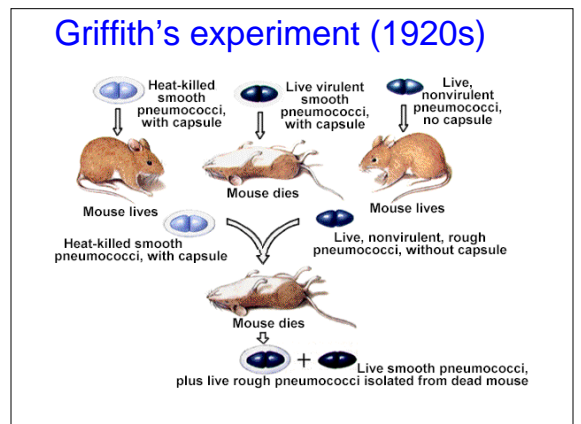
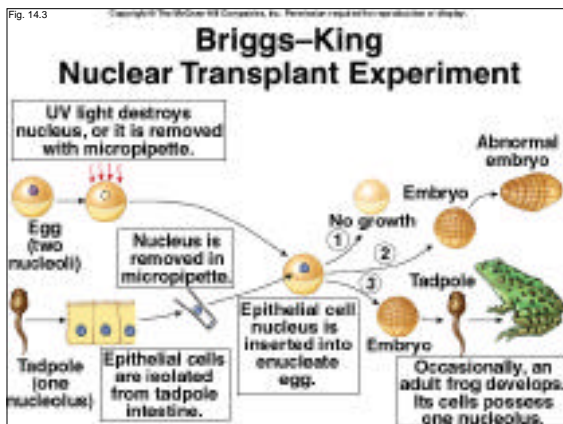
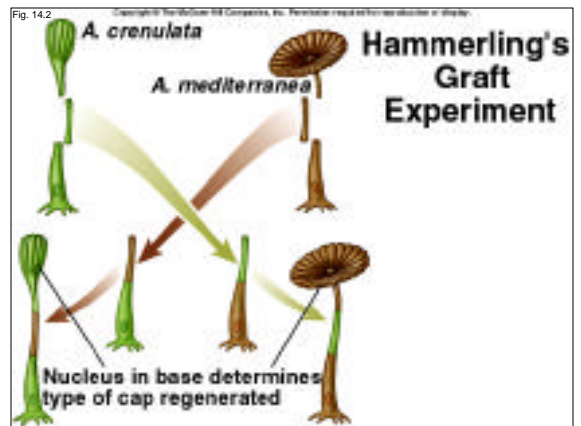
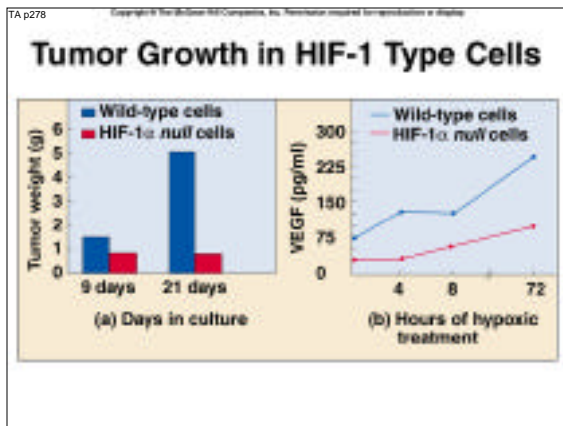
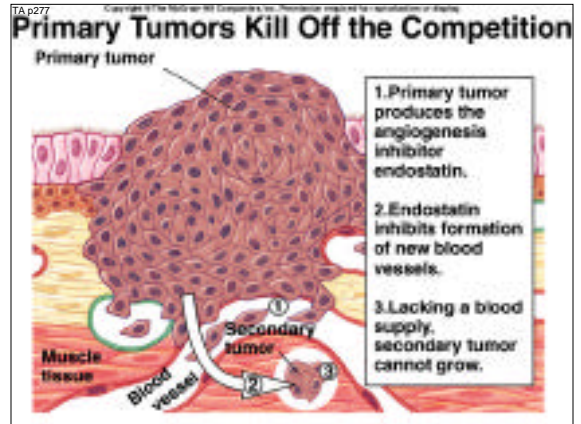
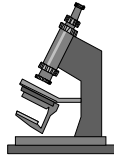
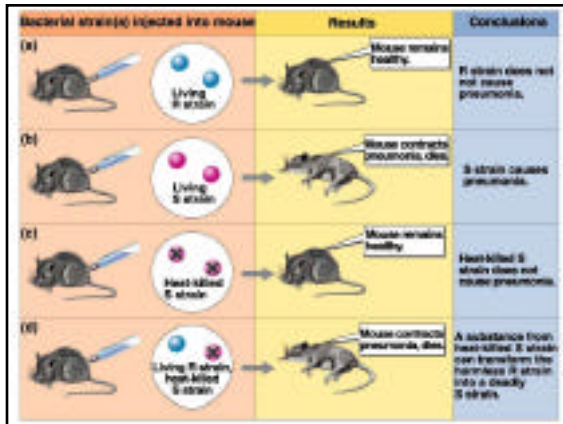


DNA structure





Smooth versus rough colonies of *Streptococcus (Diplococcus) pneumoniae*

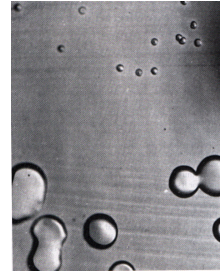


FIGURE 14.5 Transformation of *Streptococcus*. This photo, from the original publication of Avery and coworkers, shows the transformation of nonpathogenic R *Streptococcus* (the small colonies) to pathogenic S *Streptococcus* (the large colonies) in an extract prepared from heat-killed S *Streptococcus*.

Nature of DNA

✓ Protein?

⇒ Before 1944

- ↳ abundant
- ↳ Tetranucleotide hypothesis
 - ⇒ Little variability
- ↳ Active research

✓ Nucleic acid

⇒ Transforming principle

- ↳ Avery, Macleod, and McCarty that followed the work of Griffith's experiments

Avery, Macleod, and McCarty's experiments

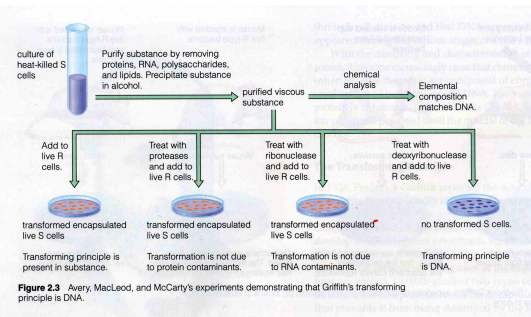
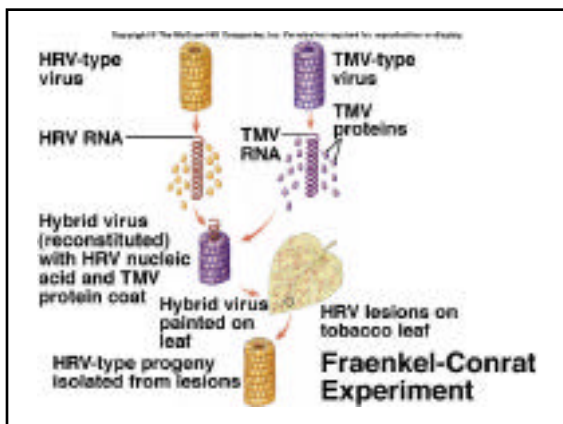
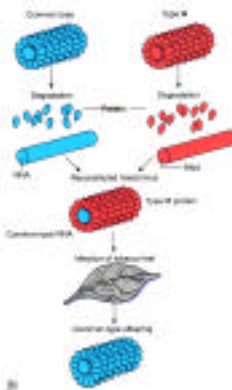


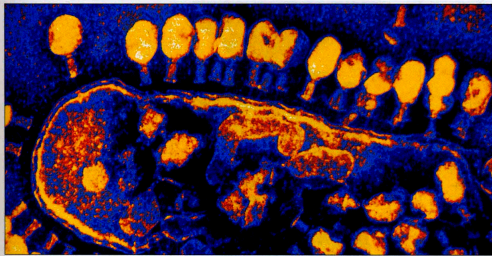
Figure 2.3 Avery, MacLeod, and McCarty's experiments demonstrating that Griffith's transforming principle is DNA.



RNA is the genomic material of the TMV

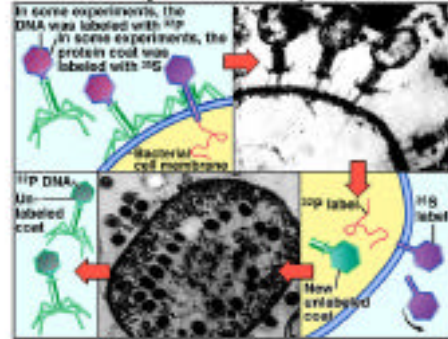


T2 phages

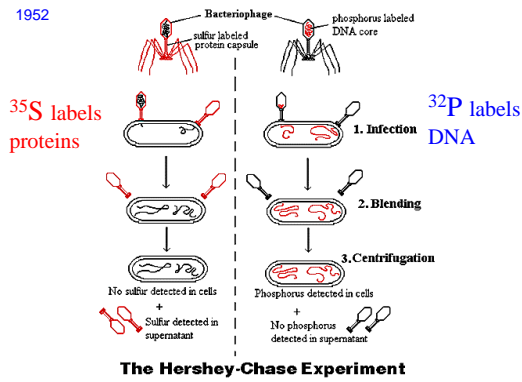


a The micrograph shows T2 bacteriophages infecting an *E. coli* cell. © 2005 Sinauer Associates, Inc.

Hershey-Chase Experiment



1952



Building blocks of DNA

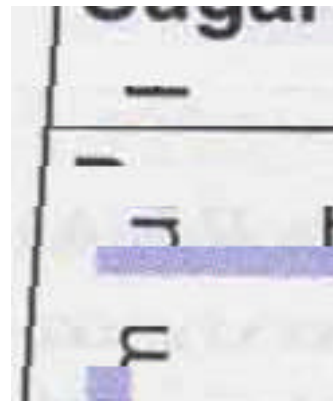


Fig. 14.6

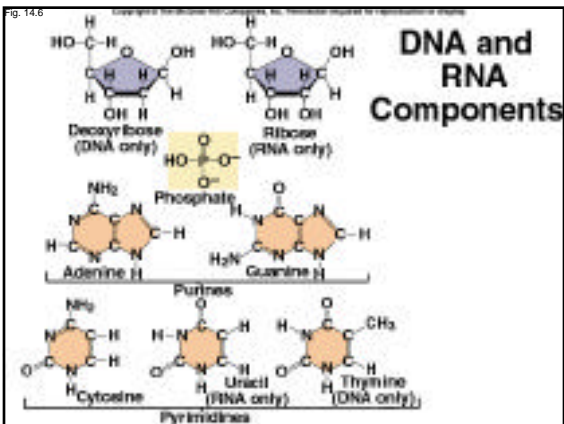
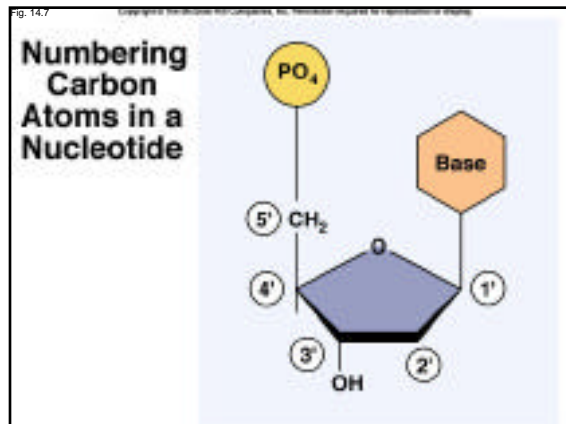
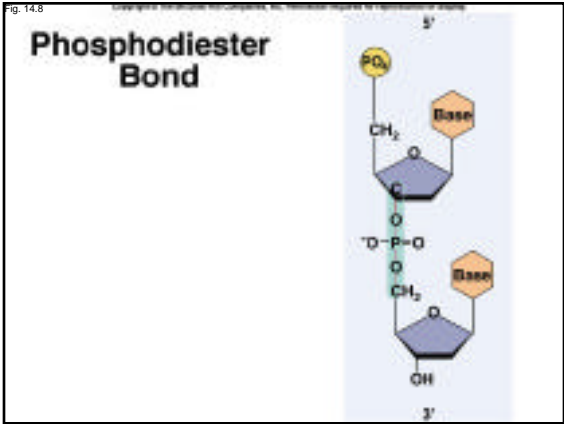


Fig. 14.7



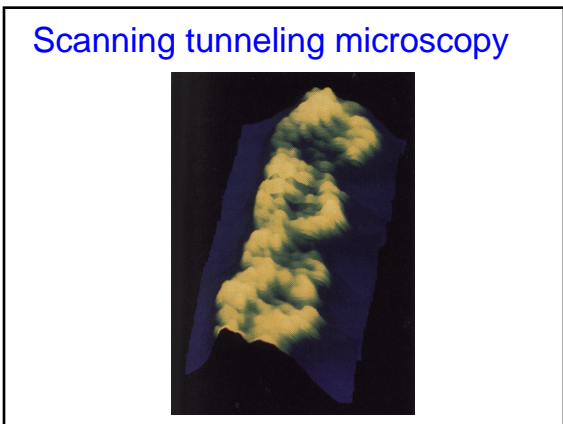
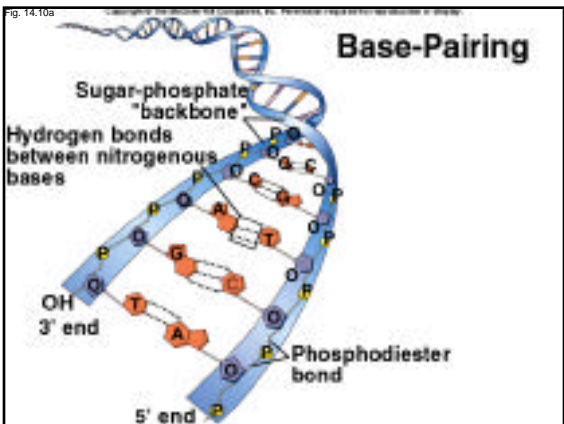
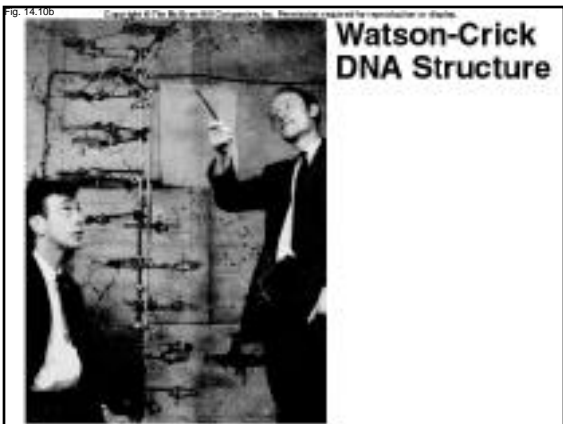
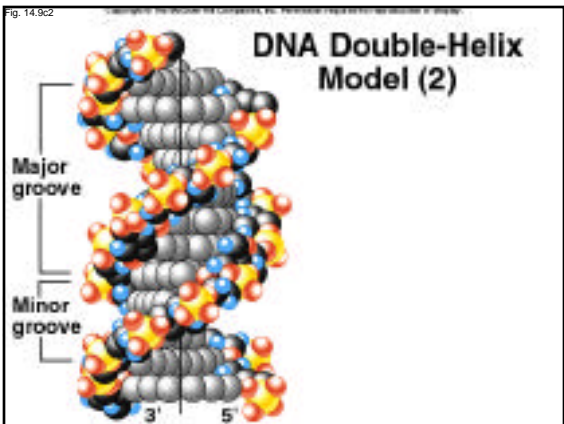
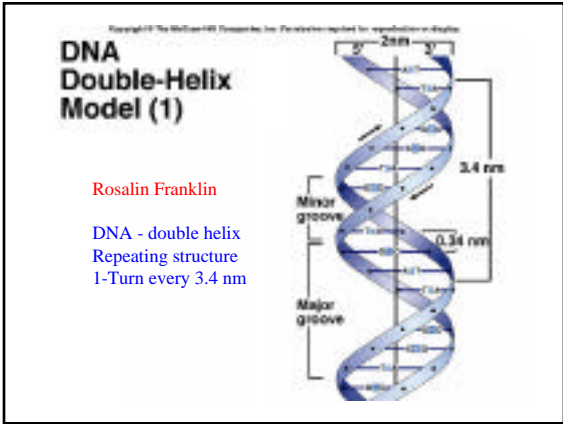
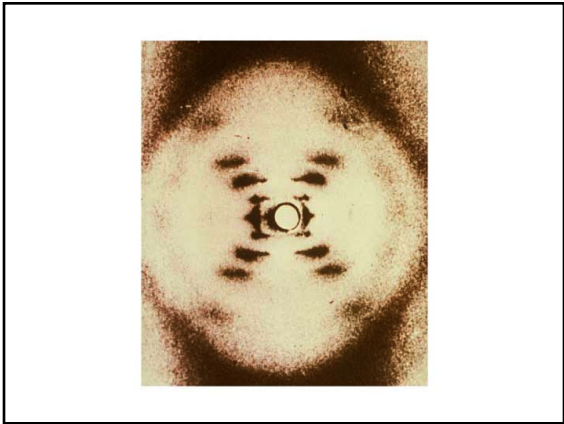


Ratio of DNA bases?

✓ Tetranucleotide hypothesis
 ⇒ DNA is a tetramer of equal quantities of bases - 1:1:1:1 ratio

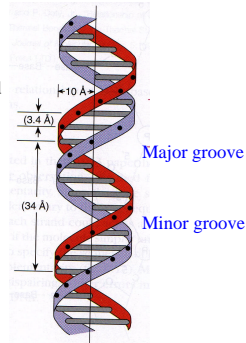
✓ Chargaff's rule
 ⇒ A 1:1 correspondence exists between the purine and pyrimidine bases

Species	Adenine	Thymine	Guanine	Cytosine
Human being (liver)	30.3%	30.3%	19.5%	19.9%
Mycobacterium tuberculosis	15.1%	14.6%	34.9%	35.4%

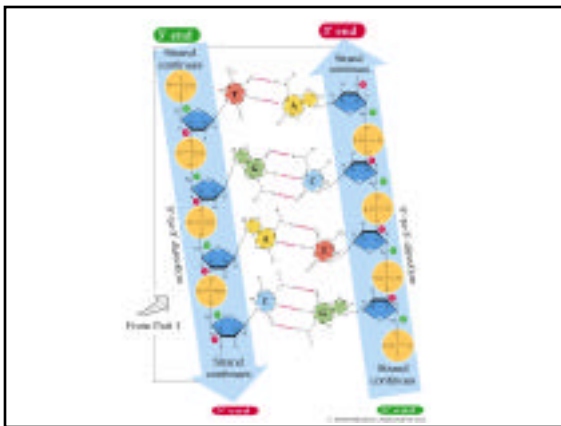
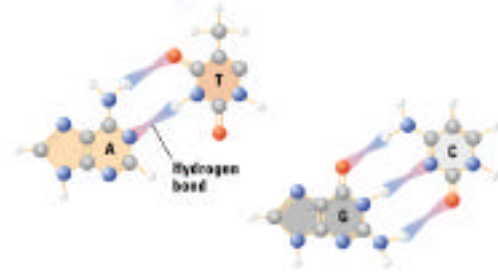


Watson & Crick DNA structure

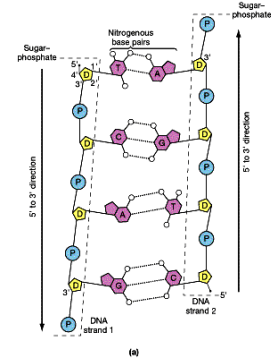
Right-handed double helix
 Antiparallel
 Bases are stacked - 3.4 Å
 Nitrogenous bases are H-bonded
 One complete turn every 10 bases or 34 Å
 Major groove and minor groove
 Double helix measures 20 Å in diameter



Bases connect or pair in the middle



Structure of DNA

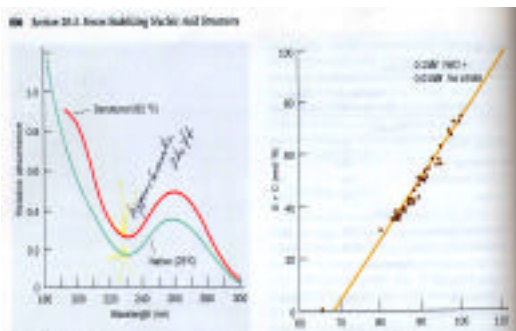


Eukaryotic evidence

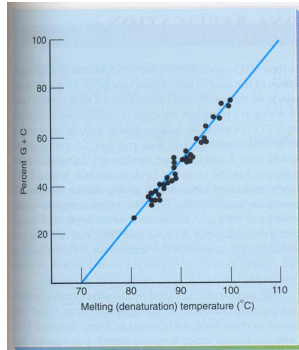
✓ Indirect

- ⇒ DNA is found primarily where genetic function is found
- ⇒ UV mutagenesis
 - DNA absorbs best at 260 nm
 - Protein absorbs best at 280 nm

Hyperchromatic shift

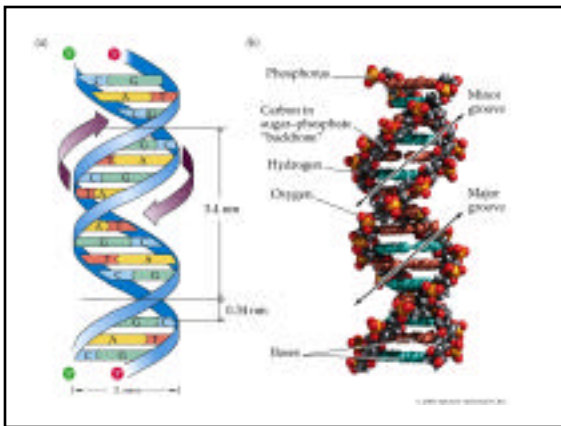
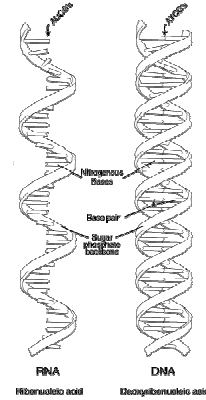


Percent G+C verses melting temperature



Structure of RNA

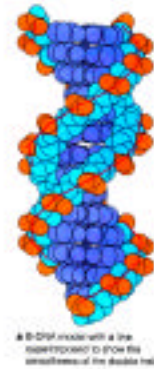
RNA is "single stranded"
 Ribose replaces Deoxyribose
 Uracil replace thymine



B-DNA

Right handed helix
 Diameter - 20 Å
 Base pairs/turn - 10
 Helix pitch - 34 Å
 Helix rise/bp - 3.4 Å

Most DNA



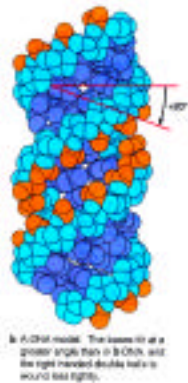
A-DNA

Right handed helix
 Diameter - 26 Å
 bp/turn - 11
 Helix pitch - 28 Å
 Helix rise/bp - 2.6 Å

Not normally found in living cells

High humidity

RNA-DNA hybrid and RNA-RNA helices



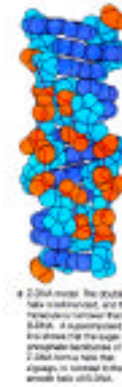
Z-DNA

Left handed helix
 Diameter - 18 Å
 bp/turn - 12
 Helix pitch - 45 Å
 Helix rise/bp - 3.7 Å

Limited regions of Z-DNA in living cells

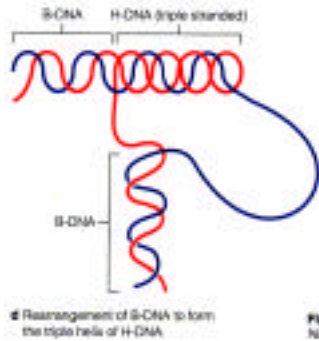
Alternating purine-pyrimidine (Gs & Cs)

Bases form a zig-zag

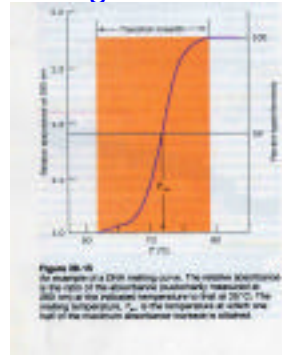


H-DNA

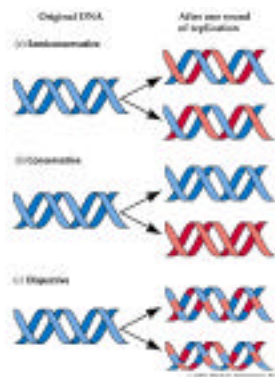
Test tube
Recombination?
DNA repair?



DNA melting curve

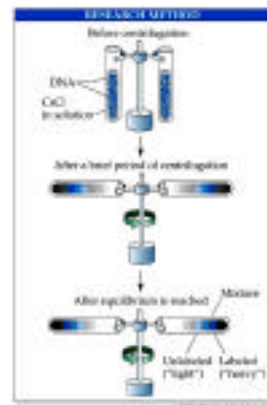


Three possible models for DNA replication

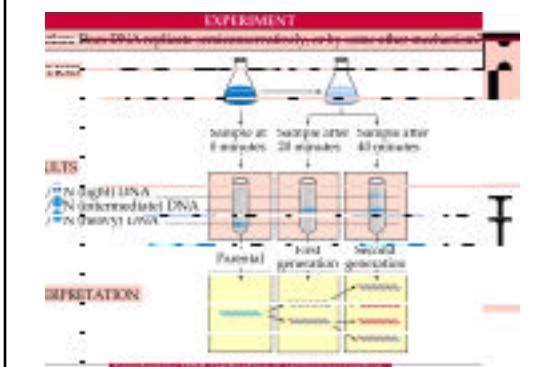


Centrifuging DNA

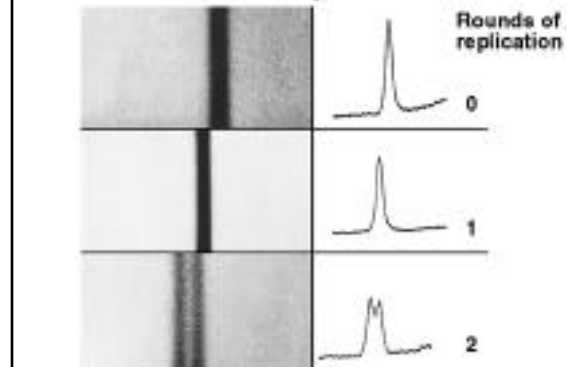
Svedberg coefficient (S)

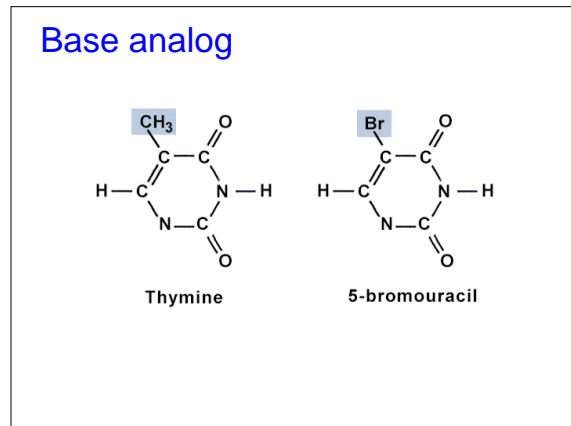
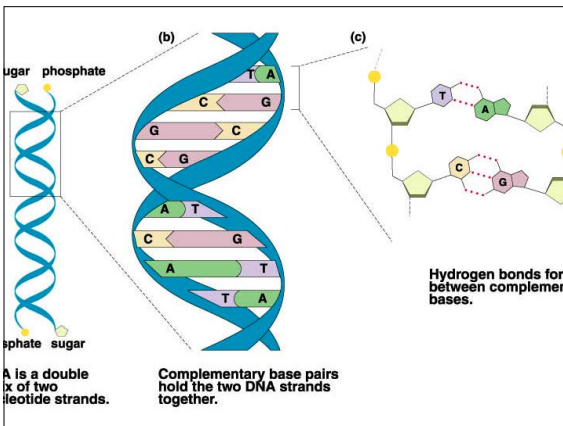
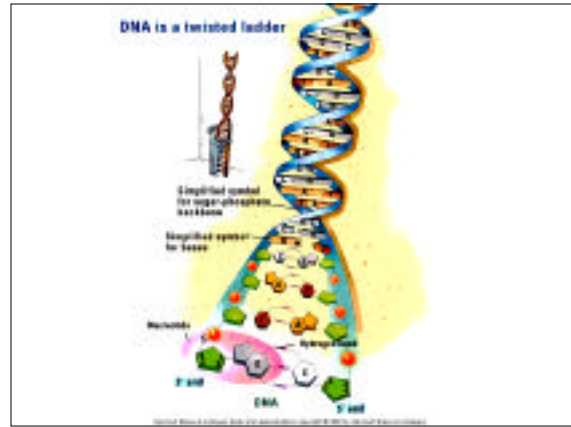
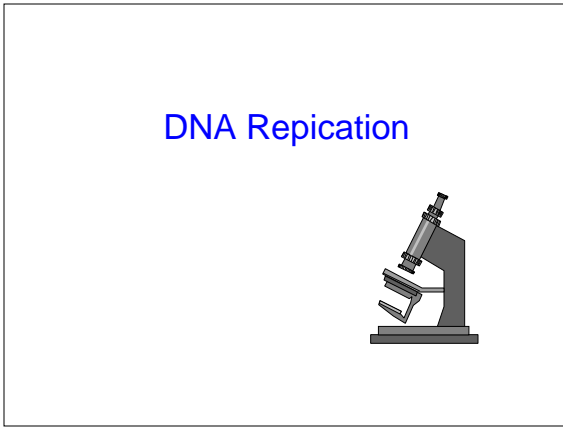
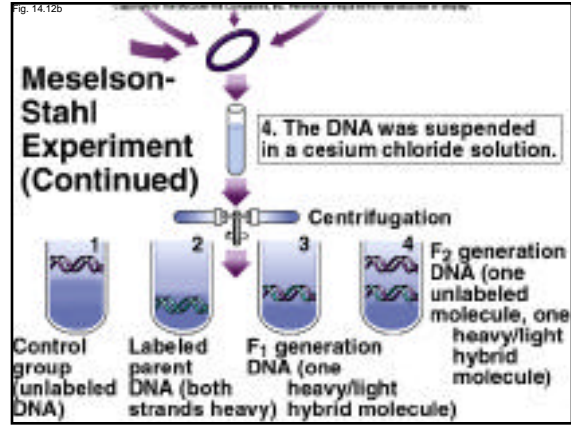
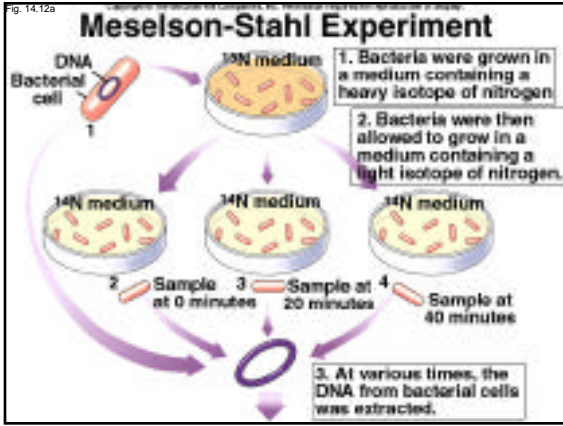


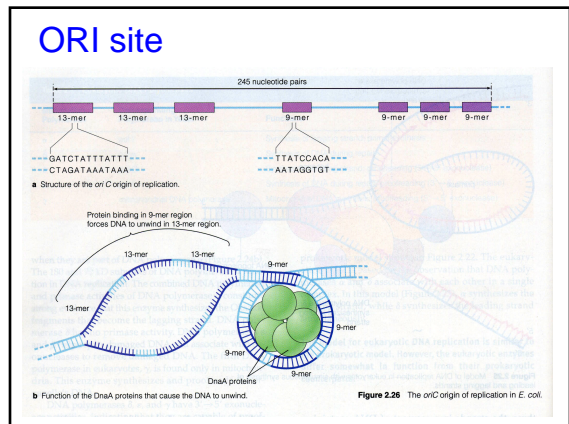
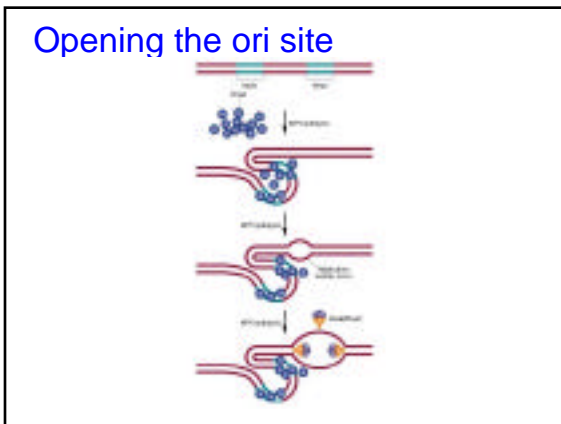
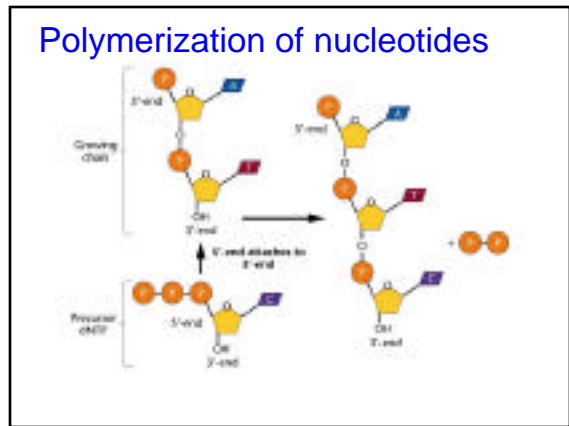
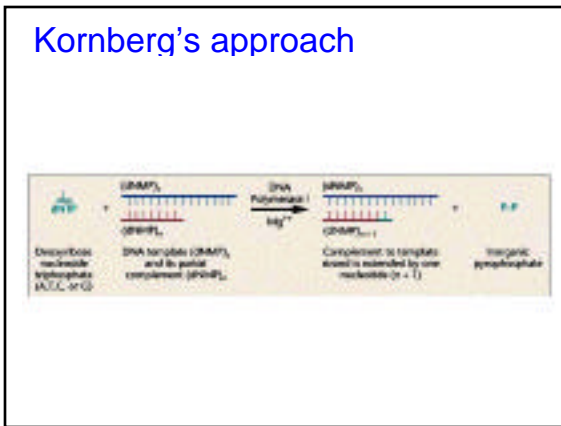
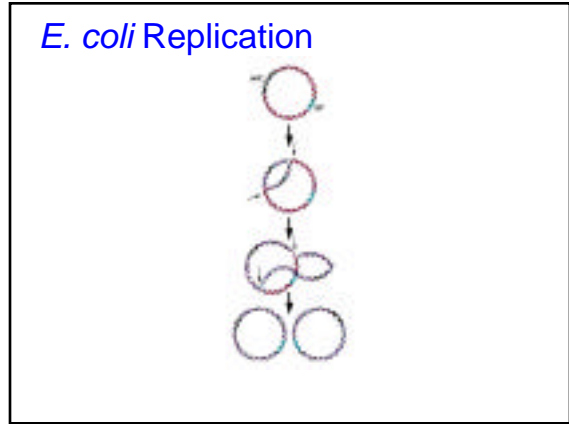
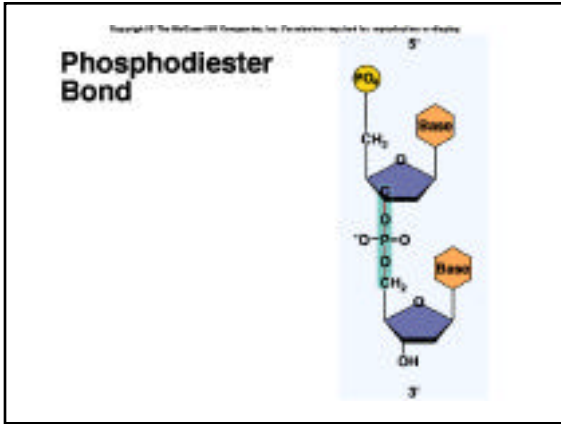
Meselson and Stahl



Meselson-Stahl Experiment Result







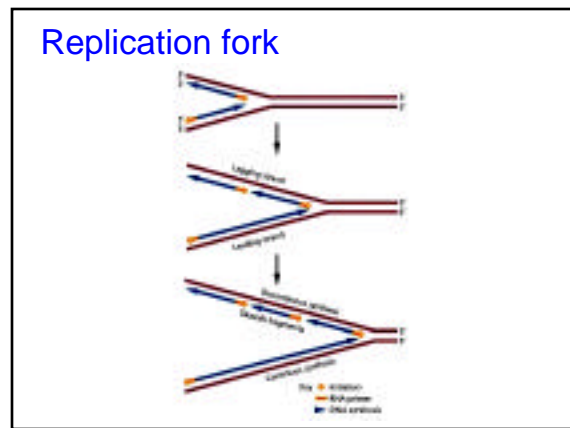
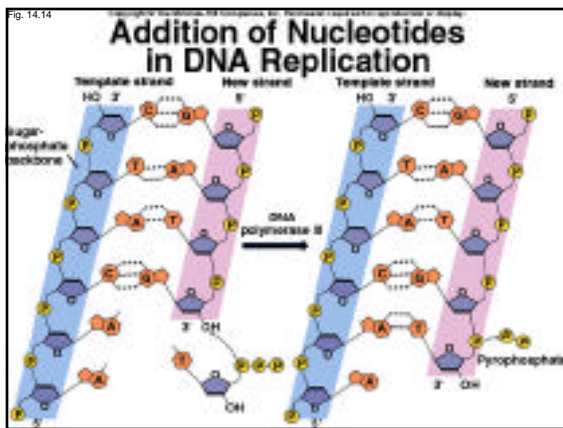
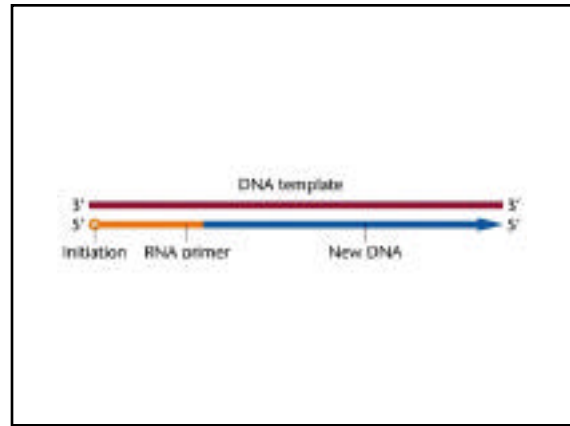
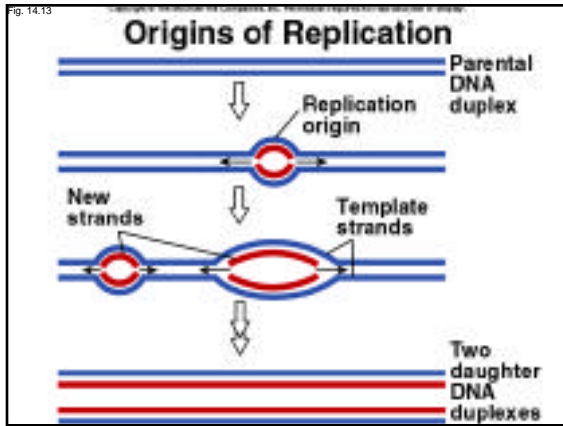
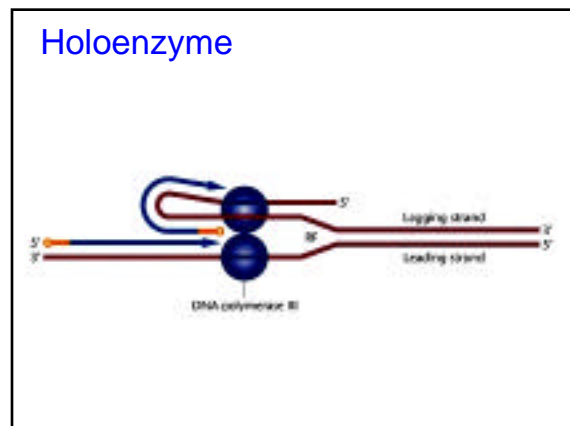
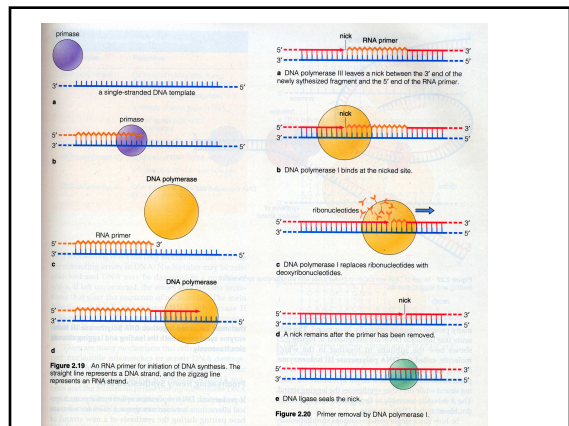
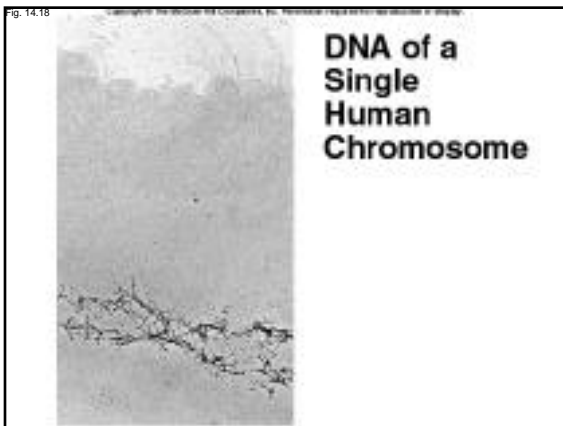
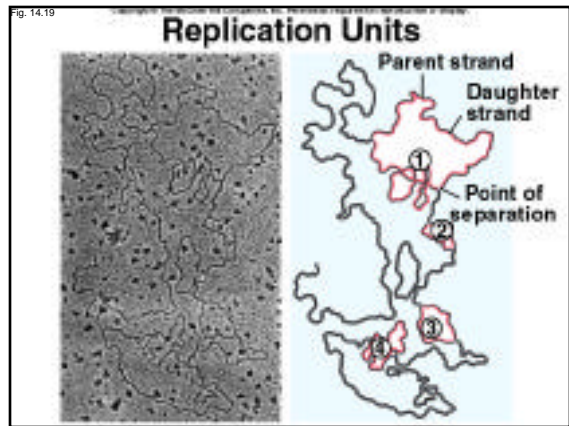
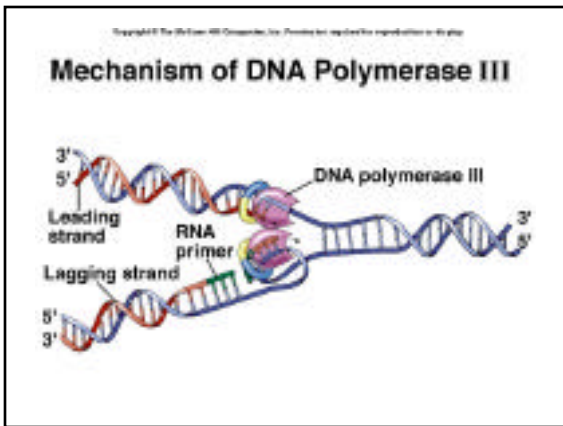
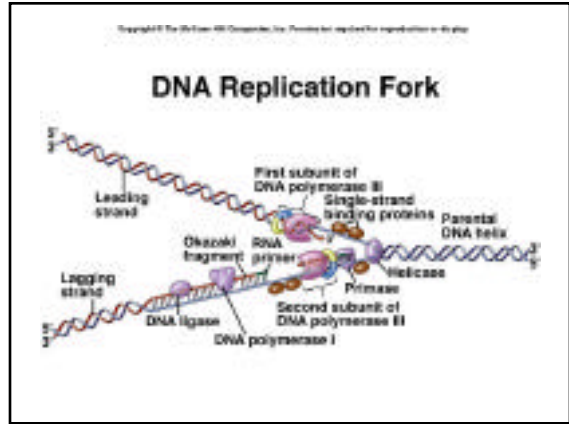
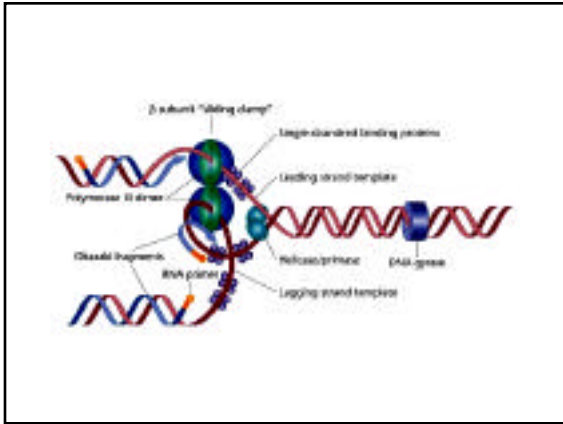
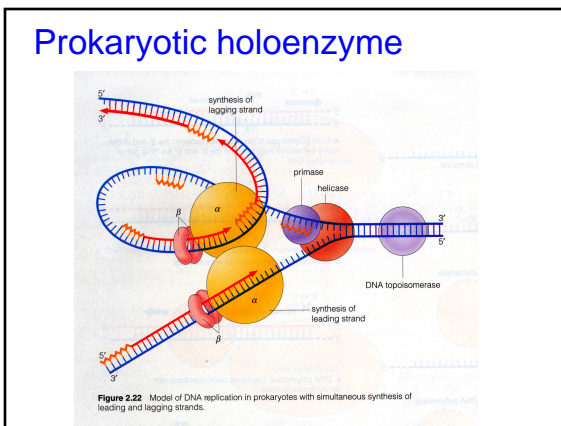
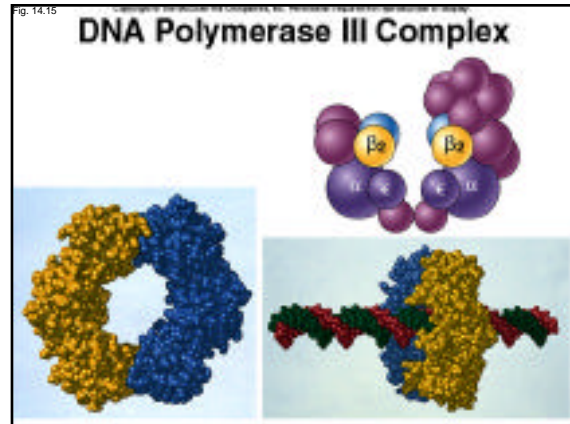
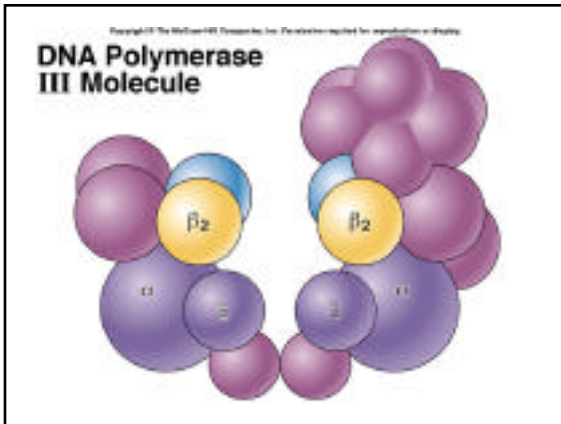


Table 14.2 DNA Replication Proteins of *E. coli*

Protein	Role	Size (kd)	Molecules per Cell
Helicase	Unwinds the double helix	300	20
Primase	Synthesizes RNA primers	60	50
Single-strand binding protein	Stabilizes single-stranded regions	74	300
DNA gyrase	Relieves torque	400	250
DNA polymerase III	Synthesizes DNA	~900	20
DNA polymerase I	Erases primer and fills gaps	103	300
DNA ligase	Joins the ends of DNA segments	74	300

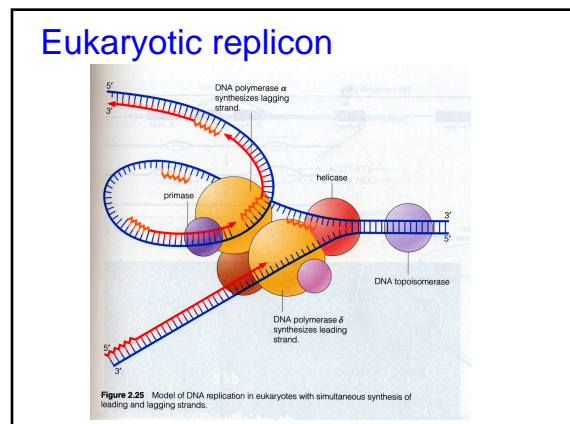
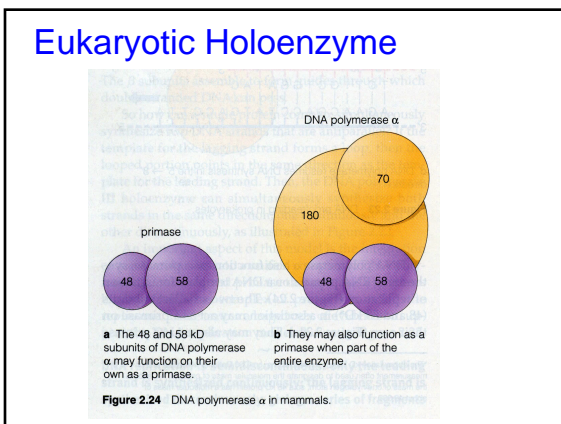






Prokaryotic polymerases

Polymerase	Functions
DNA polymerase I	Removal of nucleotides during DNA repair (5' → 3' exonuclease); synthesis of DNA during repair; synthesis of short gaps in DNA; primer removal (5' → 3' exonuclease); proofreading (3' → 5' exonuclease)
DNA polymerase II	Synthesis of DNA during repair; proofreading (3' → 5' exonuclease)
DNA polymerase III	DNA synthesis; proofreading (3' → 5' exonuclease)



Eukaryotic DNA polymerases

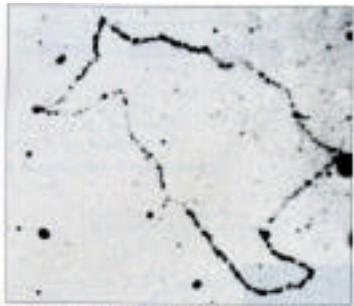
Enzyme	Corresponding Polymerase in Yeast	Function
pol I	Pol I	Synthesis of lagging strand, primer synthesis
pol II	Pol II	Synthesis of DNA autophagen
pol III	Pol III	Synthesis of leading strand, proofreading (3' → 5' exonuclease)
pol IV	Pol IV	Synthesis of DNA autophagen, proofreading (3' → 5' exonuclease)
pol V	Pol V	Synthesis of DNA autophagen, proofreading (3' → 5' exonuclease)

E. coli replication fork



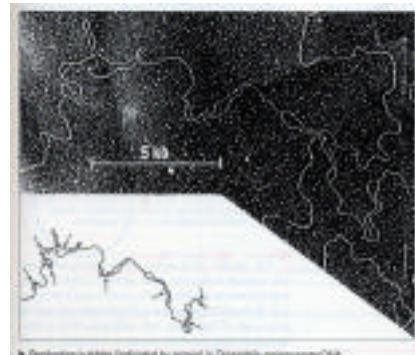
Figure 1.18 Electron micrograph of a replication fork in *E. coli*. (From Ben Cairns, J. 1987. The chromosome of *Escherichia coli*. Cold Spring Harbor: Cold Spring Harbor Laboratory Press, 20-40. Reprinted by permission of the publisher.)

E. coli replicon



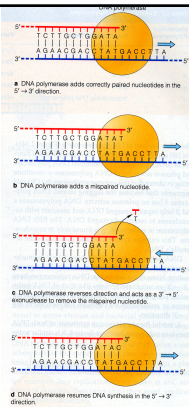
The bacterial DNA labeled with high-level radioactivity appears from 3000-5000 of 1% developed. It is the DNA labeled with low-level radioactivity.

Drosophila replicons

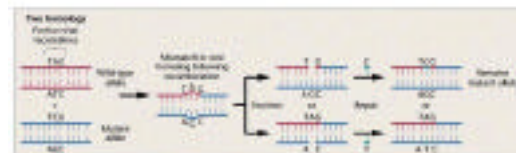


Drosophila replicons labeled by use of ³²P-methylthymine.

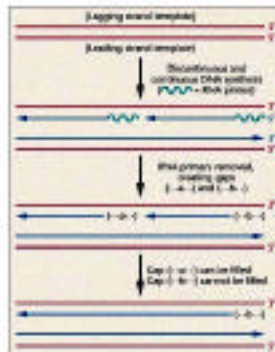
Proofreading



Repair



Telomer problem



Telomers replicated

