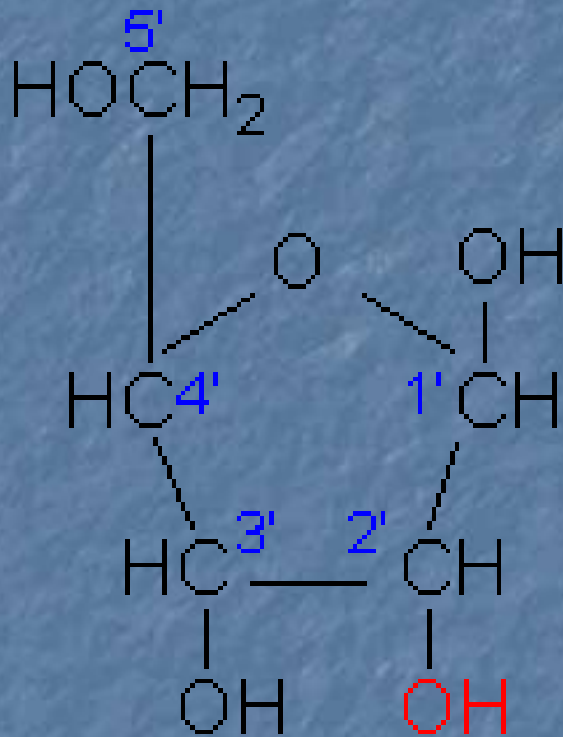


DNA STRUCTURE

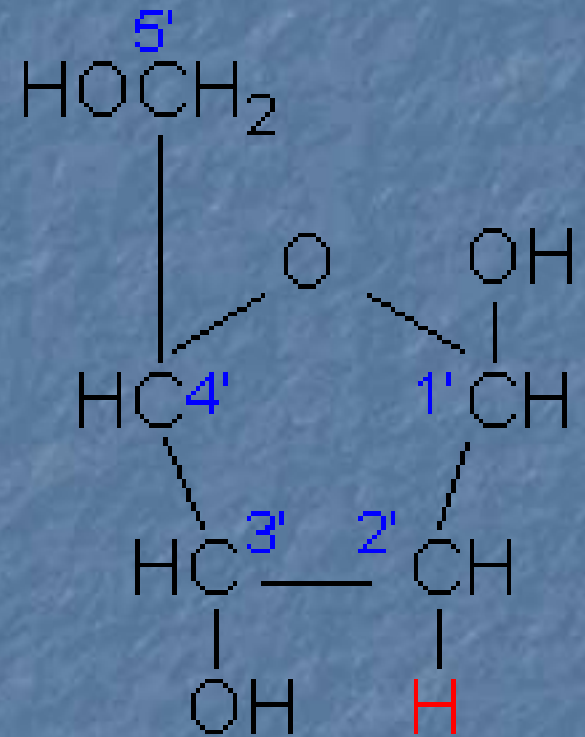
NUCLEIC ACIDS

- Nucleic acids are polymers
 - Monomer---nucleotides
 - Nitrogenous bases
 - Purines
 - Pyrimidines
 - Sugar
 - Ribose
 - Deoxyribose
 - Phosphates
 - +nucleoside=nucleotide
- } Nucleosides

The Sugars

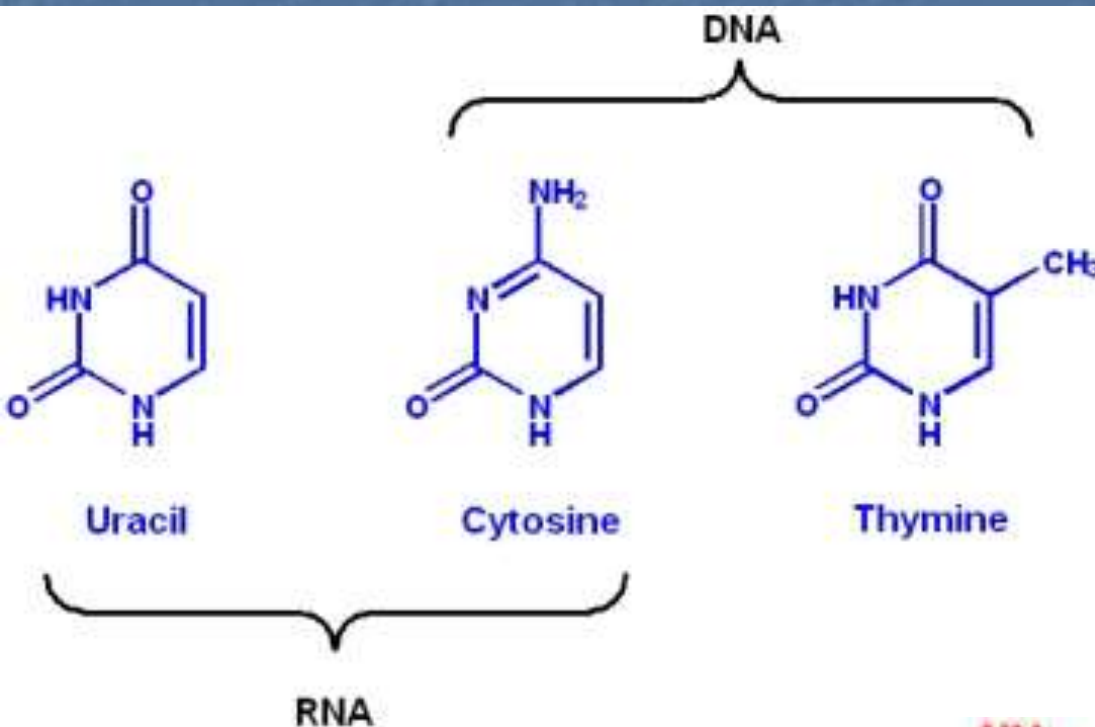


Ribose
(in RNA)



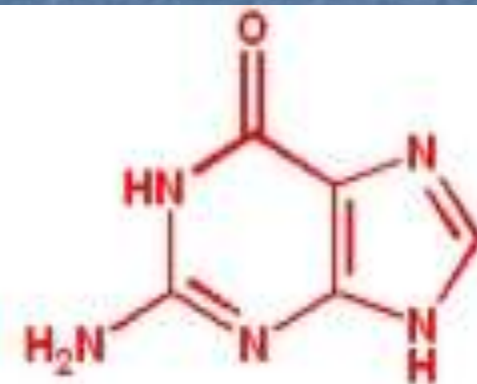
2-Deoxyribose
(in DNA)

The Bases



← PYRIMIDINES

PURINES →

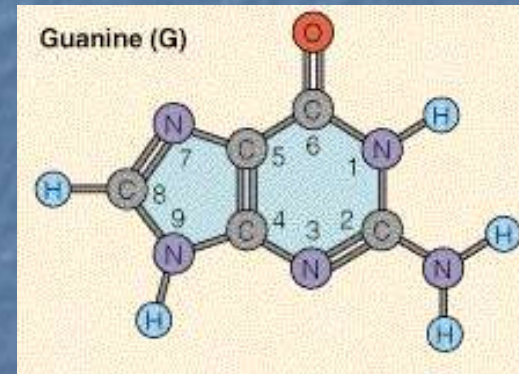
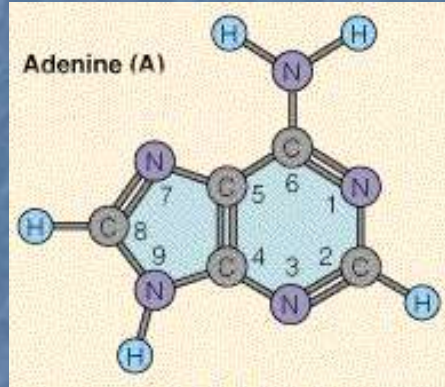


Adenine

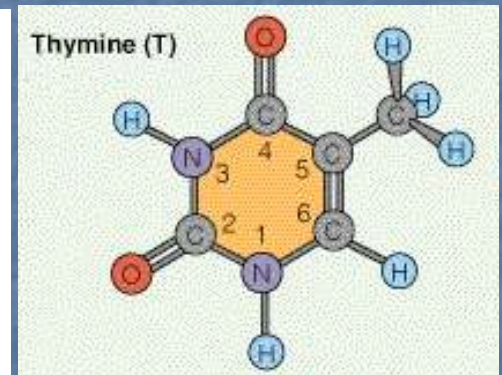
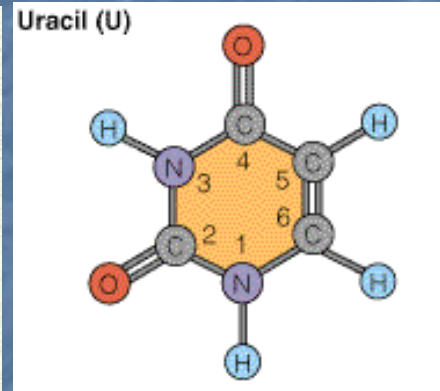
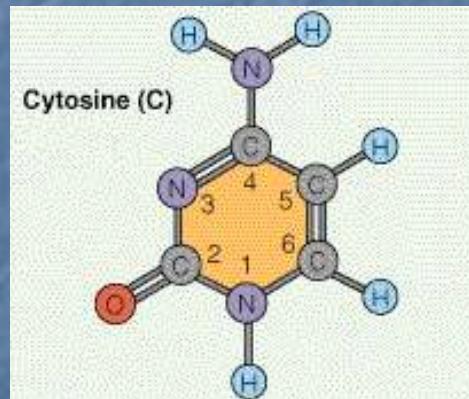
Guanine

Bases of DNA (and RNA)

Purines:



Pyrimidines:

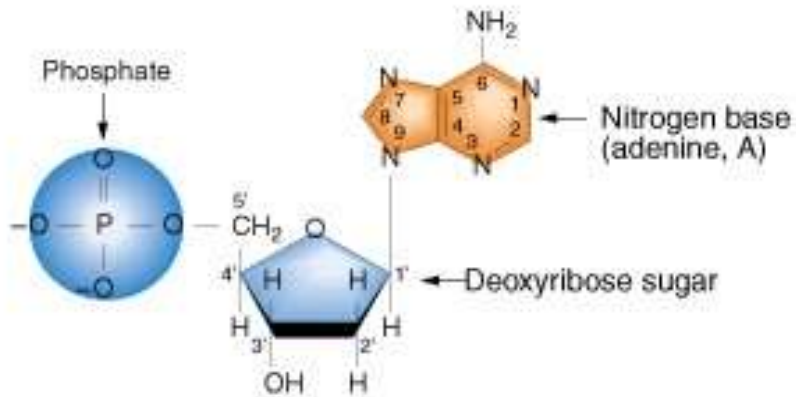


RNA only

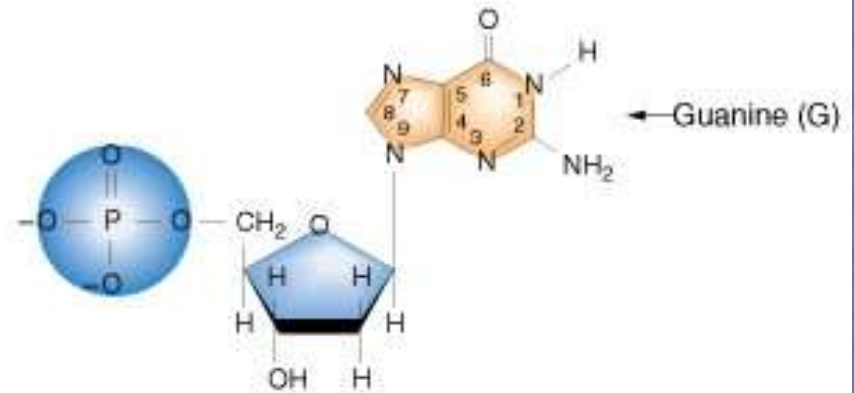
DNA only

Nucleotides and Nucleosides

Purine nucleotides

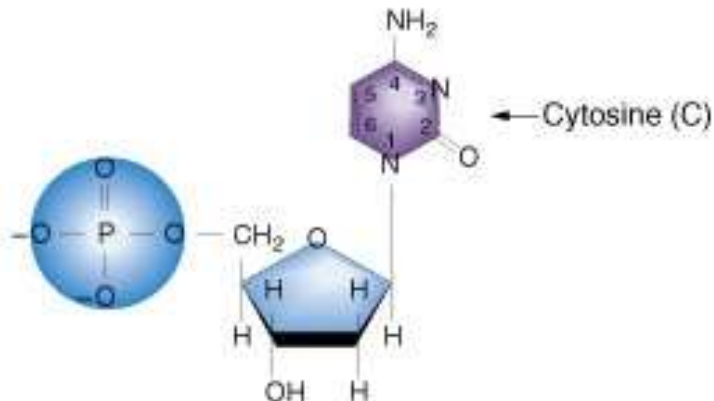


Deoxyadenosine 5'-phosphate (dAMP)

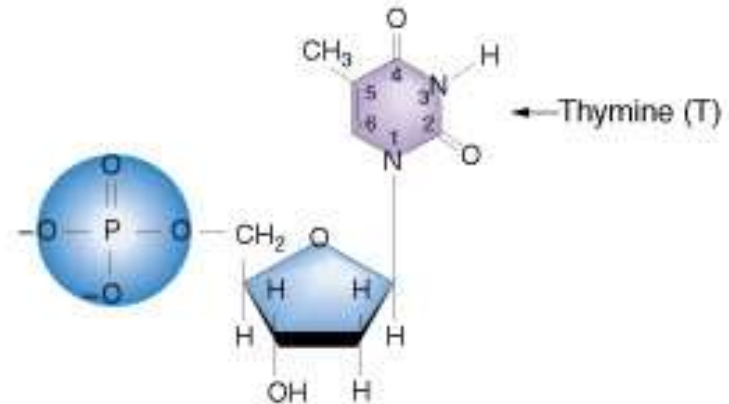


Deoxyguanosine 5'-phosphate (dGMP)

Pyrimidine nucleotides



Deoxycytidine 5'-phosphate (dCMP)



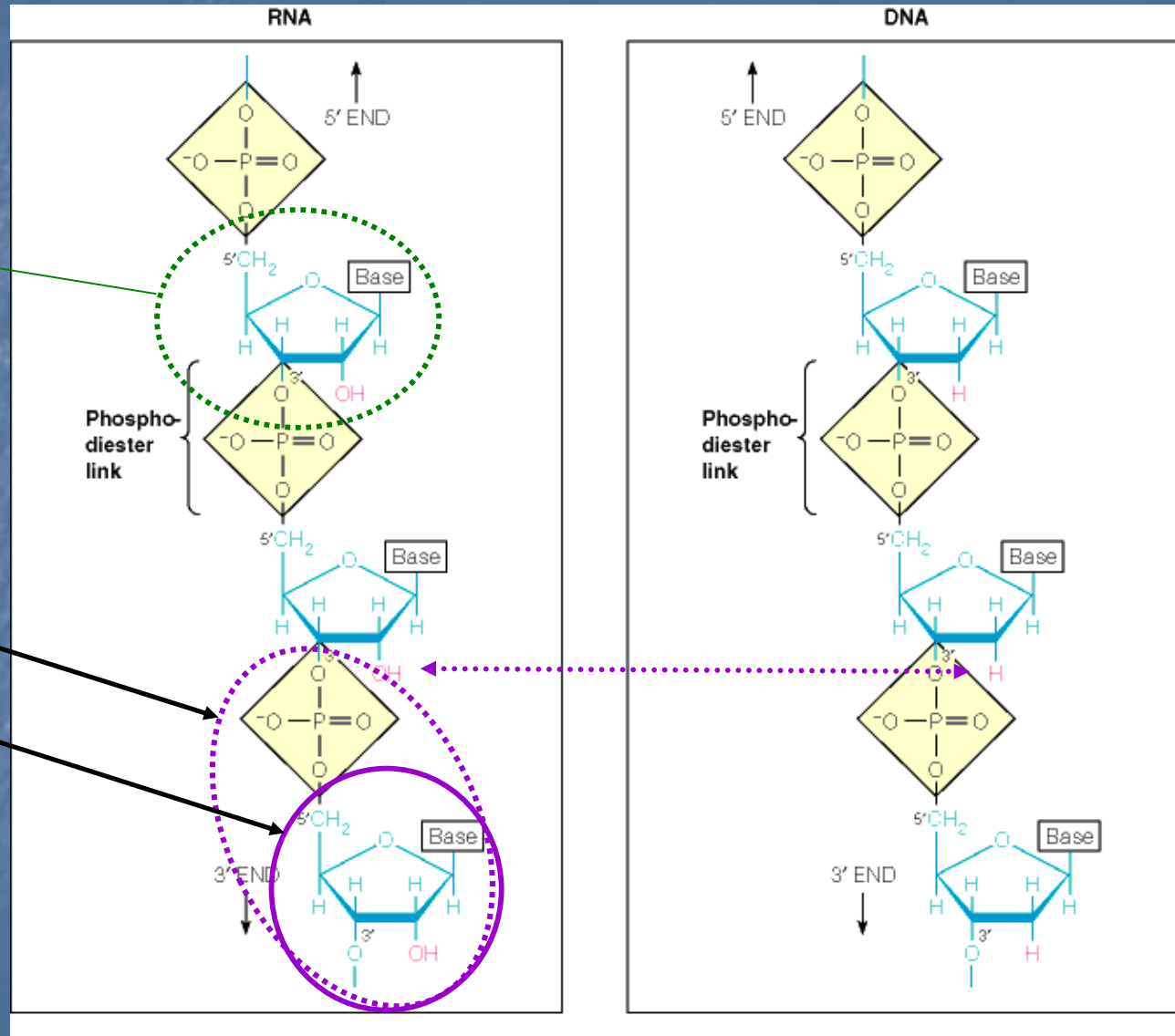
Deoxythymidine 5'-phosphate (dTMP)

Chemical Structure of DNA and RNA

The C is named 1'-5'

Nucleotide

Nucleoside

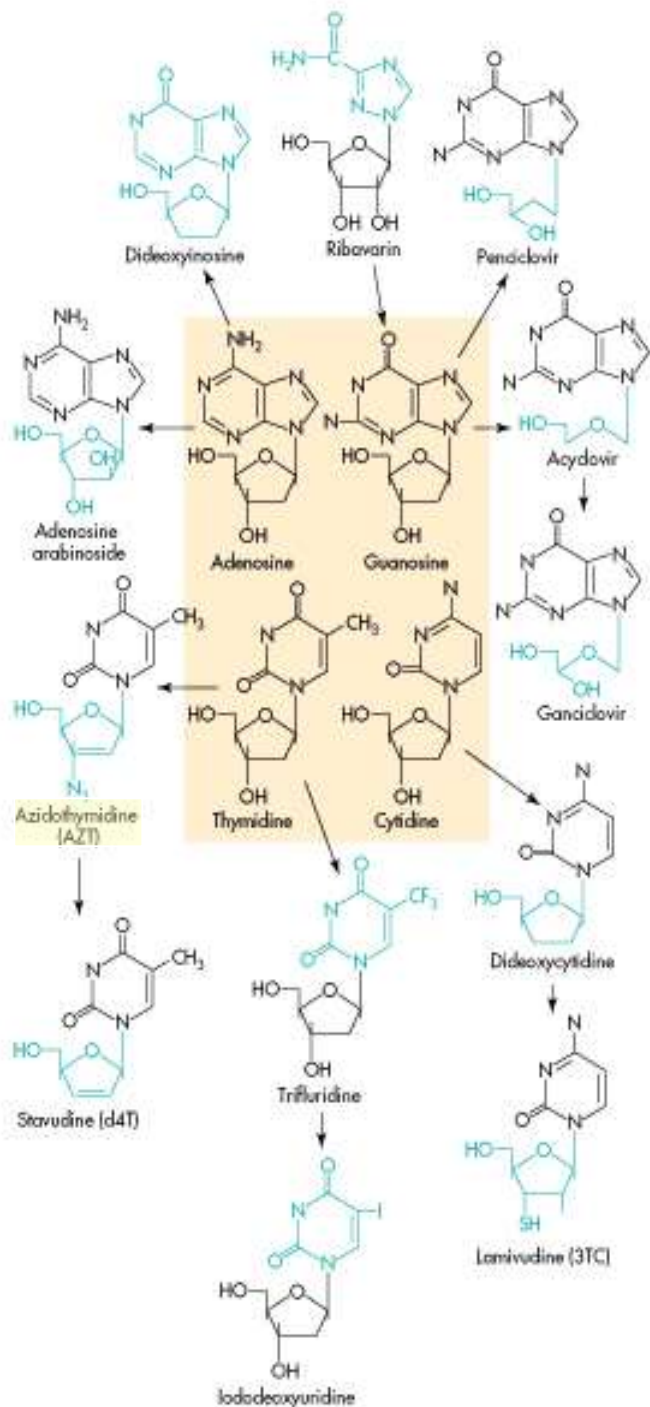


Nucleotides and Nucleosides

BASE	NUCLEOSIDE	DEOXYNUCLEOSIDE
Adenine	Adenosine	2-deoxyadenosine
Guanine	Guanosine	2-deoxyguanosine
Cytosine	Cytidine	2-deoxycytidine
Uracil	Uridine	Not usually found
Thymine	Not usually found	2-deoxythymidine

Nucleotides are nucleosides + phosphate

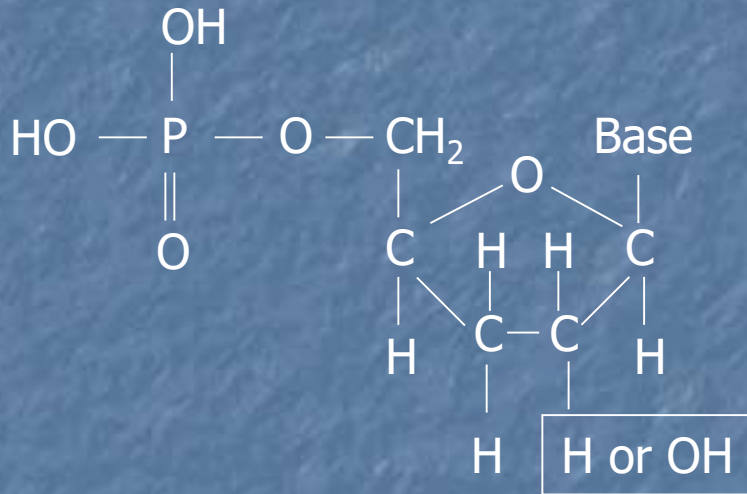
Nucleotide Analogues as Drugs



Nucleic Acids

make up 13-34% of the dry weight in bacteria
deoxyribonucleic acid (DNA) and ribonucleic acid (RNA)

Nucleotide: a building block



Nucleoside: base + sugar

Sugar:

- RNA – ribose (OH)
- DNA – deoxyribose (H)

Bases:

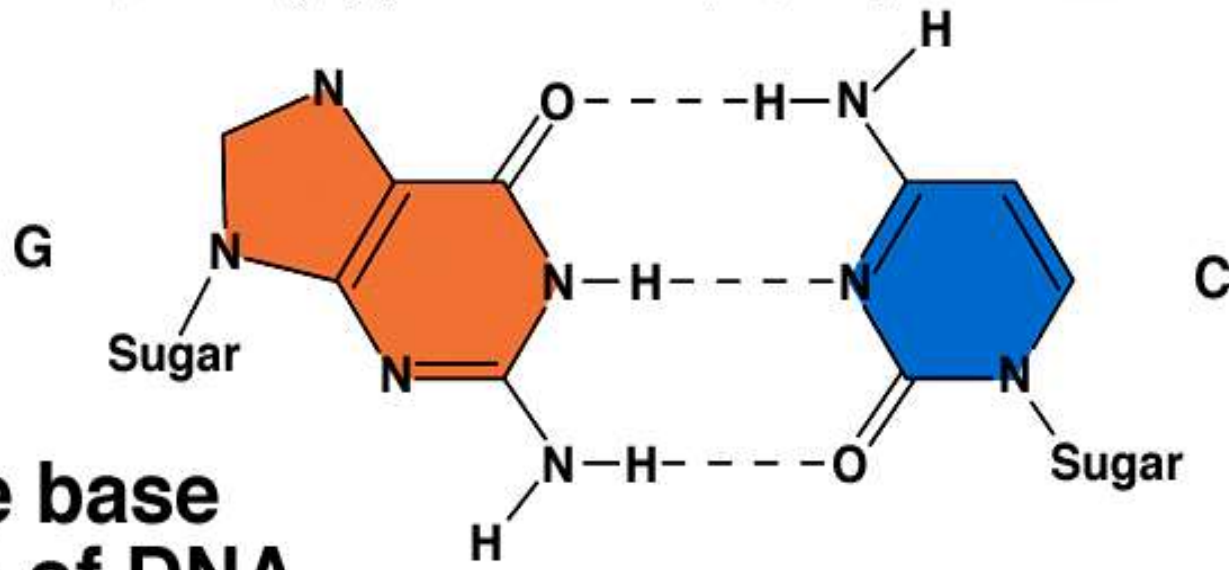
- adenine (A), cytosine (C), guanine (G), thymine (T)
- RNA uses uracil (U) instead of thymine

- certain nucleotides serve as a storage of energy and reducing power
e.g. **ATP -> ADP -> AMP**

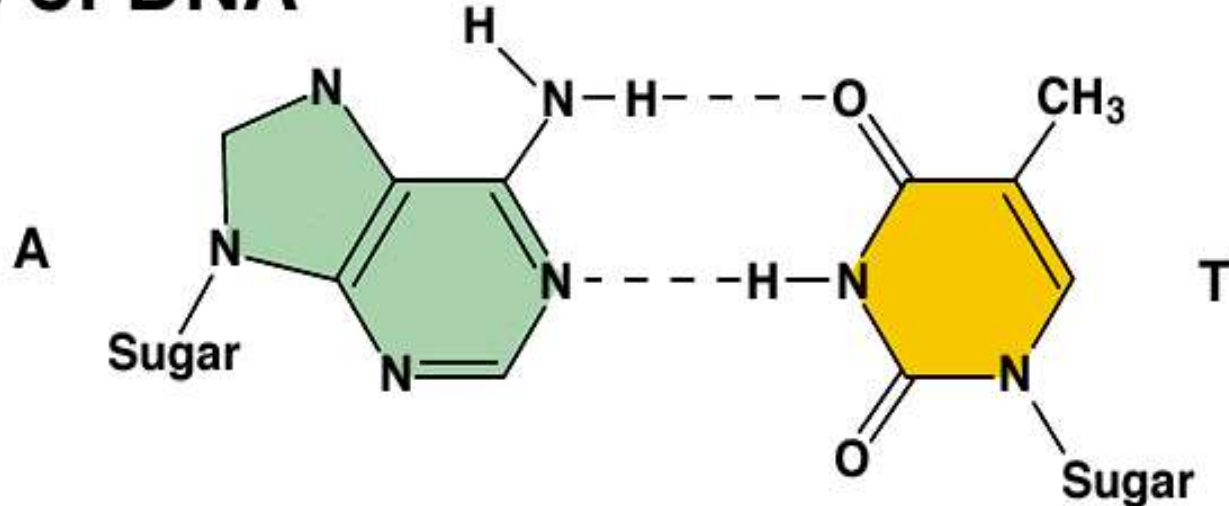
hydrolysis (energy is released)

DNA Stabilization– Complementary Base Pairing

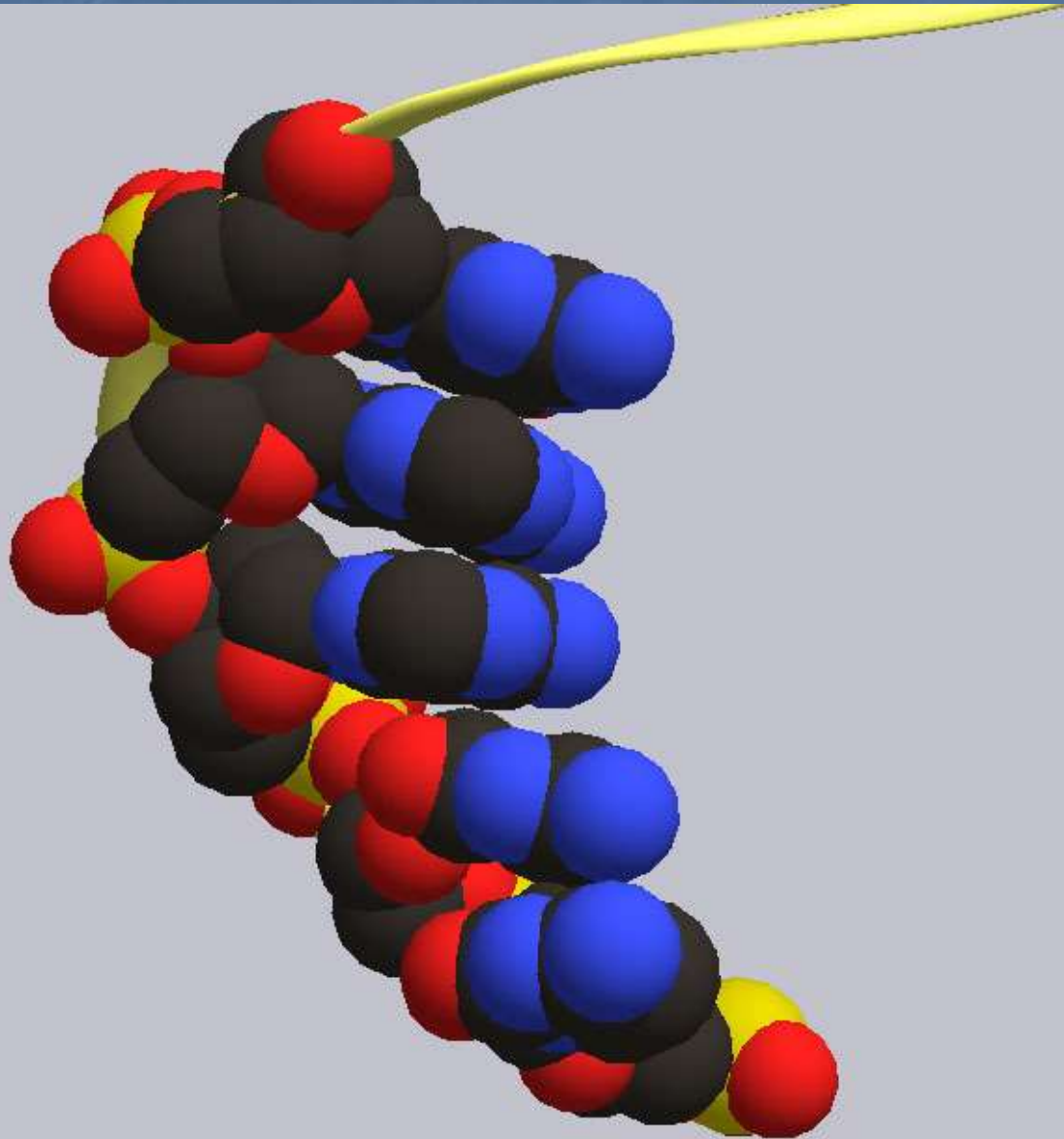
Robert Weaver, *Molecular Biology*, Copyright © 1999. The McGraw-Hill Companies, Inc. All rights reserved.



The base pairs of DNA

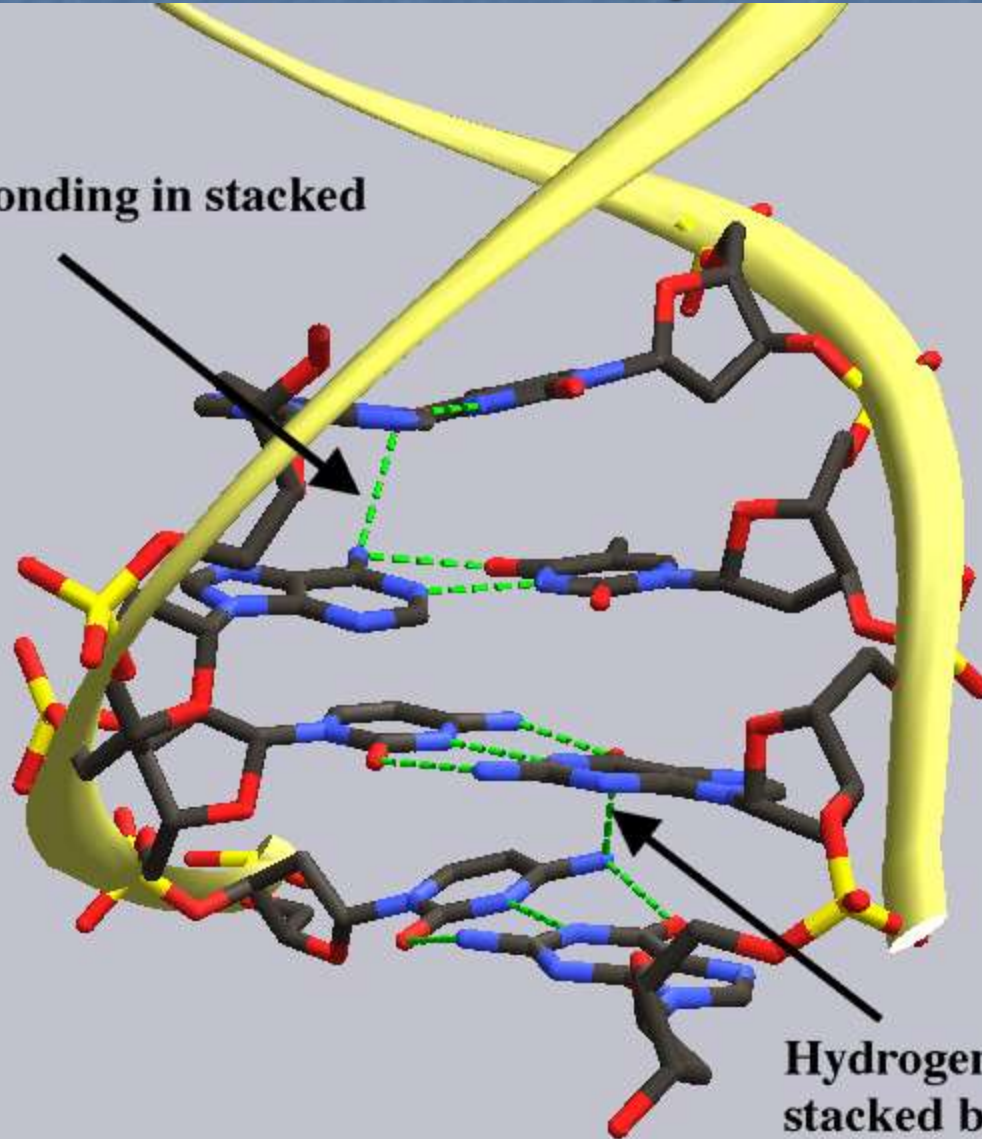


DNA Stabilization-Base Stacking



DNA Stabilization--H-bonding between DNA base pair stacks

Hydrogen bonding in stacked
base pairs.

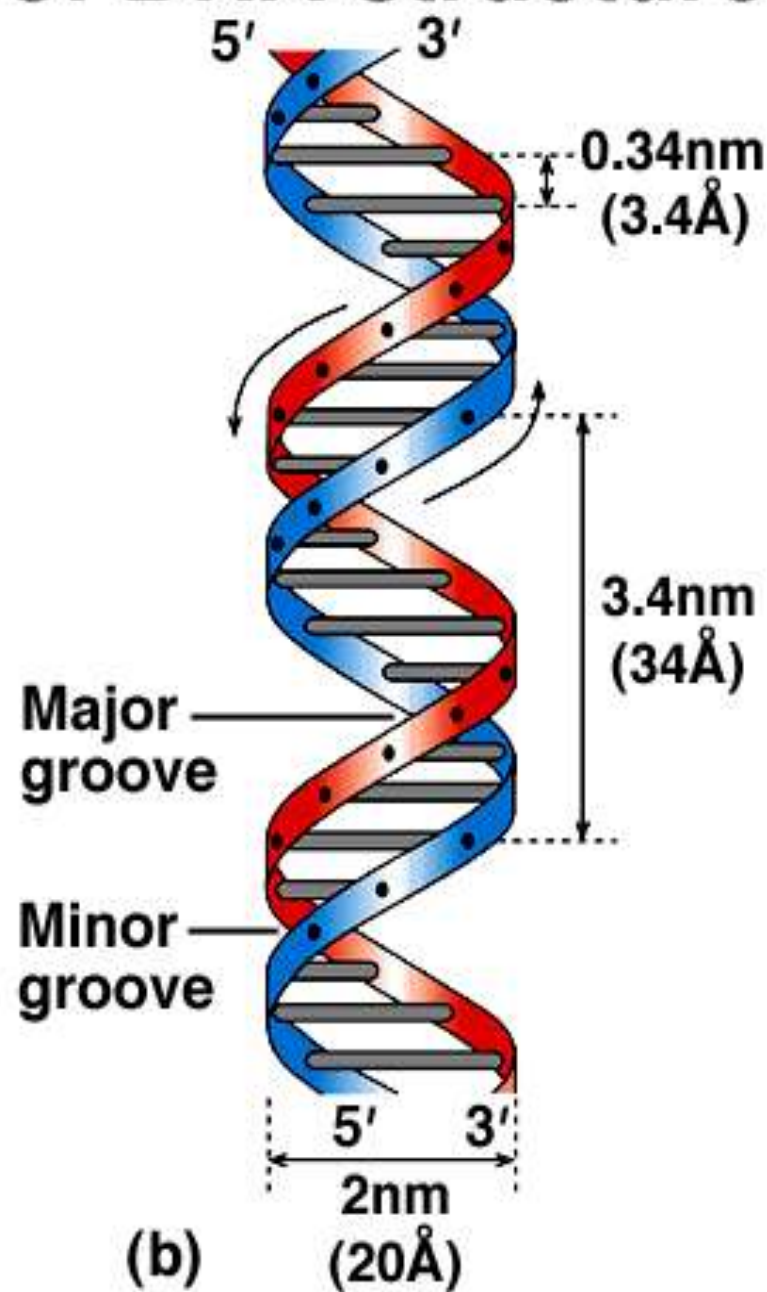
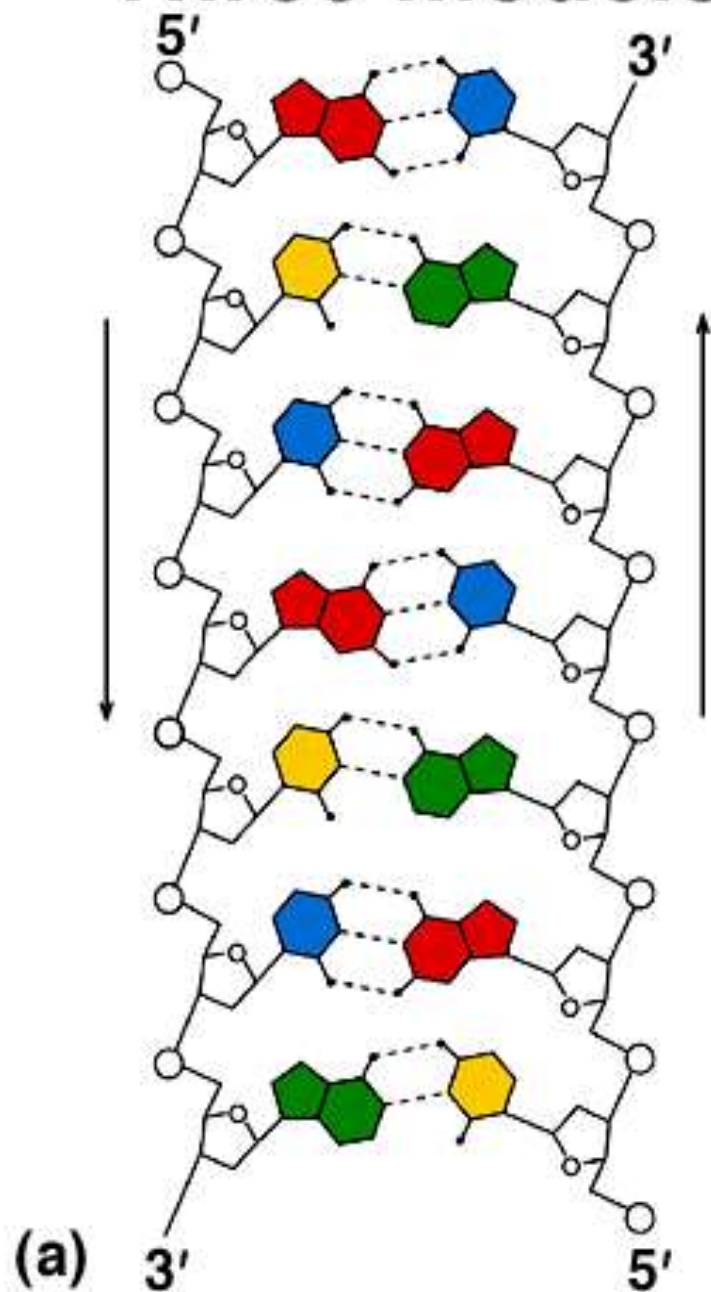


Hydrogen bonding in
stacked base pairs.

Advantages to Double Helix

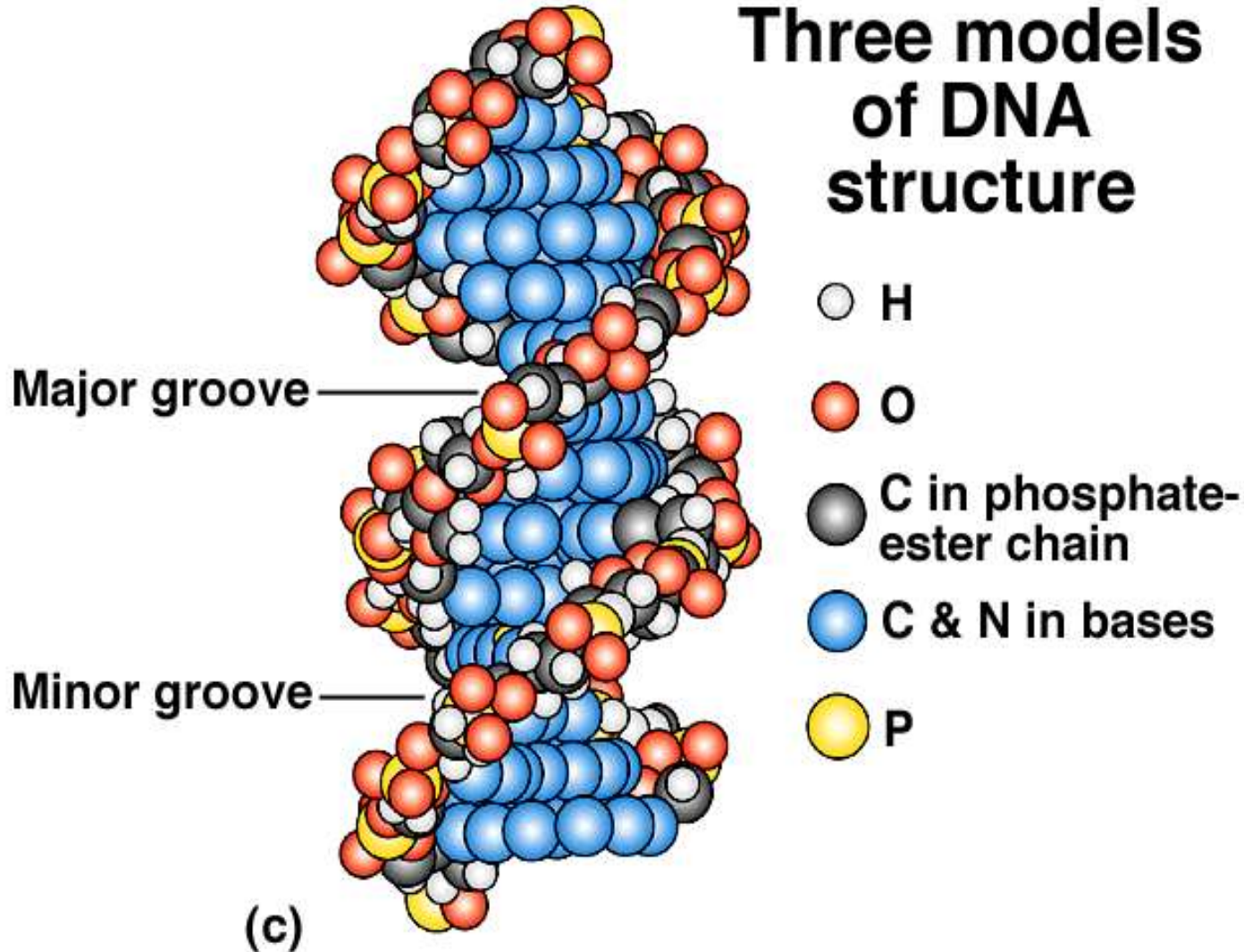
- Stability---protects bases from attack by H_2O soluble compounds and H_2O itself.
- Provides easy mechanism for replication

Three models of DNA structure



Physical Structure (cont'd)

Robert Weaver, *Molecular Biology*, Copyright © 1999. The McGraw-Hill Companies, Inc. All rights reserved.



G-C Content

- $A=T$, $G=C$, but $AT \neq GC$
- Generally $GC \sim 50\%$, but extremely variable
- EX.
 - Slime mold $\sim 22\%$
 - Mycobacterium $\sim 73\%$
- Distribution of GC is not uniform in genomes

CONSEQUENCES OF GC CONTENT

- GC slightly denser
 - ∴ Higher GC DNA moves further in a gradient
- Higher # of base pairs = more stable DNA, i.e. the strands don't separate as easily.

FORMS OF DNA



A-DNA

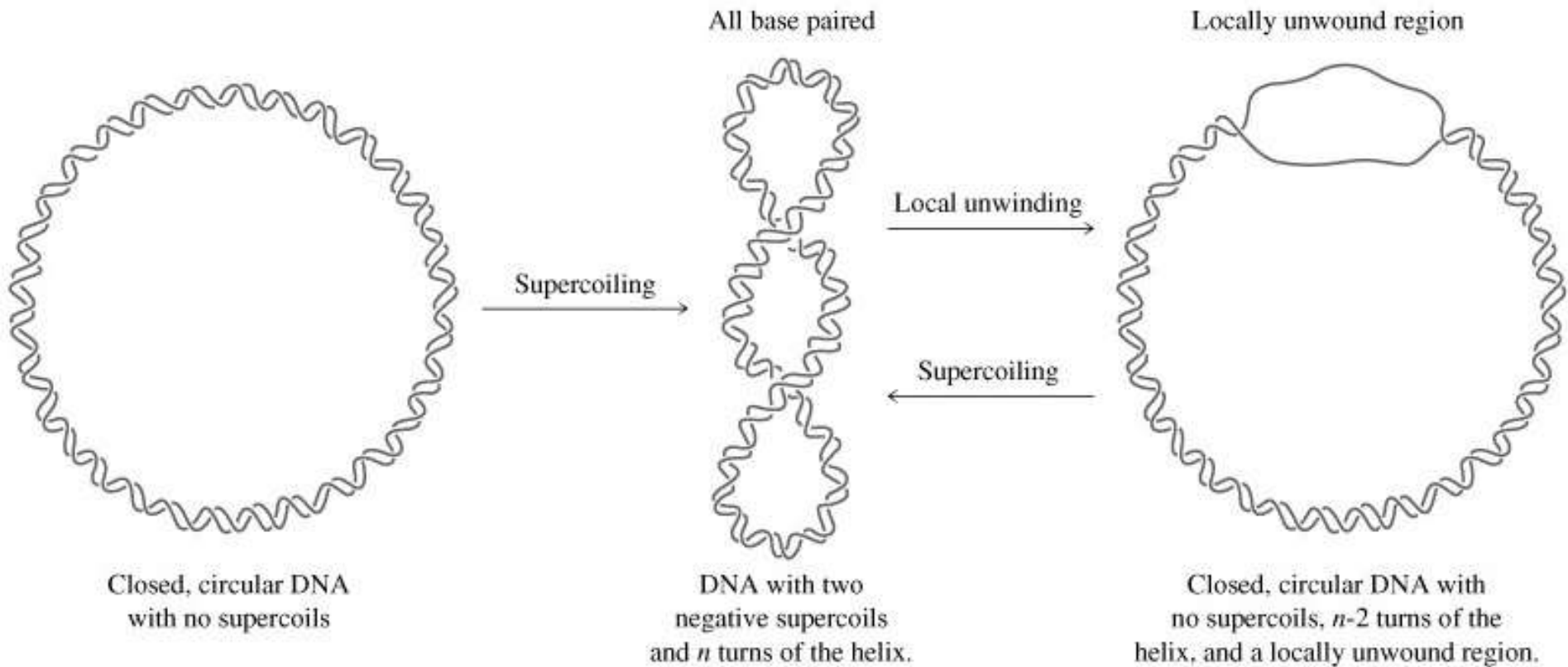


B-DNA

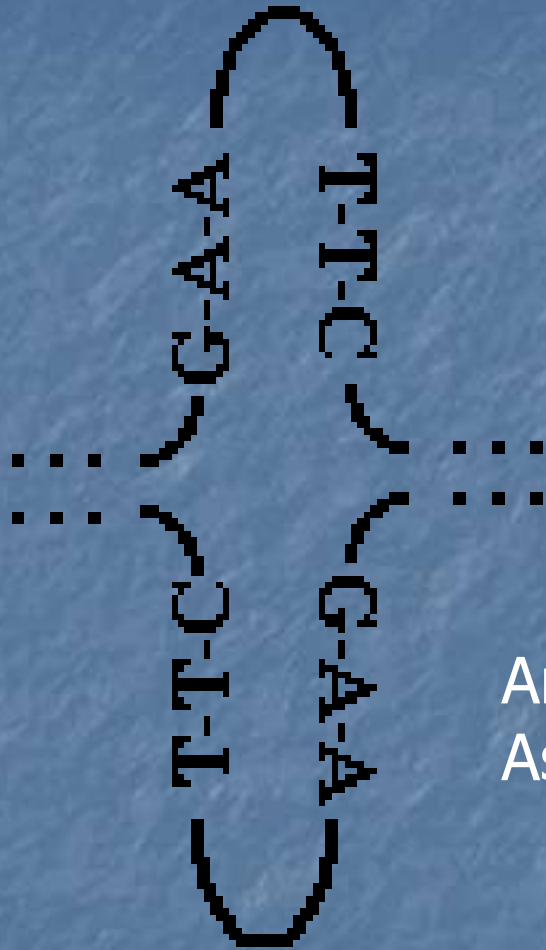


Z-DNA

Supercoiling



Cruciform Structures



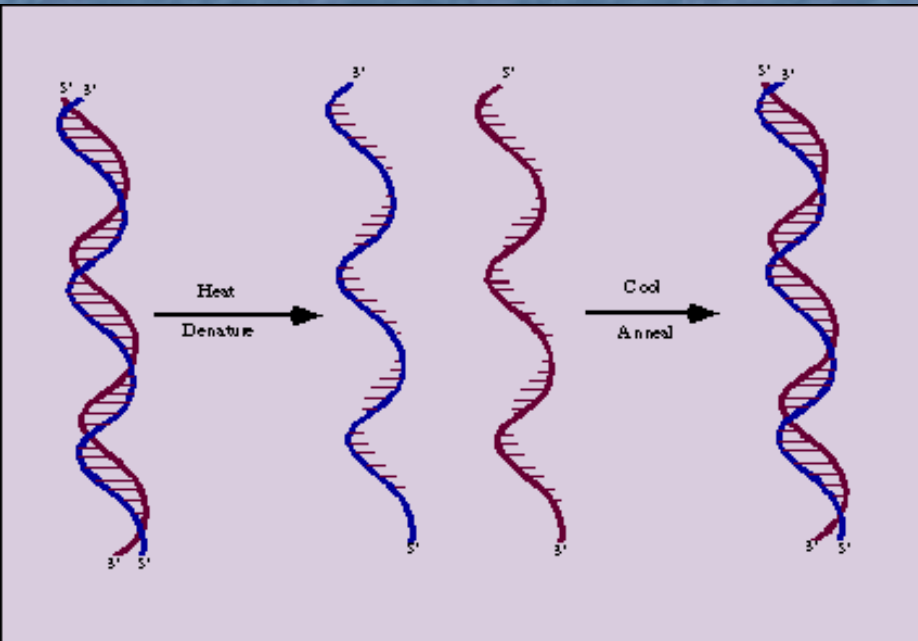
Another adaptation to supercoiling
Associated with palindromes

DNA is Dynamic

- Like proteins, DNA has 3^o structure
- Why so many deviations from normal conformation?
 - Effects on transcription (gene expression)
 - Enhances responsiveness
 - May also serve in packaging
- NOTE: most cellular DNA exists as protein containing supercoils

Denaturation of DNA

- Denaturation by heating.
- How observed?



The T at which $\frac{1}{2}$ the DNA sample is denatured is called the melting temperature (T_m)

- A_{260}
- For dsDNA,
 $A_{260}=1.0$ for $50 \mu\text{g/ml}$
- For ssDNA and RNA
 $A_{260}=1.0$ for $38 \mu\text{g/ml}$
- For ss oligos
 $A_{260}=1.0$ for $33 \mu\text{g/ml}$
- Hyperchromic shift

Importance of T_m

- Critical importance in any technique that relies on complementary base pairing
 - Designing PCR primers
 - Southern blots
 - Northern blots
 - Colony hybridization

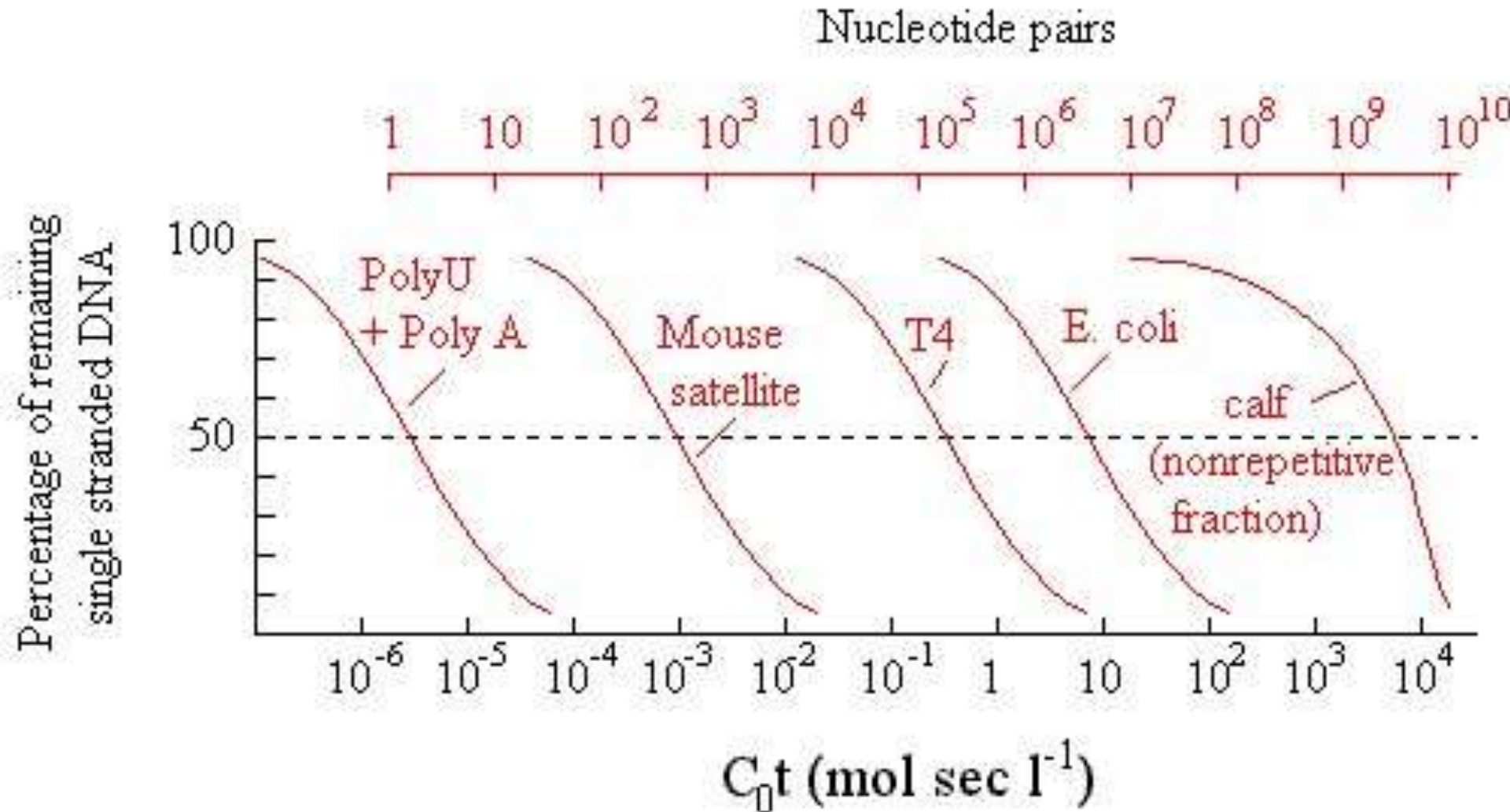
Factors Affecting T_m

- G-C content of sample
- Presence of intercalating agents (anything that disrupts H-bonds or base stacking)
- Salt concentration
- pH
- Length

Renaturation

- Strands can be induced to renature (anneal) under proper conditions. Factors to consider:
 - Temperature
 - Salt concentration
 - DNA concentration
 - Time

C_0t Curves



What Do C_0t Curves Reveal?

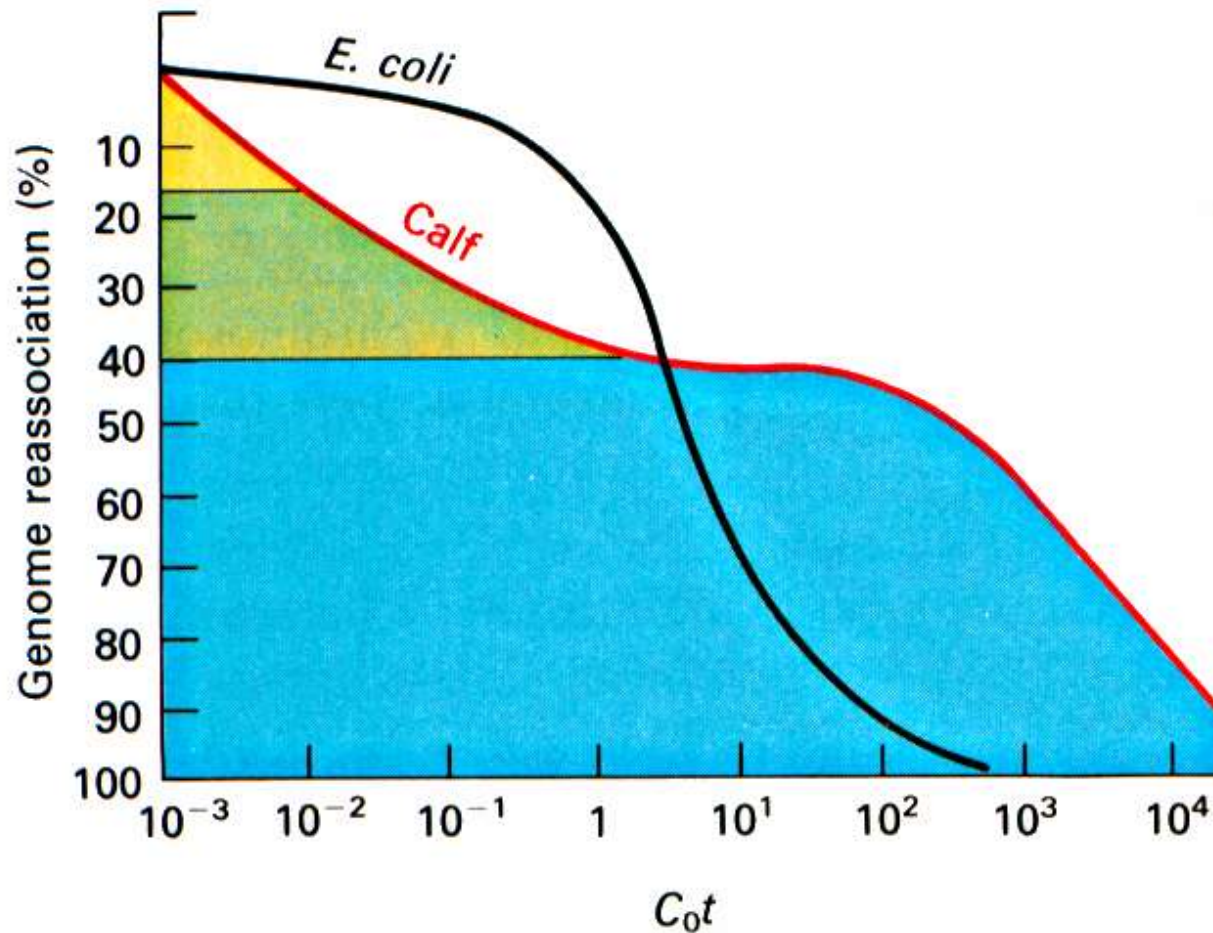
- Complexity of DNA sample
- Reveals important info about the physical structure of DNA
- Can be used to determine T_m for techniques that complementary base pairing.

Complexity of DNA- Factors

Repetitive Sequences

- Single Copy Genes
- Highly repetitive (hundreds to millions)
 - Randomly dispersed or in tandem repeats
 - Satellite DNA
 - Microsatellite repeats
 - Miniisatellite repeats
- Middle repetitive (10- hundreds)
 - Clustered
 - Dispersed
- Slightly repetitive (2-10 copies)

Renaturation curves of *E. coli* and calf DNA



- Highly repetitive sequences
- Middle repetitive sequences
- Unique sequences

RNA

- Types
 - mRNA
 - tRNA
 - rRNA
- It's still an RNA world
 - snRNA
 - siRNA
 - Ribozymes

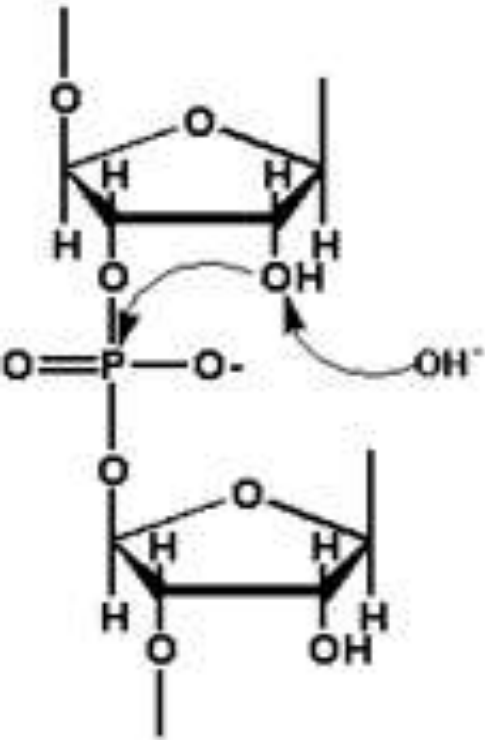
Behavior in Acids

- Dilute or mild acidic conditions
- Intermediate conditions. EX. 1N HCl @ 100°C for 15m : Depurination
- Harsher treatment-EX. 2-6N HCl, higher temps: Depyrimidination.
- NOTE: some phosphodiester bond cleavage observed during depurination, much more during depyrimidination

Behavior in Bases

- N-glycosidic bonds stable in mild alkaline conditions
- DNA melts
- Phosphodiester linkages in DNA and RNA show very different behavior in weak bases (EX 0.3 N KOH @37°C ~1 hr.)

RNA Hydrolysis in Alkaline Solutions

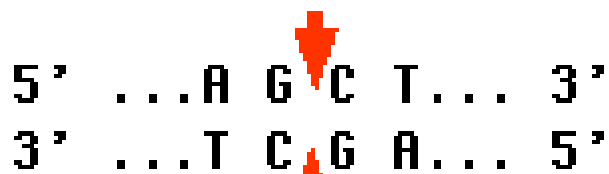


Hydrolysis by Enzymes

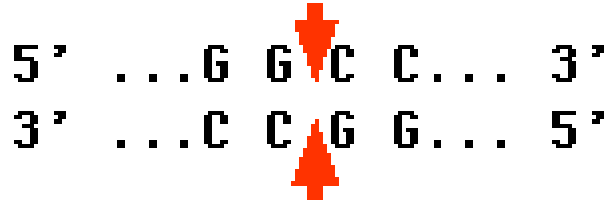
- Nuclease—catalyzes hydrolysis of phosphodiester backbone
 - Exonucleases
 - Endonucleases
 - General. Ex DNase I
 - Specific Ex. Restriction endonucleases
- Ribozymes

Restriction Enzymes

AluI



HaeIII



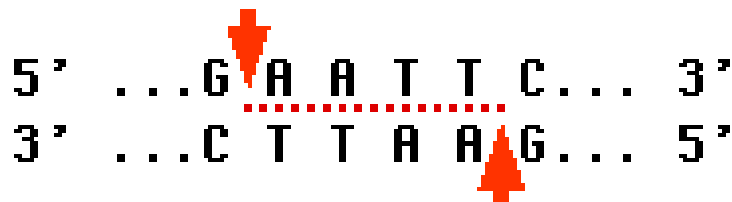
BamHI



HindIII

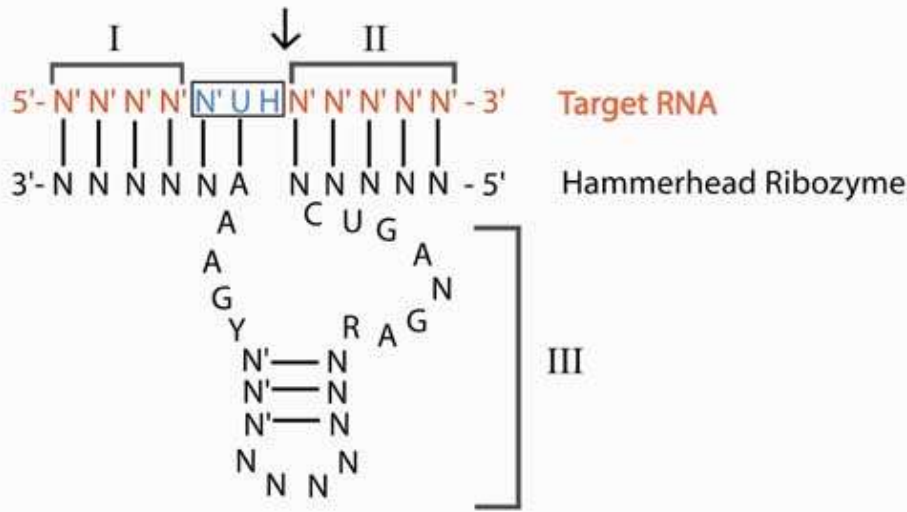
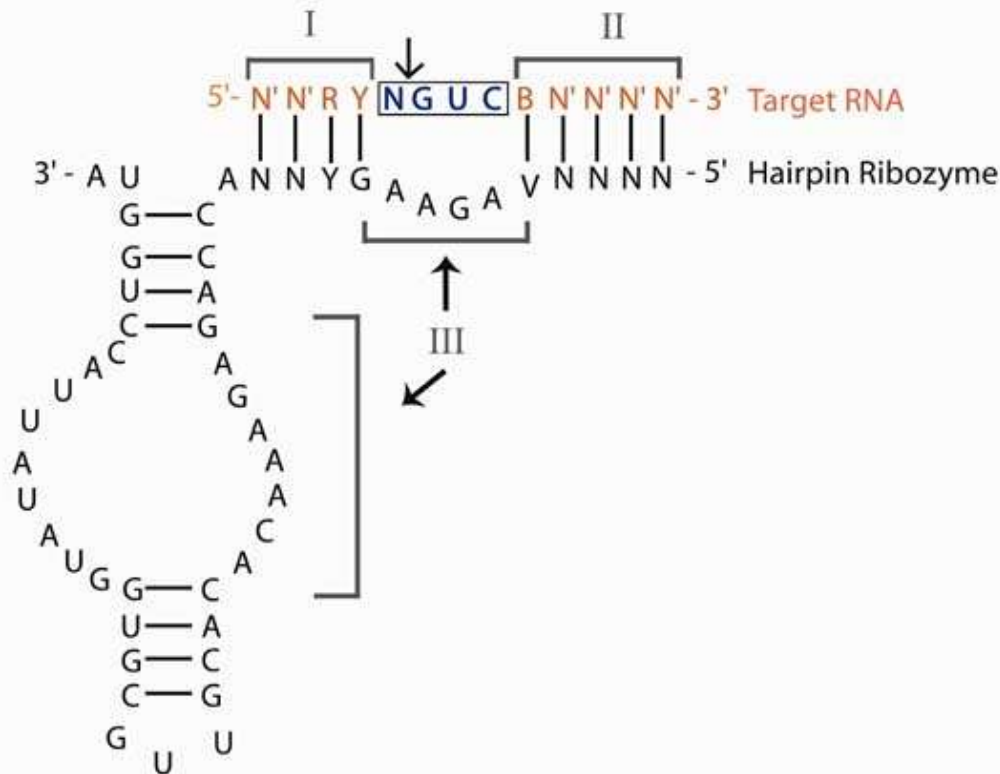


EcoRI



AluI and **HaeIII** produce blunt ends

BamHI **HindIII** and **EcoRI** produce "sticky" ends

A**B**

RIBOZYMES

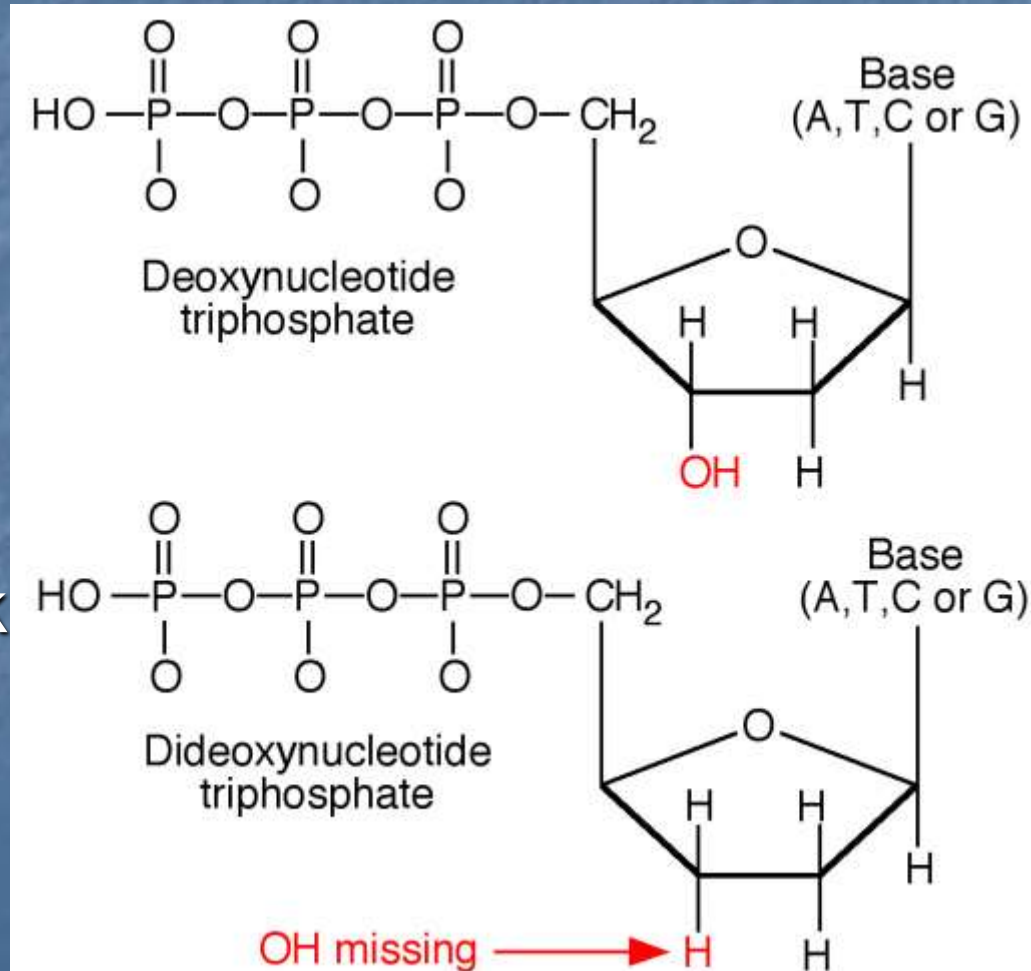
- Catalytic RNA
- Can work alone or with proteins
- Therapeutic applications?

SEQUENCING

- Purpose—determine nucleotide sequence of DNA
- Two main methods
 - Maxam & Gilbert, using chemical sequencing
 - Sanger, using *dideoxynucleotides*

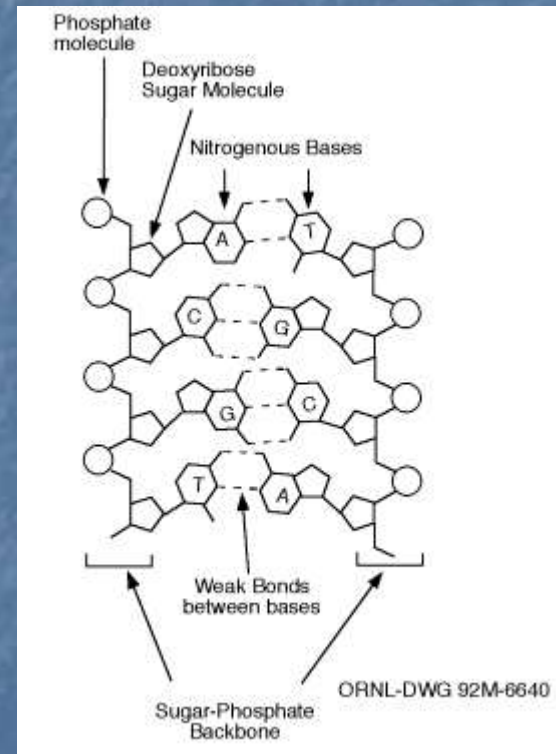
The Sanger Technique

- Uses dideoxynucleotides (dideoxyadenine, dideoxyguanine, etc)
- These are molecules that resemble normal nucleotides but lack the normal -OH group.



- Because they lack the -OH (which allows nucleotides to join a growing DNA strand), replication stops.

Normally, this would be where another phosphate is attached, but with no -OH group, a bond can not form and replication stops



The Sanger Method Requires

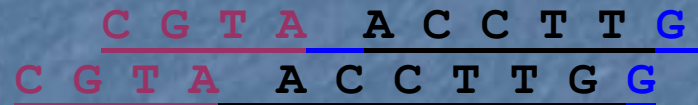
- Multiple copies of single stranded **template DNA**
- A suitable **primer** (a small piece of DNA that can pair with the template DNA to act as a starting point for replication)
- **DNA polymerase** (an enzyme that copies DNA, adding new nucleotides to the 3' end of the template)
- A 'pool' of **normal nucleotides**
- A small proportion of **dideoxynucleotides** labeled in some way (radioactively or with fluorescent dyes)

- The template DNA pieces are replicated, incorporating normal nucleotides, but **occasionally and at random** dideoxy (DD) nucleotides are taken up.
- This stops replication on that piece of DNA
- The result is a **mix of DNA lengths**, each ending with a particular labeled DDnucleotide.
- Because the different lengths 'travel' at different rates during electrophoresis, their order can be determined.

Termination during Replication

DNA SEQUENCE 3'	G	C	A	T	T	G	G	G	A	A	C	C
PRIMER 5'	C	G	T	A								
NO OF BASES	1	2	3	4	5	6	7	8	9	10	11	12

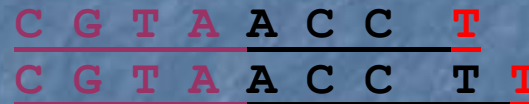
G terminated



A terminated



T terminated



C terminated



Sanger ddNTP Chain Termination Sequencing

Template 3' GCATTGGGAACC 5'
 Prime 5' CGTA 3'

