

Figure 1.1

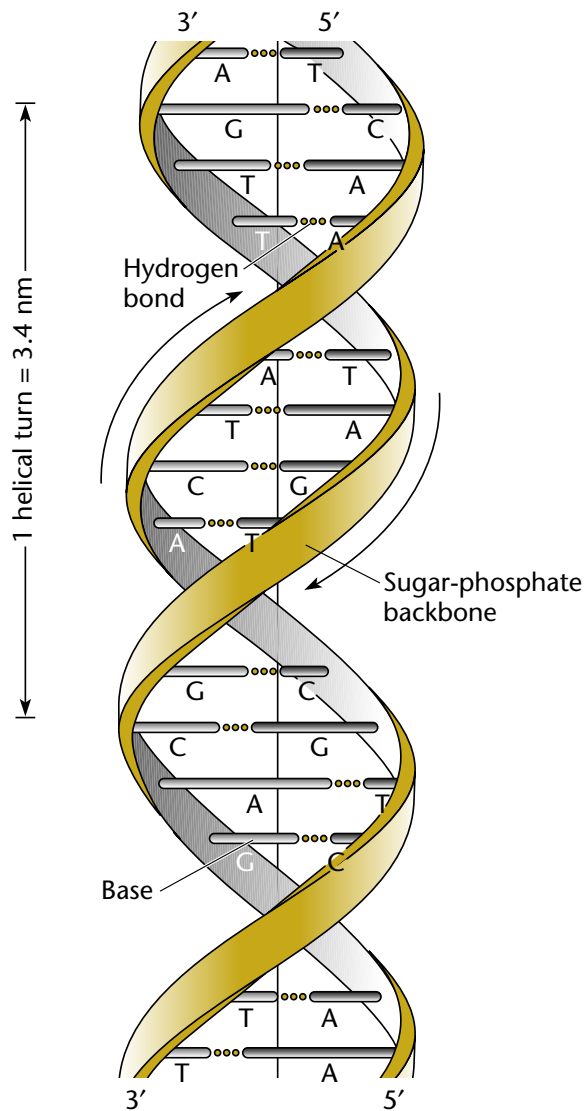
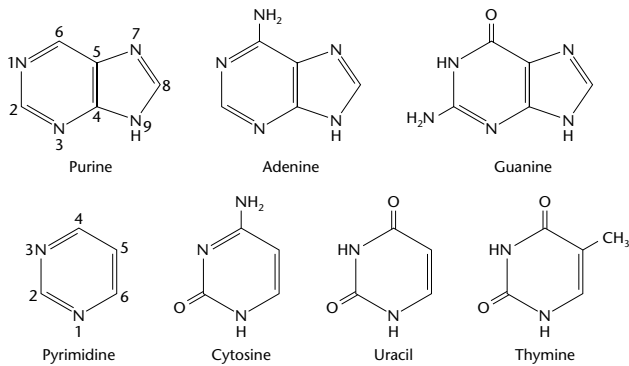
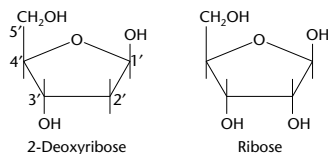


Figure 1.2

Bases



Sugars



Nucleotides

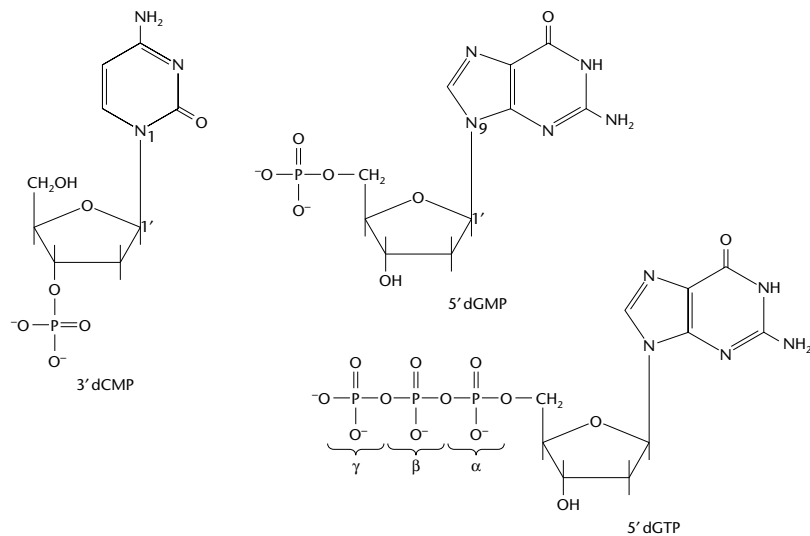
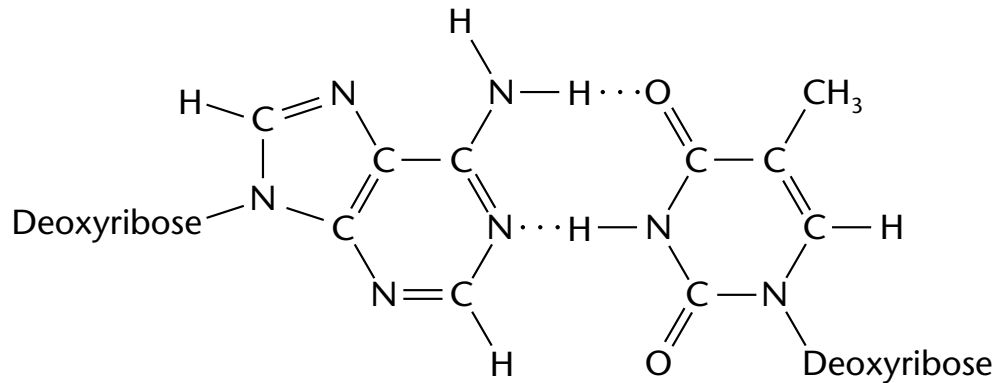
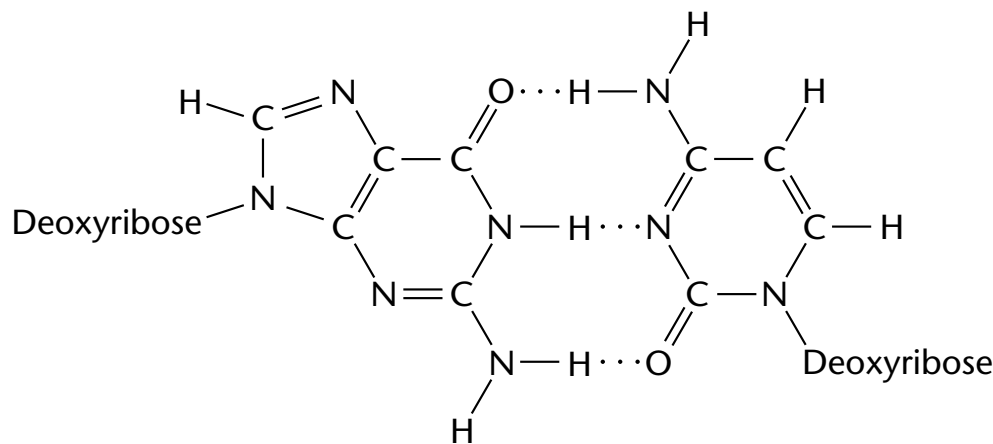


Figure 1.4



Adenine

Thymine



Guanine

Cytosine

Figure 1.6

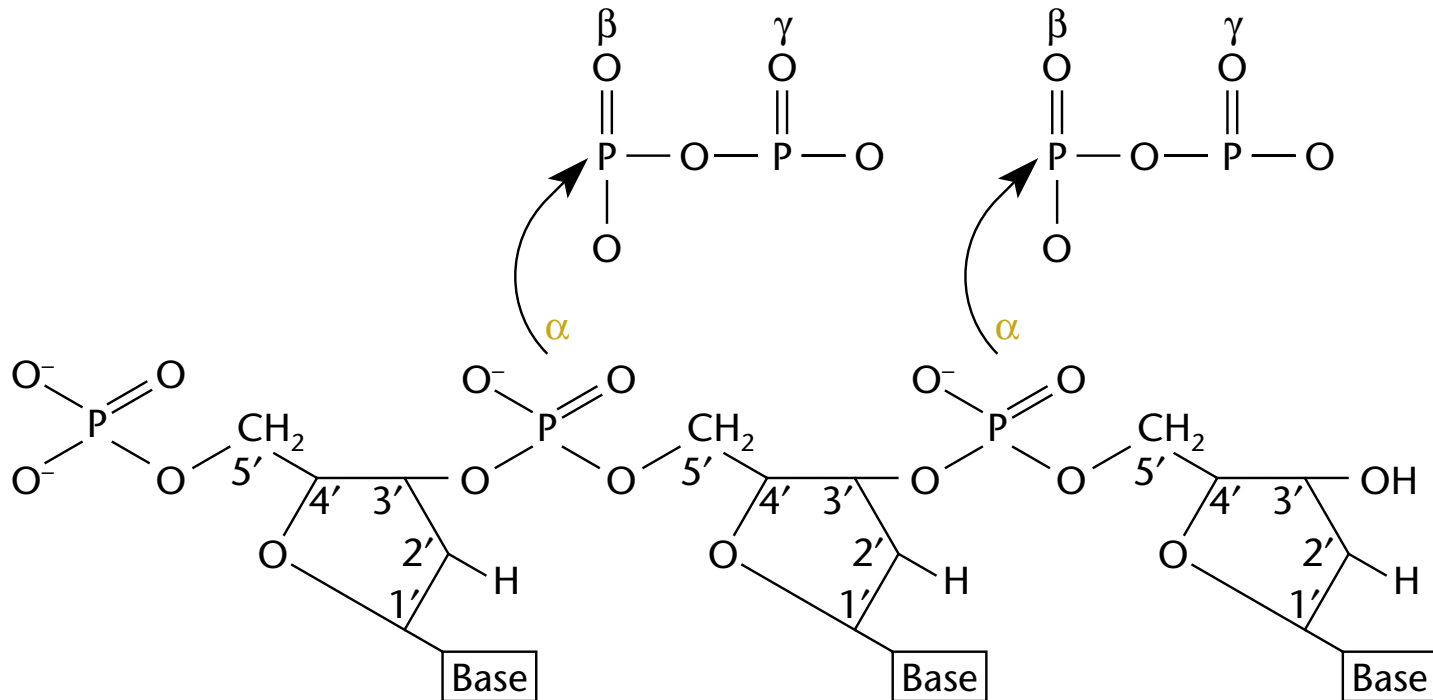


Figure 1.7

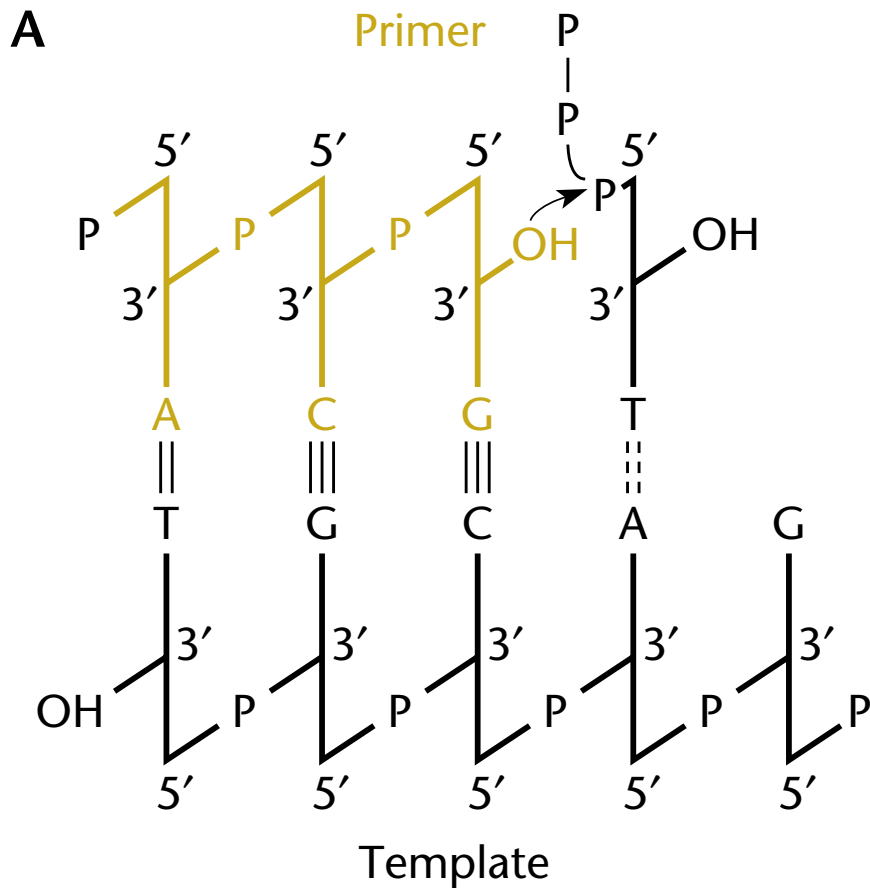


Table 1.1

TABLE 1.1 Proteins involved in <i>E. coli</i> DNA replication		
Protein	Gene	Function
DnaA	<i>dnaA</i>	Initiator protein; primosome (priming complex) formation
DnaB	<i>dnaB</i>	DNA helicase
DnaC	<i>dnaC</i>	Delivers DnaB to replication complex
SSB	<i>ssb</i>	Binding to single-stranded DNA
Primase	<i>dnaG</i>	RNA primer synthesis
DNA Pol I	<i>polA</i>	Primer removal; gap filling
DNA Pol III (holoenzyme)		
α	<i>dnaE</i>	Polymerization
ε	<i>dnaQ</i>	3' → 5' editing
RNase H	<i>rnhA</i>	Removes RNA primers
θ	<i>holE</i>	Present in core (αεθ)
β	<i>dnaN</i>	Sliding clamp
τ ^a	<i>dnaX</i>	Organizes complex; joins leading and lagging DNA PolIII
γ ^b	<i>dnaX</i>	Binds clamp loaders and SSB protein
δ	<i>holA</i>	Clamp loading
δ'	<i>holB</i>	Clamp loading
χ	<i>holC</i>	Binds SSB
ψ	<i>holD</i>	Binds SSB
DNA ligase	<i>lig</i>	Sealing DNA nicks
DNA gyrase		
α	<i>gyrA</i>	Nick closing
β	<i>gyrB</i>	ATPase

^aFull-length product of the *dnaX* gene.

^bShorter product of the *dnaX* gene produced by translational frameshifting (see Box 2.4).



Figure 1.8

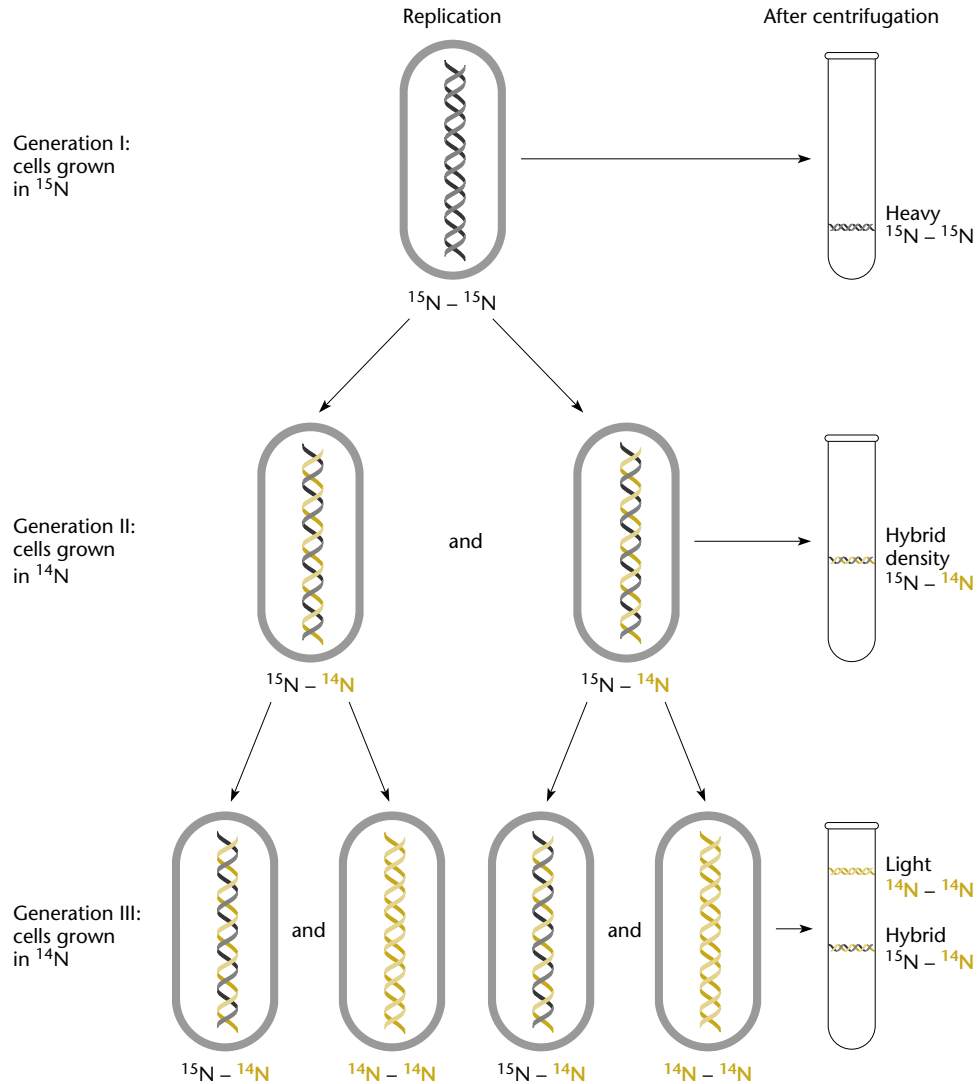


Figure 1.9

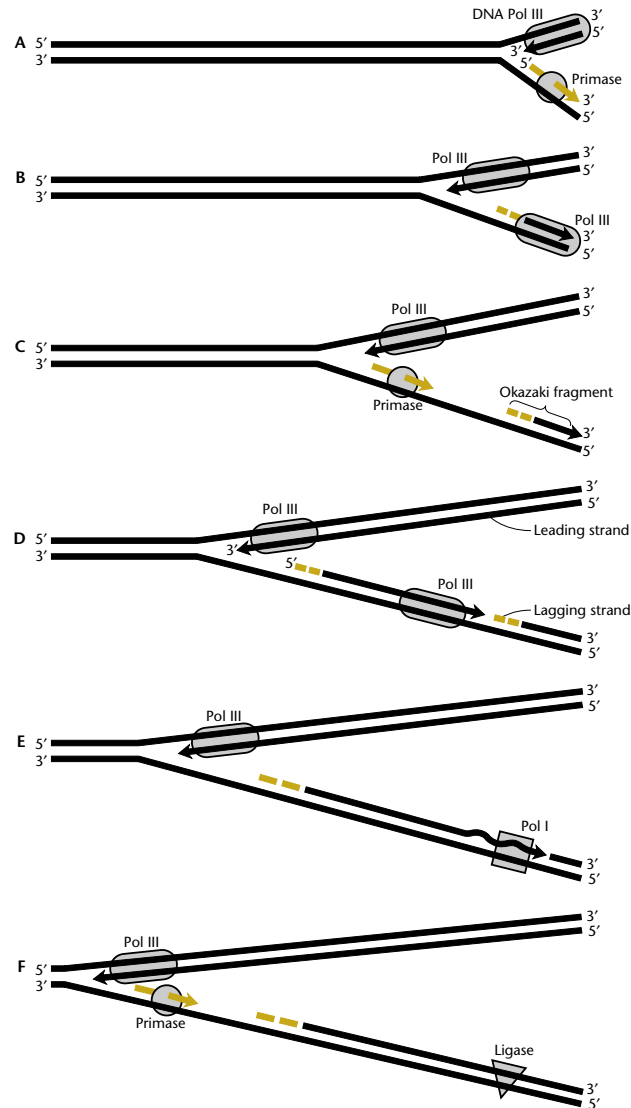


Figure 1.10

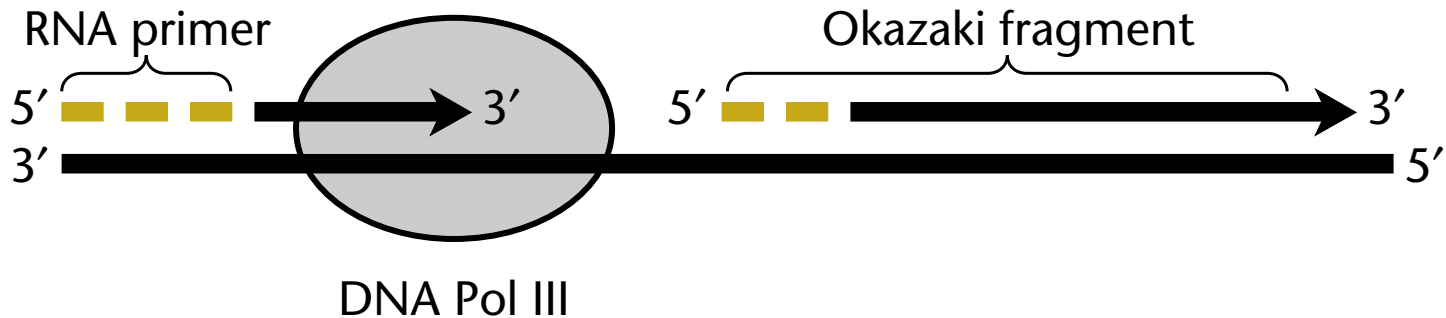


Figure 1.11

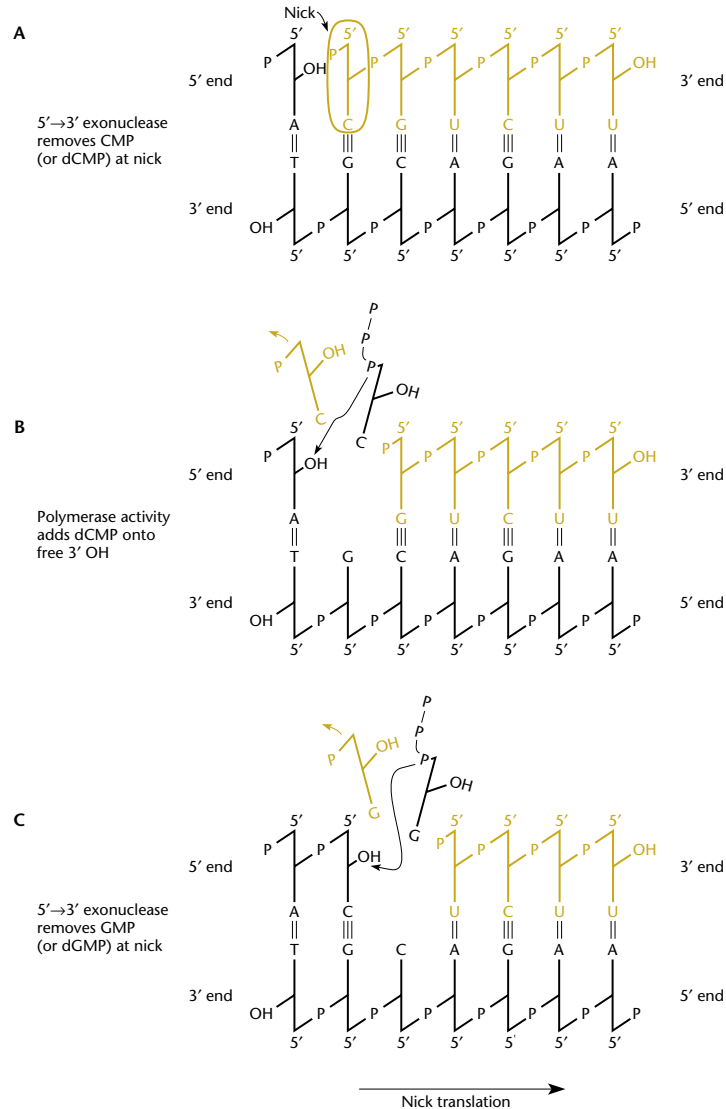


Figure 1.12

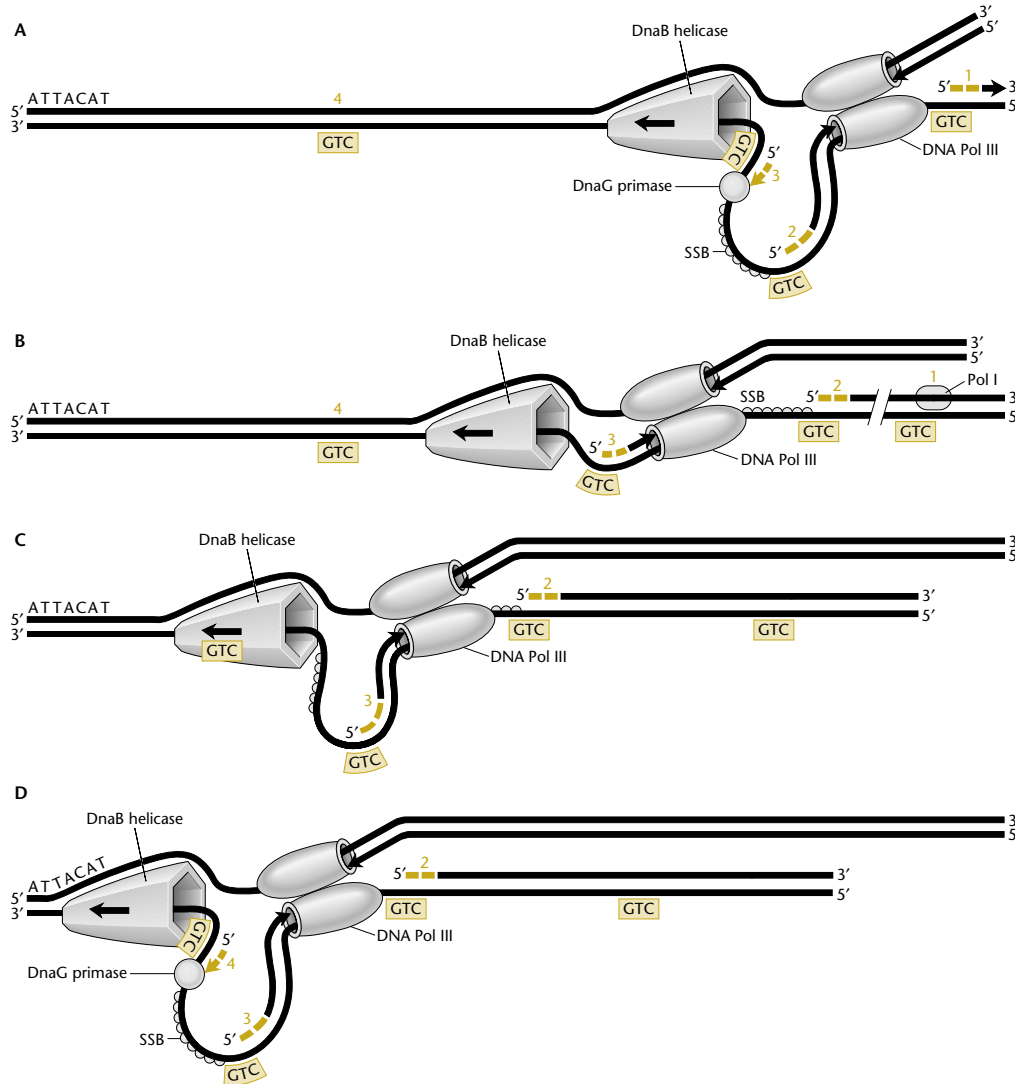




Figure 1.13

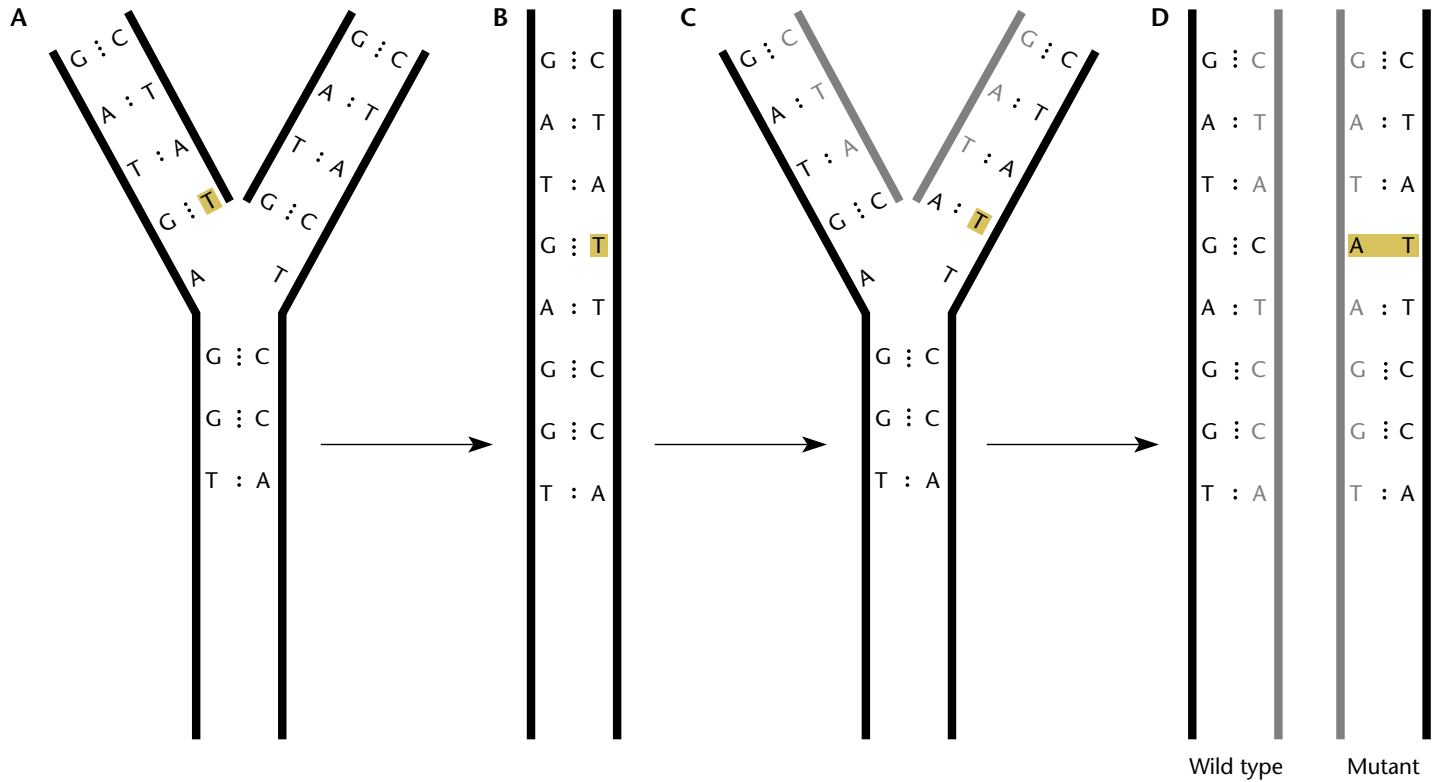


Figure 1.14

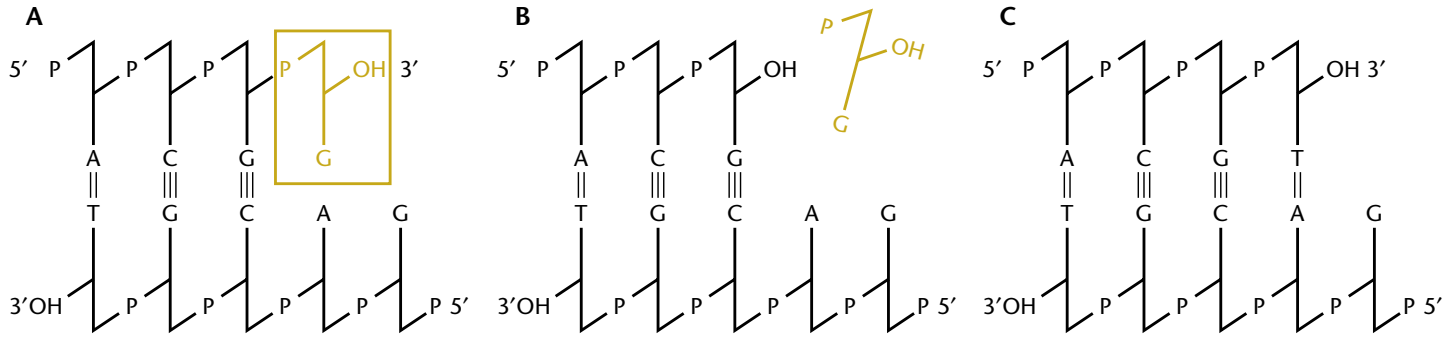


Figure 1.15

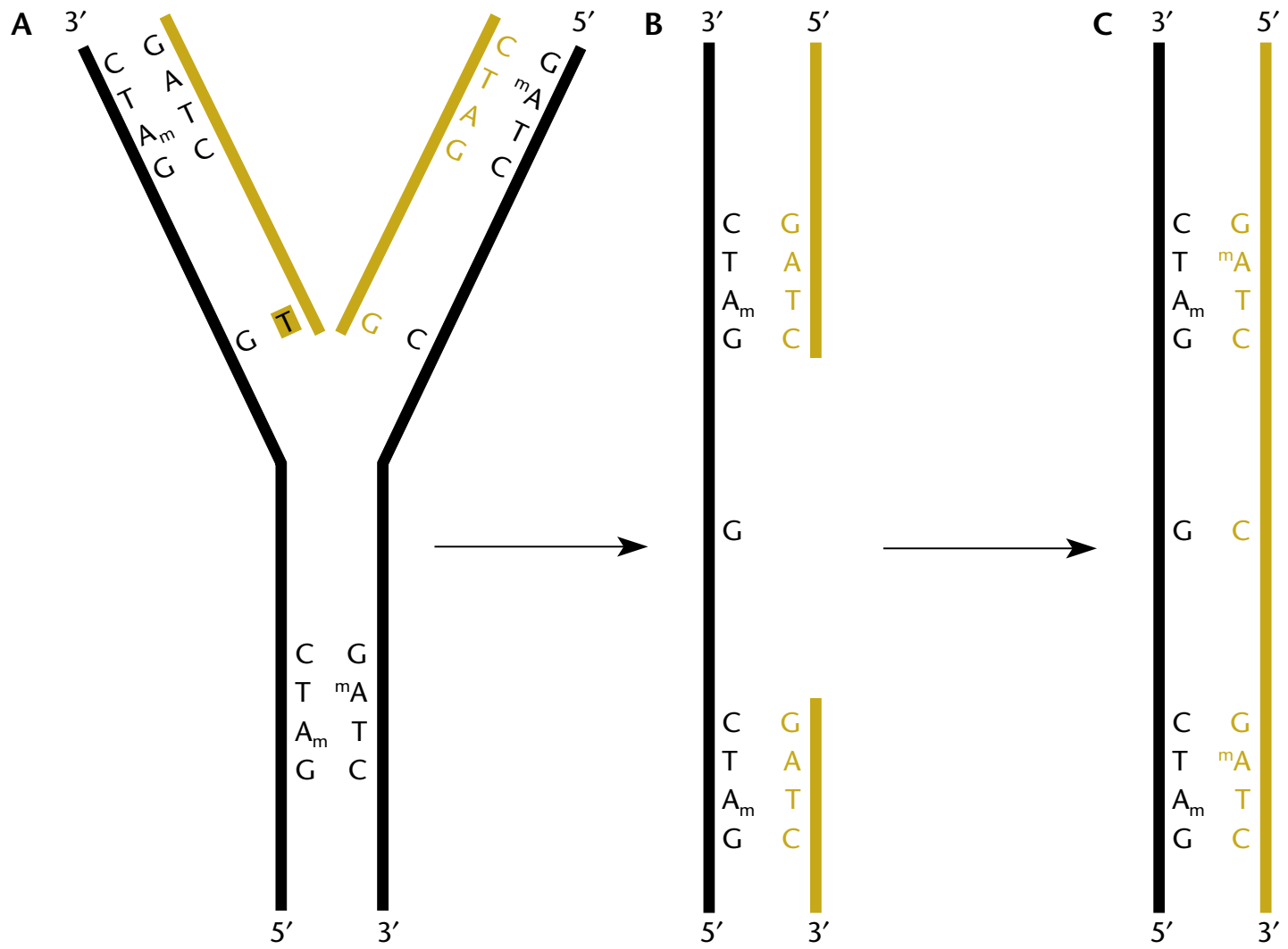




Figure 1.16

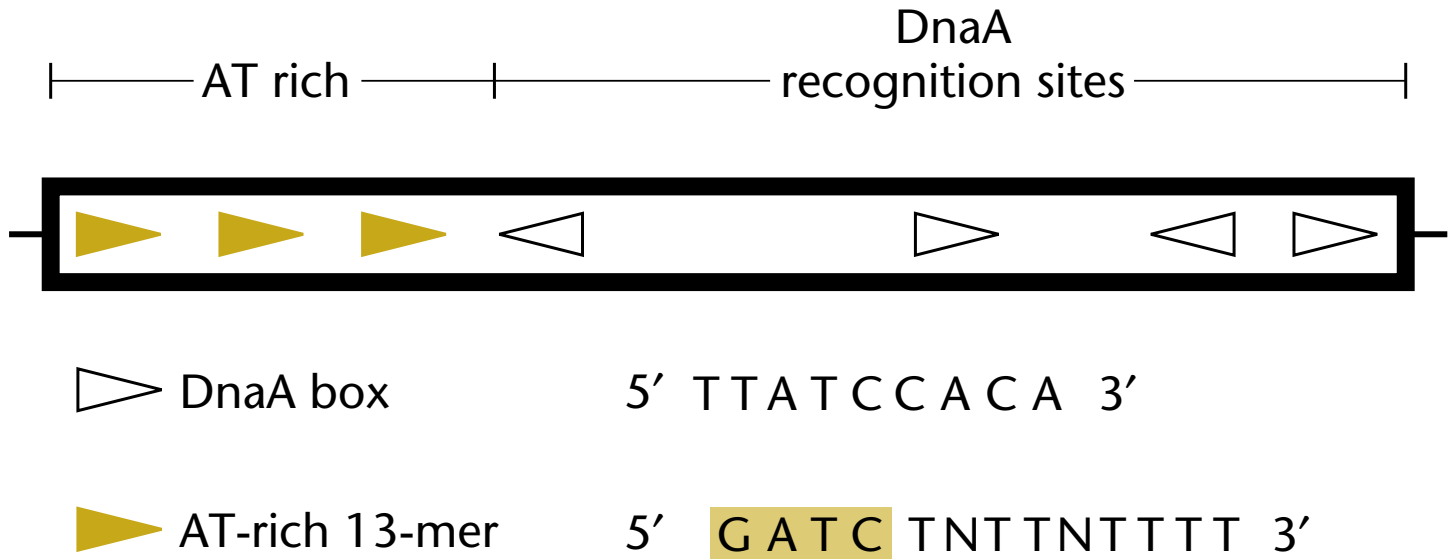


Figure 1.17

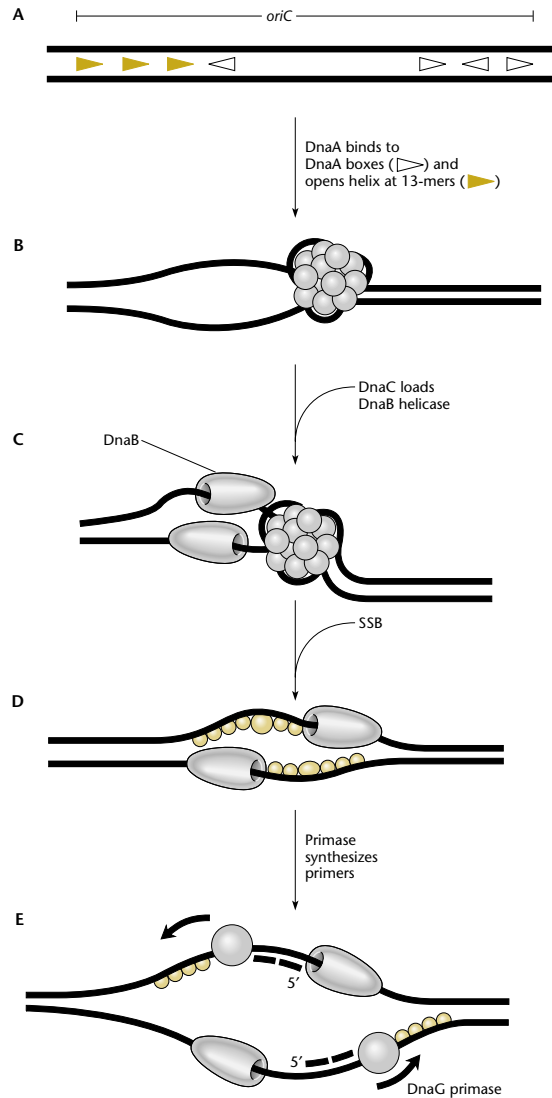
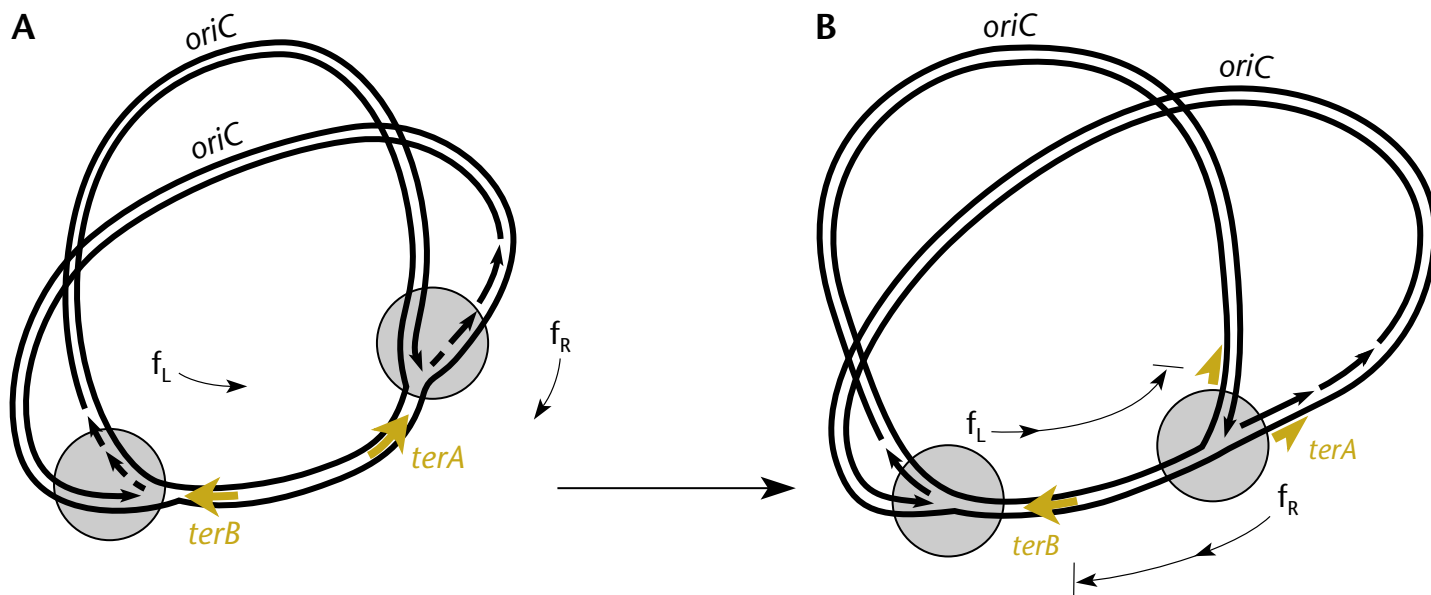


Figure 1.18



Box 1.2

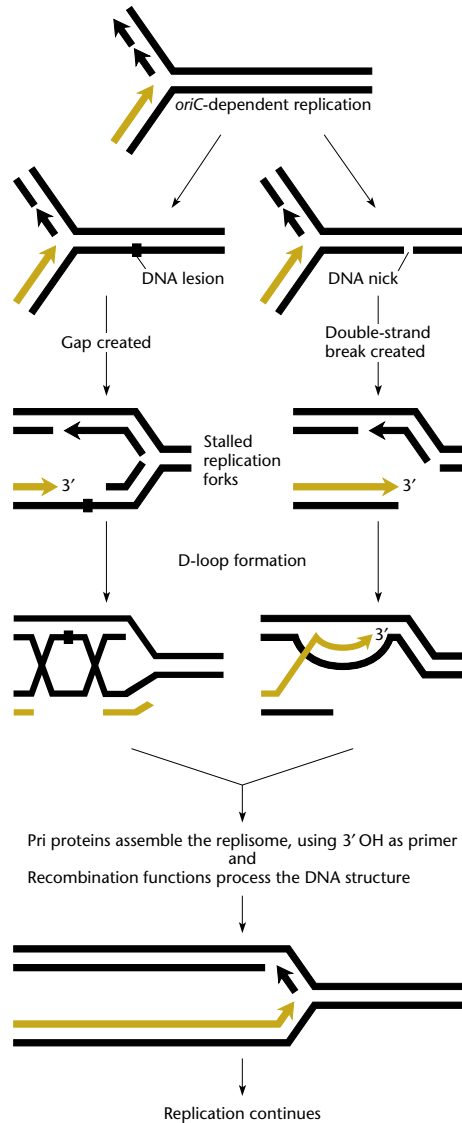


Figure 1.19

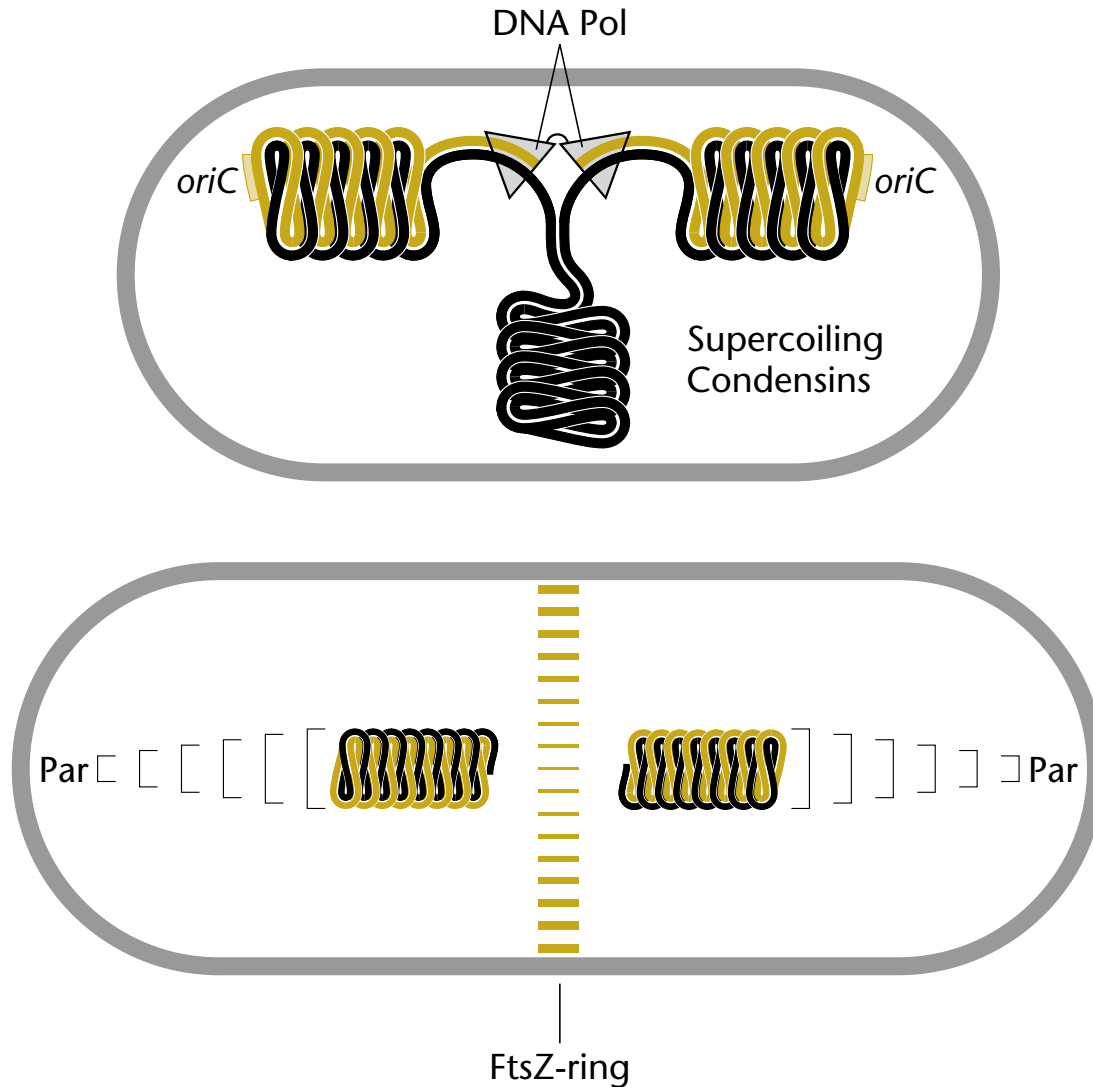


Figure 1.20

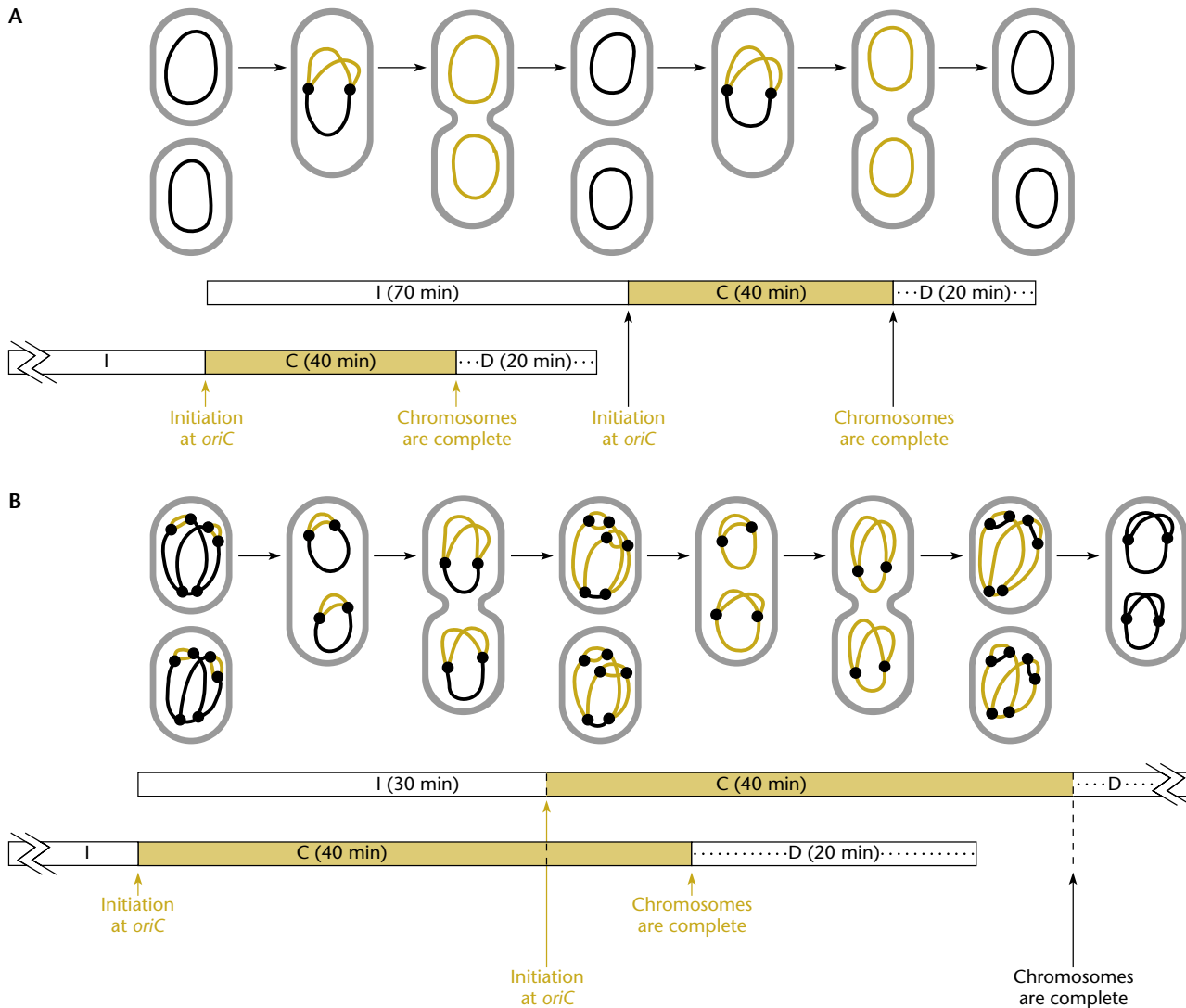


Figure 1.21

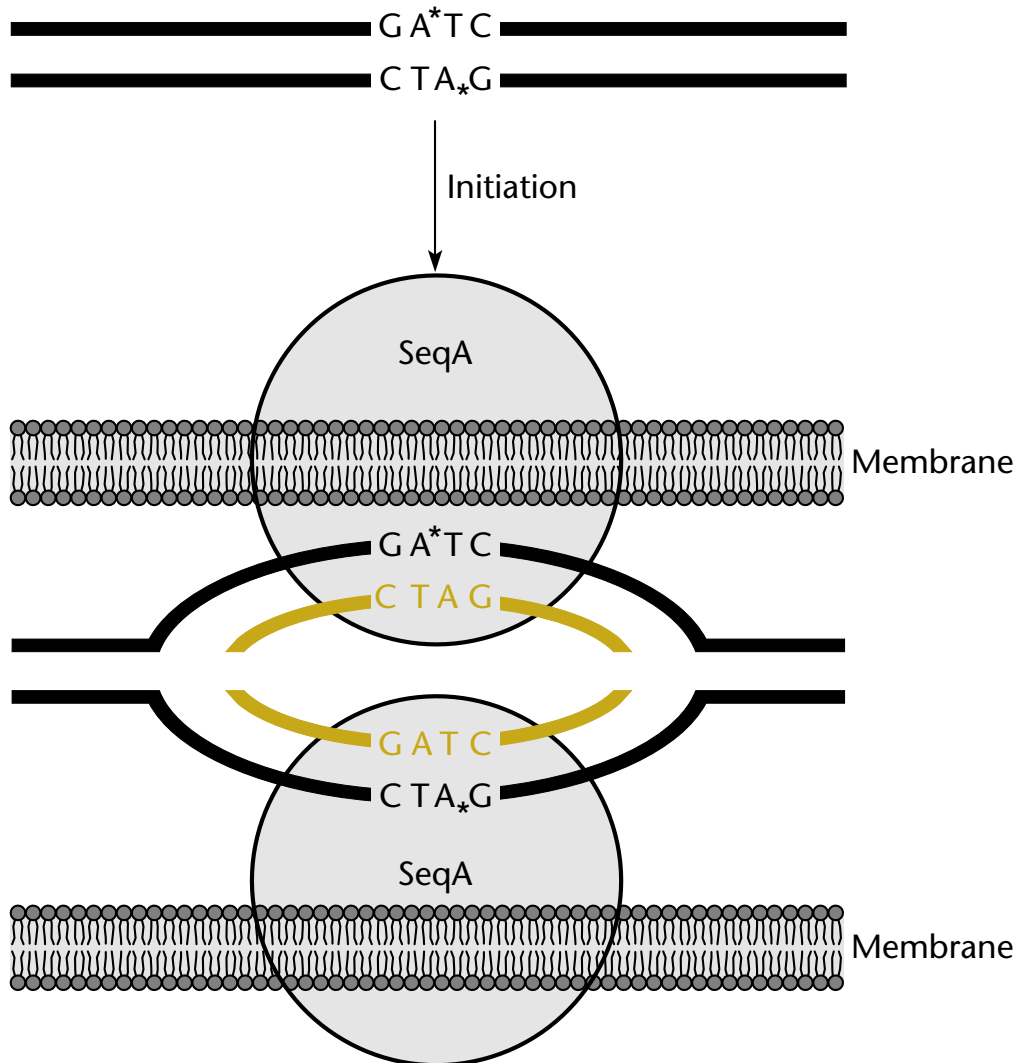


Figure 1.22

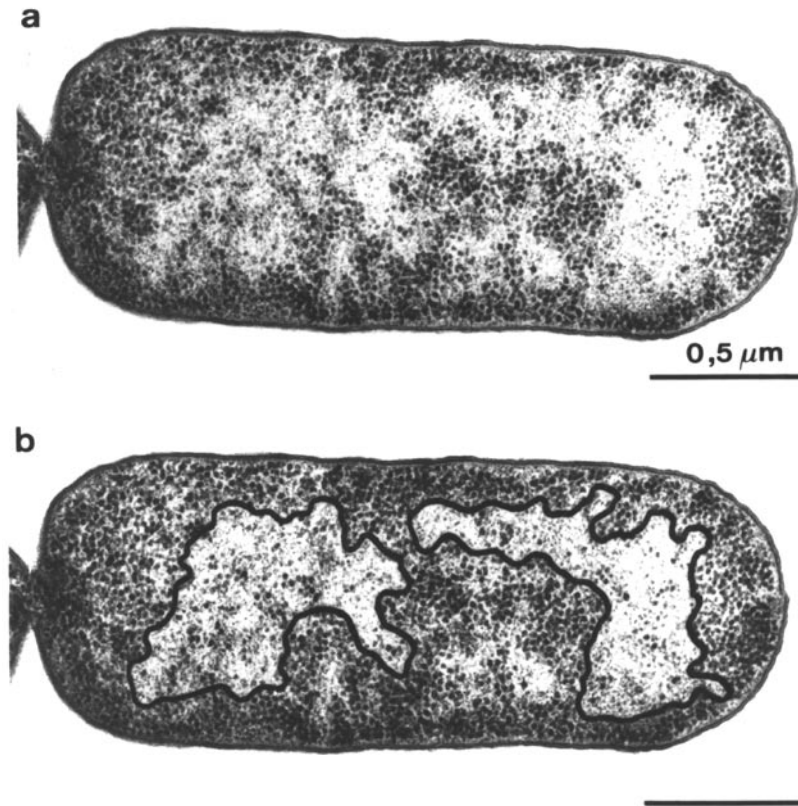


Figure 1.23

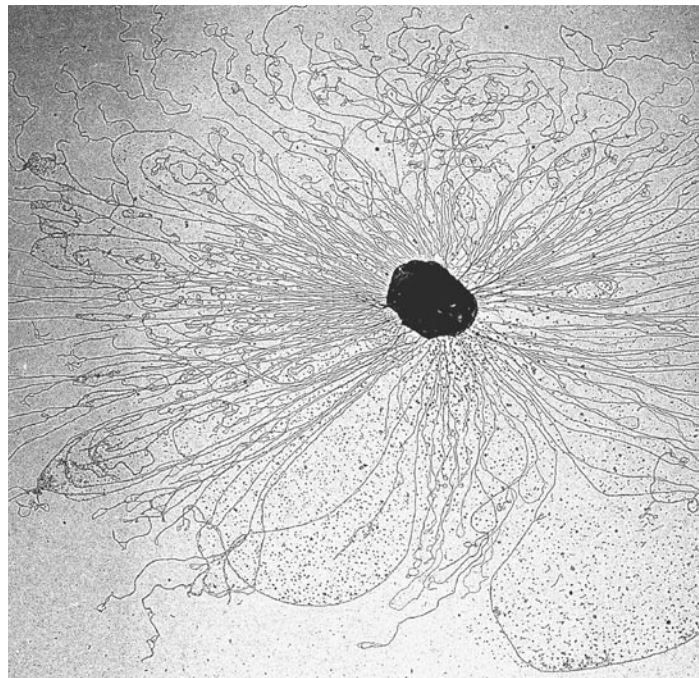
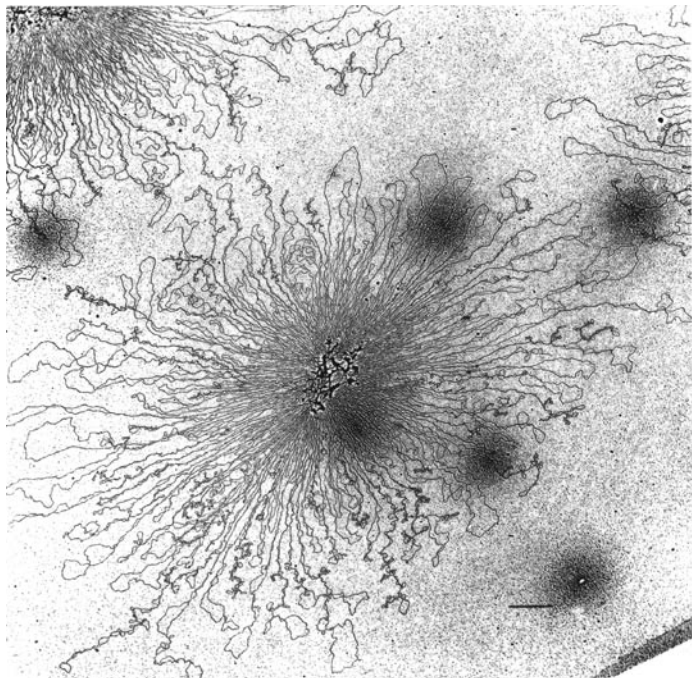


Figure 1.24

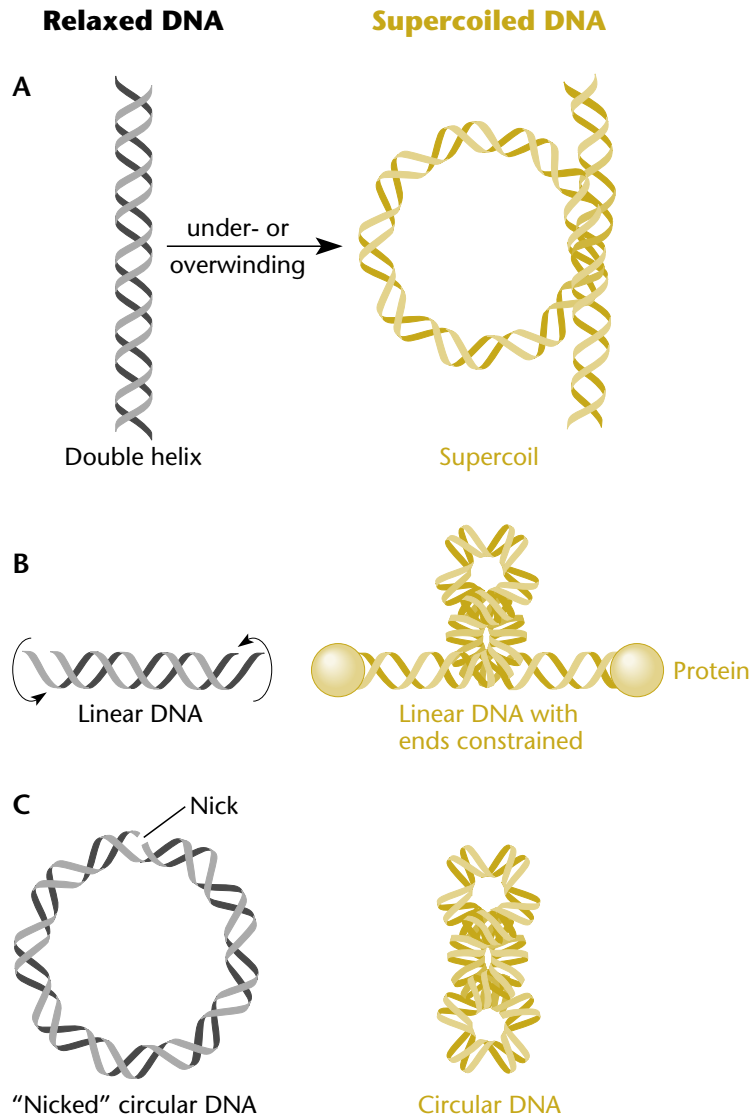


Figure 1.25

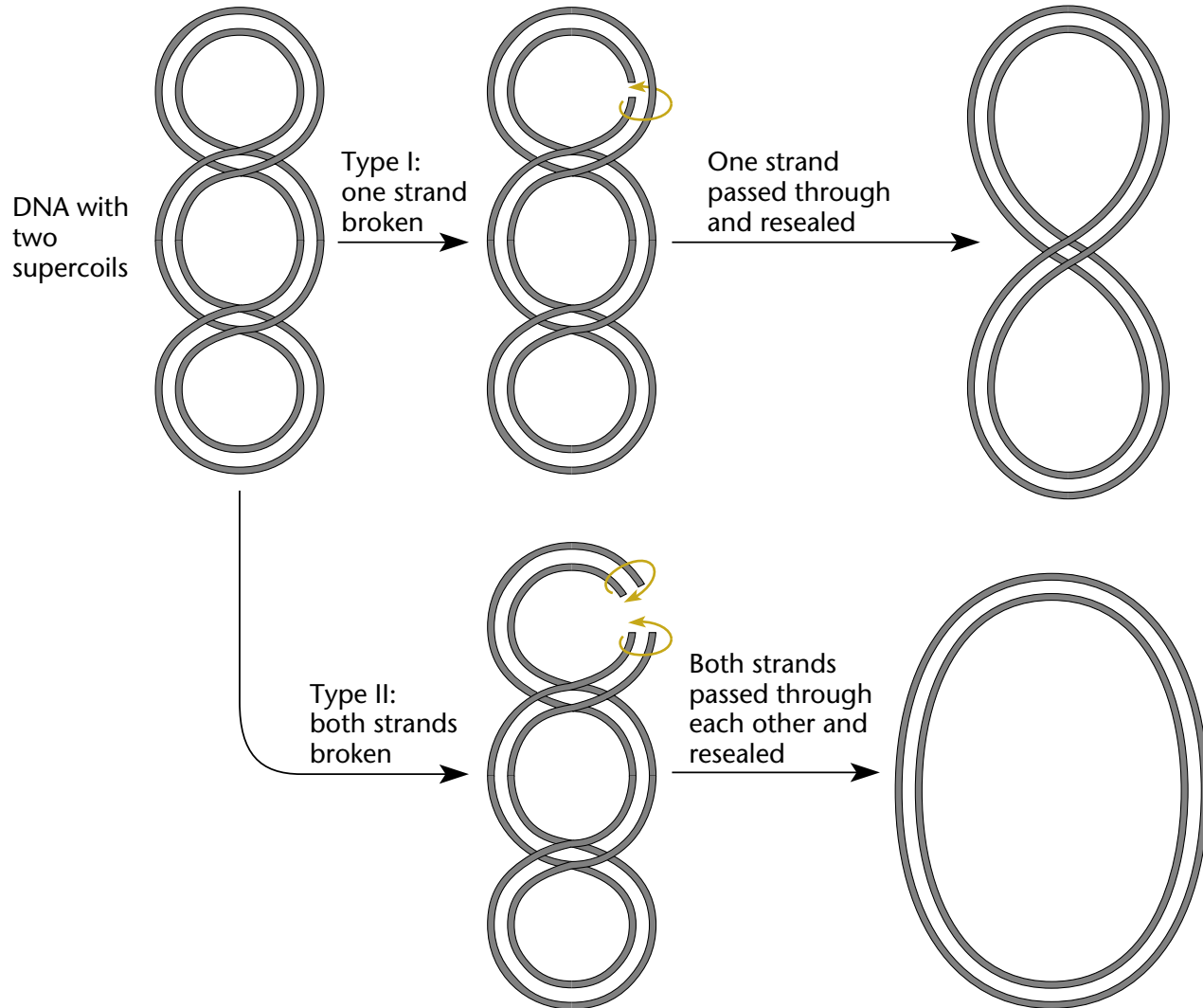


Table 1.2

TABLE 1.2 Antibiotics that block replication		
Antibiotic	Source	Target
Trimethoprim	Chemically synthesized	Dihydrofolate reductase
Hydroxyurea	Chemically synthesized	Ribonucleotide reductase
5-Fluorodeoxyuridine	Chemically synthesized	Thymidylate synthetase
Nalidixic acid	Chemically synthesized	<i>gyrA</i> subunit of gyrase
Novobiocin	<i>Streptomyces sphaeroides</i>	<i>gyrB</i> subunit of gyrase
Mitomycin C	<i>Streptomyces caespitosus</i>	Cross-links DNA

Table 1.3

Enzyme	Recognition sequence ^a
<i>Sau3A</i>	*GATC/CTAG*
<i>BamHI</i>	G*GATCC/CCTAG*G
<i>EcoRI</i>	G*AATTC/CTTAA*G
<i>PstI</i>	CTGCA*G/G*ACGTC
<i>HindIII</i>	A*AGCTT/TTCGA*A
<i>SmaI</i>	CCC*GGG/GGG*CCC
<i>NotI</i>	GC*GGCCGC/CGCCGG*CG

^aAsterisks indicate where the endonucleases cut.

Figure 1.26

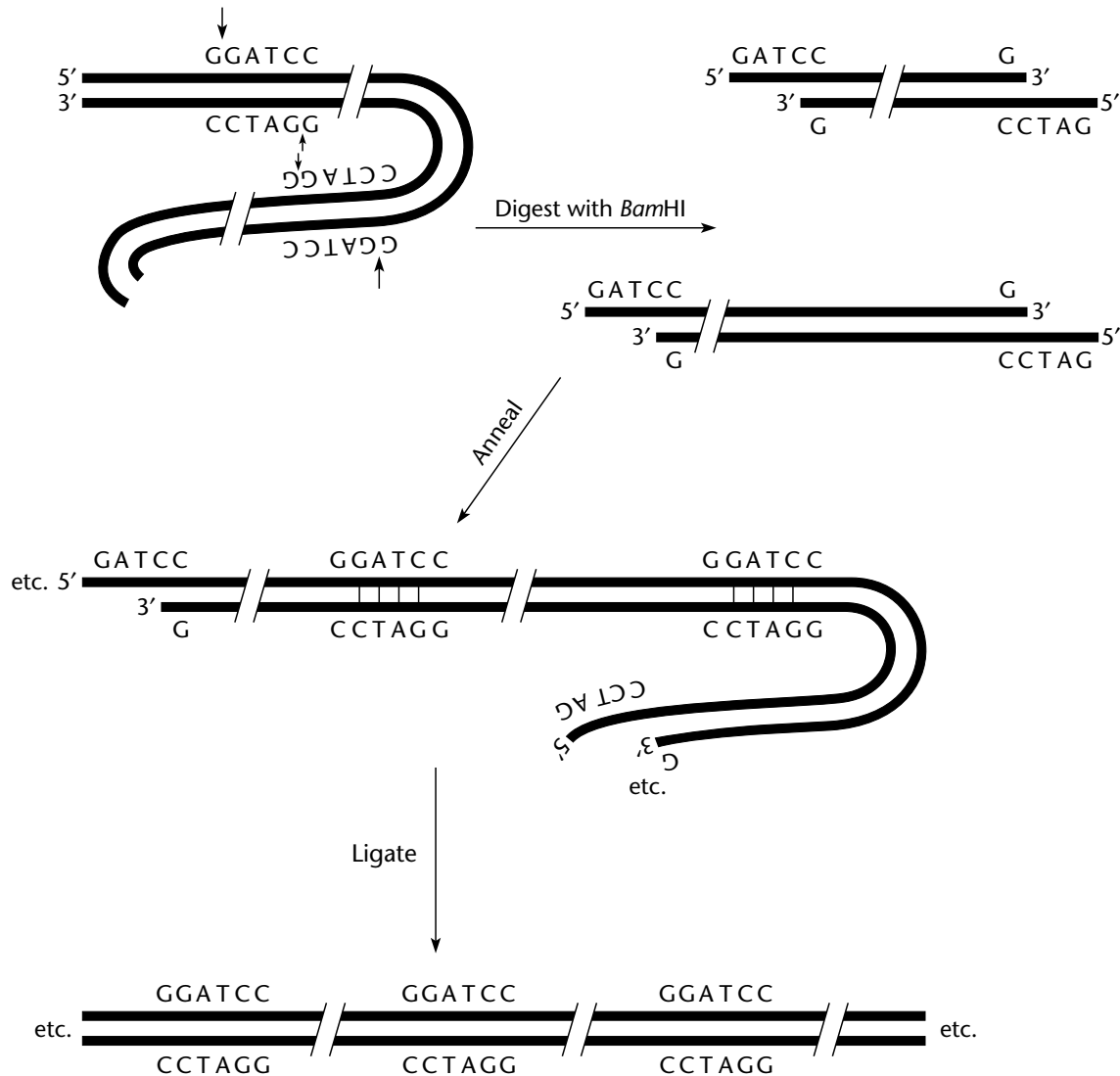




Figure 1.27

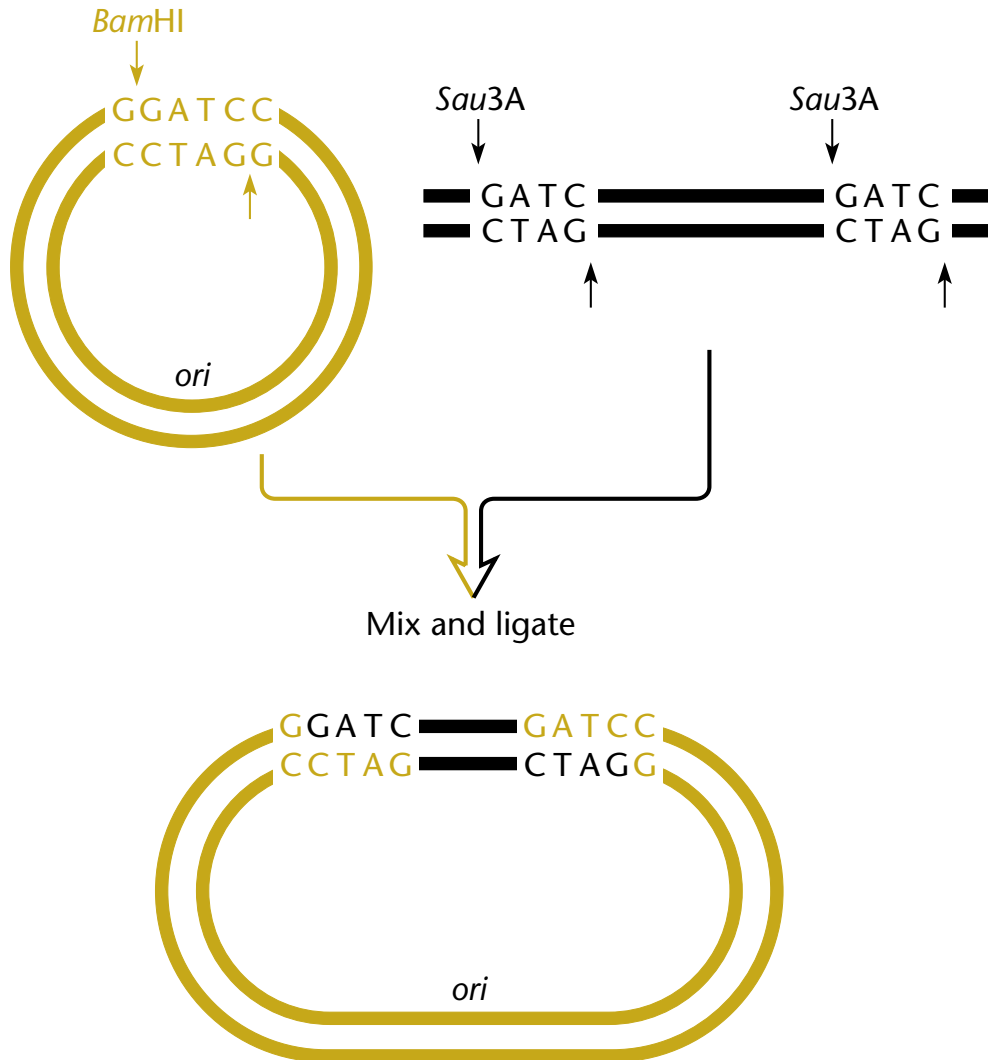


Figure 1.28

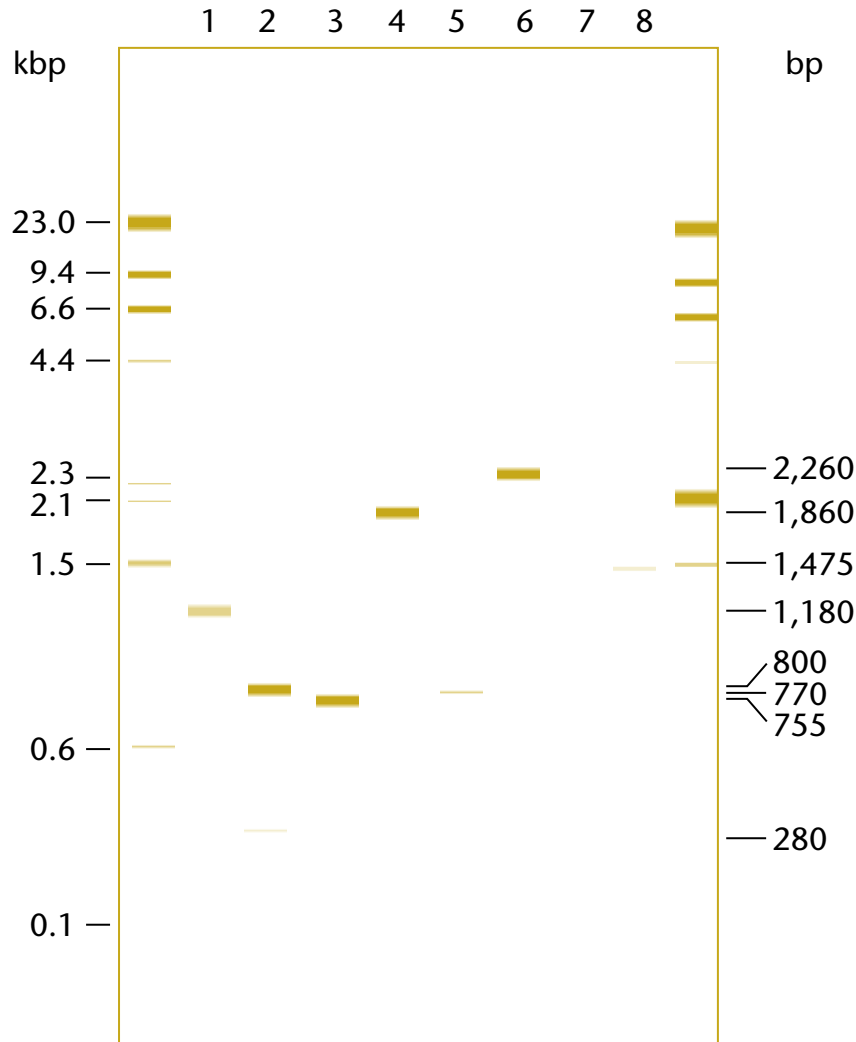


Figure 1.29

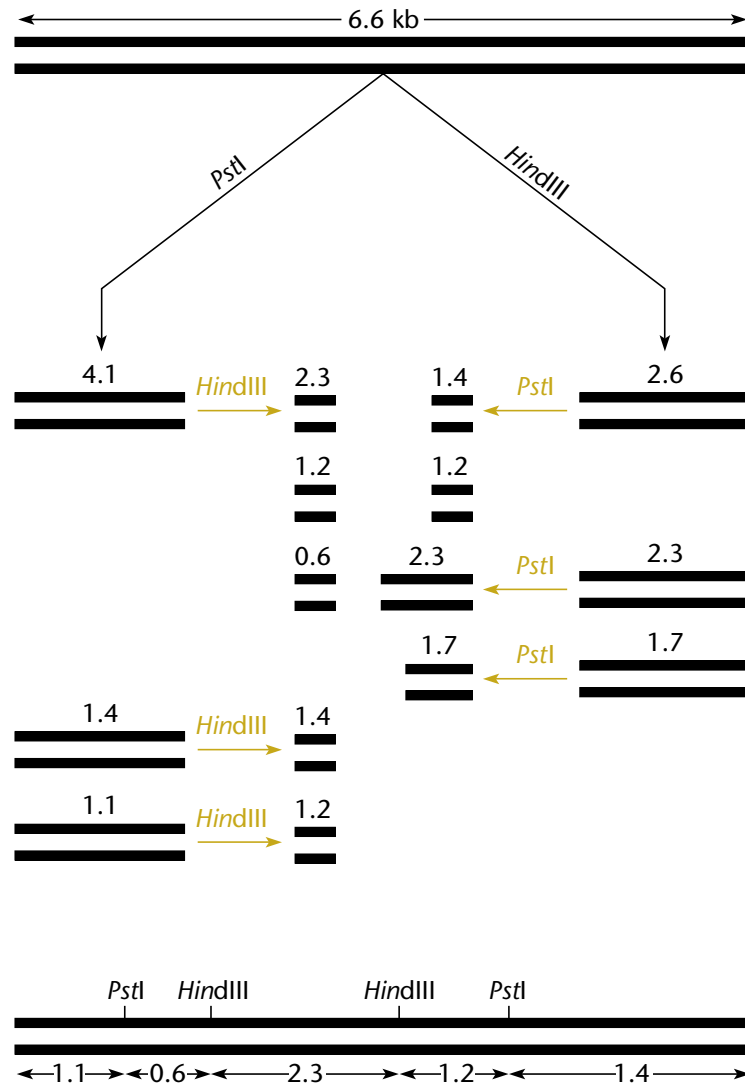
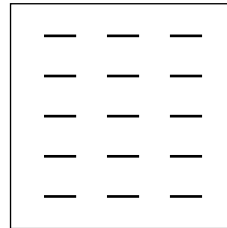


Figure 1.30

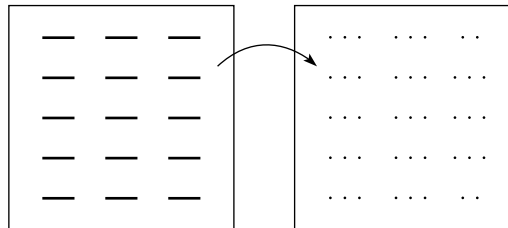
A Step 1 DNA isolation and digestion



Step 2 DNA electrophoresis



Step 3 DNA transfer



Step 4 DNA hybridization

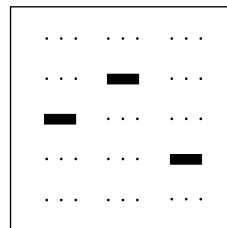


Figure 1.30 cont.

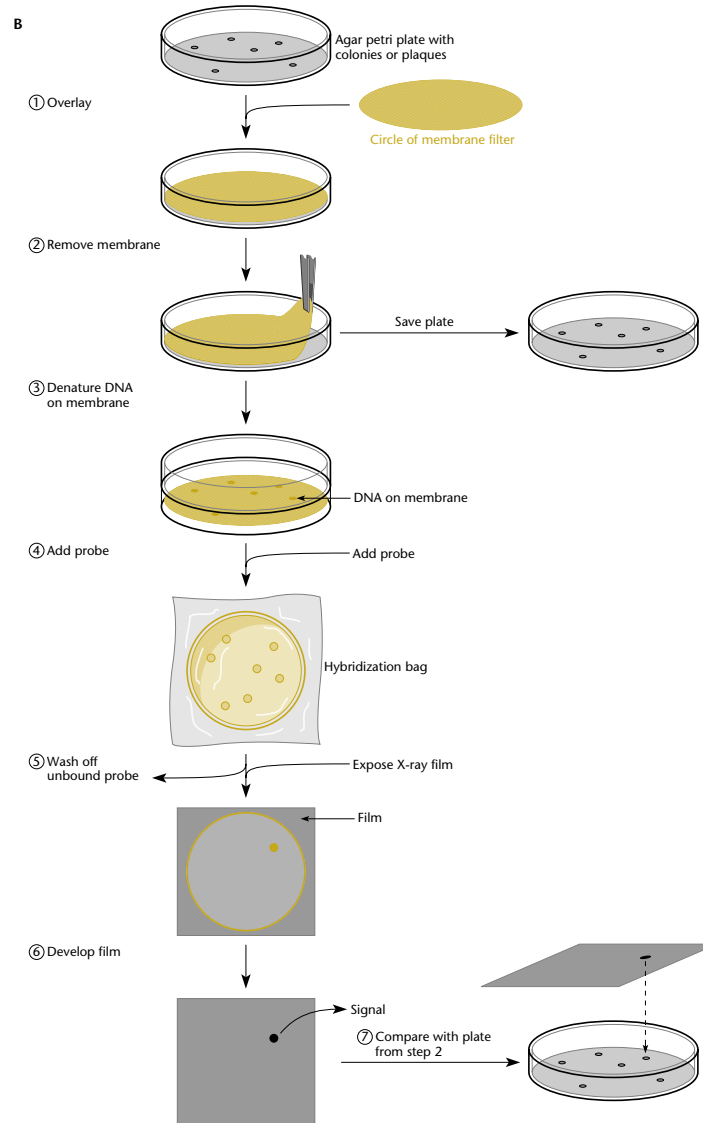
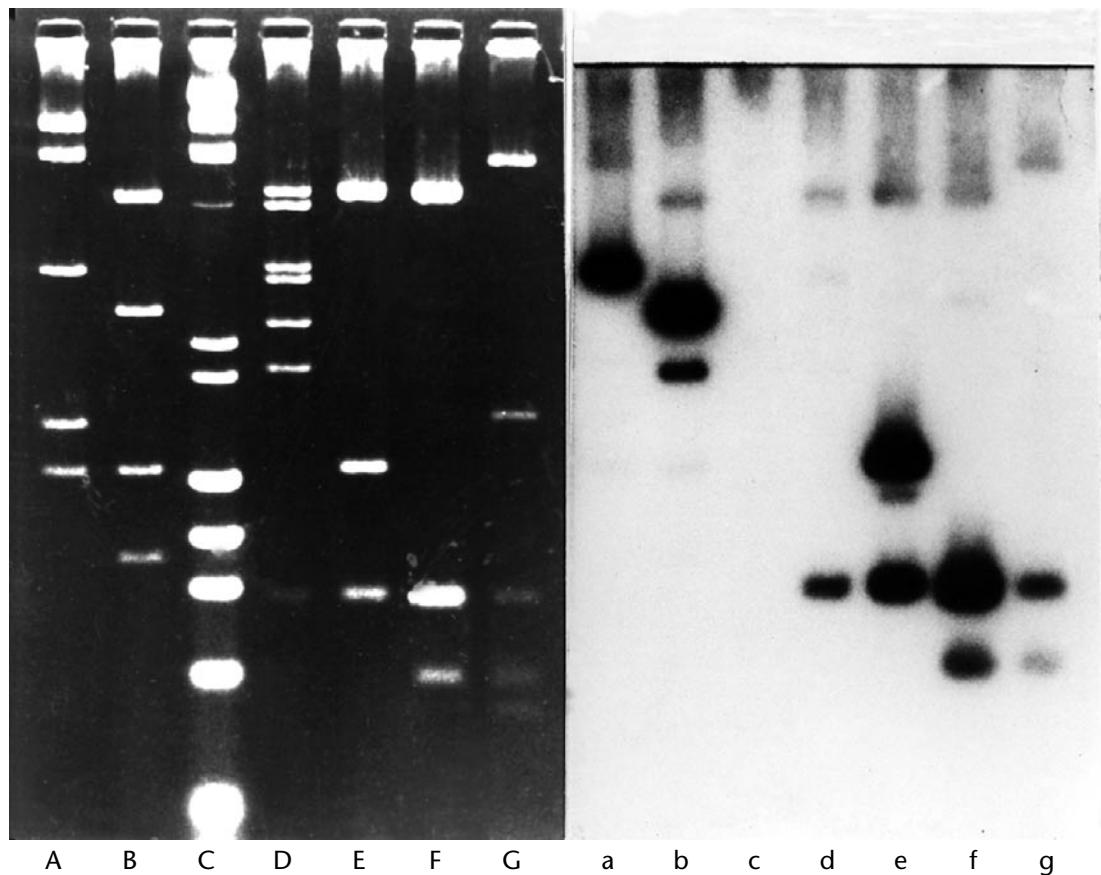


Figure 1.31





Box 1.4

Flowchart for Genomic Sequencing

- 1 Isolate genomic DNA**
 - DNA should be in pieces of >20 kb
- 2 Shear DNA**
 - DNA fragments will be of random lengths
- 3 Size fractionate DNA**
 - Collect fragments in size range from 1.5 to 2 kb
- 4 Construct plasmid library**
 - Inserts are the 1.5- to 2-kb genomic DNA
- 5 Randomly sequence inserts**
 - Sequencing process is highly automated
 - Need ~15,000 sequence runs of ~500 to 600 bases each per megabase of genome DNA
- 6 Assemble randomly generated sequence information in contiguous segments (“contigs”)**
- 7 Close gaps with directed sequencing**
 - Several hundreds of reactions needed
- 8 Analyze sequence**
 - Bioinformatics allows “annotation” of ORFs, etc.

Size Range of Genomes

Organism	Size (Mbp)	Comments
<i>Mycoplasma genitalium</i>	0.58	Smallest cell genome
<i>Treponema pallidum</i>	1.14	Causes syphilis
<i>Helicobacter pylori</i>	1.67	Causes duodenal ulcers
<i>Sulfolobus solfataricus</i>	2.25	Found in Yellowstone hot springs
<i>Bacillus subtilis</i>	4.20	Soil bacterium; “model” for development
<i>Escherichia coli</i>	4.64	Intestinal bacterium; “model” for genetics and physiology
<i>Pseudomonas aeruginosa</i>	6.26	Causes respiratory infections
<i>Streptomyces coelicolor</i>	8.4	Antibiotic-producing soil bacterium

Figure 1.32

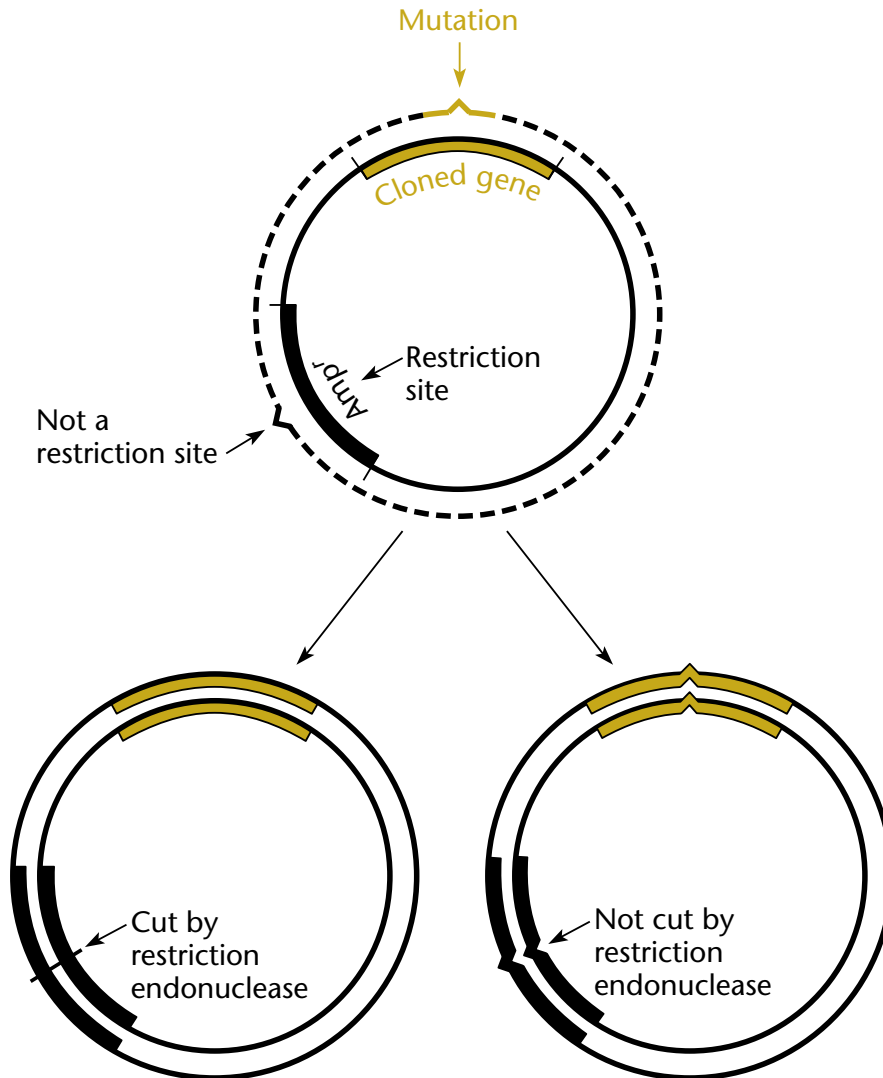


Figure 1.33

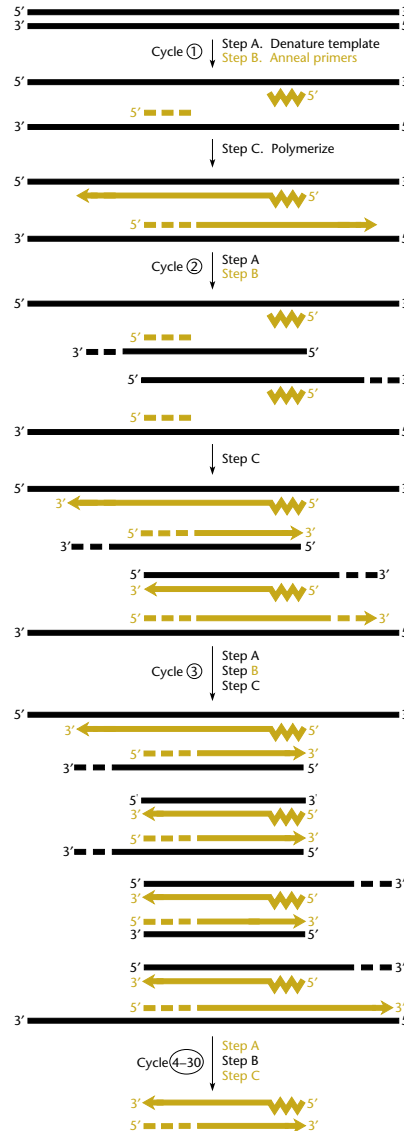




Figure 1.34

