Table 2.1

TABLE 2.1 The genetic code

First position (5′ end)	Second position				Third position (3′ end)
	U	C	A	G	
U	Phe	Ser	Tyr	Cys	U
	Phe	Ser	Tyr	Cys	C
	Leu	Ser	Stop	Stop	A
	Leu	Ser	Stop	Trp	G
C	Leu	Pro	His	Arg	U
	Leu	Pro	His	Arg	C
	Leu	Pro	Gln	Arg	A
	Leu	Pro	Gln	Arg	G
A	Ile	Thr	Asn	Ser	U
	Ile	Thr	Asn	Ser	C
	Ile	Thr	Lys	Arg	A
	Met	Thr	Lys	Arg	G
G	Val	Ala	Asp	Gly	U
	Val	Ala	Asp	Gly	C
	Val	Ala	Glu	Gly	A
	Val	Ala	Glu	Gly	G

Figure 2.1

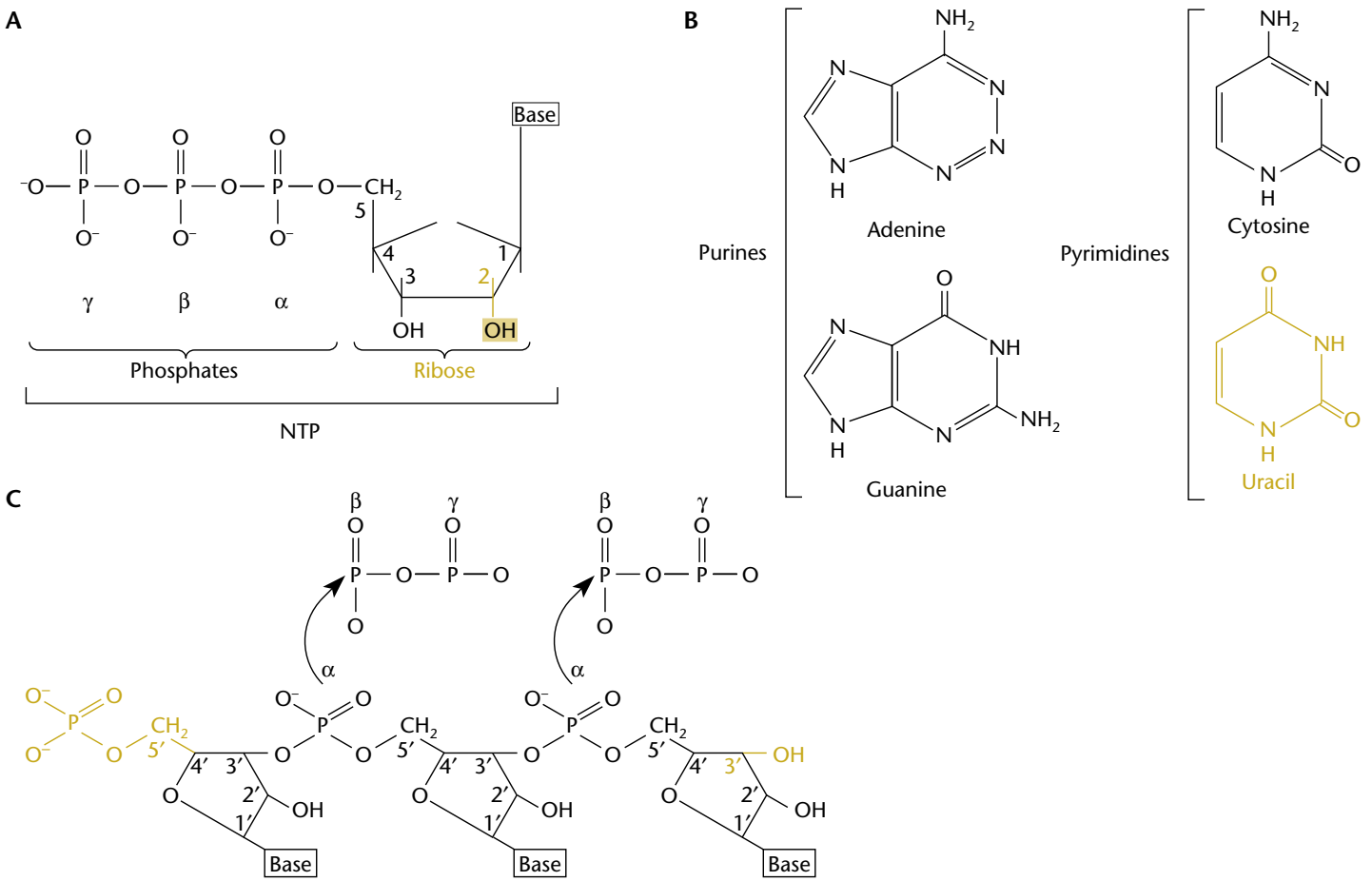
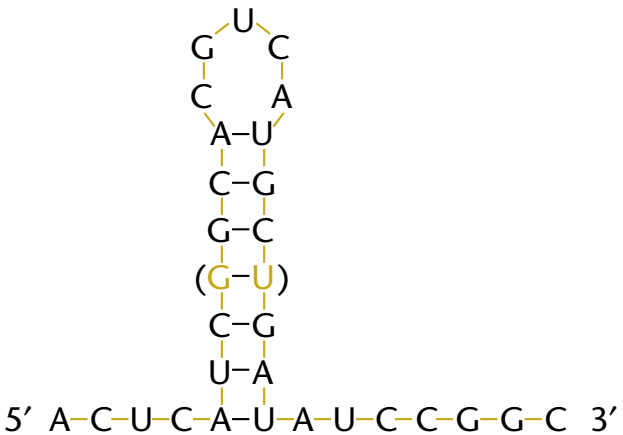
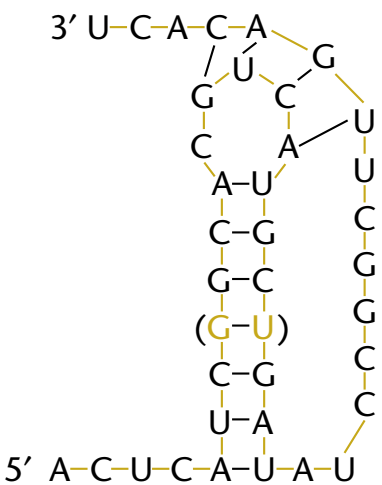

A
Base
γ
β
α
Phosphates
Ribose
NTP
B
Purines
Adenine
Guanine
Pyrimidines
Cytosine
Uracil
C
Base

Figure 2.2

A **Hairpin**



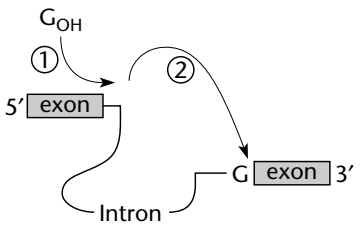
B **Pseudoknot**



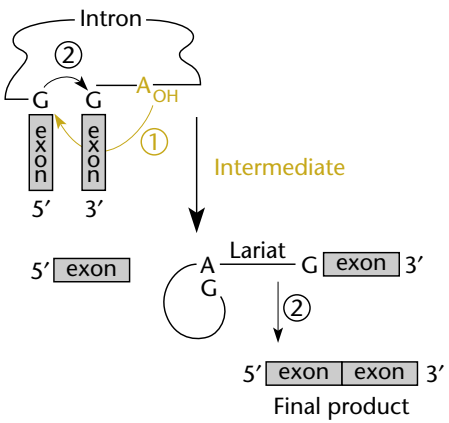
Box 2.2

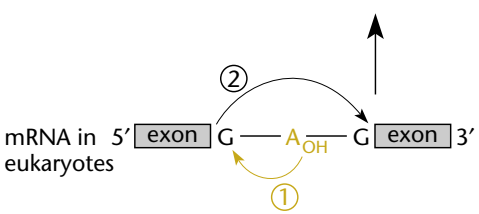
A RNA Introns

Group I



Group II





B Protein inteins

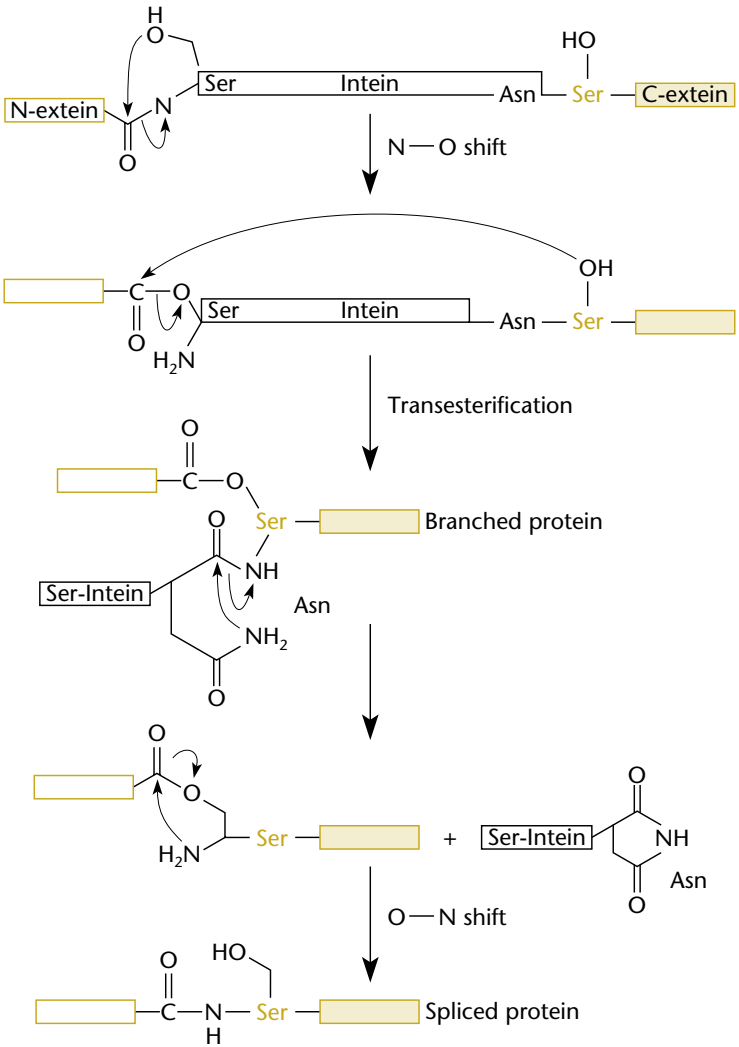


Figure 2.3

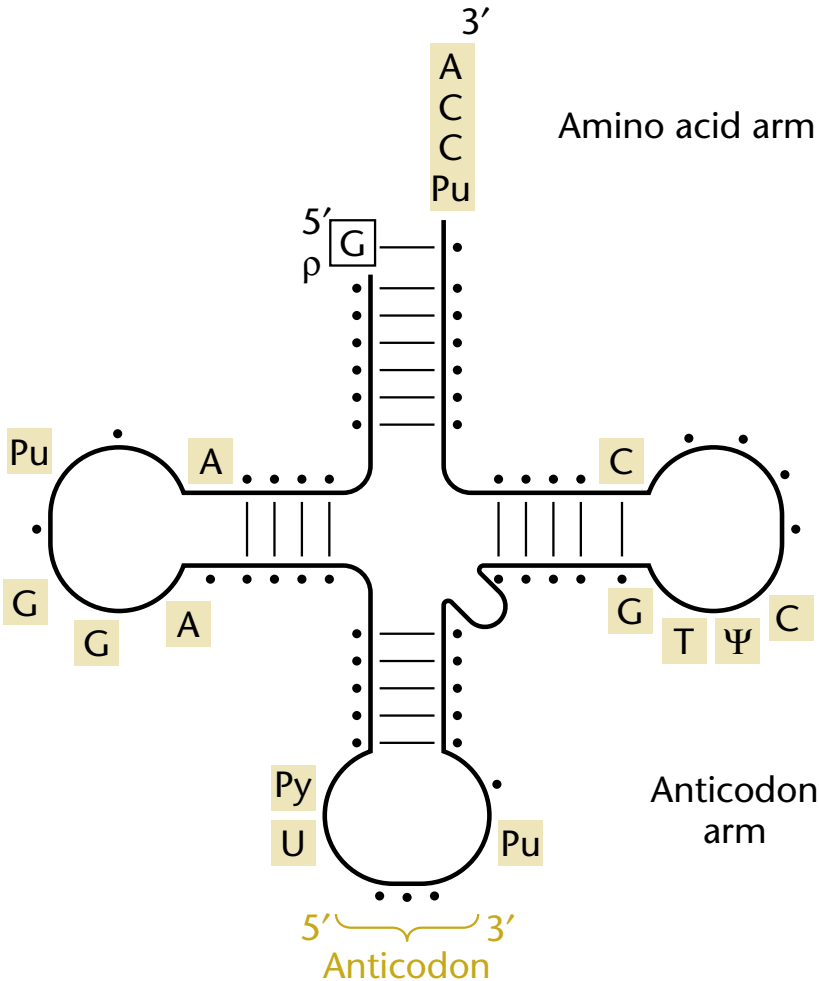

3′
A
C
C
Pu
Amino acid arm
5′
ρ
G
Pu
A
C
G
G
A
G
T
Ψ
C
Py
U
Pu
Anticodon arm
5′
3′
Anticodon

Figure 2.4

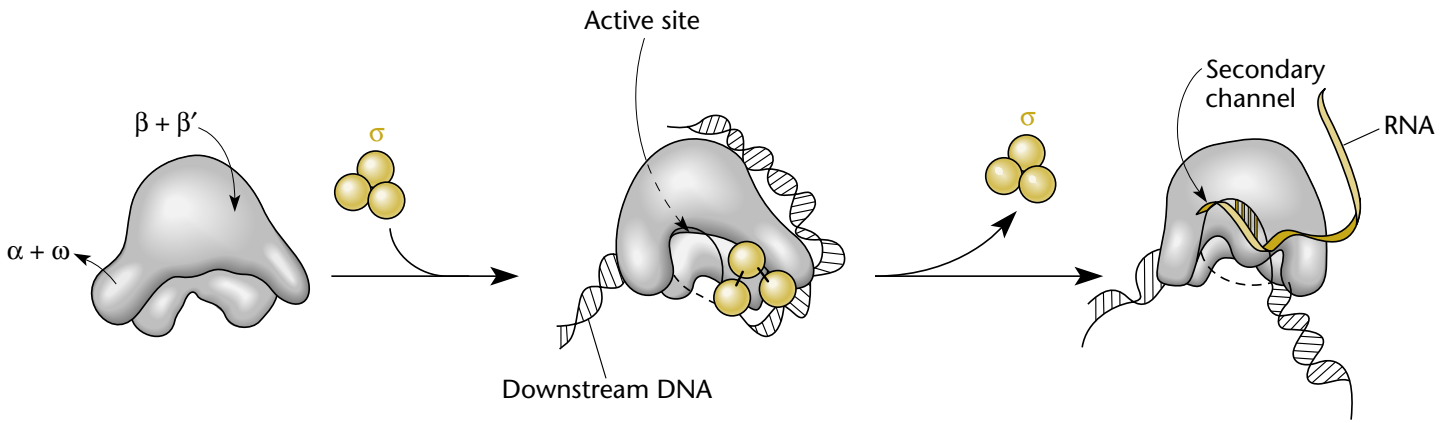

β + β′
α + ω
σ
Active site
Downstream DNA
σ
Secondary channel
RNA
RNA Pol core
Promoter complex with RNA Pol holoenzyme
Elongation complex

Figure 2.5

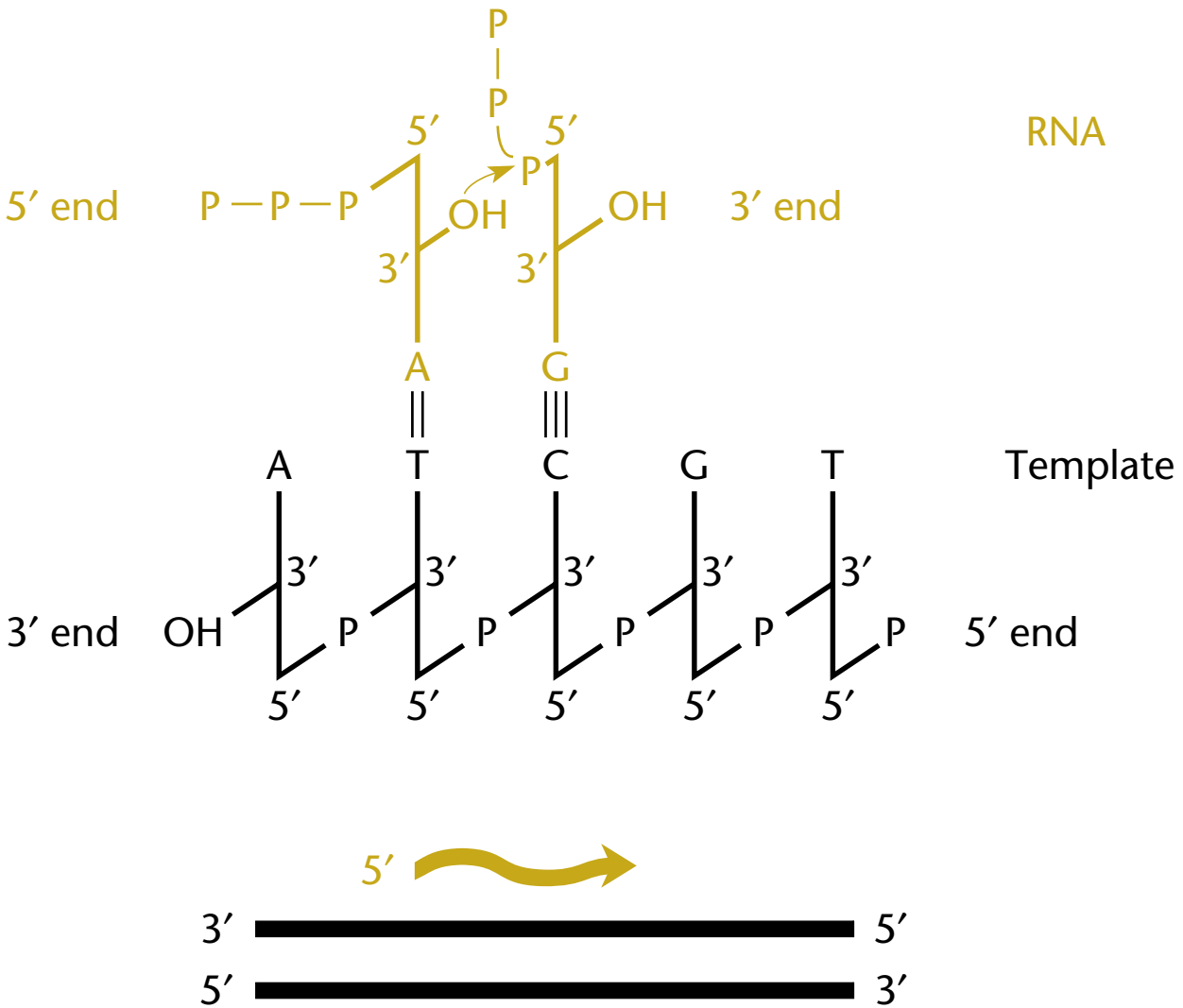

P
P
5′
5′
RNA
5′ end
P—P—P
OH
P
OH
3′ end
3′
3′
A
G
A
T
C
G
T
Template
3′
3′
3′
3′
3′
3′ end
OH
P
P
P
P
P
5′ end
5′
5′
5′
5′
5′
5′
5′
3′
5′
5′
3′

Figure 2.6

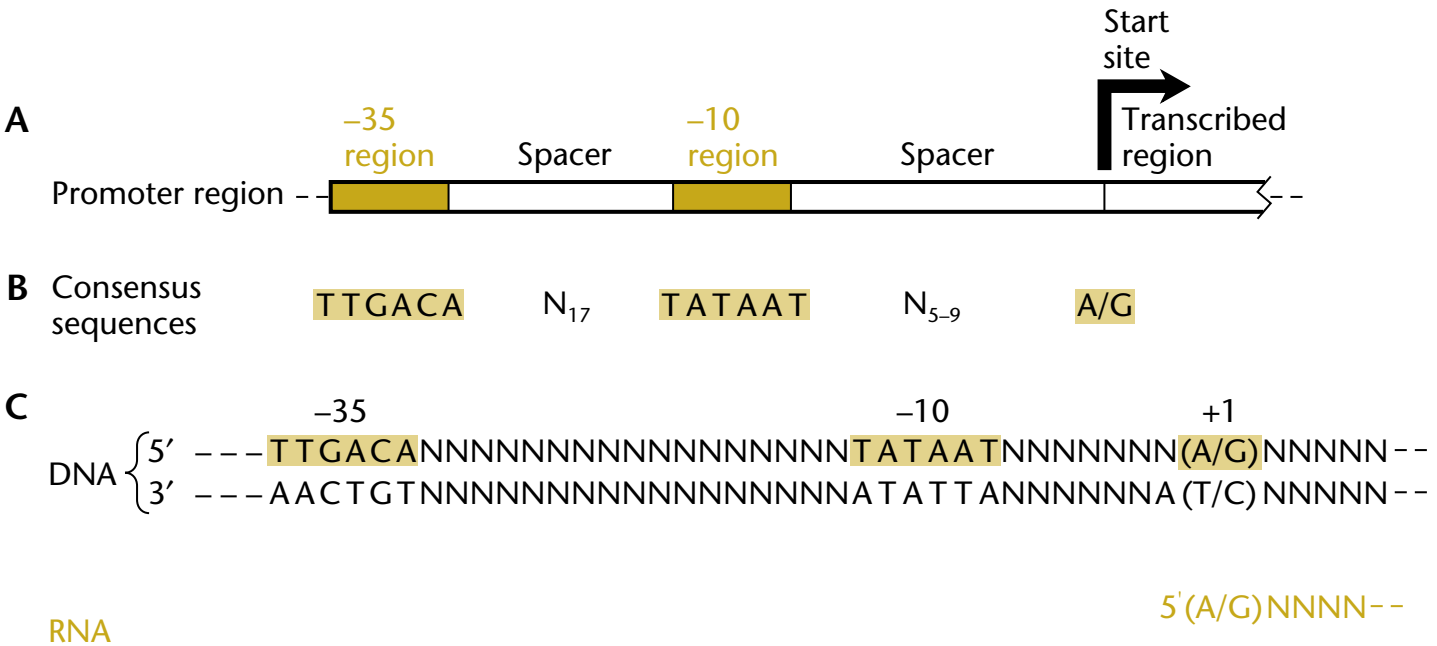

A
Start site
–35 region
Spacer
–10 region
Spacer
Transcribed region
Promoter region
B
Consensus sequences
TTGACA
N17
TATAAT
N5–9
A/G
C
–35
–10
+1
DNA
5′ – – – TTGACANNNNNNNNNNNNNNNNNTATAATNNNNNNN(A/G)NNNNN – –
3′ – – – AACTGTNNNNNNNNNNNNNNNNNATATTANNNNNNA(T/C)NNNNN – –
RNA
5′(A/G)NNNN – –

Figure 2.7


A
DNA
5′ A T T A C G A C C T A C G C A T 3′ Coding strand
3′ T A A T G C T G G A T G C G T A 5′ Template strand
RNA 5′ A U U A C G A C C U A C G C A U 3′
B
DNA
5′ 3′
3′ 5′
RNA 5′

Figure 2.8

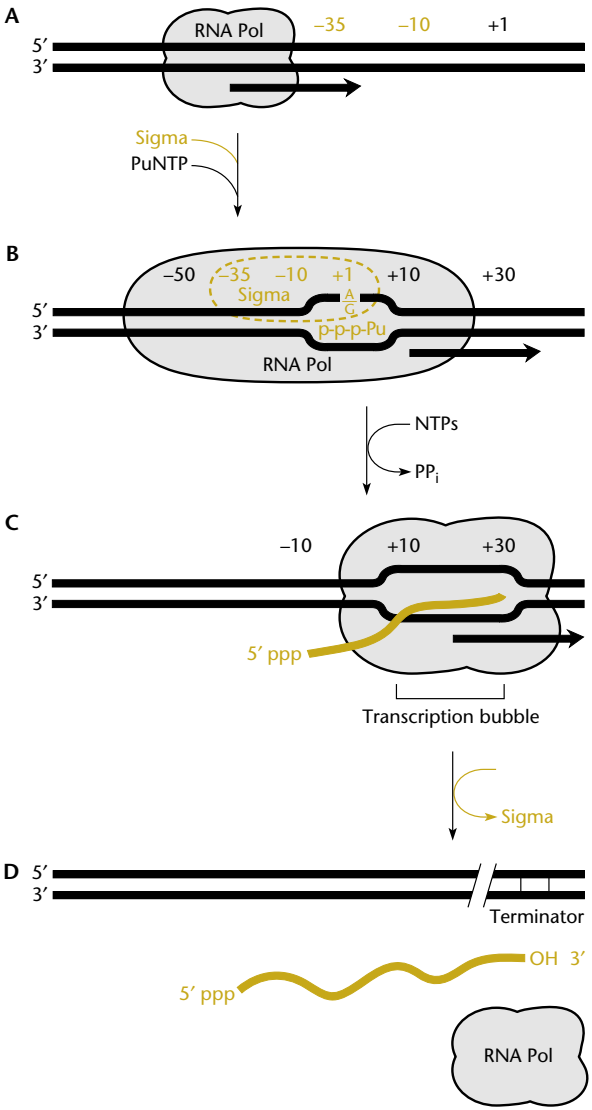

A
RNA Pol
–35
–10
+1
5′
3′
Sigma
PuNTP
B
–50
–35
–10
+1
+10
+30
Sigma
A
G
5′
3′
p-p-p-Pu
RNA Pol
NTPs
PPi
C
–10
+10
+30
5′
3′
5′ ppp
Transcription bubble
Sigma
D
5′
3′
Terminator
5′ ppp
OH 3′
RNA Pol

Figure 2.9

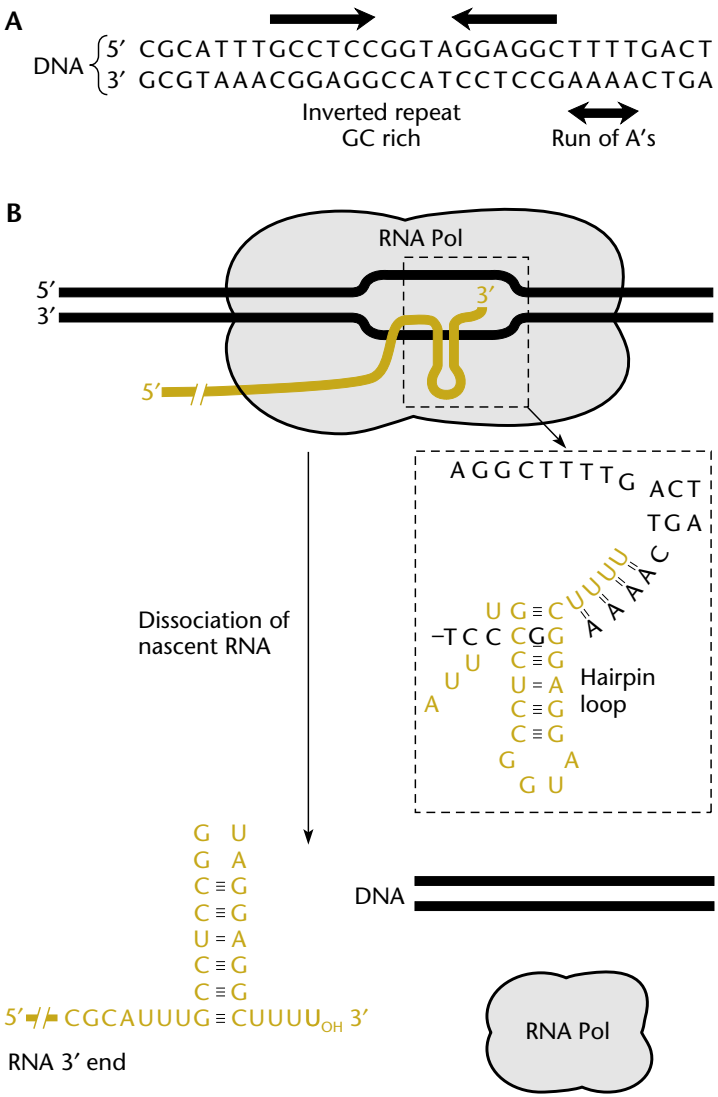

A
DNA
5′ CGCATTTGCCTCCGGTAGGAGGCTTTTGACT
3′ GCGTAAACGGAGGCCATCCTCCGAAAACTGA
Inverted repeat
GC rich
Run of A's
B
RNA Pol
5′
3′
3′
5′
AGGCTTTTG ACT
TGA
Dissociation of
nascent RNA
Hairpin
loop
DNA
RNA Pol
5′ CGCAUUUG CUUUU OH 3′
RNA 3′ end

Figure 2.10

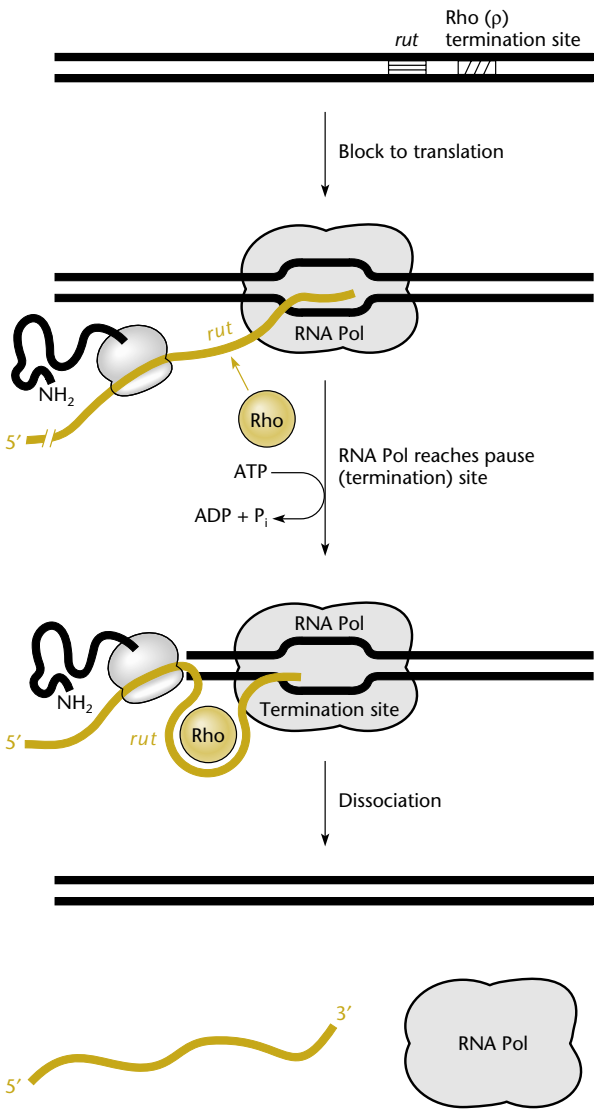

Rho (ρ)
termination site
rut
Block to translation
RNA Pol
rut
NH2
5′
Rho
RNA Pol reaches pause
(termination) site
ATP
ADP + Pi
RNA Pol
Termination site
NH2
5′
rut
Rho
Dissociation
3′
5′
RNA Pol

Figure 2.11

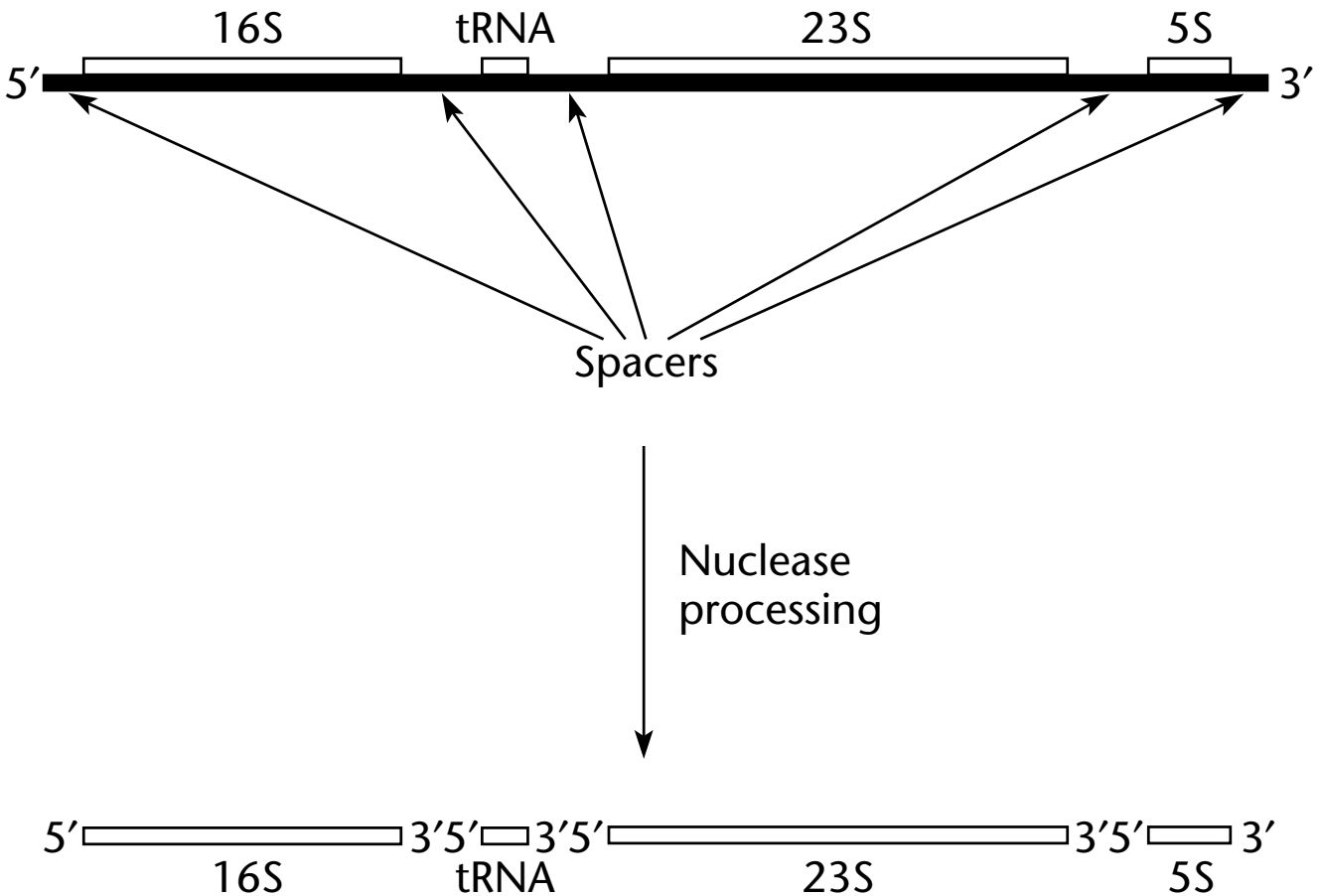

16S
tRNA
23S
5S
5′
3′
Spacers
Nuclease
processing
5′
3′5′
3′5′
3′5′
3′
16S
tRNA
23S
5S

Figure 2.12

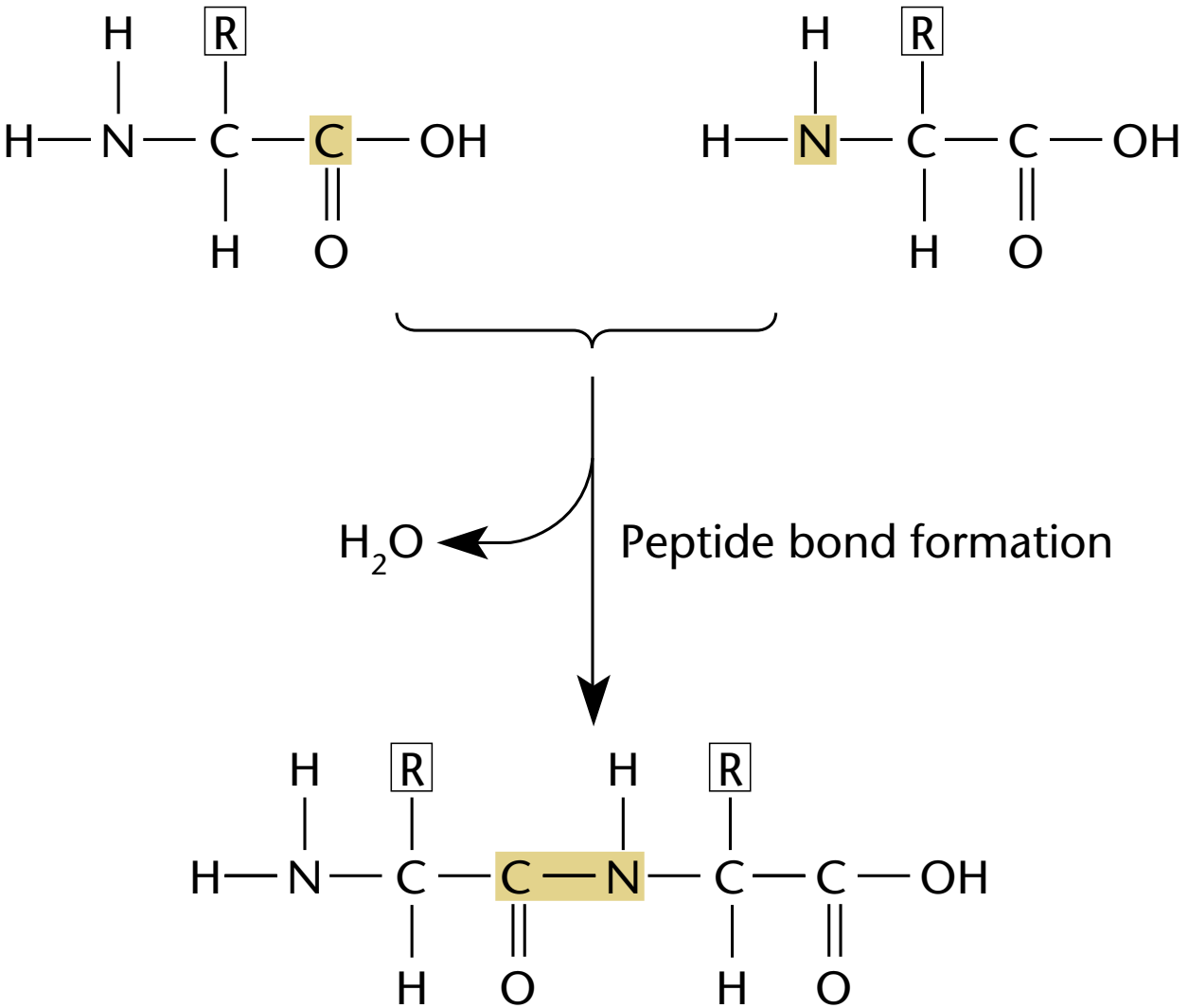
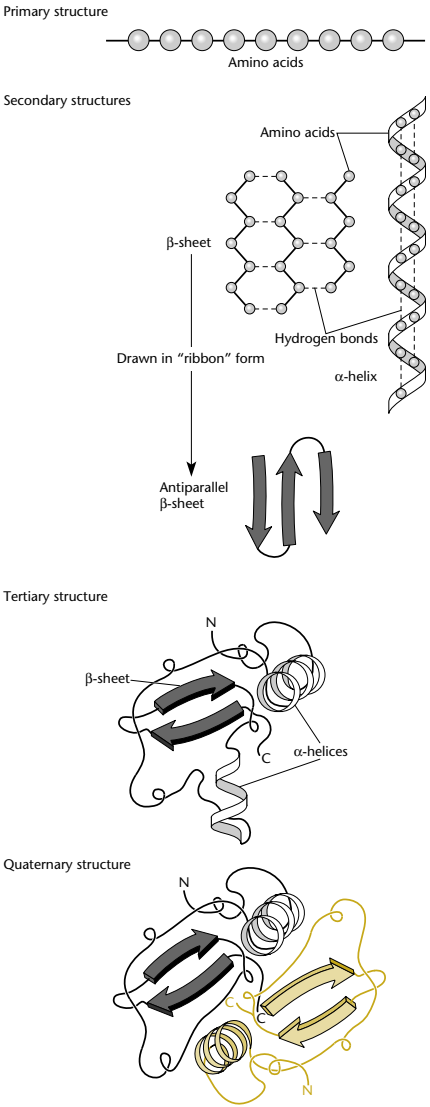

H
R
H—N—C—C—OH
H
O
H
R
H—N—C—C—OH
H
O
H_2O
Peptide bond formation
H
R
H
R
H—N—C—C—N—C—C—OH
H
O
H
O

Figure 2.13


Primary structure
Amino acids
Secondary structures
Amino acids
β-sheet
Hydrogen bonds
Drawn in "ribbon" form
α-helix
Antiparallel
β-sheet
Tertiary structure
N
β-sheet
α-helices
C
Quaternary structure
N
C
C
N

Box 2.3

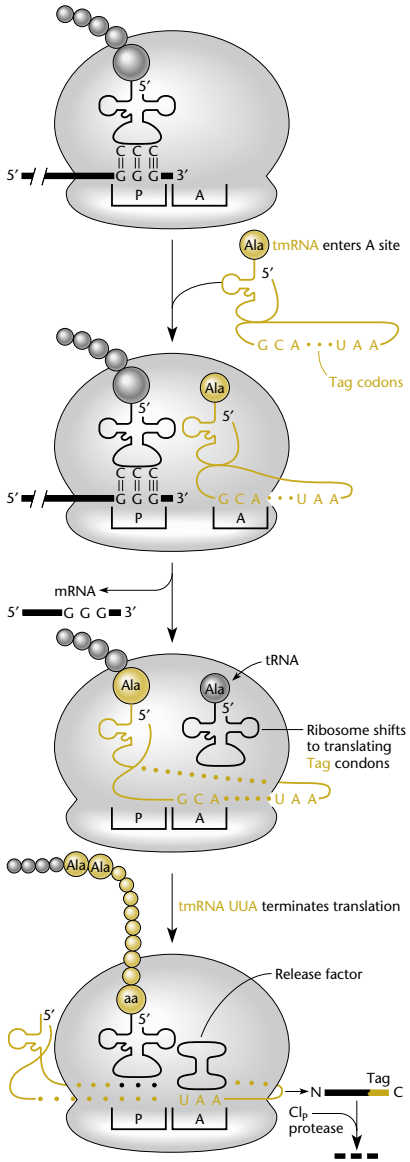

5′
C C C
G G G
5′
3′
P
A
Ala
tmRNA enters A site
5′
G C A • • • U A A
Tag codons
Ala
5′
5′
C C C
G G G
3′
G C A • • • U A A
P
A
mRNA
5′ G G G 3′
tRNA
Ala
Ala
5′
5′
Ribosome shifts
to translating
Tag condons
G C A • • • • • U A A
P
A
Ala Ala
tmRNA UUA terminates translation
Release factor
aa
5′
5′
U A A
N
Tag
C
P
A
Cl
P
protease

Figure 2.14

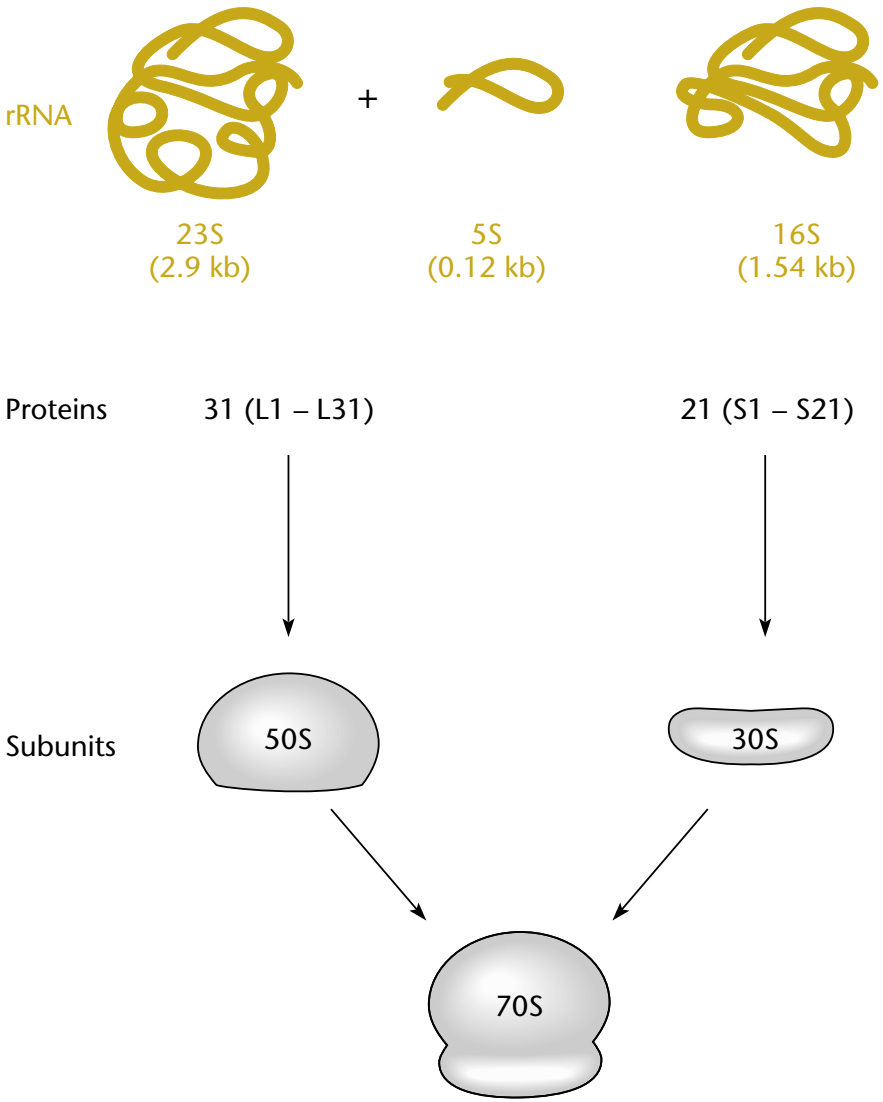

rRNA
+
23S
(2.9 kb)
5S
(0.12 kb)
16S
(1.54 kb)
Proteins
31 (L1 – L31)
21 (S1 – S21)
Subunits
50S
30S
70S

Figure 2.15

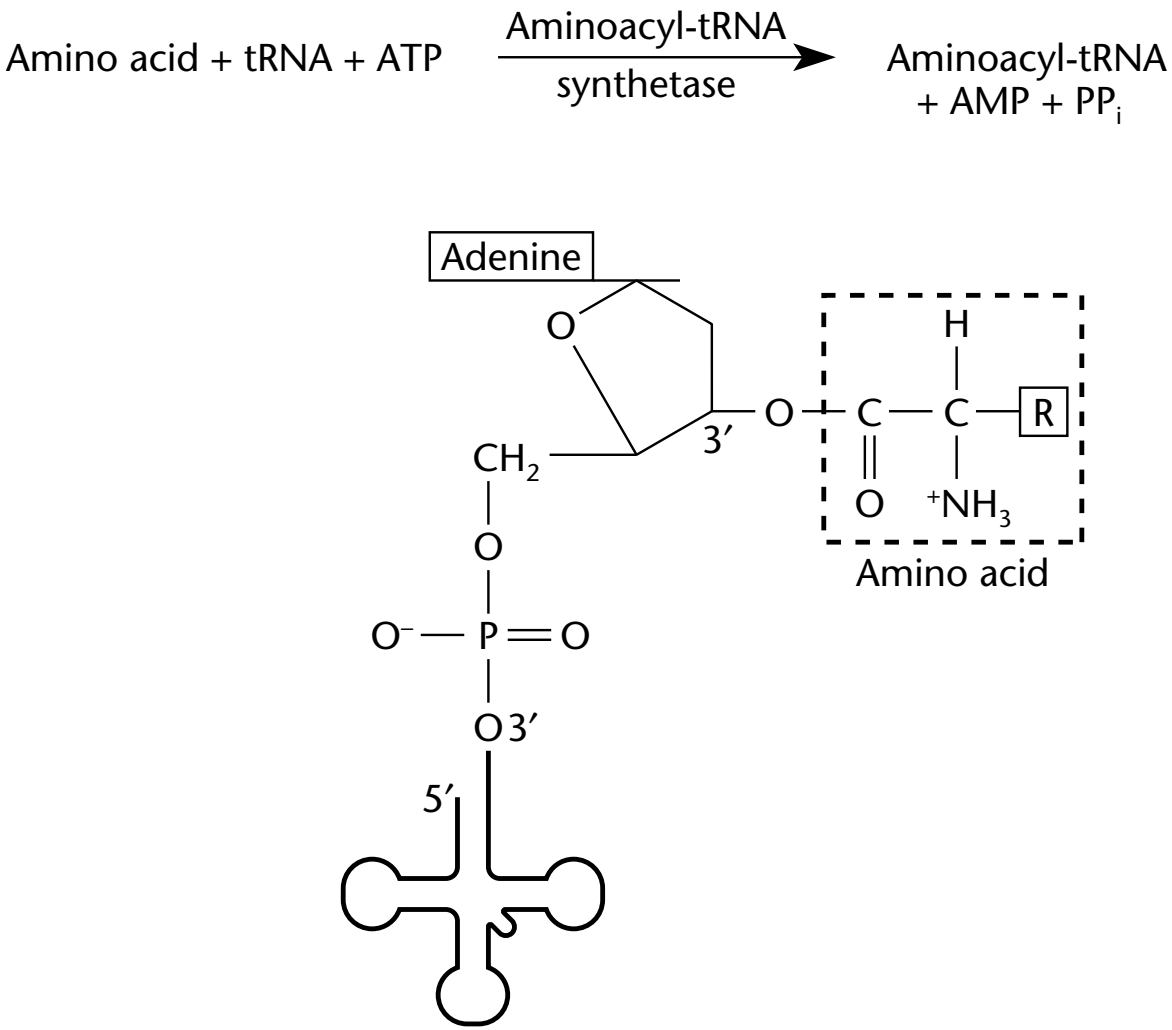

Amino acid + tRNA + ATP
Aminoacyl-tRNA synthetase
Aminoacyl-tRNA + AMP + PPi
Adenine
O
3′
O
H
C
C
R
CH2
O
+NH3
Amino acid
O
O⁻ P O
O 3′
5′

Figure 2.16

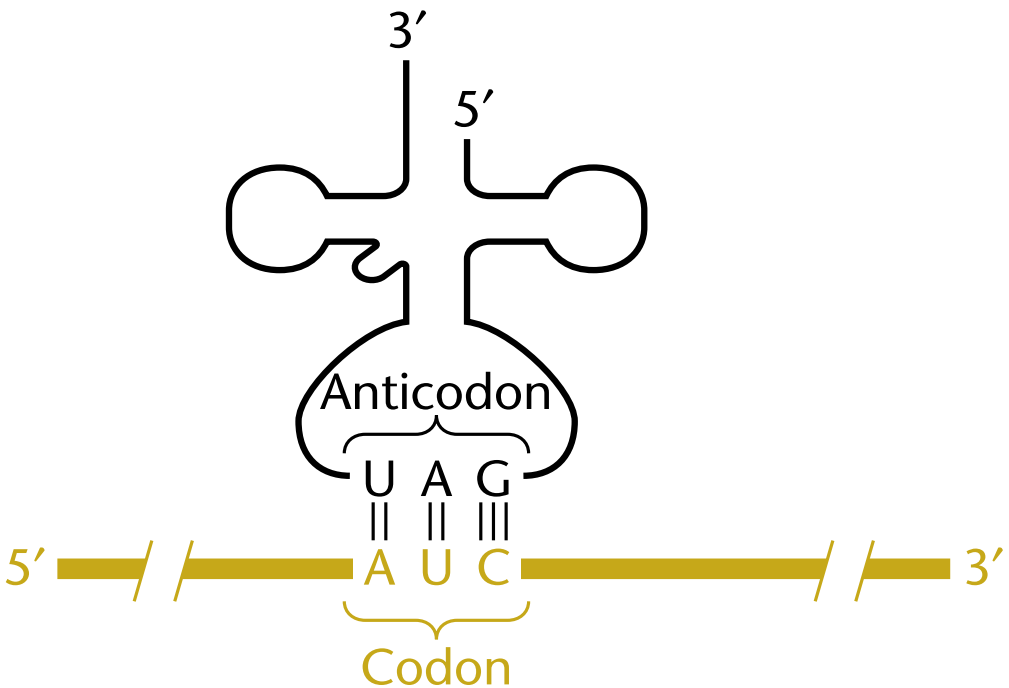


Figure 2.17

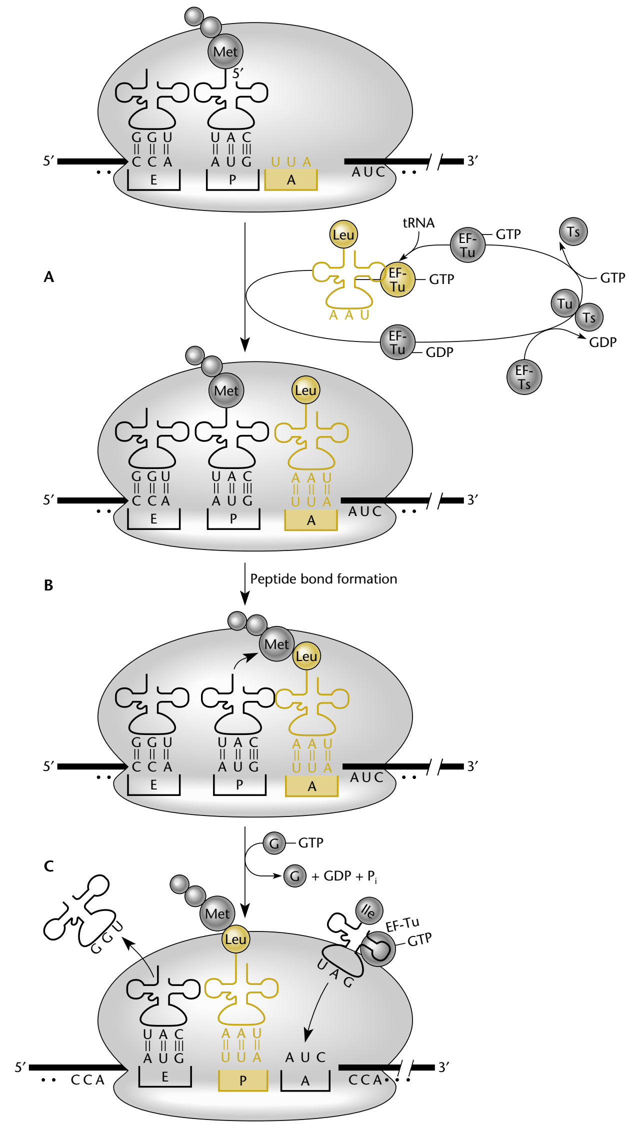

Met
5′
G G U
C C A
U A C
A U G
U U A
5′
AUC
3′
E
P
A
A
tRNA
Leu
EF-Tu
GTP
EF-Tu
GTP
Ts
GTP
A A U
Tu
Ts
EF-Tu
GDP
GDP
EF-Ts
Met
Leu
B
Peptide bond formation
C
G
GTP
G
+ GDP + P_i
Ile
EF-Tu
GTP
U A G
C C A

Figure 2.18

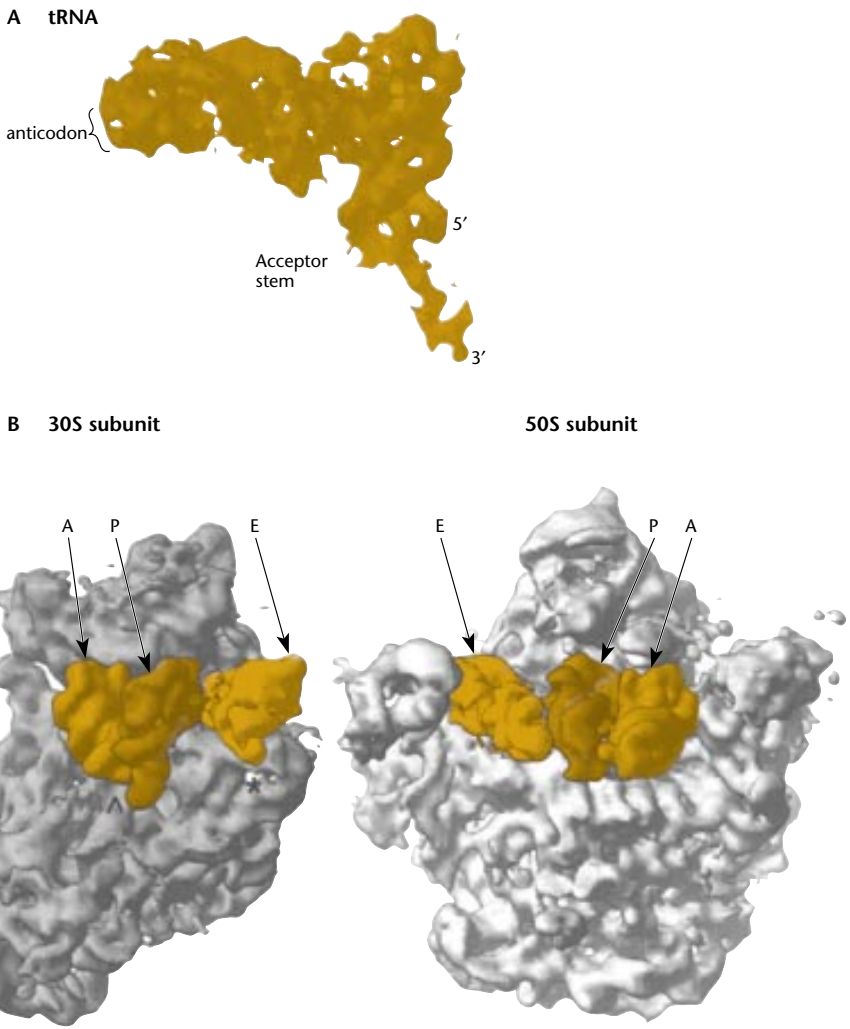

A tRNA
anticodon
5′
Acceptor stem
3′
B 30S subunit
50S subunit
A
P
E
E
P
A

Figure 2.19

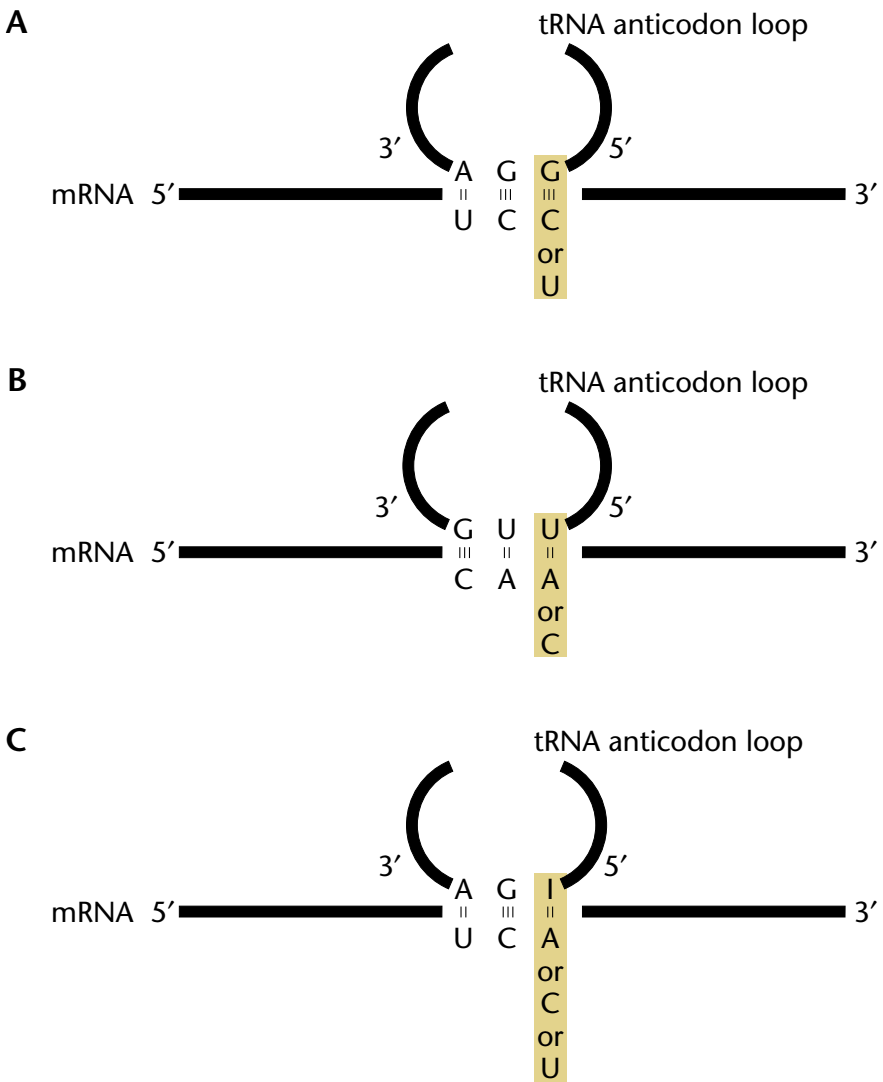

A
tRNA anticodon loop
3′
5′
mRNA 5′
A
U
G
C
G
C
or
U
3′
B
tRNA anticodon loop
3′
5′
mRNA 5′
G
C
U
A
U
A
or
C
3′
C
tRNA anticodon loop
3′
5′
mRNA 5′
A
U
G
C
I
A
or
C
or
U
3′

Figure 2.20

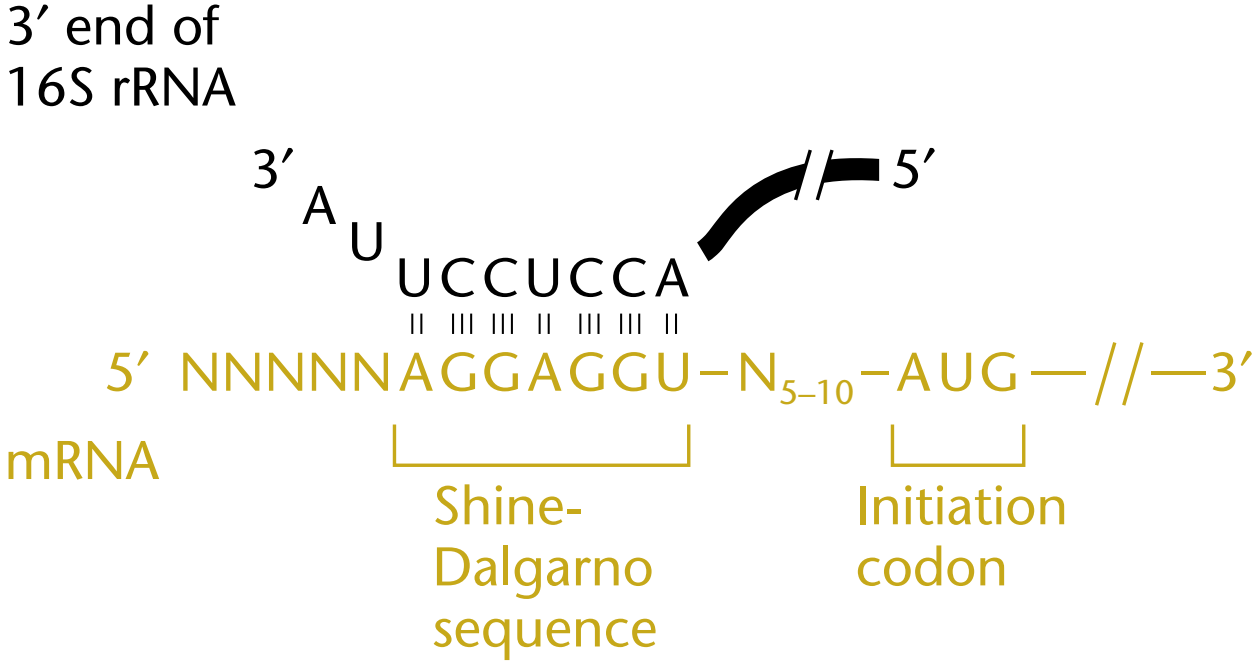

3′ end of
16S rRNA
3′
A
U
UCCUCCA
5′
5′ NNNNNAGGAGGU–N5–10–AUG—//—3′
mRNA
Shine-
Dalgarno
sequence
Initiation
codon

Figure 2.21

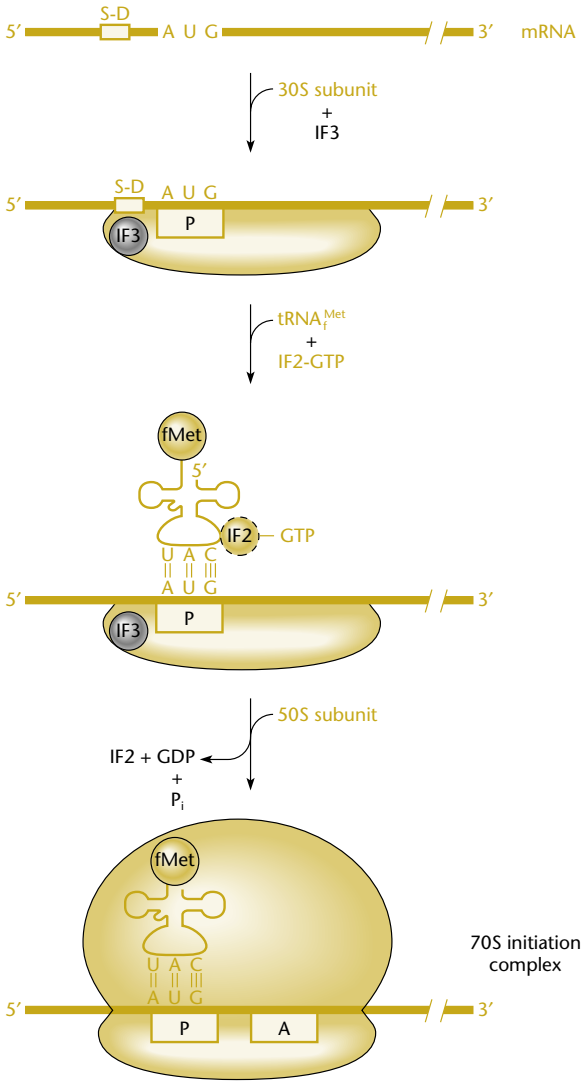
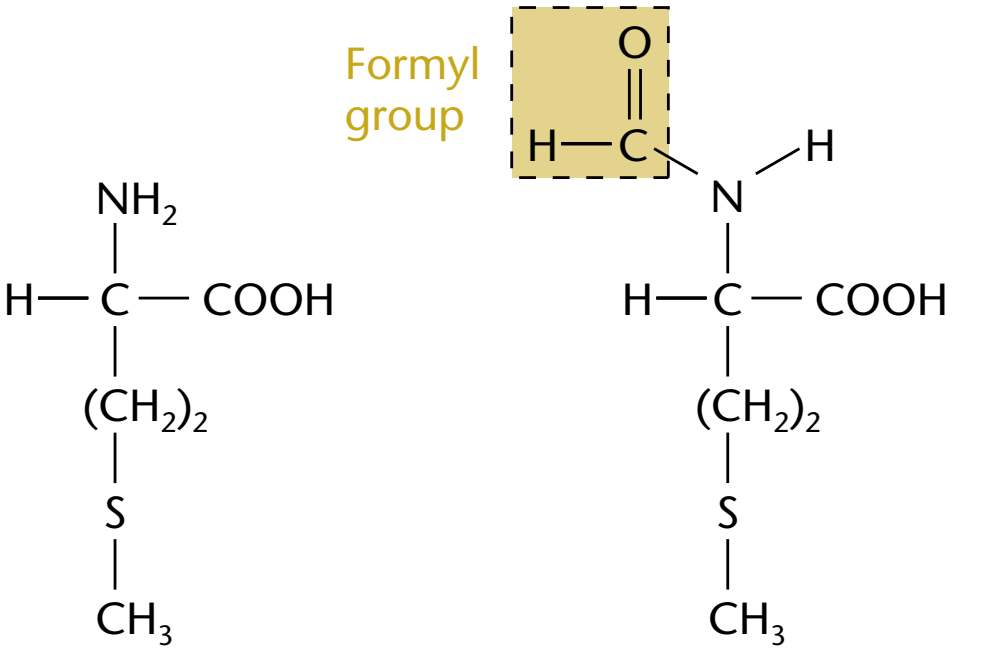

S-D
5′
A U G
3′
mRNA
30S subunit
+
IF3
S-D
A U G
5′
3′
IF3
P
tRNA$_f^{Met}$
+
IF2-GTP
fMet
5′
IF2
GTP
U A C
A U G
5′
3′
IF3
P
50S subunit
IF2 + GDP
+
P_i
fMet
U A C
A U G
70S initiation
complex
5′
3′
P
A

Figure 2.22



Methionine

N-Formylmethionine

Figure 2.23

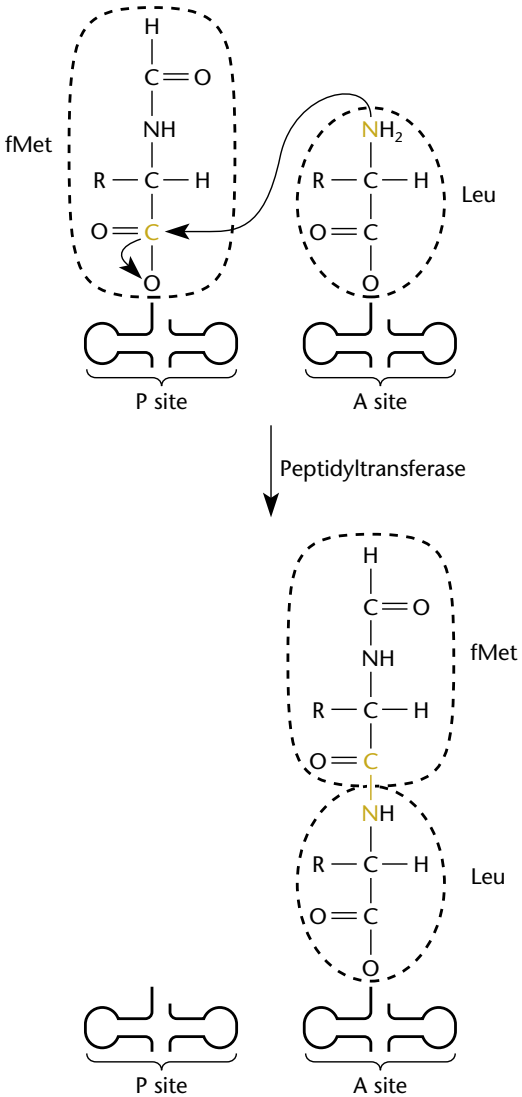

fMet
Leu
P site
A site
Peptidyltransferase
fMet
Leu
P site
A site

Figure 2.24

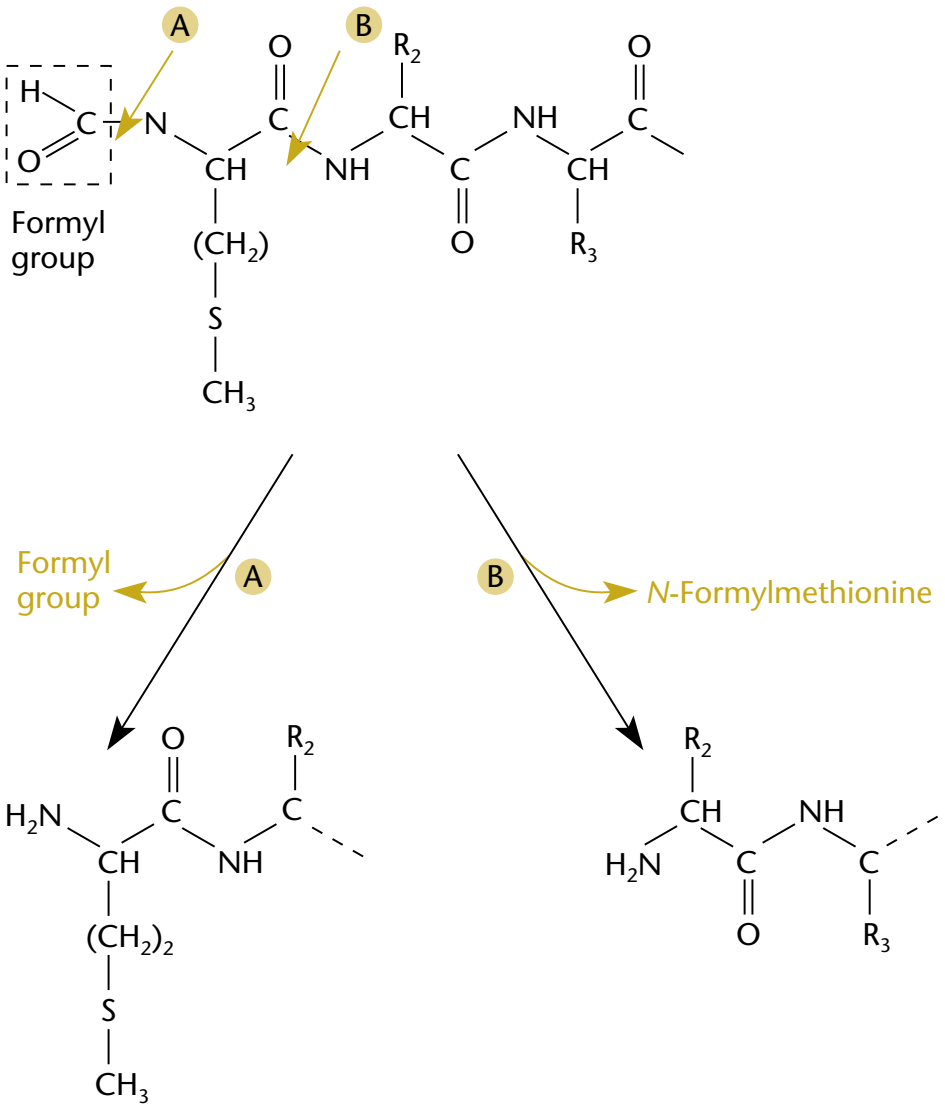


Figure 2.25

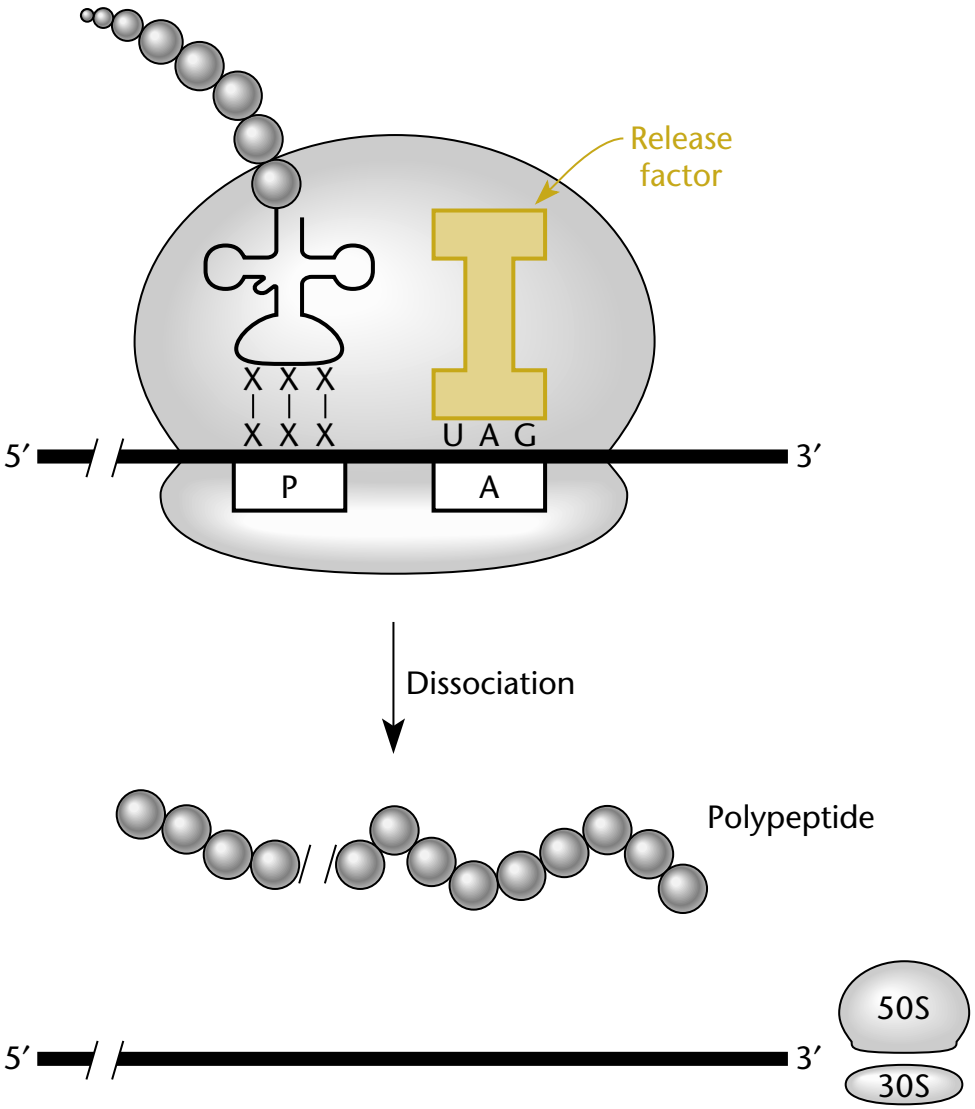

Release factor
X X X
X X X
U A G
5′
3′
P
A
Dissociation
Polypeptide
5′
3′
50S
30S

Figure 2.26

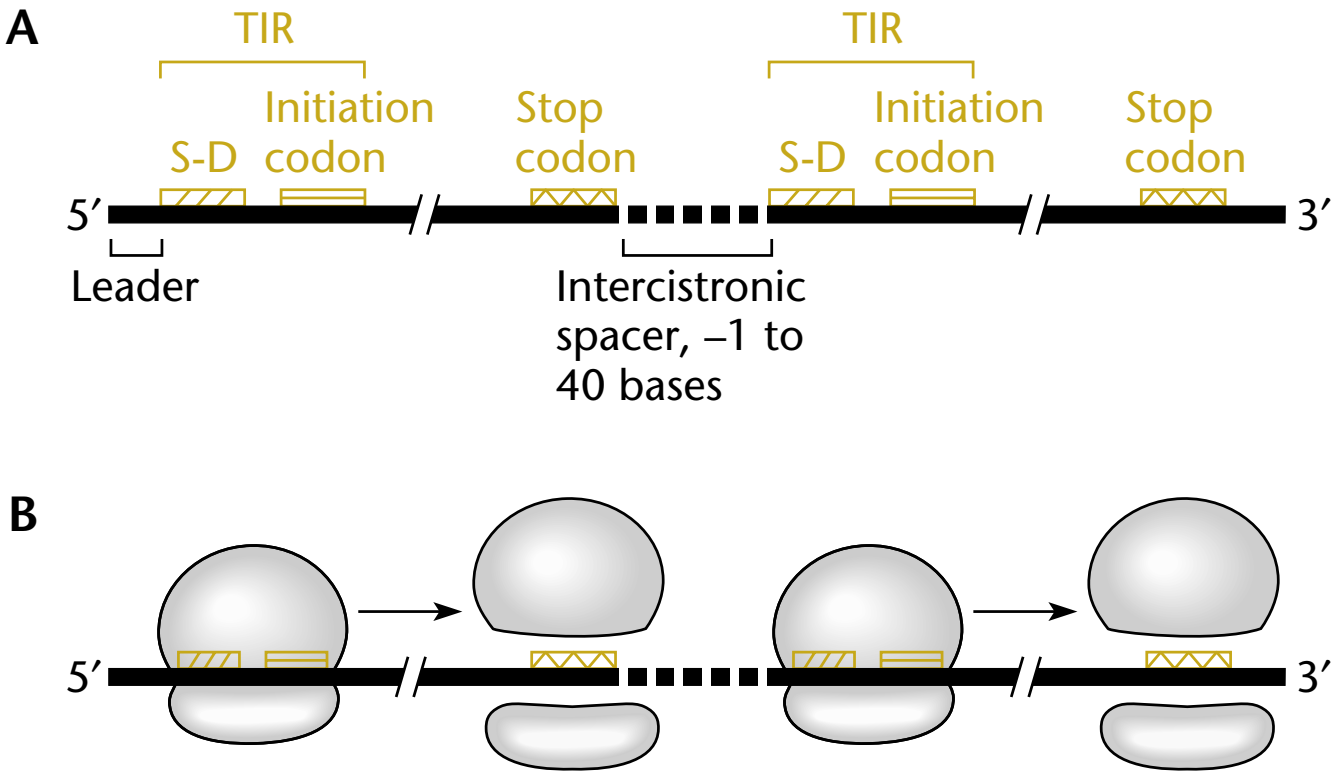

A
TIR
TIR
Initiation codon
S-D
Stop codon
Initiation codon
S-D
Stop codon
5′
3′
Leader
Intercistronic spacer, –1 to 40 bases
B
5′
3′

Figure 2.27

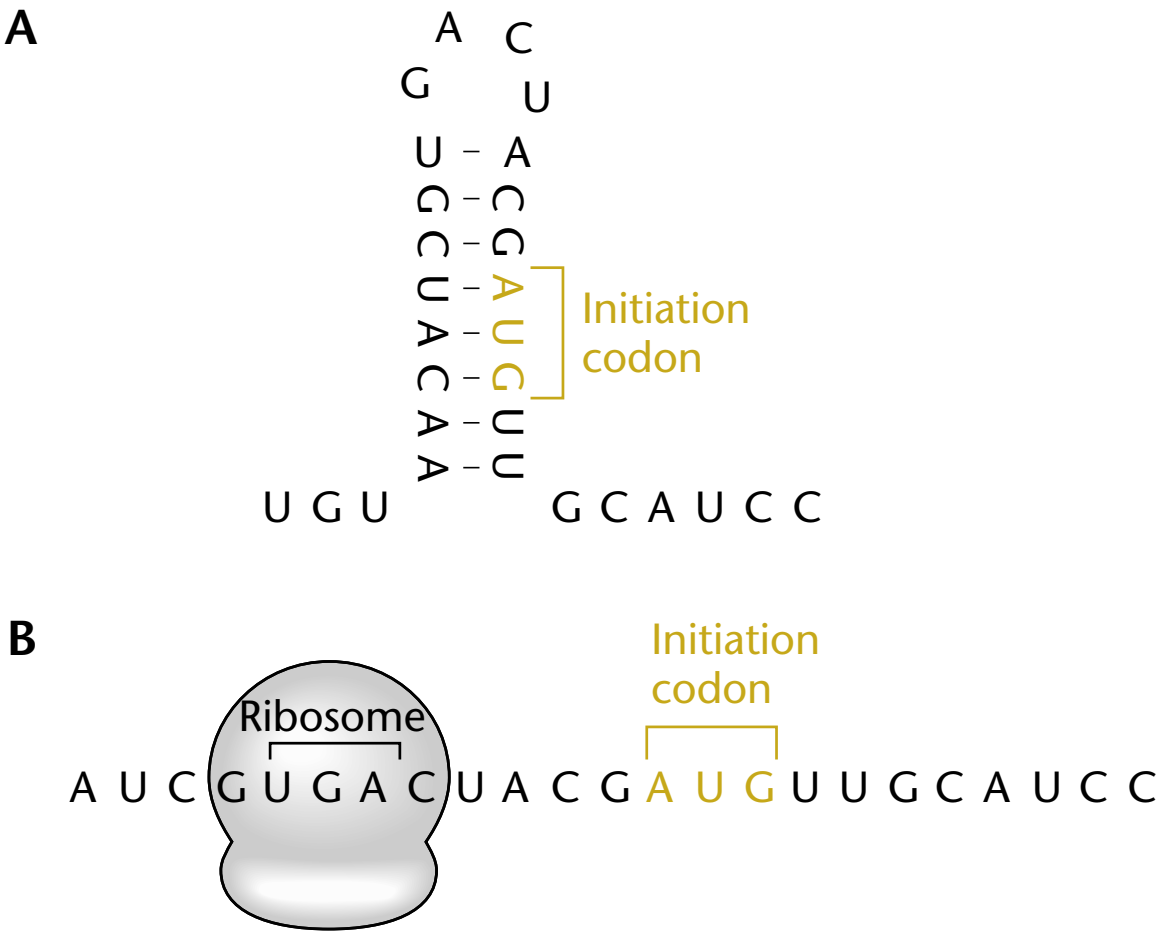

A
A C
G U
U – A
G – C
C – G
U – A
A – U
C – G
A – U
U – U
U G U
G C A U C C
Initiation codon
B
Ribosome
Initiation codon
A U C G U G A C U A C G A U G U U G C A U C C

Figure 2.28

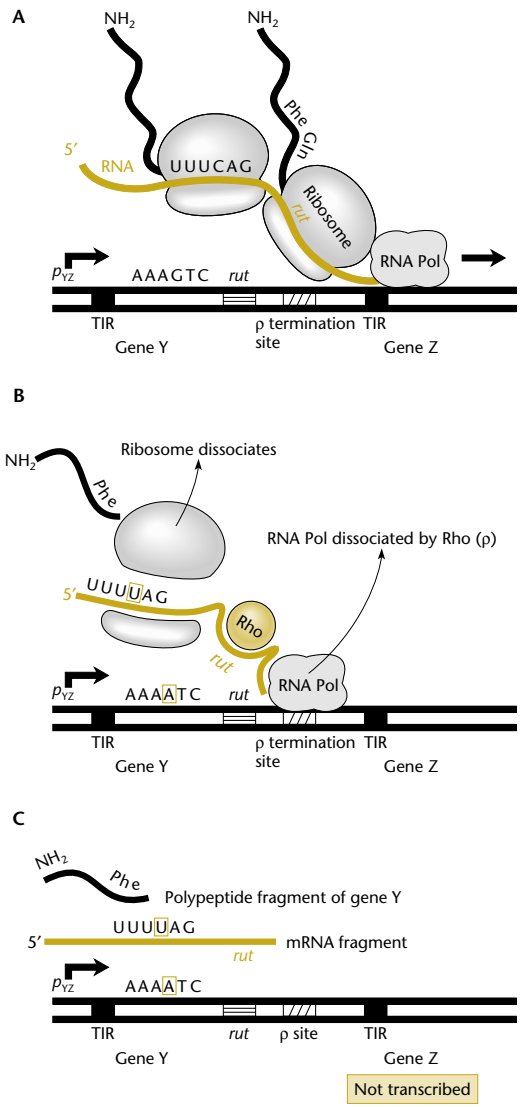

A
NH2
NH2
Phe
Gln
5′
RNA
UUUCAG
Ribosome
rut
RNA Pol
pYZ
AAAGTC
rut
TIR
Gene Y
ρ termination site
TIR
Gene Z
B
Ribosome dissociates
NH2
Phe
RNA Pol dissociated by Rho (ρ)
5′
UUUUAG
Rho
rut
pYZ
AAAATC
rut
RNA Pol
TIR
Gene Y
ρ termination site
TIR
Gene Z
C
NH2
Phe
Polypeptide fragment of gene Y
5′
UUUUAG
mRNA fragment
rut
pYZ
AAAATC
TIR
Gene Y
rut
ρ site
TIR
Gene Z
Not transcribed

Figure 2.29

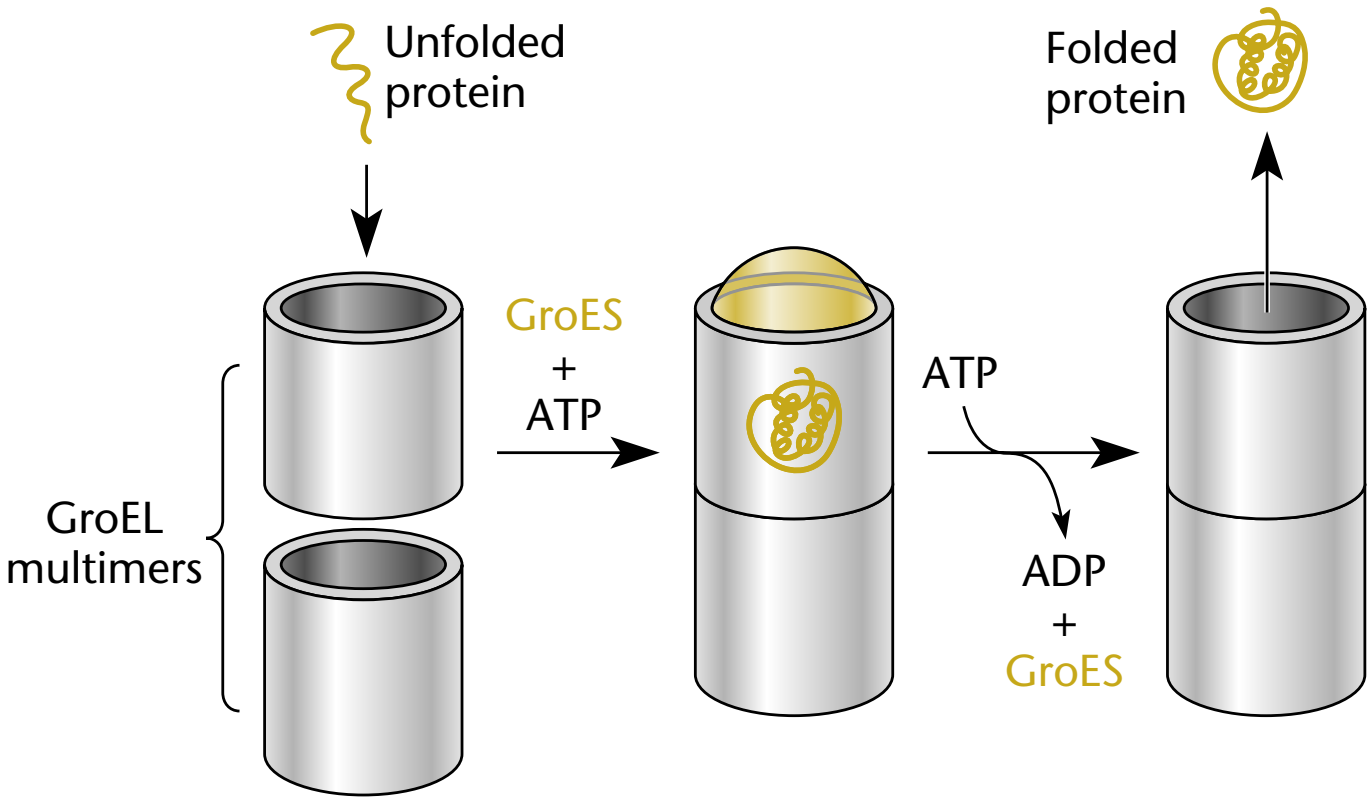
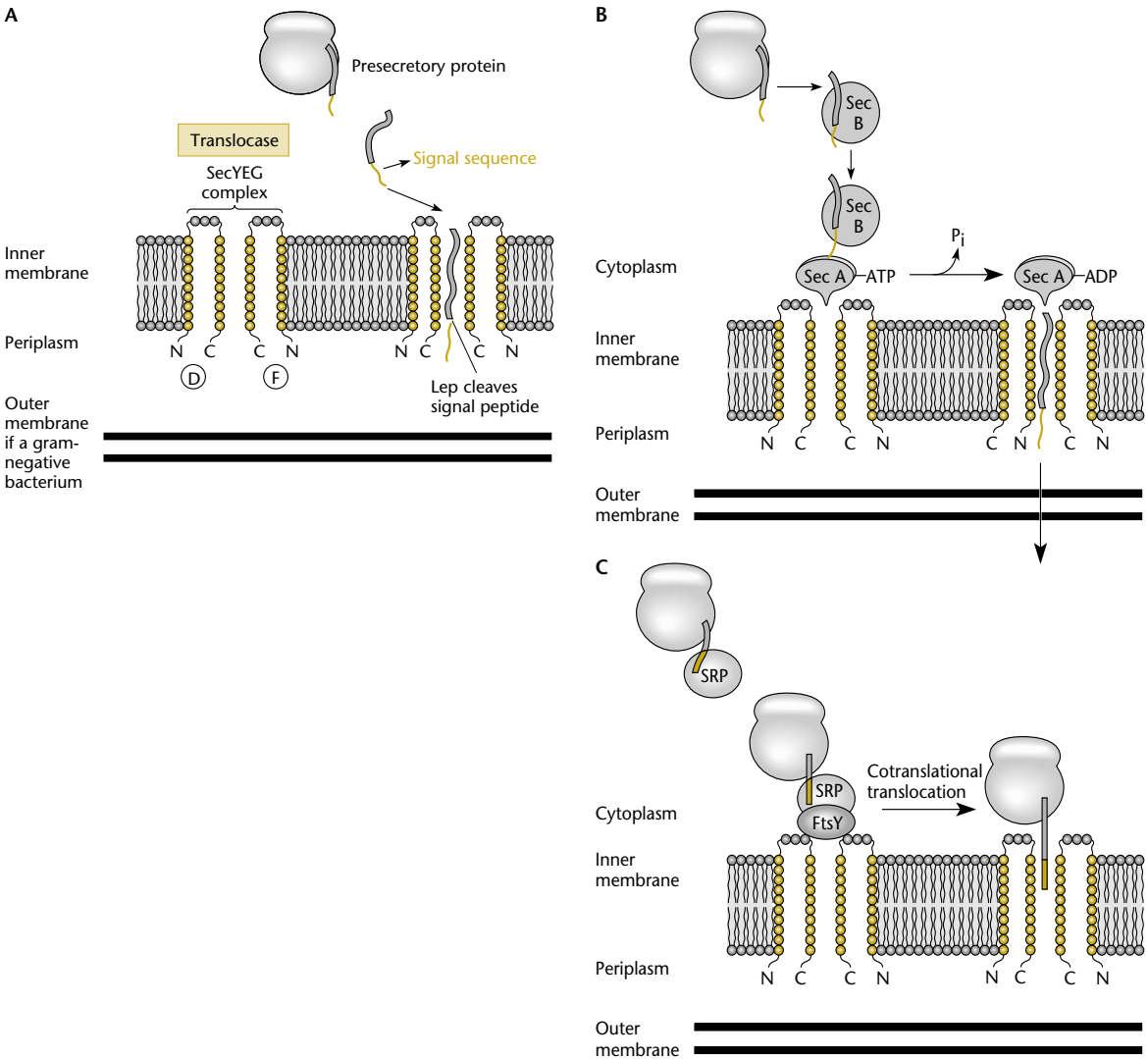

Unfolded protein
Folded protein
GroES
+
ATP
ATP
GroEL multimers
ADP
+
GroES

Figure 2.30


A
Presecretory protein
Translocase
Signal sequence
SecYEG complex
Inner membrane
Periplasm
N C C N
D
F
N C C N
Lep cleaves signal peptide
Outer membrane if a gram-negative bacterium
B
Sec B
Sec B
Cytoplasm
Sec A ATP
Pi
Sec A ADP
Inner membrane
Periplasm
N C C N
C N C N
Outer membrane
C
SRP
SRP
FtsY
Cotranslational translocation
Cytoplasm
Inner membrane
Periplasm
N C C N
N C C N
Outer membrane

Box 2.6

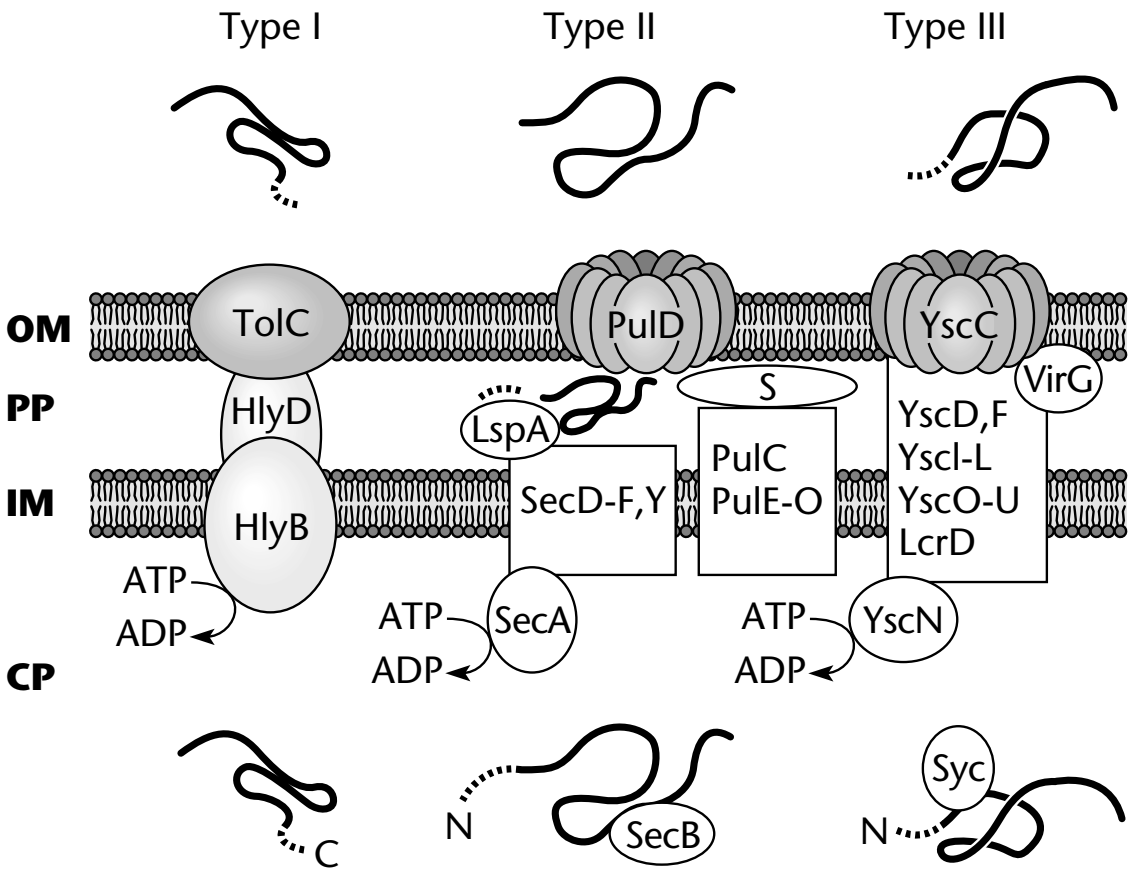

Type I
Type II
Type III
OM
PP
IM
CP
TolC
HlyD
HlyB
ATP
ADP
PulD
LspA
SecD-F,Y
S
PulC
PulE-O
SecA
ATP
ADP
YscC
VirG
YscD,F
YscI-L
YscO-U
LcrD
YscN
ATP
ADP
C
N
SecB
Syc
N

Figure 2.31

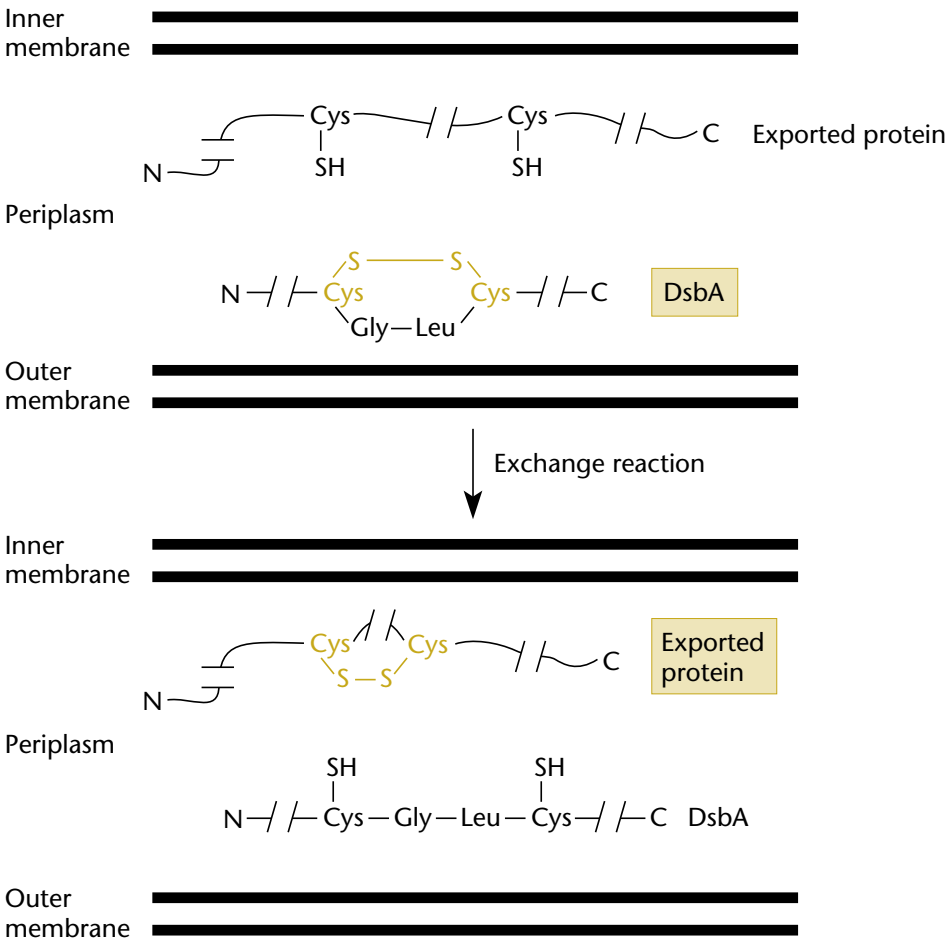

Inner membrane
Cys
SH
Cys
SH
N
C
Exported protein
Periplasm
S
S
N
Cys
Cys
C
Gly—Leu
DsbA
Outer membrane
Exchange reaction
Inner membrane
Cys
Cys
S—S
N
C
Exported protein
Periplasm
SH
SH
N
Cys—Gly—Leu—Cys
C
DsbA
Outer membrane

Figure 2.32

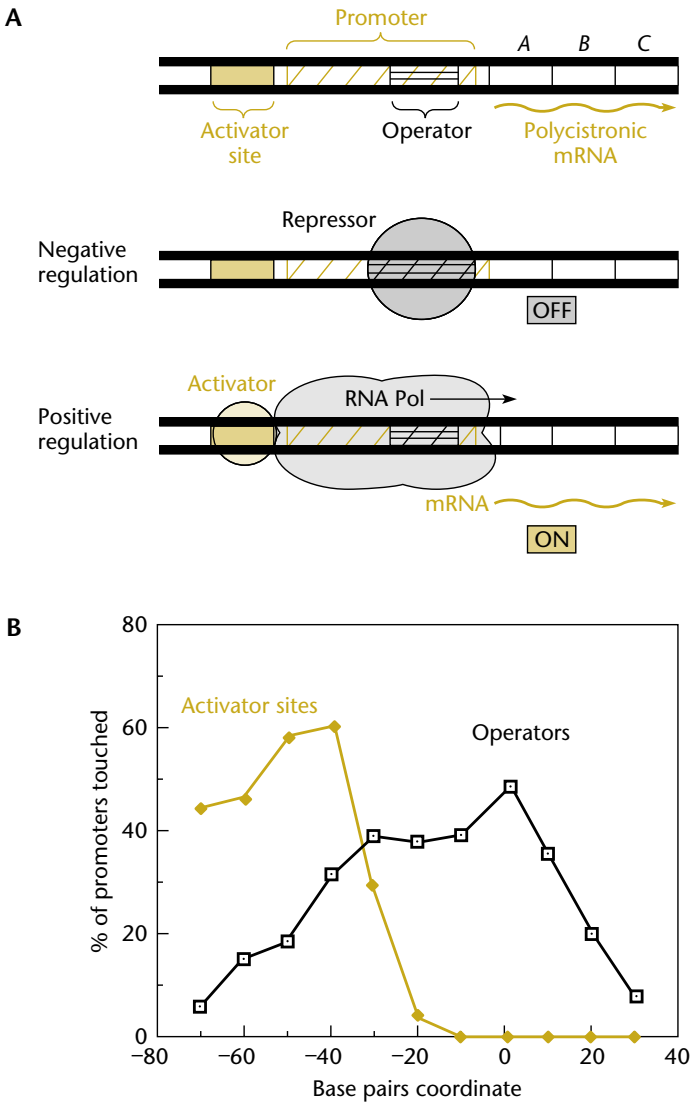

A
Promoter
A
B
C
Activator site
Operator
Polycistronic mRNA
Repressor
Negative regulation
OFF
Activator
RNA Pol
Positive regulation
mRNA
ON
B
Activator sites
Operators
% of promoters touched
80
60
40
20
0
−80
−60
−40
−20
0
20
40
Base pairs coordinate

Figure 2.33

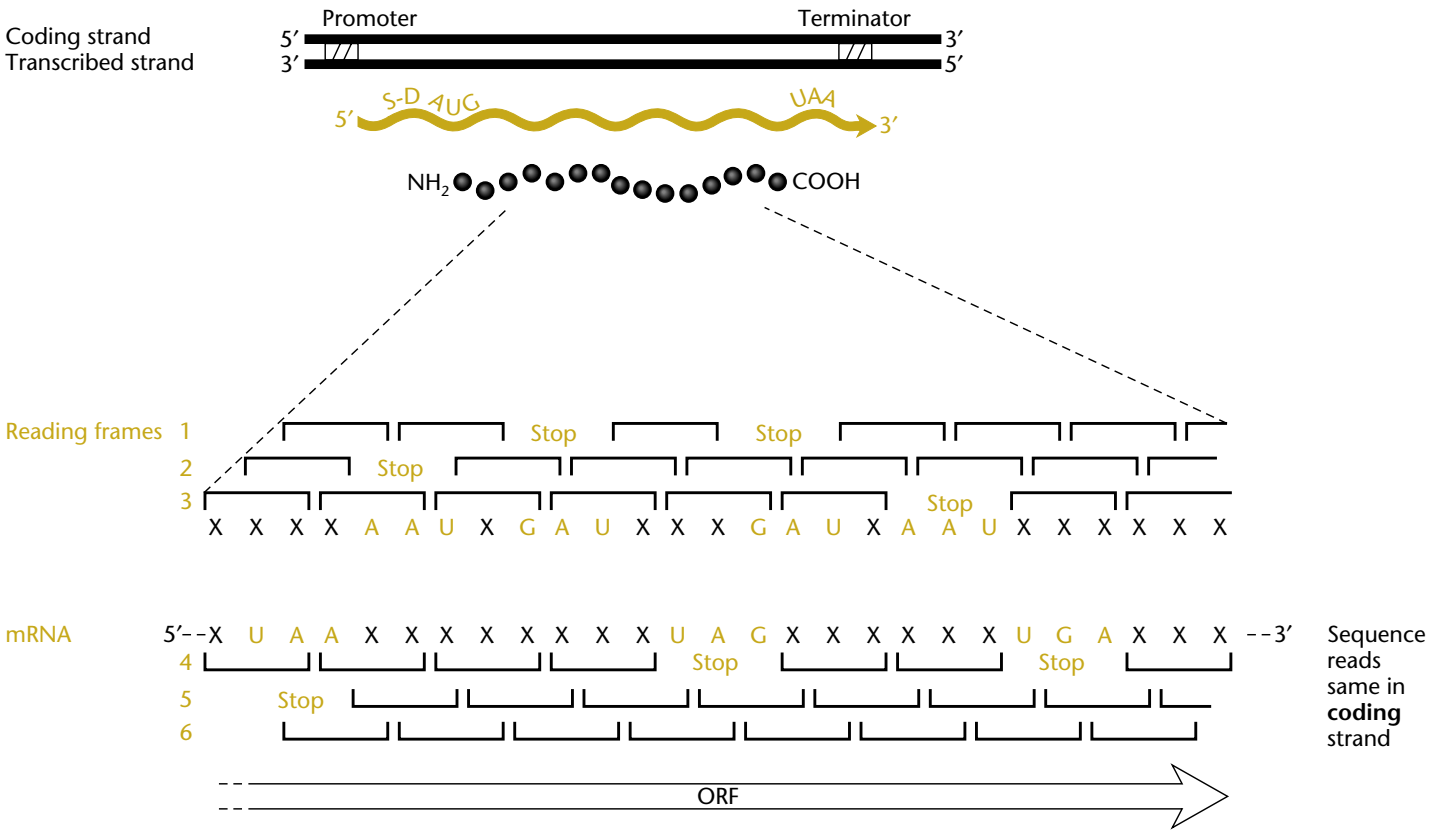
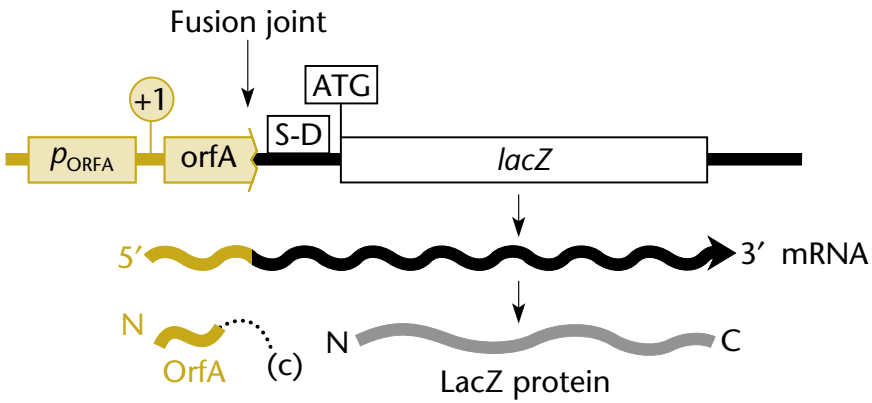

Coding strand
Transcribed strand
Promoter
Terminator
5′
3′
3′
5′
S-D
AUG
UAA
5′
3′
NH2
COOH
Reading frames
1
2
3
Stop
Stop
Stop
Stop
X X X X A A U X G A U X X X G A U X A A U X X X X X X
mRNA
5′--X U A A X X X X X X X X U A G X X X X X X U G A X X X --3′
4
5
6
Stop
Stop
Stop
Stop
ORF
Sequence reads same in **coding** strand

Figure 2.34

A Transcriptional fusion:

Promoter and transcription +1 site: *orfA* gene
TIR : *lacZ* gene

Protein : LacZ



B Translational fusion:

Promoter and transcription +1 site: *orfA* gene
TIR : *orfA* gene

Protein : OrfA′ - ′LacZ

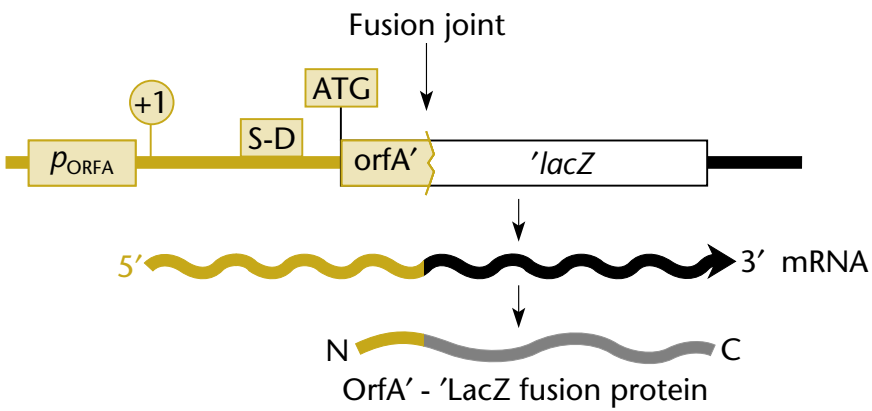
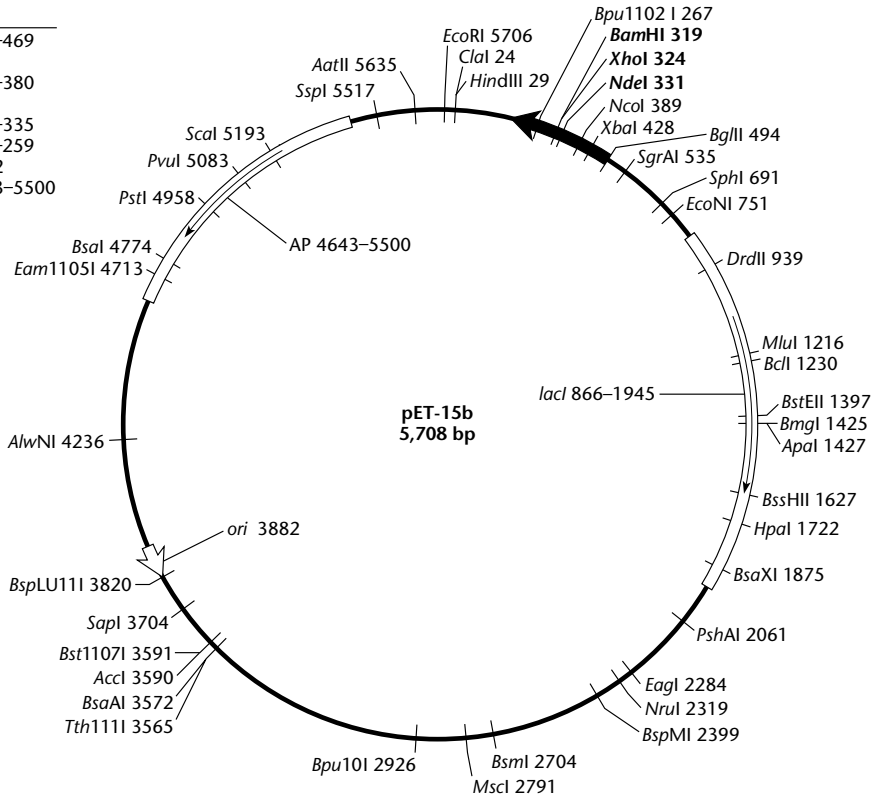


Figure 2.35

pET-15b sequence landmarks

T7 promoter	453–469
T7 transcription start	452
His·Tag coding sequence	362–380
Multiple cloning sites (*Nde*I - *Bam*HI)	319–335
T7 terminator	213–259
pBR322 origin	3882
bla coding sequence	4643–5500



BglII — T7 promoter — *lac* operator — XbaI — RBS

AGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCCCTCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGA

NcoI — His·Tag — NdeI — XhoI — BamHI

TATACCATGGGCAGCAGCCATCATCATCATCATCACAGCAGCGGCCTGGTGCCGCGCGGCAGCCATATGCTCGAGGATCCGGCTGCTAACAAAGCCCGA

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro Arg Gly Ser His Met Leu Glu Asp Pro Ala Ala Asn Lys Ala Arg

Bpu1102I — Thrombin — T7 terminator

AAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTG

Lys Glu Ala Glu Leu Ala Ala Ala Thr Ala Glu Gln End

TABLE 2.2 Antibiotics that block RNA synthesis

Antibiotic	Source	Target or action
Streptolydigin	*Streptomyces lydicus*	β subunit of RNA polymerase
Actinomycin D	*Streptomyces antibioticus*	Binds DNA
Rifampin	*Nocardia mediterranei*	β subunit of RNA polymerase
Bleomycin	*Streptomyces verticulus*	Cuts DNA

TABLE 2.3 Antibiotics that block translation

Antibiotic	Source	Target
Puromycin	*Streptomyces alboniger*	A site of ribosome
Kanamycin	*Streptomyces kanamyceticus*	16S rRNA
Neomycin	*Streptomyces fradiae*	16S rRNA
Streptomycin	*Streptomyces griseus*	30S ribosome
Thiostrepton	*Streptomyces azureus*	23S rRNA
Gentamicin	*Micromonospora purpurea*	16S rRNA
Tetracycline	*Streptomyces rimosus*	A site of ribosome
Chloramphenicol	*Streptomyces venezuelae*	Peptidyltransferase
Erythromycin	*Saccharopolyspora erythraea*	23S rRNA
Fusidic acid	*Fusidium coccinuem*	Translation elongation factor G
Kirromycin	*Streptomyces collinus*	Translation elongation factor Tu