

1. eIF₃ loaded at the side of small subunit (SSU) → prevent binding of large subunit (LSU)
2. eIF₁ loaded at "A" site → prevent tRNA from binding at "A"
3. tRNA_i^{methionine} binds to "P" site with eIF₂ -----→
- 4.
5. mRNA is untangled by eIF₄ -----→
-eIF₄ = helicase
6. Ribosome with bound tRNA_i^{methionine} and eIF₂ binds to m⁷G – 5' end of mRNA (ribosome binding site)
7. ATP is hydrolysed to ADP and P_i → tRNA_i moves along mRNA searching for the first AUG -----→

Energy intensive → because anabolising a.a. into highly ordered polypeptides decreases **entropy**!

8. eIF₂ (GTPase) hydrolyses GTP to GDP and P_i → Release of initiation factors → Dissociation of eIF₃ allows LSU to bind → ready for elongation -----→

- c. **Elongation**: Adding charged tRNA to "A" with elongation factors → ribosome moves every 3 nucleotides → peptide bond formation

-EF1 (eukaryotes) = EF-TU (bacteria), EF2 (eukaryotes) = EF-G

9. EF1/EF-TU brings 2nd charged tRNA to "A" site and proofreads translation;
 - Checks whether the tRNA-amino acid match is correct
 - Correct matches have a narrowly-defined affinity for EF-TU → allow EF-TU to discriminate and select the correct ones into the ribosome
 - Monitors interaction (hydrogen bond) between anticodon of aminoacyl-tRNA and codon on mRNA at "A"
 - As aminoacyl-tRNA bends when bound to GTP-form of EF-TU → codon pairing, BUT not peptide bond formation → correct codon pairing gives GTP hydrolysis → EF-TU releases tRNA and amino acid is donated for protein synthesis -----

10. LSU catalyses peptide bond formation between 1st and 2nd amino acids

