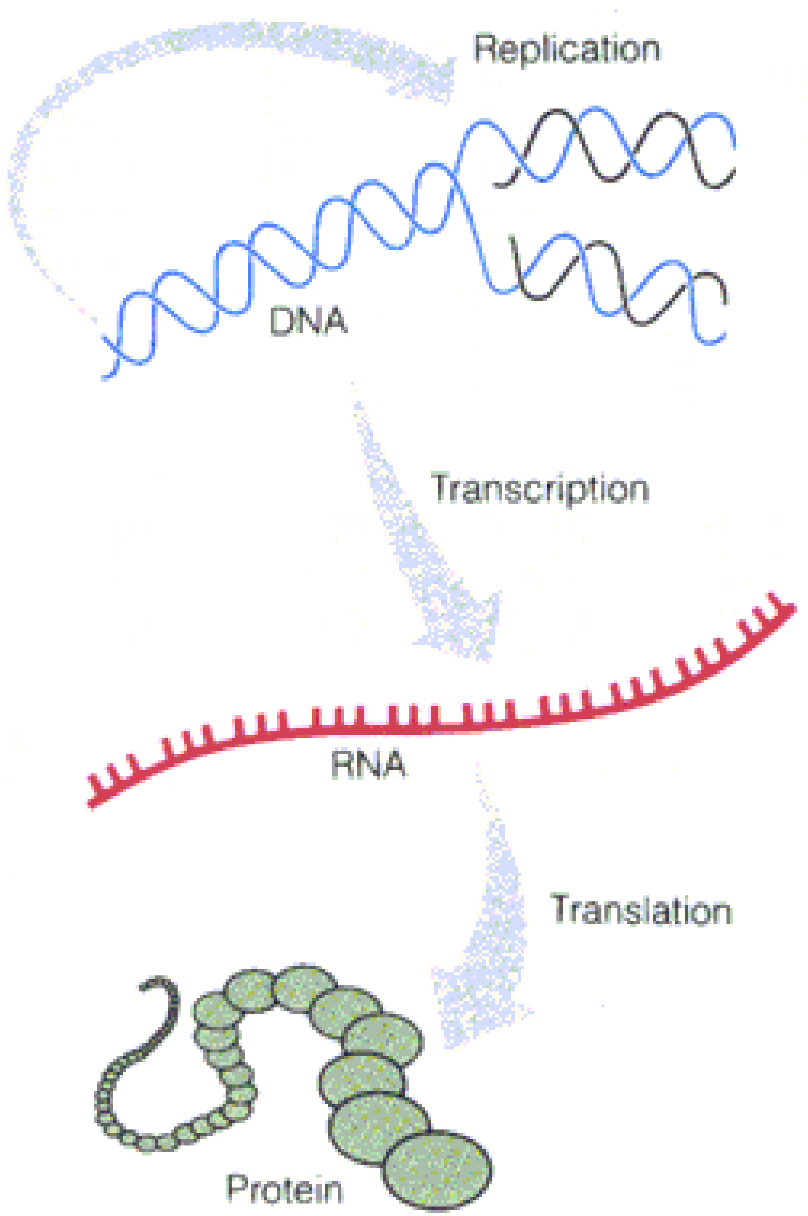
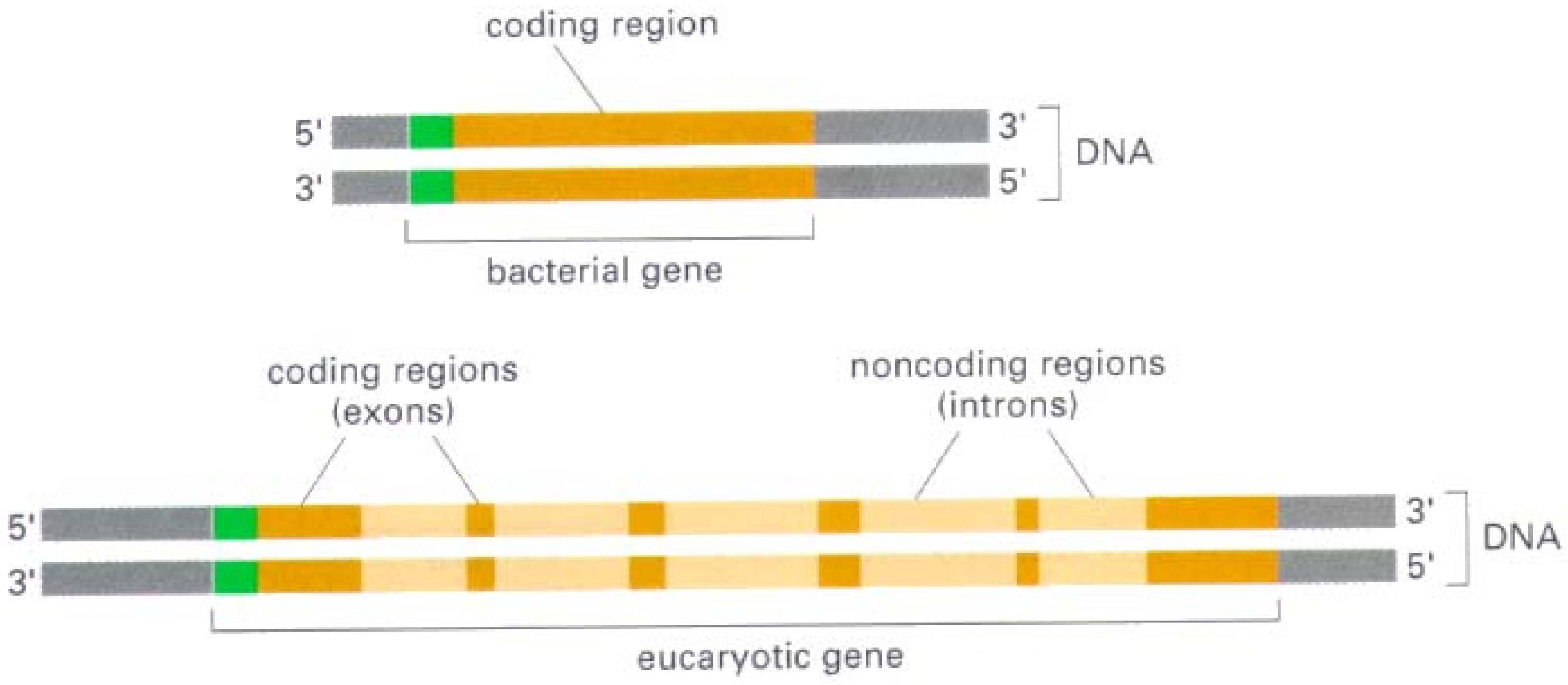
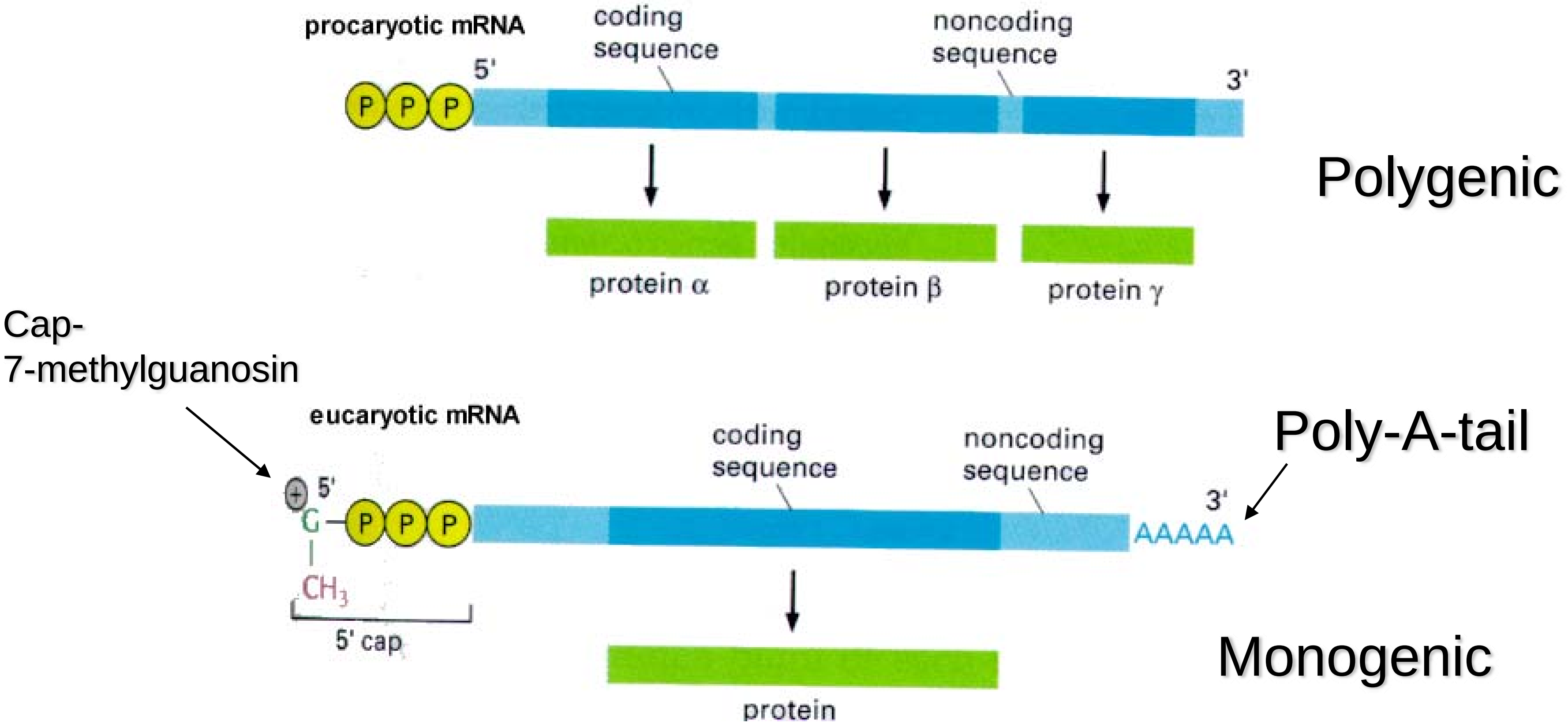
Gene Expression
-Translation-


Replication
DNA
Transcription
RNA
Translation
Protein

Comparison of a Bacterial Gene with a Eucaryotic Gene



A Comparison of Procaryotic and Eucaryotic mRNAs



Summary: From Gene to Protein

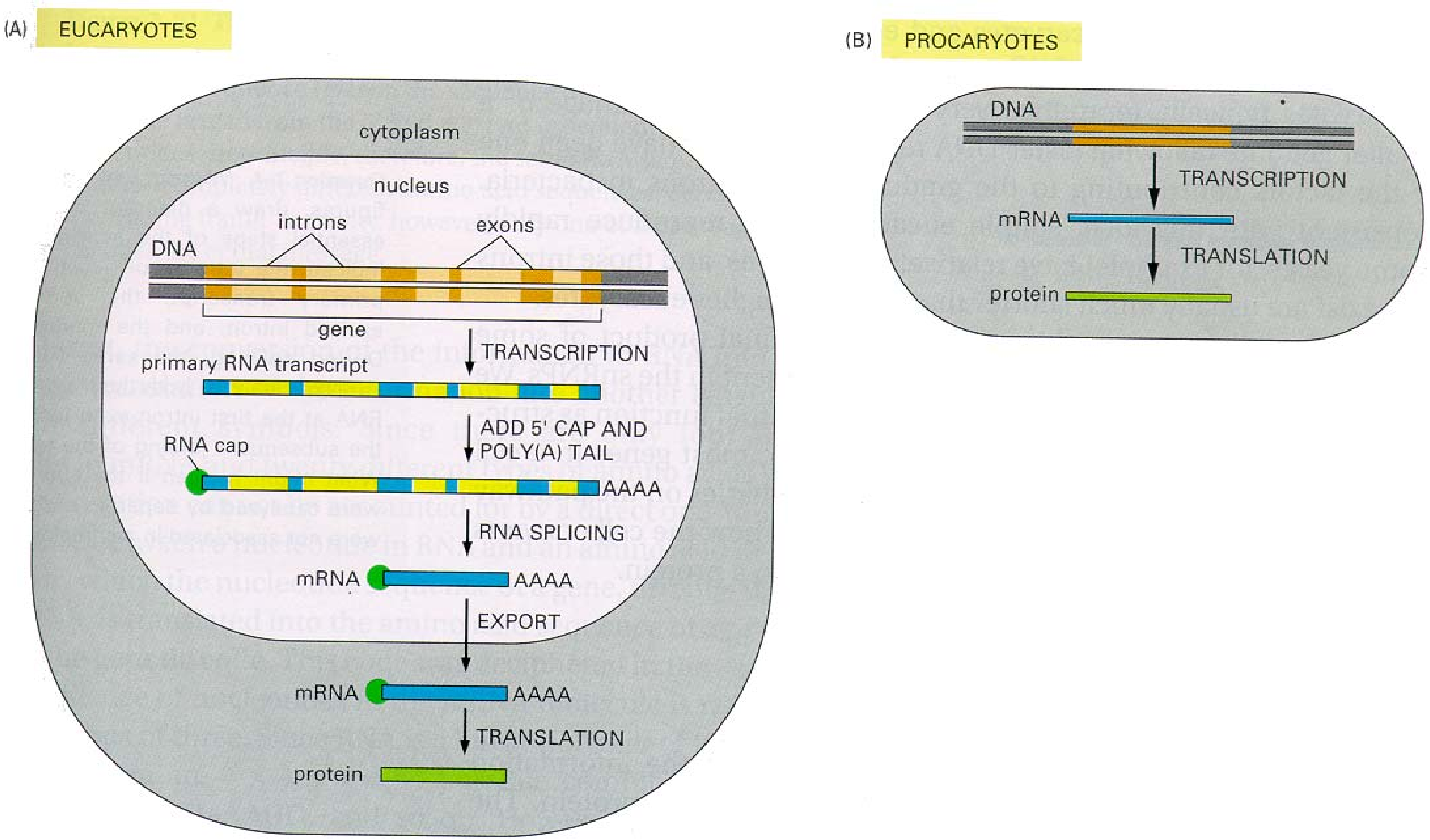


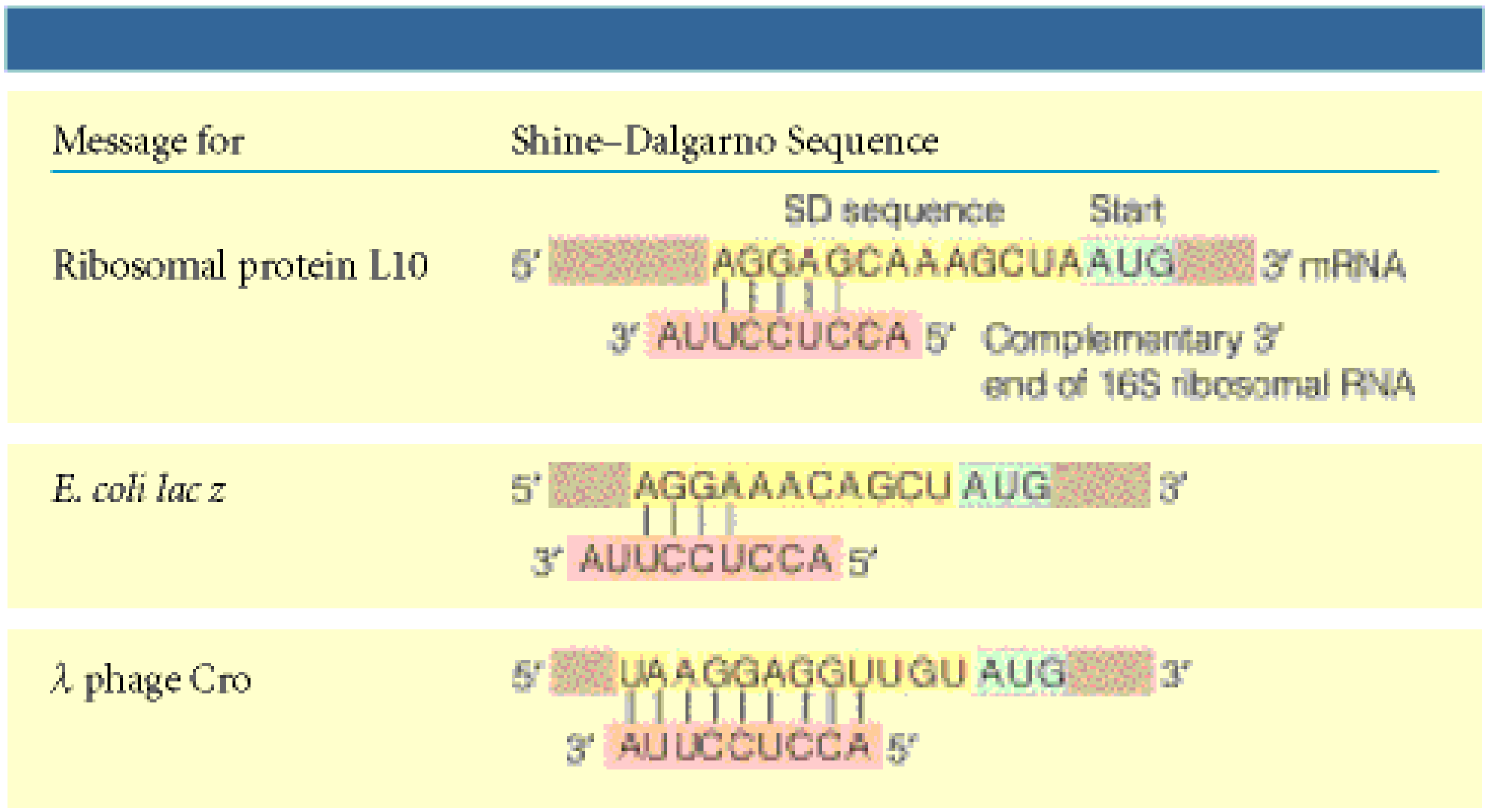
Table 6.6 Ribosome Structure

Property	Prokaryote	Eukaryote
Overall Size	70S	80S
Small subunit	30S	40S
No. of proteins	~21	~30
RNA size (No. of bases)	16S (1500)	18S (2300)
Large subunit	50S	60S
No. of proteins	~34	~50
RNA size (No of bases)	23S (2900)	28s (4200
	5S (120	5.8S (160)
		5S (120)

Shine-Dalgarno Sequences

Help align ribosomes on mRNA to properly start translation

Can base-pair with a sequence contained in the ribosomal RNA



The Genetic Code

$4^n > 20$, when $n=\{3,4,5,\ldots\}$

First position (5′ end)	Second position: U	C	A	G	Third position (3′ end)
U	UUU Phe	UCU Ser	UAU Tyr	UGU Cys	U
U	UUC Phe	UCC Ser	UAC Tyr	UGC Cys	C
U	UUA Leu	UCA Ser	UAA Stop	UGA Stop	A
U	UUG Leu	UCG Ser	UAG Stop	UGG Trp	G
C	CUU Leu	CCU Pro	CAU His	CGU Arg	U
C	CUC Leu	CCC Pro	CAC His	CGC Arg	C
C	CUA Leu	CCA Pro	CAA Gln	CGA Arg	A
C	CUG Leu	CCG Pro	CAG Gln	CGG Arg	G
A	AUU Ile	ACU Thr	AAU Asn	AGU Ser	U
A	AUC Ile	ACC Thr	AAC Asn	AGC Ser	C
A	AUA Ile	ACA Thr	AAA Lys	AGA Arg	A
A	AUG Met	ACG Thr	AAG Lys	AGG Arg	G
G	GUU Val	GCU Ala	GAU Asp	GGU Gly	U
G	GUC Val	GCC Ala	GAC Asp	GGC Gly	C
G	GUA Val	GCA Ala	GAA Glu	GGA Gly	A
G	GUG Val	GCG Ala	GAG Glu	GGG Gly	G

Triplet code (why?)

Non-overlapping, unpunctuated

Nearly universal

Codon = group of three consecutive nucleotides

Start codon (in green)

- AUG

Stop codons (in orange)

- UAA
- UAG
- UGA

Redundant (usually the 3rd letter)

TABLE 6.5 The genetic code as expressed by triplet base sequences of mRNA[a]

Codon	Amino acid	Codon	Amino acid	Codon	Amino acid	Codon	Amino acid
UUU	Phenylalanine	UCU	Serine	UAU	Tyrosine	UGU	Cysteine
UUC	Phenylalanine	UCC	Serine	UAC	Tyrosine	UGC	Cysteine
UUA	Leucine	UCA	Serine	UAA	None (stop signal)	UGA	None (stop signal)
UUG	Leucine	UCG	Serine	UAG	None (stop signal)	UGG	Tryptophan
CUU	Leucine	CCU	Proline	CAU	Histidine	CGU	Arginine
CUC	Leucine	CCC	Proline	CAC	Histidine	CGC	Arginine
CUA	Leucine	CCA	Proline	CAA	Glutamine	CGA	Arginine
CUG	Leucine	CCG	Proline	CAG	Glutamine	CGG	Arginine
AUU	Isoleucine	ACU	Threonine	AAU	Asparagine	AGU	Serine
AUC	Isoleucine	ACC	Threonine	AAC	Asparagine	AGC	Serine
AUA	Isoleucine	ACA	Threonine	AAA	Lysine	AGA	Arginine
AUG (start)[b]	Methionine	ACG	Threonine	AAG	Lysine	AGG	Arginine
GUU	Valine	GCU	Alanine	GAU	Aspartic acid	GGU	Glycine
GUC	Valine	GCC	Alanine	GAC	Aspartic acid	GGC	Glycine
GUA	Valine	GCA	Alanine	GAA	Glutamic acid	GGA	Glycine
GUG	Valine	GCG	Alanine	GAG	Glutamic acid	GGG	Glycine

a The boxes of codons are colored according to the scheme: ionizable: acidic, ionizable: basic, nonionizable polar, and nonpolar (Figure 2.12). The nucleotide on the left is at the 5′-end of the triplet.

b AUG encodes *N*-formylmethionine at the beginning of mRNAs of Bacteria.

Transfer RNAs (tRNAs)

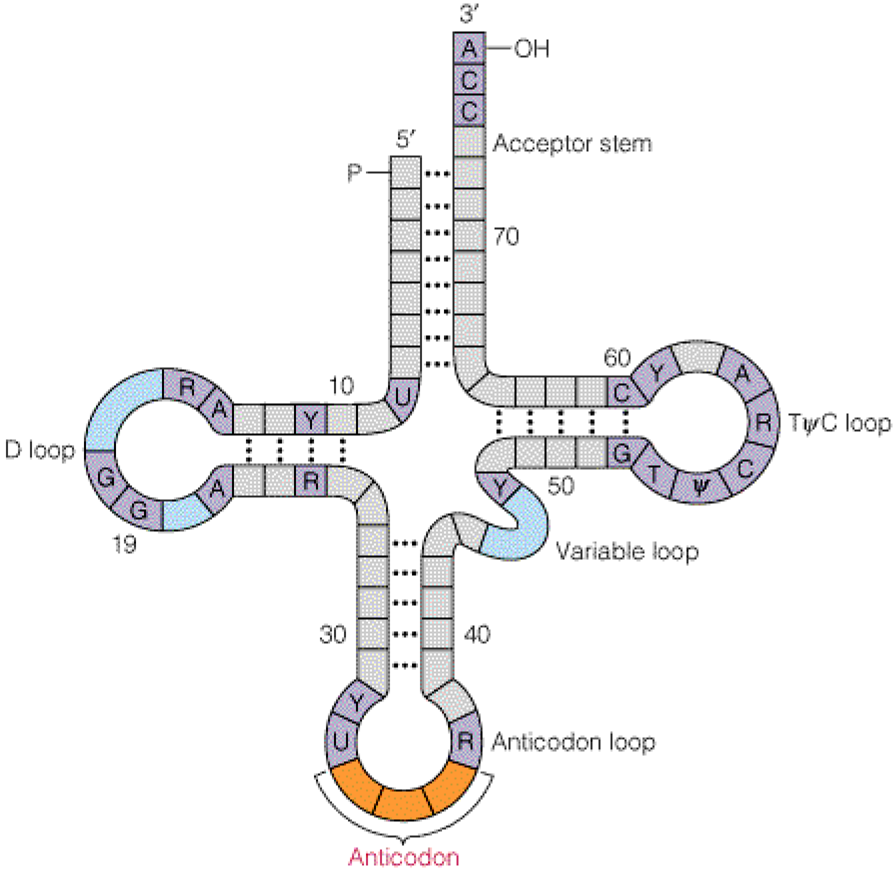
Adaptor molecules that match amino acids to codons in mRNA.

Any cell contains different types of tRNA molecules sufficient to incorporate all 20 amino acids into protein.

Some tRNAs can recognise more than one codon.

About 80 nucleotides in length.

Structures of tRNAs

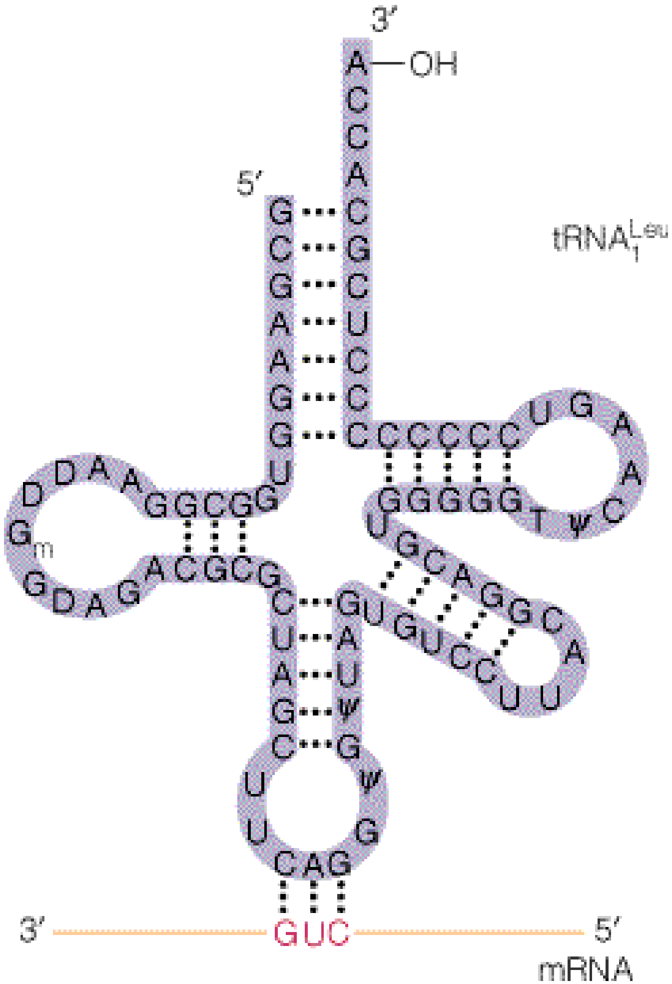


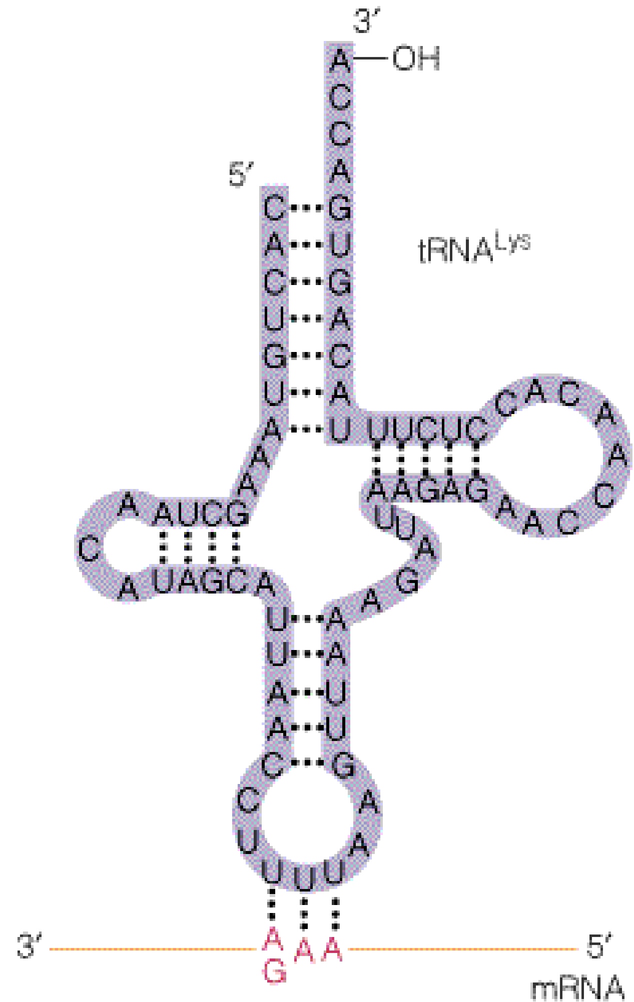
All tRNAs share a general common structure that includes:

- an anticodon triplet loop (pairs with mRNA codons)

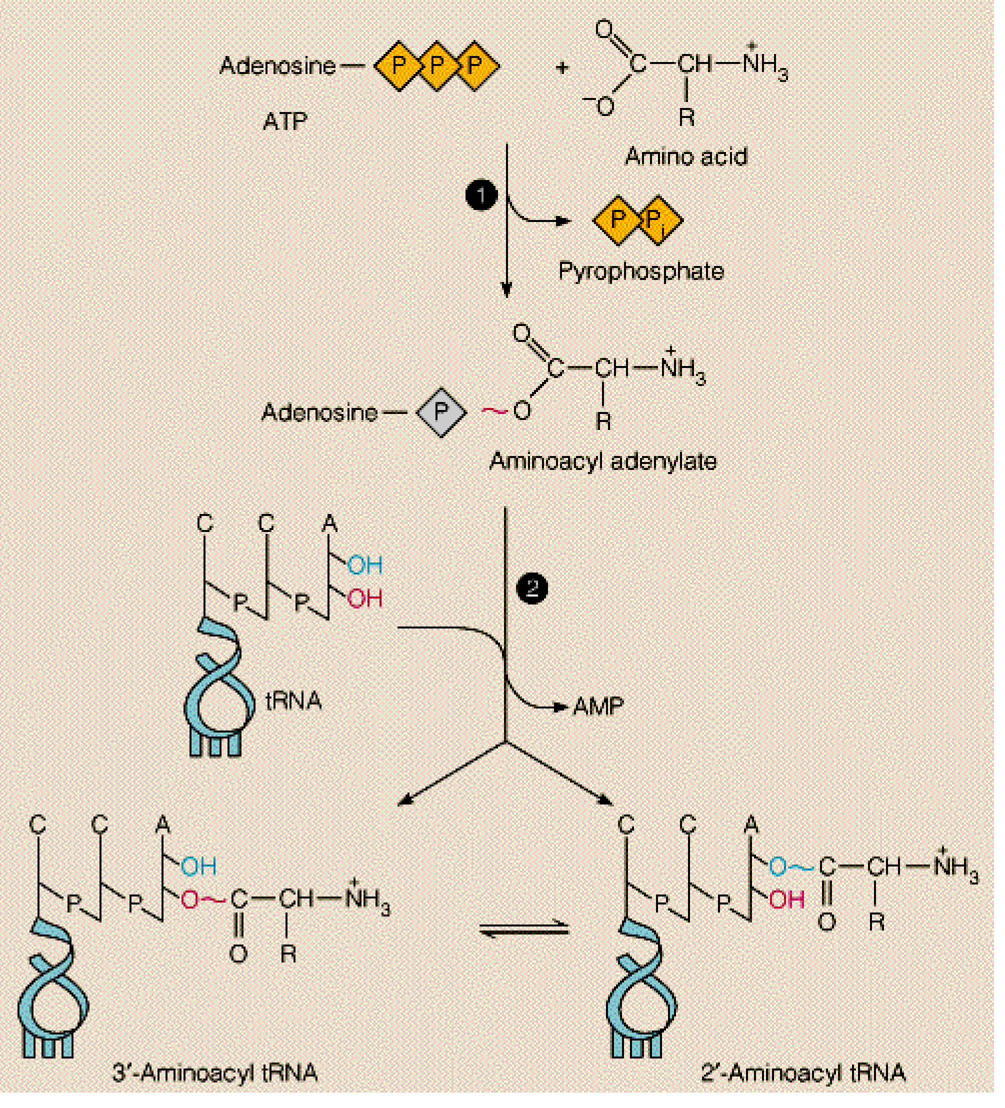
- an acceptor stem (to which the amino acid is attached)

Structures of tRNAs





Coupling of amino acids to tRNAs

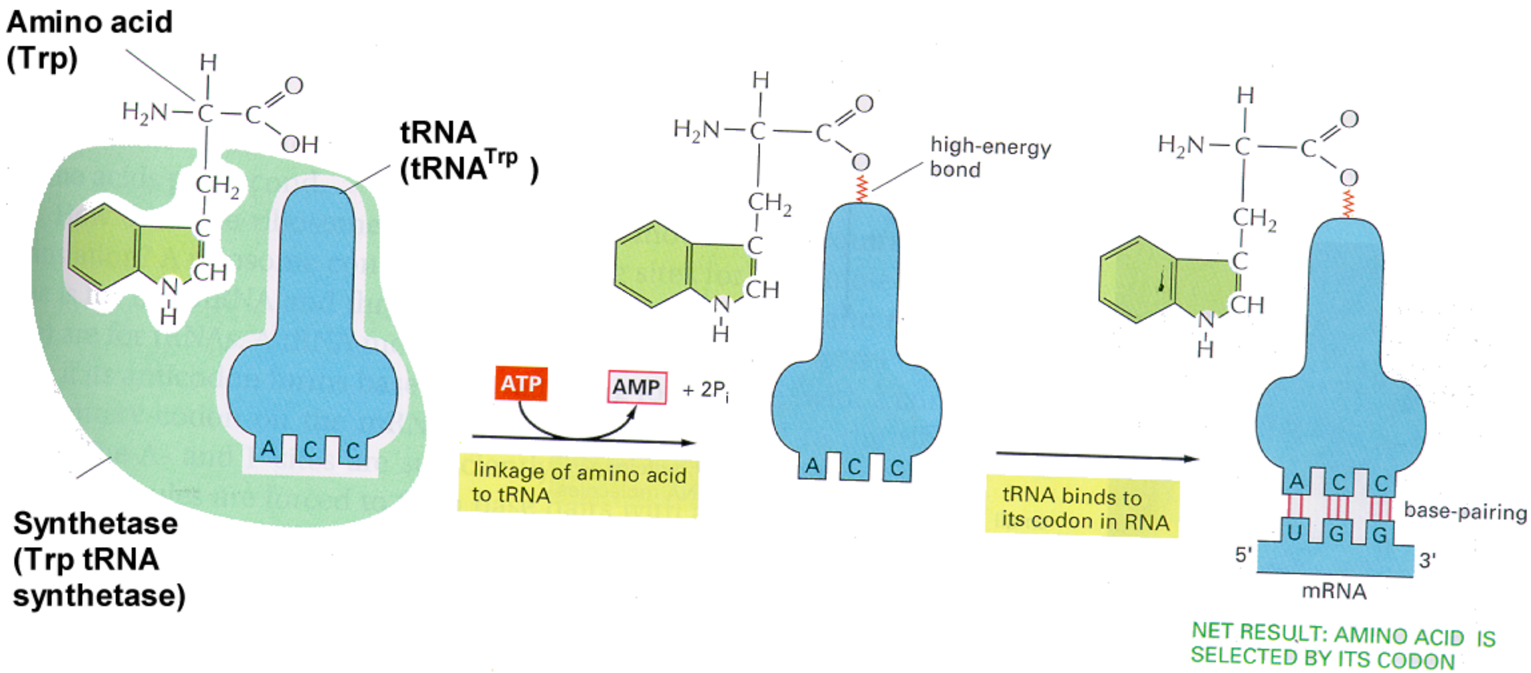


1. The amino acid is accepted by the aminoacyl-tRNA synthetase enzyme and is adenylated

2. The proper tRNA is accepted by the enzyme and the amino acid residue is transferred to the 2’ or 3’ OH of the 3’-terminal residue of the RNA

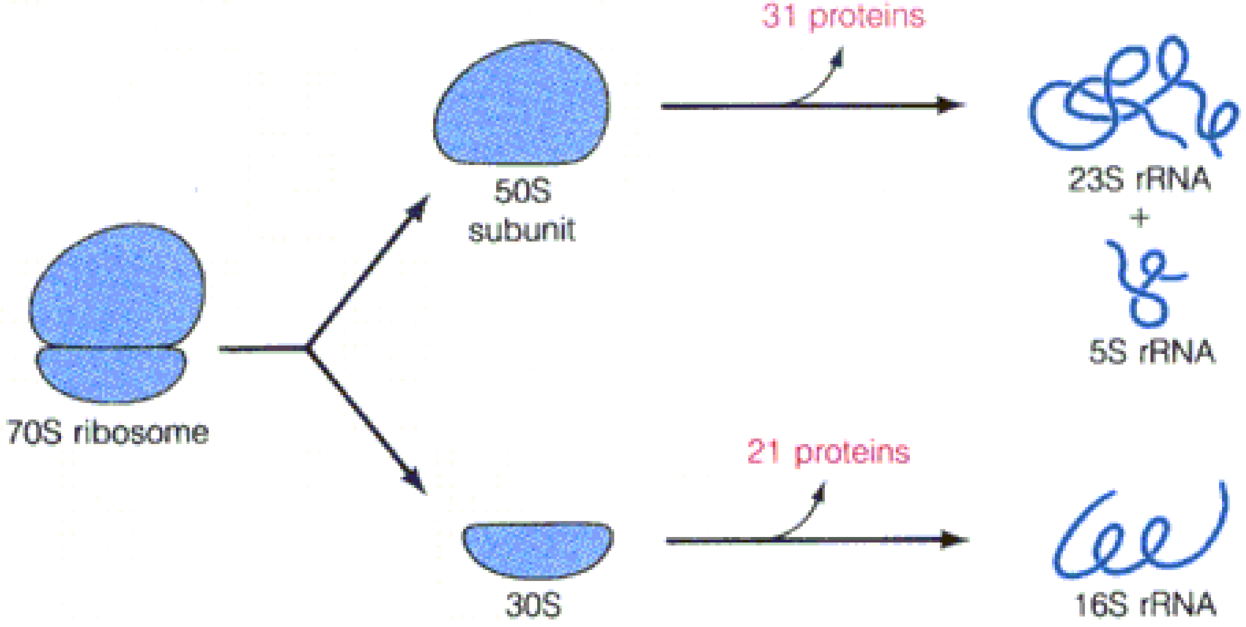
All reactions occur on the synthetase enzyme.

The Two Steps of Decoding



The genetic code is translated by means of two adaptors that act one after another.

The Procaryotic Ribosome

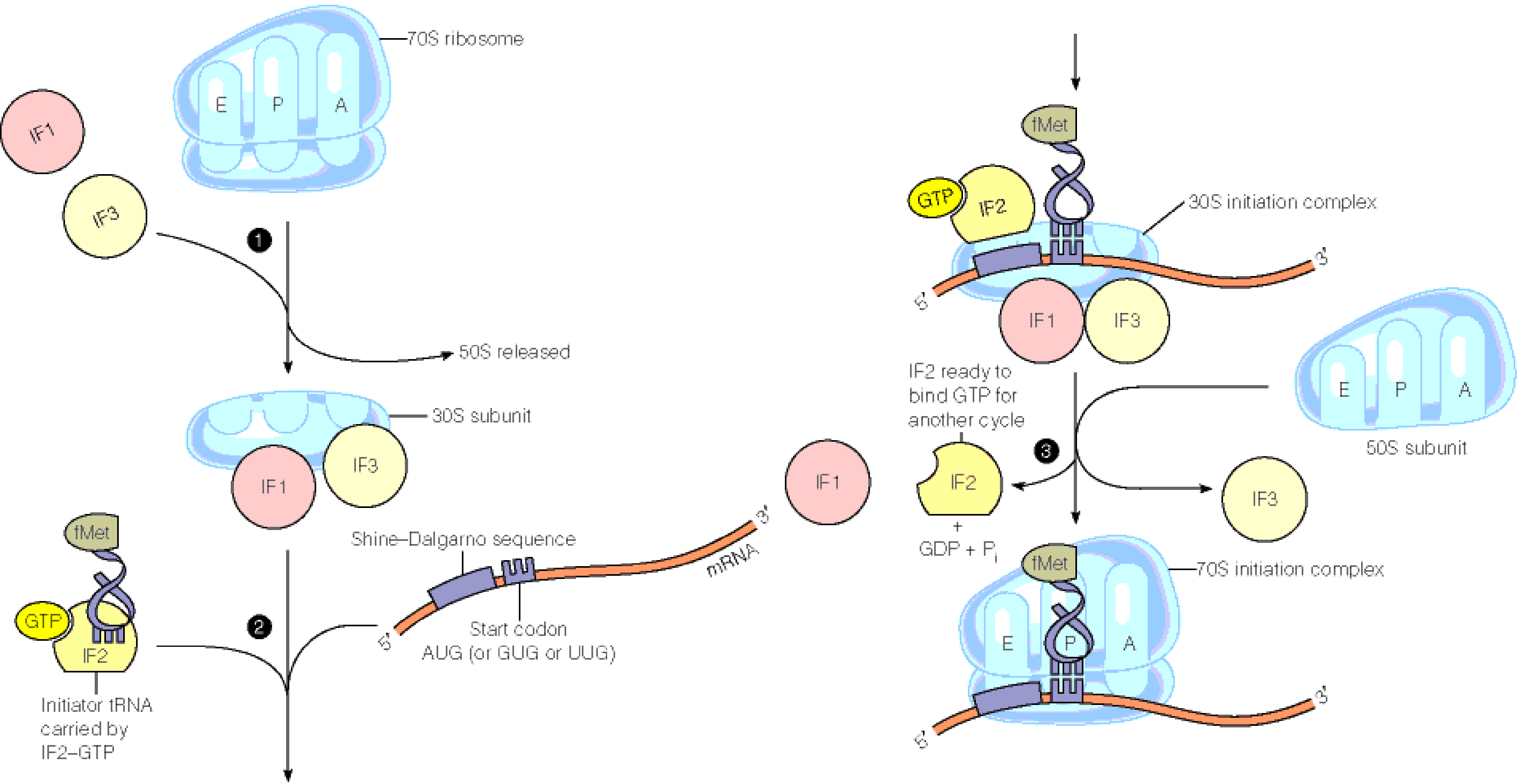


Synthesises polypeptides under the direction of mRNA templates

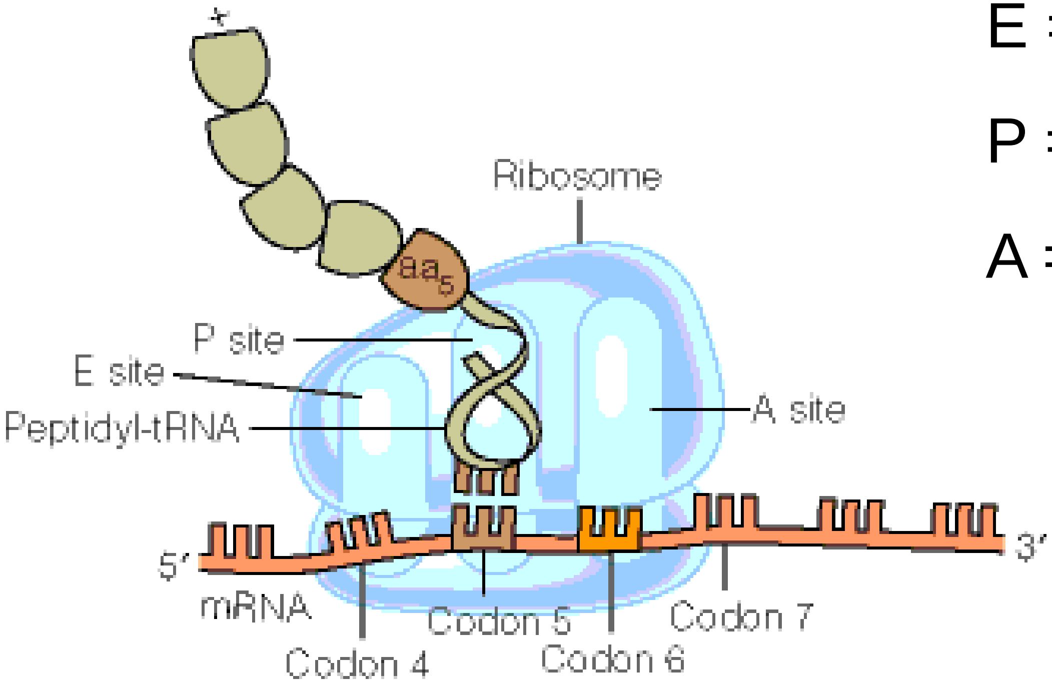
Translation = decoding of the information written in RNA into the amino acid sequence of the protein

The Mechanism of Translation

Initiation in Procaryotes



The Mechanism of Translation
Elongation in Procaryotes (1)



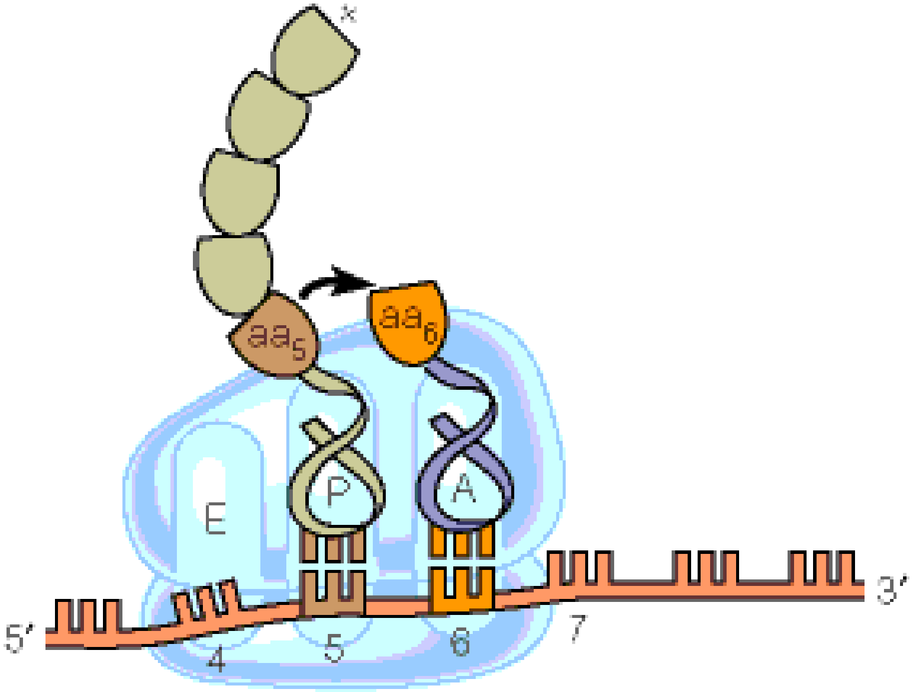
E = exit site

P = peptidyl binding site

A = aminoacyl binding site

The Mechanism of Translation

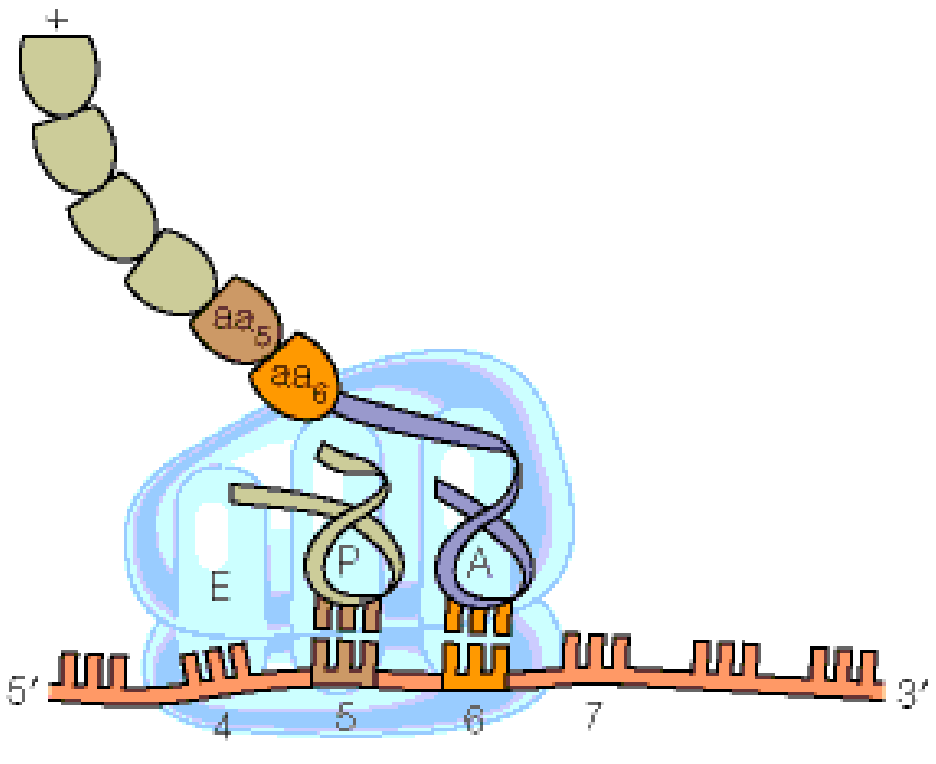
Elongation in Procaryotes (2)



Binding of a spesific amino acid tRNA to A site

The Mechanism of Translation

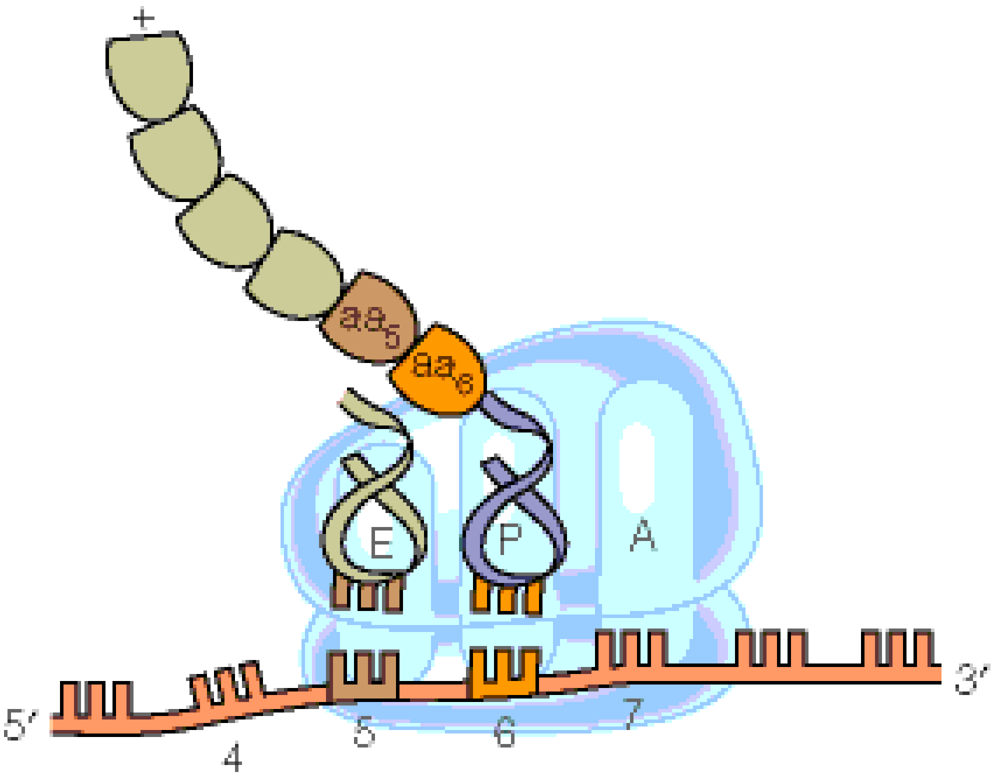
Elongation in Procaryotes (3)



Peptide bond formation: chain transfer from peptidyl tRNA to aminoacyl tRNA

The Mechanism of Translation

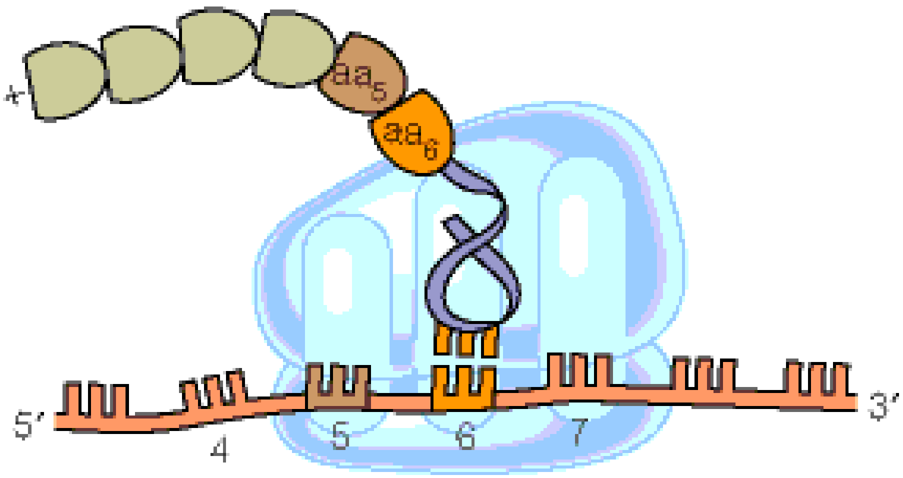
Elongation in Procaryotes (4)



Translocation of peptidyl tRNA from A site to P site. Ribosome moves one codon to the right, and the now uncharged tRNA moves from P site to E site.

The Mechanism of Translation

Elongation in Procaryotes (5)

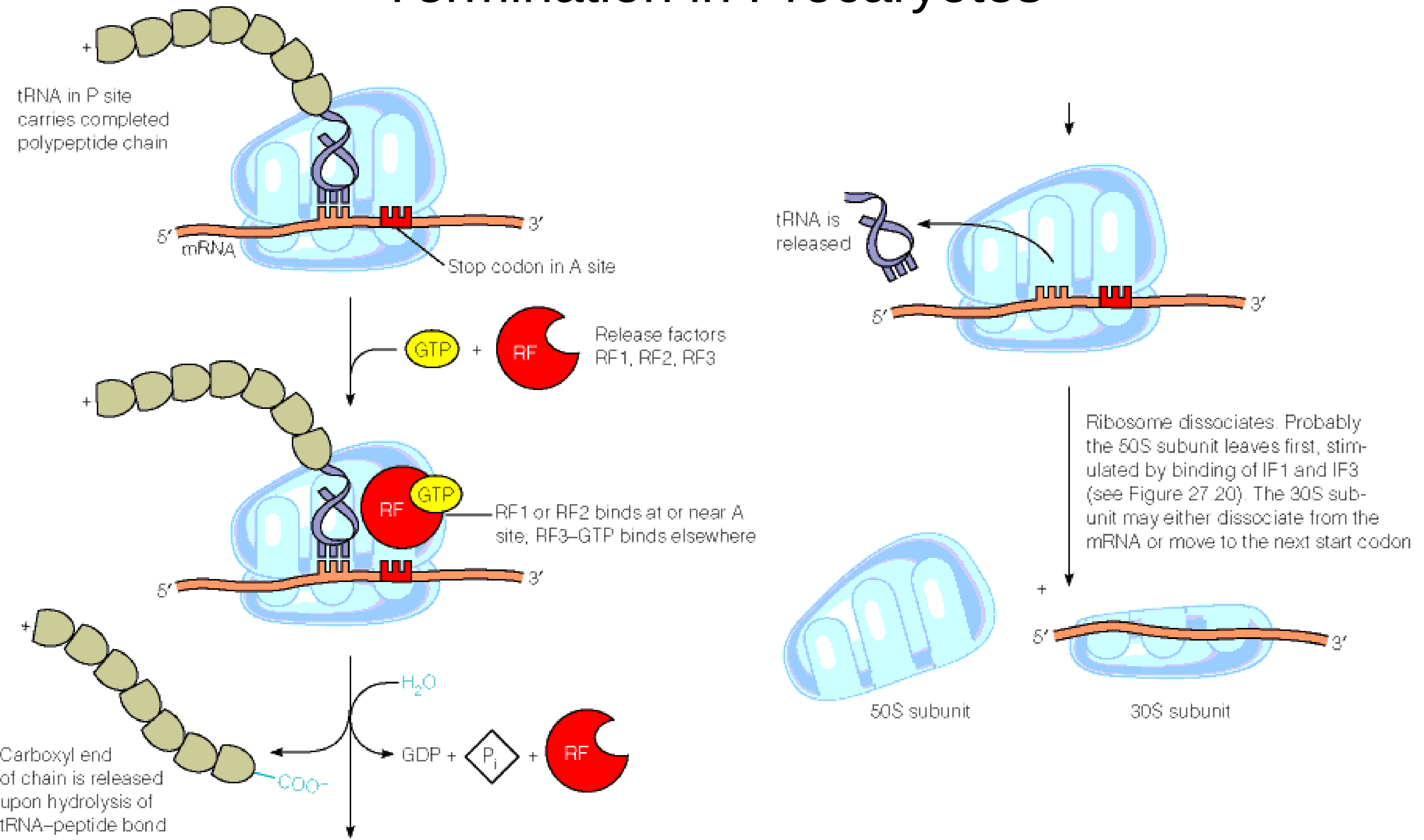


Ribosome is ready to start another cycle.

The cycles will continue until a termination codon is reached.

The Mechanism of Translation

Termination in Procaryotes



The Regulation of Protein Synthesis

When translation is regulated, it is generally done at the initiation state:

1. The tertiary structure of the mRNA can prevent its attachment to the ribosomal subunit
2. Proteins may bind to the mRNA, blocking initiation
3. Anti-sense RNA may block initiation

The Wobble Concept

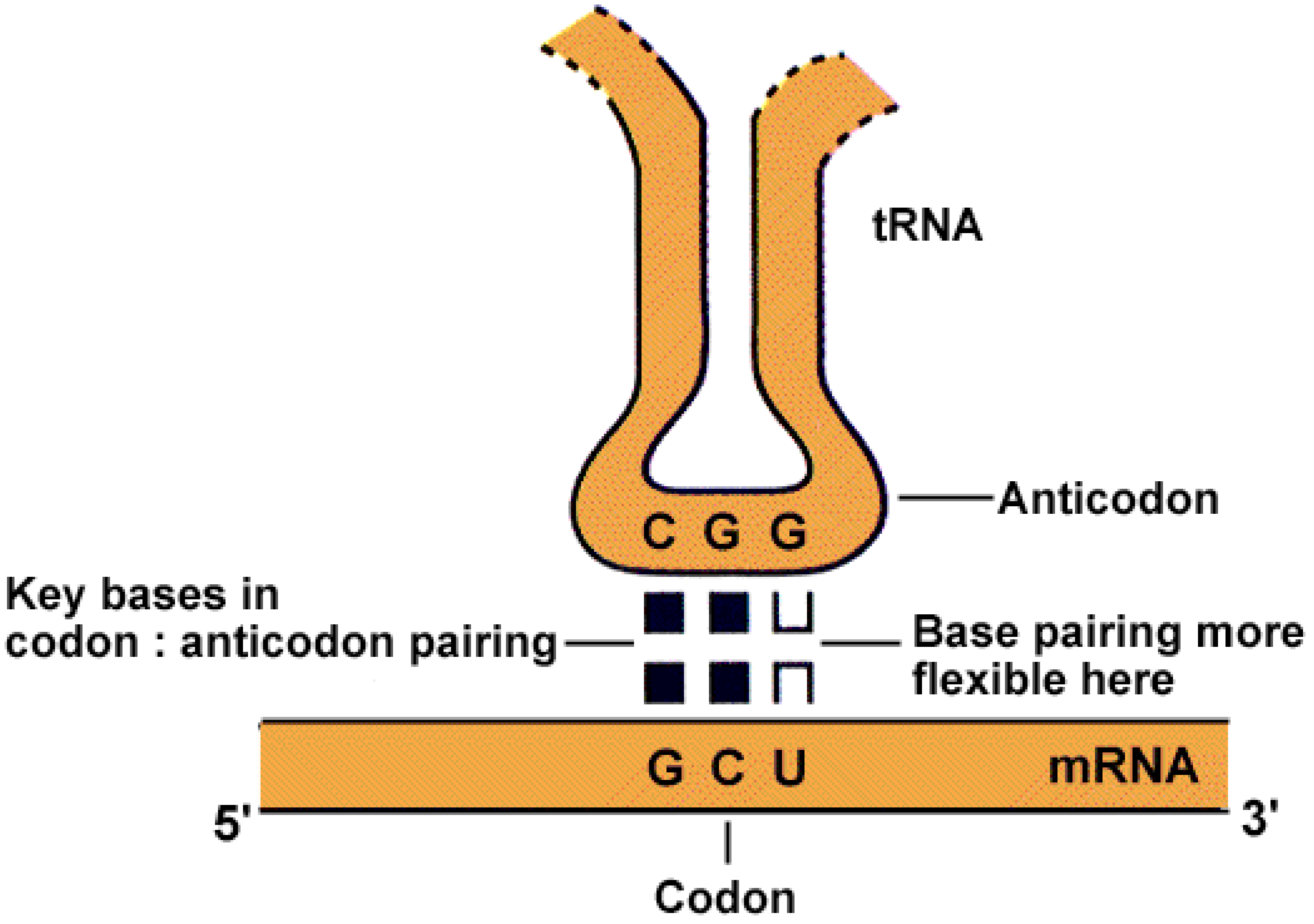


Figure 6.34

3 Different Reading Frames

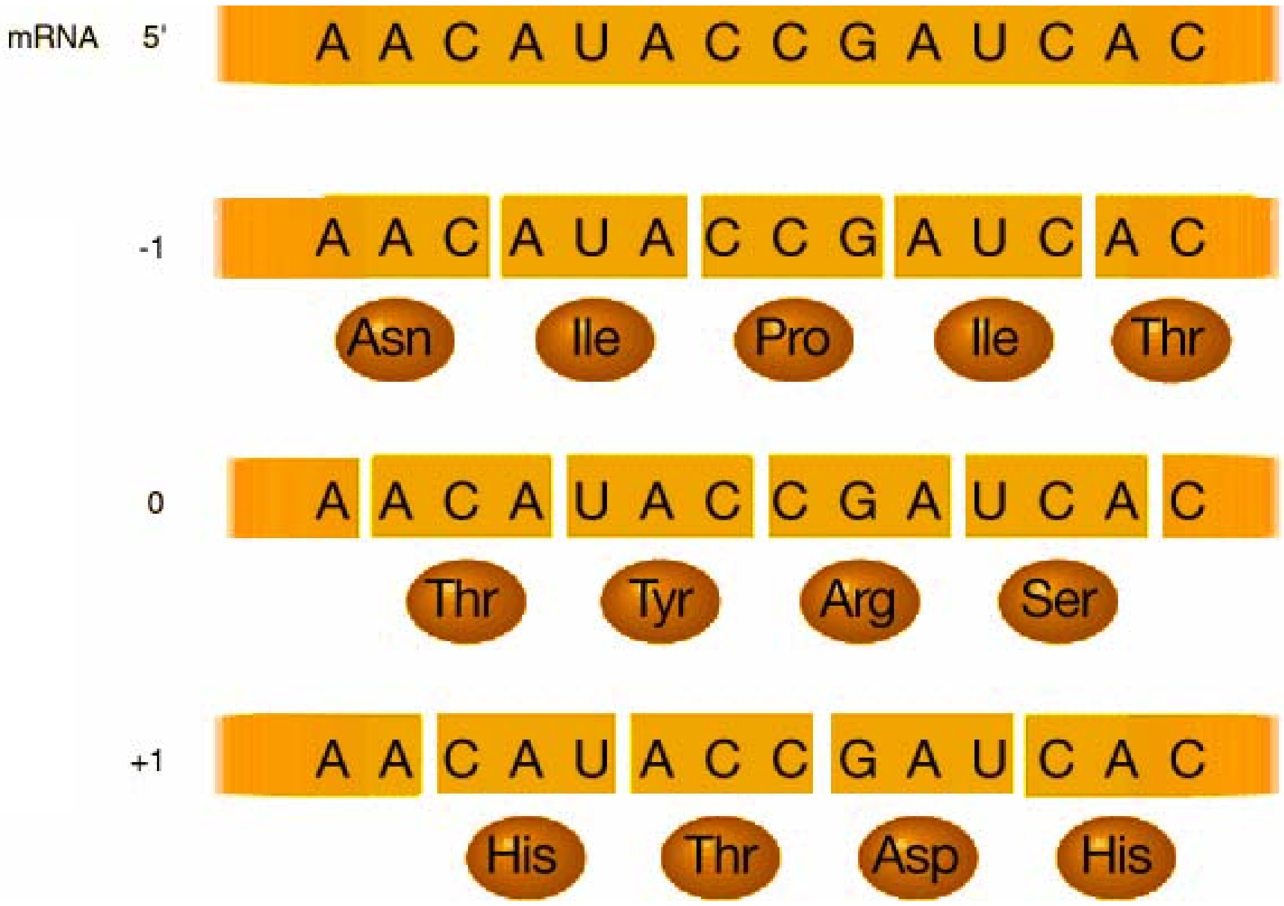


Figure 6.35

Structure of Transfer RNA

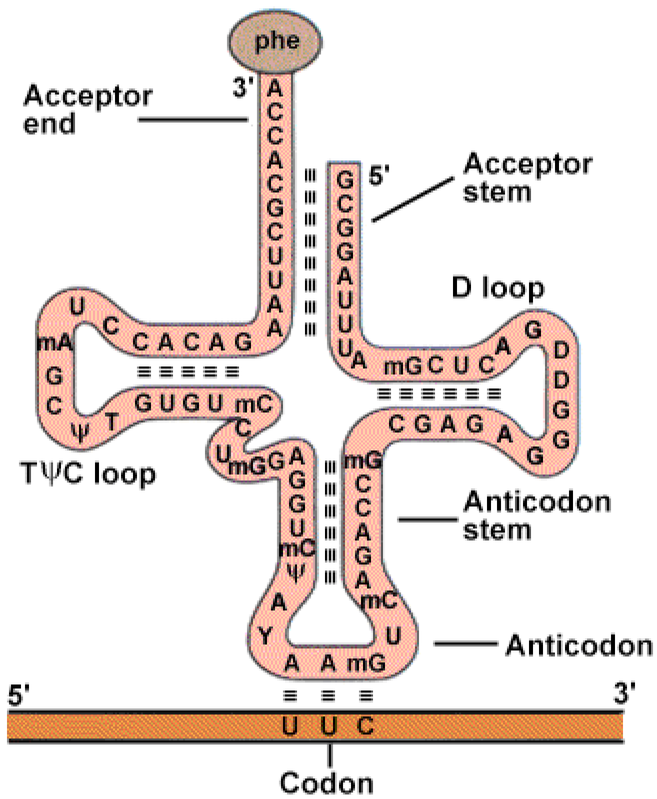


Figure 6.36a

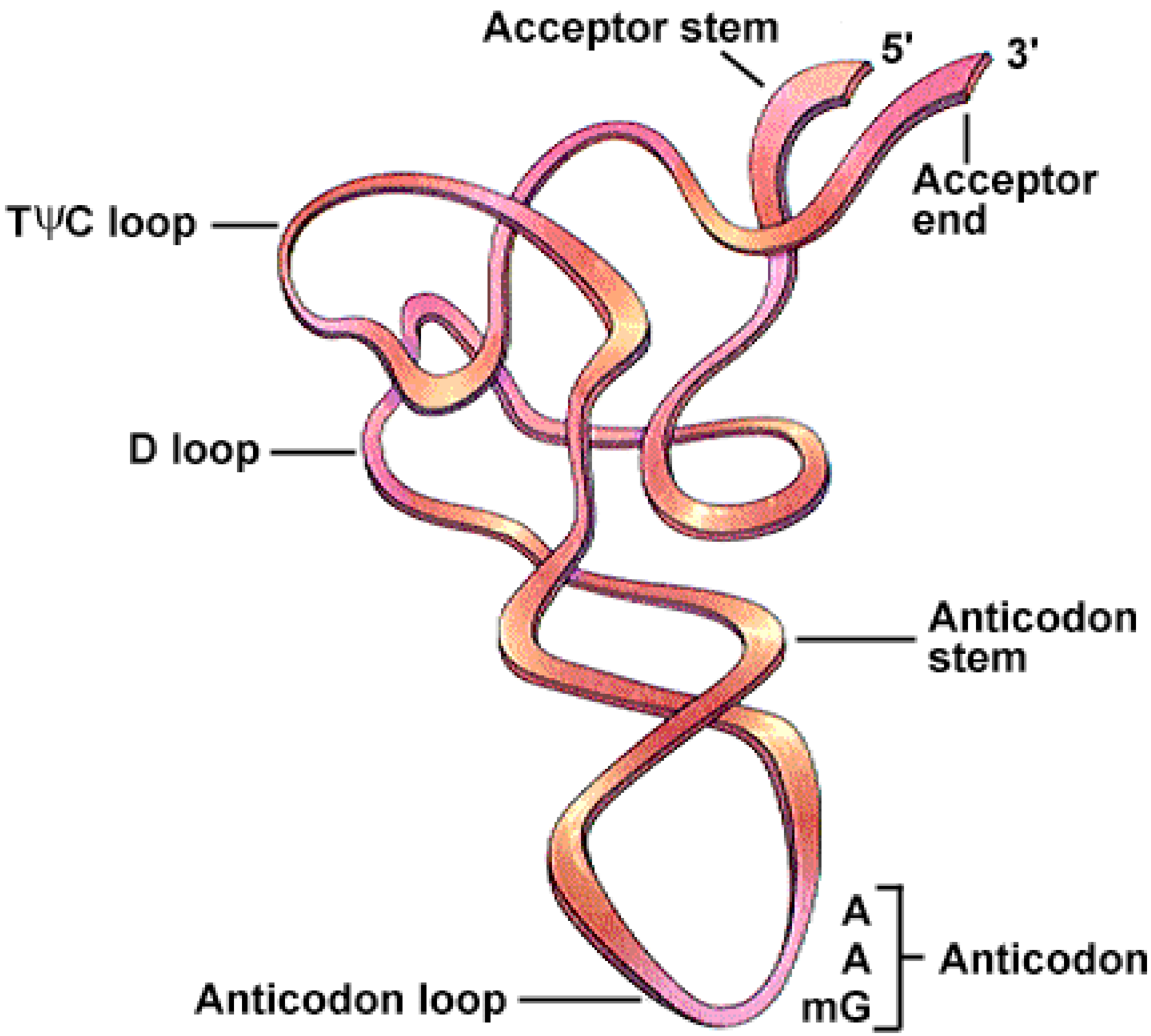

Acceptor stem
5'
3'
Acceptor
end
TΨC loop
D loop
Anticodon
stem
A
A
mG
Anticodon
Anticodon loop

Figure 6.36b

Aminoacyl-tRNA synthetase activity

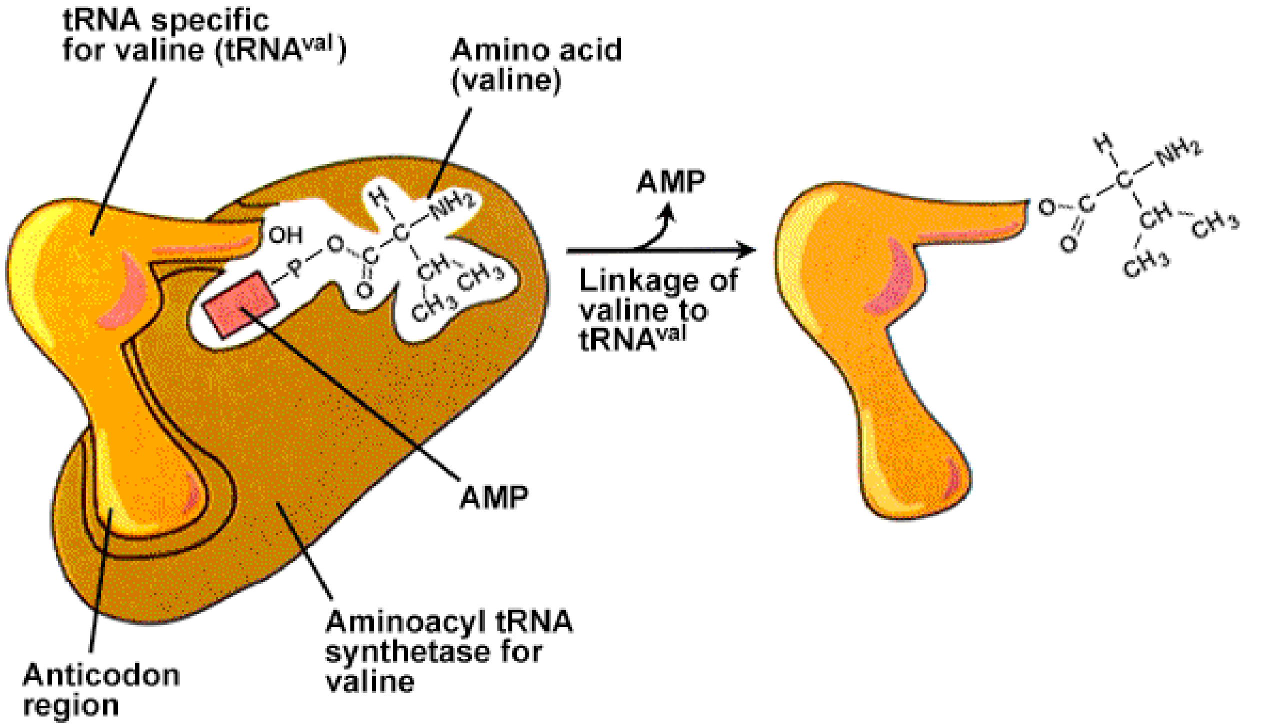
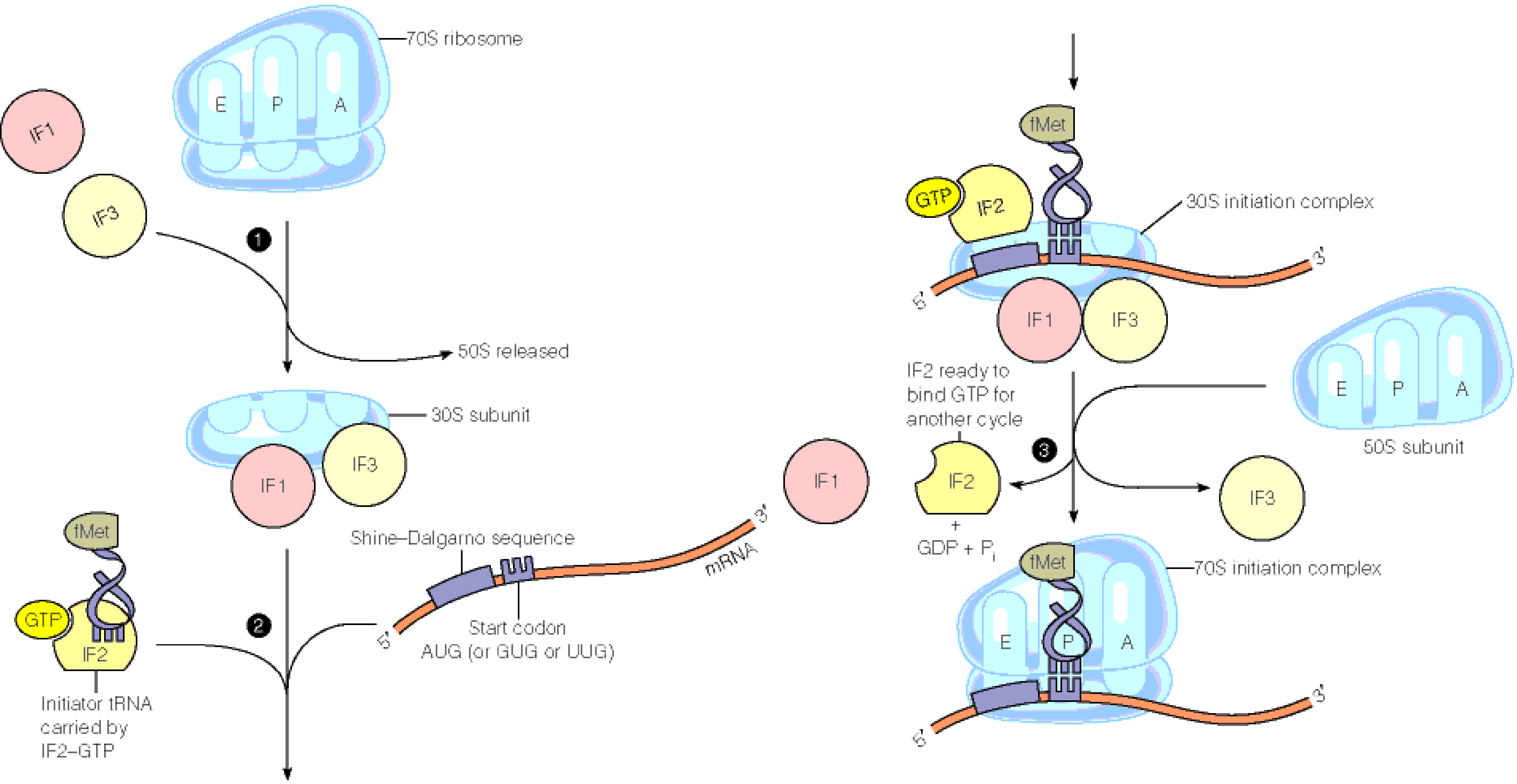


Figure 6.37

The Mechanism of Translation

Initiation in Procaryotes



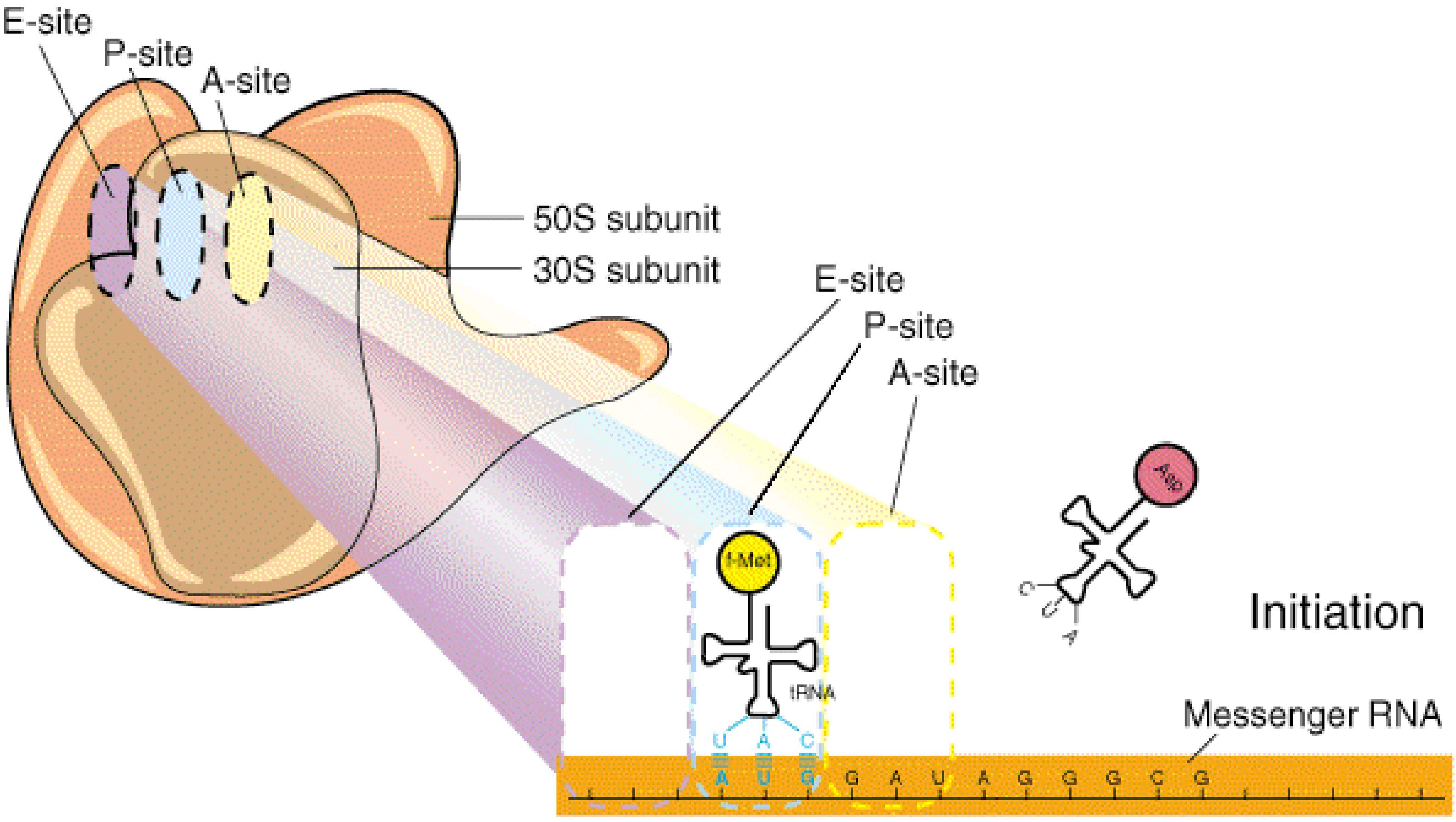
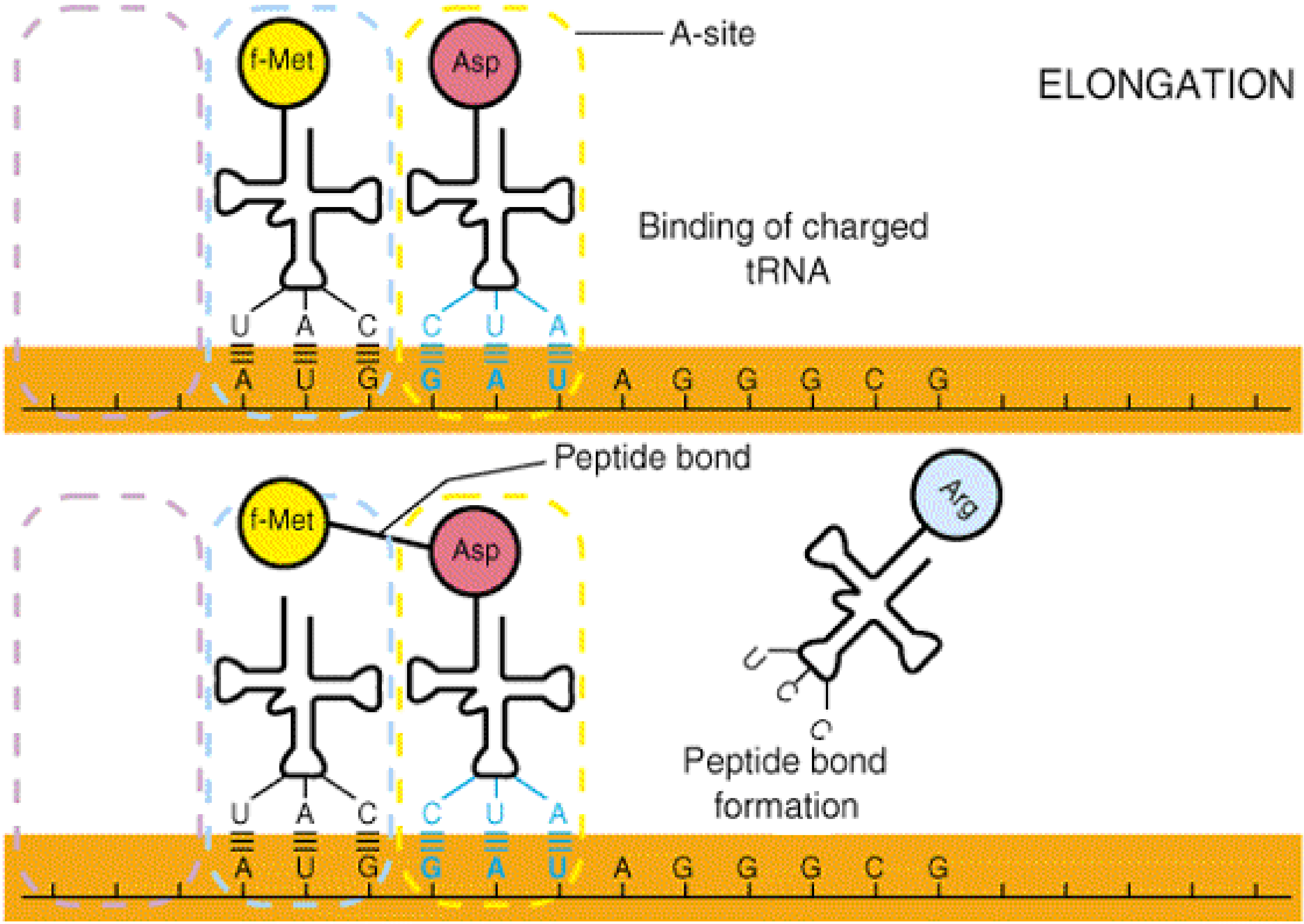
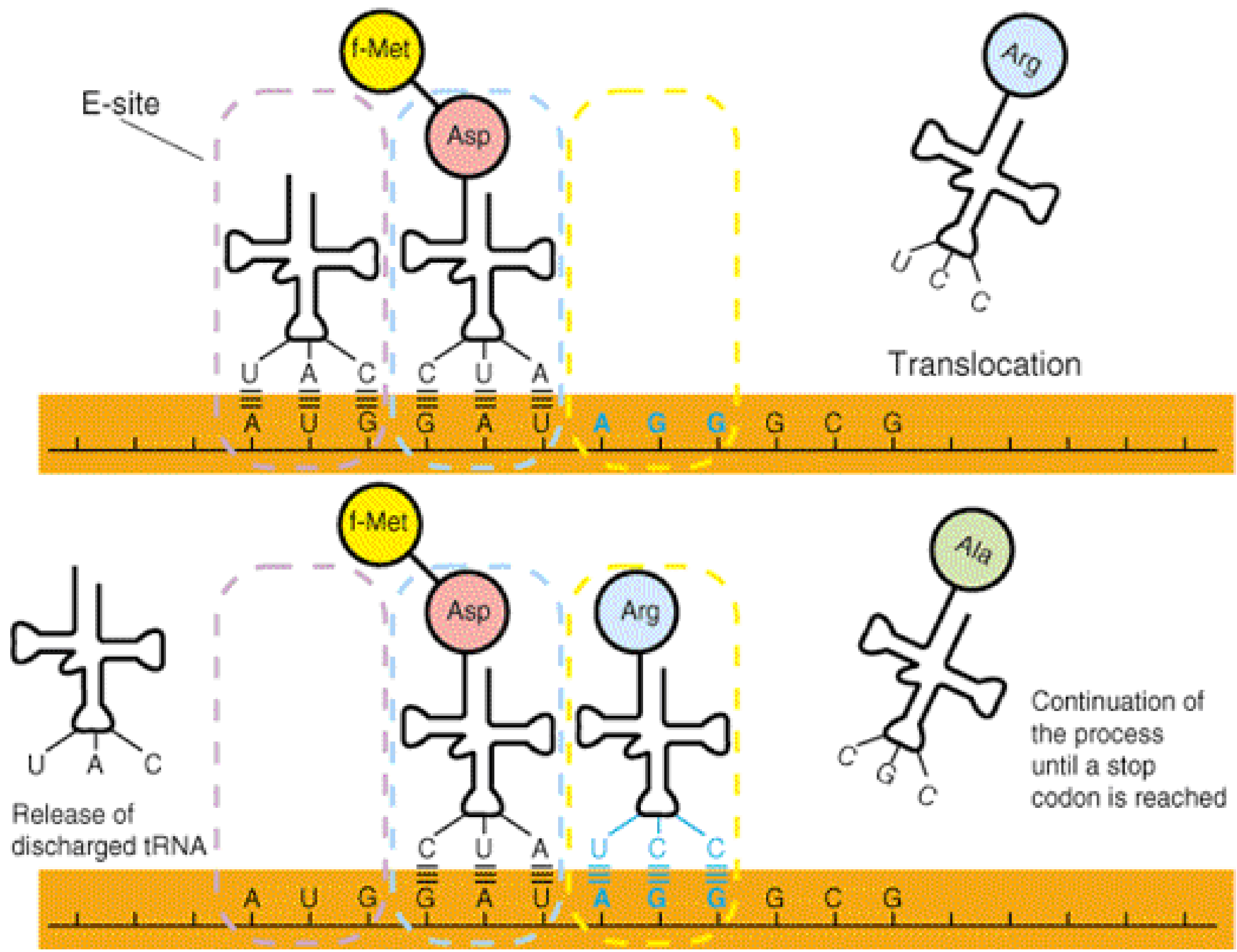

E-site
P-site
A-site
50S subunit
30S subunit
E-site
P-site
A-site
f-Met
tRNA
U A C
A U G G A U A G G G C G
Asp
Initiation
Messenger RNA

Figure 6.38


ELONGATION
A-site
f-Met
Asp
Binding of charged tRNA
U A C
C U A
A U G
G A U
A G G G C G
Peptide bond
f-Met
Asp
Arg
U
C
C
Peptide bond formation
U A C
C U A
A U G
G A U
A G G G C G



E-site
f-Met
Asp
Arg
U A C
C U A
A U G G A U A G G G C G
Translocation
U C C
f-Met
Asp
Arg
Ala
U A C
Release of
discharged tRNA
C U A
U C C
A U G G A U A G G G C G
C G C
Continuation of
the process
until a stop
codon is reached

Polysome

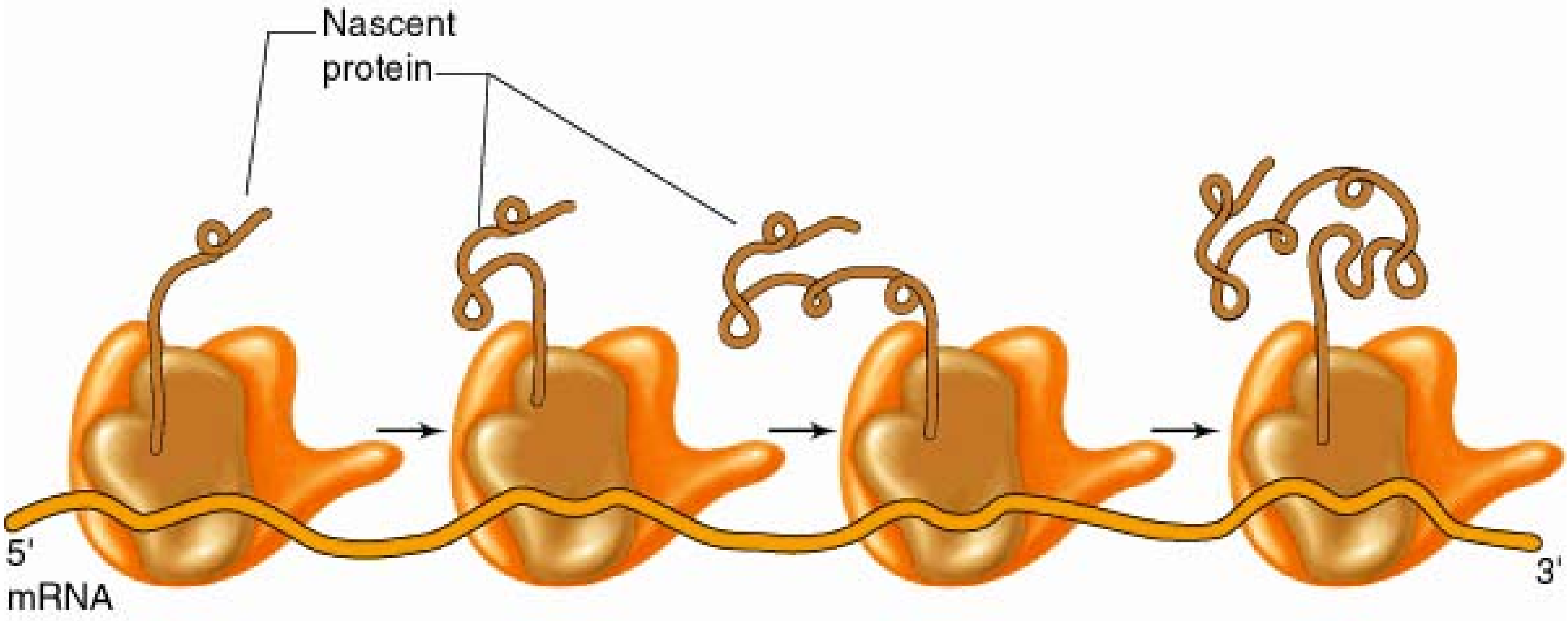


Figure 6.39

Molecular Chaperone

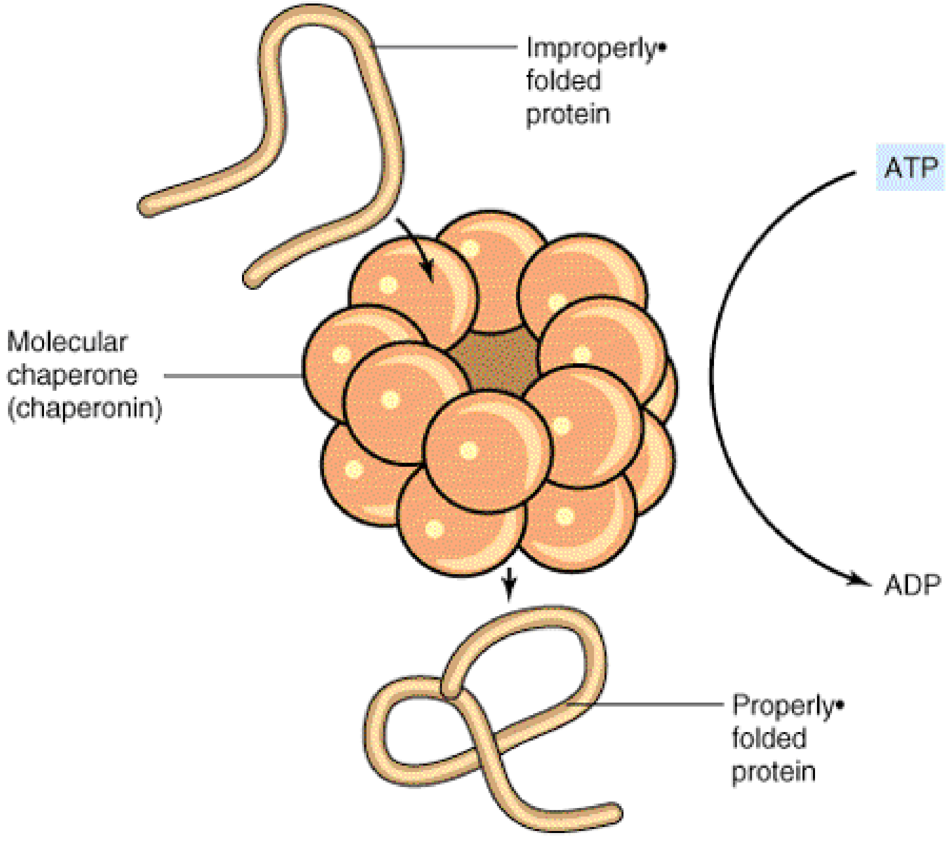


Figure 6.40

TABLE 6.7 Variations in the genetic code[a]

Codon	Universal code	Other codes in cellular chromosomes			Other mitochondrial codes		
		Mycoplasma	*Paramecium*	*Euplotes*	Yeast	Protozoa	Mammals
UGA	Stop	Tryptophan	Stop	Cysteine	Tryptophan	Tryptophan	Tryptophan
UAA/UAG	Stop	Stop	Glutamine	Stop	Stop	Stop	Stop
AUA	Isoleucine	Isoleucine	Isoleucine	Isoleucine	Methionine	Methionine	Methionine
CUA	Leucine	Leucine	Leucine	Leucine	Threonine	Leucine	Leucine
AGA/AGG	Arginine	Arginine	Arginine	Arginine	Arginine	Arginine	Stop

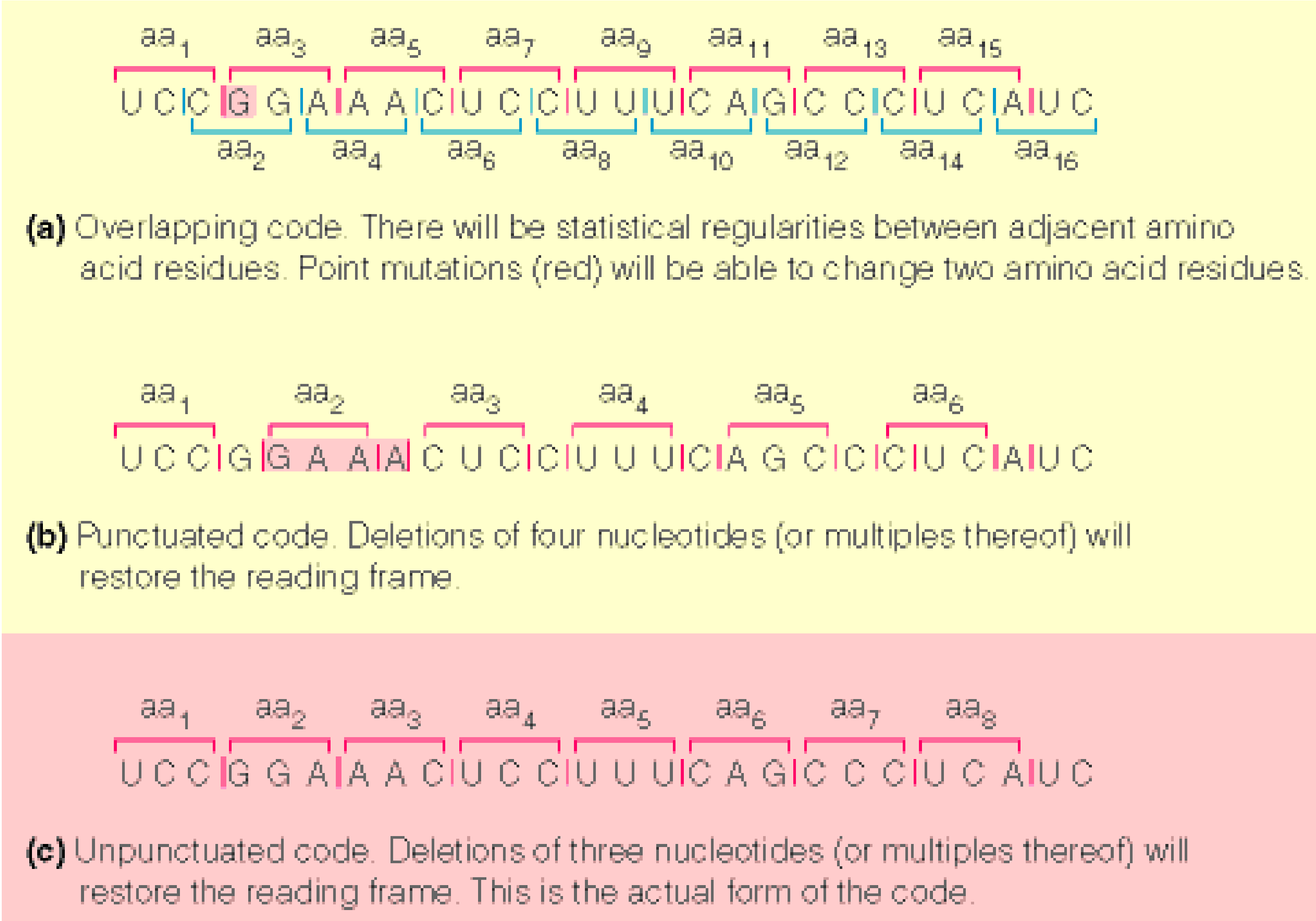
a The universal genetic code is used in the chromosomes of most cells, chloroplasts, plant mitochondria, and their viruses and plasmids. A few organisms use slightly different codes in their chromosomes (in the nucleus). The examples of these other nuclear codes are from *Mycoplasma* (Bacteria) and two different ciliated protozoa (Eukarya). All nonplant mitochondria use variations of the universal code, whereas plant mitochondria use the universal code. The examples here are only a few of the different types known.

Codon Usage

- ✍Organisms have preferred codons for each amino acid
- ✍For a given organism, some codons are used very often, while others are used rarely
- ✍This codon preference is a unique trait of the organism
- ✍Codon preference can be used to determine whether a newly sequenced region actually encodes a gene

The Genetic Code

Three Conceivable Kinds of Genetic Codes

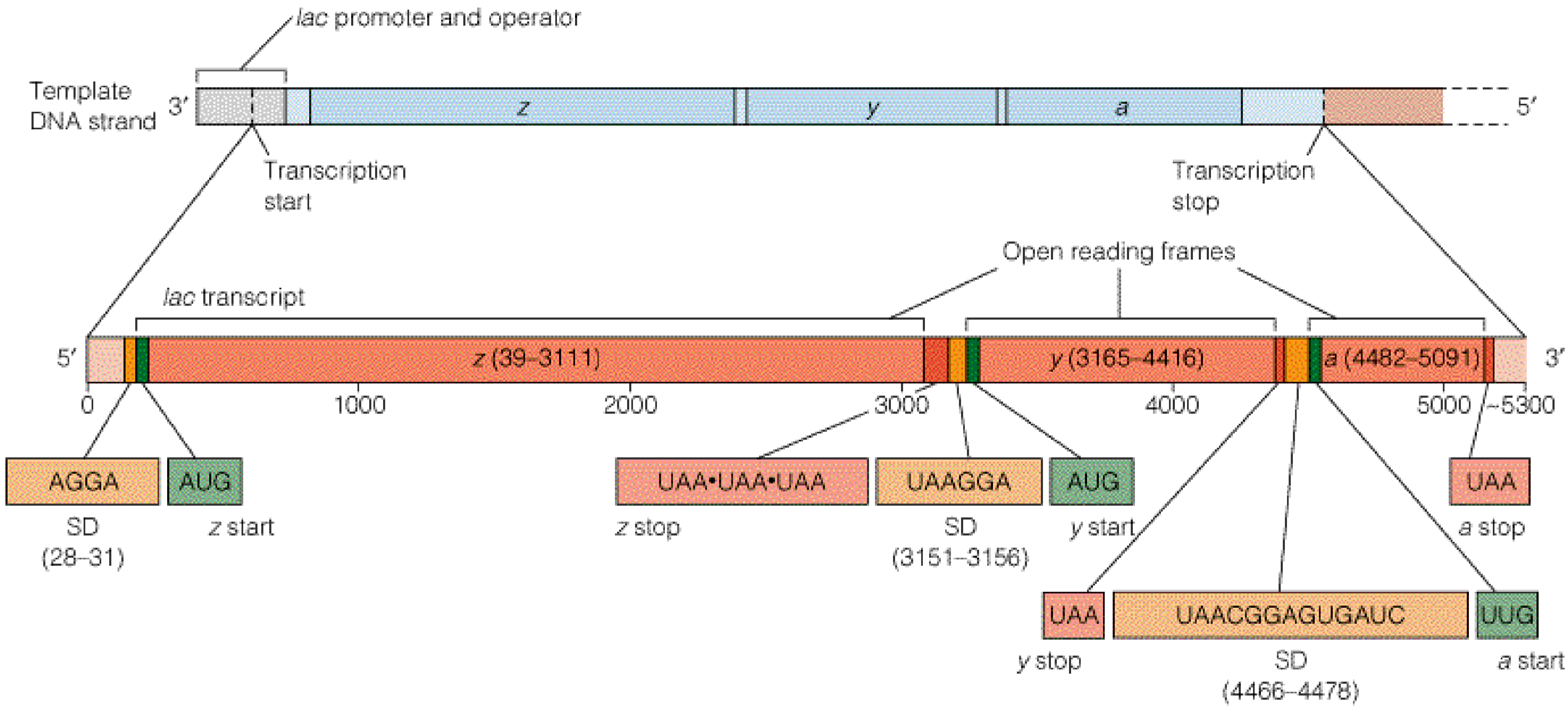


(a) Overlapping code. There will be statistical regularities between adjacent amino acid residues. Point mutations (red) will be able to change two amino acid residues.

(b) Punctuated code. Deletions of four nucleotides (or multiples thereof) will restore the reading frame.

(c) Unpunctuated code. Deletions of three nucleotides (or multiples thereof) will restore the reading frame. This is the actual form of the code.

Structure of Procaryotic mRNAs



mRNA has also regions that do not encode for a protein

Shine-Dalgarno sequence (SD) = Ribosome Binding Site (RBS)

The first AUG after SD-sequence is interpreted as the start site of translation