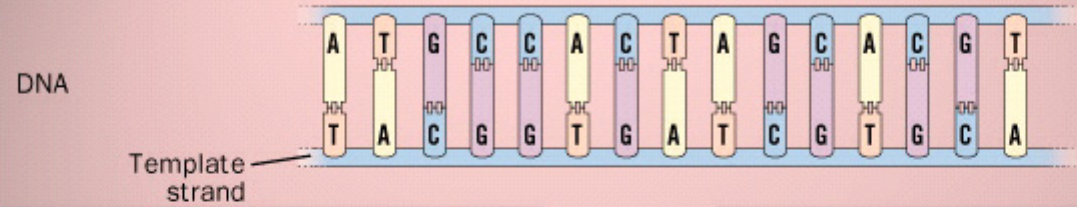
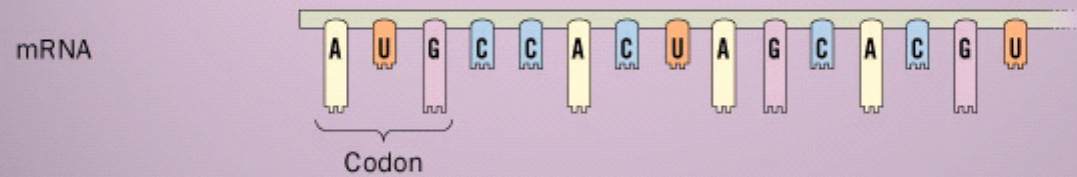


Síntesis de Proteínas (Traducción)

Gene expression

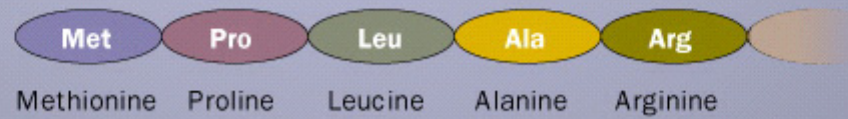


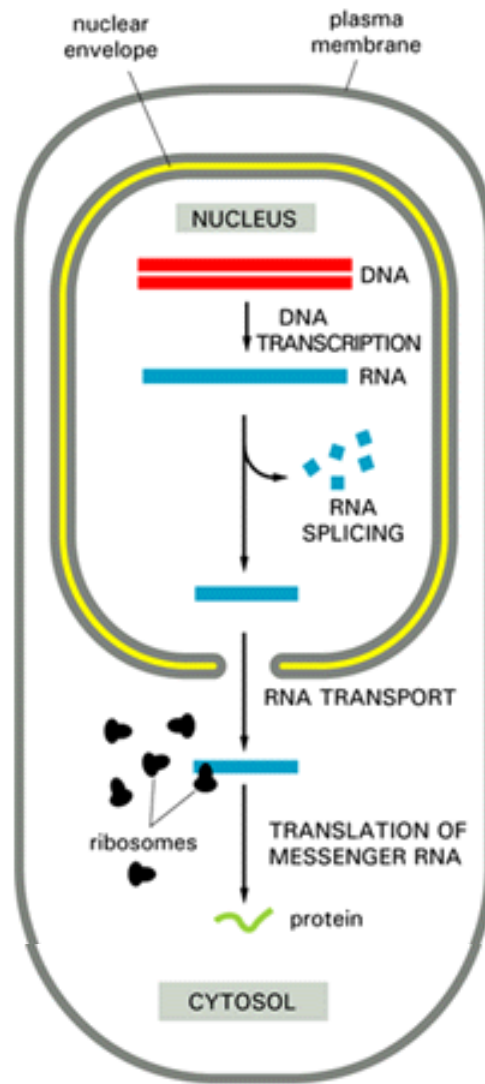
Transcription



Translation

Protein
(amino
acid chain)





Cómo se alinean los nucleótidos en el mRNA templado?

Experimentos (síntesis de proteínas in vitro):

1) Extracto celular + polímero poli U (UUUUUU) + sistema de síntesis in vitro



Producto: polímero con un solo aminoácido: fenilalanina

2) Extracto celular + polímero poli UG + sistema de síntesis in vitro



**Producto: polímero con 2 aminoácidos: GUG UGU GUG
UGU.....
y así sucesivamente**

CÓDIGO GENÉTICO

		Second base					
		U	C	A	G		
First base	U	UUU Phe UUC UUA Leu UUG	UCU UCC Ser UCA UCG	UAU Tyr UAC UAA Stop UAG Stop	UGU Cys UGC UGA Stop UGG Trp	U C A G	Third base
	C	CUU CUC Leu CUA CUG	CCU CCC Pro CCA CCG	CAU His CAC CAA Gln CAG	CGU CGC Arg CGA CGG	U C A G	
	A	AUU AUC Ile AUA AUG Met/Start	ACU ACC Thr ACA ACG	AAU Asn AAC AAA Lys AAG	AGU Ser AGC AGA Arg AGG	U C A G	
	G	GUU GUC Val GUA GUG	GCU GCC Ala GCA GCG	GAU Asp GAC GAA Glu GAG	GGU GGC Gly GGA GGG	U C A G	

Características del Código Genético:

- 1. Cada codón está formado por 3 nucleótidos**
- 2. Un codón = un aminoácido**
- 3. Algunos aminoácidos son codificados por más de un codón: redundancia**
- 4. Hay solo un codón de iniciación: AUG: metionina**
- 5. Posibilidades: $4 \times 4 \times 4 = 64$**
De ellos, 61 codifican para algún aminoácido
3 codones son de término: UAA UAG UGA
- 6. El código es universal**

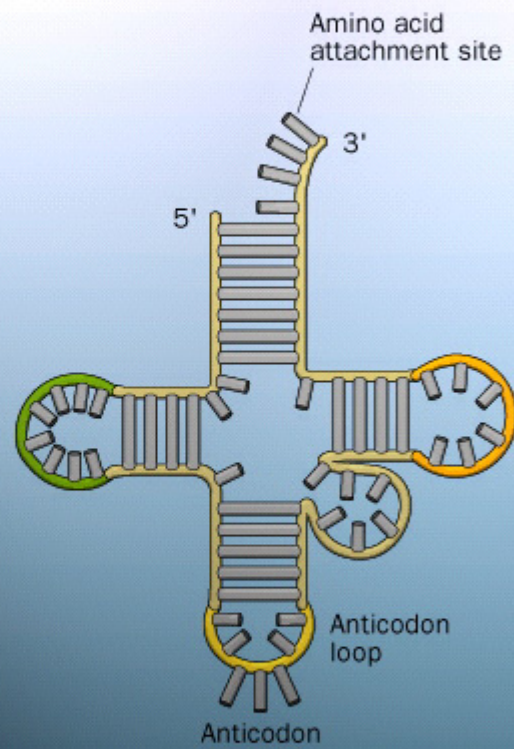
Qué factor determina cuál aminoácido se agrega a la cadena en la síntesis proteica??

**Existe un adaptador que reconoce a los nucleótidos y a los aminoácidos al mismo tiempo:
RNA de transferencia: tRNA**

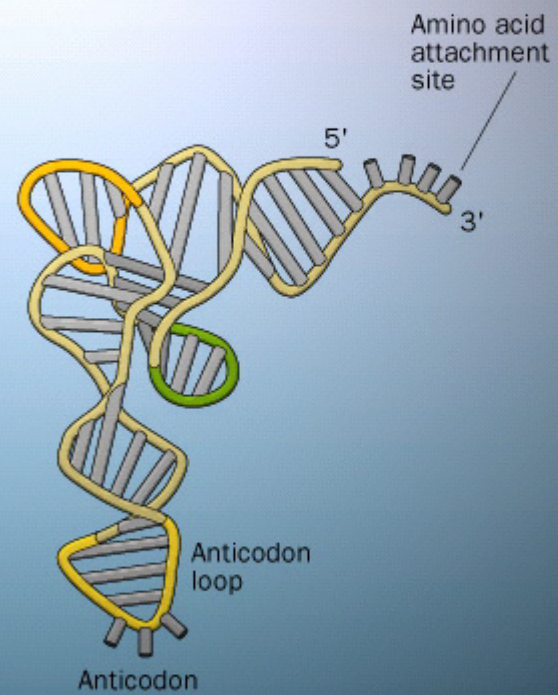
**Cada tRNA transporta un aminoácido:
tRNA^{gli} tRNA^{ala}, etc**

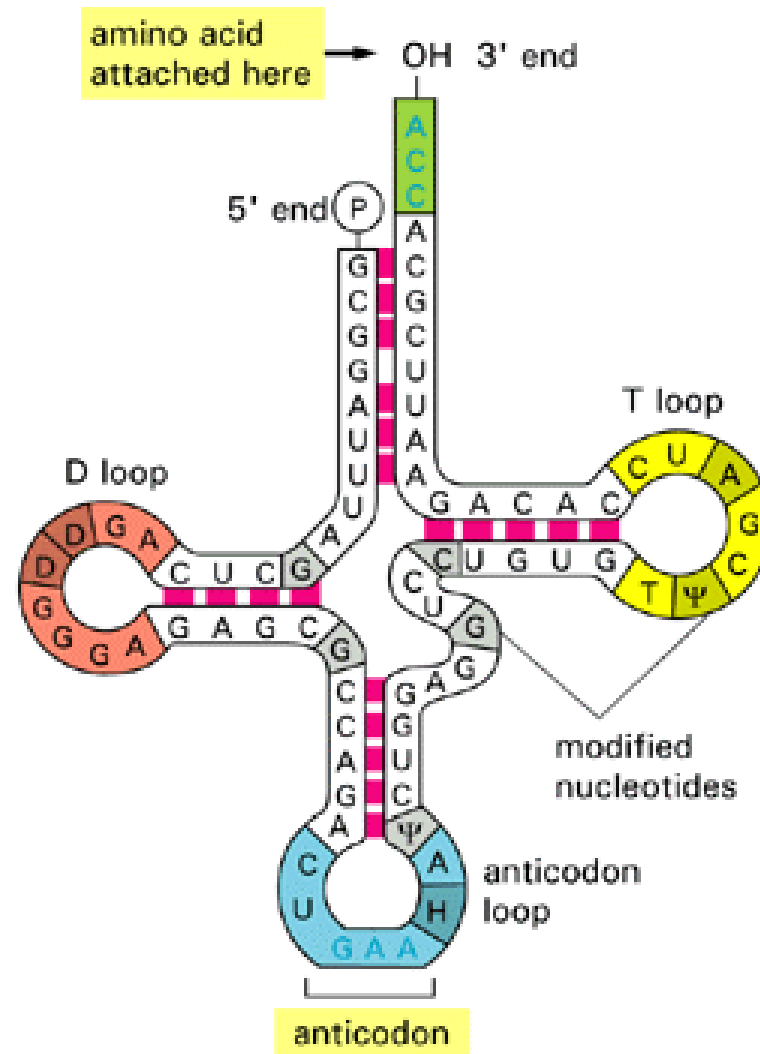
Se han encontrado 31 tRNA diferentes

tRNA ("cloverleaf" model)



tRNA (folded model)



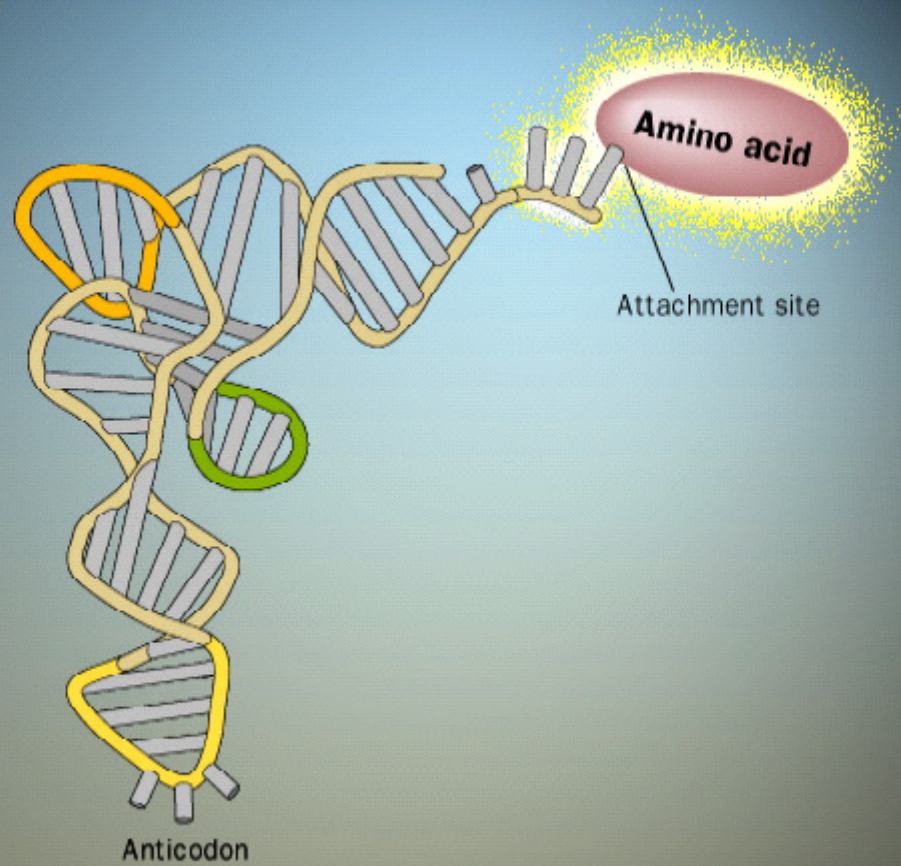


tRNA

Funciones de los tRNA:

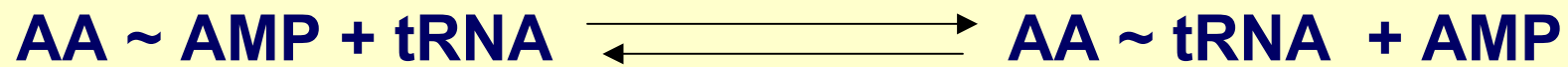
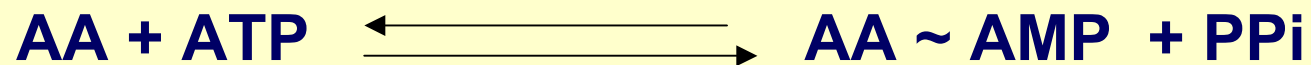
- 1.- Unir covalentemente un aminoácido al tRNA que contiene una secuencia de nucleótidos (anticodón) complementaria al codón que especifica ese aminoácido sobre el mRNA**
- 2.- Activar al aminoácido generando un enlace altamente energético en el extremo COOH para que reaccione con el aminoácido siguiente en la secuencia de la cadena y forme el enlace peptídico**

Charged tRNA

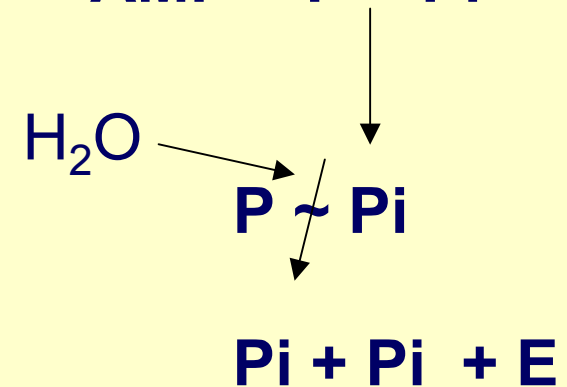


Activación del aminoácido

Ocurre en 2 etapas en el citosol



$$\Delta G = 0$$



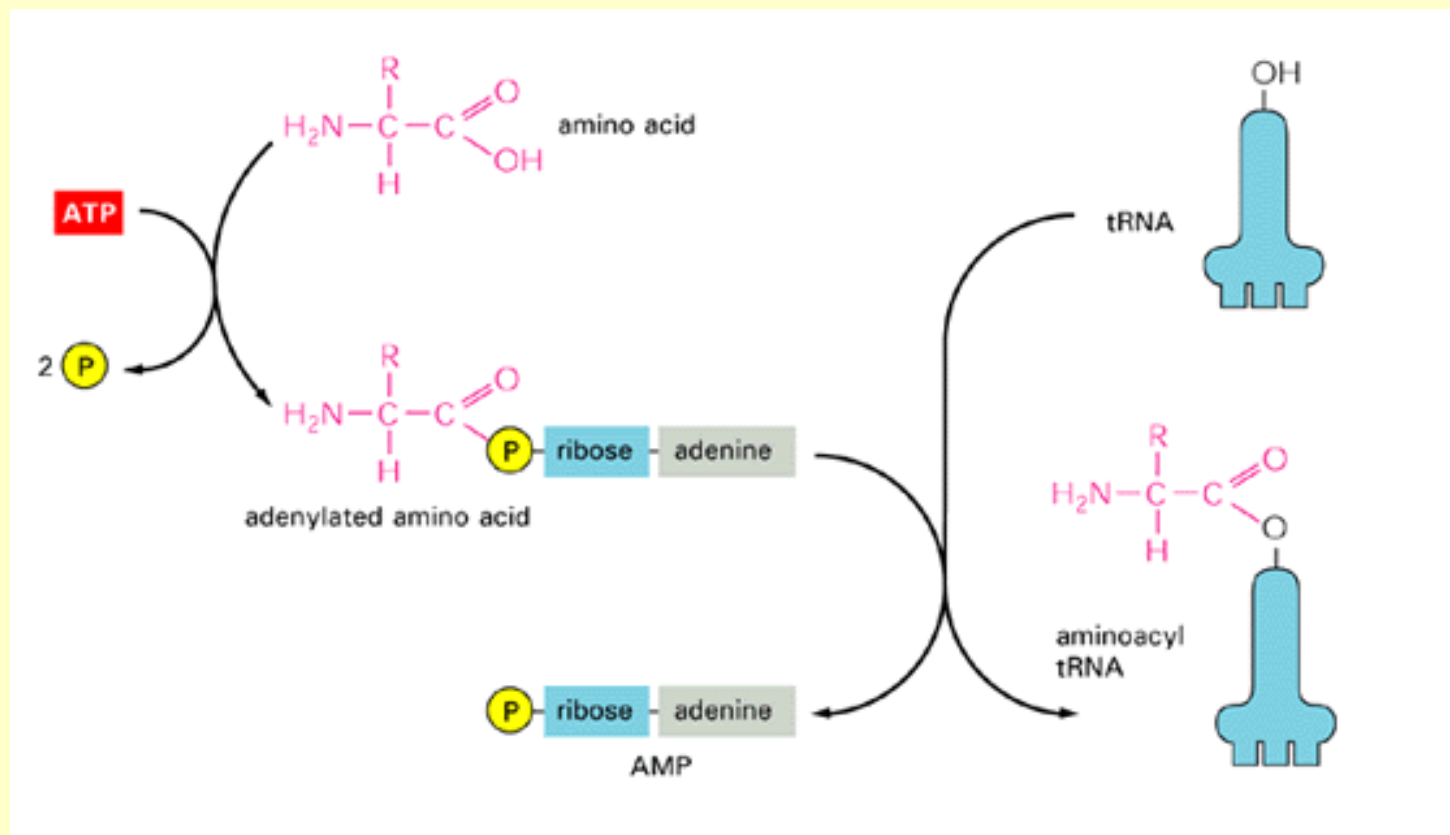
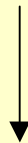


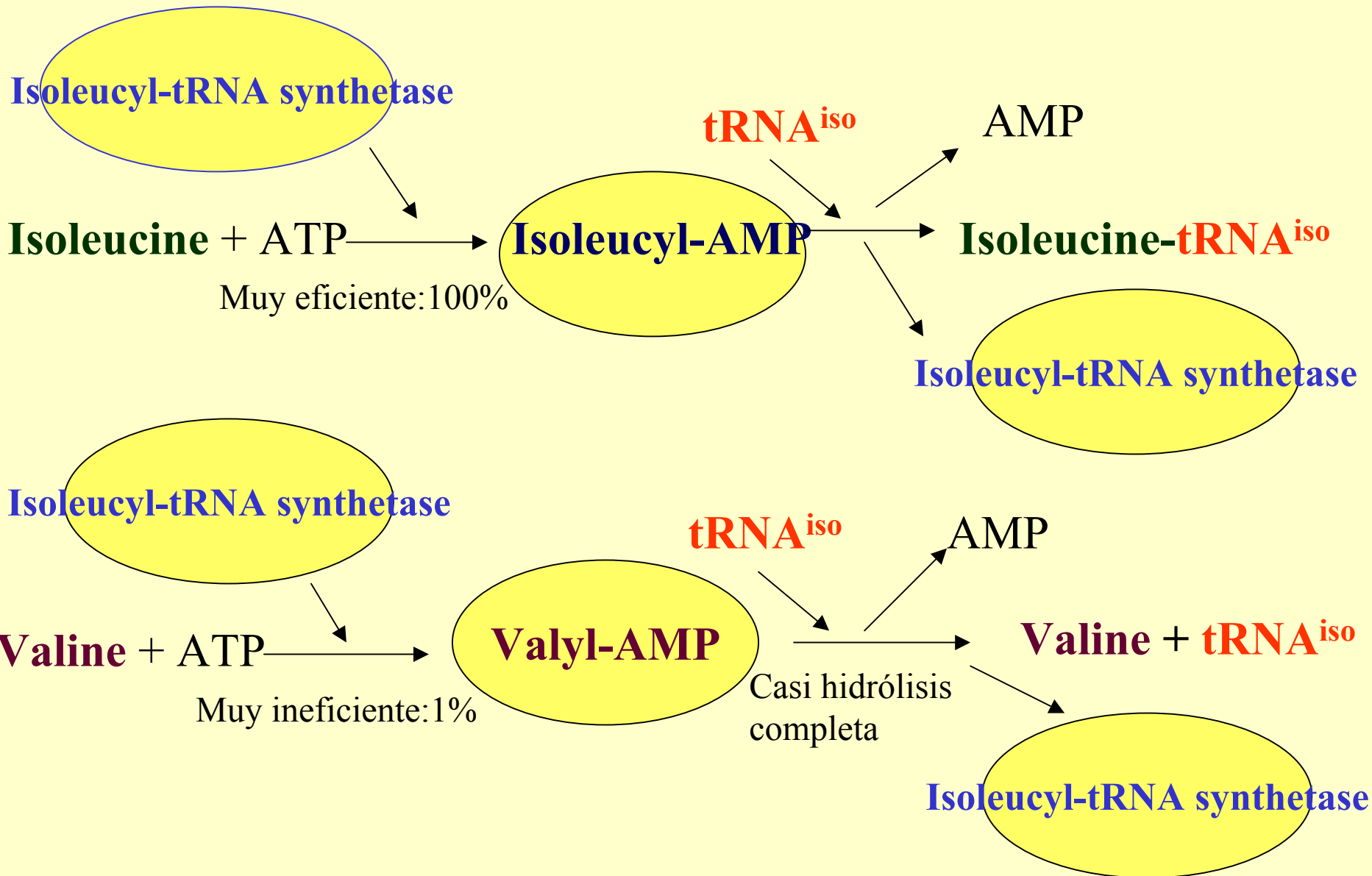
Figure 6-11. Amino acid activation. The two-step process in which an amino acid (with its side chain denoted by R) is activated for protein synthesis by an aminoacyl-tRNA synthetase enzyme is shown. As indicated, the energy of ATP hydrolysis is used to attach each amino acid to its tRNA molecule in a high-energy linkage. The amino acid is first activated through the linkage of its carboxyl group directly to an AMP moiety, forming an *adenylated amino acid*; the linkage of the AMP, normally an unfavorable reaction, is driven by the hydrolysis of the ATP molecule that donates the AMP. Without leaving the synthetase enzyme, the AMP-linked carboxyl group on the amino acid is then transferred to a hydroxyl group on the sugar at the 3' end of the tRNA molecule. This transfer joins the amino acid by an activated ester linkage to the tRNA and forms the final aminoacyl-tRNA molecule. The synthetase enzyme is not shown in these diagrams.

Funciones de la aminoacil- tRNA sintetasa

- 1.- Cataliza la unión del AA a su correspondiente tRNA**
- 2.-Posee un sitio de hidrólisis del aminoácido incorrecto que asegura la fidelidad en la unión del aminoácido correcto a su correspondiente tRNA**



Corrector de prueba



Mecanismo corrector de prueba de la aminoacil-tRNA sintetasa

Una vez activado el aminoácido (unido al tRNA)

el tRNA^{aa} difunde al ribosoma y comienza el

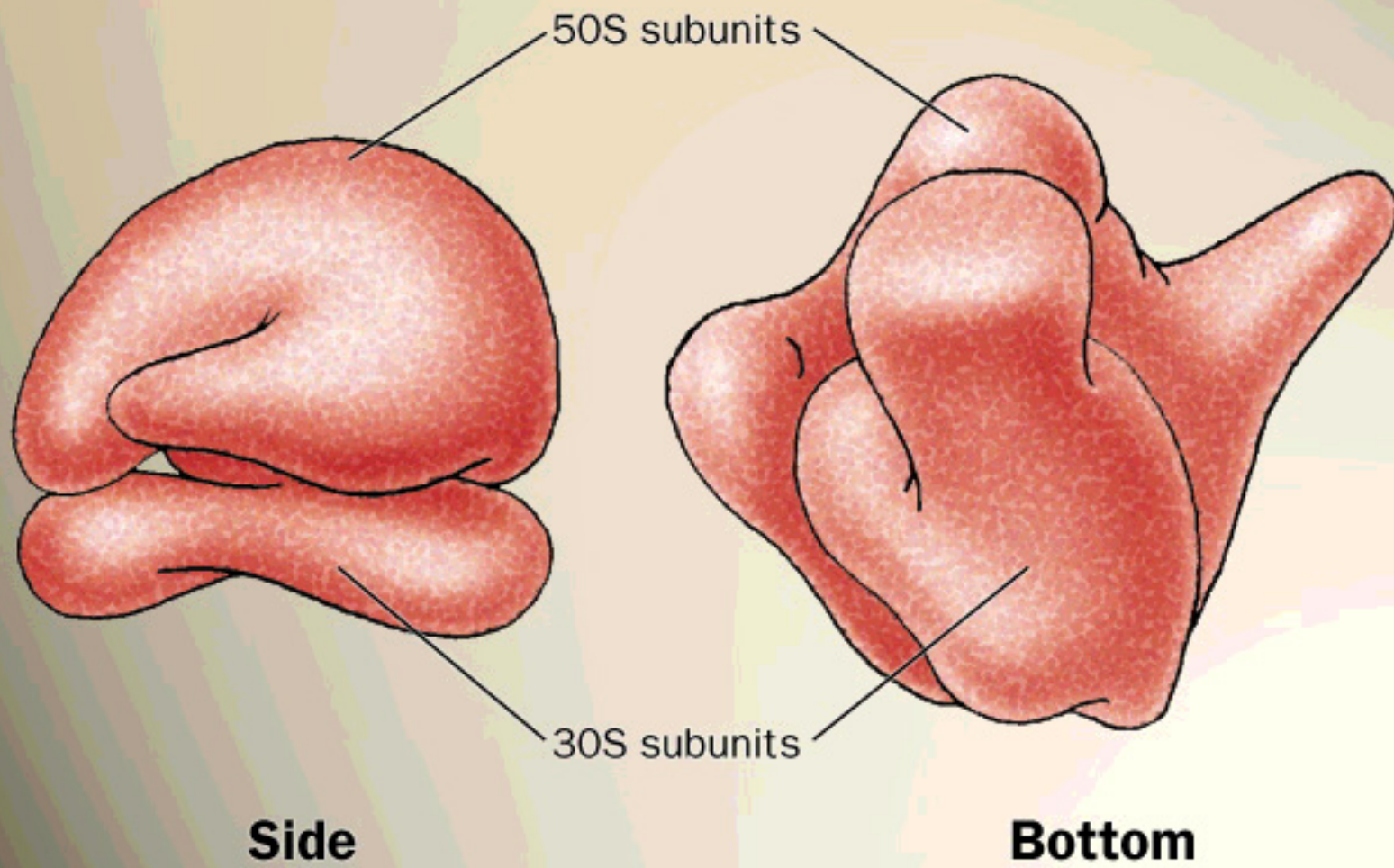
CICLO del RIBOSOMA

Iniciación

Elongación

Término

RIBOSOME



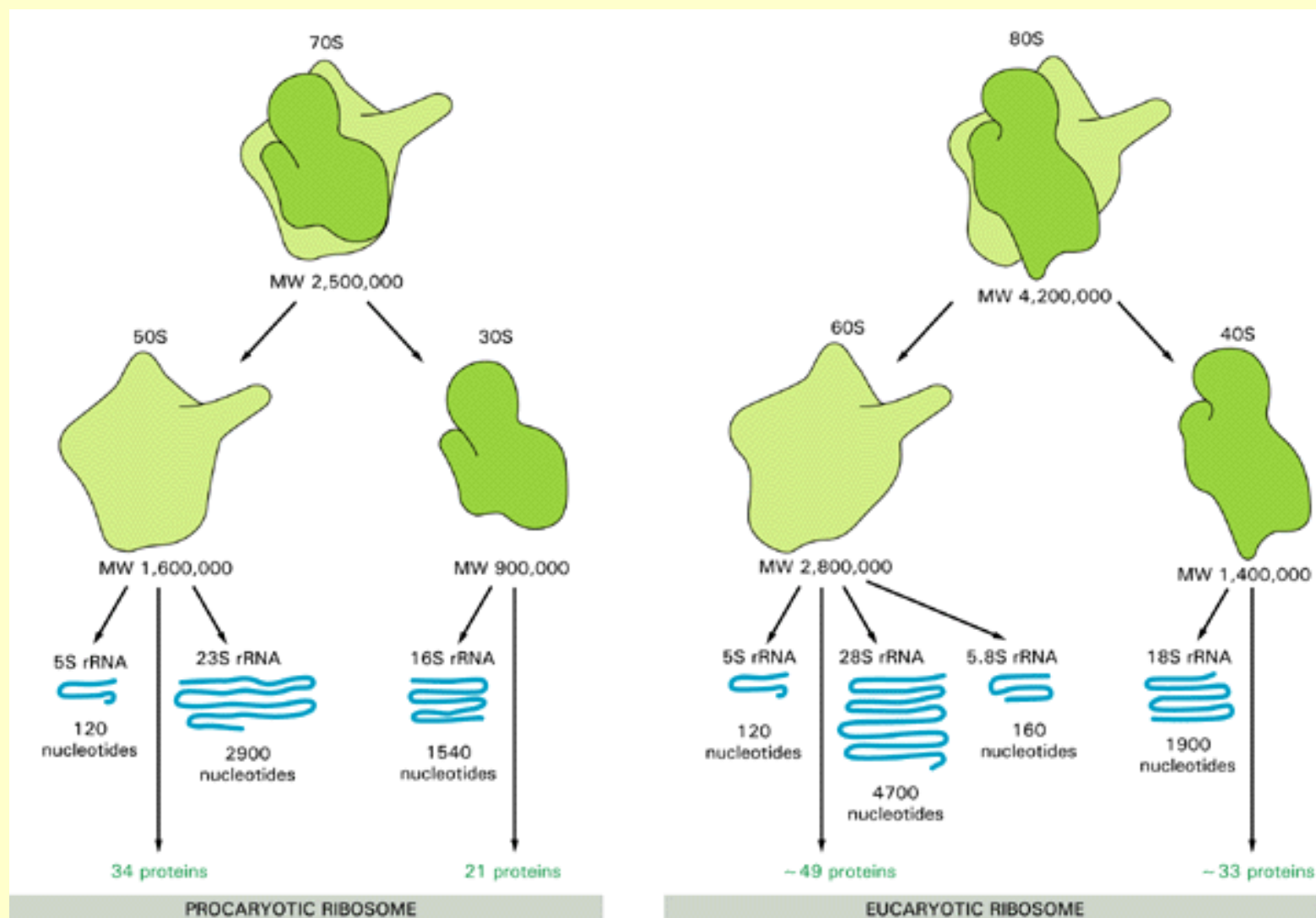
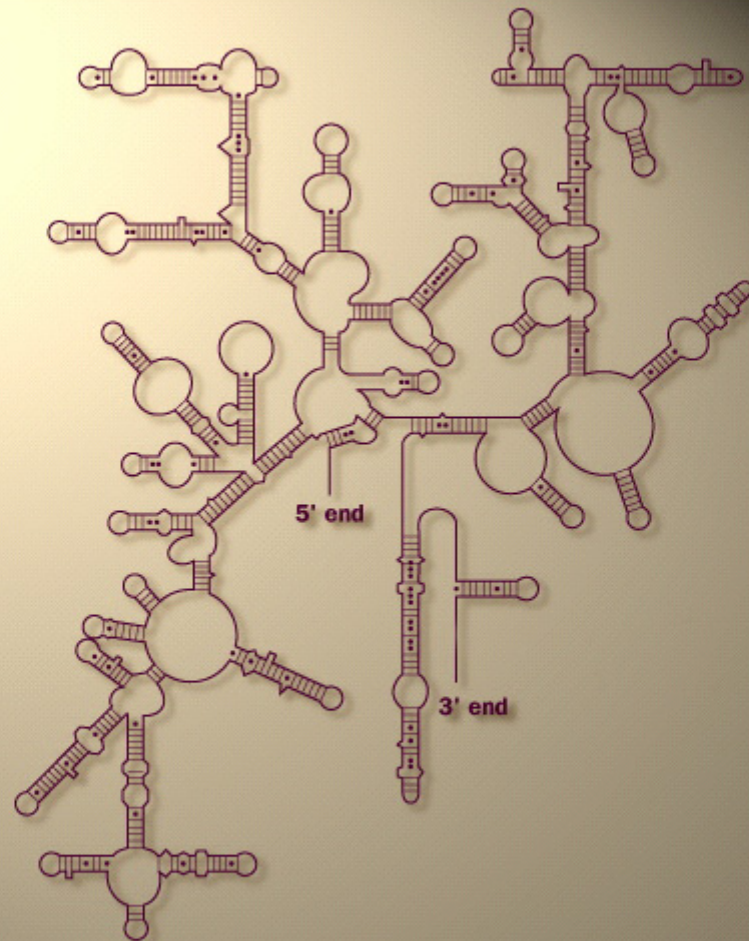


Figure 6-20. A comparison of the structures of procaryotic and eucaryotic ribosomes.

Ribosomal components are commonly designated by their "S values," which indicate their rate of sedimentation in an ultracentrifuge. Despite the differences in the number and size of their rRNA and protein components, both types of ribosomes have nearly the same structure and they function in very similar ways. Although the 18S and 28S rRNAs of the eucaryotic ribosome contain many extra nucleotides not present in their bacterial counterparts, these nucleotides are present as multiple insertions that are thought to protrude as loops and leave the basic structure of each rRNA largely unchanged.

Ribosomal RNA



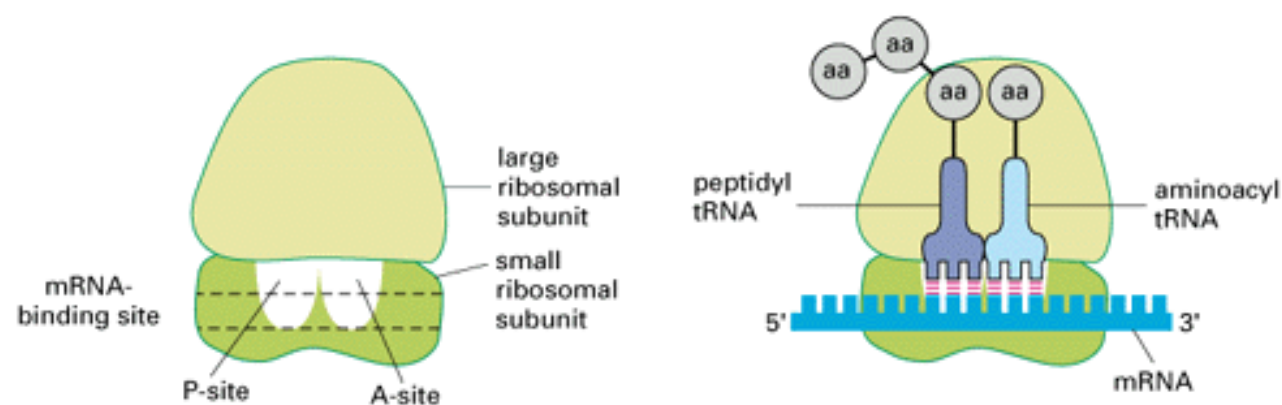
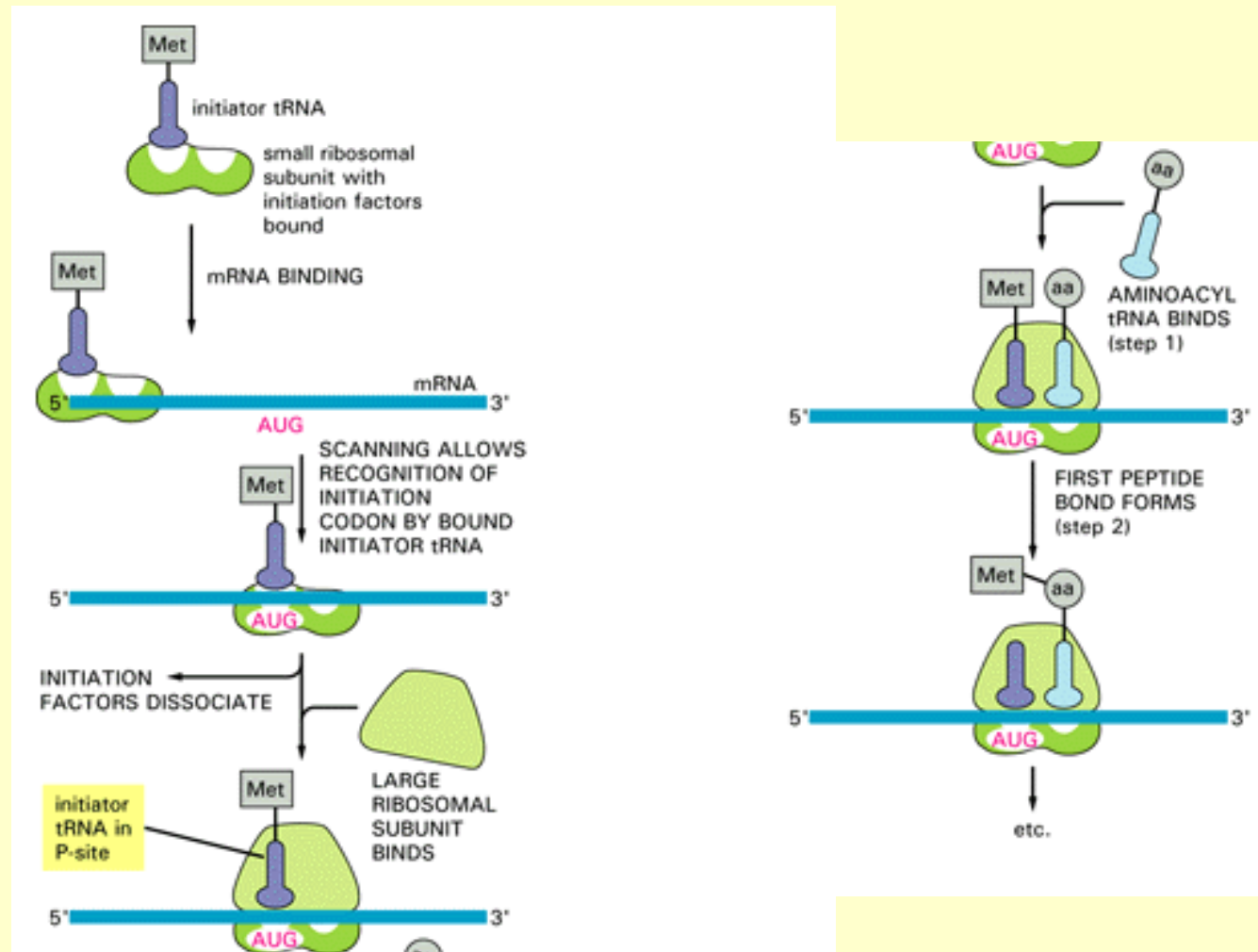


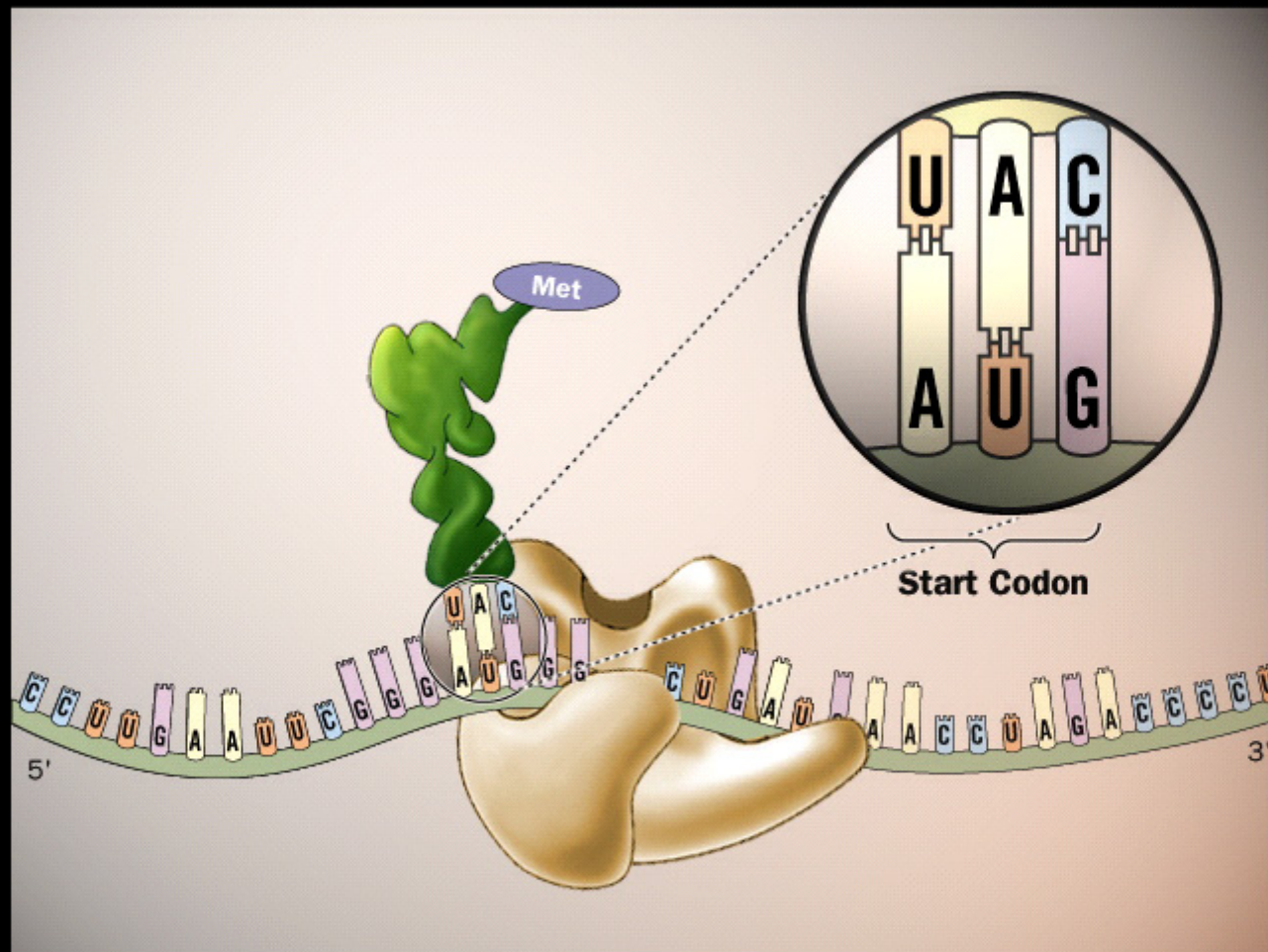
Figure 6-21. The three major RNA-binding sites on a ribosome. An empty ribosome is shown on the left and a loaded ribosome on the right. The representation of a ribosome used here and in the next three figures is highly schematic; for a more accurate view, see [Figures 6-18](#) and [6-25](#).

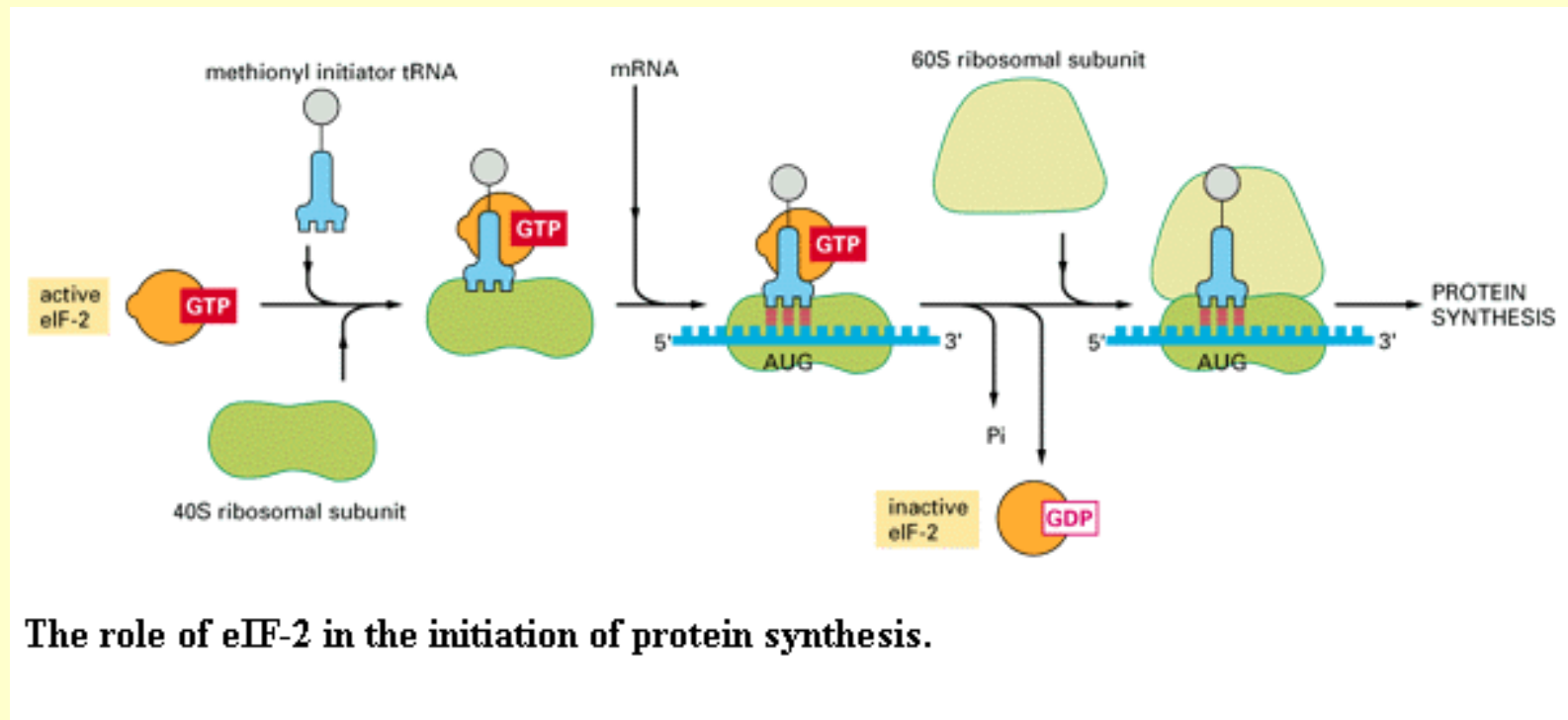
Componentes de la maquinaria biosintetizadora:

- 1.- mRNA**
- 2.- Aminoácidos**
- 3.- Energía**
- 4.- tRNA**
- 5.- Ribosomas**
- 6.- rRNA**
- 7.- Extracto celular (enzimas, factores solubles:
factores de iniciación (eIF) , elongación (eEF),
término.**

Iniciación







The role of eIF-2 in the initiation of protein synthesis.

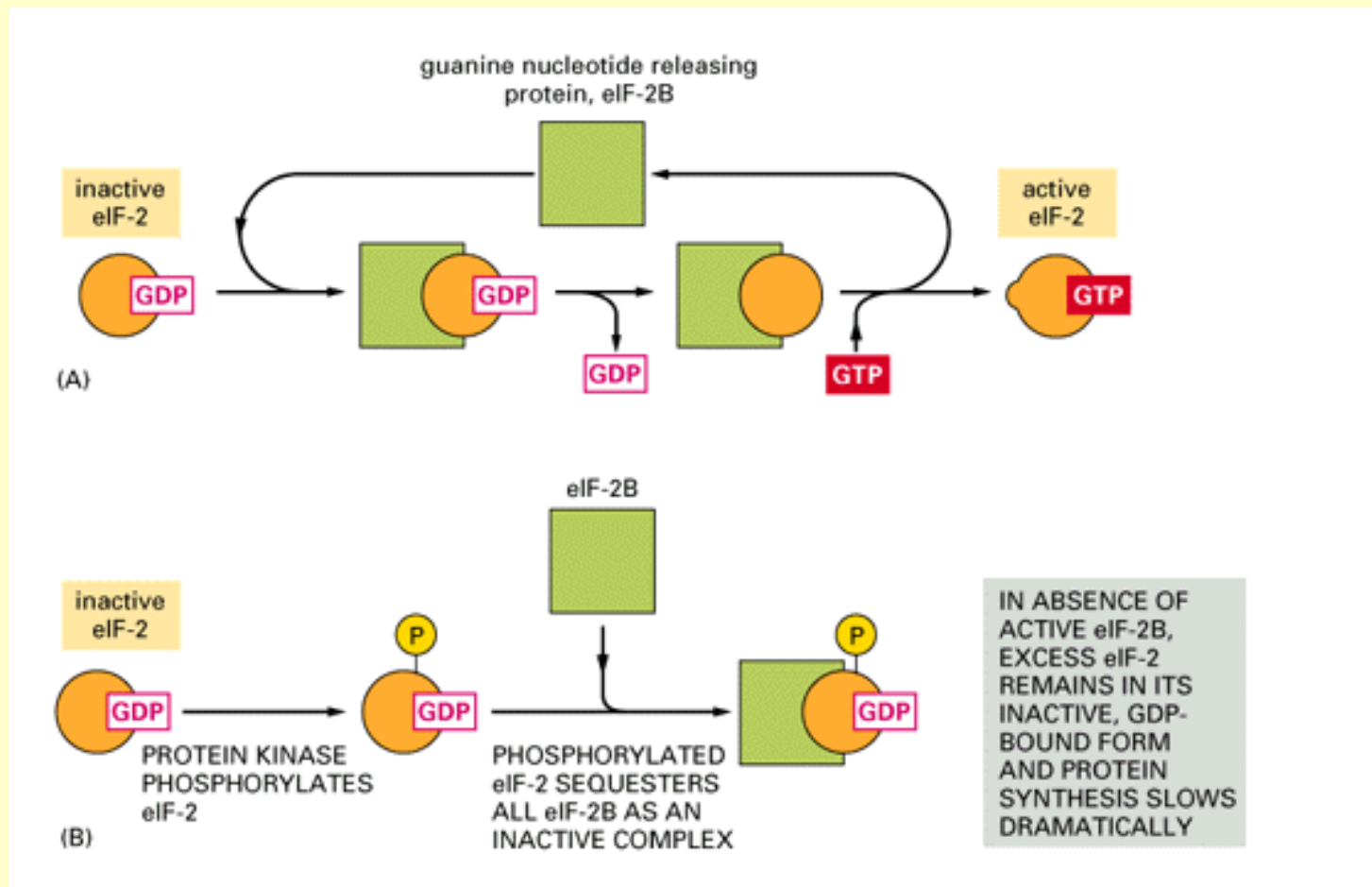
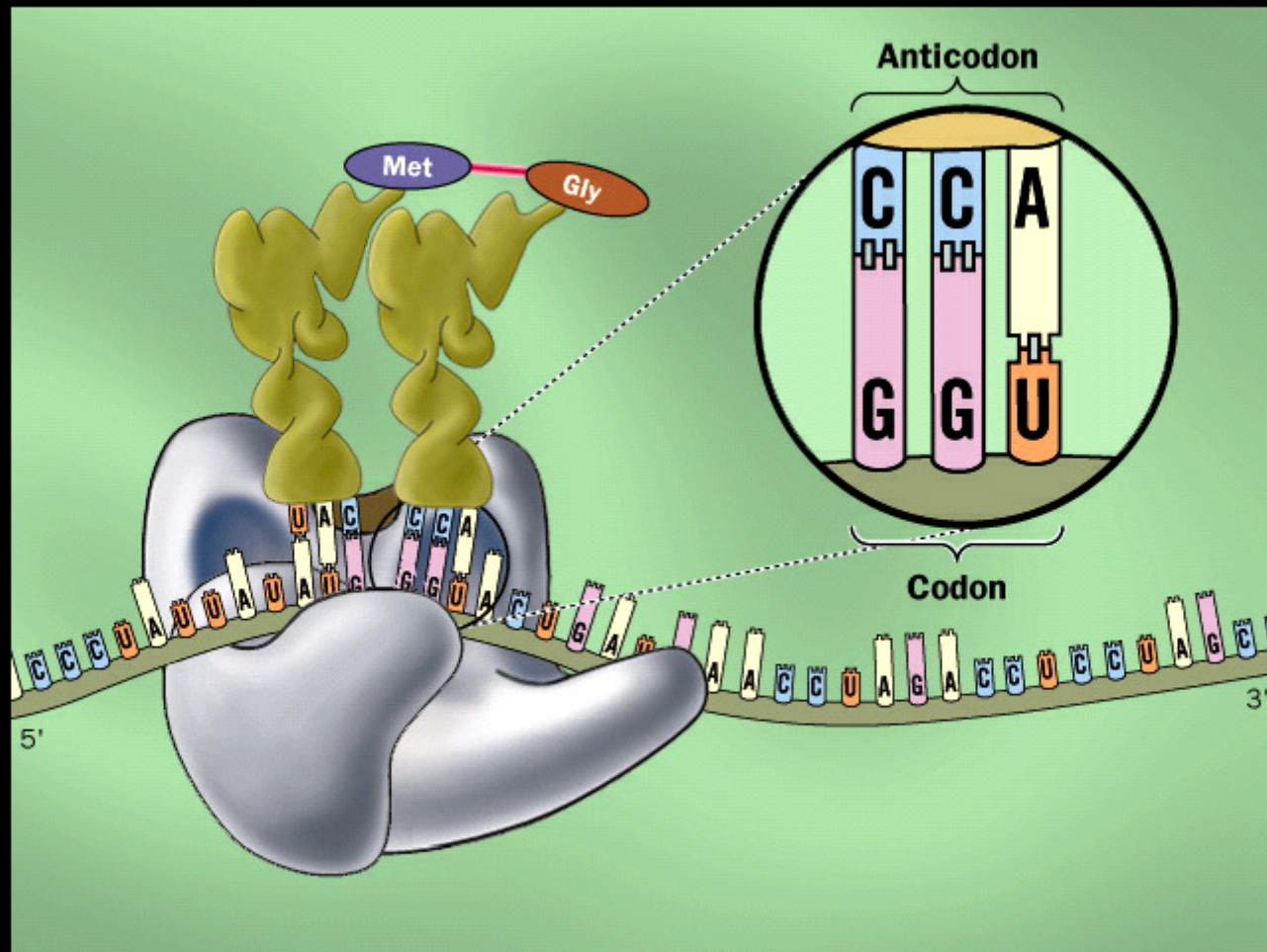
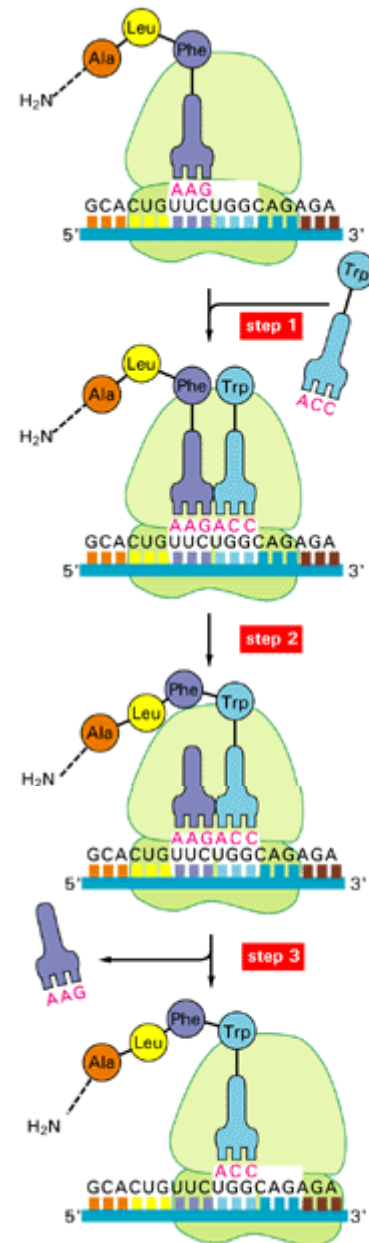


Figure 9-82. The eIF-2 cycle. (A) The recycling of used eIF-2 by a guanine nucleotide releasing protein (eIF-2B). (B) eIF-2 phosphorylation controls protein synthesis rates by tying up eIF-2B.



Elongación



Término

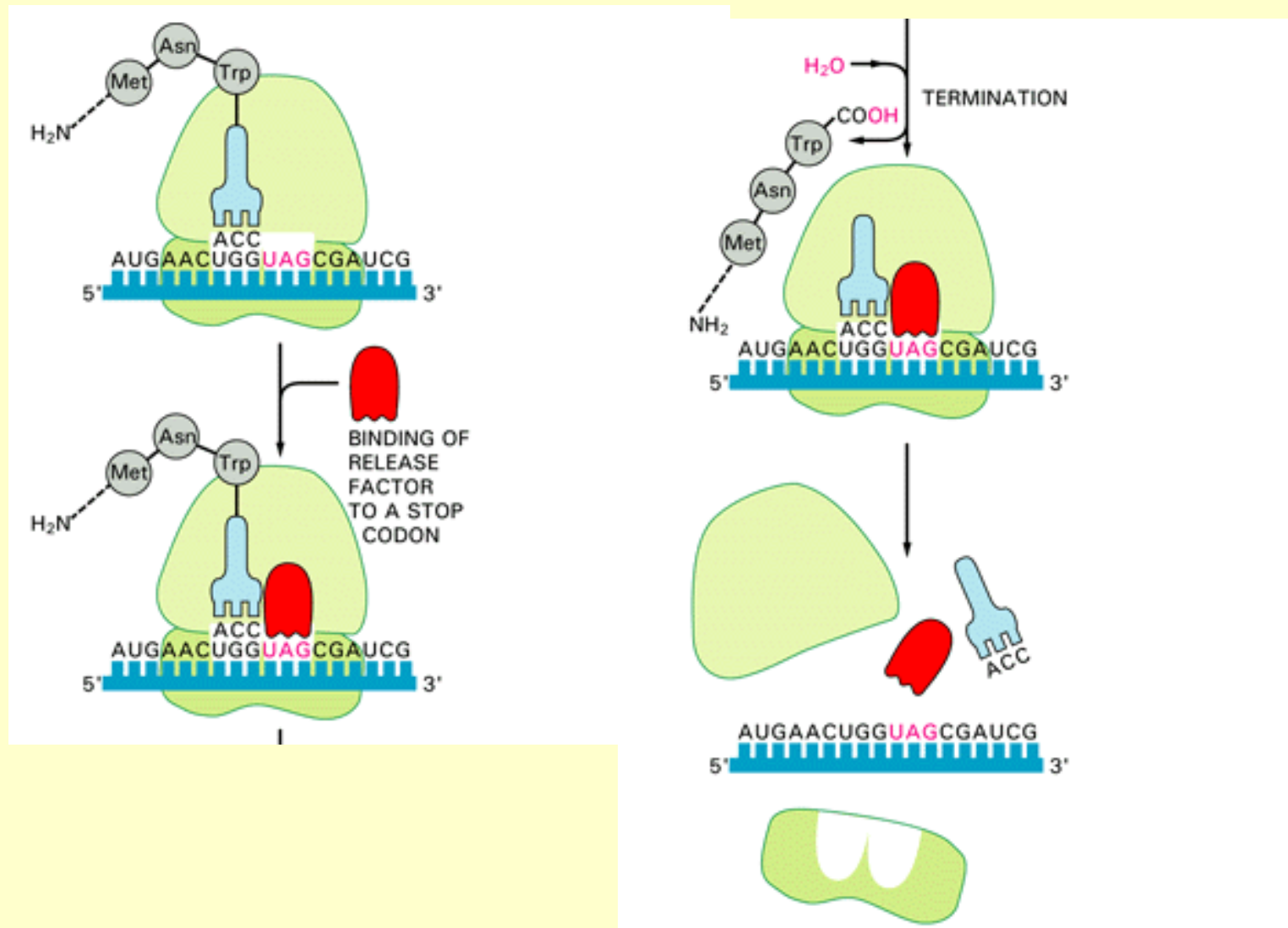
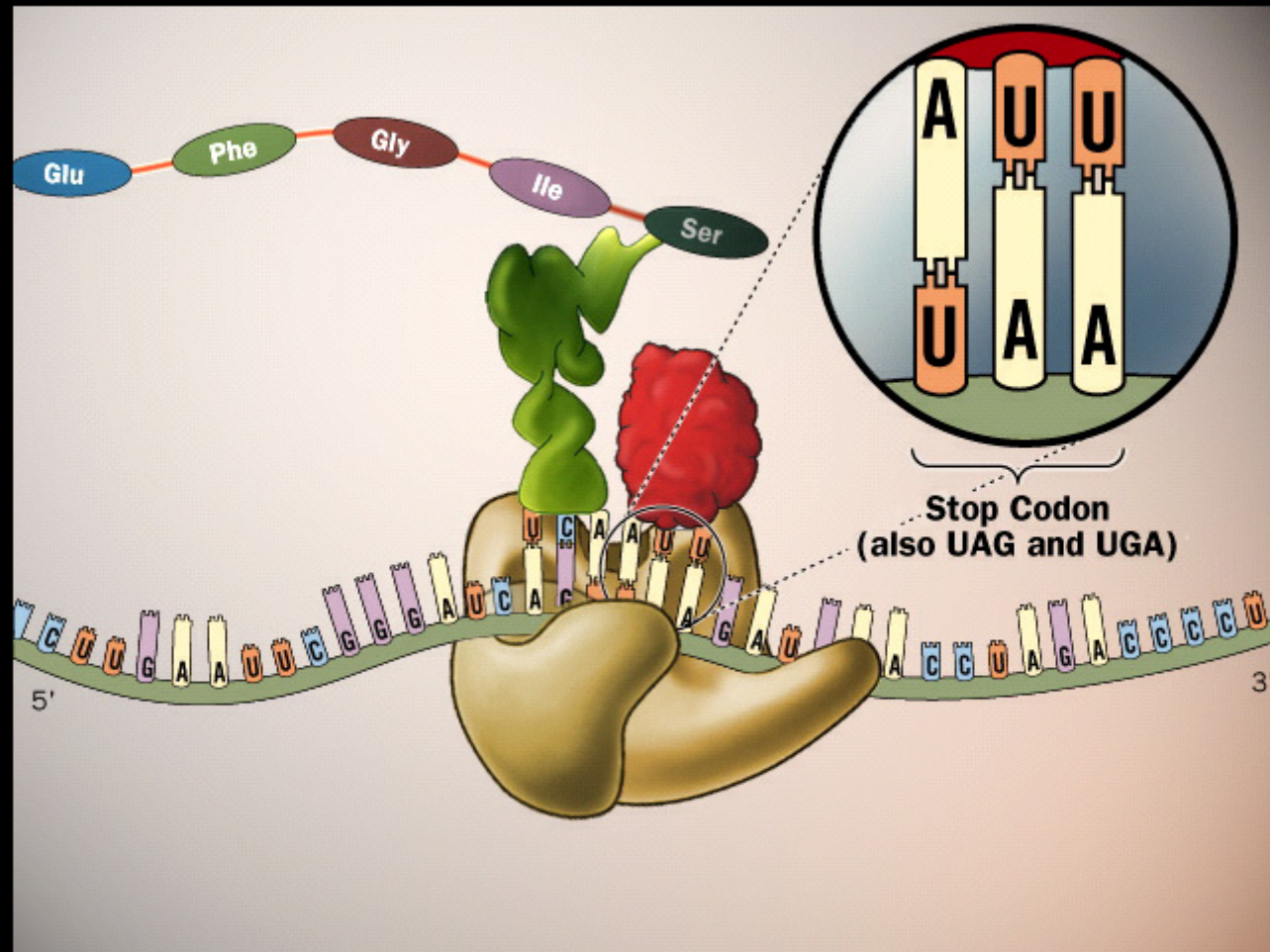
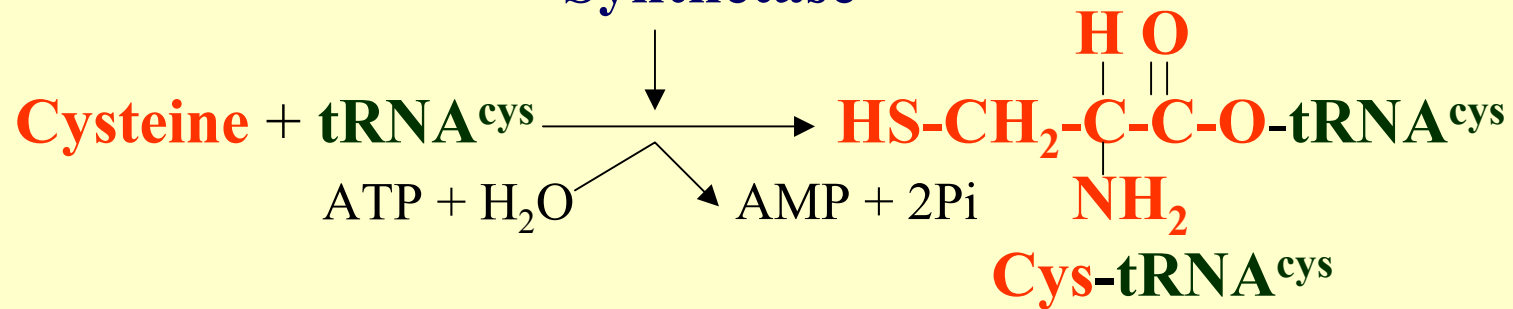


Figure 6-23. The final phase of protein synthesis. The binding of release factor to a stop codon terminates translation. The completed polypeptide is released, and the ribosome dissociates into its two separate subunits.

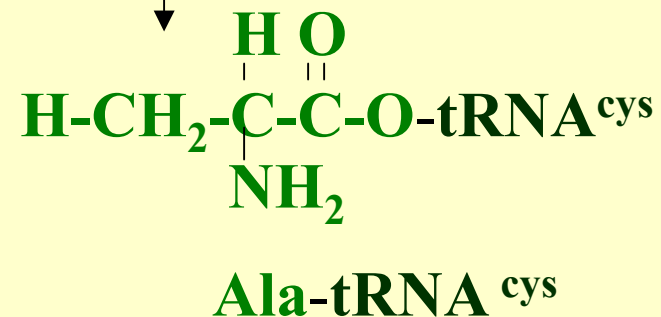


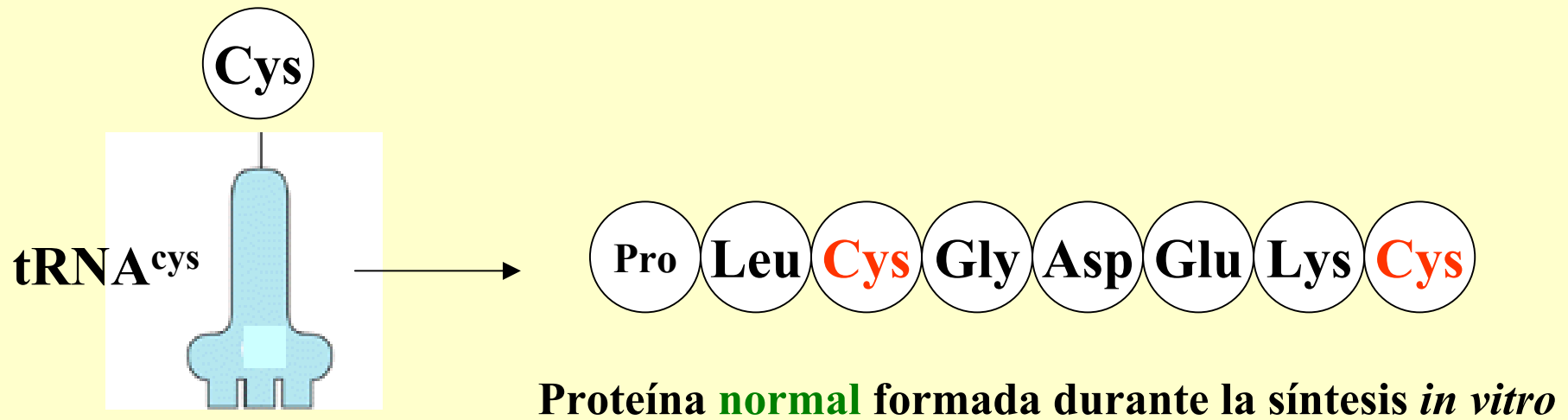
Qué funciones cumplen los aminoácidos en la síntesis proteica???

**Cysteine tRNA
Synthetase**

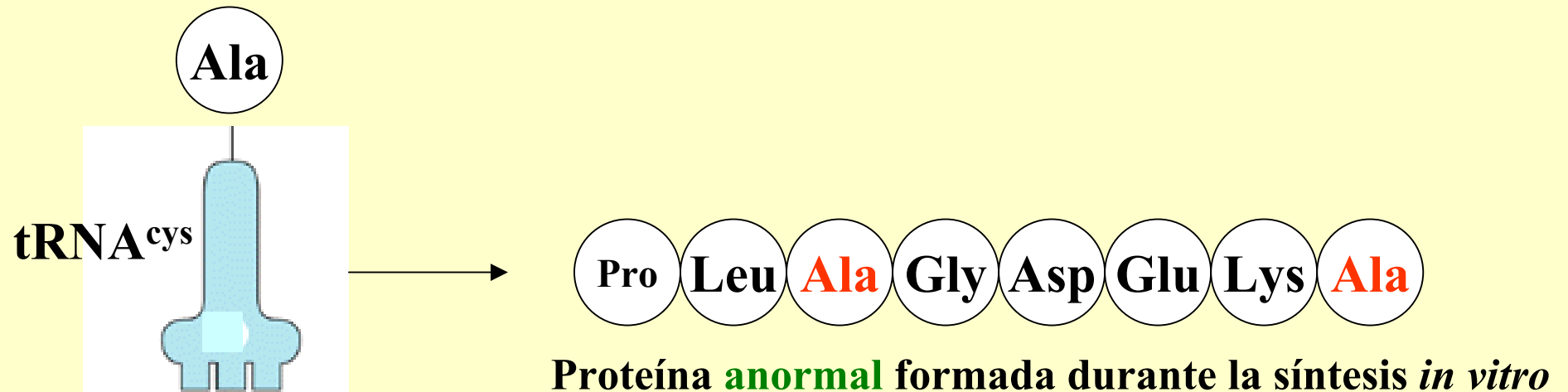


Raney Nickel





Modificación química de Cys



Ala unida a tRNA^{cys}

Factor de elongación: otro corrector de pruebas

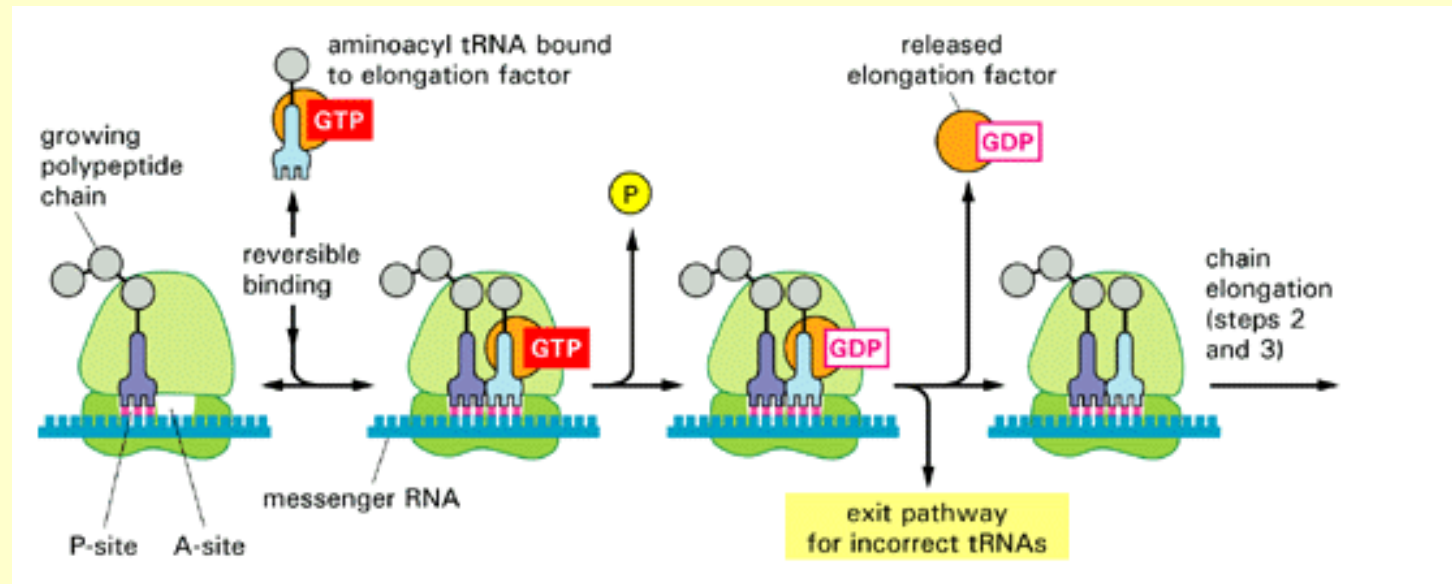
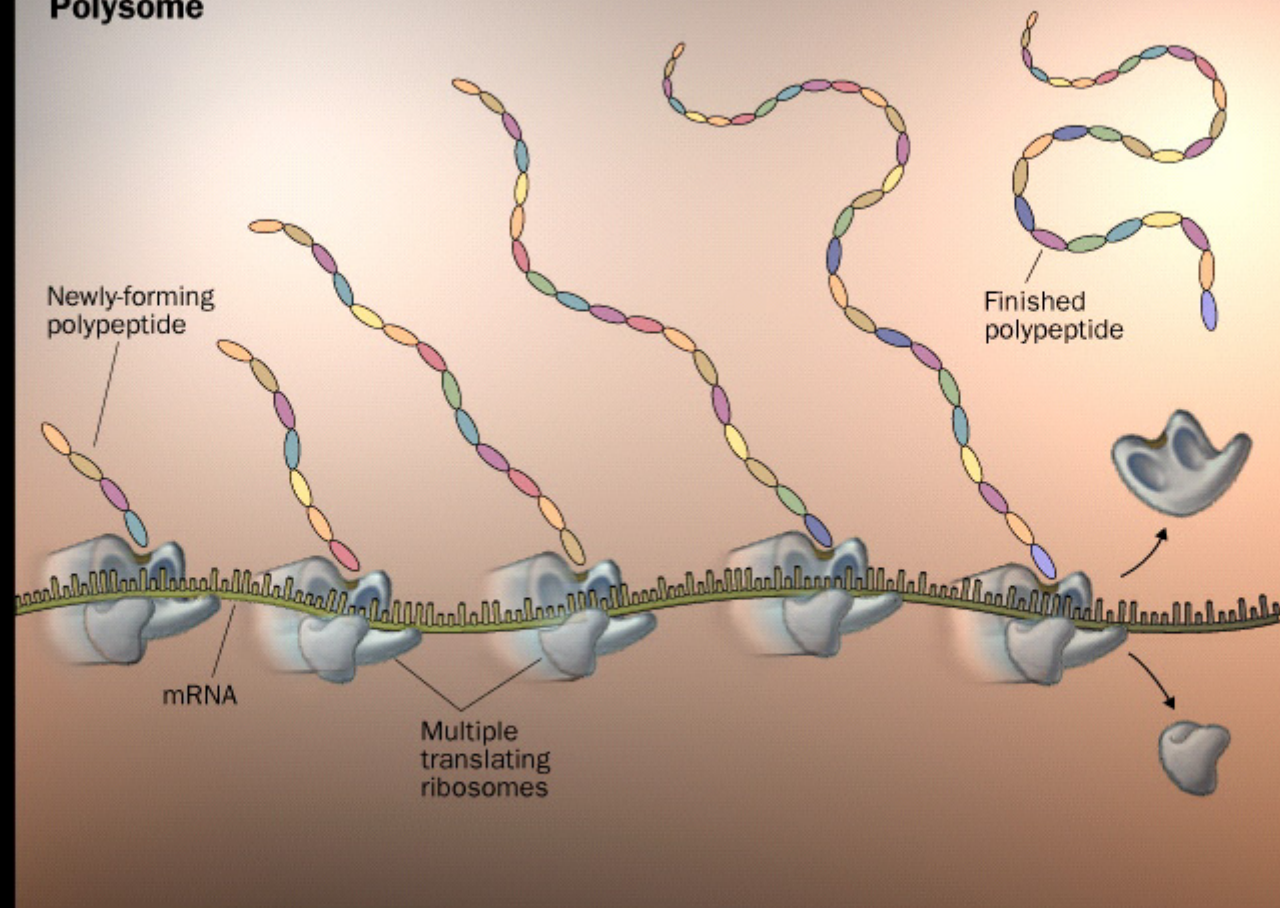


Figure 6-31. Kinetic proofreading selects for the correct tRNA molecule on the ribosome. This more detailed view of step 1 of the elongation phase of protein synthesis shows how, in the initial binding event, an aminoacyl-tRNA molecule that is tightly bound to an elongation factor pairs transiently with the codon at the A-site. This pairing triggers GTP hydrolysis by the elongation factor, enabling the factor to dissociate from the aminoacyl-tRNA molecule, which can now participate in chain elongation (see [Figure 6-22](#)). A delay between aminoacyl tRNA binding and its availability for protein synthesis is thereby inserted into the protein synthesis mechanism. As a result, only those tRNAs with the correct anticodon are likely to remain paired to the mRNA long enough to be added to the growing polypeptide chain. The elongation factor, which is an abundant protein, is called EF-Tu in procaryotes and EF-1 in eucaryotes. The dramatic change in the three-dimensional structure of EF-Tu that is caused by GTP hydrolysis is illustrated in [Figure 5-20](#).

Polysome



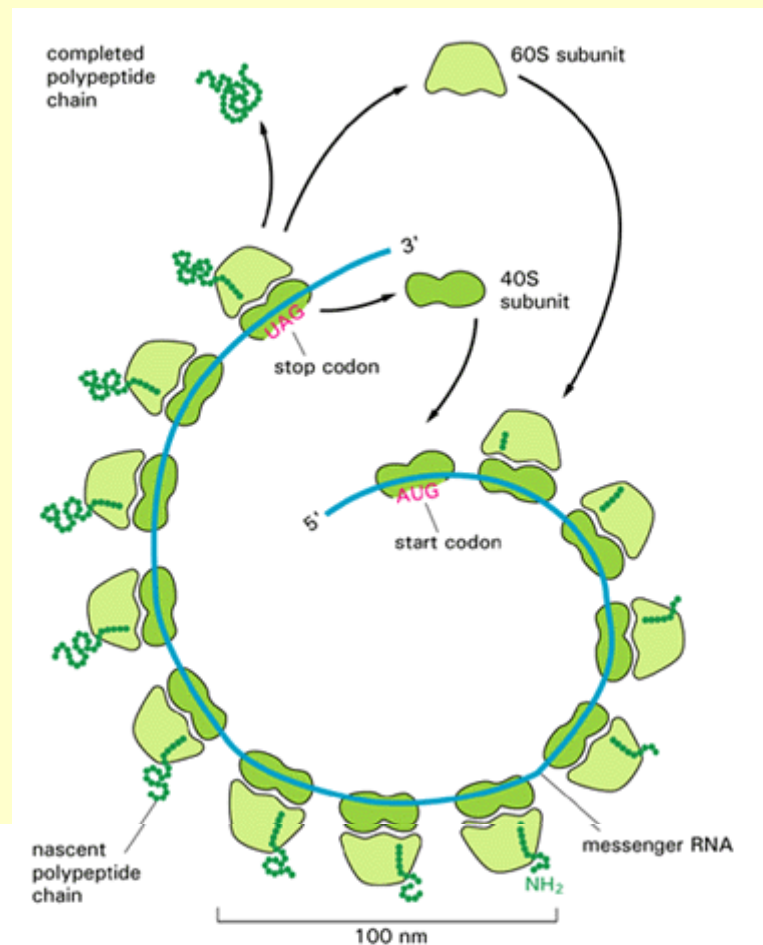
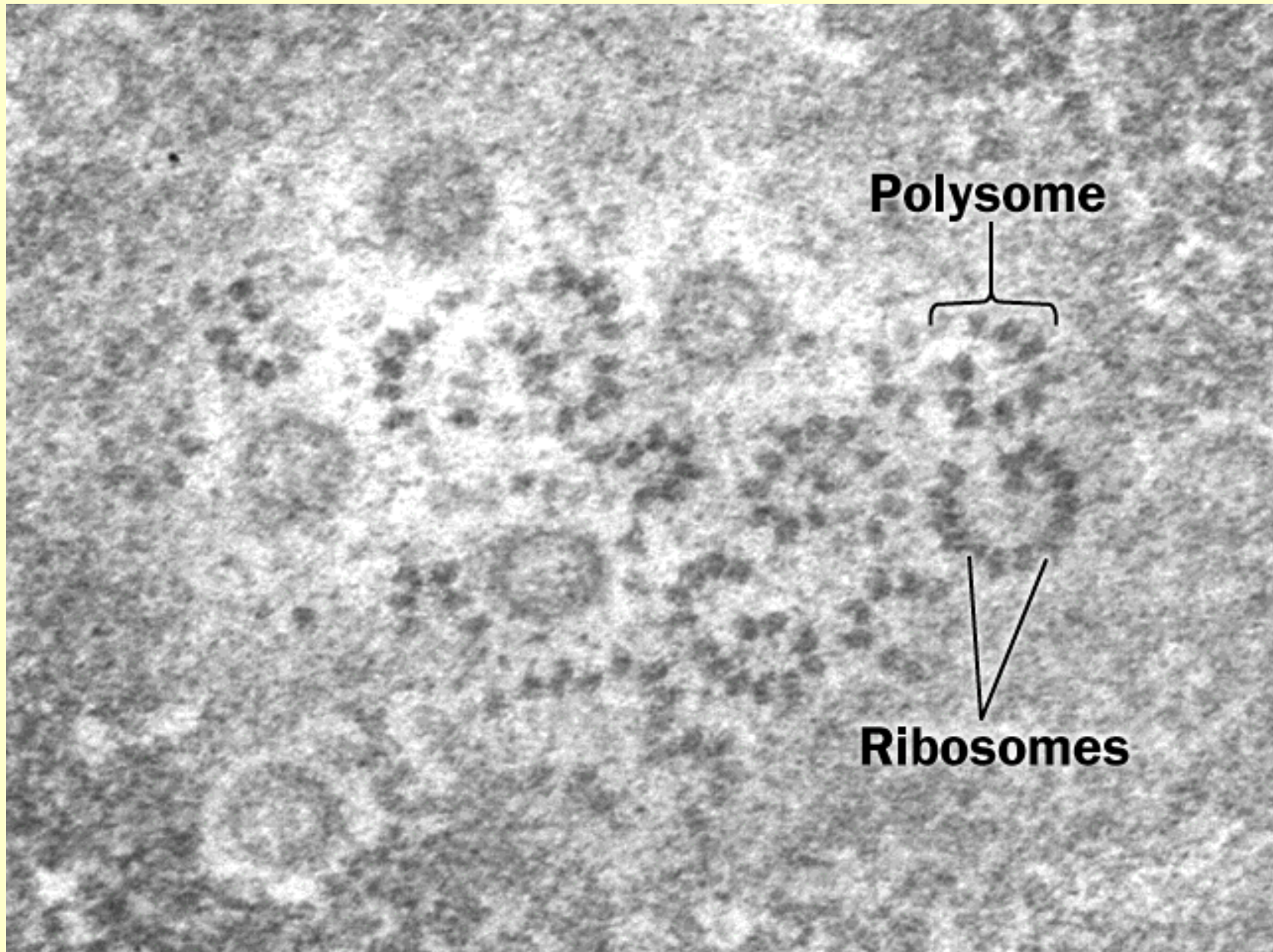
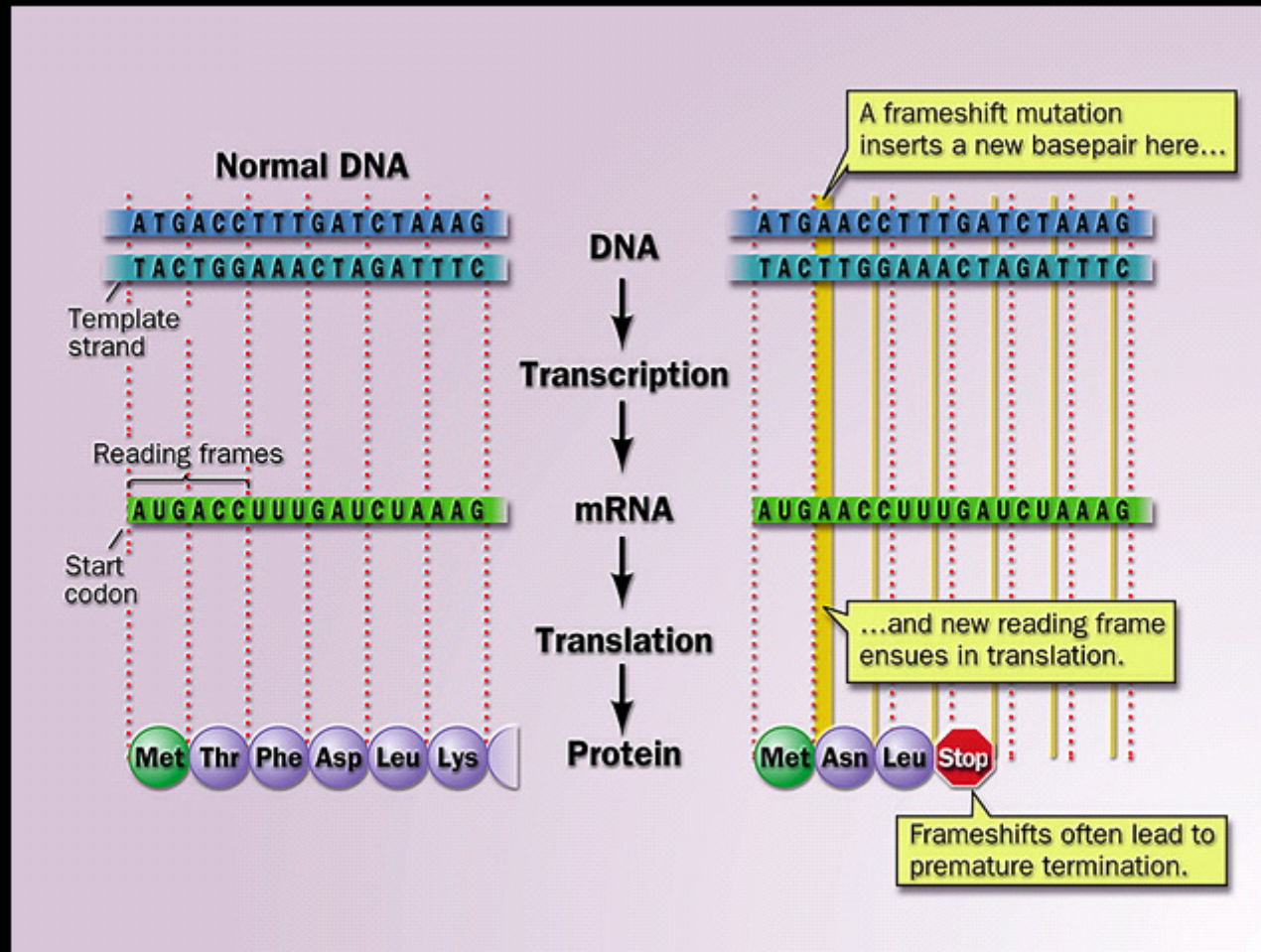
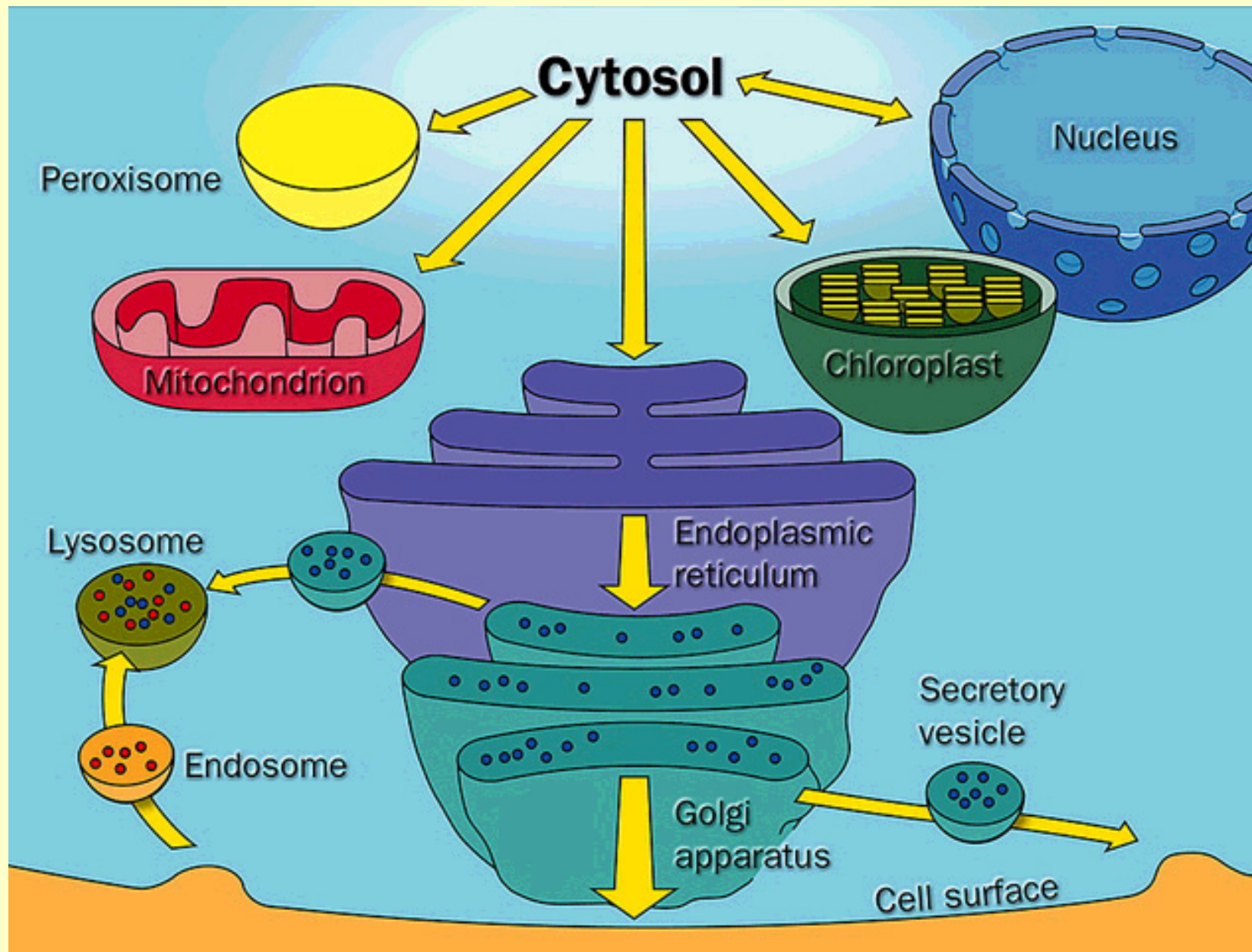


Figure 6-28. A polyribosome. Schematic drawing showing how a series of ribosomes can simultaneously translate the same mRNA molecule.







Destino de las proteínas que se están sintetizando:

RER, Golgi, membrana plasmática, secreción

