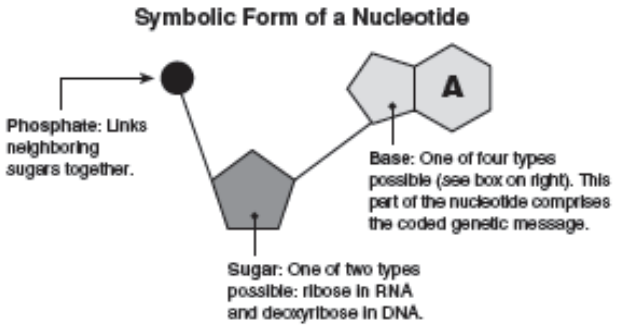
CHAPTER 16: DNA, RNA, PROTEINS

NUCLEIC ACIDS (DNA & RNA) = "Information" molecules



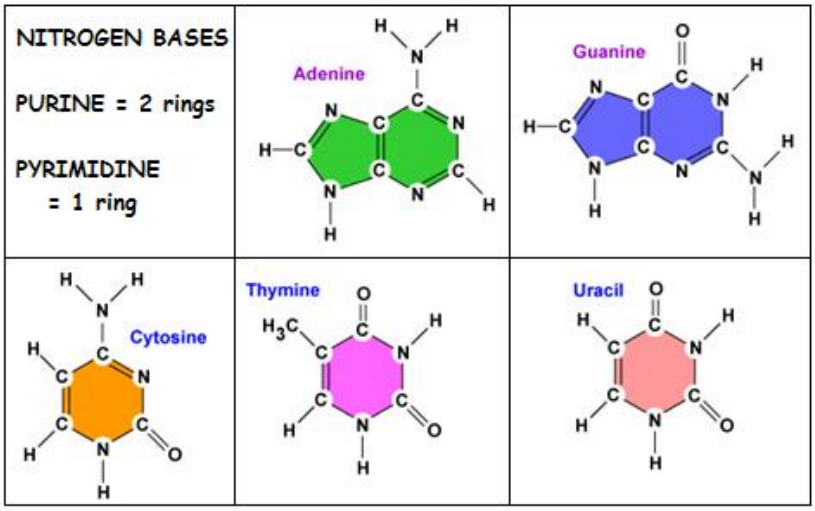
NUCLEOTIDE SUBUNITS

SUGAR = Ribose (RNA)

OR Deoxyribose (DNA)

NITROGEN BASES:

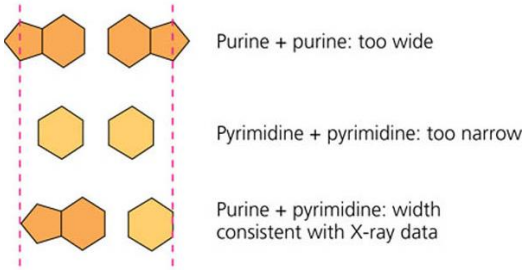
DNA	RNA
Adenine	Adenine
Guanine	Guanine
Cytosine	Cytosine
Thymine	Uracil



CHARGAFF'S RULES:

A = T and G = C

A Purine always bonds to a Pyrimidine

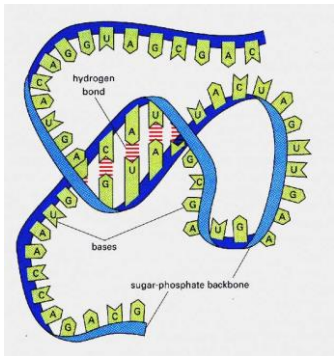


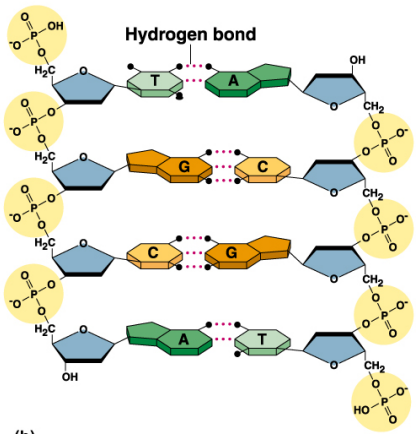
RIBONUCLEIC ACID (RNA)

- Single stranded
- Sugar = ribose
- Nitrogenous bases = A, U, G, (NO T)
- Can fold up in 3D shape

DEOXYRIBONUCLEIC ACID (DNA)

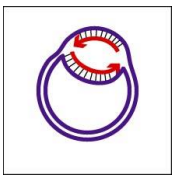
- Double stranded
- Sugar = deoxyribose
- Nitrogenous bases = A, T, G, C (NO U)
- Strands run in opposite directions (ANTIPARALLEL)
- Ladder twists into a DOUBLE HELIX
- Backbone = sugars and phosphates
- Rungs of ladder = nitrogenous bases
- Hydrogen bonds between nitrogenous bases hold sides of ladder together





REPLICATION (DNA → DNA)

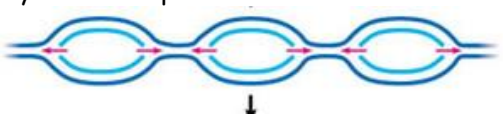
Site where it starts = **ORIGIN of REPLICATION**

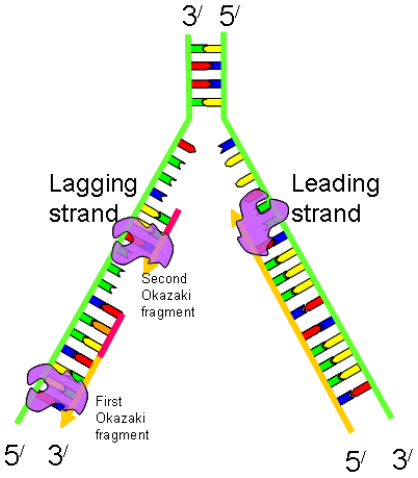


Place where nucleotides add = REPLICATION FORK

Prokaryote- single starting spot

Eukaryotes-multiple sites



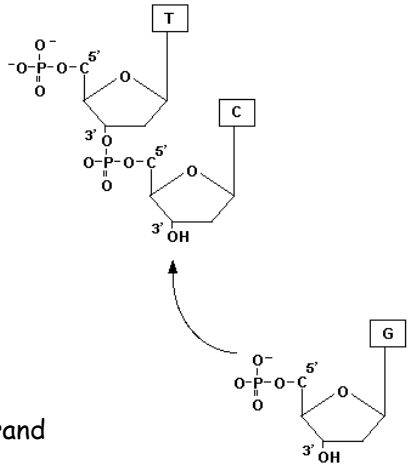


DNA POLYMERASE

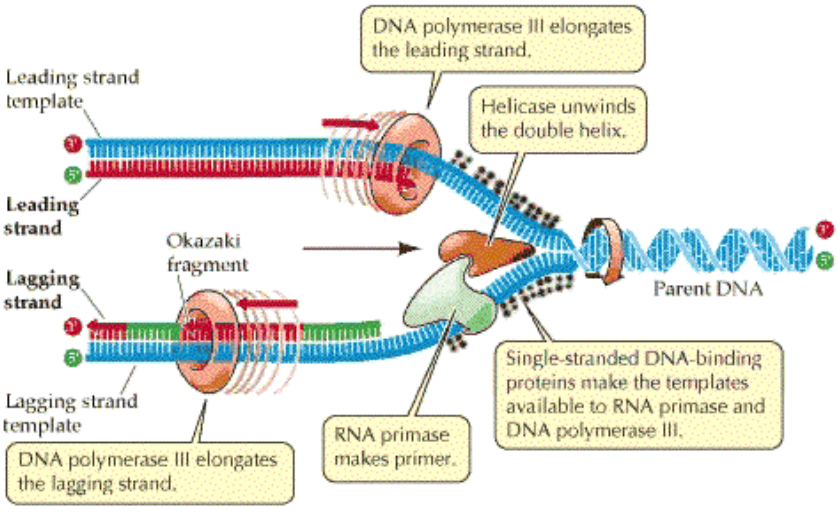
- **reads code strand in 3′ → 5′ direction**
- **builds a new strand in 5′→3′ direction**
- **adds on to 3′ end of sugar** in previous nucleotide

Splitting phosphates from **nucleotide triphosphate subunits**
provides energy for reaction

DNA POLYMERASE CAN'T START A CHAIN by itself;
can only add nucleotides **to 3′ end of an existing DNA/RNA chain**



- **HELICASE**- untwists double helix to open strands at replication forks
- **TOPOISOMERASE**- relieves strain caused by untwisting
- **SINGLE-STRAND BINDING PROTEINS-**
  stabilize unpaired strands to hold them open
- **PRIMASE**-starts segment by adding RNA primer sequence
- **DNA POLYMERASE I** -
  removes RNA primers and replaces them with DNA bases
  by adding to the 3′ end of the previous fragment
- **LIGASE**-joins Okazaki fragments together to make a continuous copied strand

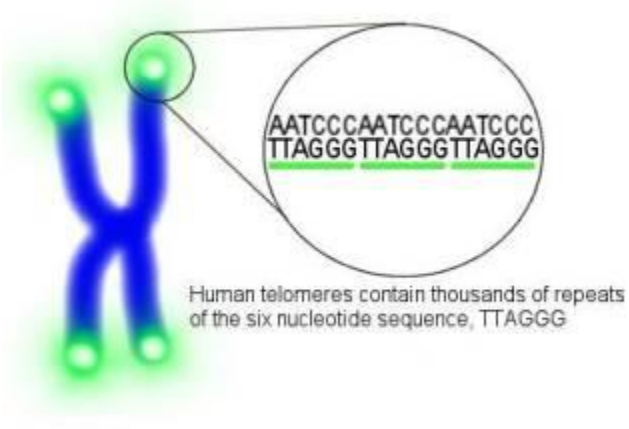


LEADING STRAND (runs 3′→ 5′)
copies toward the replication fork
PRIMASE adds **RNA primer**
to start chain
DNA POLYMERASE III
adds nucleotides in 5′ → 3′ direction

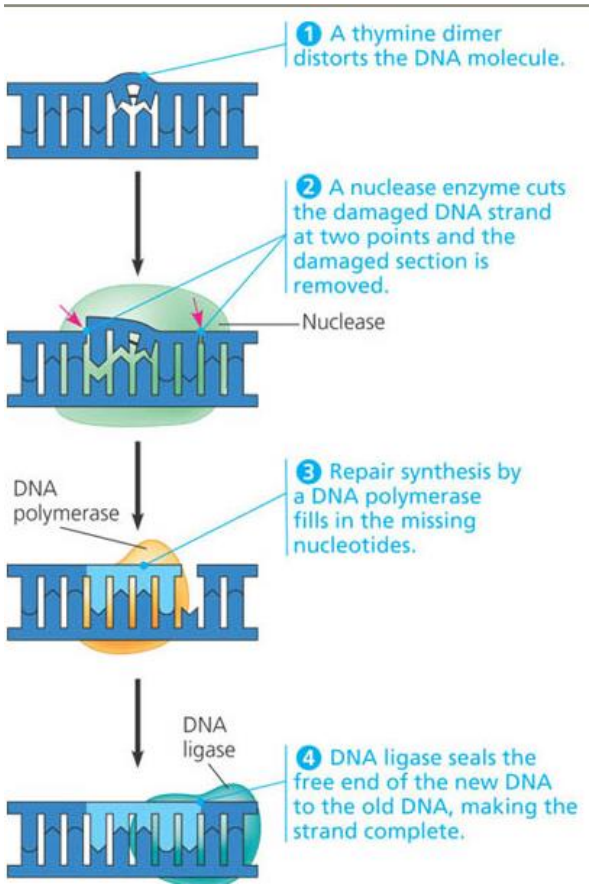
LAGGING STRAND (runs 5′→ 3′)
copies away from replication fork
PRIMASE
adds RNA primers at various spots as fork opens
DNA POLYMERASE III
adds nucleotides in 5′ → 3′ direction
short segments= **OKAZAKI FRAGMENTS**

IMPORTANT: Because DNA polymerase can't fill in last section when primer is removed from lagging strand, the code shortens with each replication

TELOMERE sequences at ends of chromosomes
prevent erosion of essential information in code with each replication
TELOMERASE = enzyme that lengthens telomeres
- found in eukaryotic germ cells that divide frequently to produce gametes
- may play a role in a aging and cancer



PROOFREADING & REPAIR



Mistakes in final DNA: 1 in 10 billion
Mistakes in initial base pairing during replication 1 in 100,000
DNA POLYMERASE proofreads each base as it's added & fixes errors
Errors can come from "proofreading mistakes" that are not caught OR environmental damage (Ex: X-rays, UV light, chemical mutagens/carcinogens)

NUCLEOTIDE EXCISION-REPAIR
- Cells continually monitor DNA and make repairs
- NUCLEASES- DNA cutting enzymes remove errors
- DNA POLYMERASE fills in gap using complimentary strand
- LIGASE seals ends

Ex: THYMINE DIMERS = joins THYMINES in same strand
- damage caused by UV light
- can be repaired

Xeroderma pigmentosum-
genetic disorder can't go out in sun
mutation in DNA enzymes that repair UV
increased skin cancer/cataracts