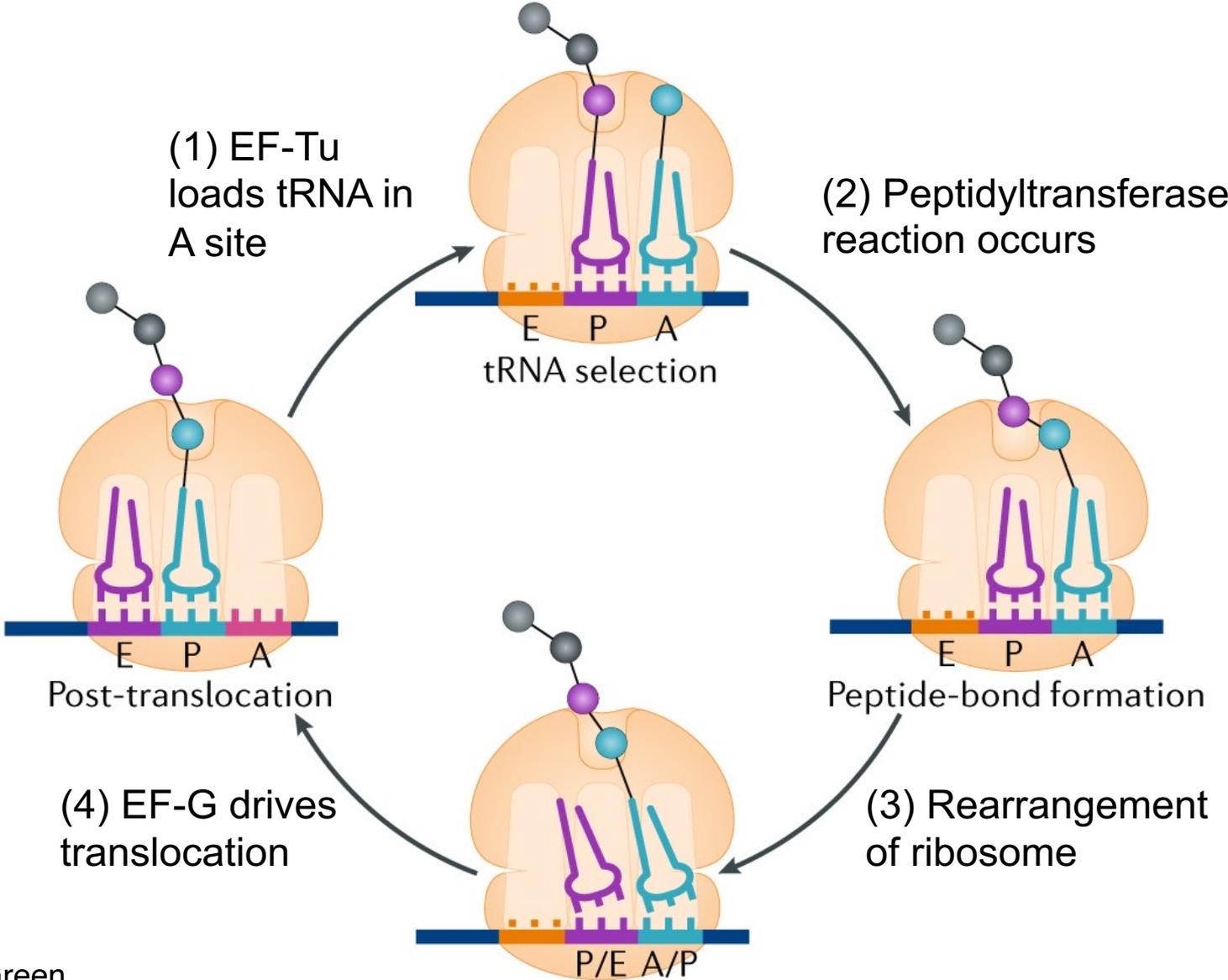
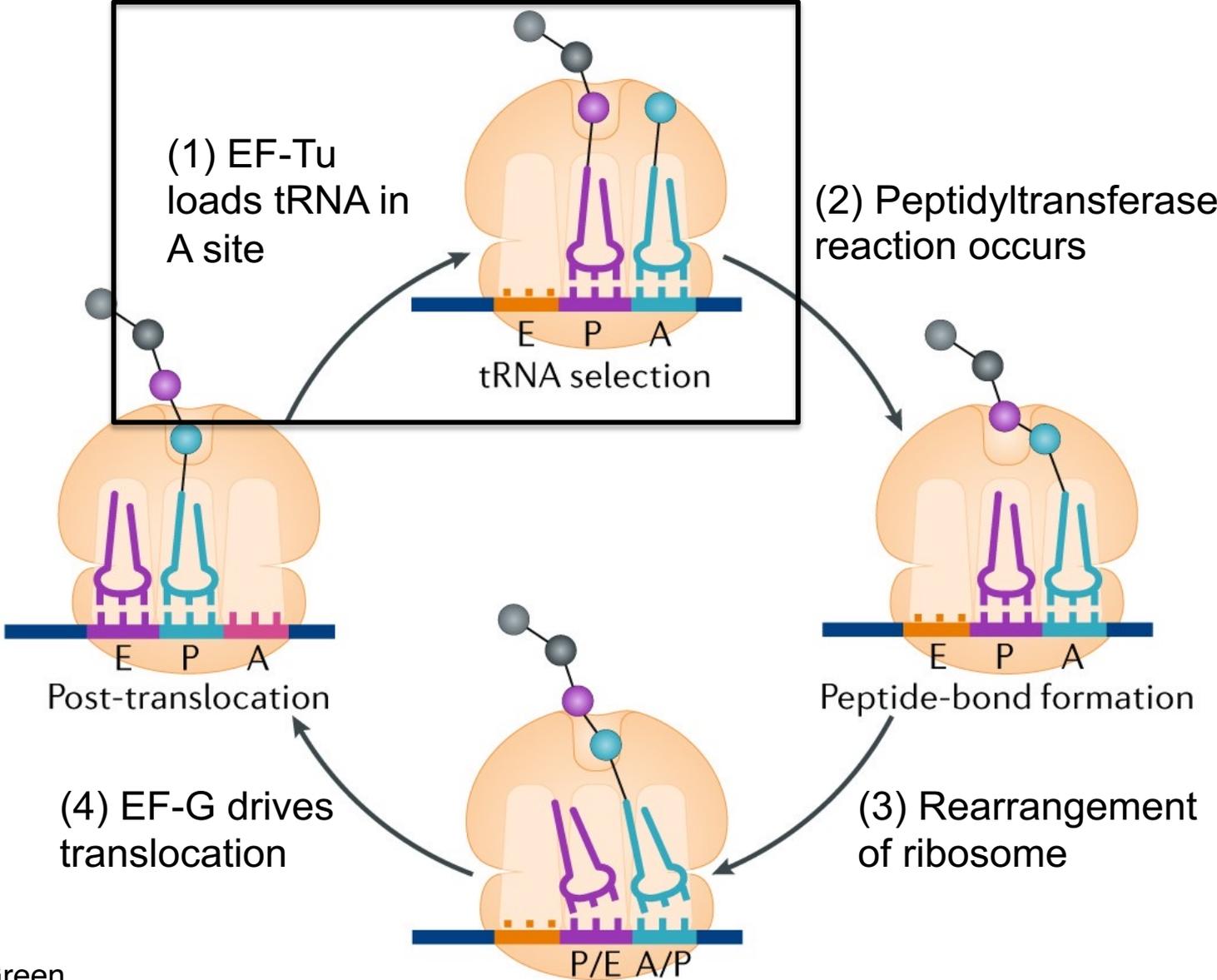


- **1% extra credit on your final grade (= 10 points on your lower midterm grade) for submitting an online evaluation for the course by the campus deadline**
- **Final exam next Wednesday at 8am in CS24**
- **Final exam is cumulative**
- **You will have all 3 hours**
- **I will have my final office hours on Monday (2pm)**
- **The TAs have extra office hours today and Saturday**
- **Review session Monday evening at 6pm**

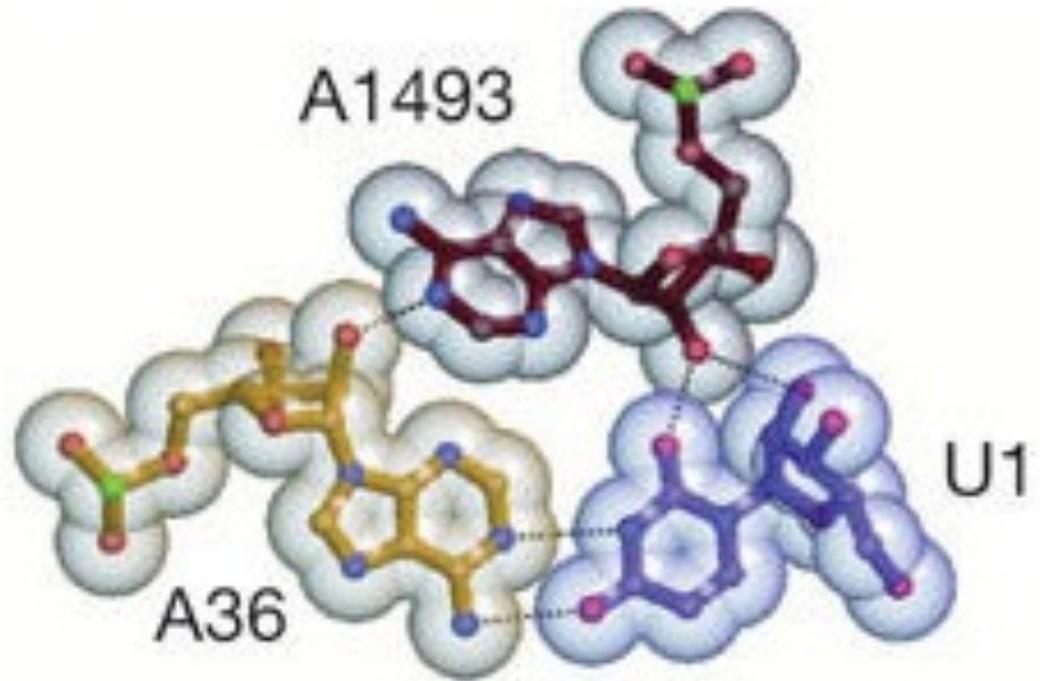
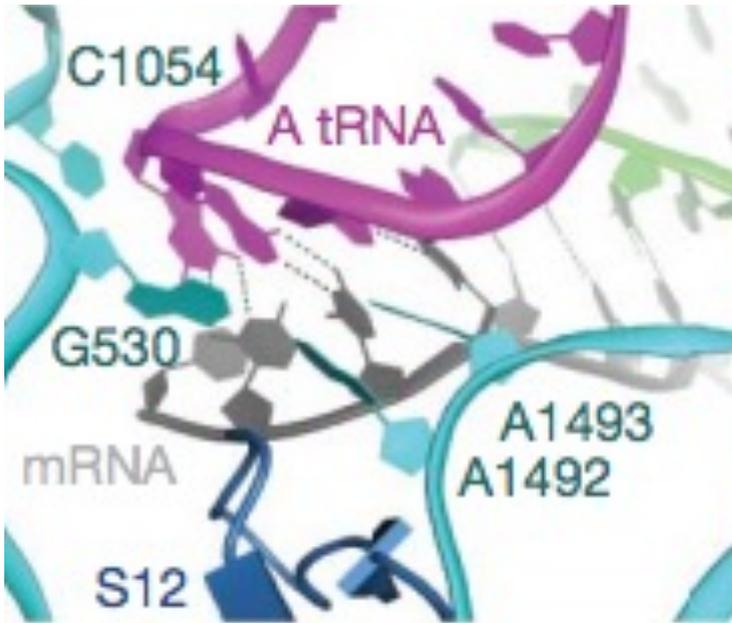
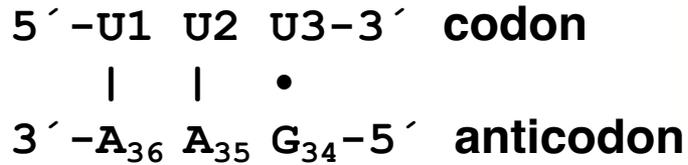
# Summary of translation elongation (similar in bacteria and eukaryotes, bacterial names shown)



# Summary of translation elongation (similar in bacteria and eukaryotes, bacterial names shown)



# The codon/anticodon interaction is stabilized in the A site through interactions with the 16S rRNA



**A-Minor interaction between A1493 of 16S rRNA and the first codon/anticodon base-pair**



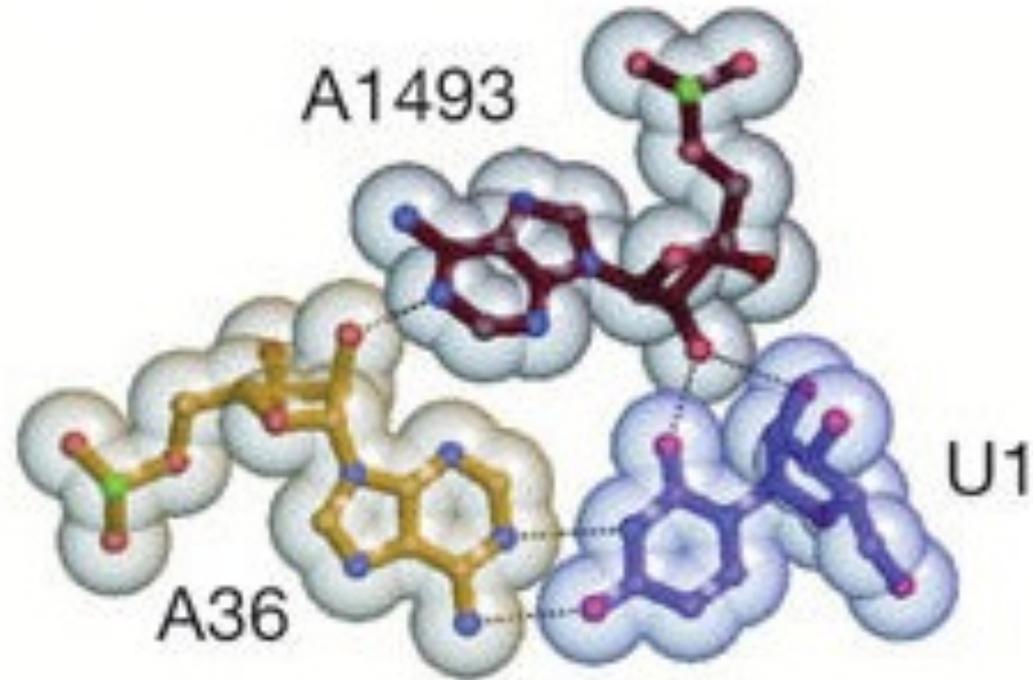
Is this interaction specific to the codons containing a U at position 1?

**A: Yes because it involves the carbonyl of U in the minor groove**

**B: No because it involves the 2' OH of both codon and anticodon**

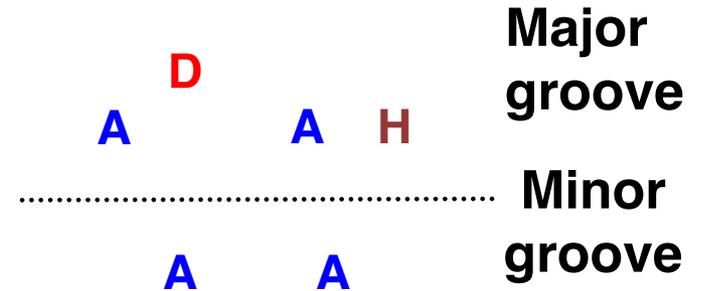
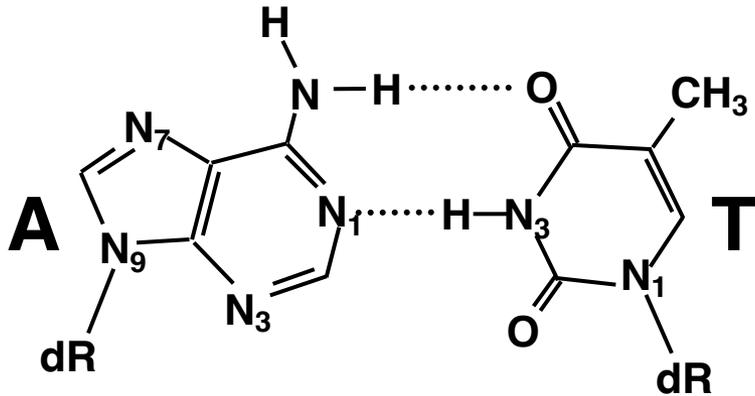
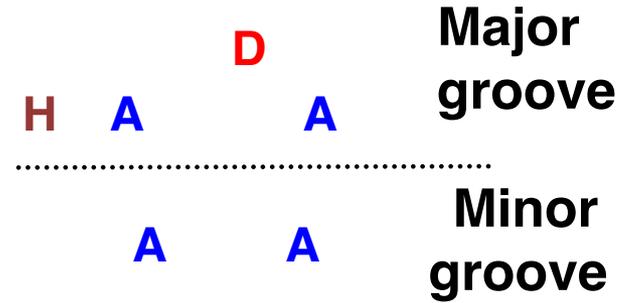
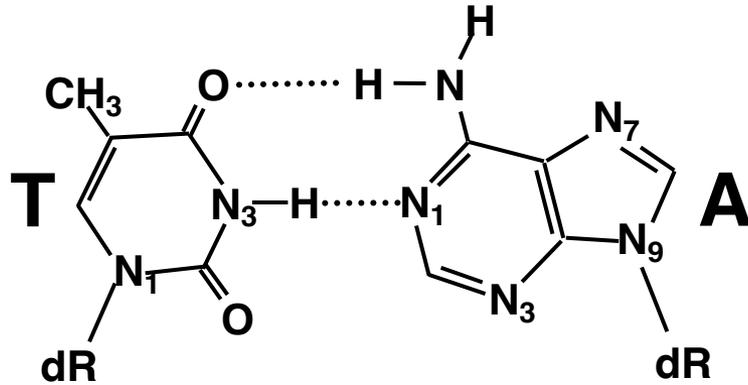
**C: Yes because a G instead of the U would sterically clash with A1493**

**D: No because you could form interactions with the H-bond acceptor in the minor groove and the 2'-OH regardless of the sequence**



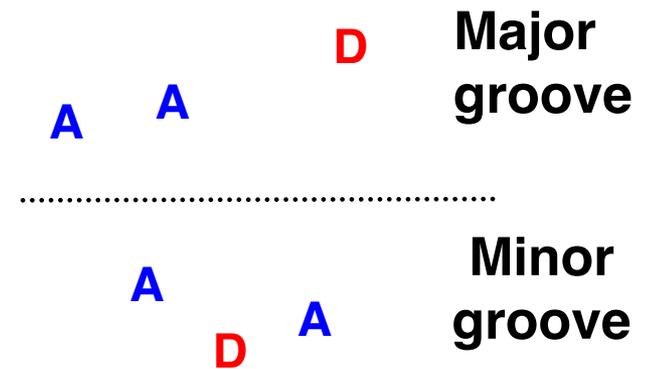
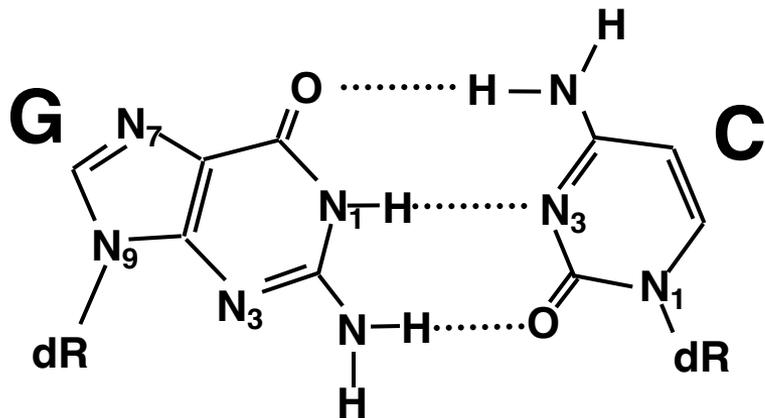
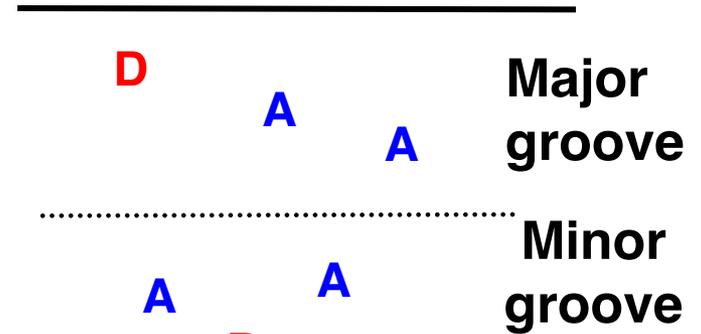
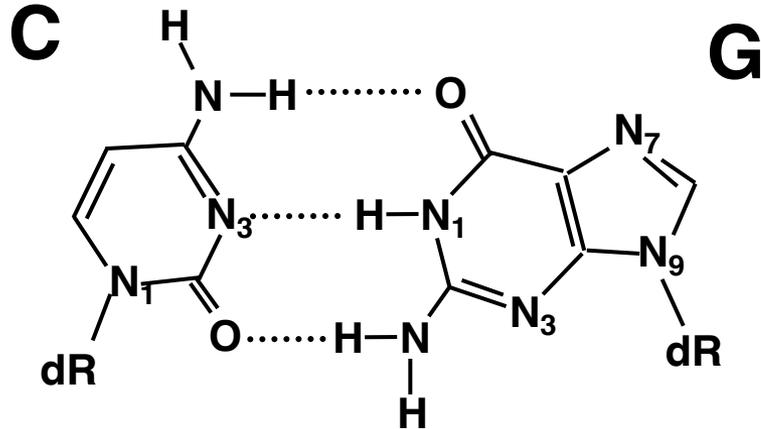
# Recognition of Specific sequences by DNA-binding proteins

Distribution of H-bonds Donors (D) Acceptors (A) and Hydrophobic groups (H) available for recognition

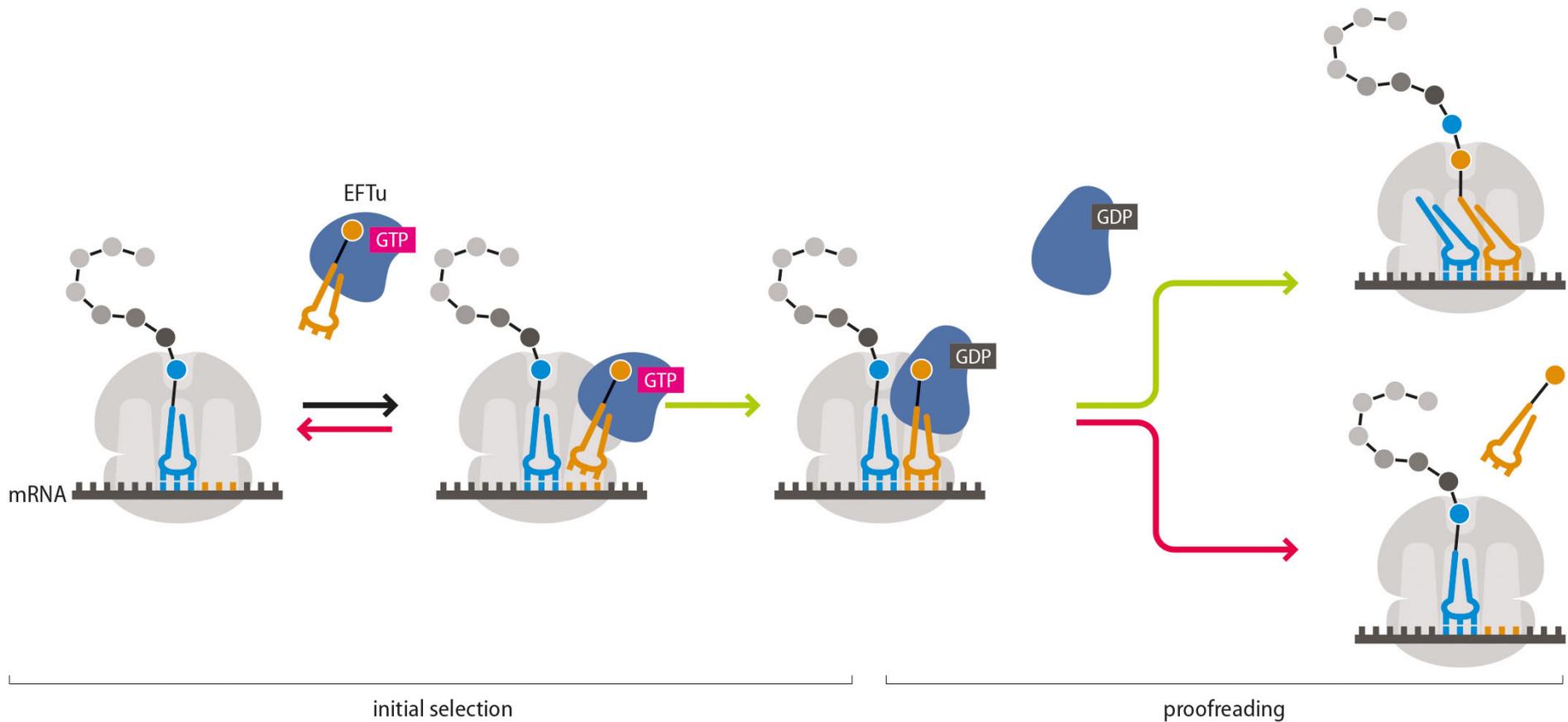


# Recognition of Specific sequences by DNA-binding proteins

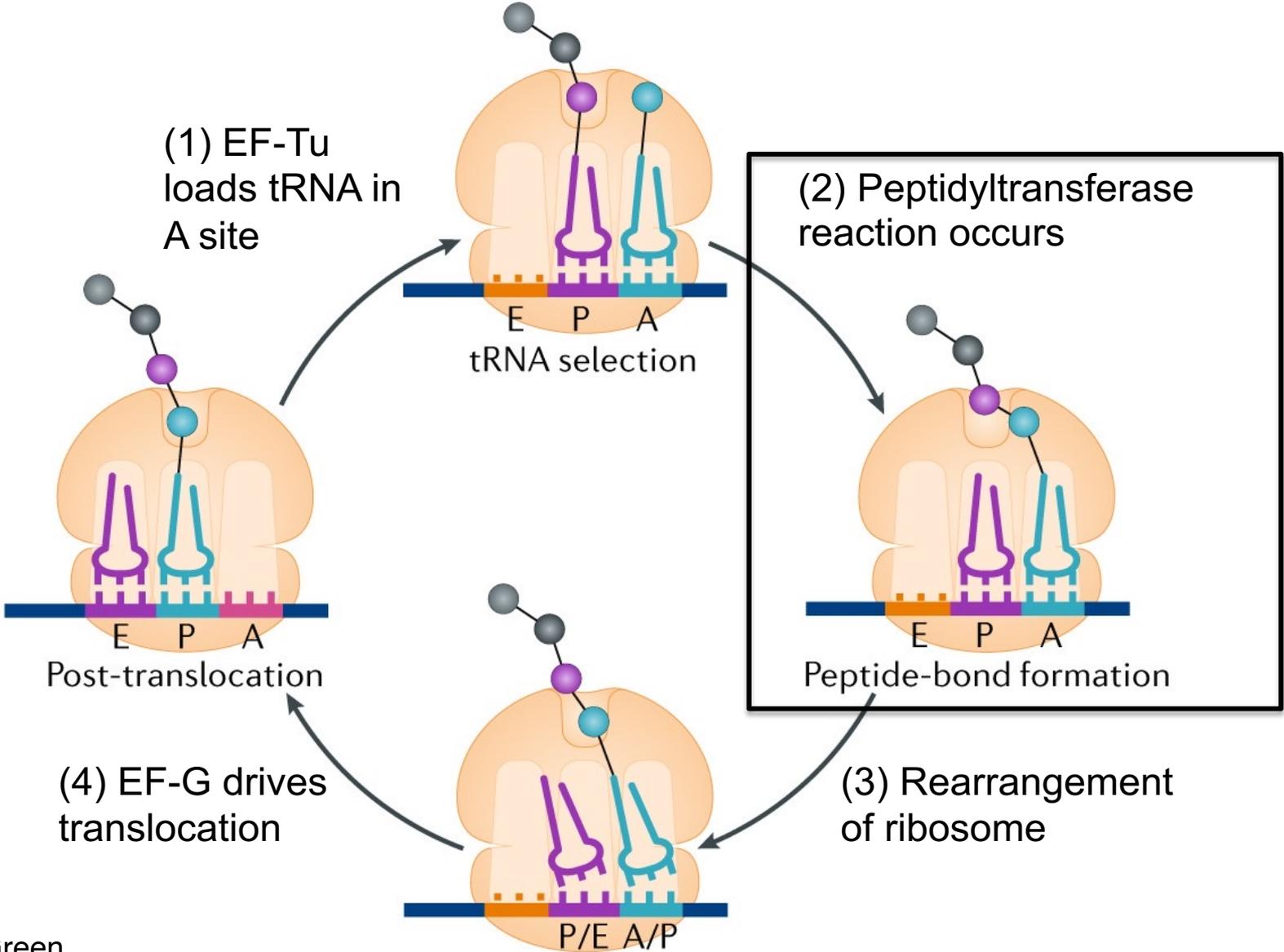
Patterns of H-bonds  
 Donors (**D**), Acceptors (**A**),  
 and Hydrophobic groups (**H**)  
 available for recognition



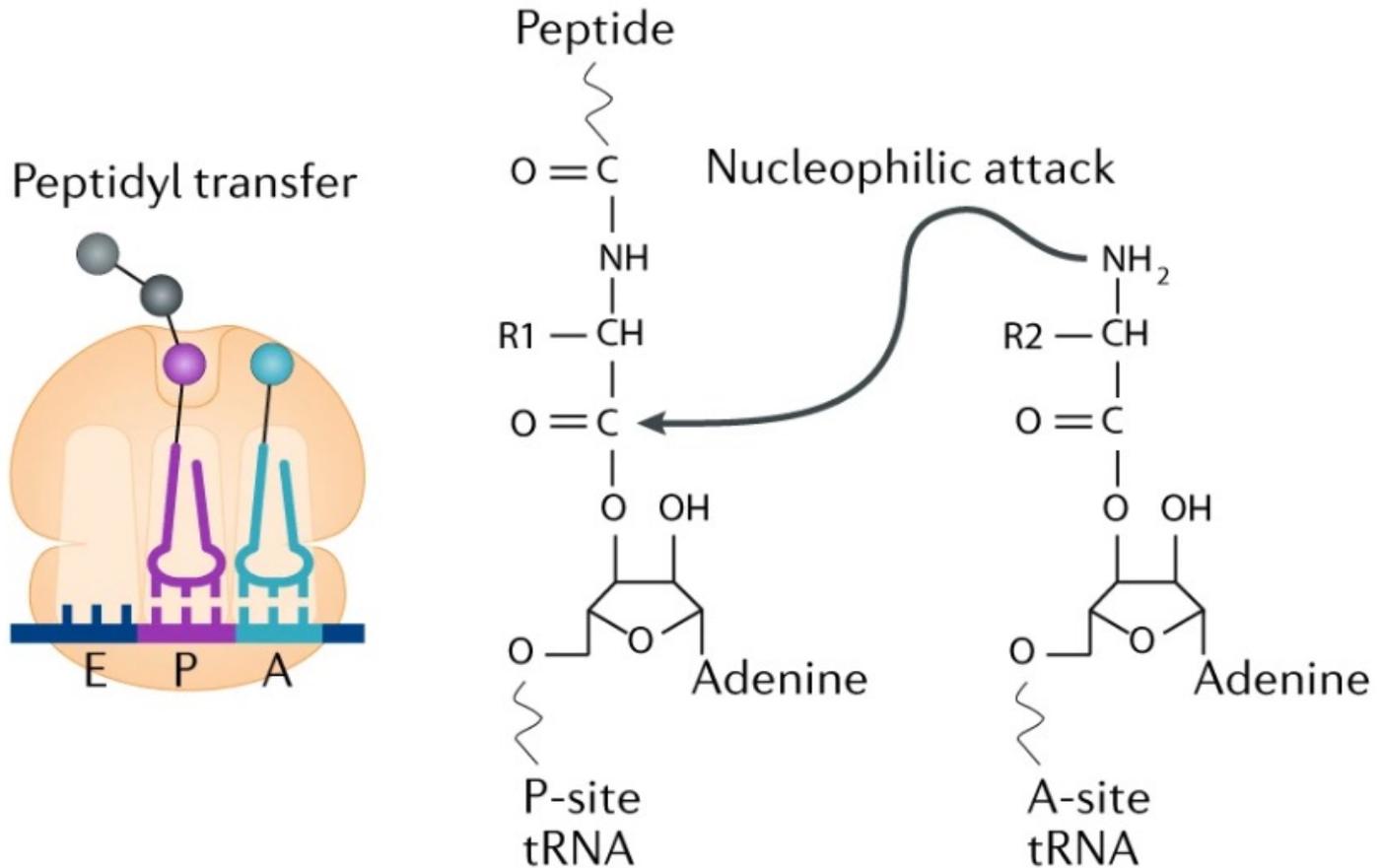
# Fidelity of A-site codon/anticodon interaction is sensed numerous times in elongation (kinetic proofreading)



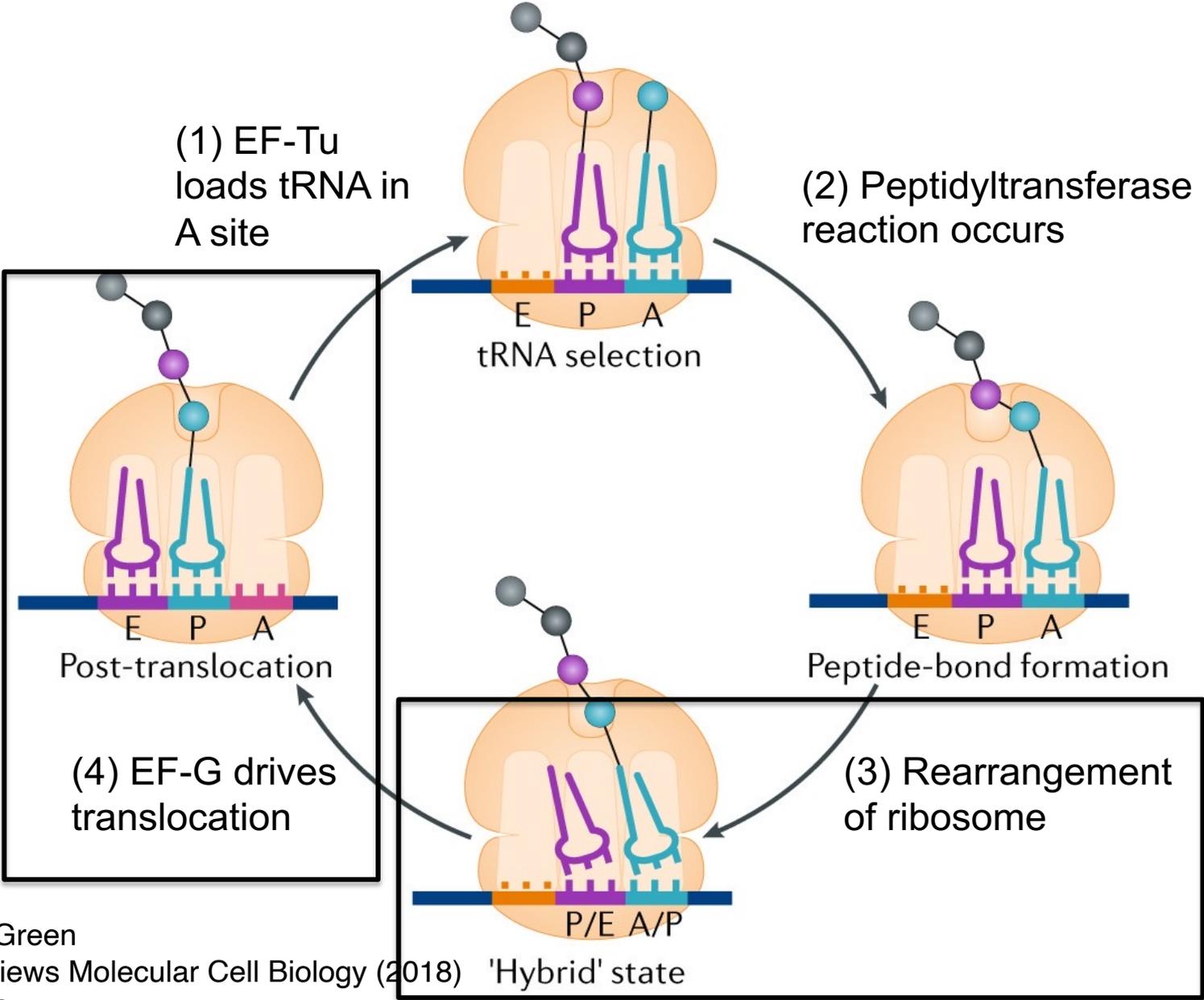
# Summary of translation elongation (similar in bacteria and eukaryotes, bacterial names shown)



# The peptidyl transferase reaction

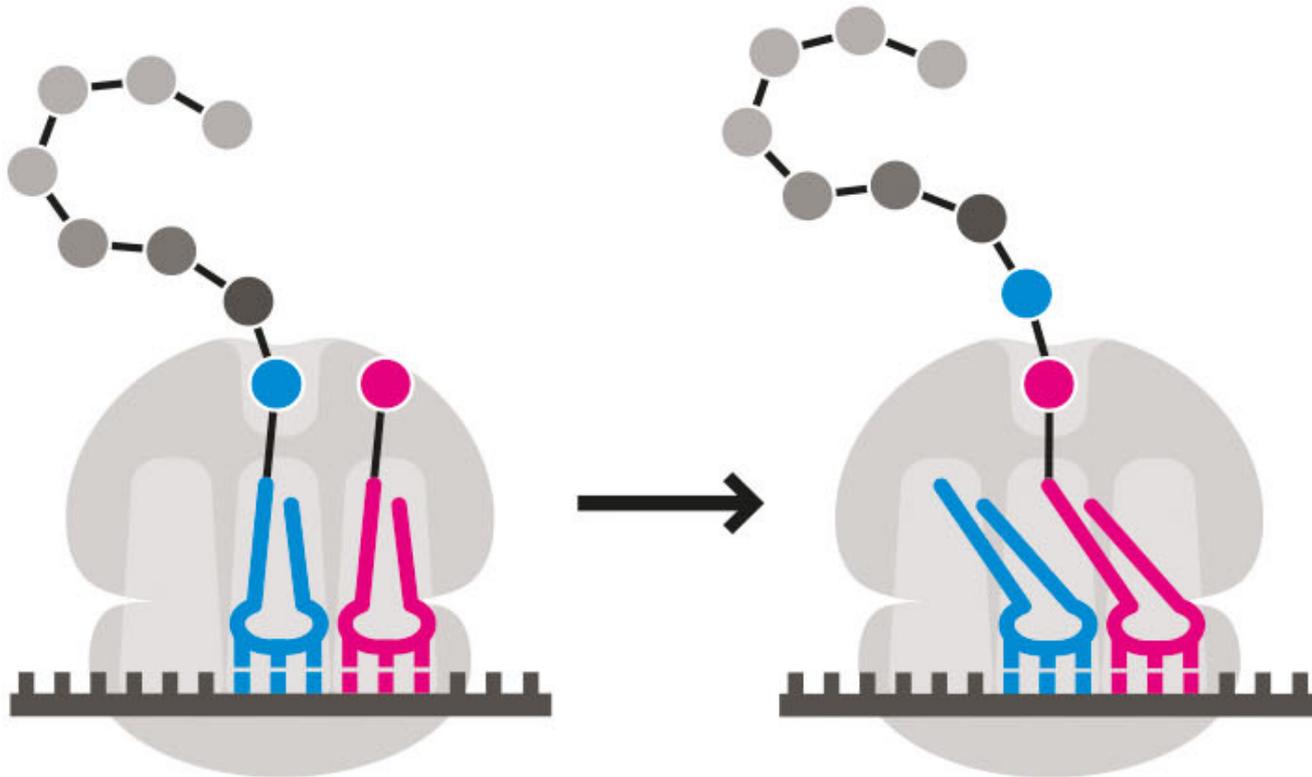


# Summary of translation elongation (similar in bacteria and eukaryotes, bacterial names shown)



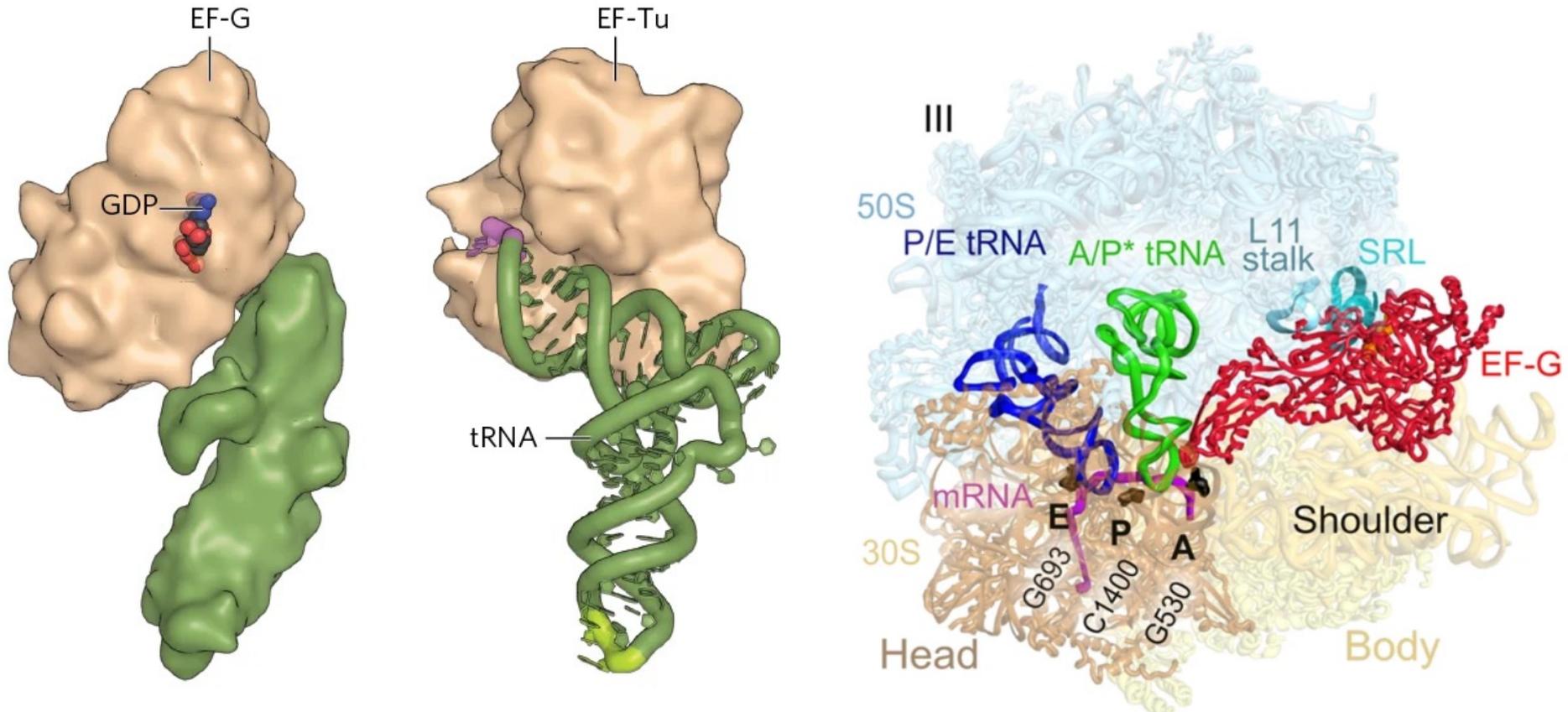
Schuller & Green  
Nature Reviews Molecular Cell Biology (2018) 'Hybrid' state

# Rearrangement to the hybrid state occurs concurrently with peptide bond formation



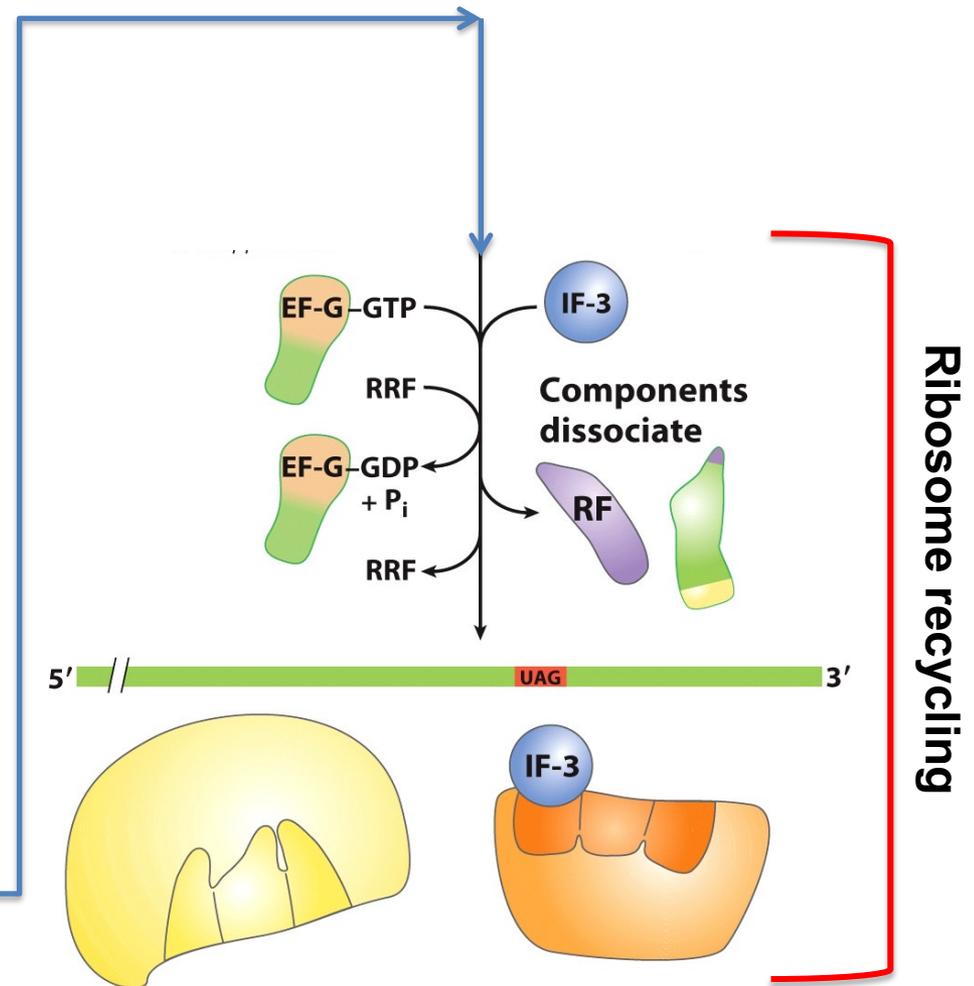
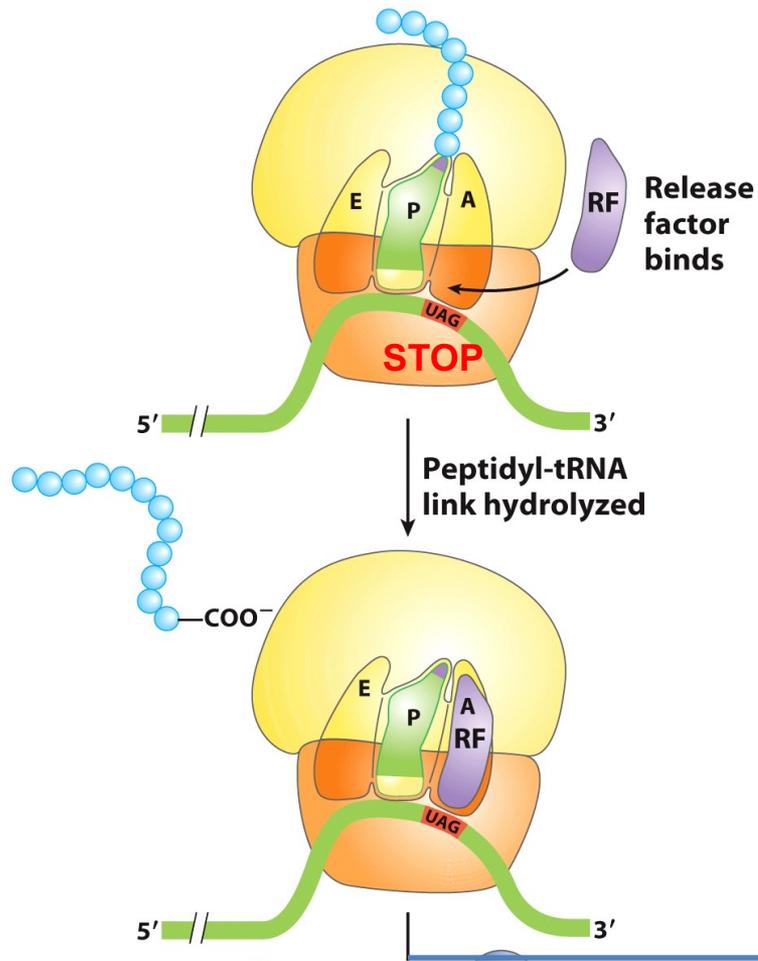
# EF-G drives translocation of tRNAs through the ribosome

EF-G is a GTPase that mimics a tRNA-EfTu complex, drives forward movement of tRNAs through ribosome



(b)

# Termination of translation (figure shows bacterial factors)



In eukaryotes:

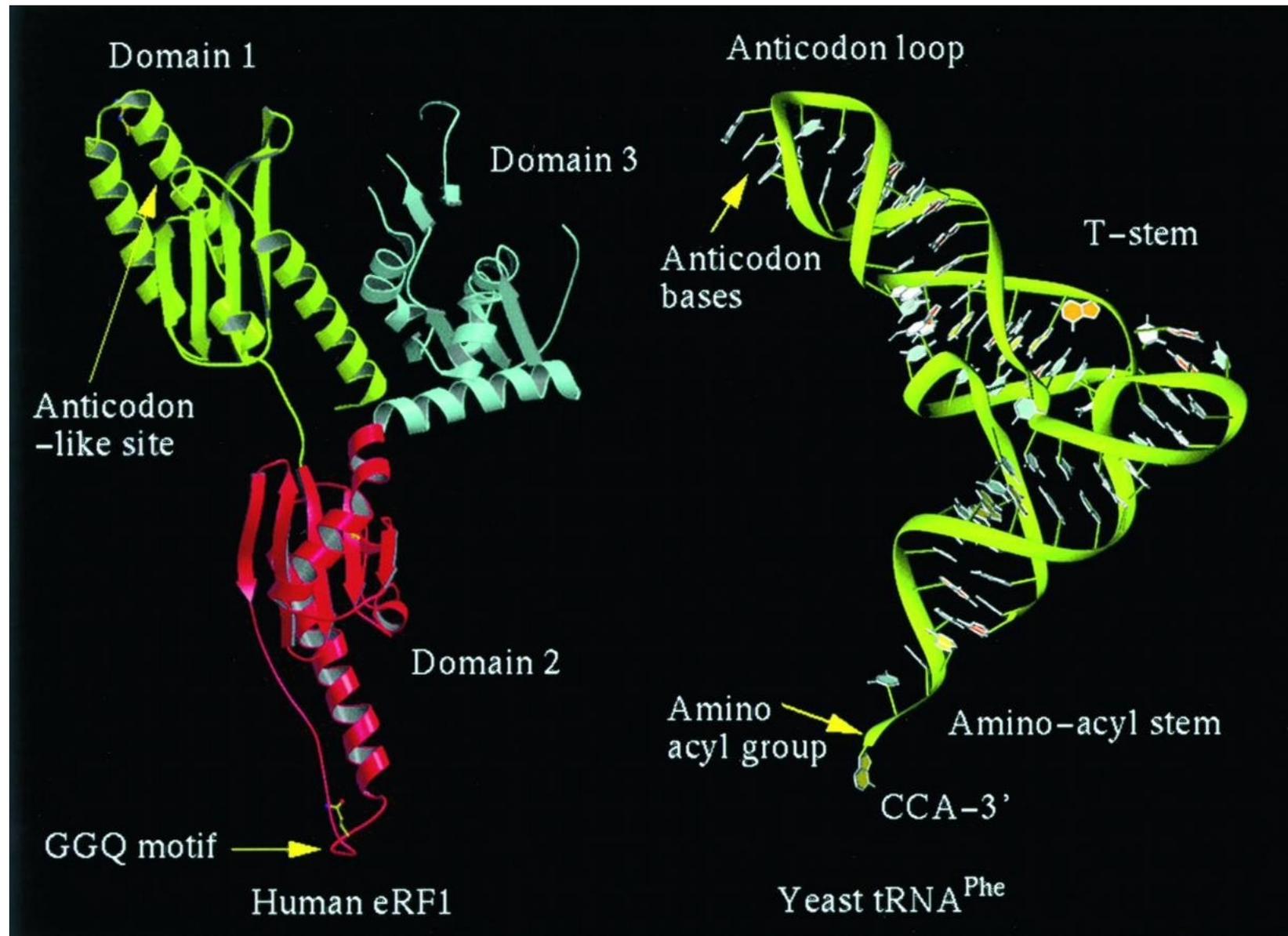
- eRF1 catalyzes peptidyl-tRNA bond cleavage (hydrolysis reaction)
- eRF3 is a GTPase that assists eRF1

Figure 27-32

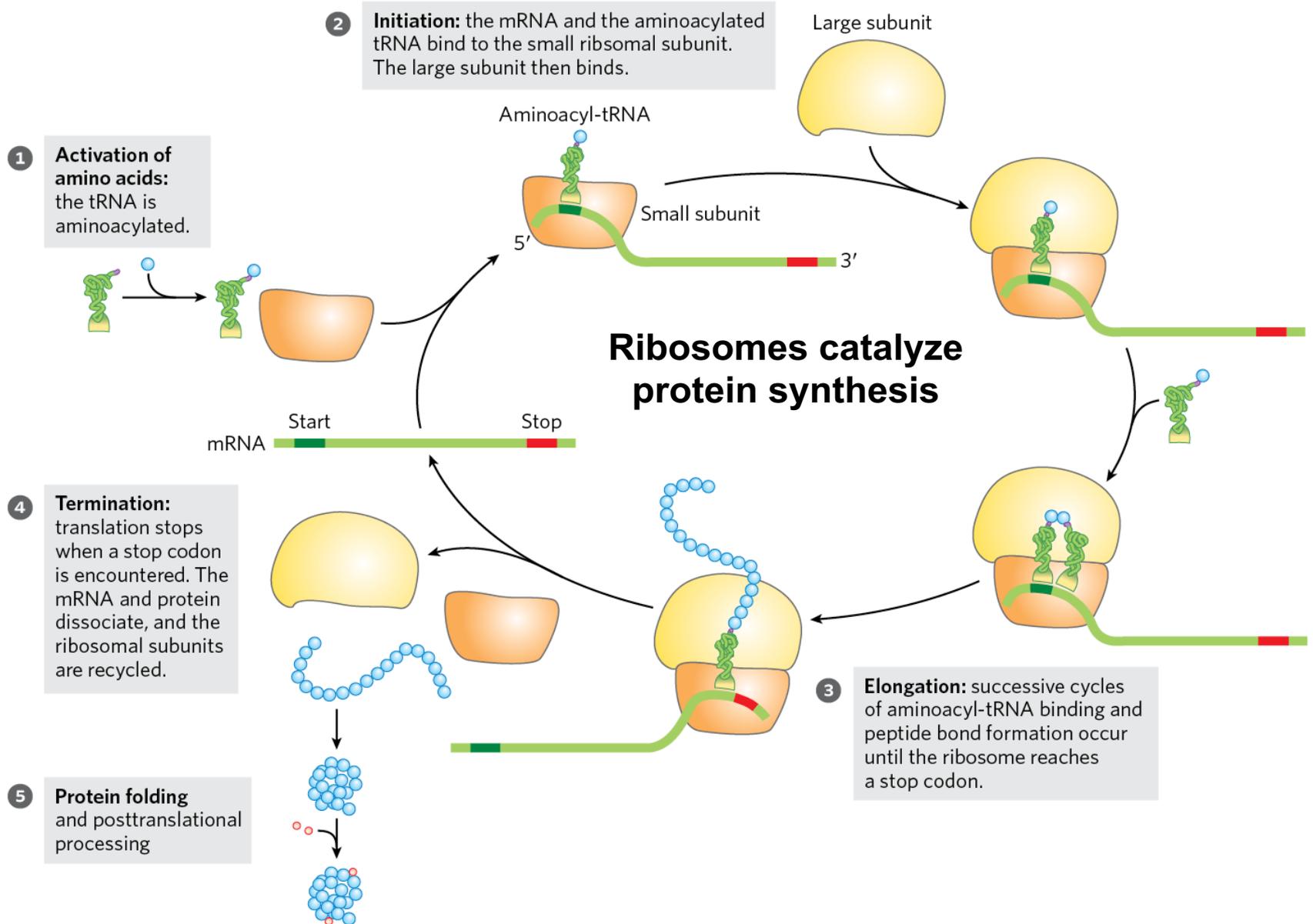
*Lehninger Principles of Biochemistry*, Sixth Edition

© 2013 W. H. Freeman and Company

# eRF1 looks just like a tRNA!!



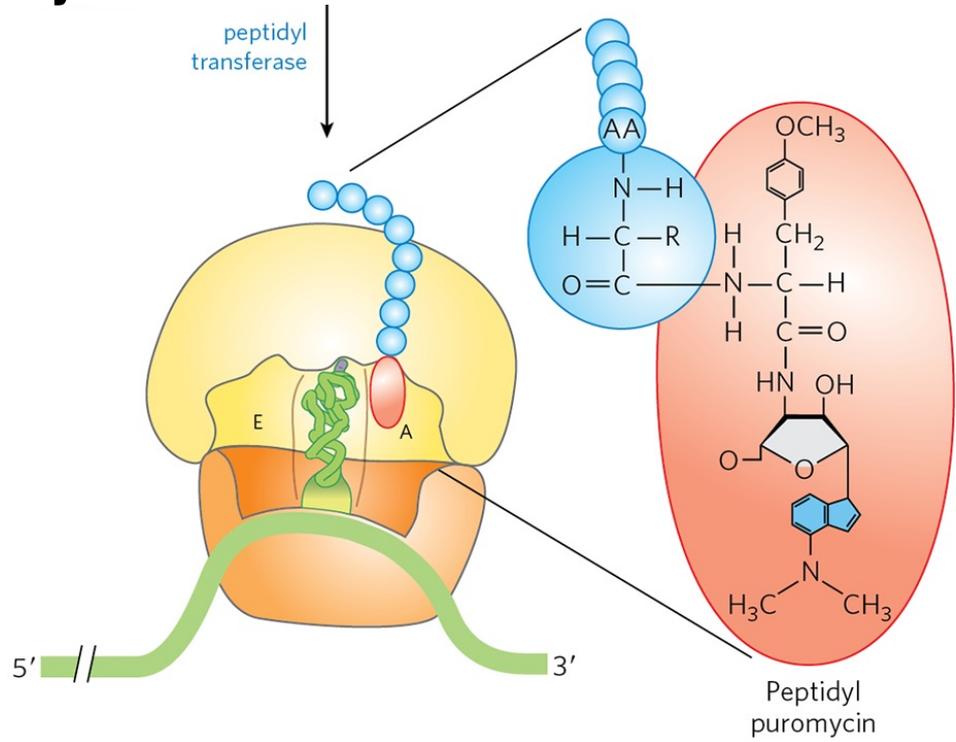
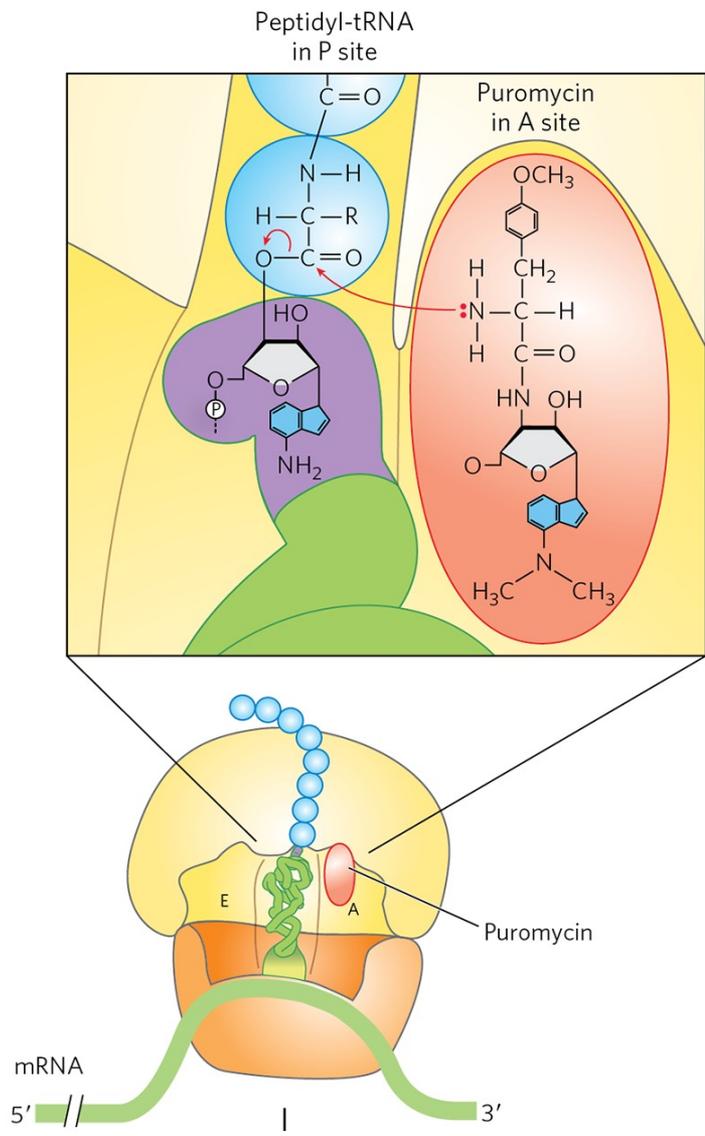
# An overview of protein synthesis



# Many antibiotics inhibit bacterial translation

## Puromycin is one of the best understood examples

- Puromycin structure is very similar to the end of an aminoacyl-tRNA
- Puromycin binds in the A site & participates in peptide bond formation → peptidyl-tRNA
- Prematurely terminates polypeptide synthesis



# Mutation terminology

- **Missense mutation**: mutation in the DNA that results in a change in the amino acid sequence of the protein
- **Nonsense mutation**: converts a codon into a stop codon
- **Silent mutation**: mutation in the DNA that does not alter the amino acid sequence of the protein
- **Frameshift mutation**: insertion or deletion that is not a multiple of 3 and thereby changes the reading frame

# Quality Control of Translation:

Quality control pathways prevent the accumulation of truncated or deficient proteins due to defects in mRNAs:

- truncated mRNAs (because of random breaks in RNAs)
- mRNAs that do not contain stop codons (because of mistakes in the 3'-end processing reactions)
- mRNAs containing premature termination codons (gene mutations, errors made by RNA polymerase, or mistakes in splicing)

**An example of translation QC in eukaryotes: “Nonstop” protein degradation in eukaryotes**

# Quality control of translation for “non-stop” mRNAs

- Non-stop mRNAs can be generated if the poly(A) tail is added before the stop codons

- The Poly(A) tail is translated as a Poly-Lysine tract

- Poly-Lysine tract sticks in the ribosome exit tunnel because of electrostatic interactions

- Ltn1 ubiquitin ligase attaches polyubiquitin chains to the nascent polypeptide stuck to the ribosome

- **This marks the aberrant protein for degradation by the proteasome**

