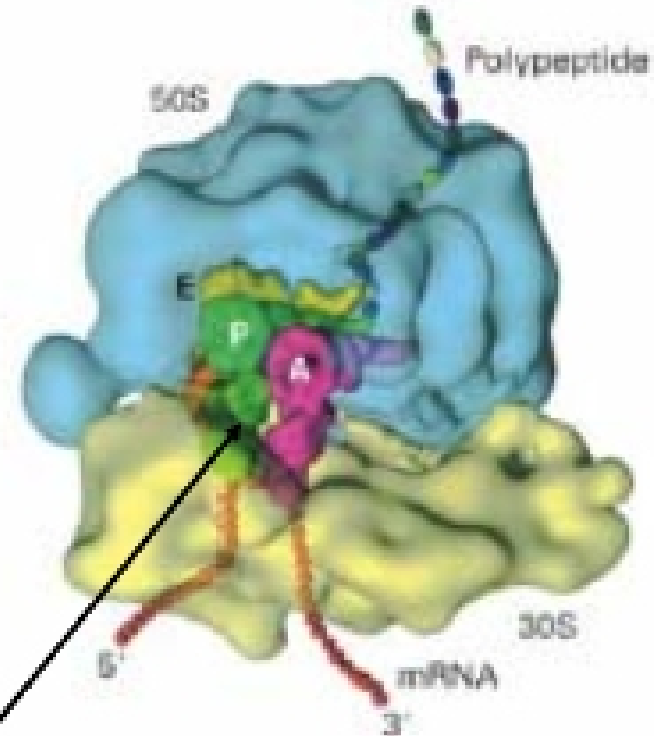
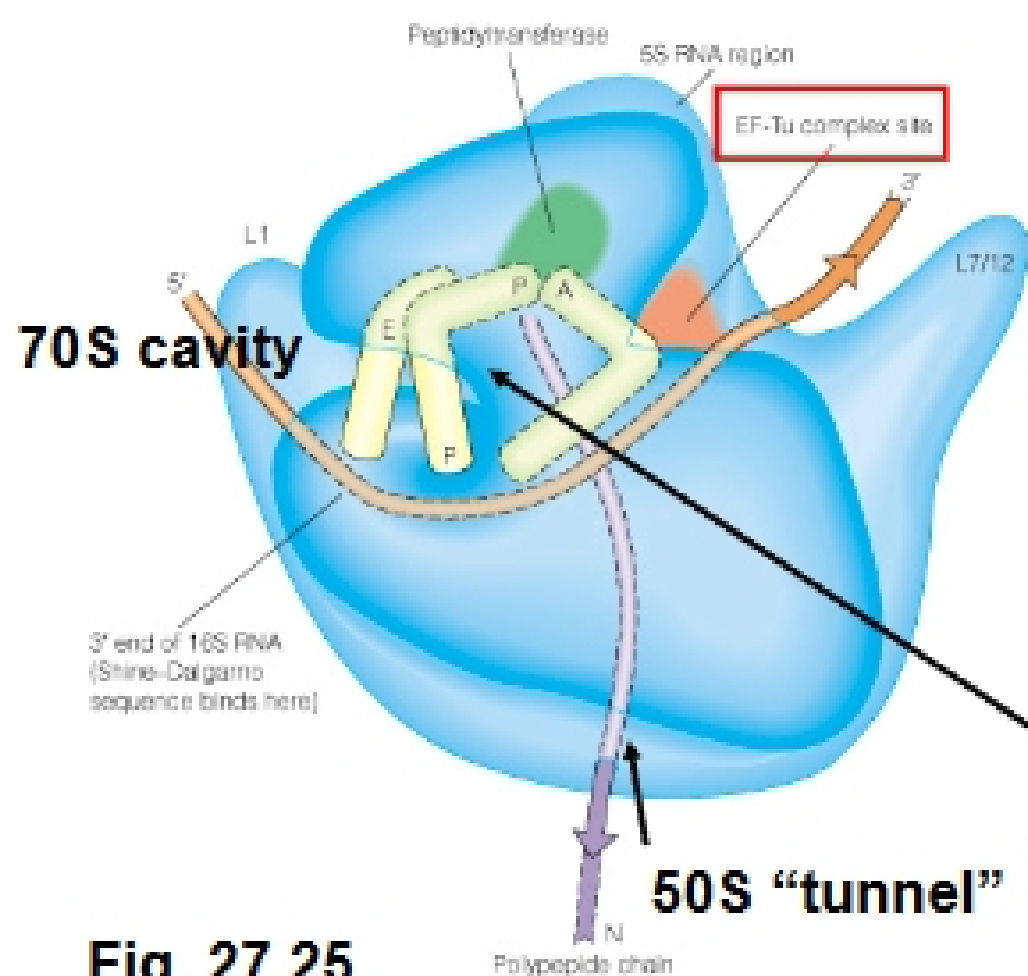


**Protein synthesis II**  
**Biochemistry 302**

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# Several idealized views of the 70S ribosomal complex during translation



Both models imagine all three binding sites (A, P, E) occupied by tRNAs. This would only be a transient occurrence during actual protein synthesis.

**Fig. 27.25**

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**View with 30S subunit in front, 50S subunit behind**

# Prokaryotic translation: Three steps of chain elongation

- **A site (AA-tRNA binding, EF-Tu-GTP hydrolysis)**
  - Loading of new AA-tRNA joined to **EF-Tu-GTP**
  - Codon positioning of AA-tRNA assisted by GTP hydrolysis
  - Dissociation of EF-Tu-GDP (Released EF-Tu “reloaded” with GTP via **EF-Ts exchange factor**)
- **A,P sites (transpeptidation in 50S subunit)**
  - $\alpha$ -amino group from A site AA-tRNA attacks the carbonyl carbon of P-site bound peptidyl-tRNA
  - Formation of new peptide bond at A/P 50S hybrid-site
  - P-site deacylated tRNA (i.e. w/o peptide) - leaving group
- **A, P, E site (translocation, EF-G-GTP hydrolysis)**
  - Rapid transfer of uncharged tRNA to E site and ejection
  - Translocation of peptidyl-(3'OH) tRNA from A site to P site via **EF-G**-mediated ribosome movement 3' to the next codon