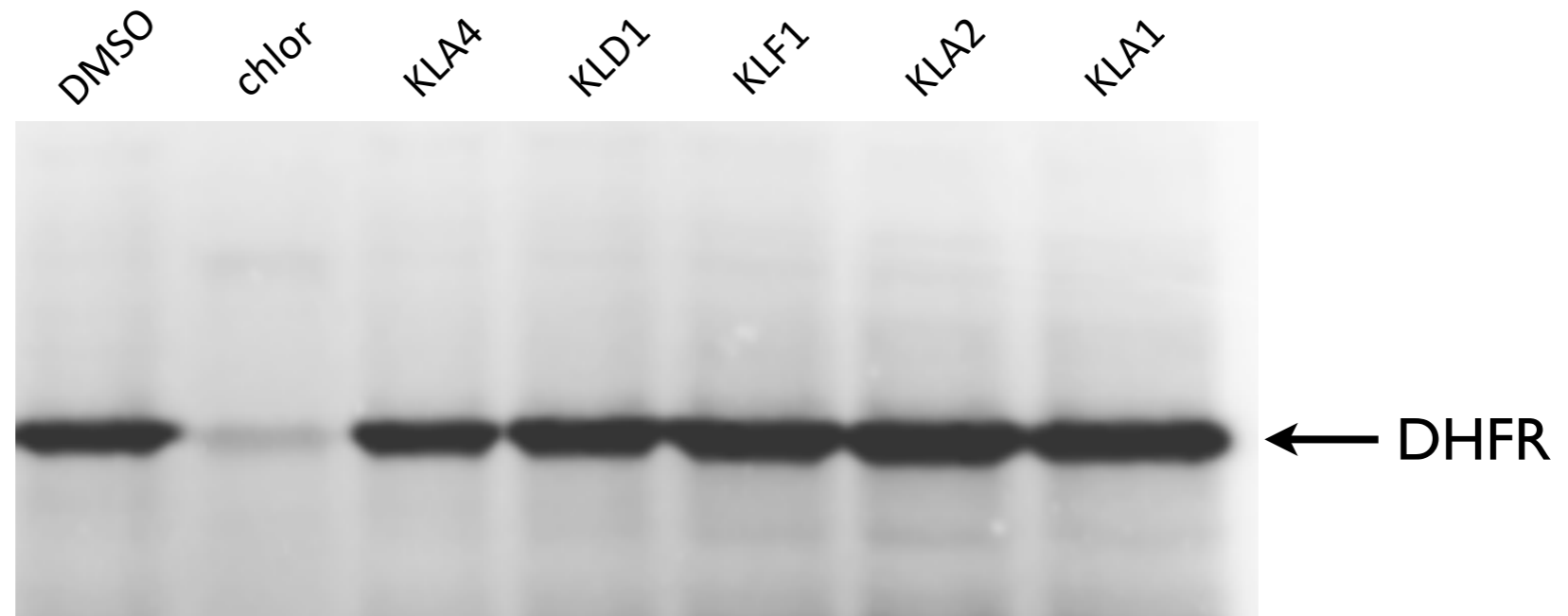




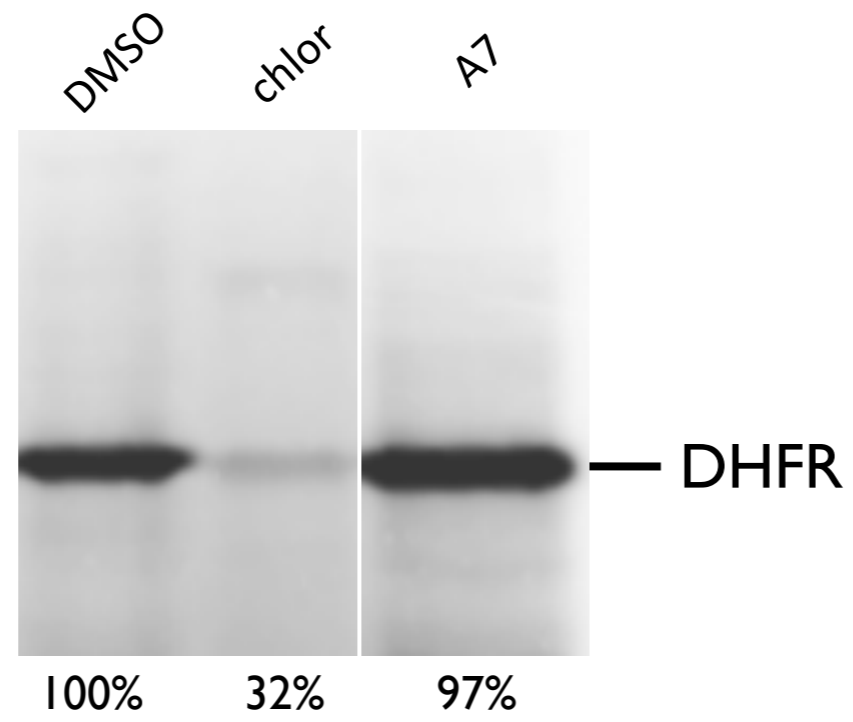


# in vitro translation is not inhibited

representative gel



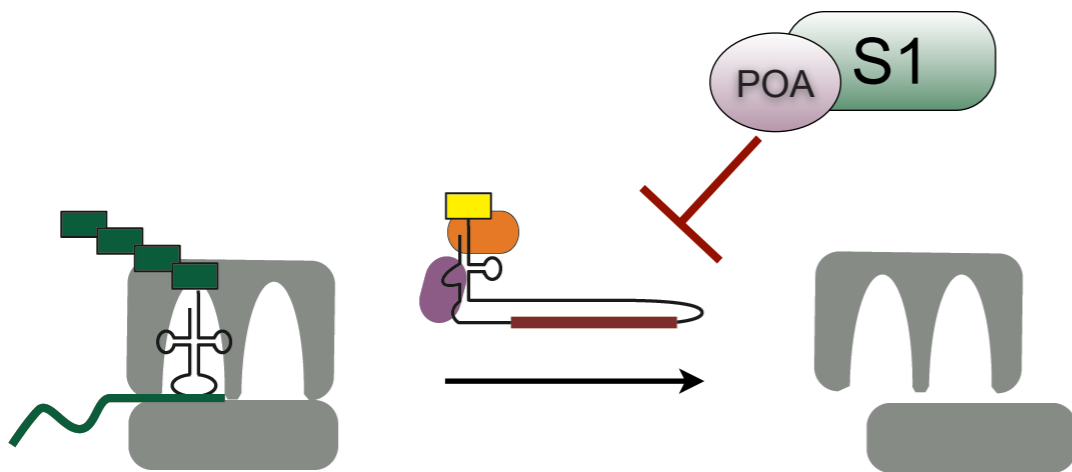
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