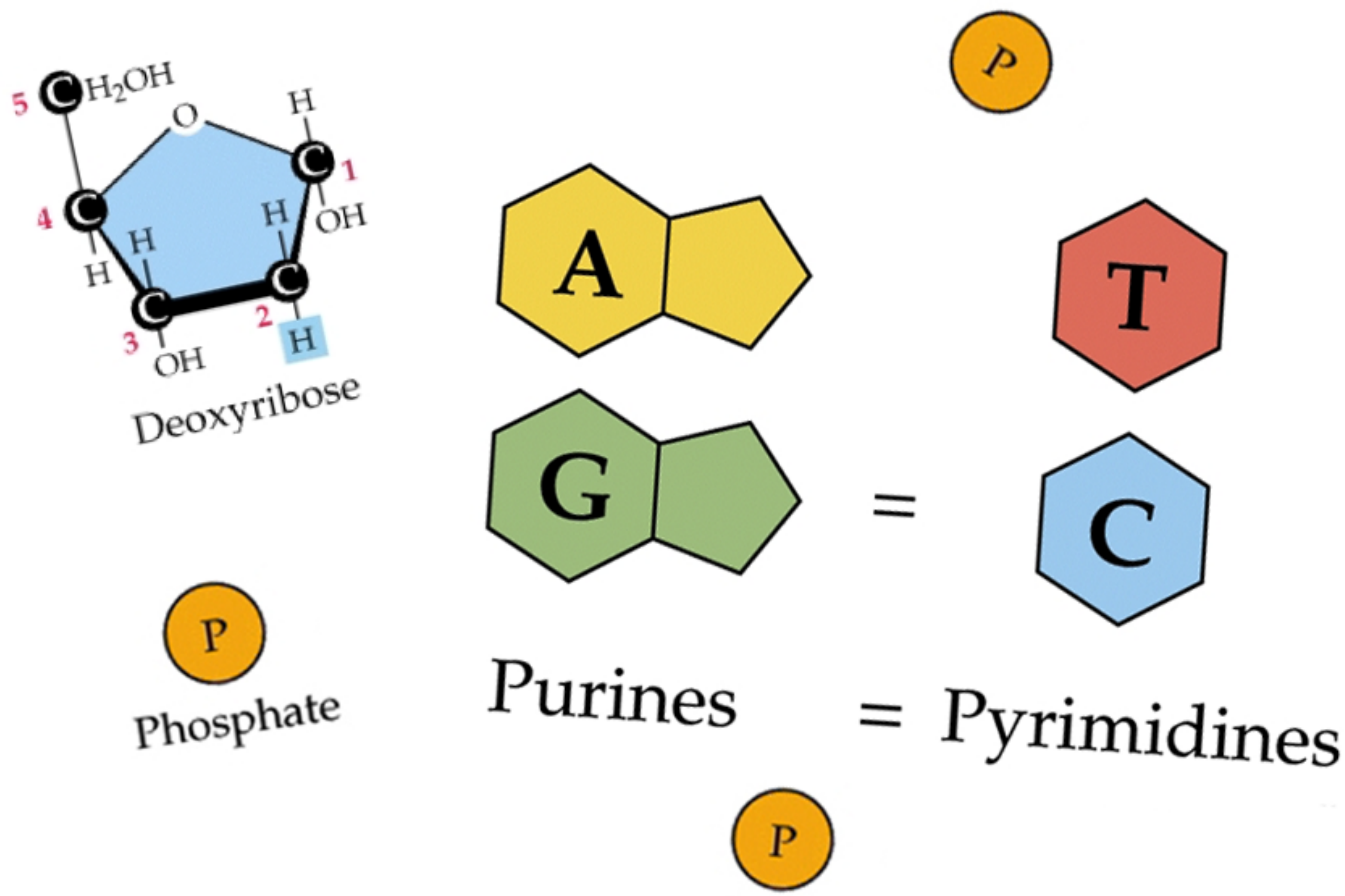
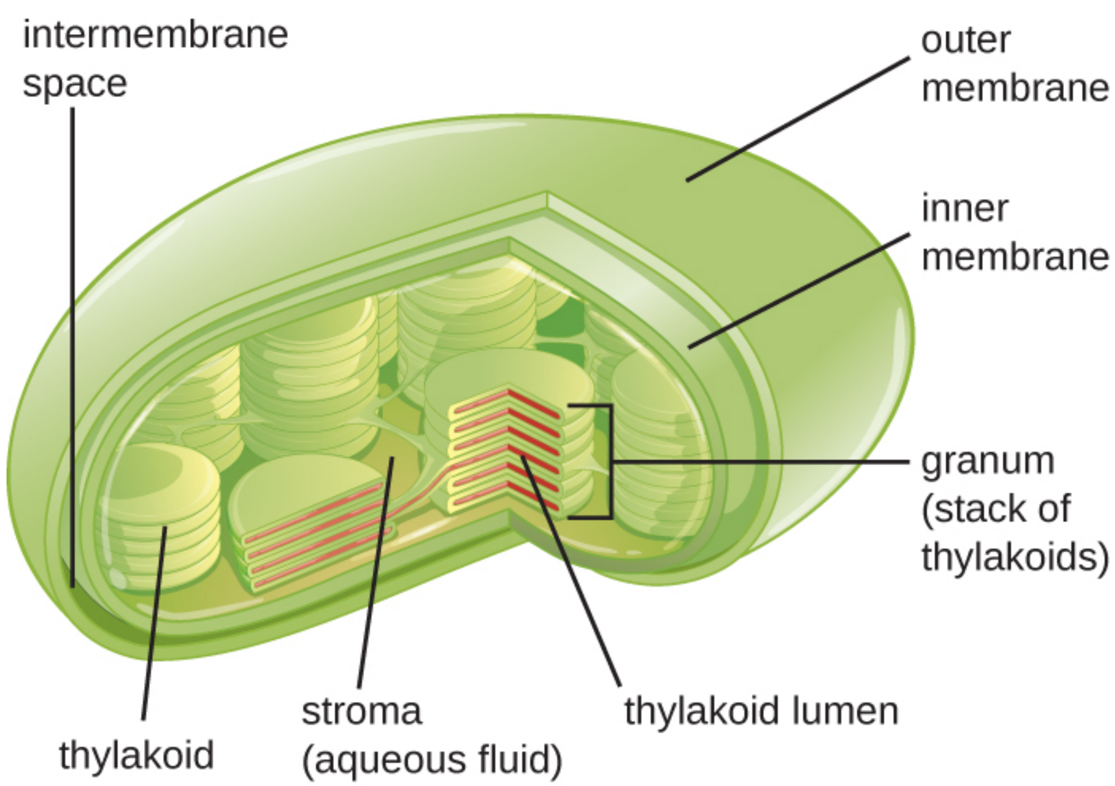
BIOL2107, Fall ’23

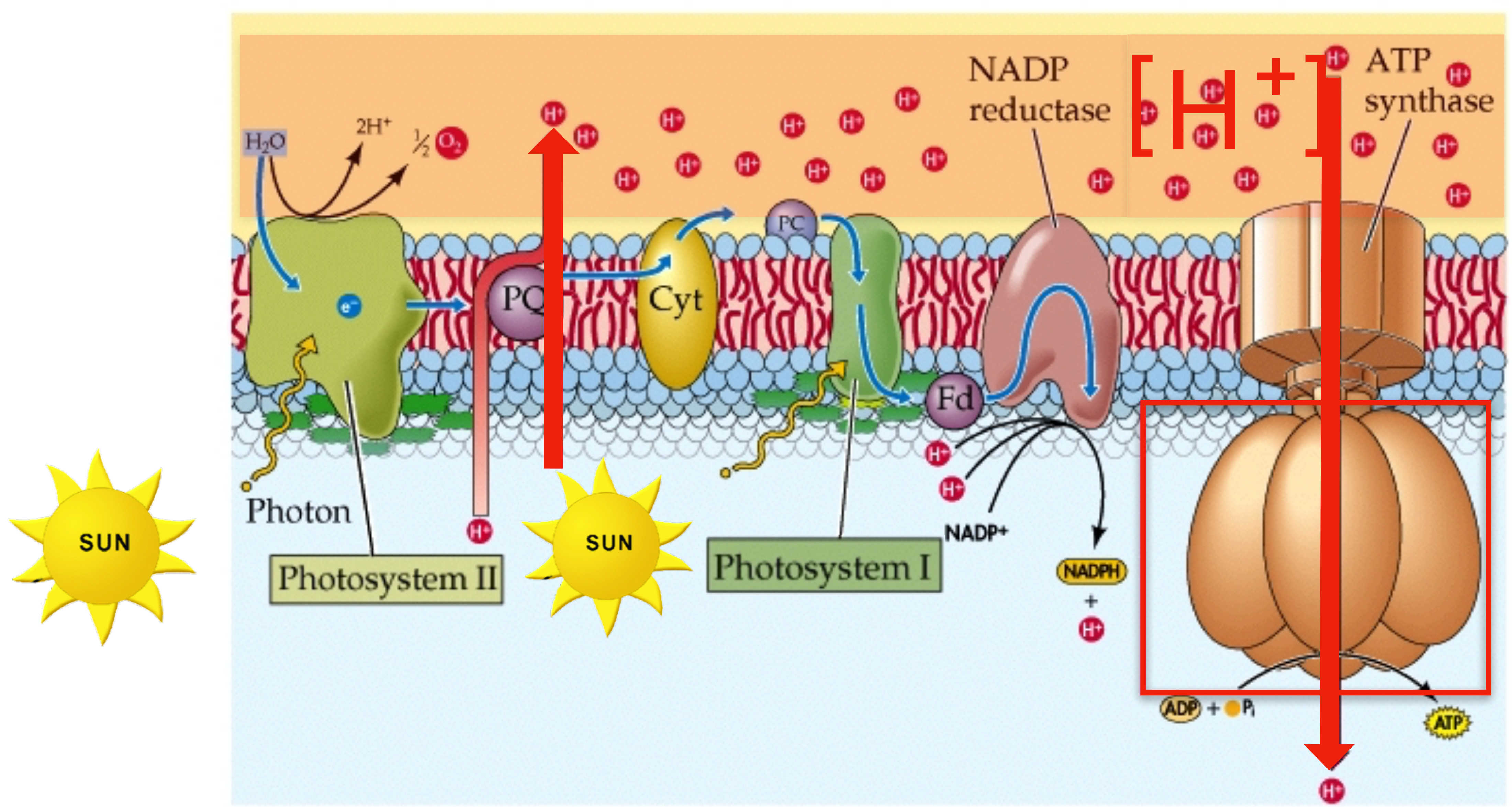
Lecture 22



Central Dogma: A little bit of history…plus

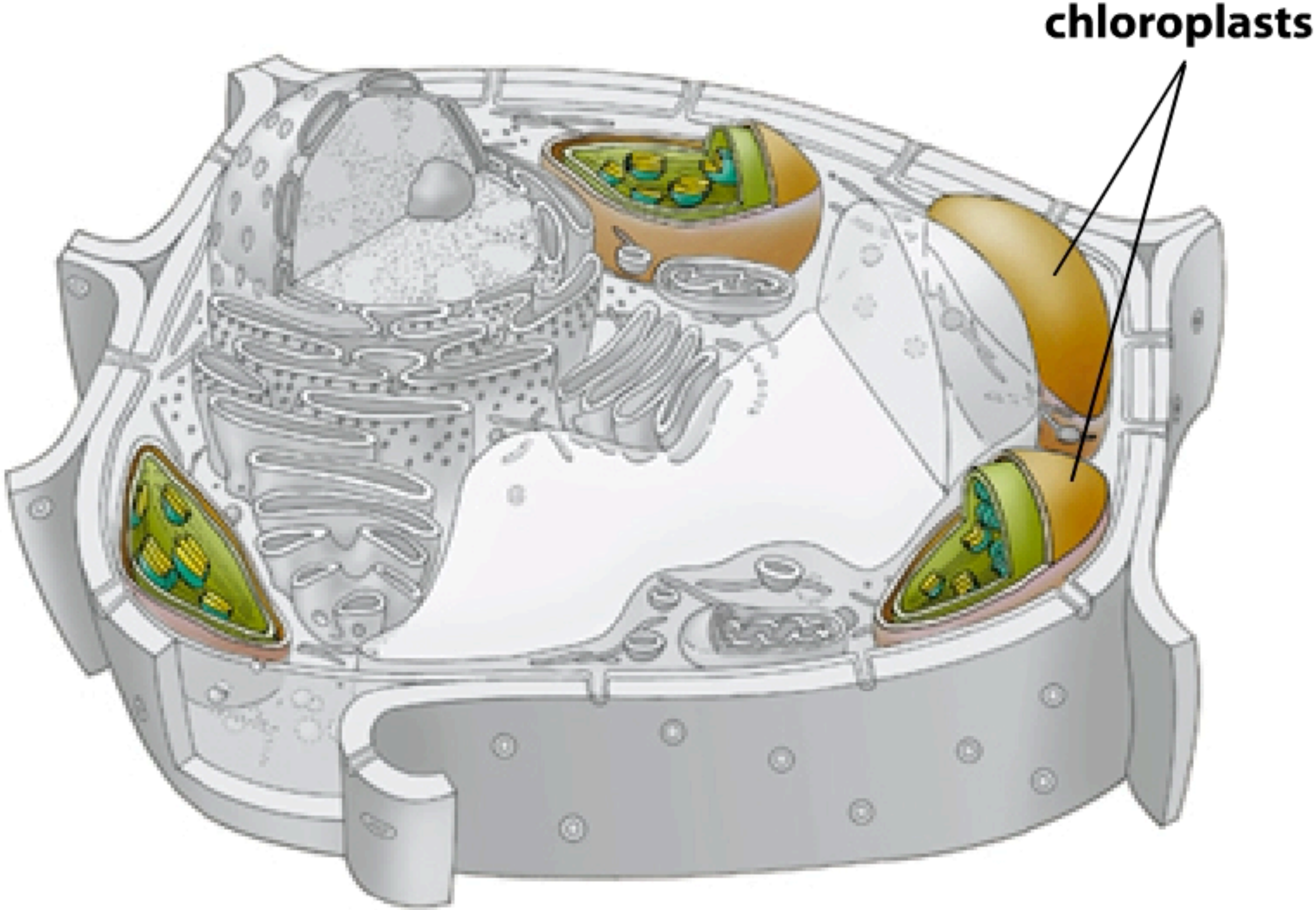


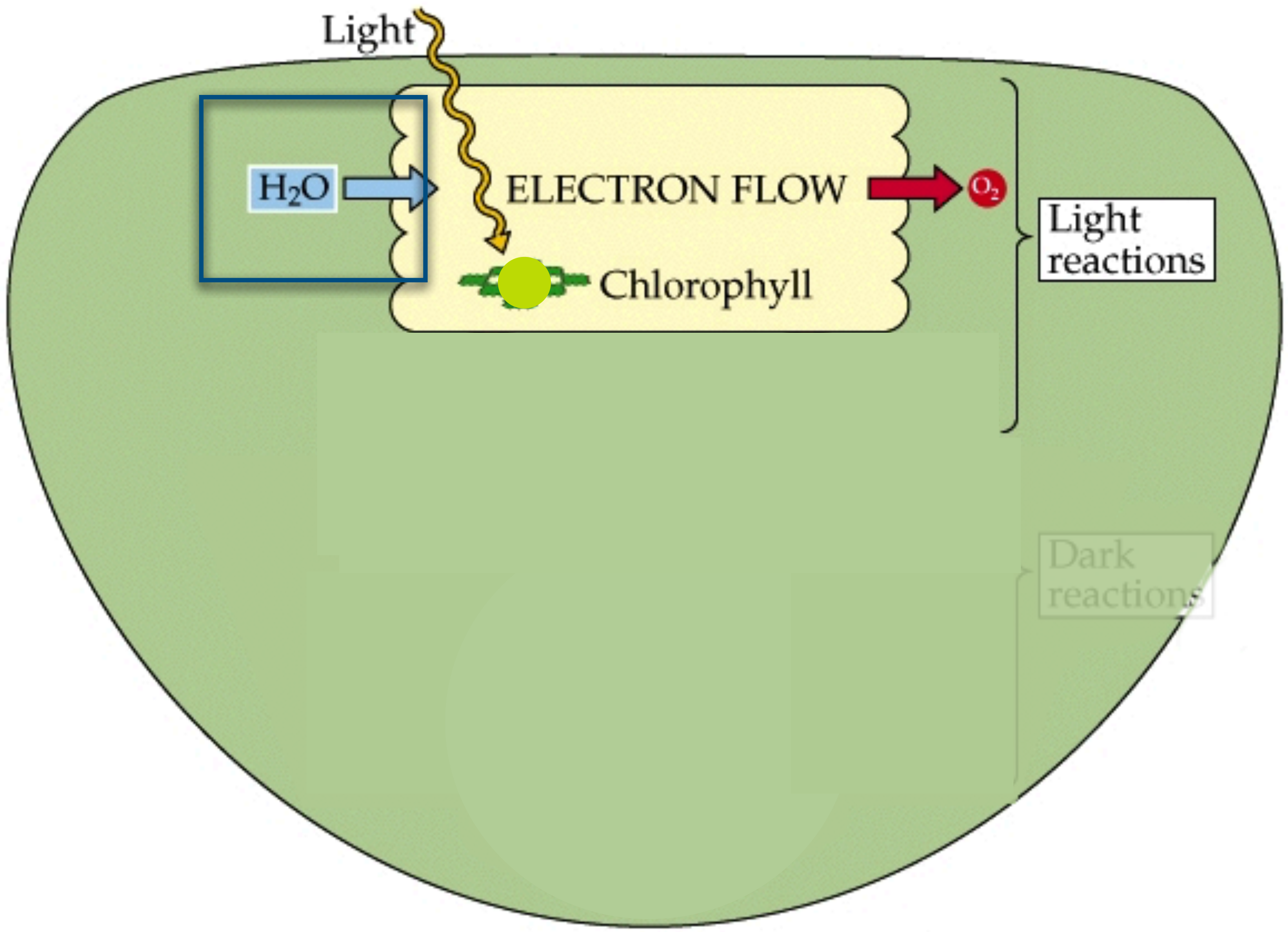
intermembrane space
outer membrane
inner membrane
granum (stack of thylakoids)
thylakoid
stroma (aqueous fluid)
thylakoid lumen

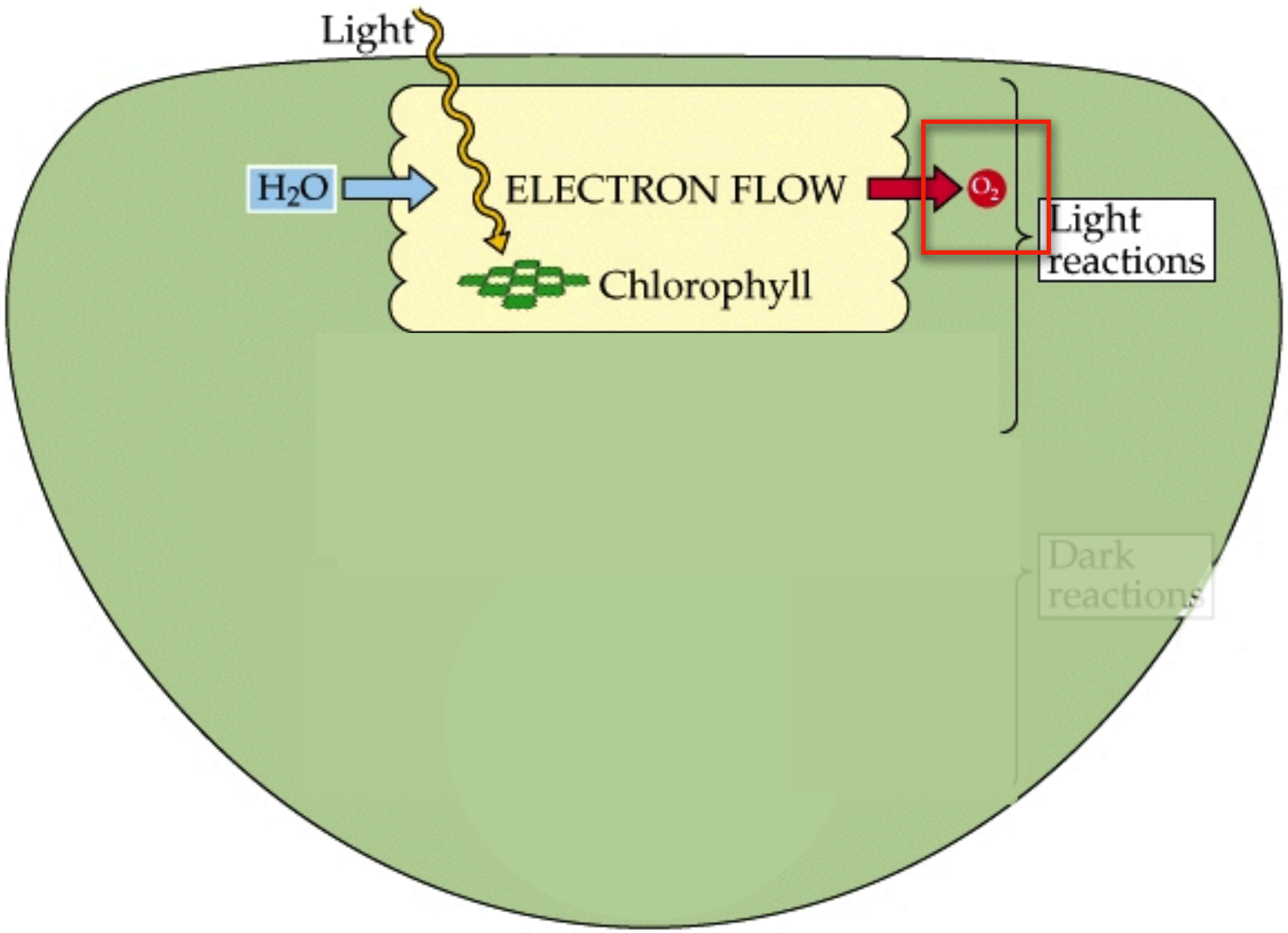


H_2O
$2H^+$
½ O_2
NADP reductase
[H^+]
ATP synthase
H^+
PQ
Cyt
PC
e^-
Fd
Photon
Photosystem II
SUN
SUN
Photosystem I
$NADP^+$
NADPH
+
ADP + P_i
ATP

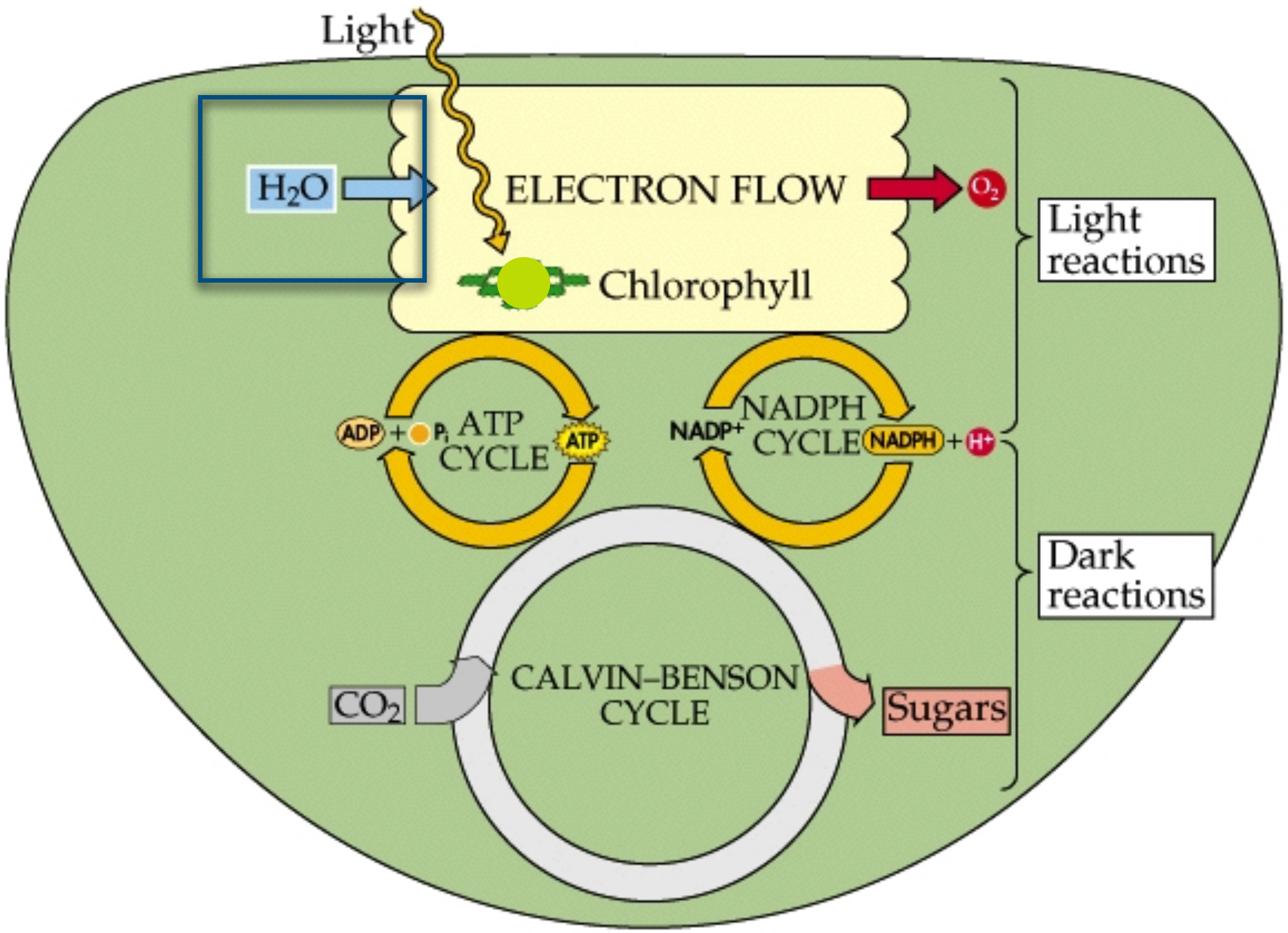
A Plant Cell



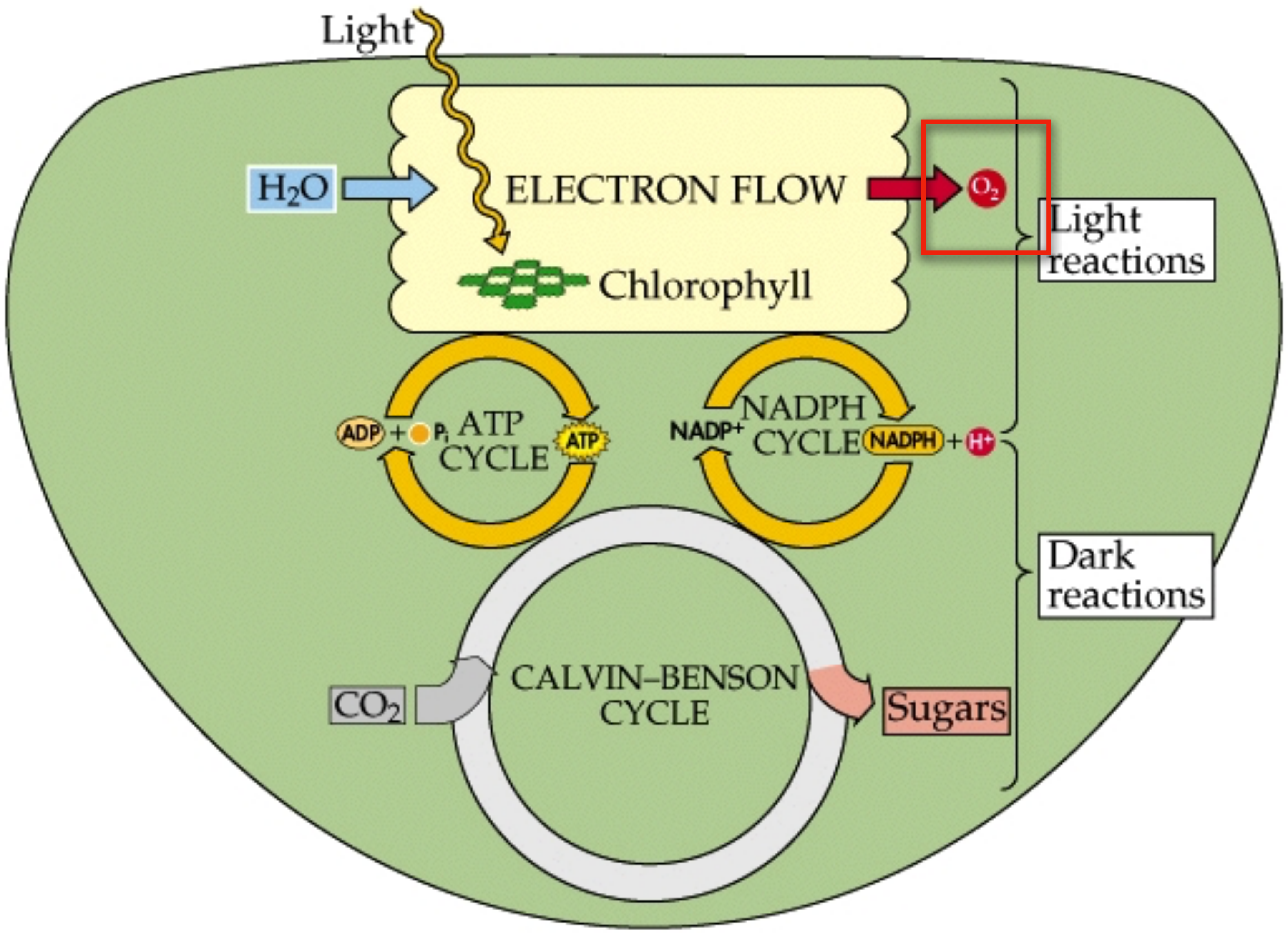

Light
H_2O
ELECTRON FLOW
O_2
Chlorophyll
Light reactions
Dark reactions



Light
H_2O
ELECTRON FLOW
O_2
Chlorophyll
Light reactions
Dark reactions



Light
H_2O
ELECTRON FLOW
O_2
Chlorophyll
Light reactions
ADP + P_i
ATP CYCLE
ATP
NADP+
NADPH CYCLE
NADPH + H+
Dark reactions
CO_2
CALVIN–BENSON CYCLE
Sugars


Light
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Light reactions
ADP + P_i
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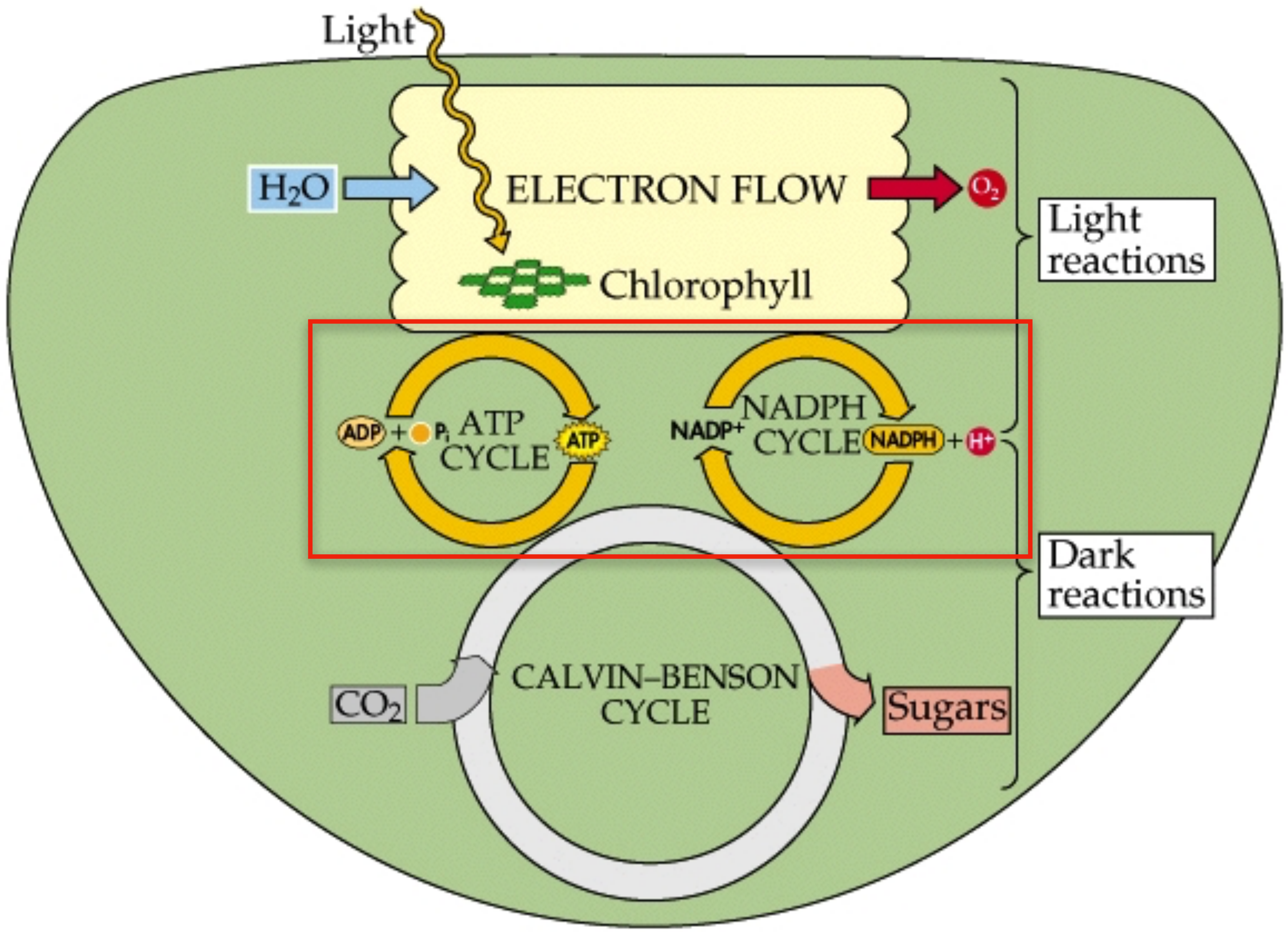
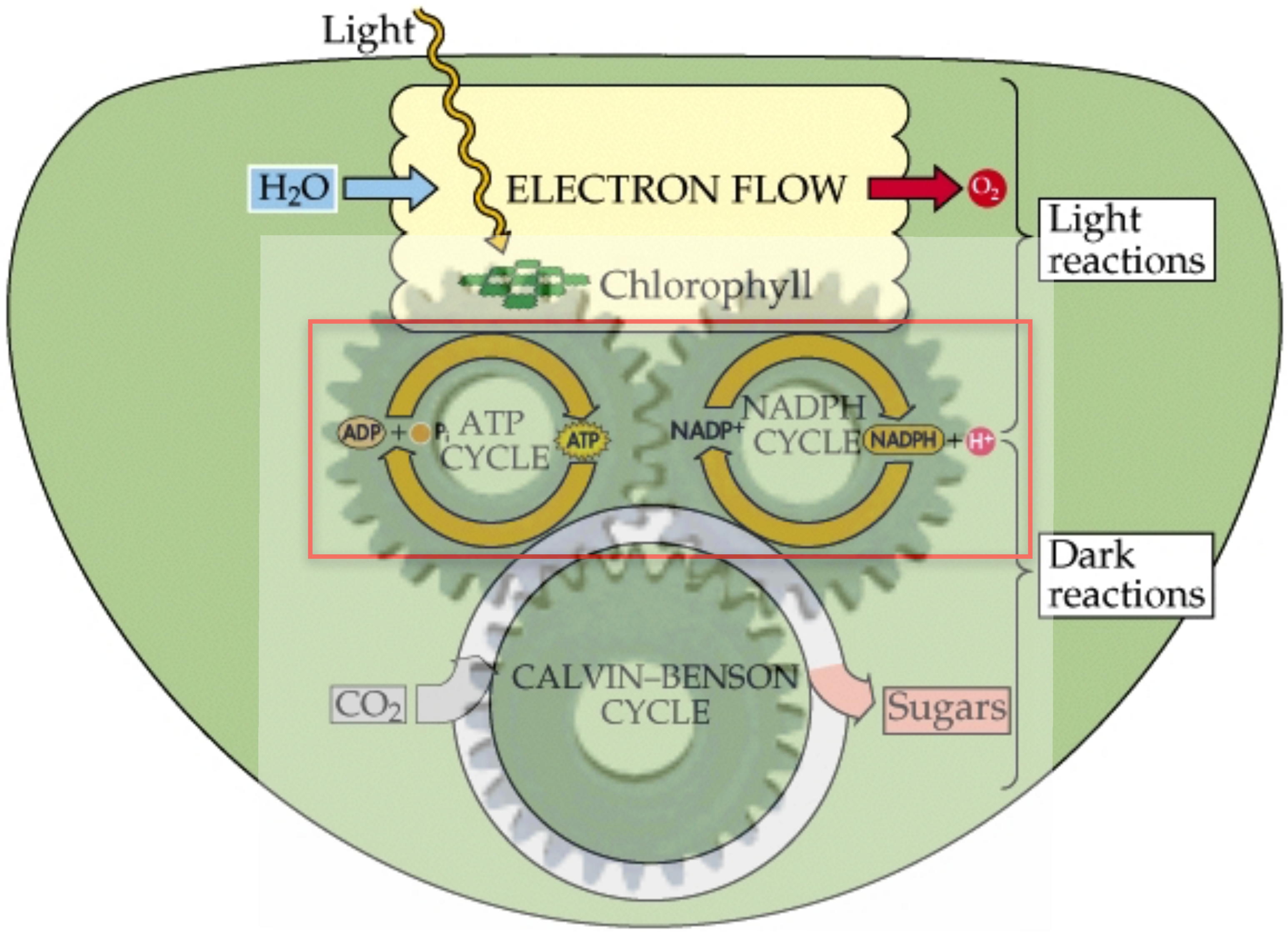
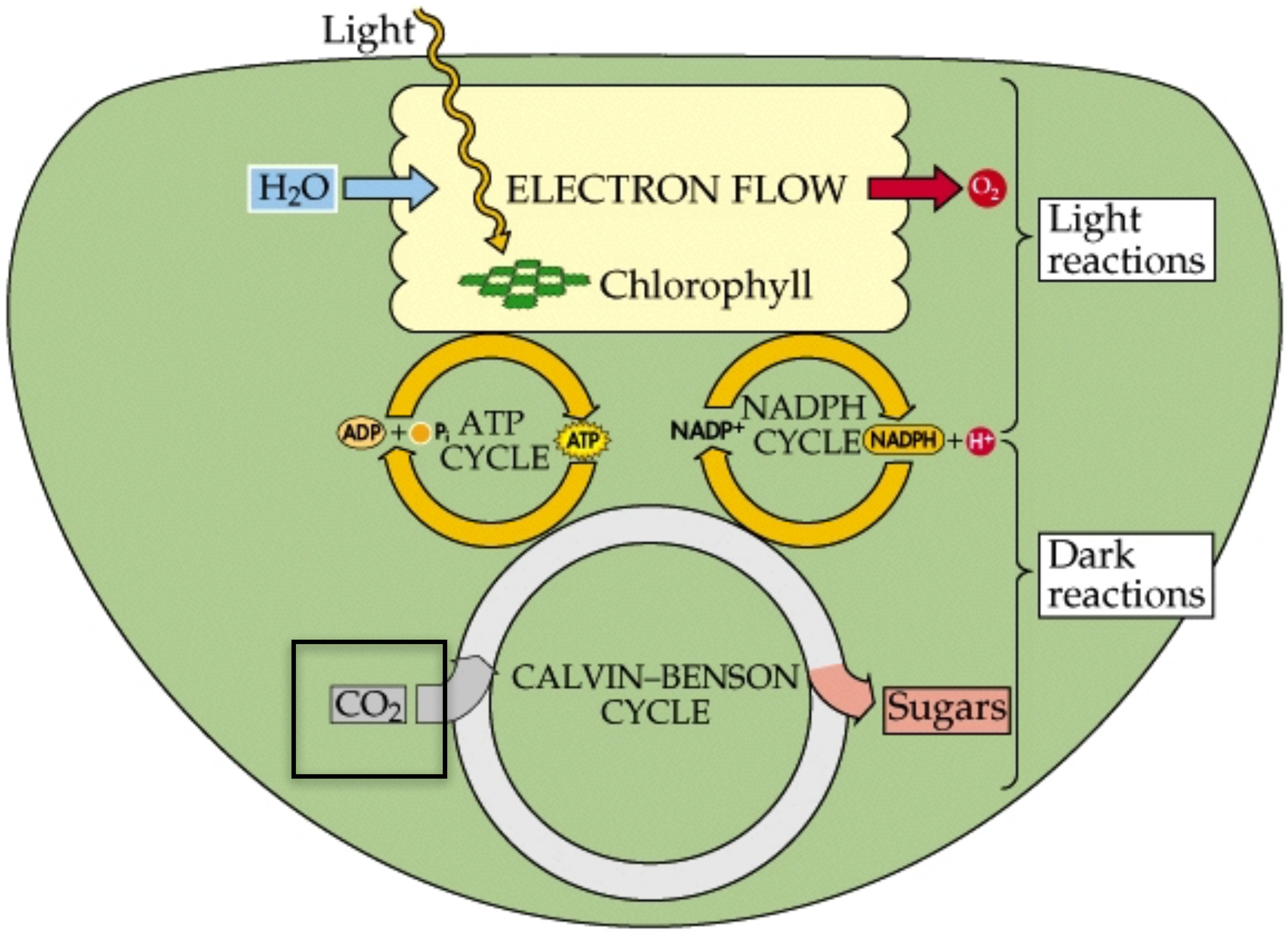


Light
H_2O
ELECTRON FLOW
O_2
Chlorophyll
Light reactions
ADP + P_i
ATP CYCLE
ATP
$NADP^+$
NADPH CYCLE
NADPH + H^+
Dark reactions
CO_2
CALVIN–BENSON CYCLE
Sugars



Light
H2O
ELECTRON FLOW
O2
Chlorophyll
Light reactions
ADP
Pi
ATP CYCLE
ATP
NADP+
NADPH CYCLE
NADPH
H+
Dark reactions
CO2
CALVIN–BENSON CYCLE
Sugars


Light
H_2O
ELECTRON FLOW
O_2
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Light reactions
ADP + P_i
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Dark reactions
CO_2
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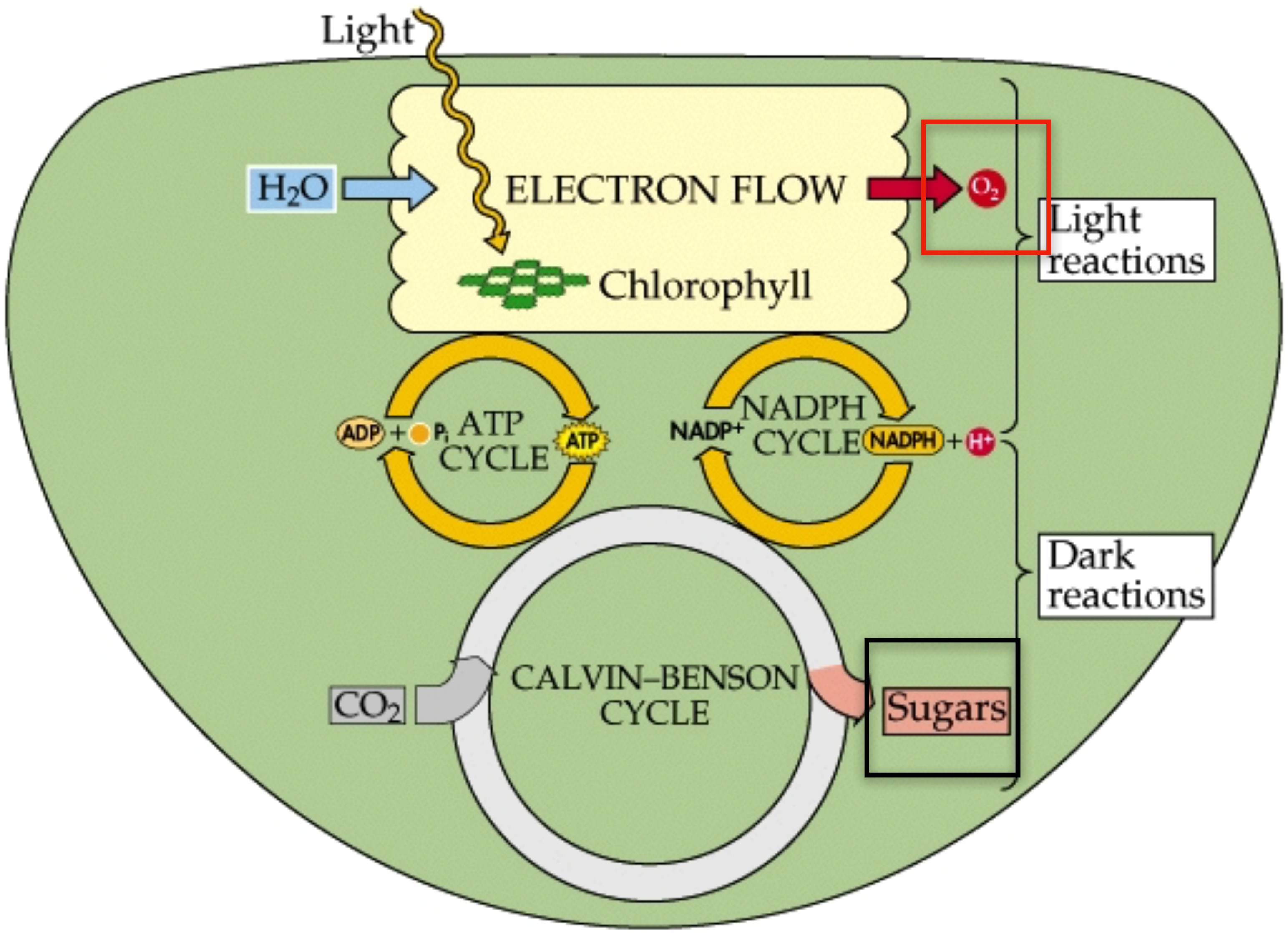
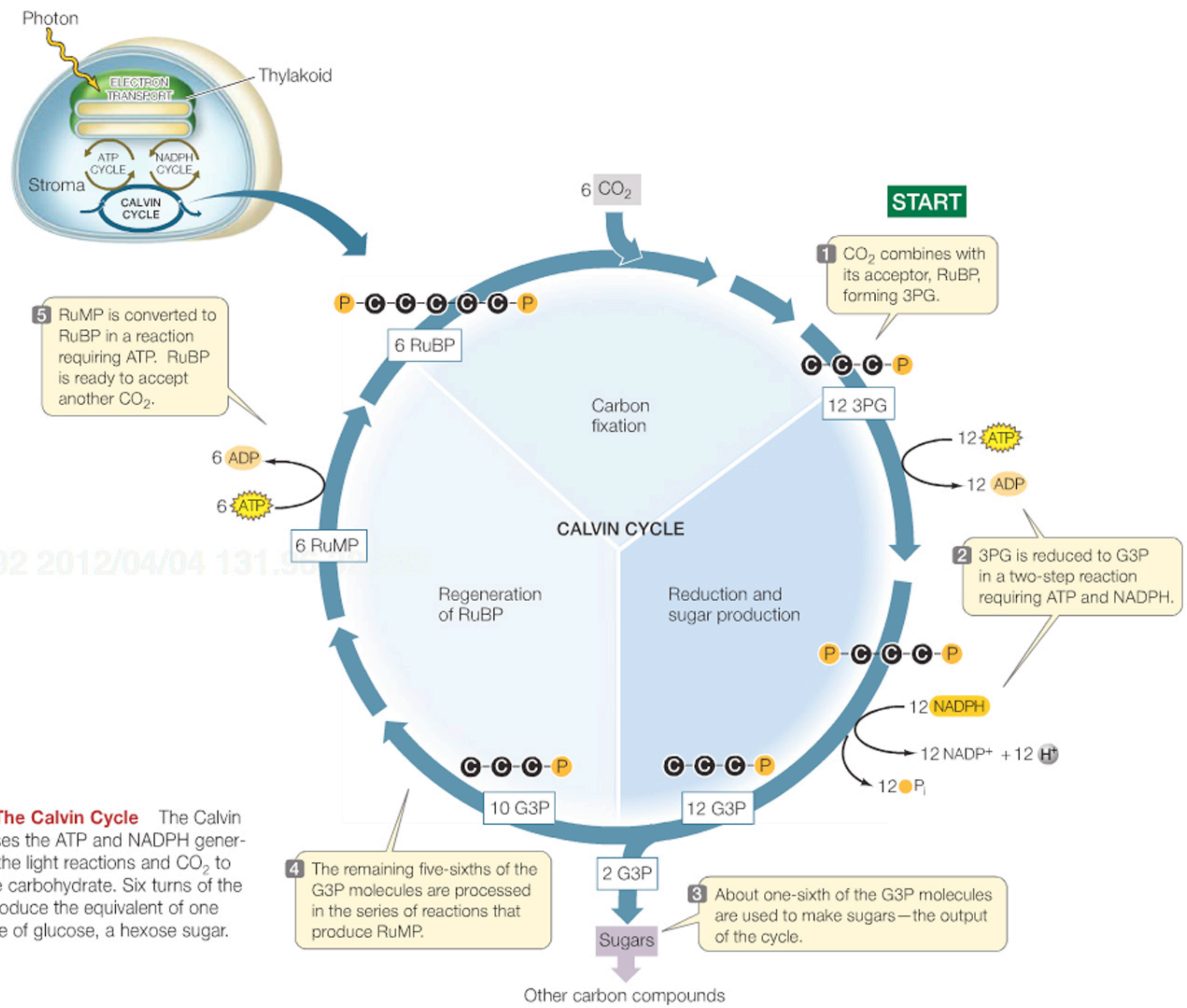
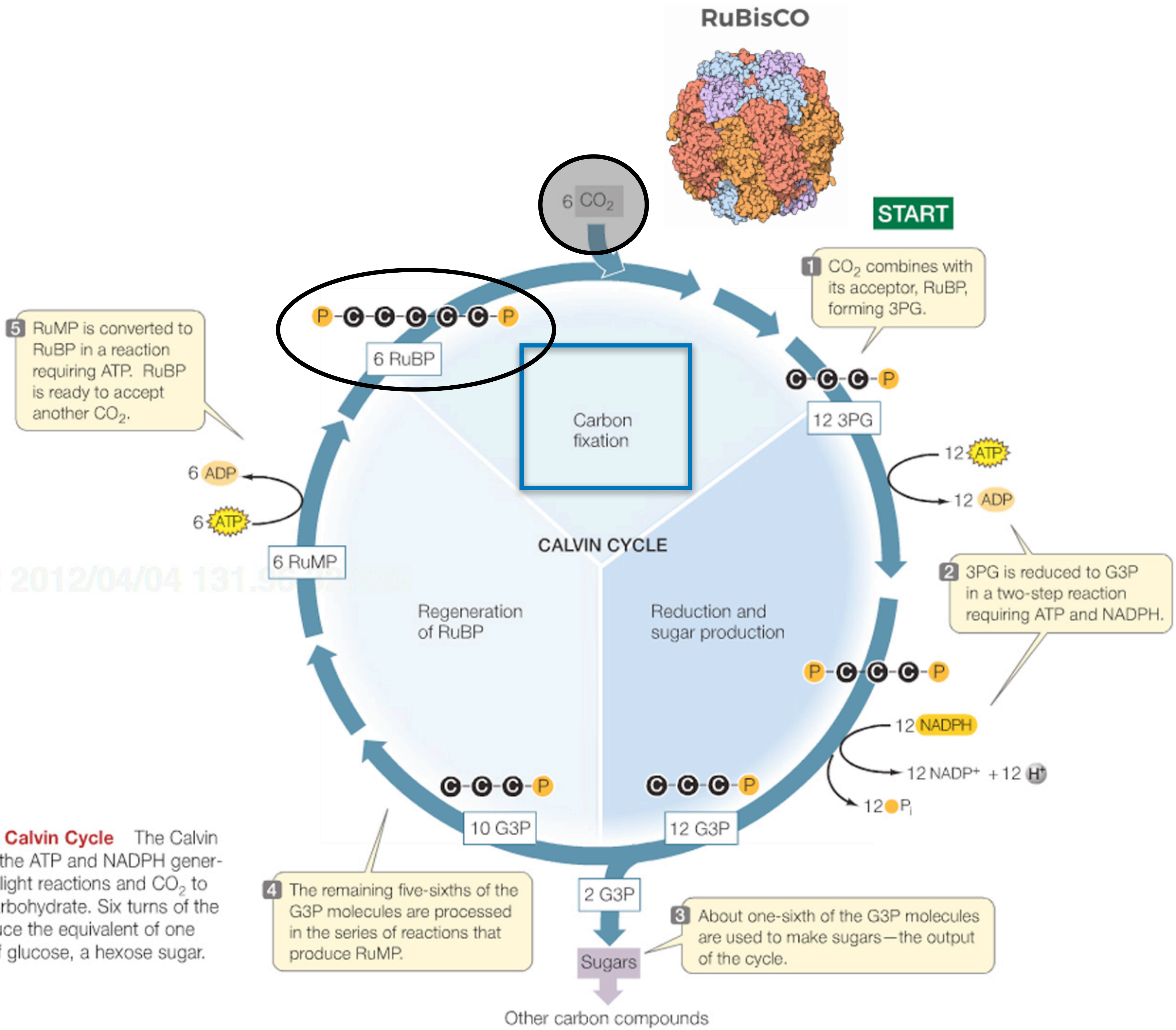


Oxygenic photosynthesis… Plants and Cyanobacteria

The **Dark Reaction....** better know as the **Calvin-Benson cycle,** which is composed of three processes to reduce CO_2 to carbohydrate (the last part of the photosynthetic equation referenced earlier).



10.15 The Calvin Cycle The Calvin cycle uses the ATP and NADPH generated in the light reactions and CO_2 to produce carbohydrate. Six turns of the cycle produce the equivalent of one molecule of glucose, a hexose sugar.



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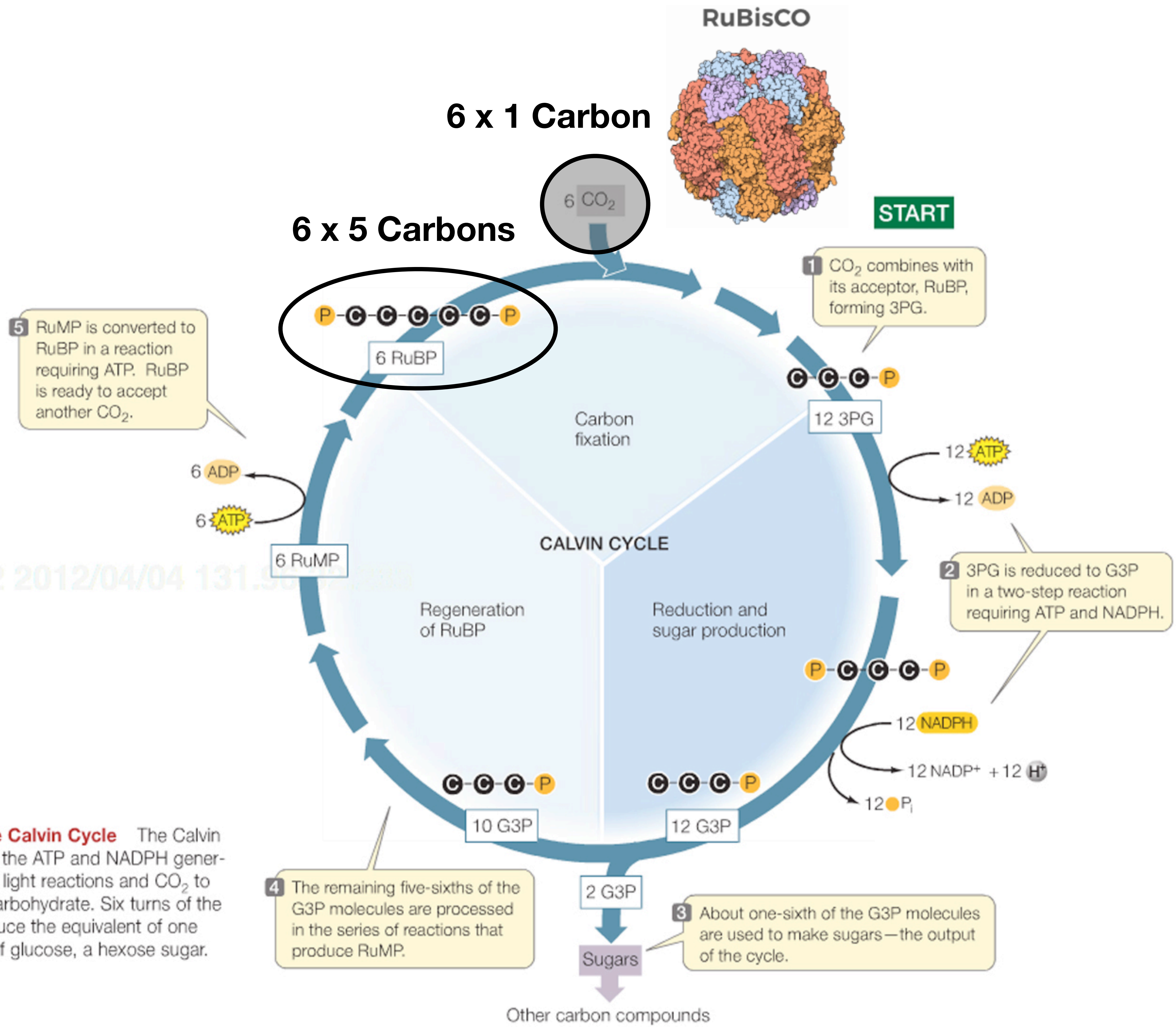

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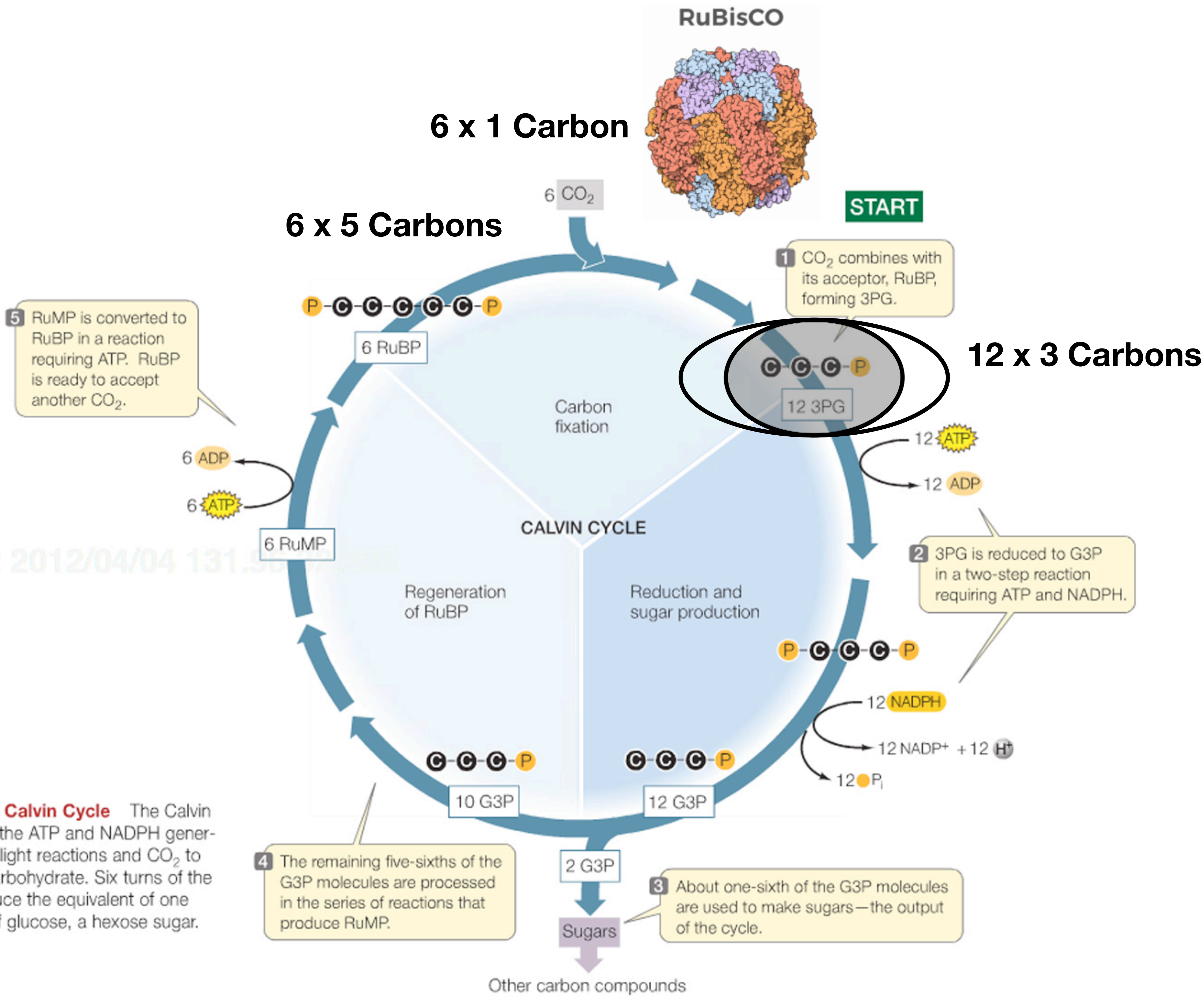

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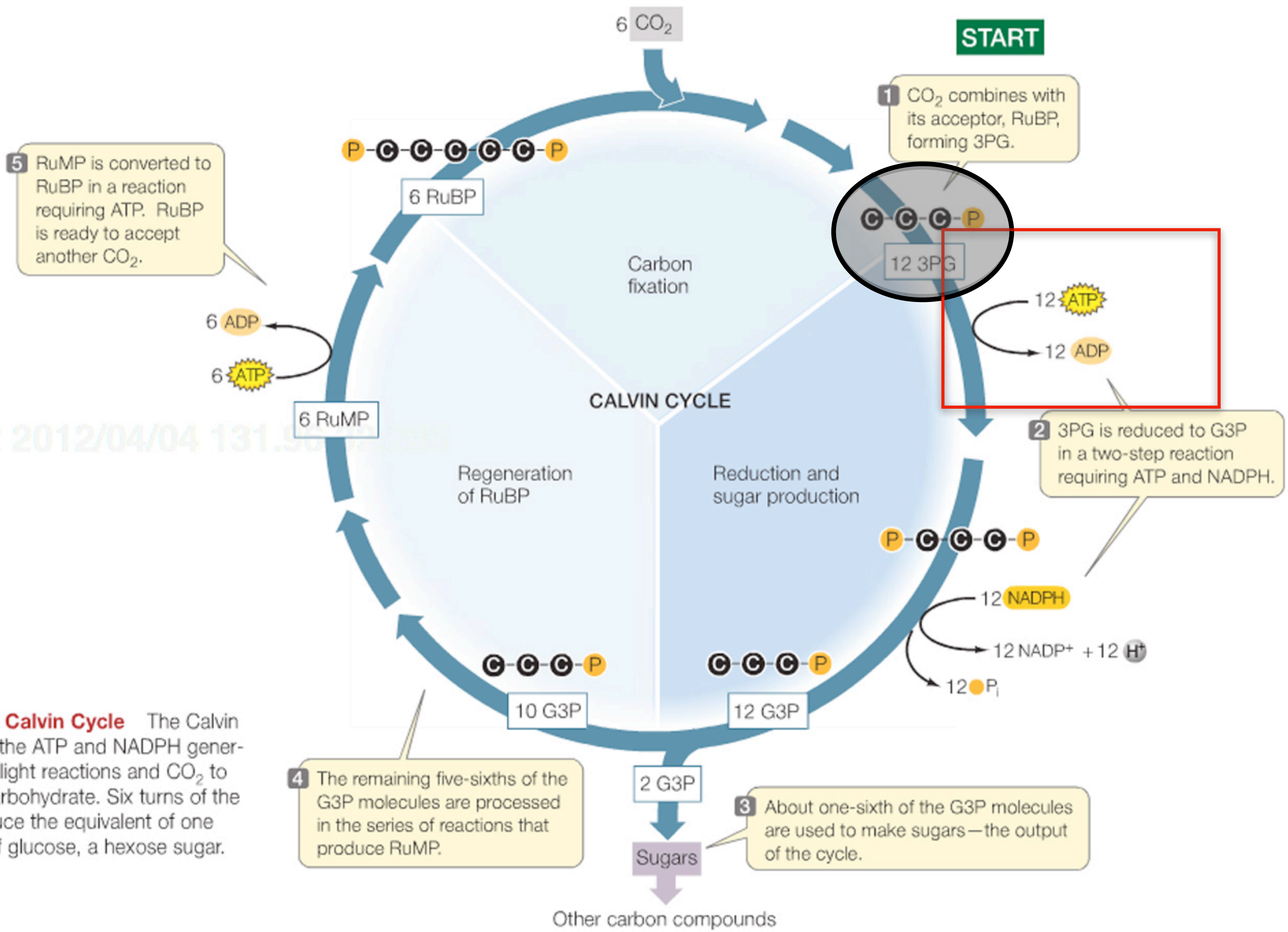

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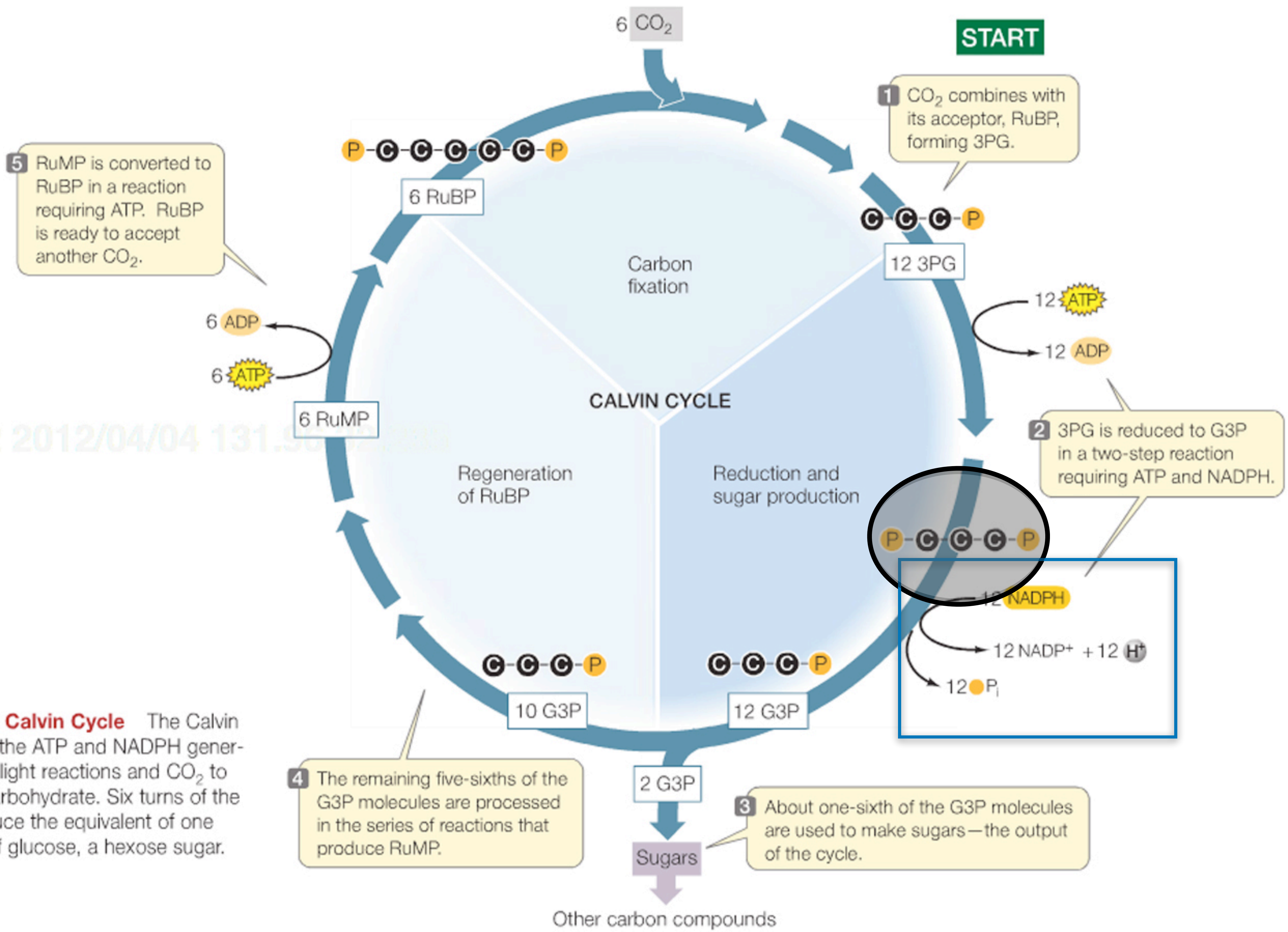

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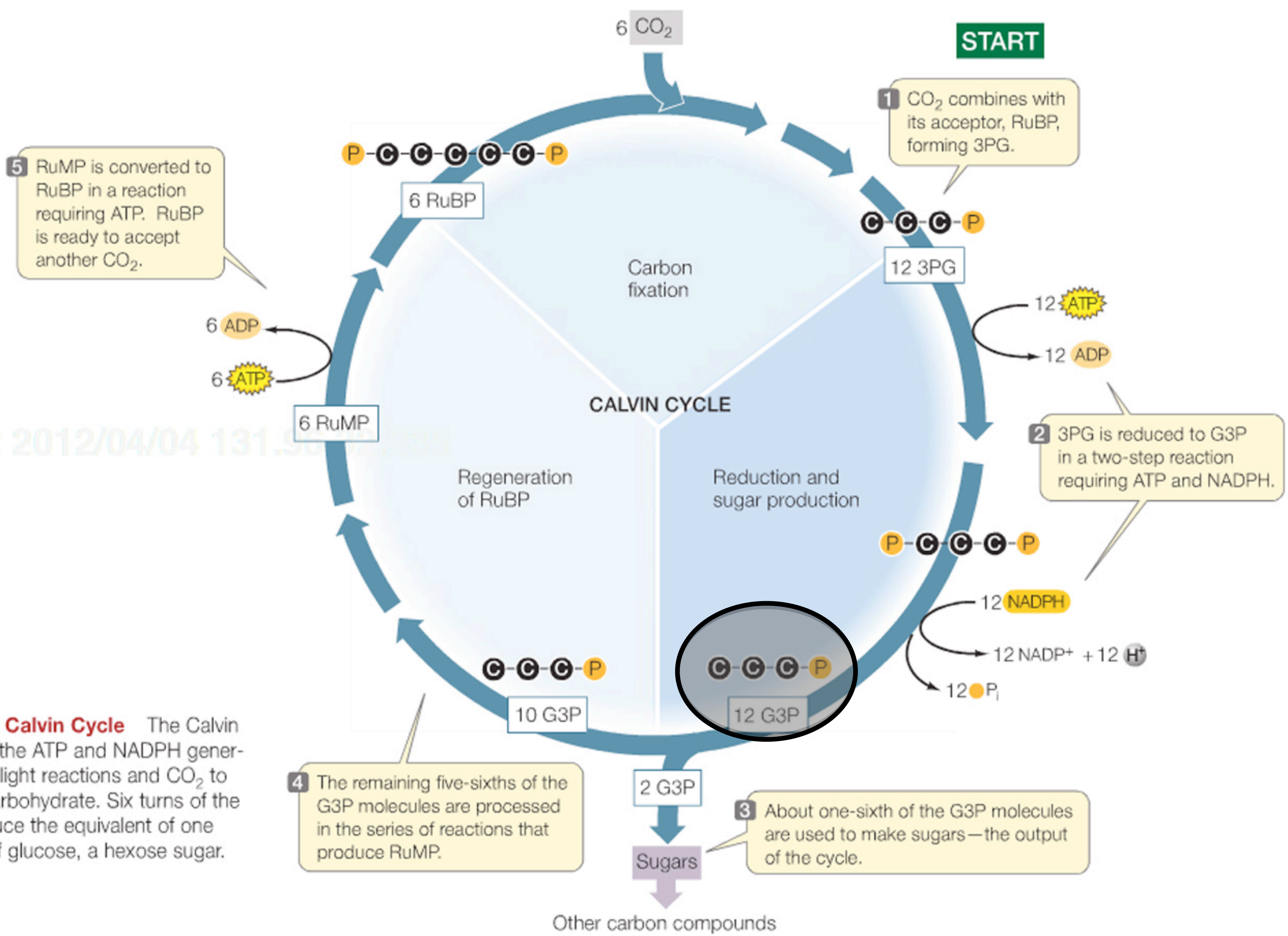

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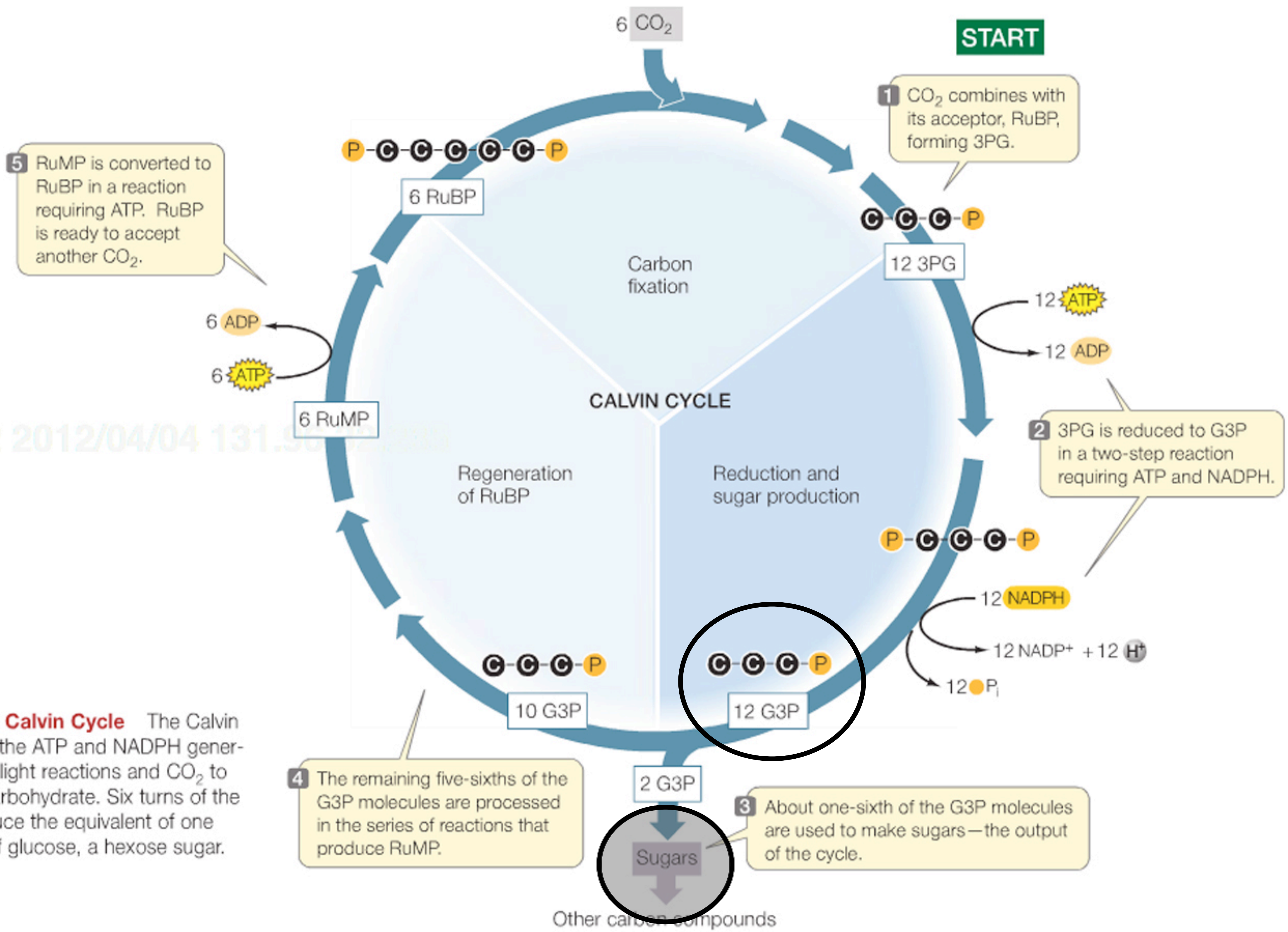

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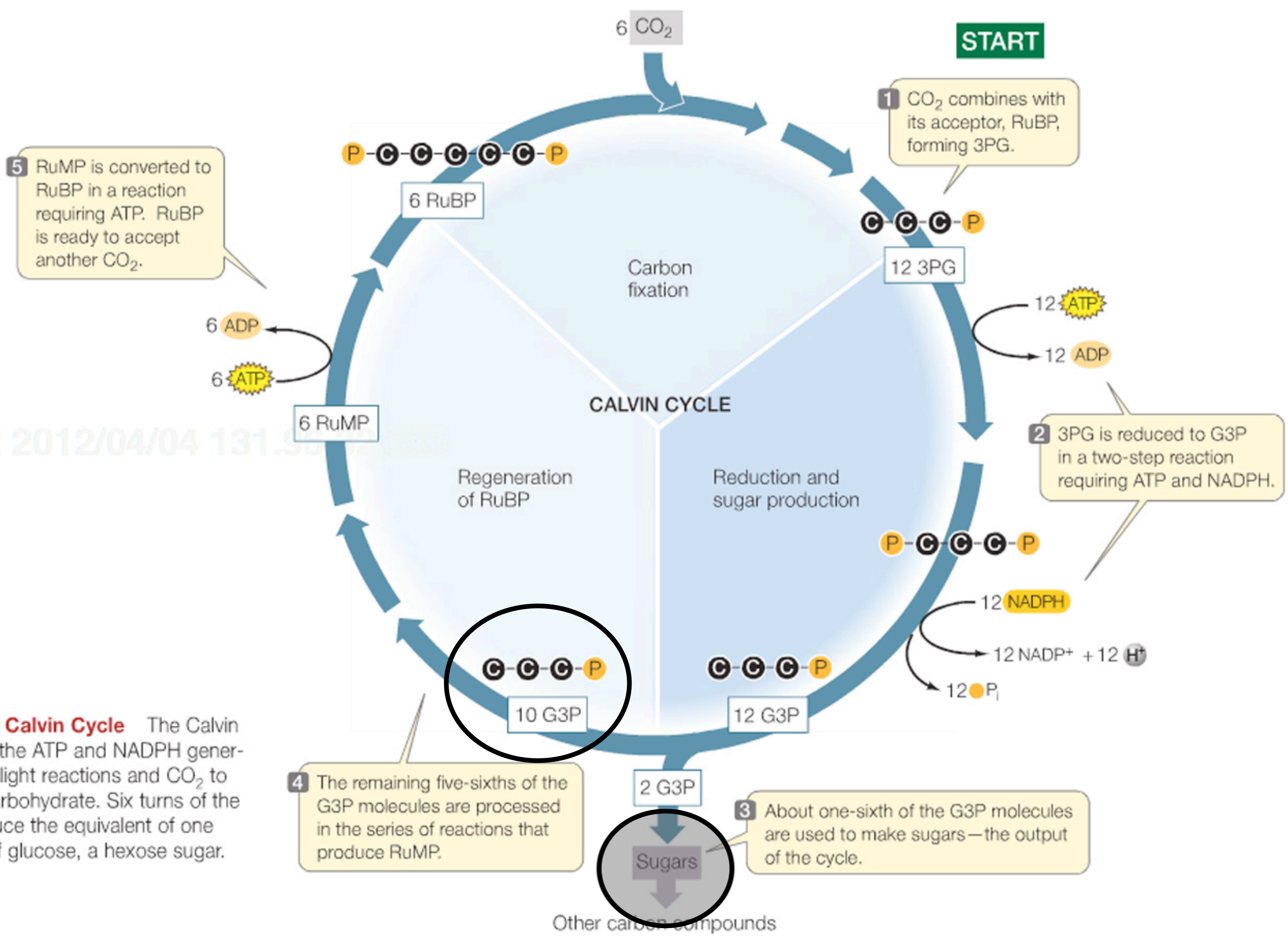

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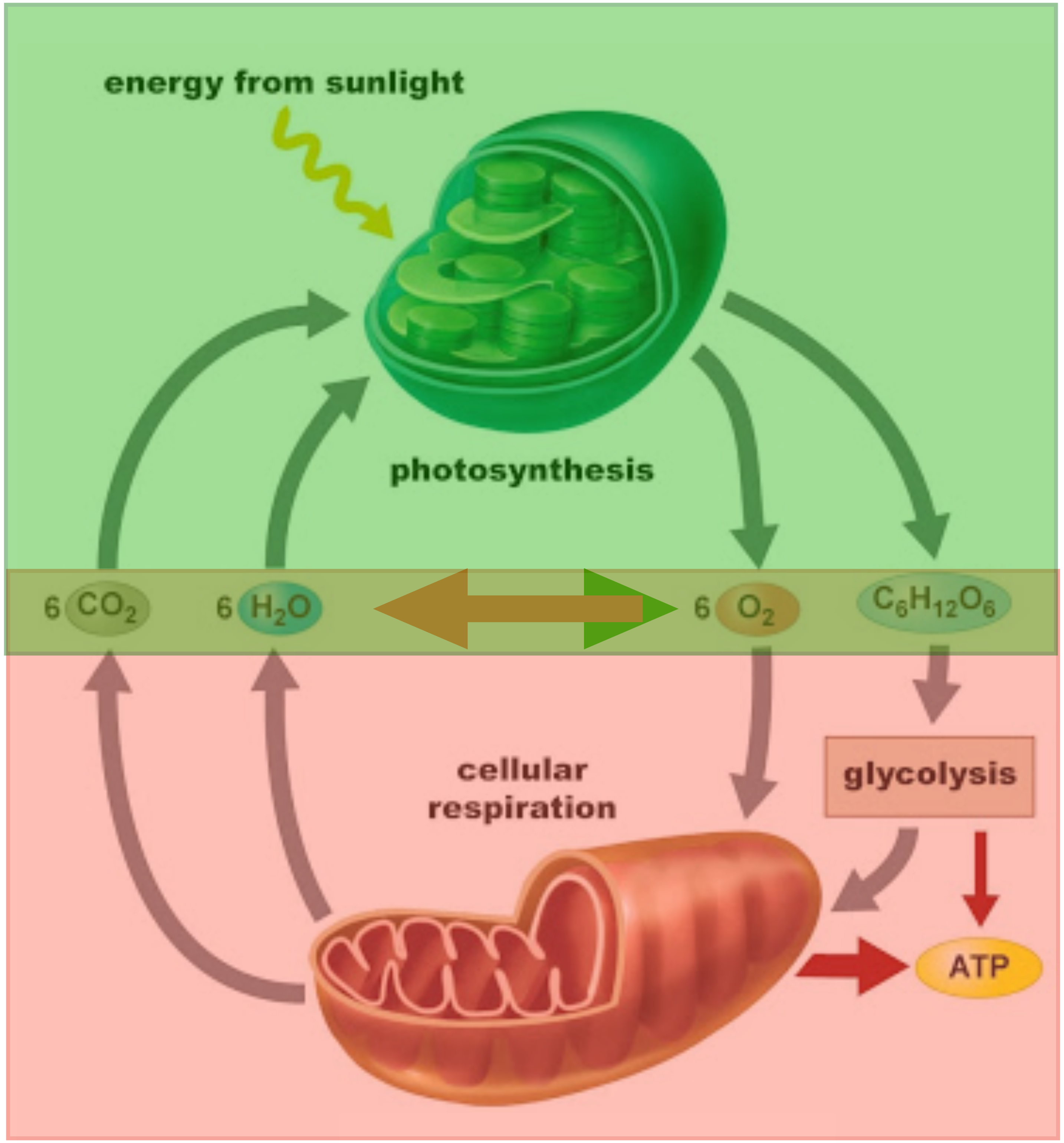
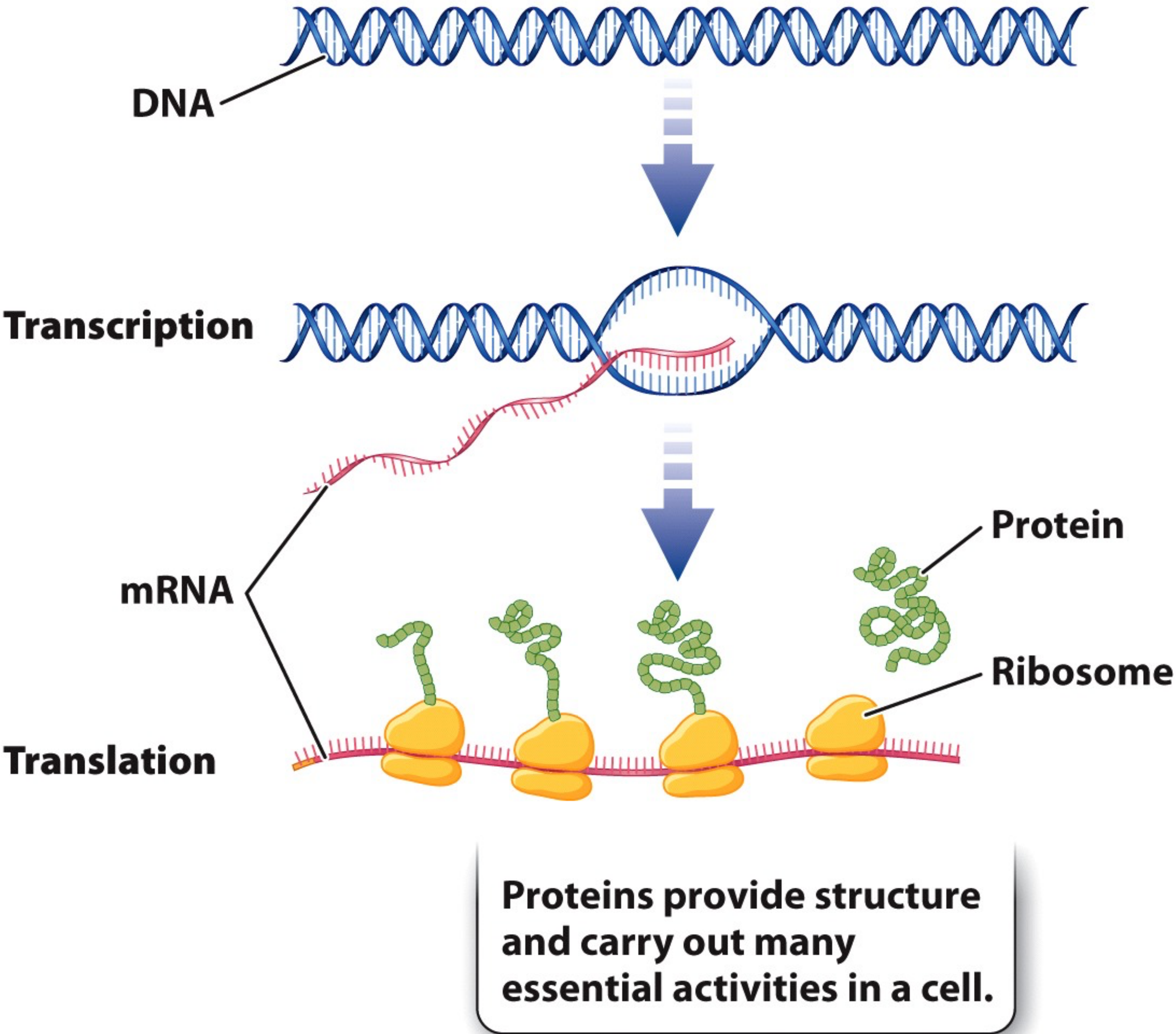
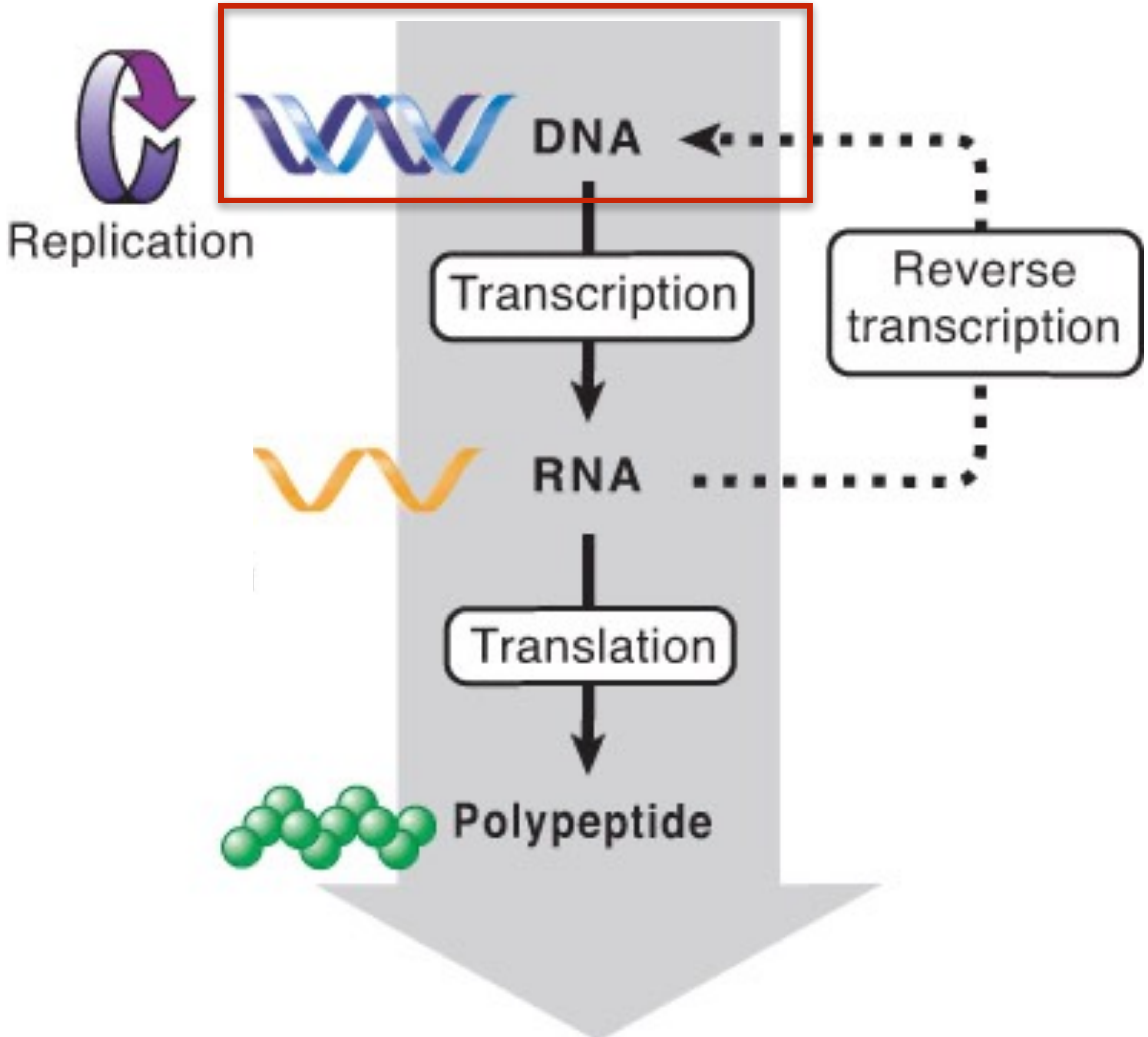
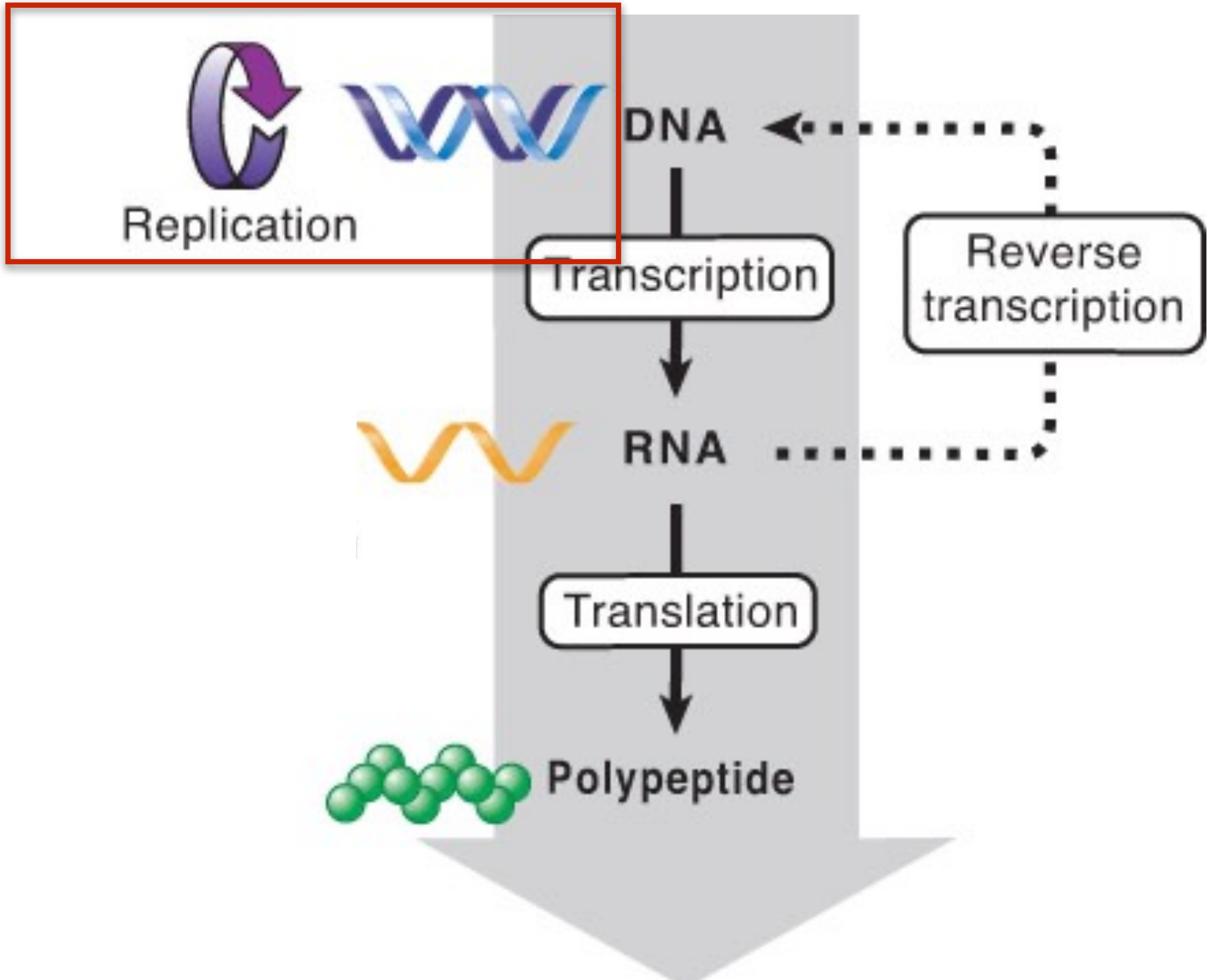


Plants do BOTH


DNA
Transcription
mRNA
Translation
Protein
Ribosome
Proteins provide structure and carry out many essential activities in a cell.



Information in nucleic acid can be perpetuated or transferred, but the transfer of information into a polypeptide is irreversible.



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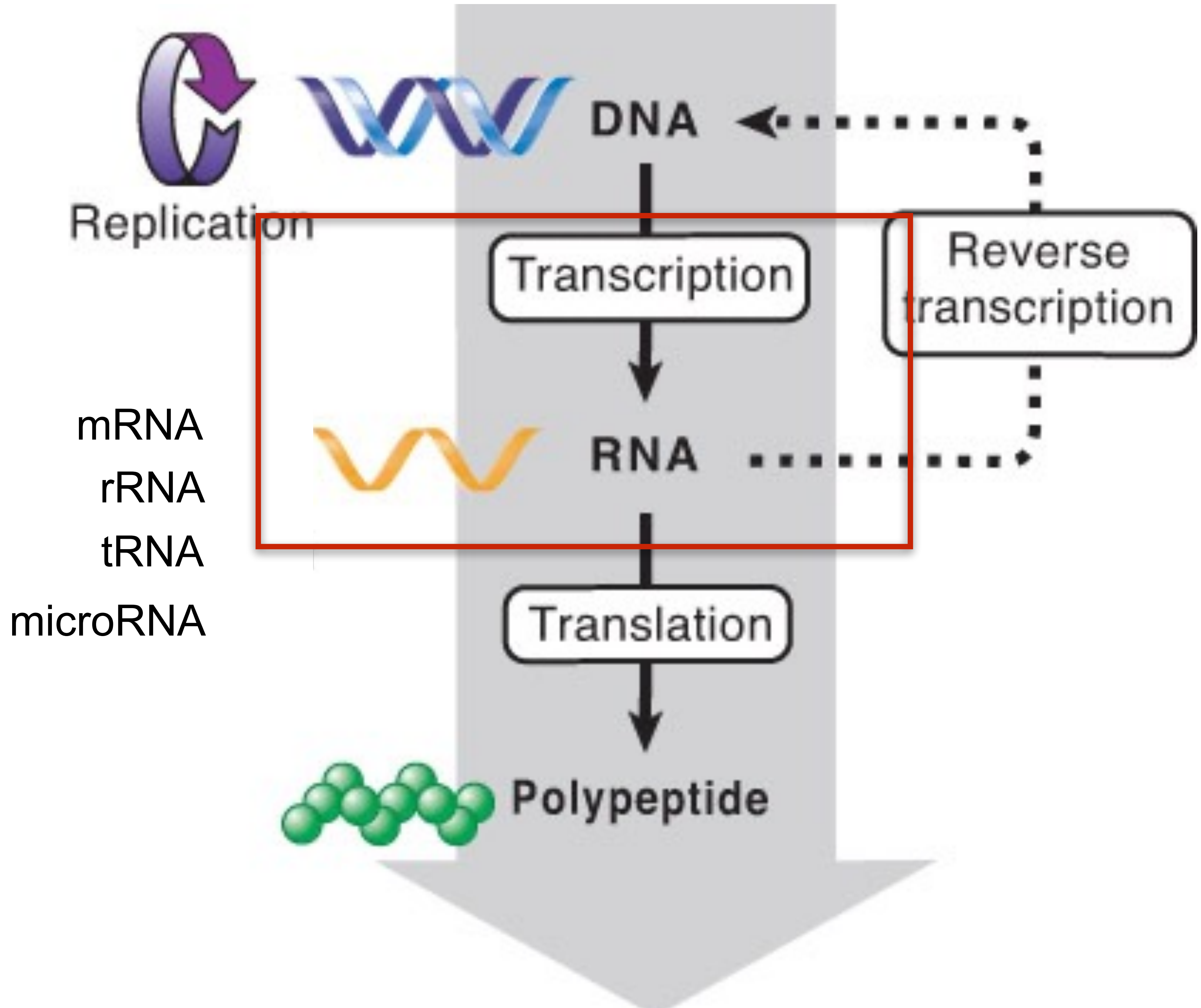

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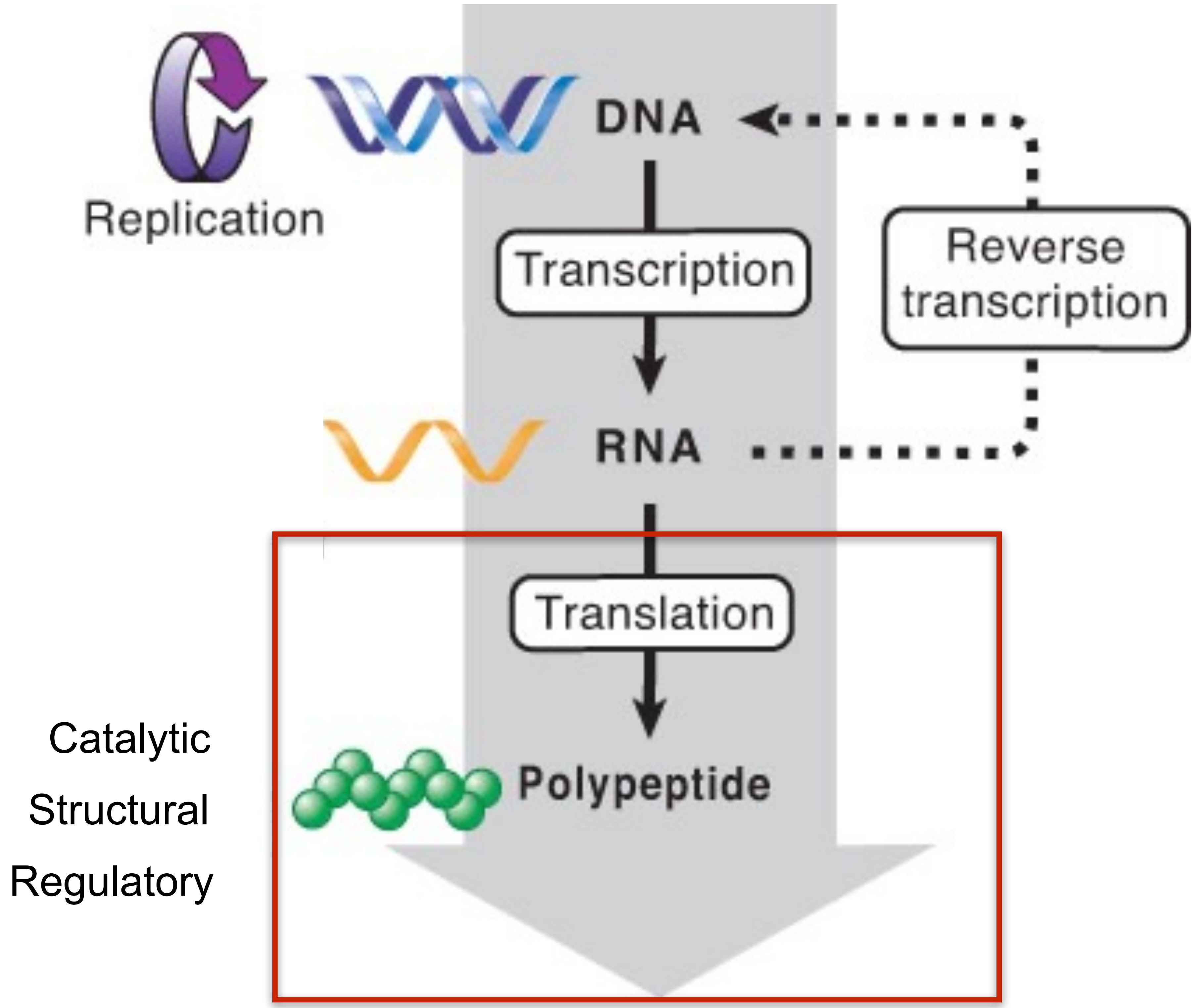

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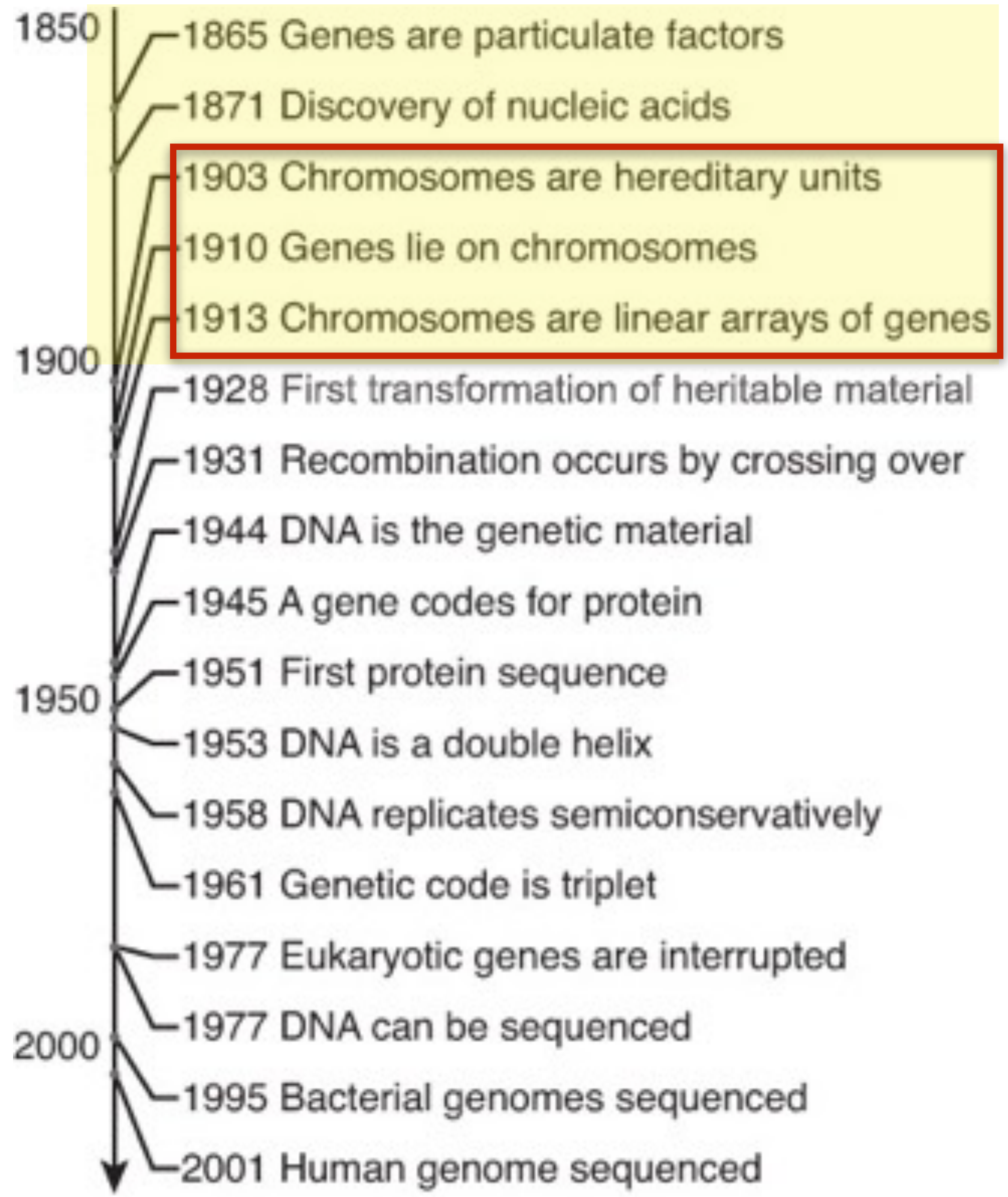
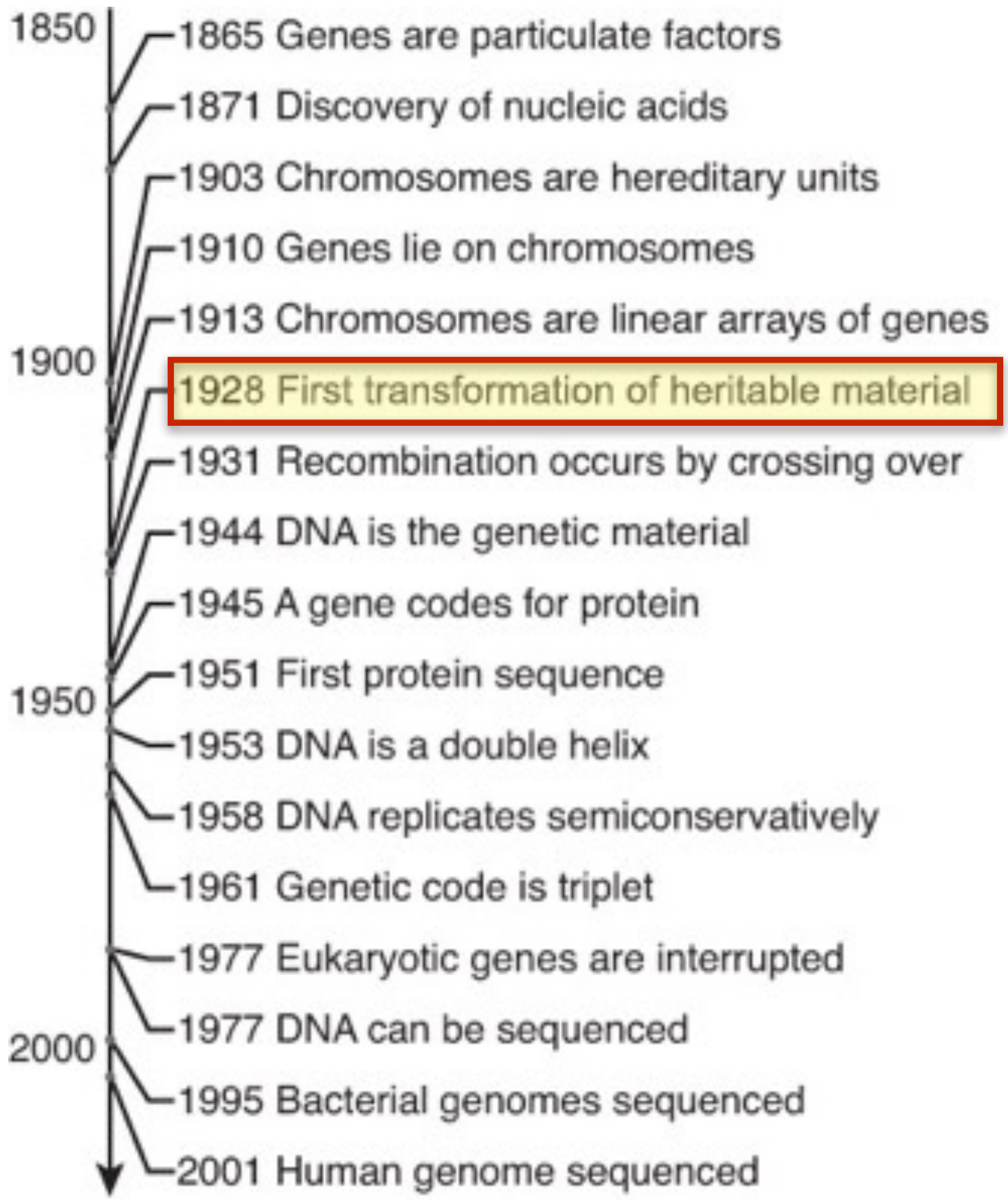


A brief history of genetics.



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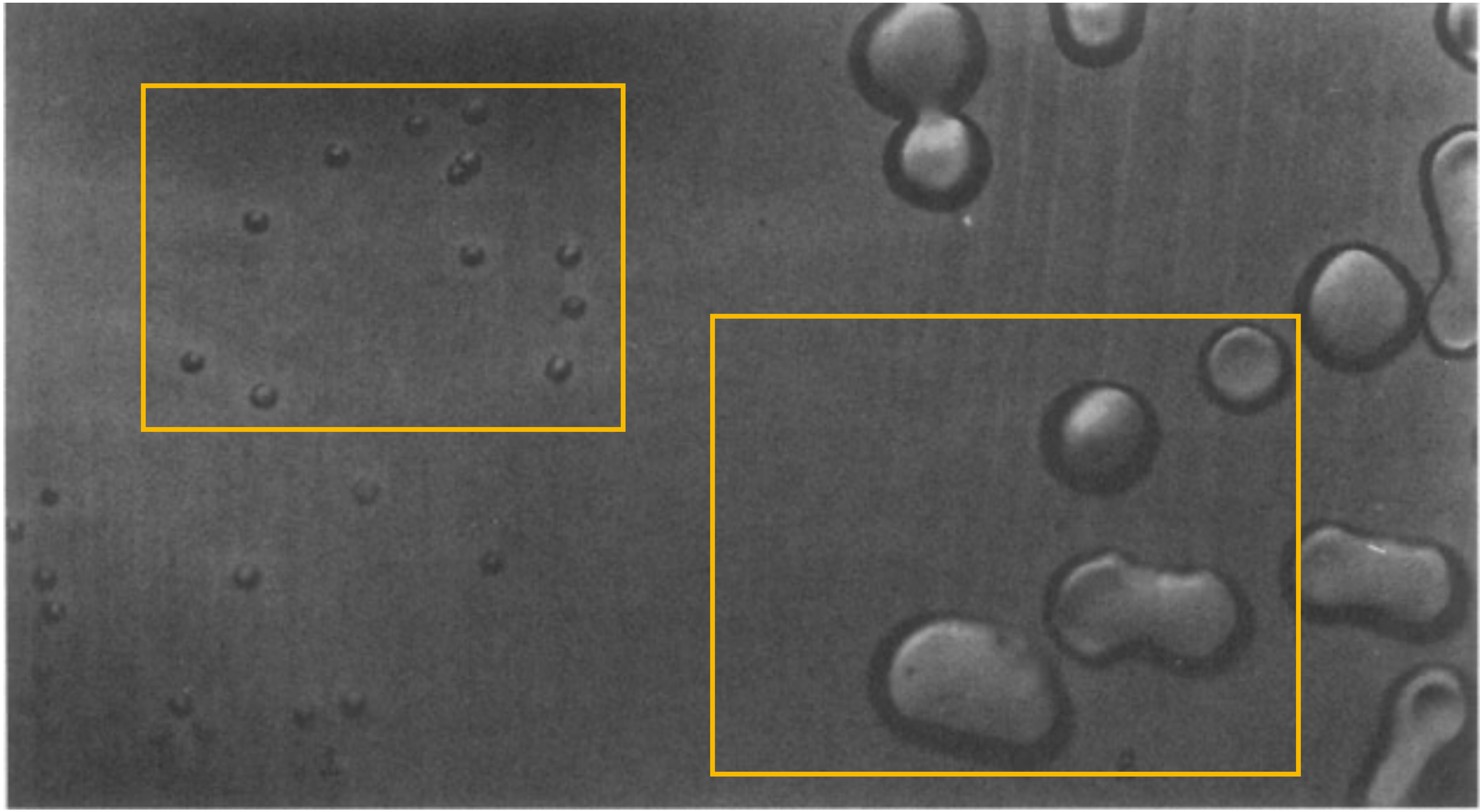
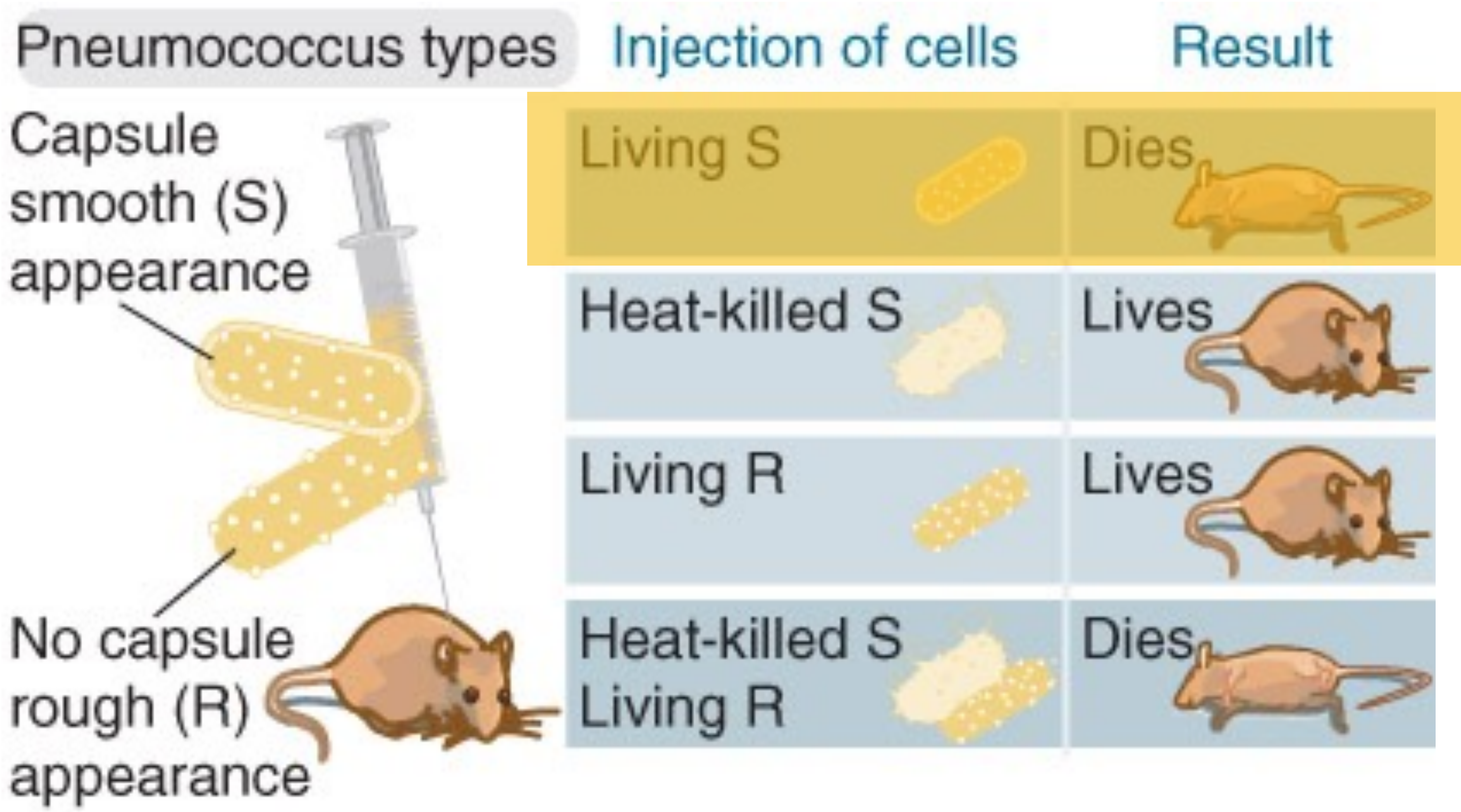
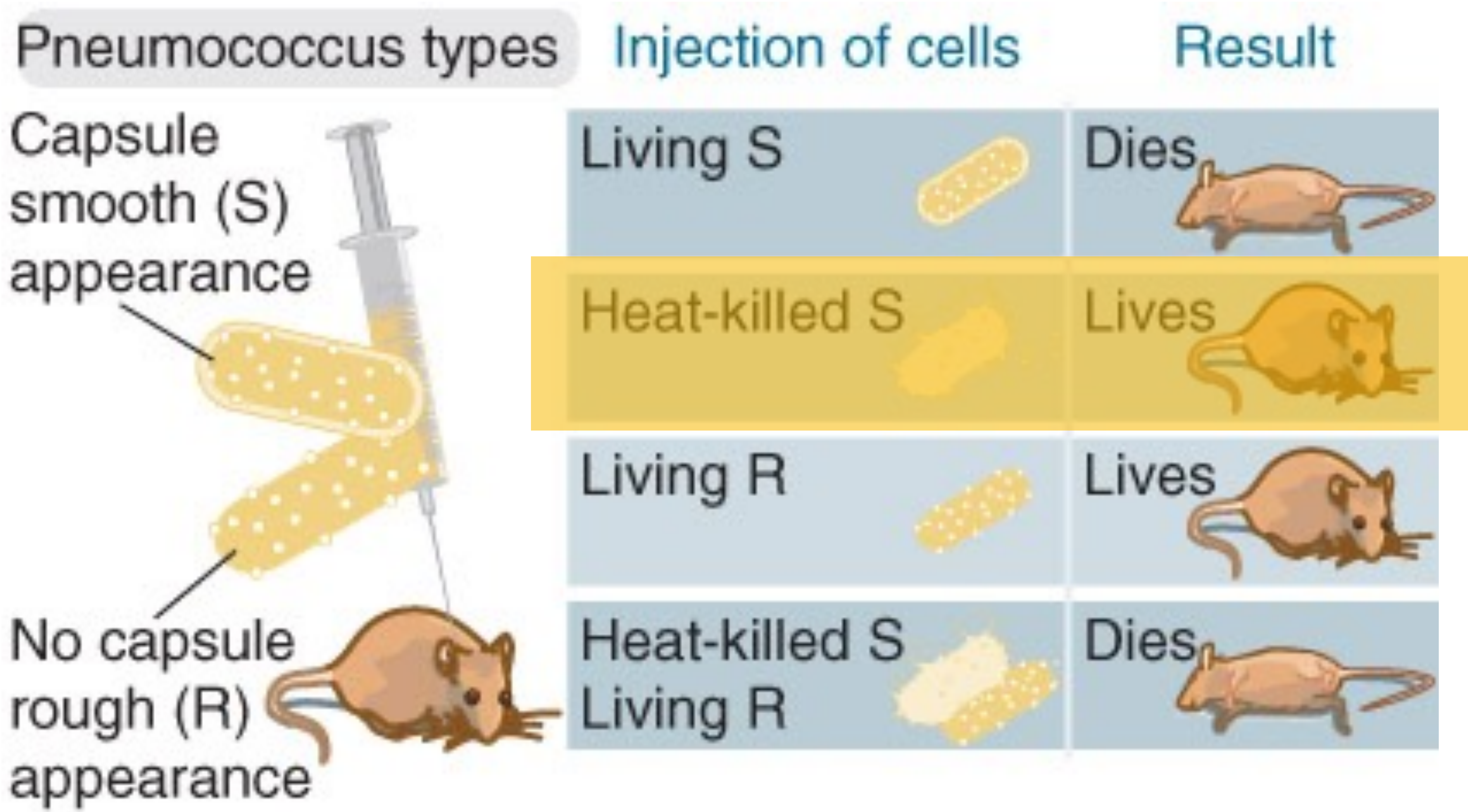


Rough (left) and smooth (right) colonies of ***S. pneumoniae.***



Simultaneous injection of both heat-killed S-type and live R-type bacteria can kill mice just as effectively as the live S-type.



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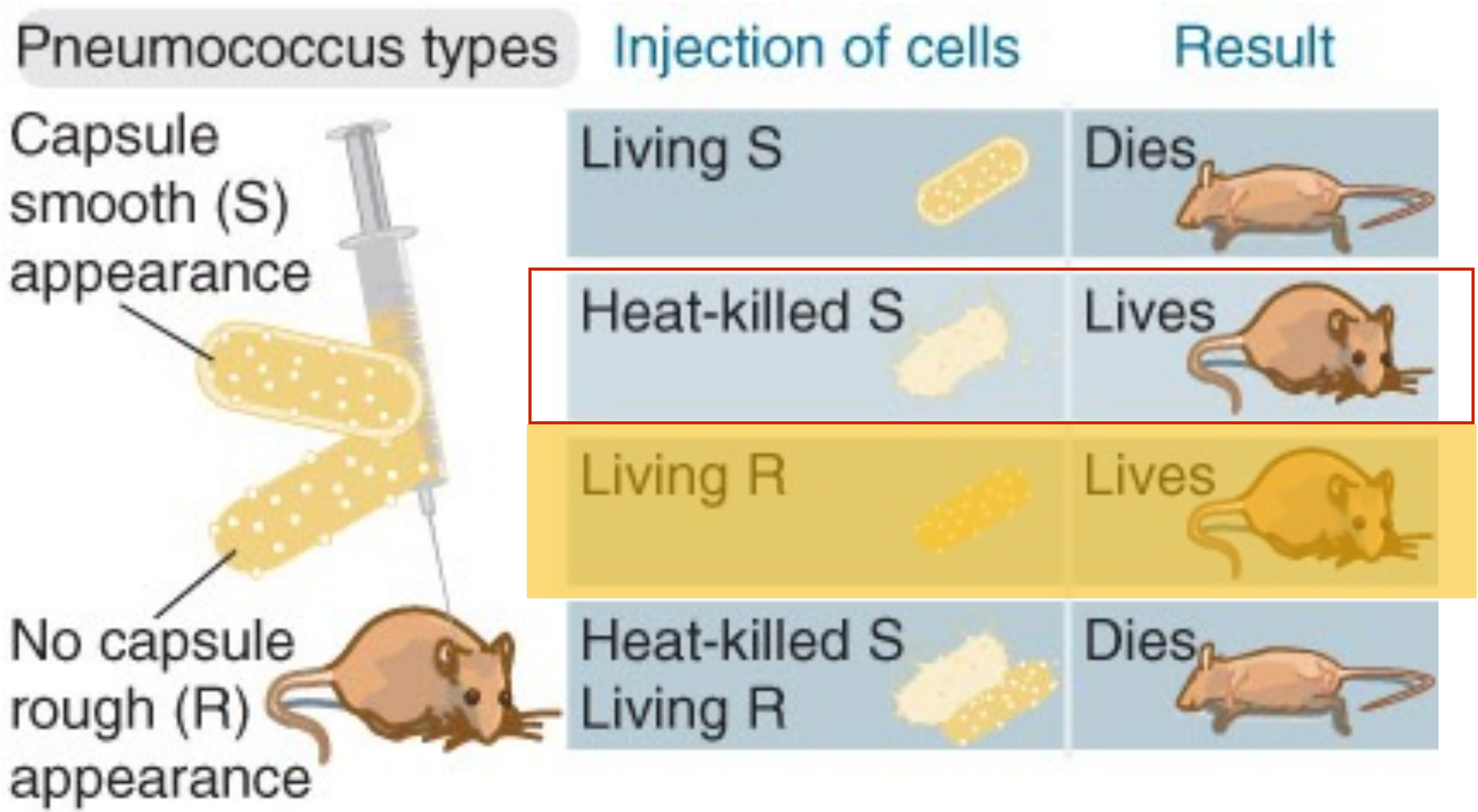

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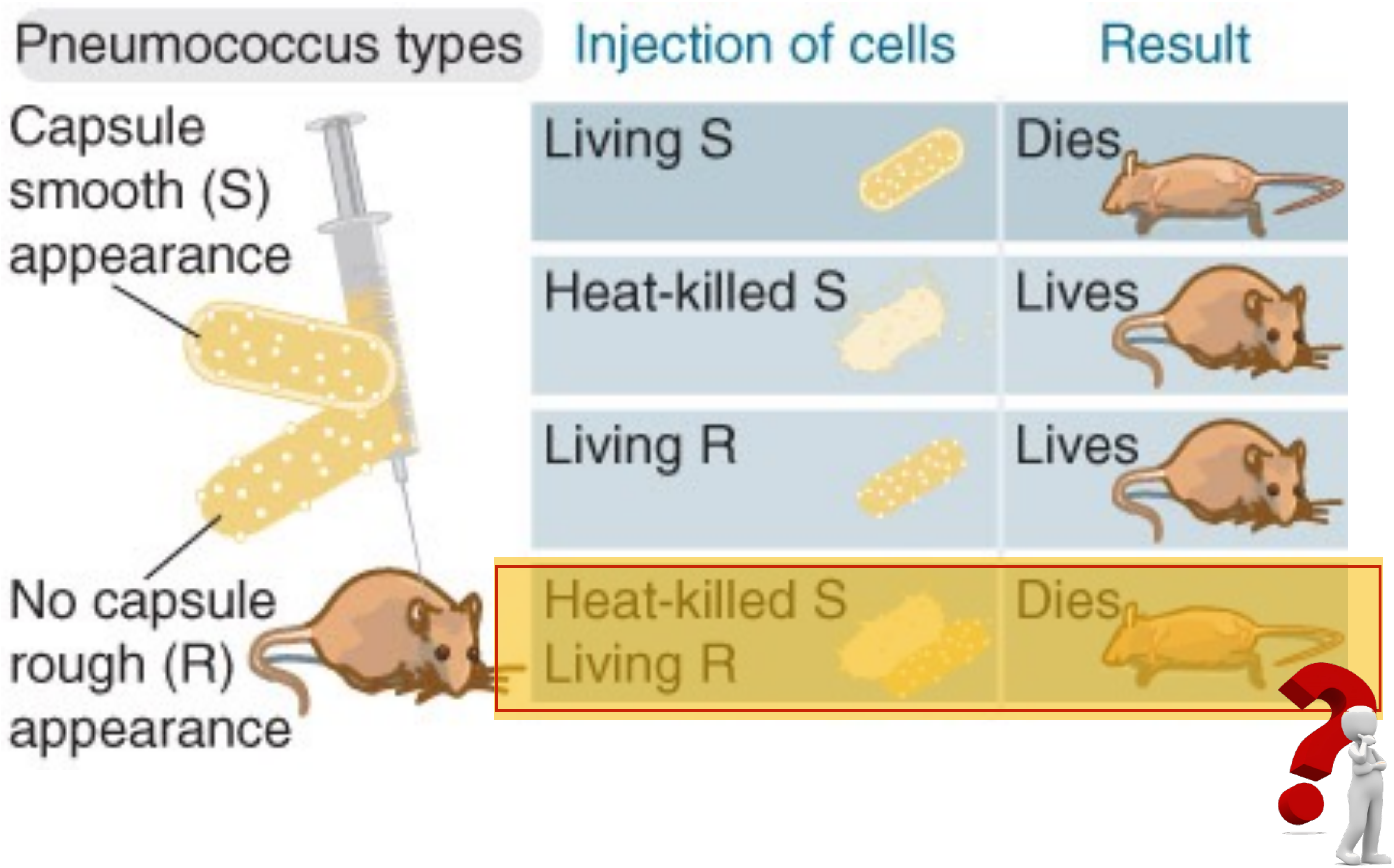

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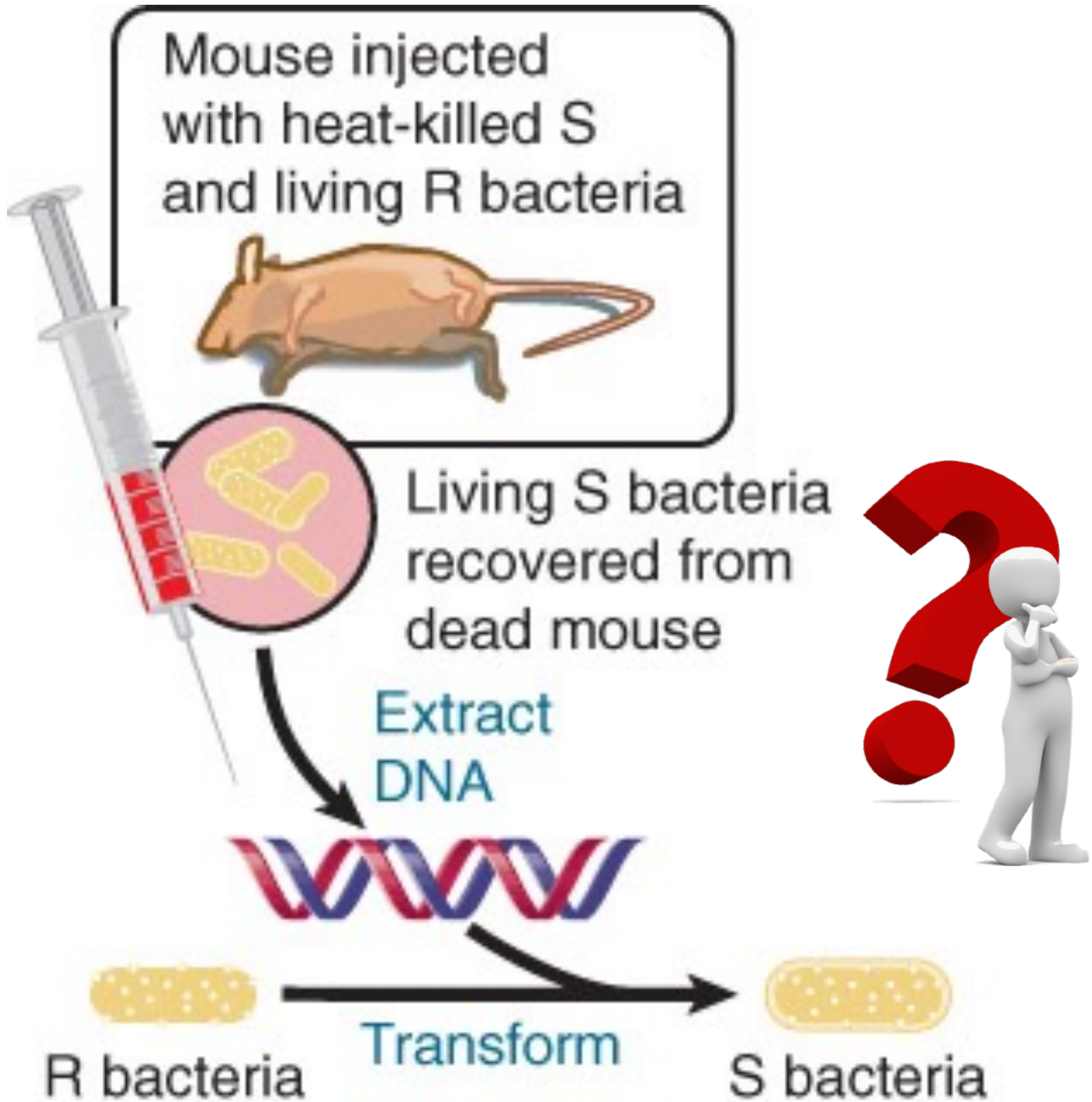
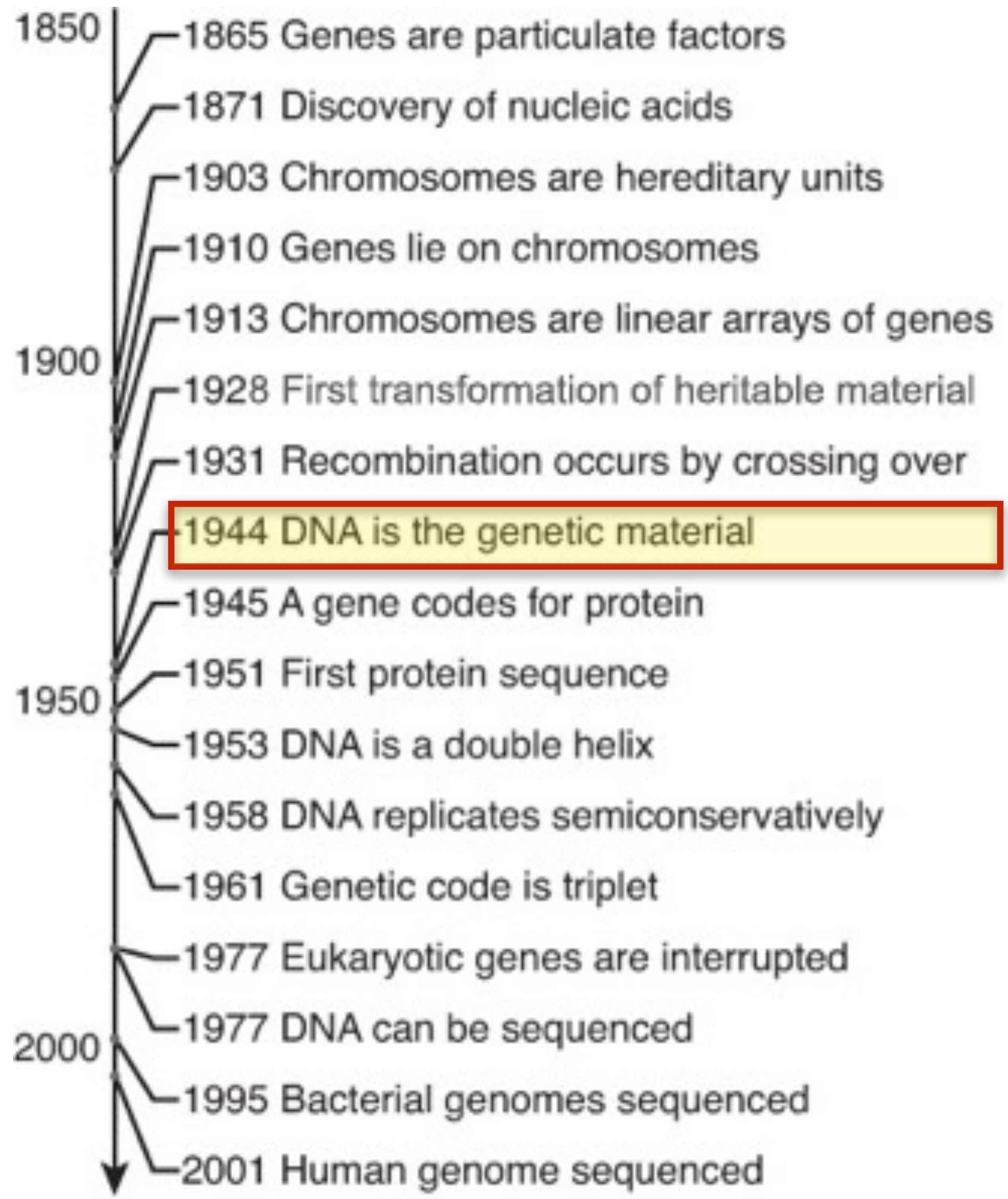


The DNA of S-type bacteria can transform R-type bacteria into the same S-type.



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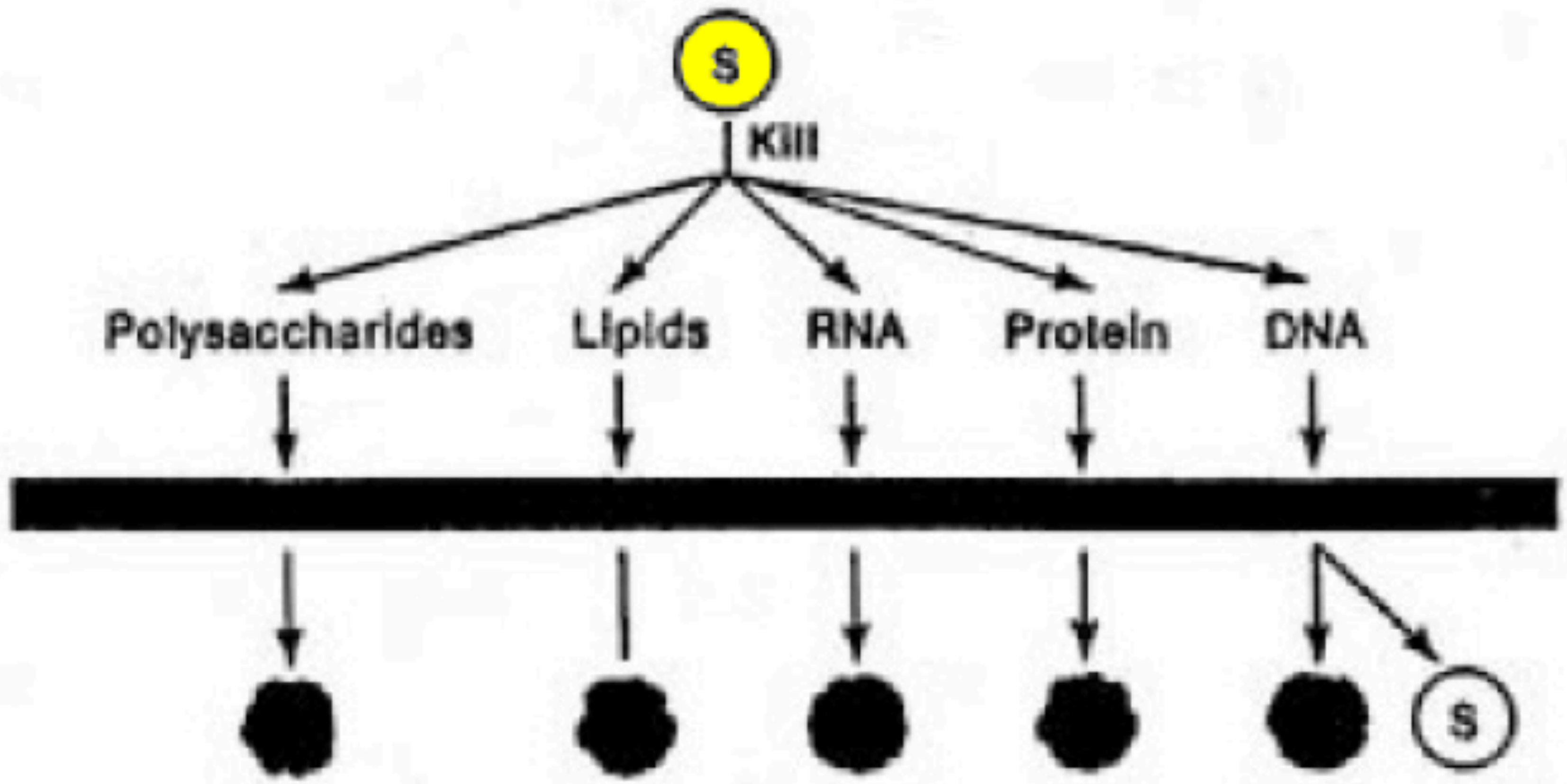
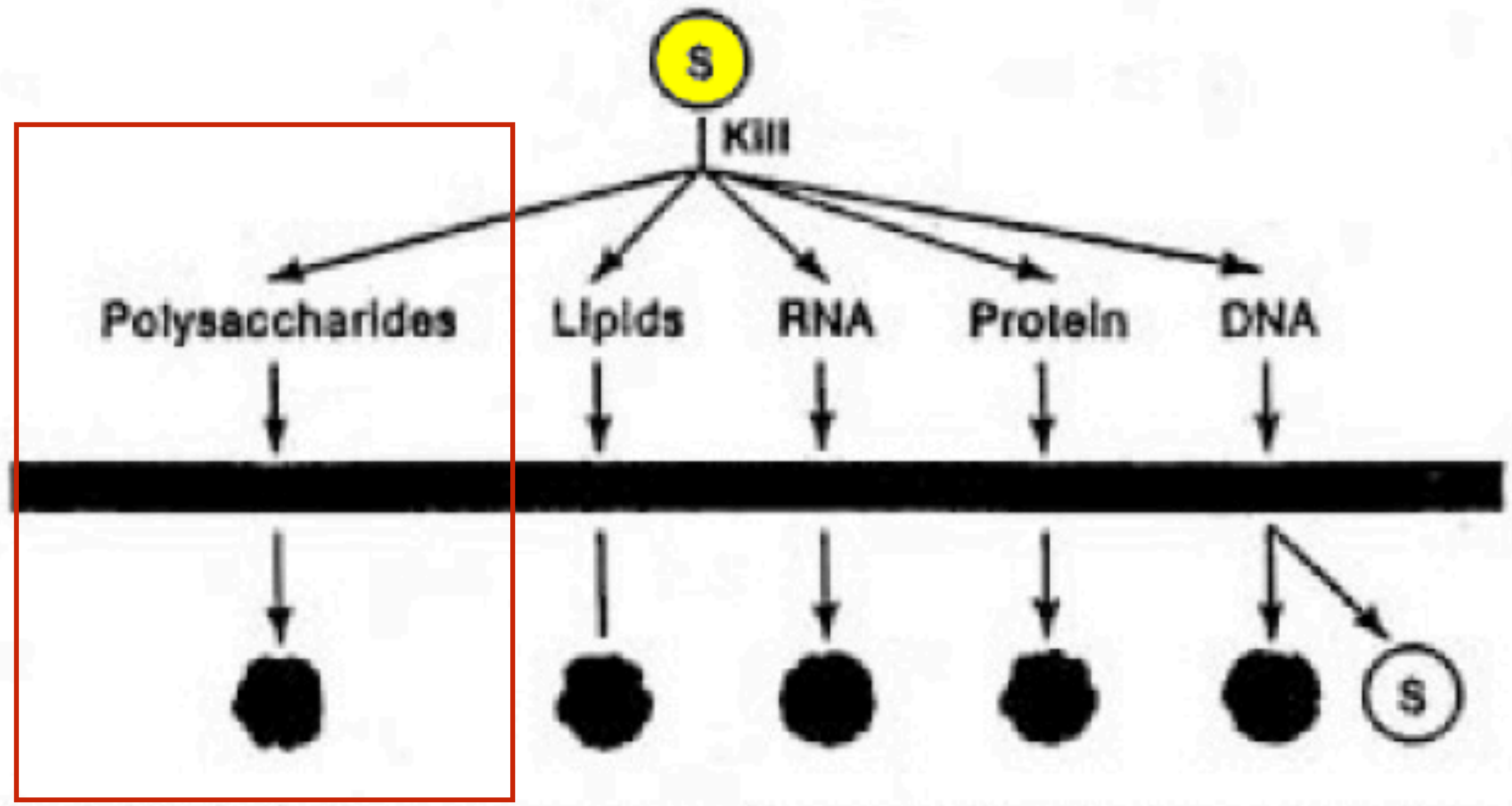


Figure 11-2. Demonstration that DNA is the transforming agent. DNA is the only agent that produces smooth (S) colonies when added to live rough (R) cells.



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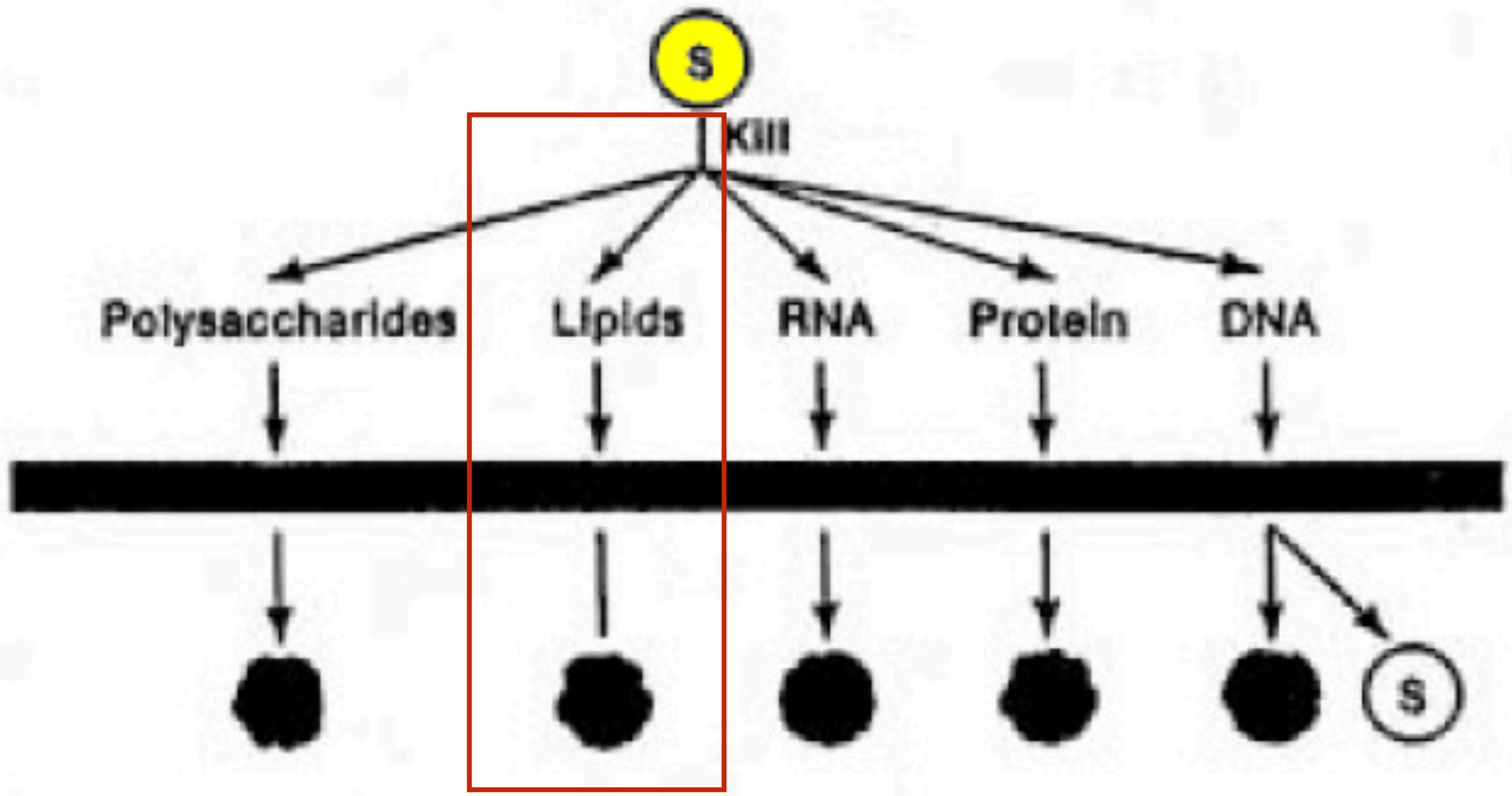

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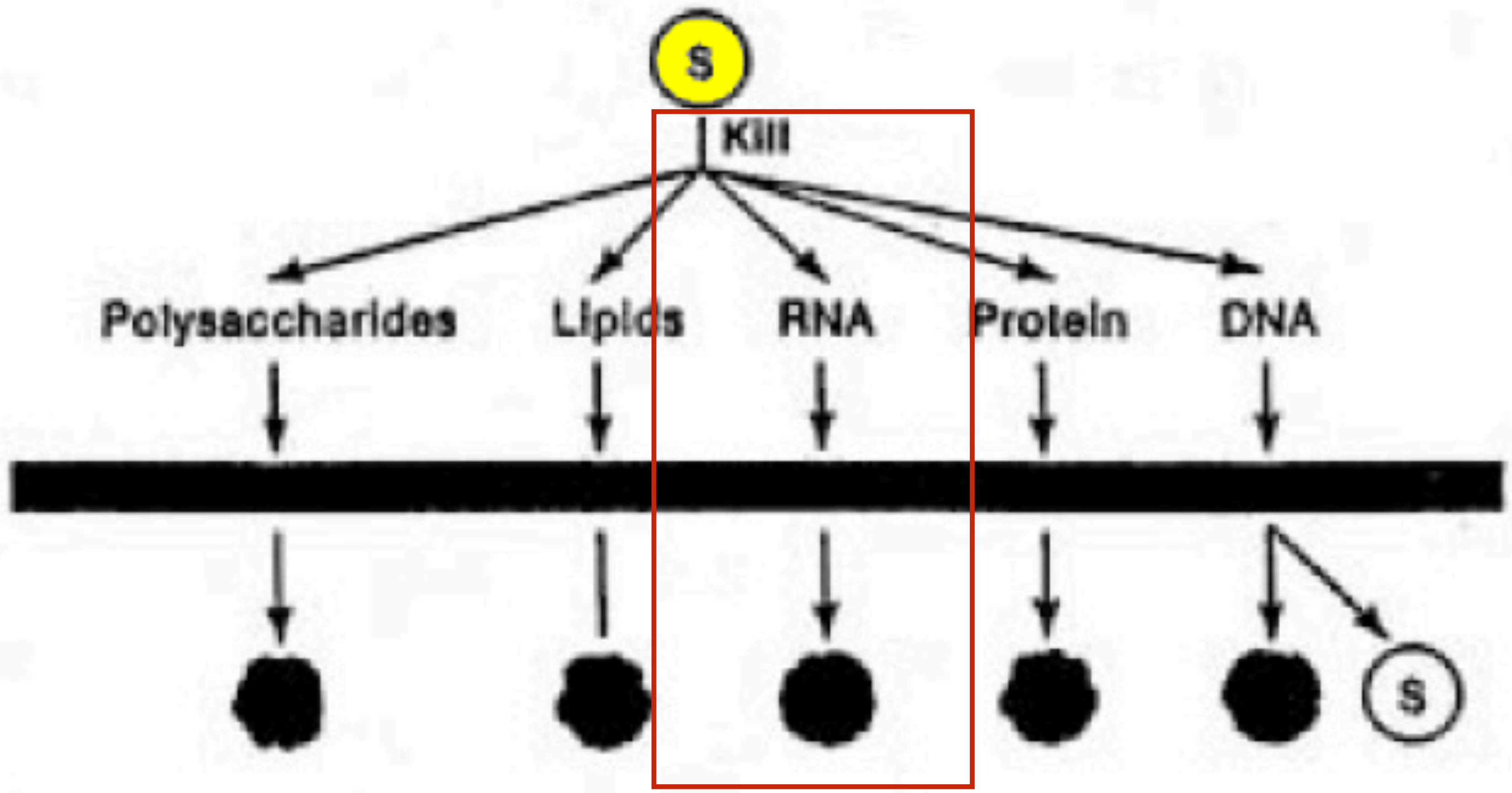

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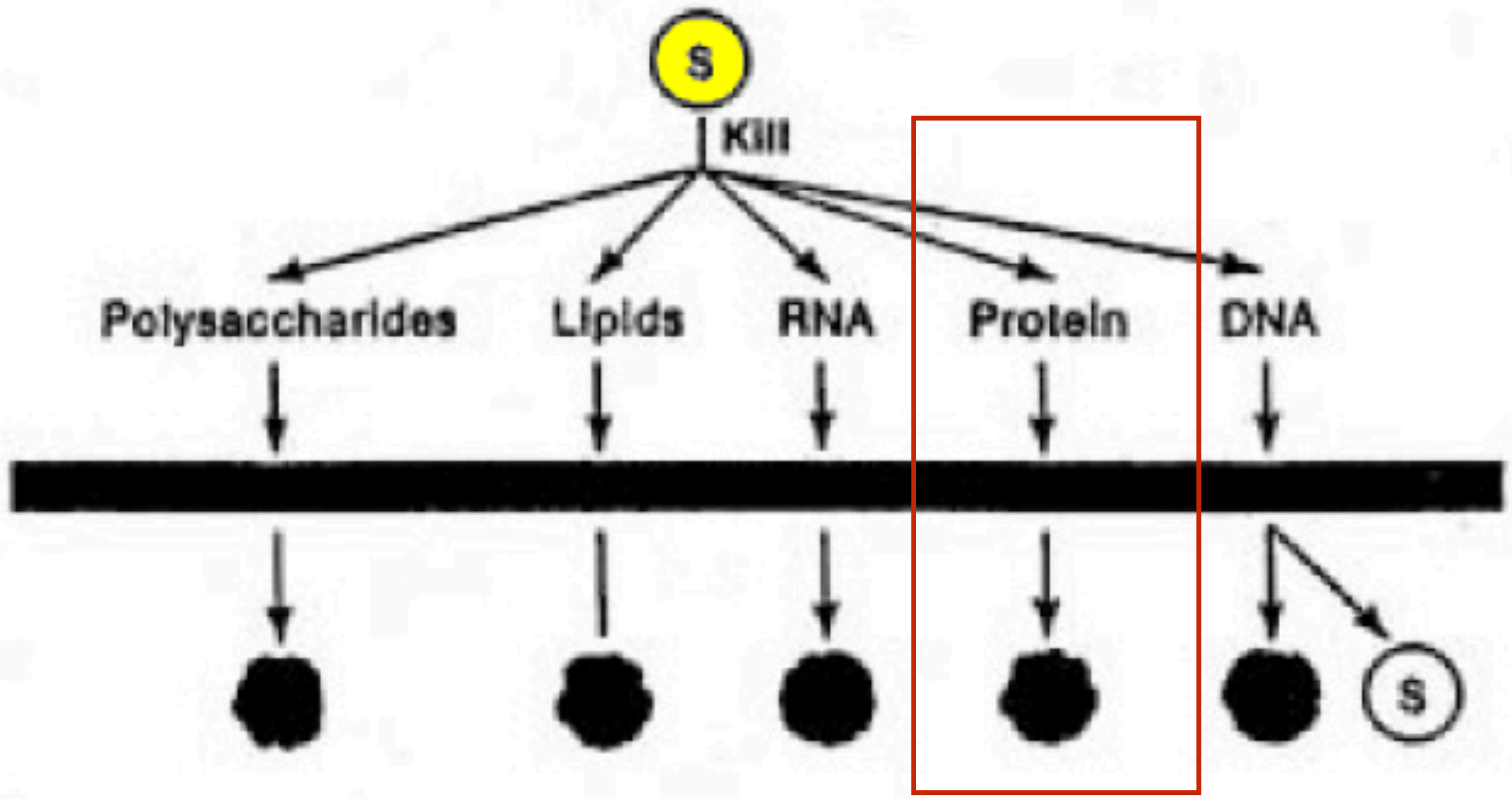

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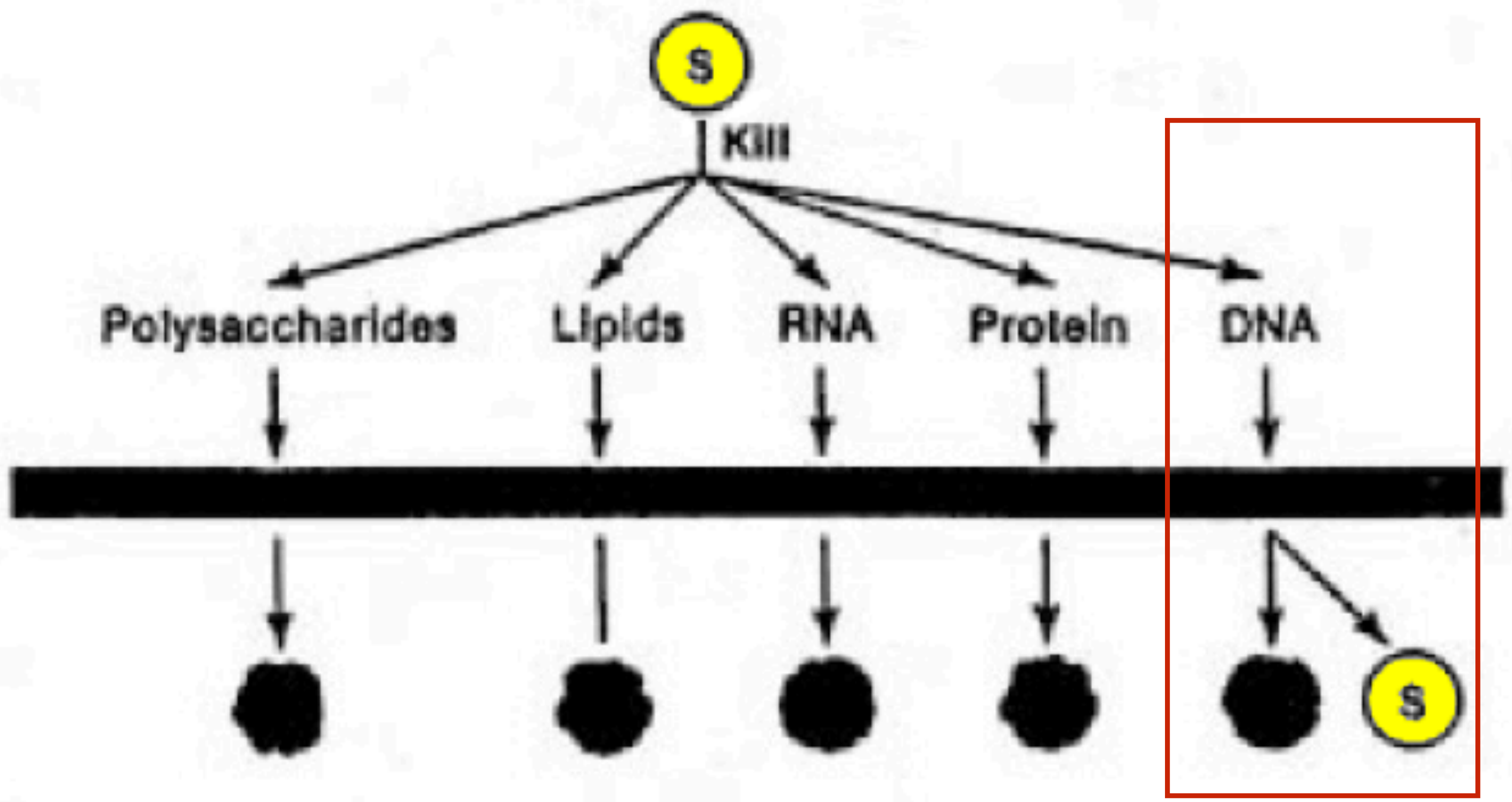

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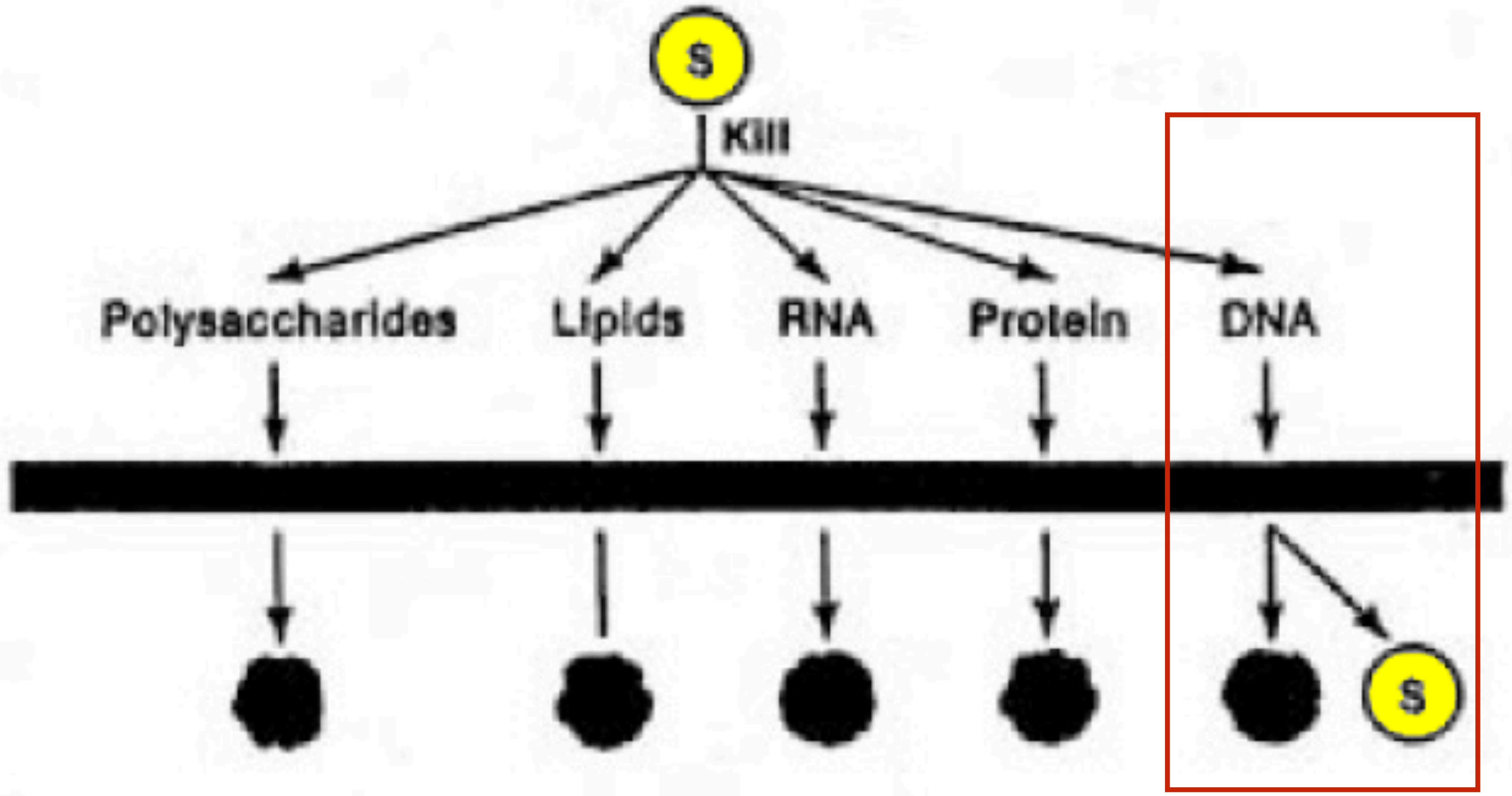

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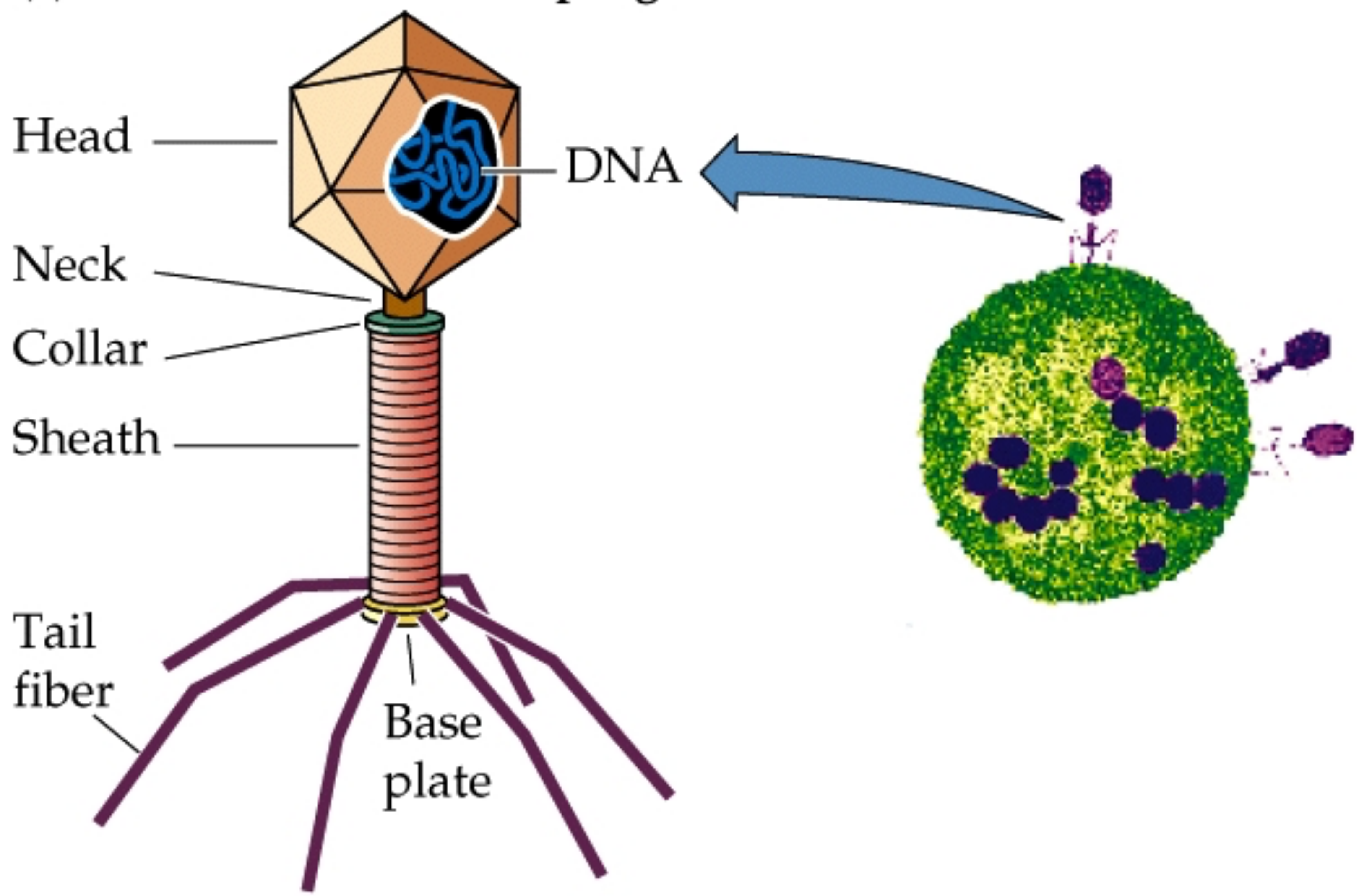
Purification technique, not good enough… still proteins in the DNA sample

(*a*) **The virus: T2 bacteriophage**



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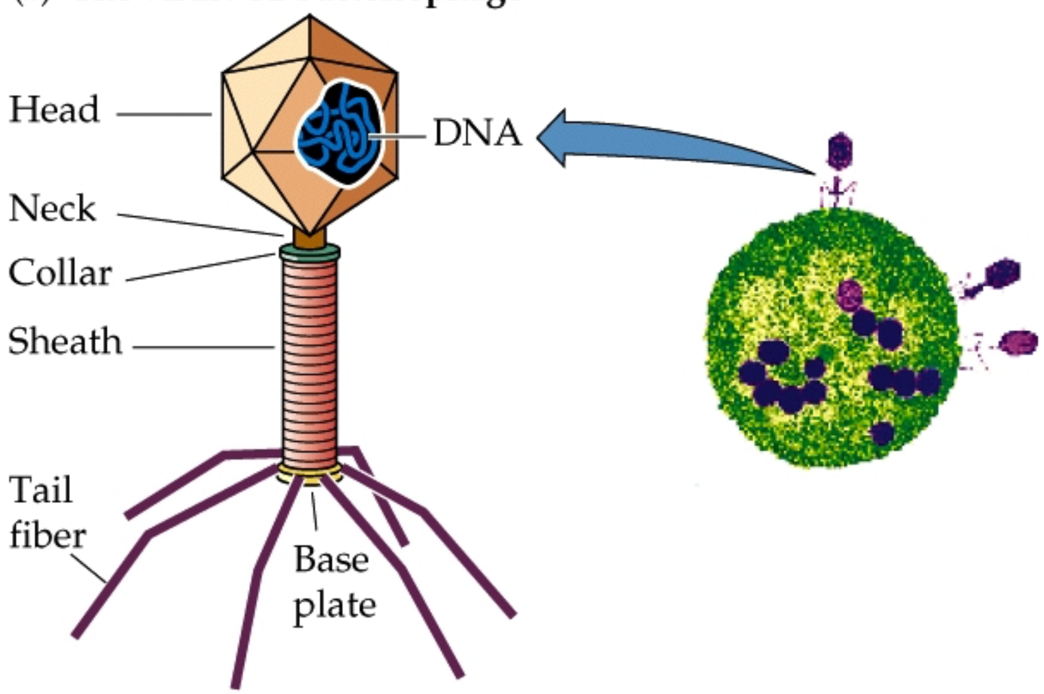
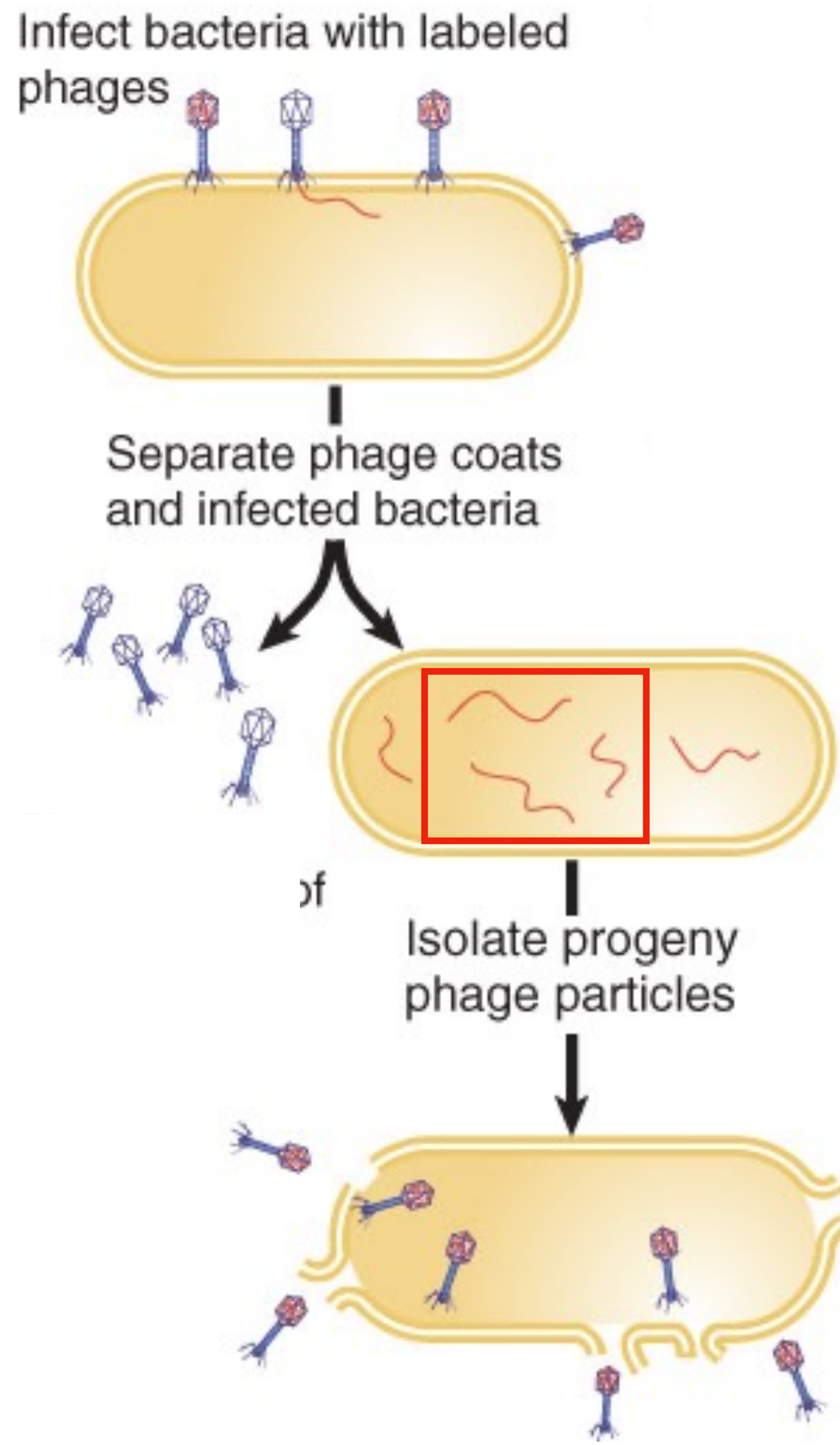
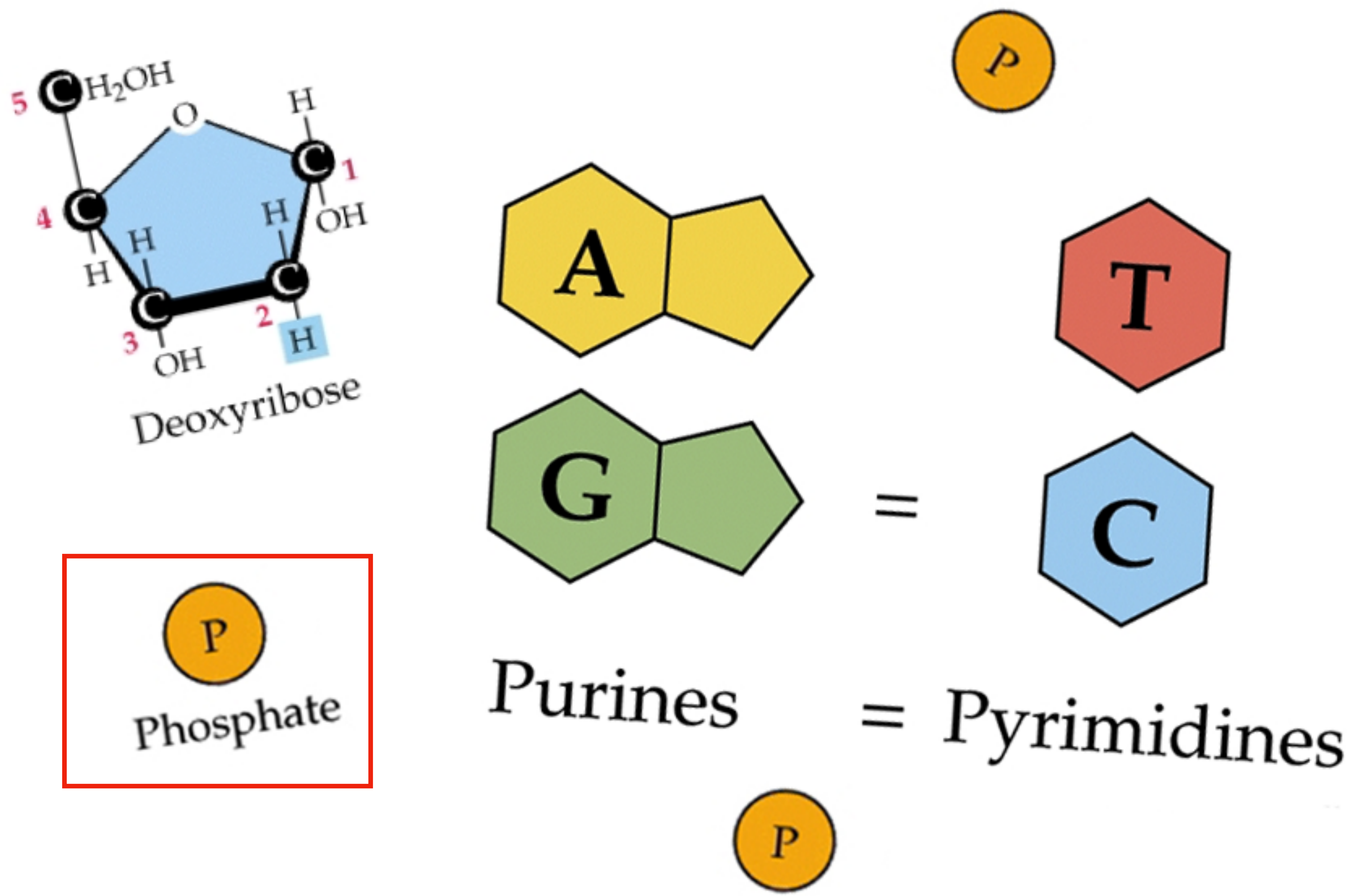
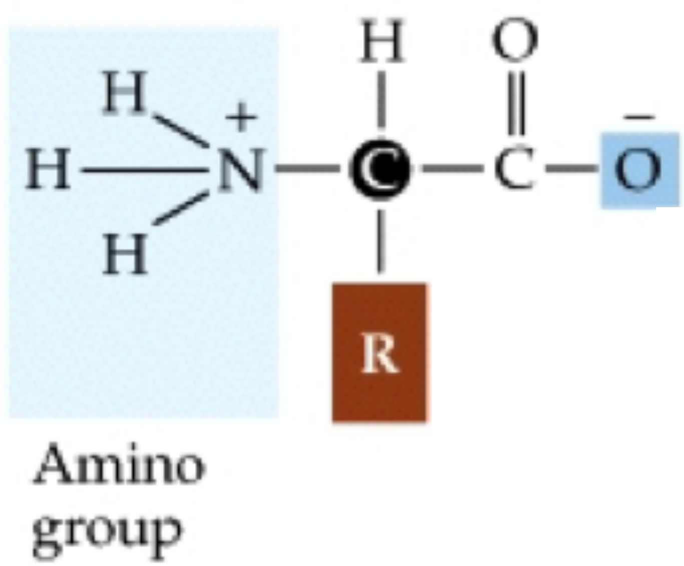
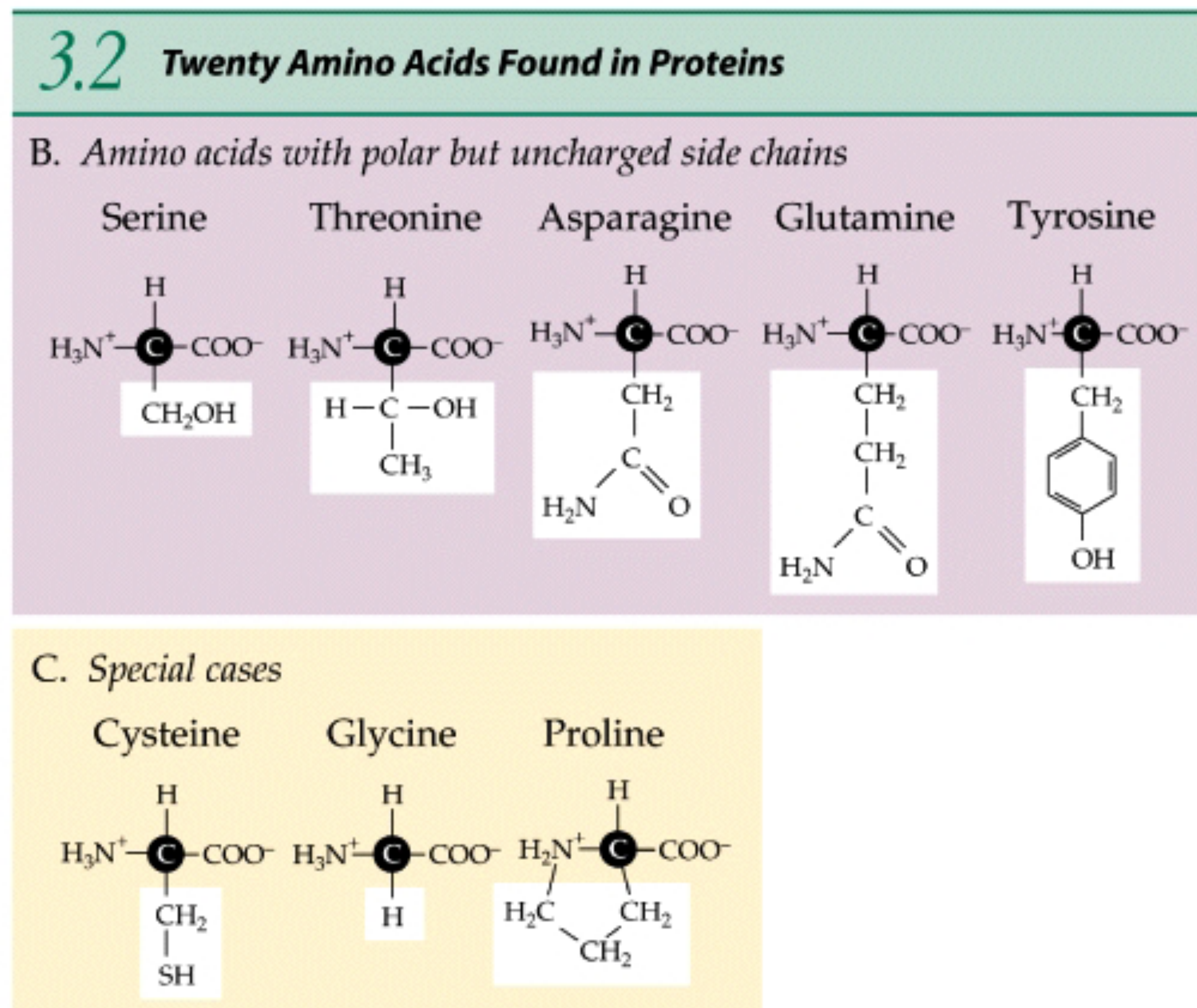






5
CH_2OH
O
H
1
4
OH
H
H
H
H
2
3
OH
H
Deoxyribose
P
Phosphate
P
A
T
G
=
C
Purines
= Pyrimidines
P

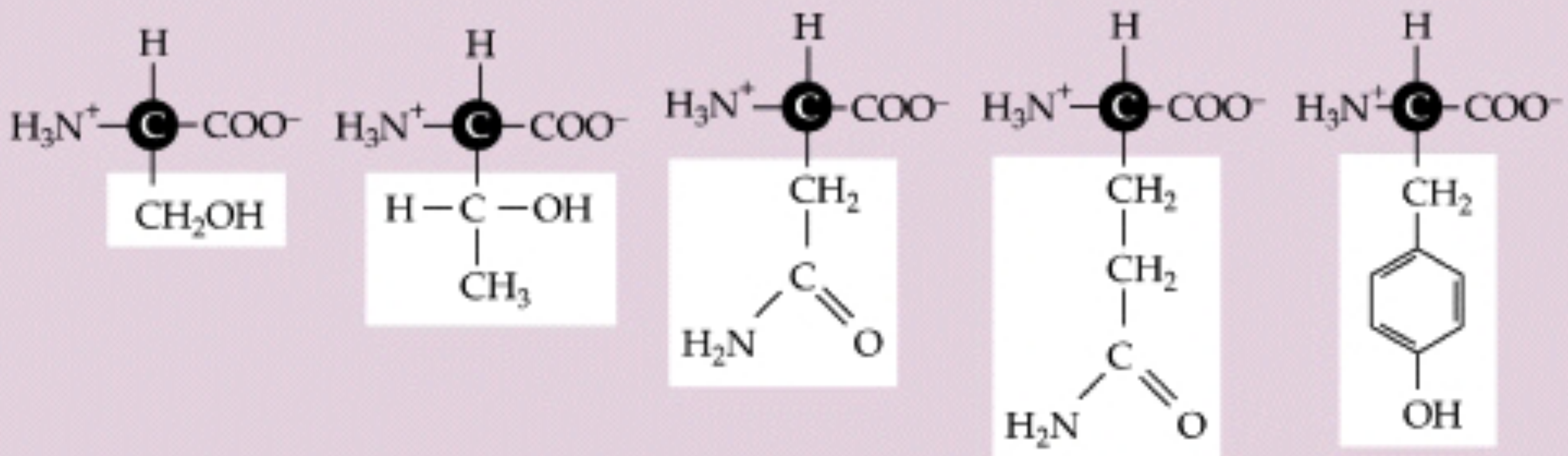

H
H
H
N
+
H
C
O
C
O
−
R
Amino group


3.2 Twenty Amino Acids Found in Proteins
B. Amino acids with polar but uncharged side chains
Serine
Threonine
Asparagine
Glutamine
Tyrosine
H_3N^+
COO−
CH_2OH
H—C—OH
CH_3
CH_2
H_2N
O
OH
C. Special cases
Cysteine
Glycine
Proline
SH
H_2N^+
H_2C
H

3.2 Twenty Amino Acids Found in Proteins

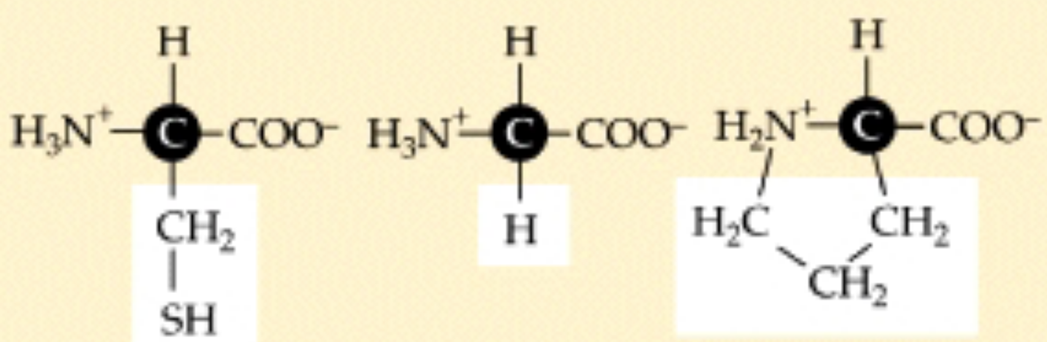
B. *Amino acids with polar but uncharged side chains*

Serine Threonine Asparagine Glutamine Tyrosine

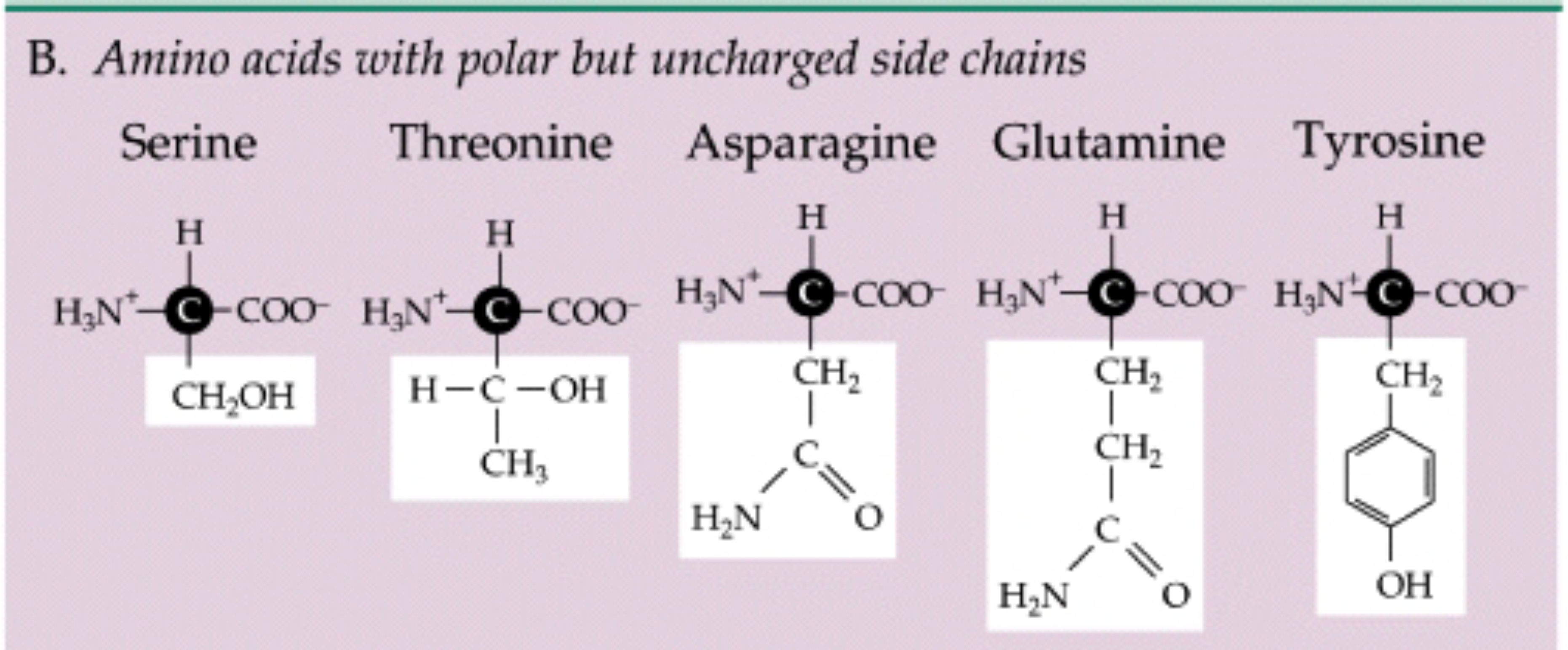


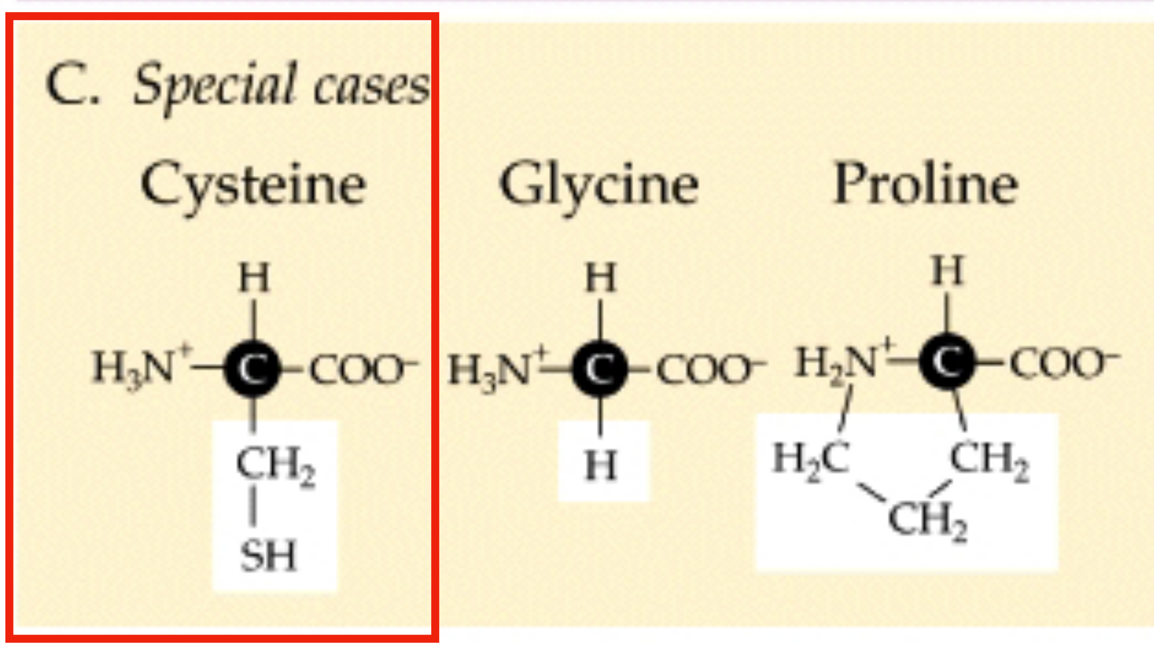
C. *Special cases*

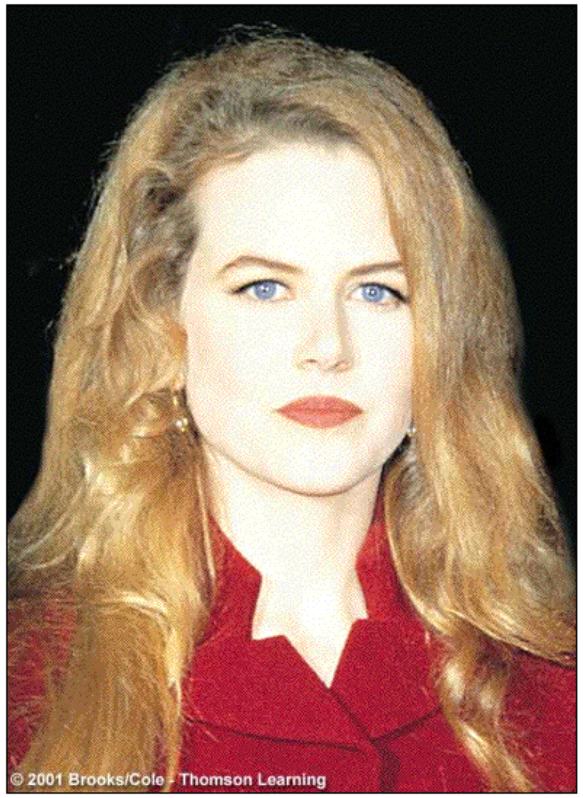
Cysteine Glycine Proline



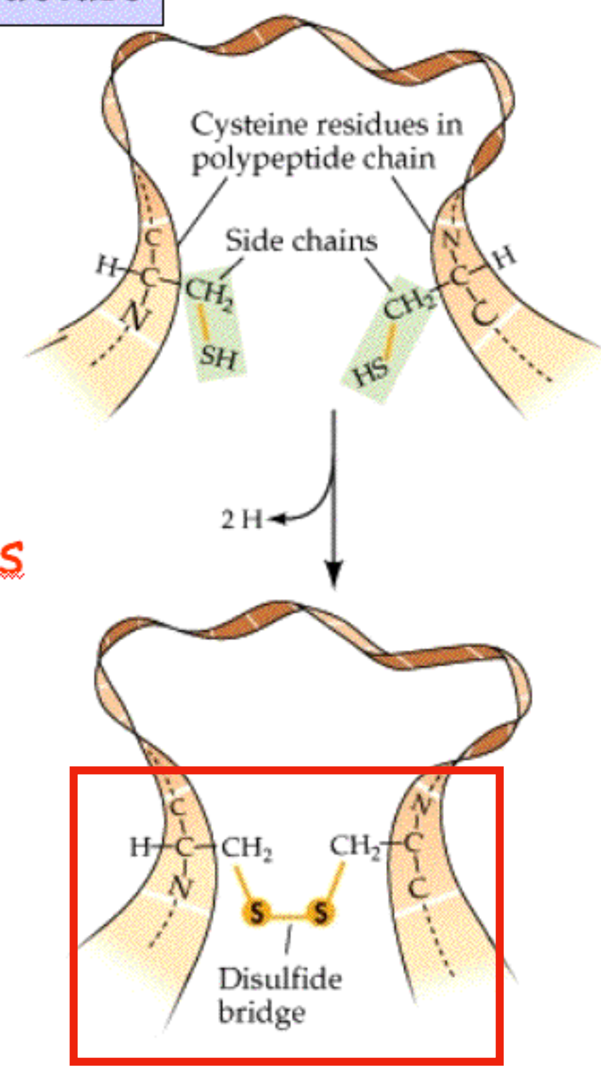
3.2 Twenty Amino Acids Found in Proteins



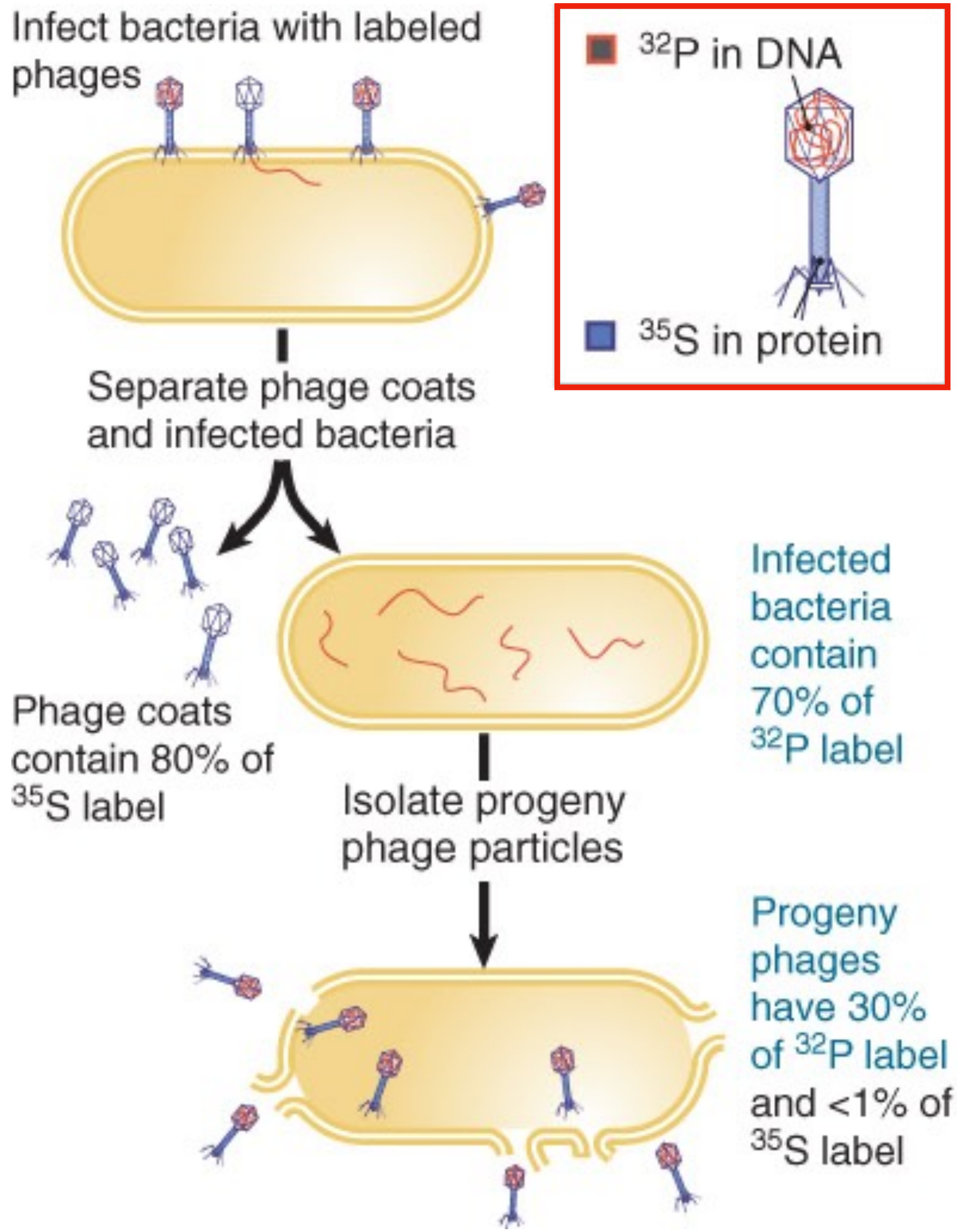




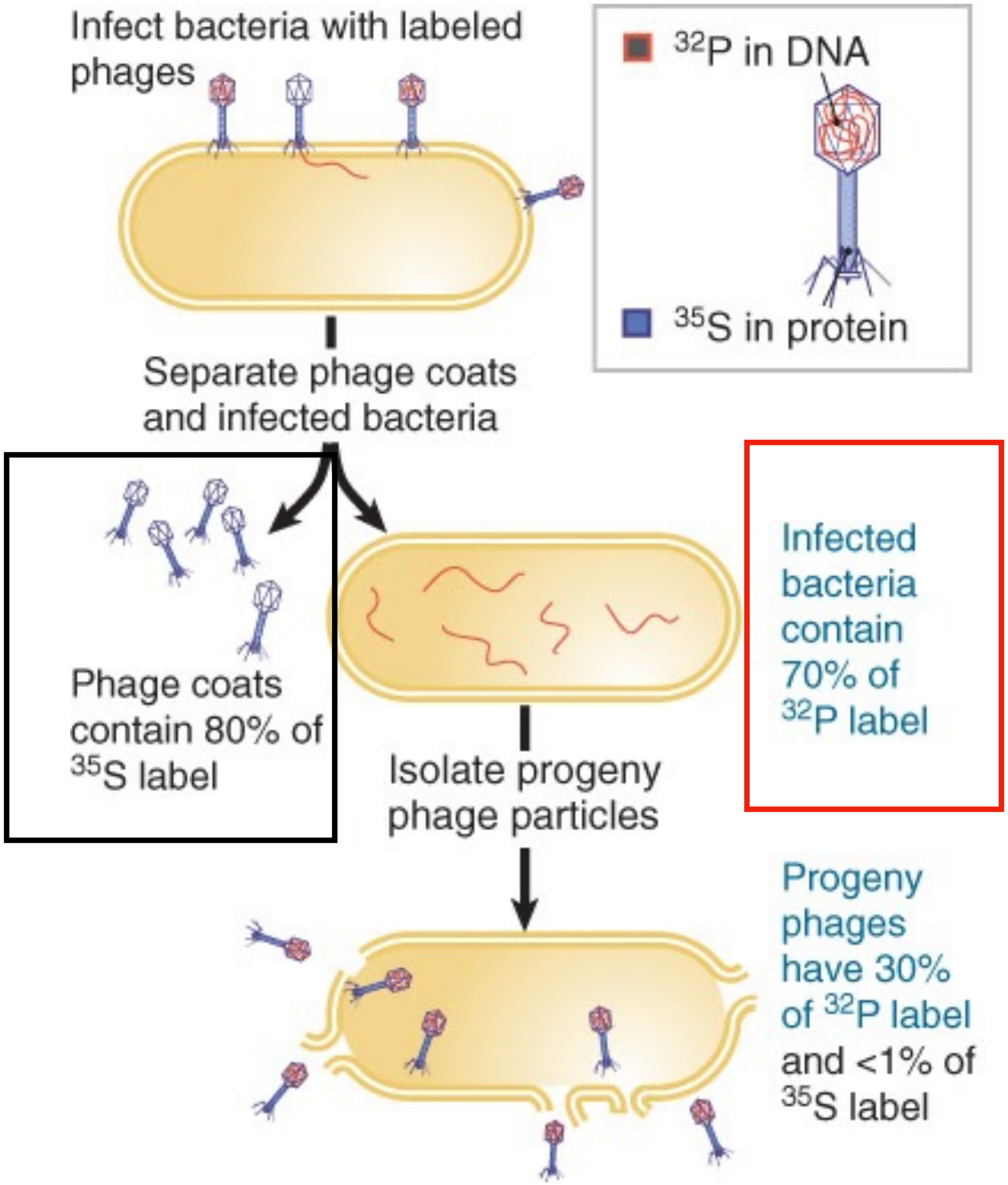
Protein structure

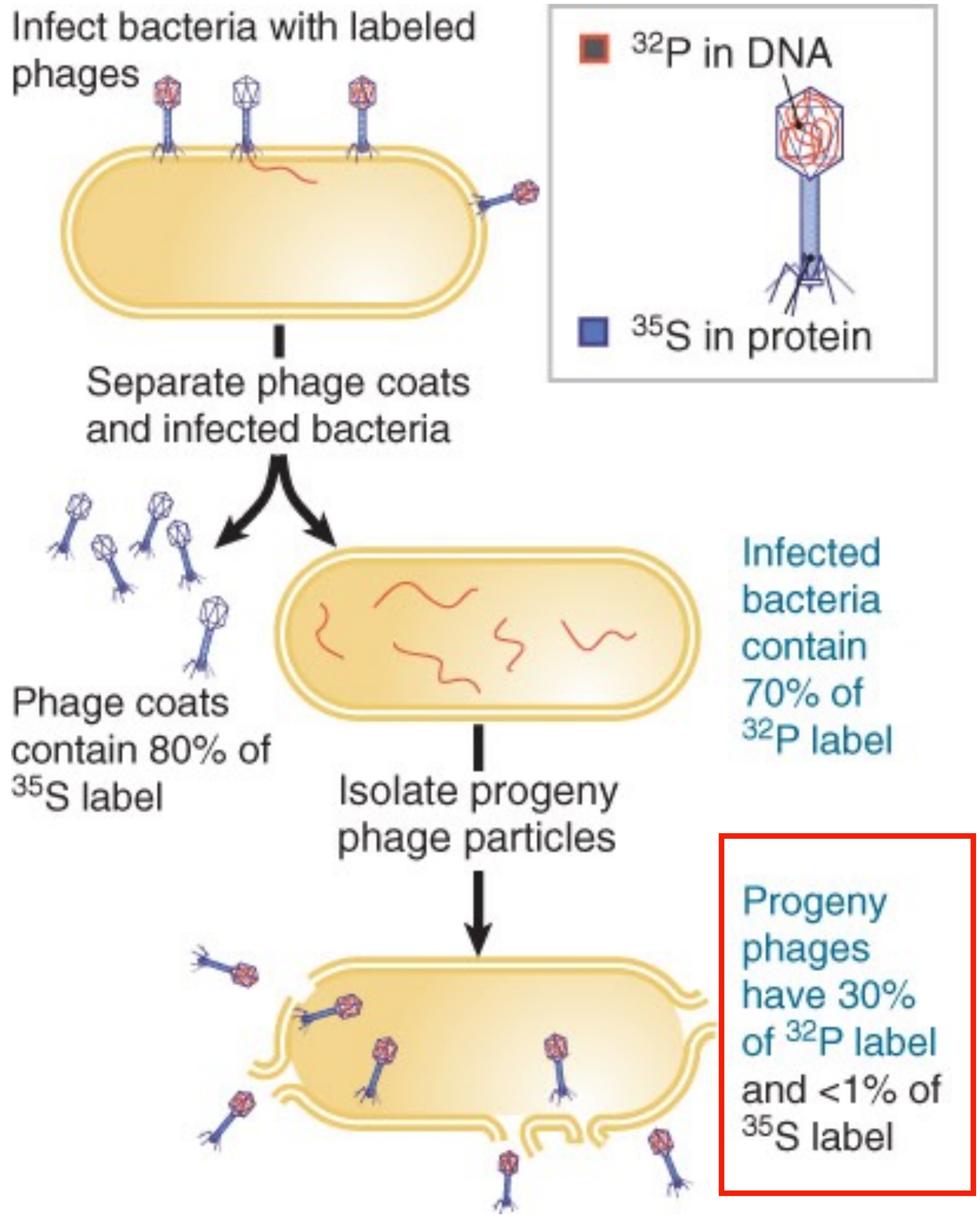


- curls in a perm are formed by making bonds between cysteines



Infect bacteria with labeled phages
^{32}P in DNA
^{35}S in protein
Separate phage coats and infected bacteria
Phage coats contain 80% of ^{35}S label
Infected bacteria contain 70% of ^{32}P label
Isolate progeny phage particles
Progeny phages have 30% of ^{32}P label and <1% of ^{35}S label


Infect bacteria with labeled phages
^{32}P in DNA
^{35}S in protein
Separate phage coats and infected bacteria
Phage coats contain 80% of ^{35}S label
Infected bacteria contain 70% of ^{32}P label
Isolate progeny phage particles
Progeny phages have 30% of ^{32}P label and <1% of ^{35}S label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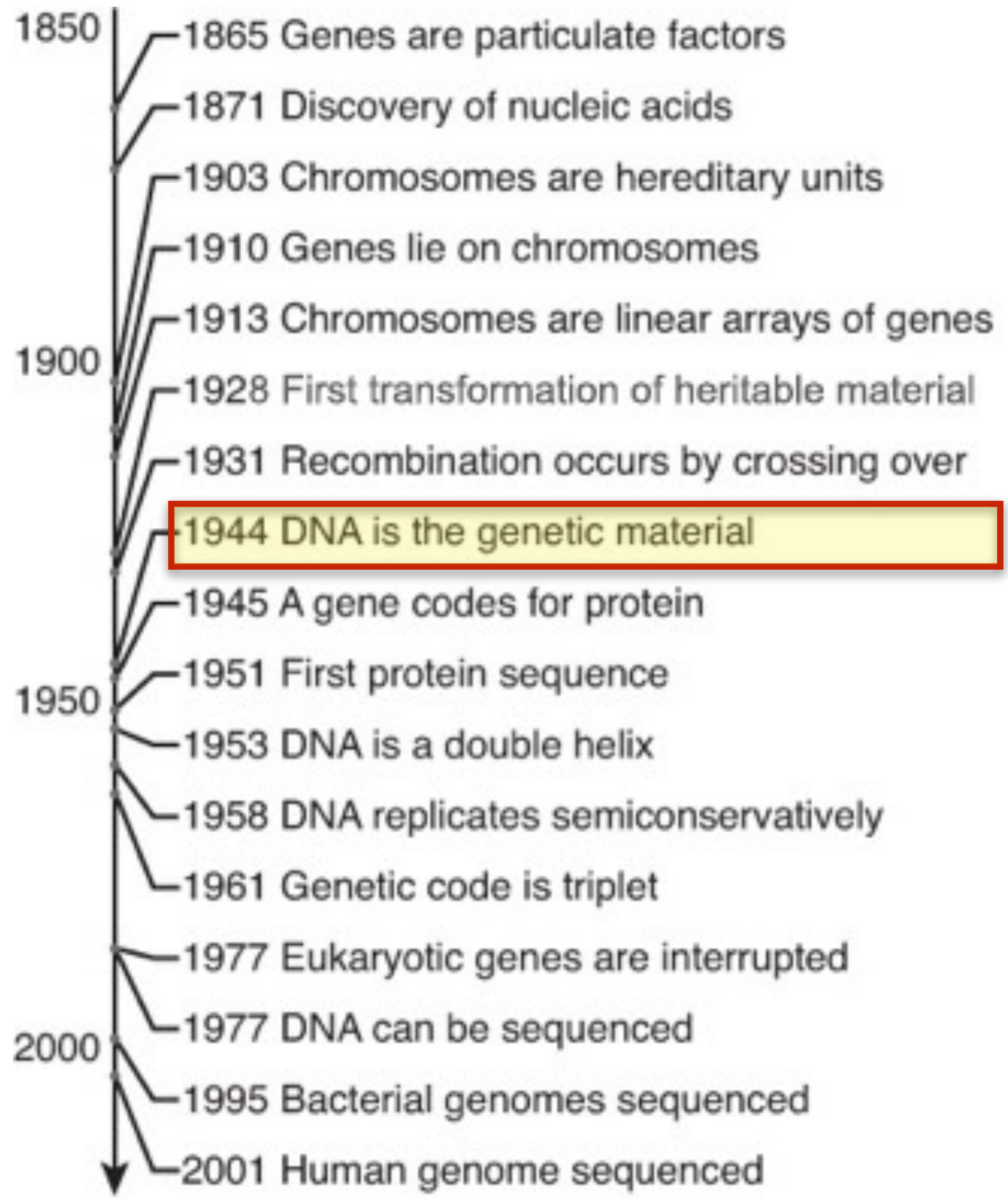
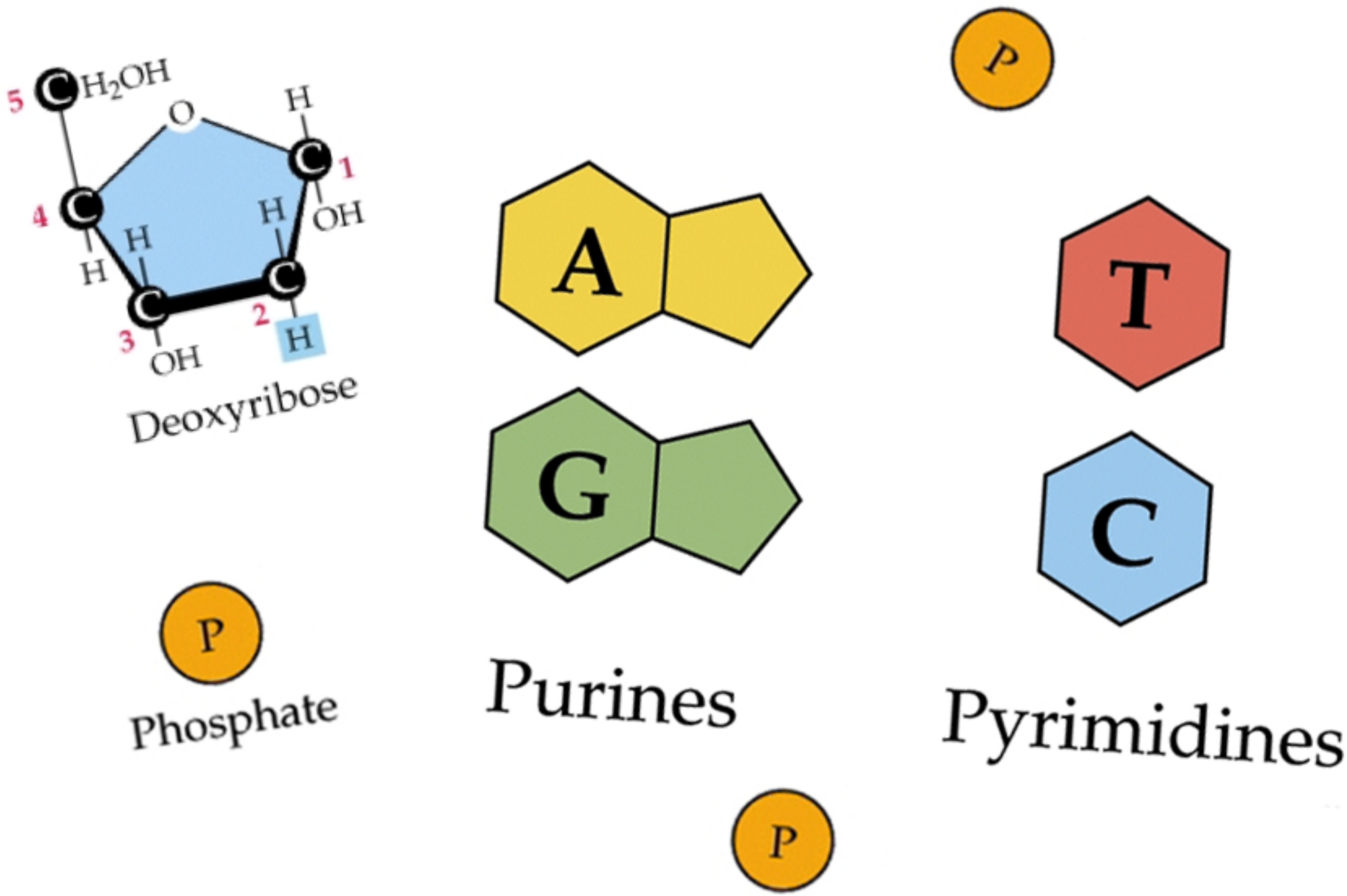
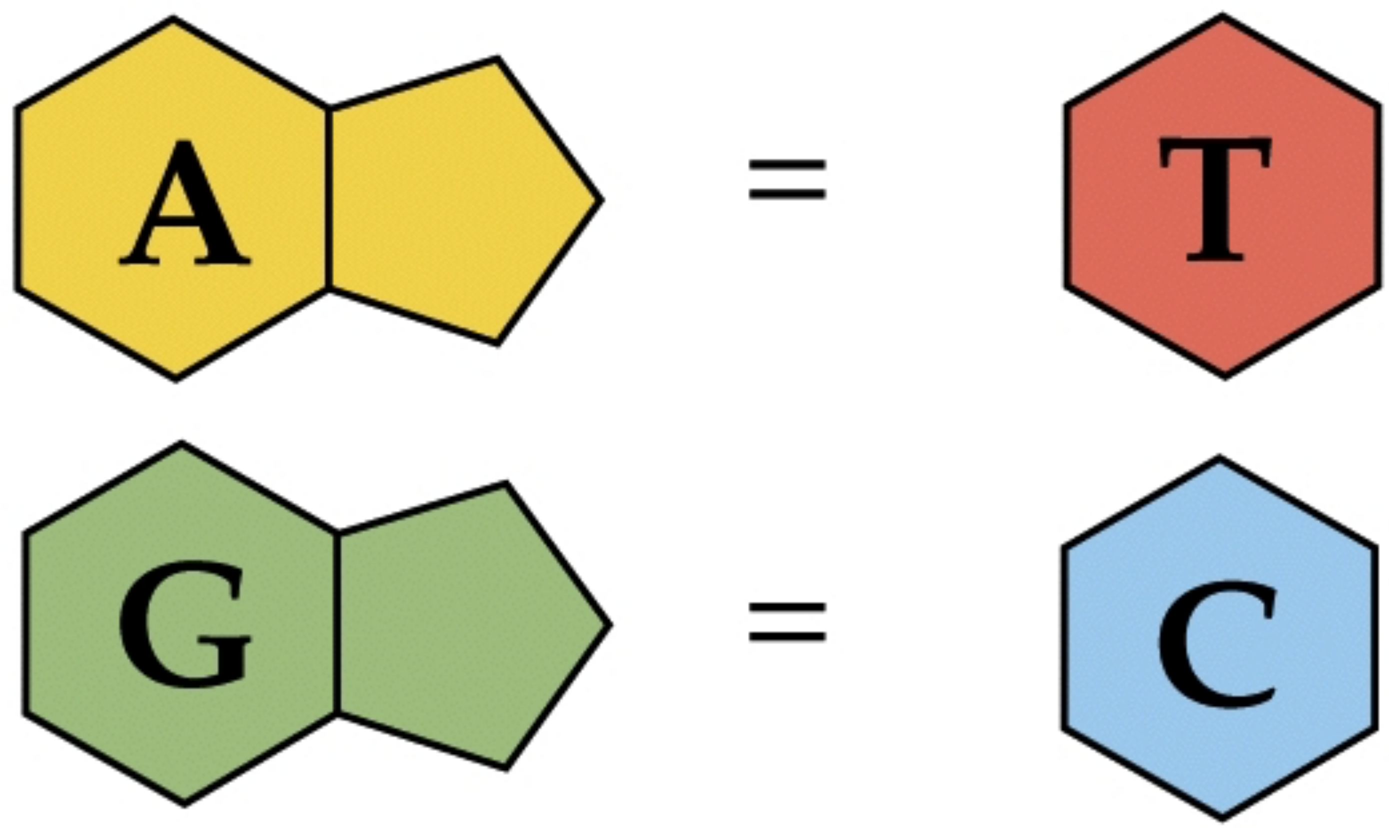
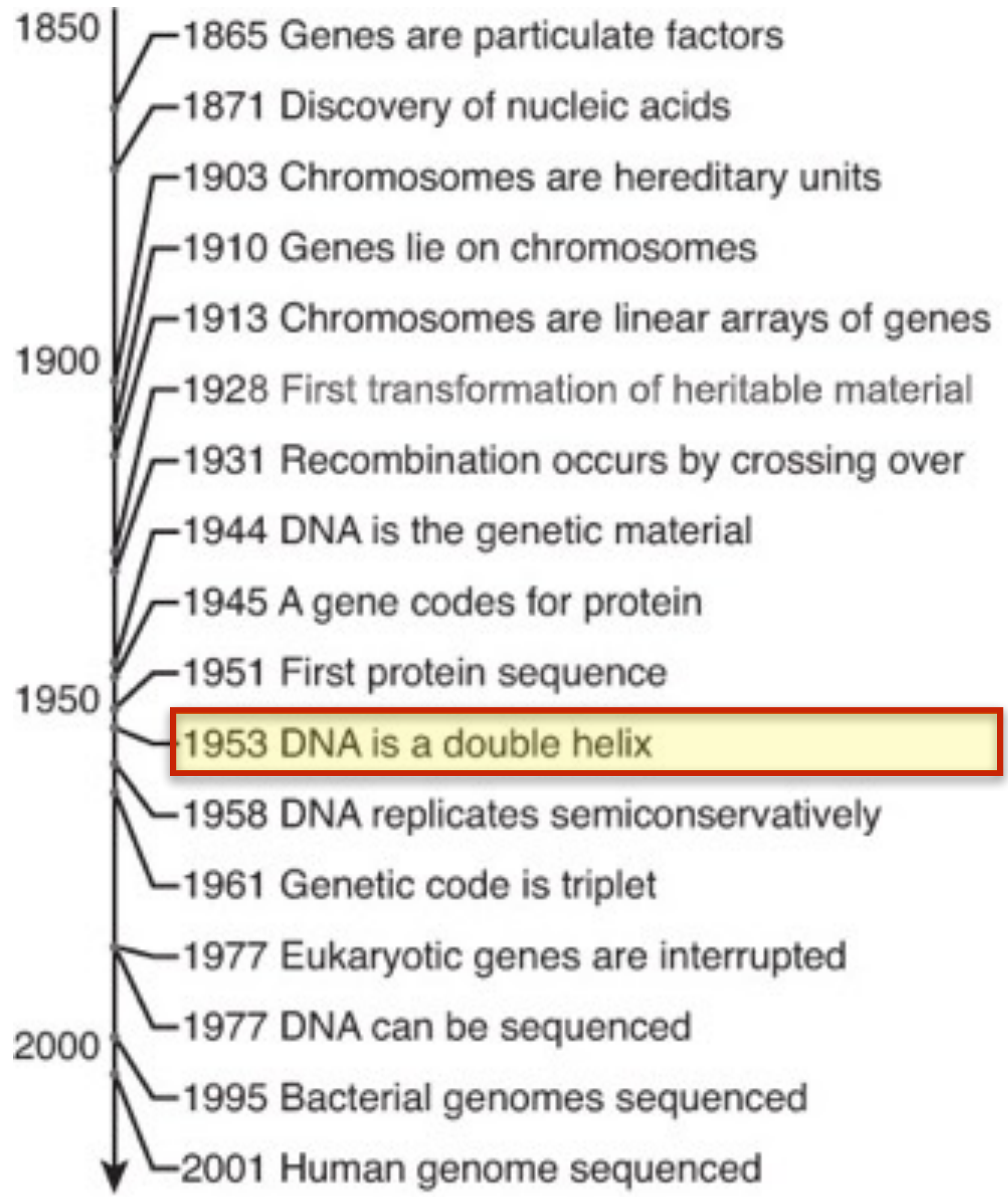


A brief history of genetics.


5
CH2OH
O
H
1
OH
4
H
H
H
2
H
3
OH
Deoxyribose
P
A
G
T
C
P
Phosphate
Purines
Pyrimidines
P



Purines = Pyrimidines



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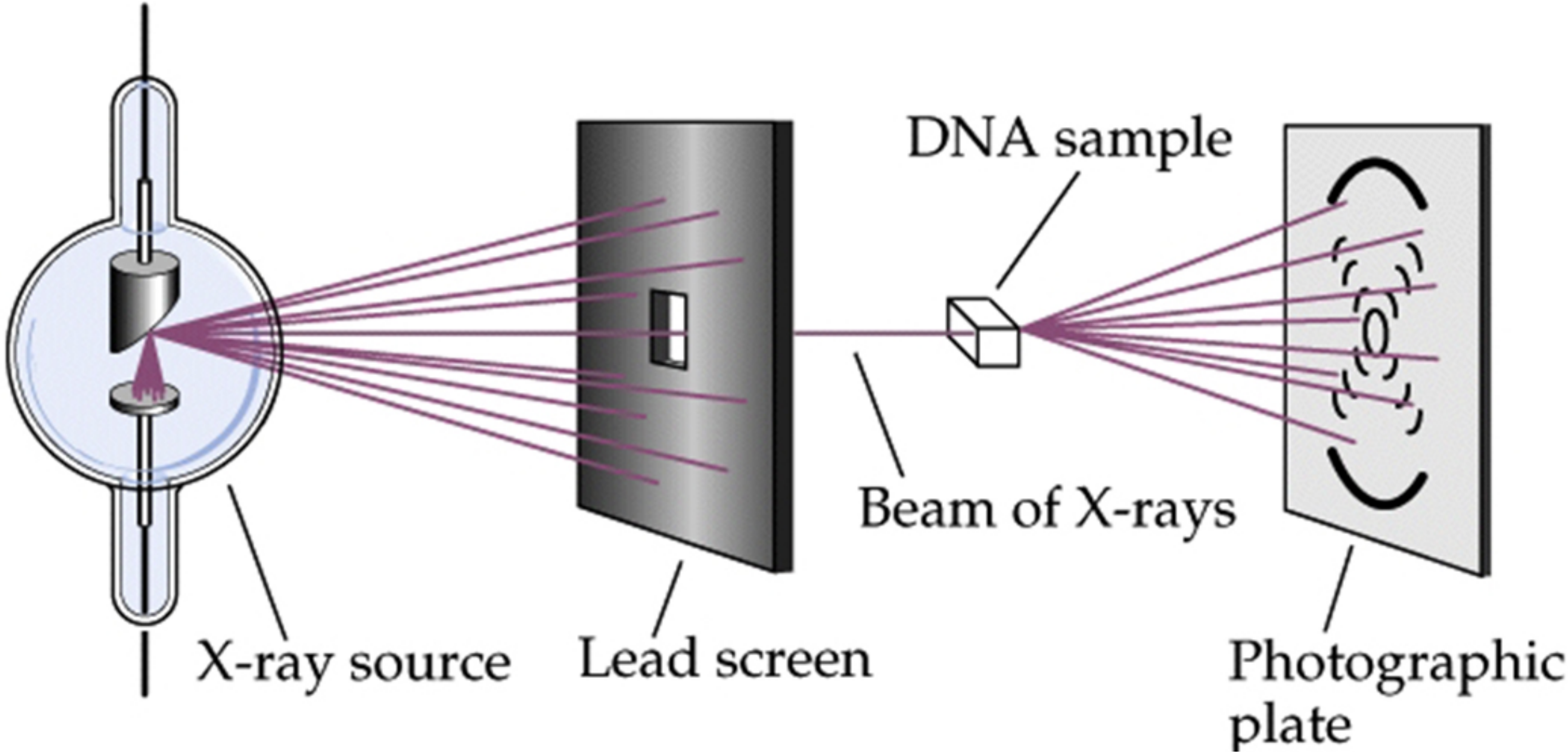
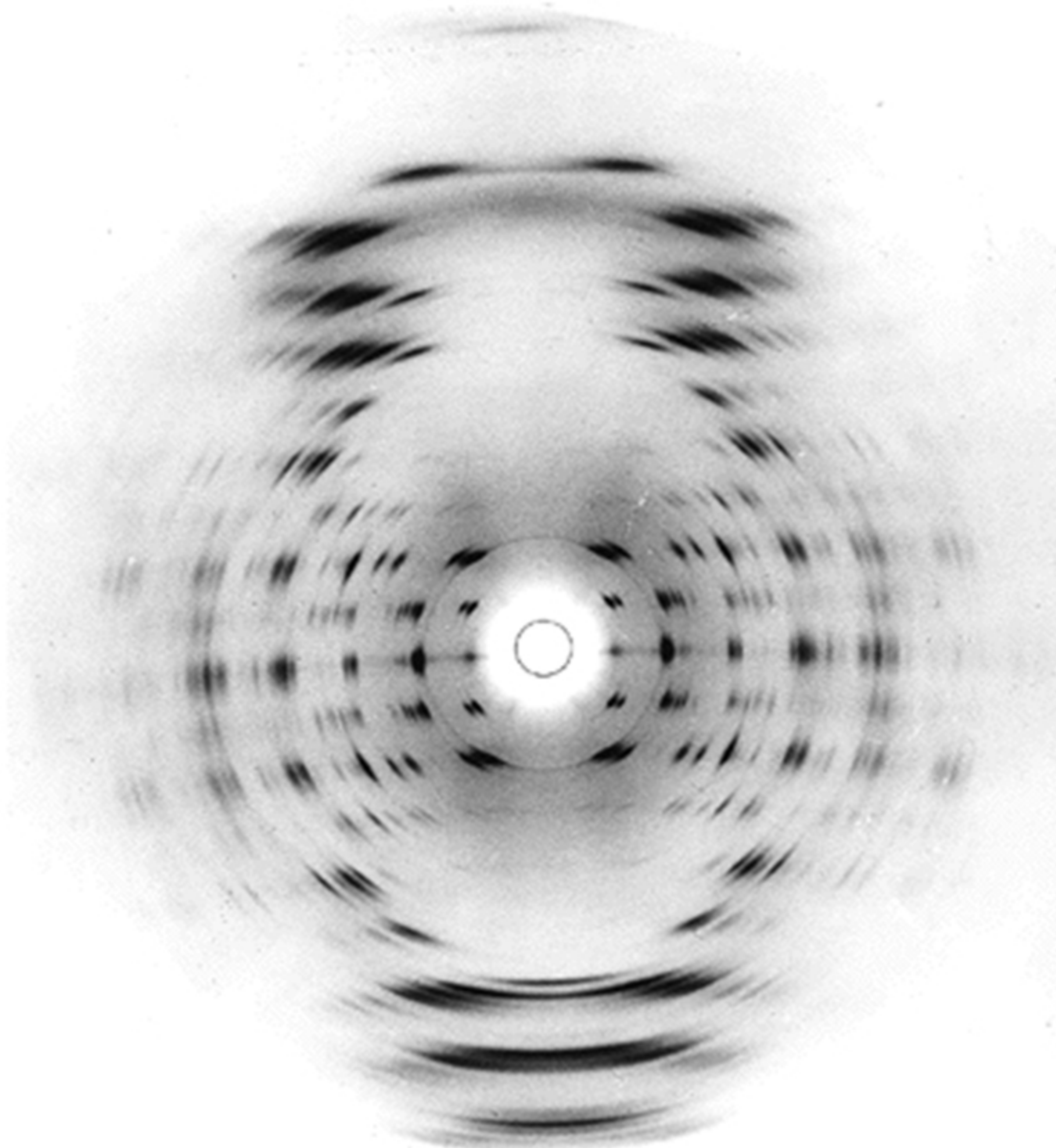
Rosalind Franklin: A Crucial Contribution

A crucial contribution. Rosalind Franklin made a crucial contribution to the discovery of the double helix structure of DNA, but some would say she got a raw deal. Biographer Brenda Maddox called her the "Dark Lady of DNA," based on a once disparaging reference to Franklin by one of her coworkers. Unfortunately, this negative appellation undermined the positive impact of her discovery. Indeed, Franklin is in the shadows of science history, for while her work on DNA was crucial to the discovery of its structure, her contribution to that landmark discovery is little known.

Rosalind Franklin

On to better things. Franklin moved to Birkbeck College where, ironically, she began working on the structure of the tobacco mosaic virus, building on research that Watson had done before his work on DNA. During the next few years she did some of the best and most important work of her life, and she traveled the world talking about coal and virus structure. However, just as her career was peaking, it was cut tragically short when she died of ovarian cancer at age 37.


DNA sample
Beam of X-rays
X-ray source
Lead screen
Photographic
plate



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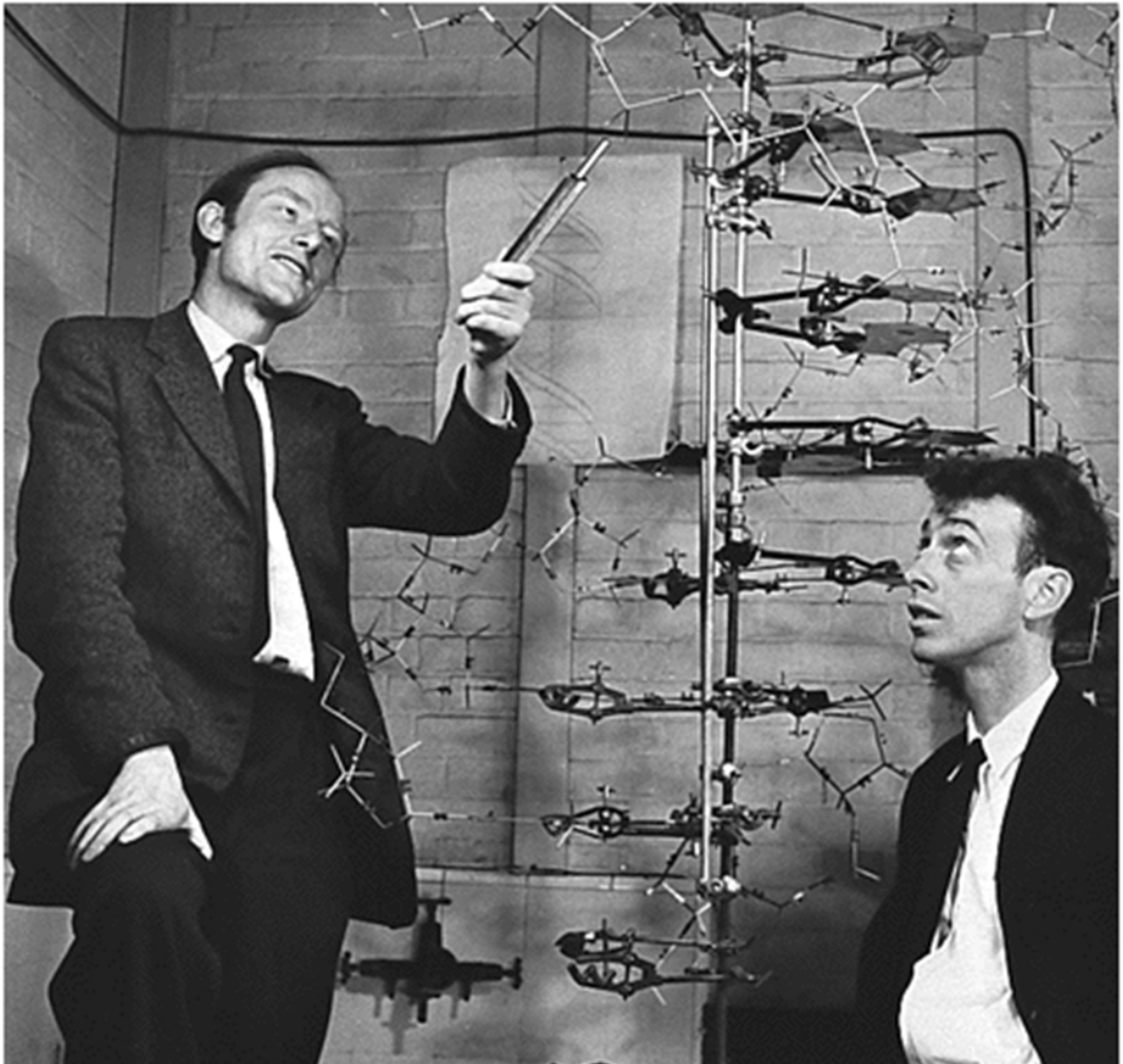
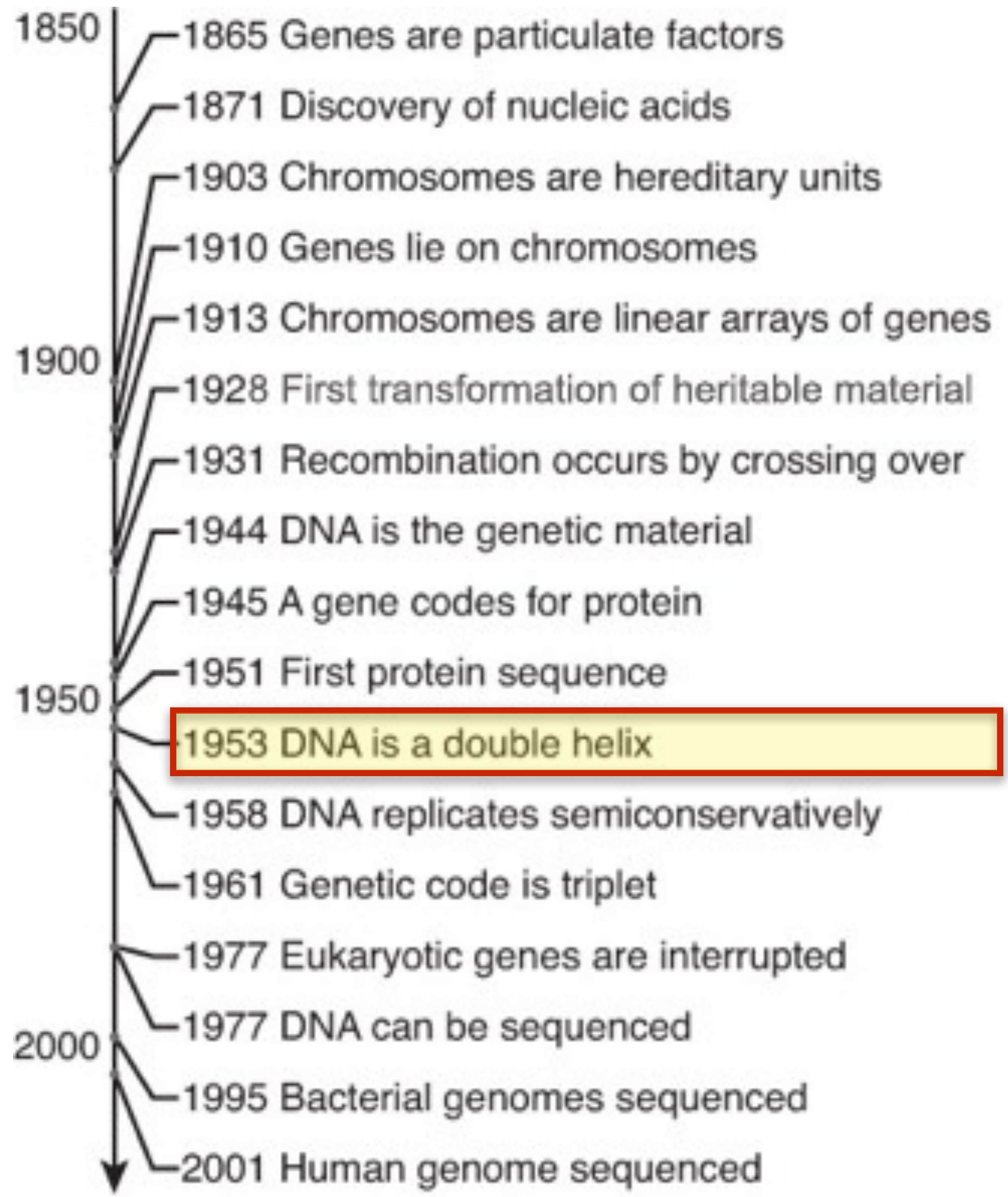




A brief history of genetics.

equipment, and to Dr. G. E. R. Deacon and the captain and officers of R.R.S. *Discovery II* for their part in making the observations.

[1] Young, F. B., Gerrard, H., and Jevons, W., *Phil. Mag.*, **40**, 149 (1920).

[2] Longuet-Higgins, M. S., *Mon. Not. Roy. Astro. Soc., Geophys. Supp.*, **5**, 285 (1949).

[3] Von Arx, W. S., Woods Hole Papers in Phys. Oceanog. Meteor., **11** (3) (1950).

[4] Ekman, V. W., *Arkiv. Mat. Astron. Fysik.* (*Stockholm*), **2** (11) (1905).

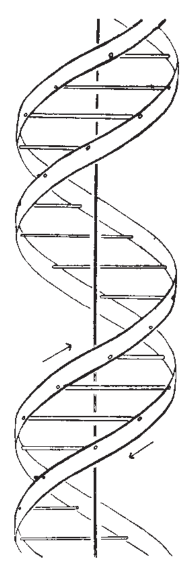
MOLECULAR STRUCTURE OF NUCLEIC ACIDS

A Structure for Deoxyribose Nucleic Acid

WE wish to suggest a structure for the salt of deoxyribose nucleic acid (D.N.A.). This structure has novel features which are of considerable biological interest.

A structure for nucleic acid has already been proposed by Pauling and Corey[1]. They kindly made their manuscript available to us in advance of publication. Their model consists of three intertwined chains, with the phosphates near the fibre axis, and the bases on the outside. In our opinion, this structure is unsatisfactory for two reasons: (1) We believe that the material which gives the X-ray diagrams is the salt, not the free acid. Without the acidic hydrogen atoms it is not clear what forces would hold the structure together, especially as the negatively charged phosphates near the axis will repel each other. (2) Some of the van der Waals distances appear to be too small.

Another three-chain structure has also been suggested by Fraser (in the press). In his model the phosphates are on the outside and the bases on the inside, linked together by hydrogen bonds. This structure as described is rather ill-defined, and for this reason we shall not comment on it.



This figure is purely diagrammatic. The two ribbons symbolize the two phosphate—sugar chains, and the horizontal rods the pairs of bases holding the chains together. The vertical line marks the fibre axis

We wish to put forward a radically different structure for the salt of deoxyribose nucleic acid. This structure has two helical chains each coiled round the same axis (see diagram). We have made the usual chemical assumptions, namely, that each chain consists of phosphate diester groups joining β-D-deoxyribofuranose residues with 3′,5′ linkages. The two chains (but not their bases) are related by a dyad perpendicular to the fibre axis. Both chains follow right-handed helices, but owing to the dyad the sequences of the atoms in the two chains run in opposite directions. Each chain loosely resembles Furberg's[2] model No. 1; that is, the bases are on the inside of the helix and the phosphates on the outside. The configuration of the sugar and the atoms near it is close to Furberg's 'standard configuration', the sugar being roughly perpendicular to the attached base. There is a residue on each chain every 3·4 A. in the z-direction. We have assumed an angle of 36° between adjacent residues in the same chain, so that the structure repeats after 10 residues on each chain, that is, after 34 A. The distance of a phosphorus atom from the fibre axis is 10 A. As the phosphates are on the outside, cations have easy access to them.

The structure is an open one, and its water content is rather high. At lower water contents we would expect the bases to tilt so that the structure could become more compact.

The novel feature of the structure is the manner in which the two chains are held together by the purine and pyrimidine bases. The planes of the bases are perpendicular to the fibre axis. They are joined together in pairs, a single base from one chain being hydrogen-bonded to a single base from the other chain, so that the two lie side by side with identical z-co-ordinates. One of the pair must be a purine and the other a pyrimidine for bonding to occur. The hydrogen bonds are made as follows: purine position 1 to pyrimidine position 1; purine position 6 to pyrimidine position 6.

If it is assumed that the bases only occur in the structure in the most plausible tautomeric forms (that is, with the keto rather than the enol configurations) it is found that only specific pairs of bases can bond together. These pairs are: adenine (purine) with thymine (pyrimidine), and guanine (purine) with cytosine (pyrimidine).

In other words, if an adenine forms one member of a pair, on either chain, then on these assumptions the other member must be thymine; similarly for guanine and cytosine. The sequence of bases on a single chain does not appear to be restricted in any way. However, if only specific pairs of bases can be formed, it follows that if the sequence of bases on one chain is given, then the sequence on the other chain is automatically determined.

It has been found experimentally[3,4] that the ratio of the amounts of adenine to thymine, and the ratio of guanine to cytosine, are always very close to unity for deoxyribose nucleic acid.

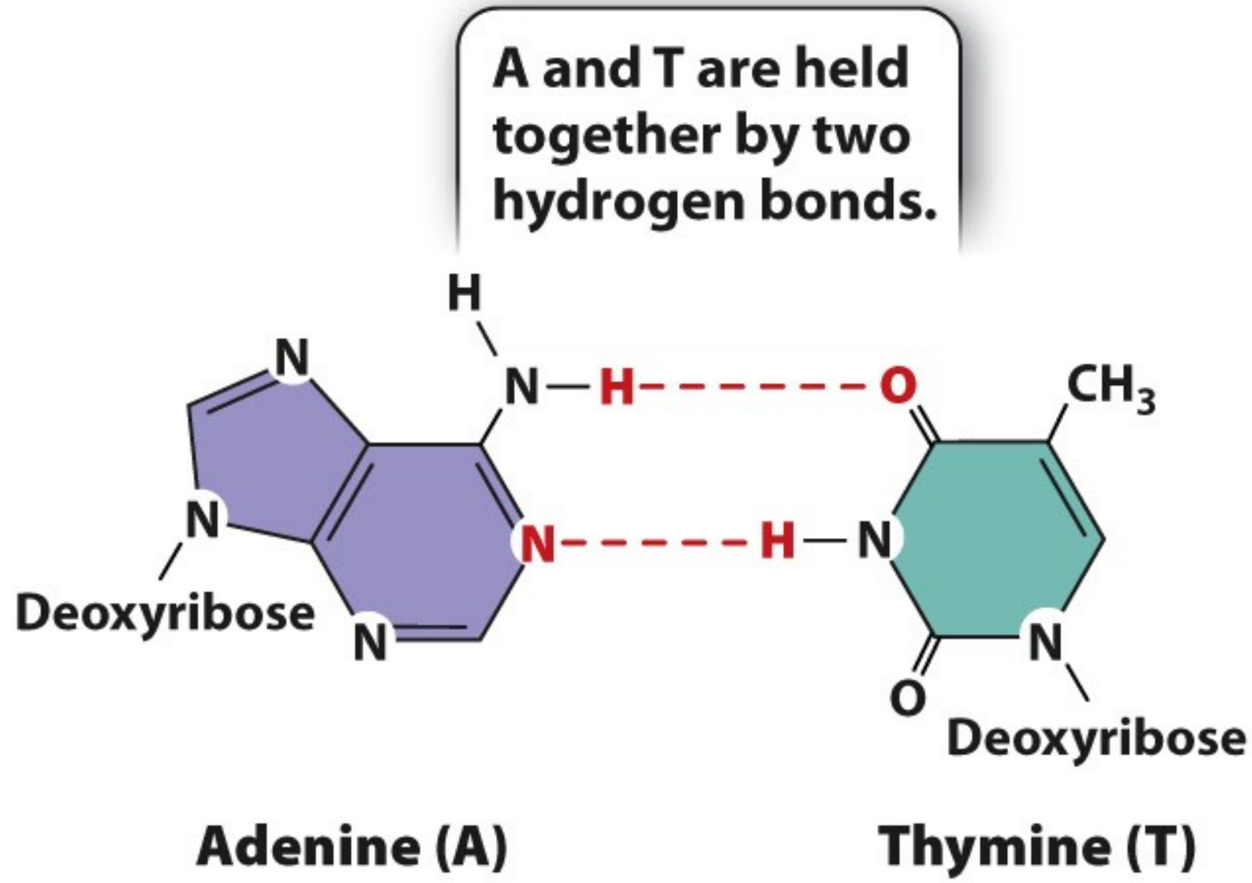
It is probably impossible to build this structure with a ribose sugar in place of the deoxyribose, as the extra oxygen atom would make too close a van der Waals contact.

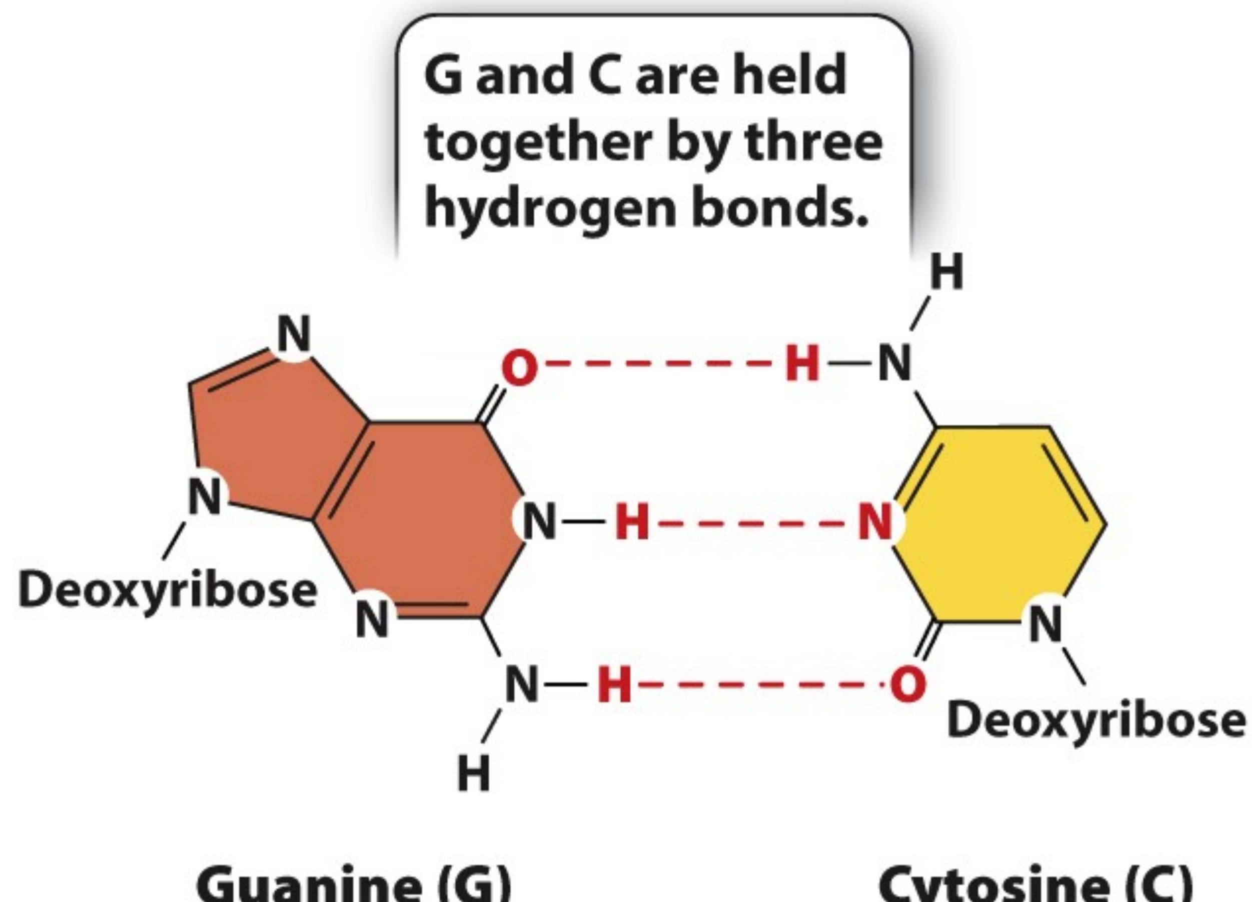
The previously published X-ray data[5,6] on deoxyribose nucleic acid are insufficient for a rigorous test of our structure. So far as we can tell, it is roughly compatible with the experimental data, but it must be regarded as unproved until it has been checked against more exact results. Some of these are given in the following communications. We were not aware of the details of the results presented there when we devised our structure, which rests mainly though not entirely on published experimental data and stereochemical arguments.

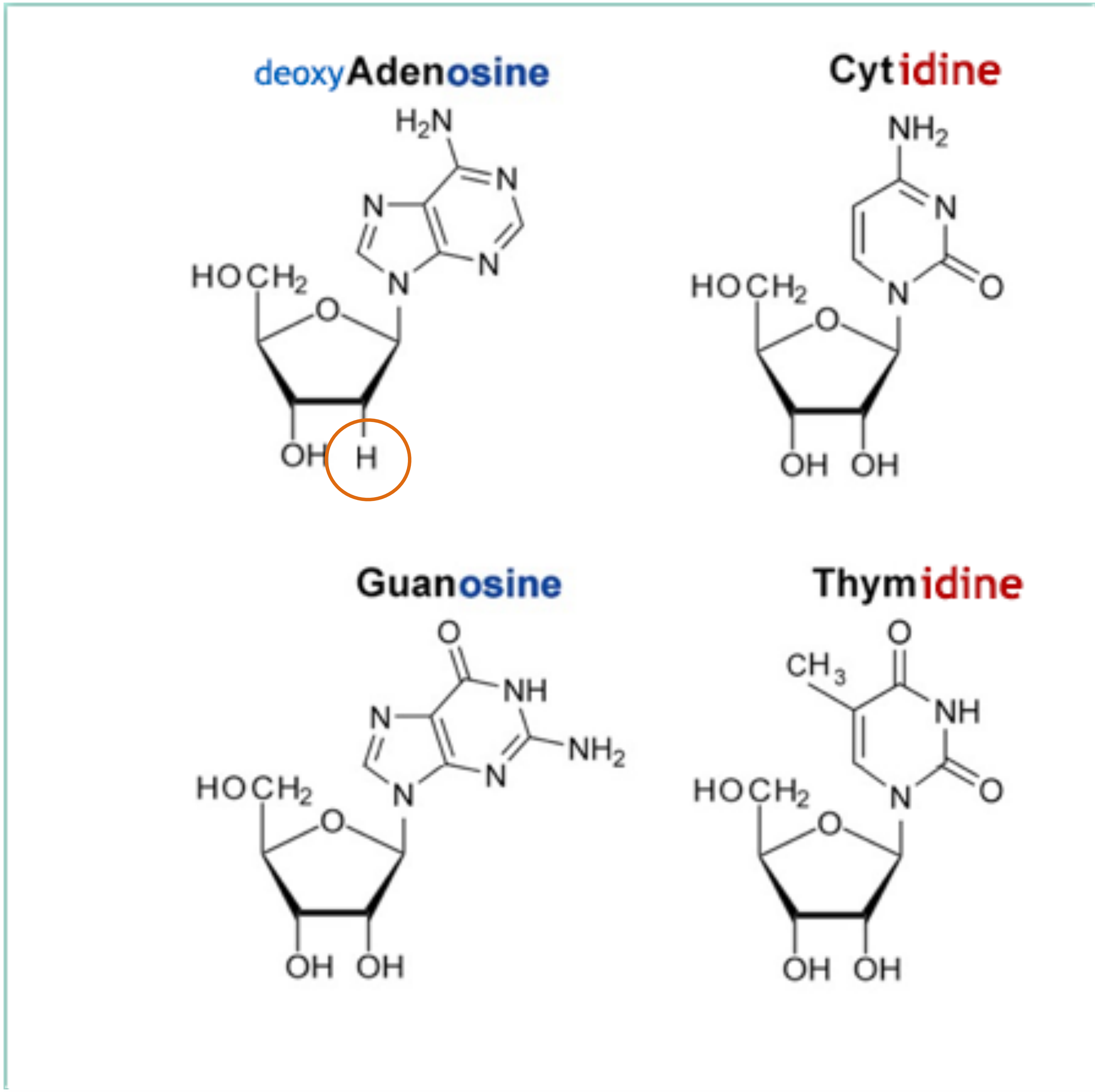
It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material.

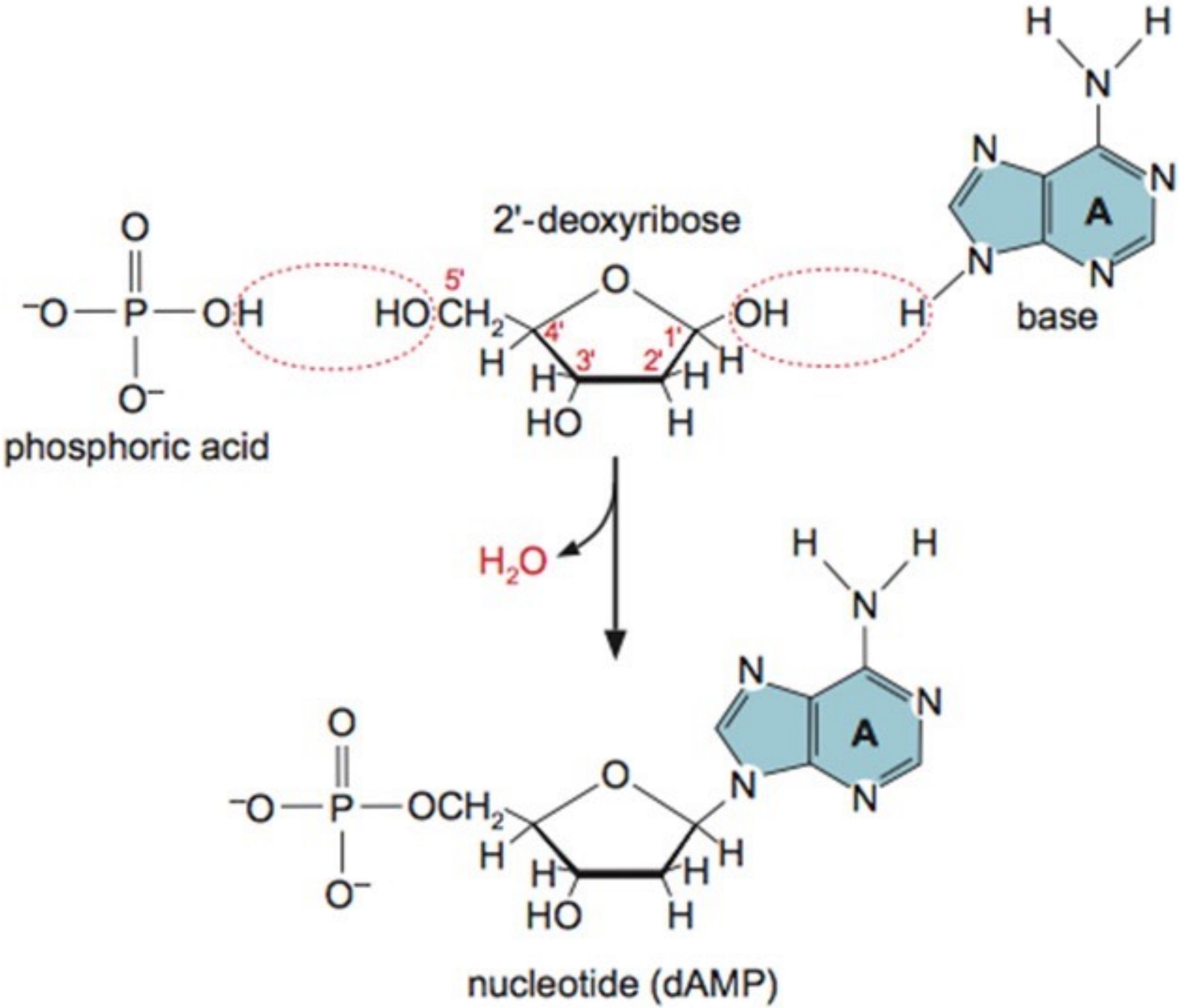
Full details of the structure, including the conditions assumed in building it, together with a set of co-ordinates for the atoms, will be published elsewhere.

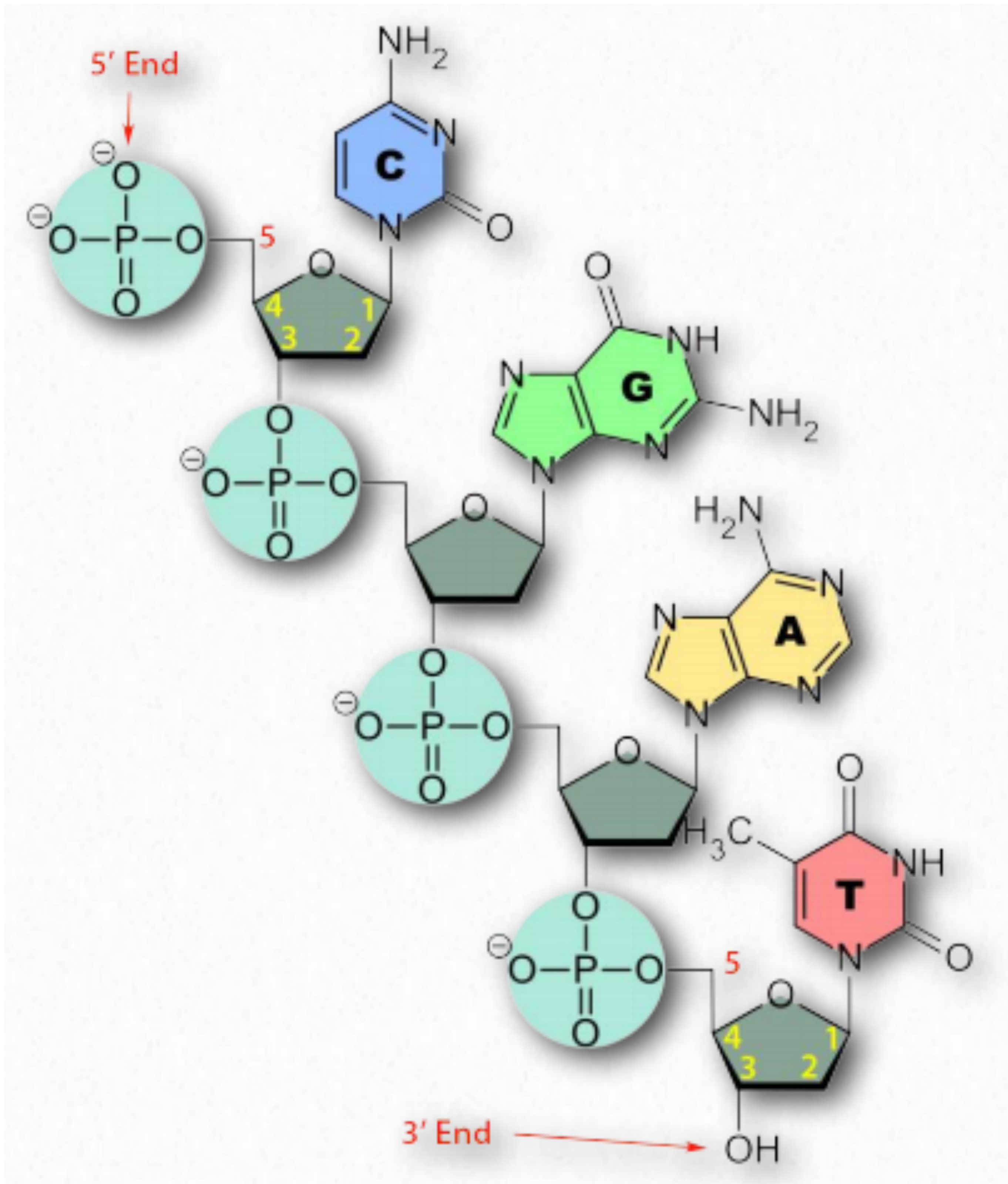
We are much indebted to Dr. Jerry Donohue for constant advice and criticism, especially on inter-atomic distances. We have also been stimulated by a knowledge of the general nature of the unpublished experimental results and ideas of Dr. M. H. F. Wilkins, Dr. R. E. Franklin and their co-workers at

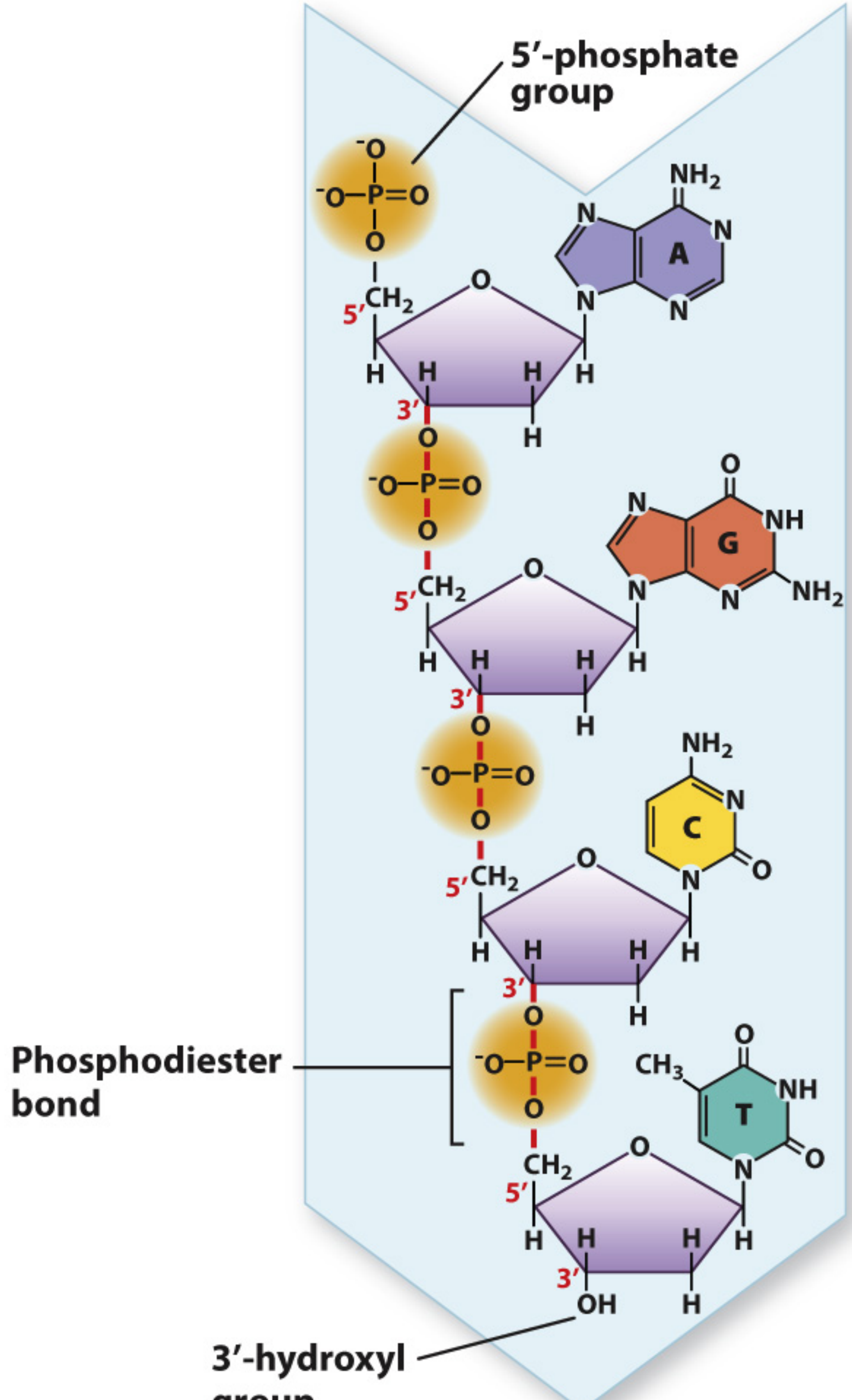

A and T are held together by two hydrogen bonds.
H
N
N—H
O
CH3
N
N
H—N
Deoxyribose
N
N
O
Deoxyribose
Adenine (A)
Thymine (T)


G and C are held together by three hydrogen bonds.
H
N
O
H—N
N
N—H
N
Deoxyribose
N
N
N—H
O
Deoxyribose
H
Guanine (G)
Cytosine (C)


deoxyAdenosine
Cytidine
Guanosine
Thymidine


2'-deoxyribose
phosphoric acid
base
5'
4'
3'
2'
1'
A
H2O
nucleotide (dAMP)


5′ End
3′ End
C
G
A
T
OH



5′-phosphate group
A
G
C
T
5′
3′
Phosphodiester bond
3′-hydroxyl group

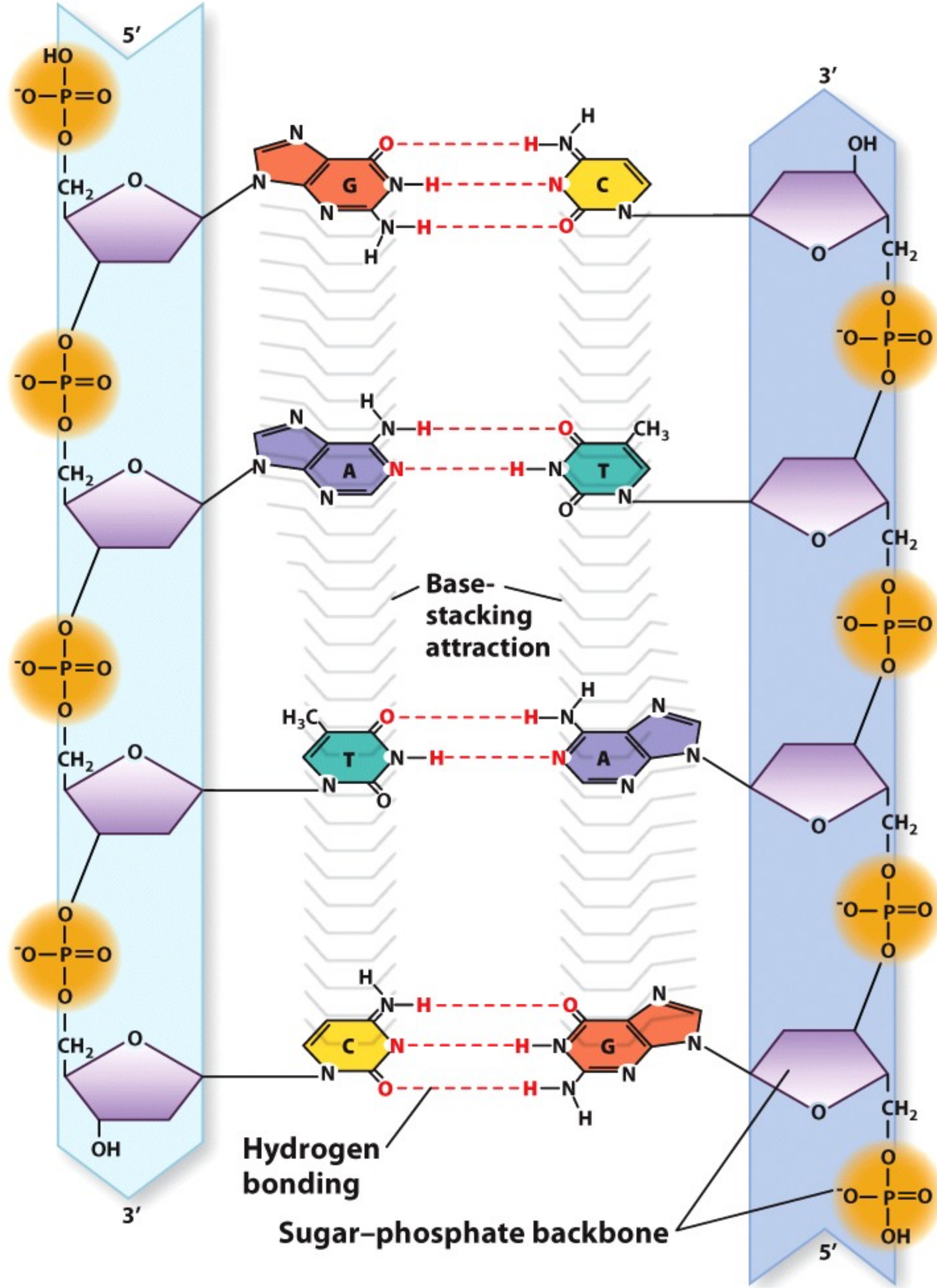
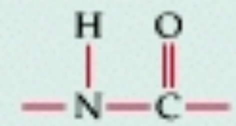
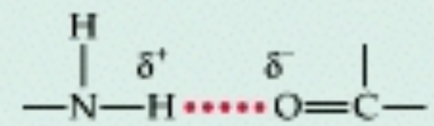
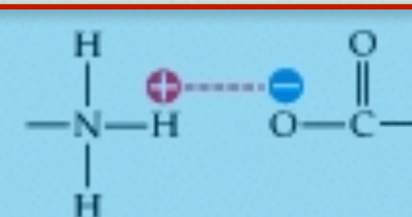
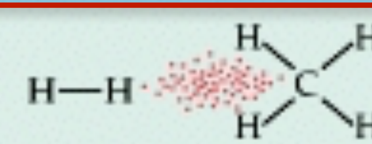
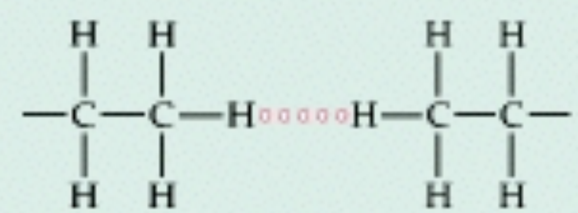


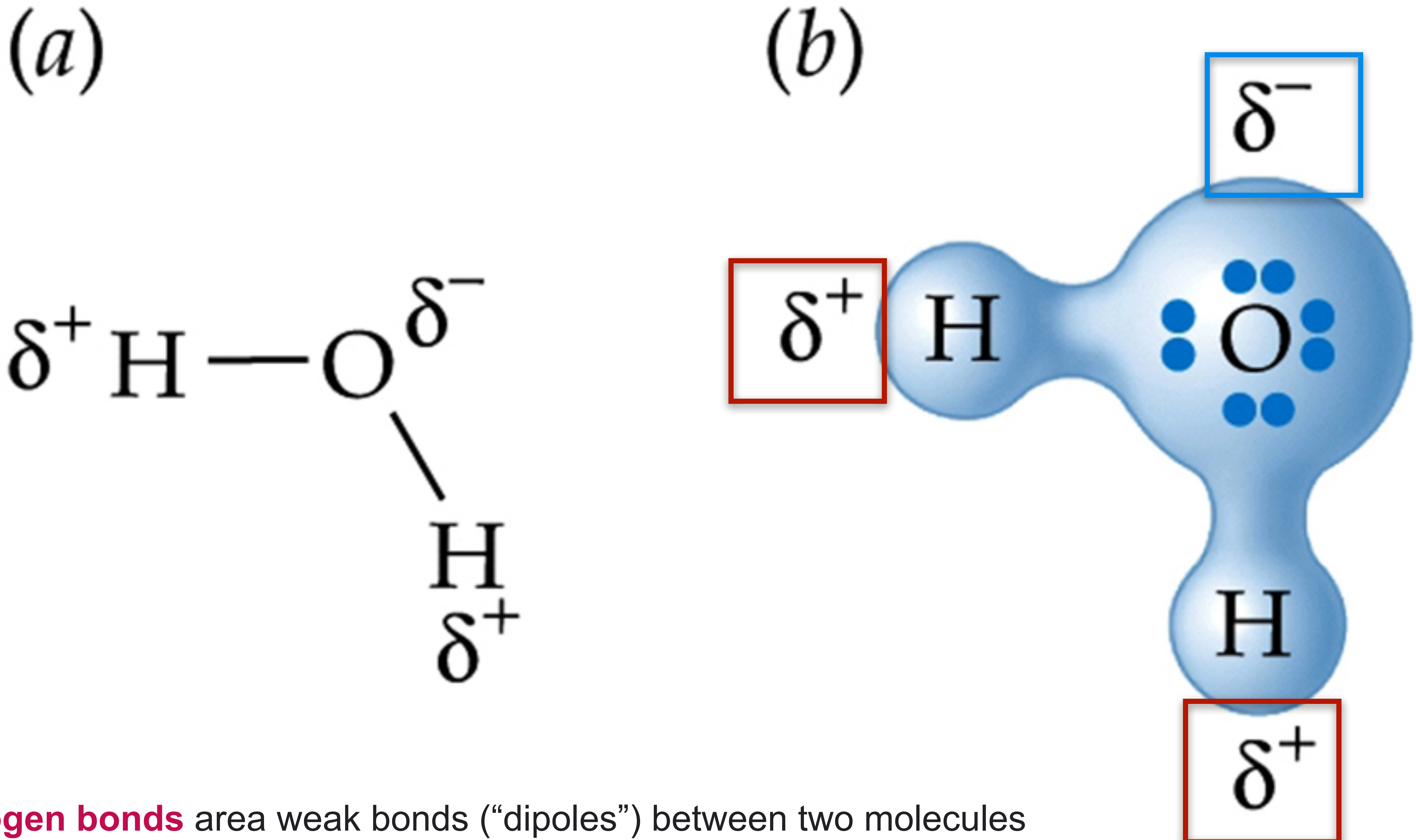
Figure 3.10

Biology: How Life Works

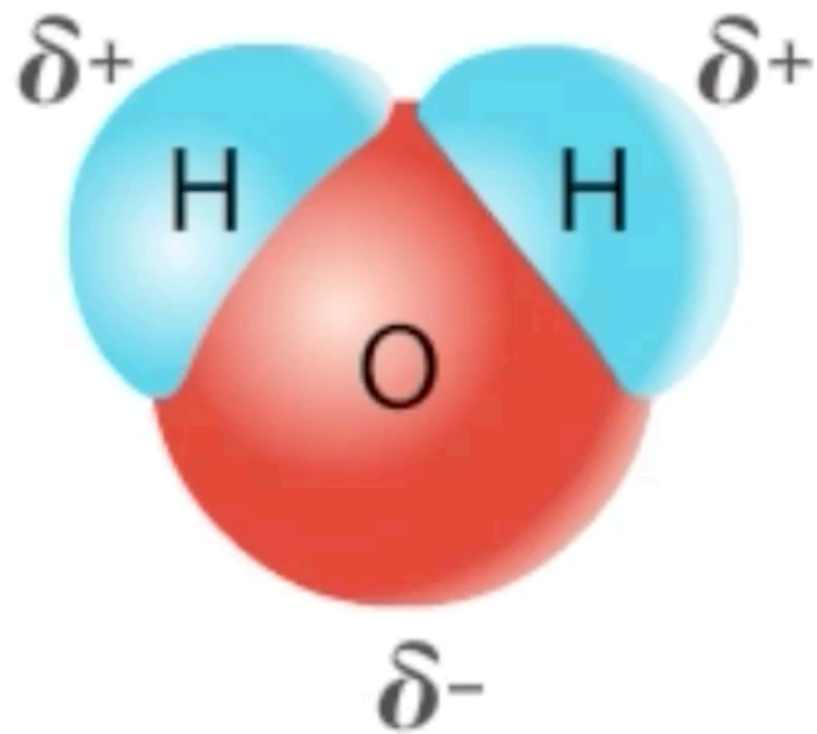
2.1 Chemical Bonds and Interactions

NAME	BASIS OF INTERACTION	STRUCTURE	BOND ENERGY[a] (KCAL/MOL)
Covalent bond	Sharing of electron pairs		50–110
Hydrogen bond	**Weak electrostatic interactions**		3–7
Ionic interaction	Attraction of opposite charges		3–7
van der Waals interaction	Interaction of electron clouds		1
Hydrophobic interaction	Interaction of nonpolar substances		1–2

[a]*Bond energy* is the amount of energy needed to separate two bonded or interacting atoms under physiological conditions.



Hydrogen bonds area weak bonds (“dipoles”) between two molecules -resulting from electrostatic attractions between a proton in one molecule and an electronegative region of a molecule in the other.


δ+
δ+
H
H
O
δ−

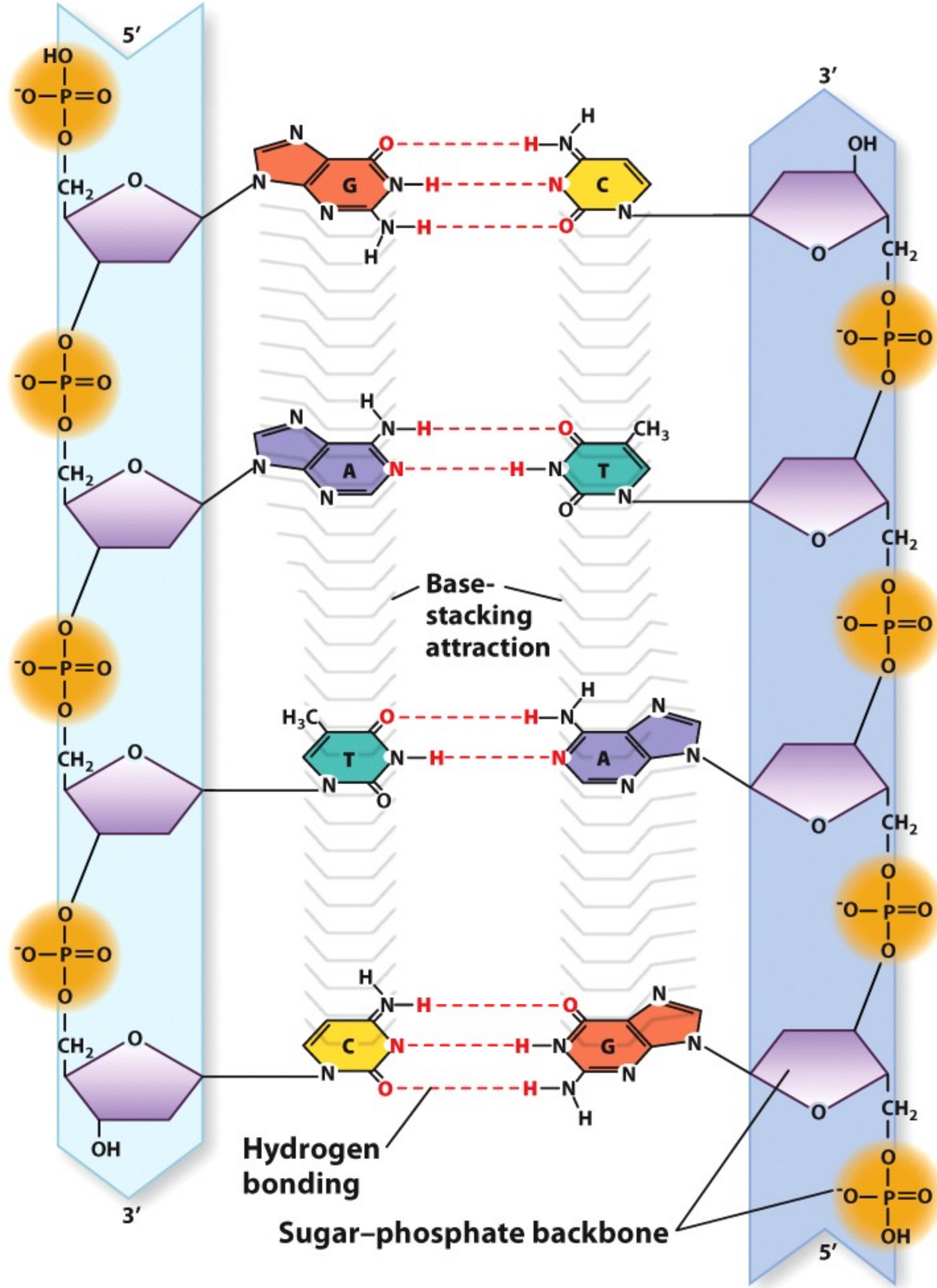
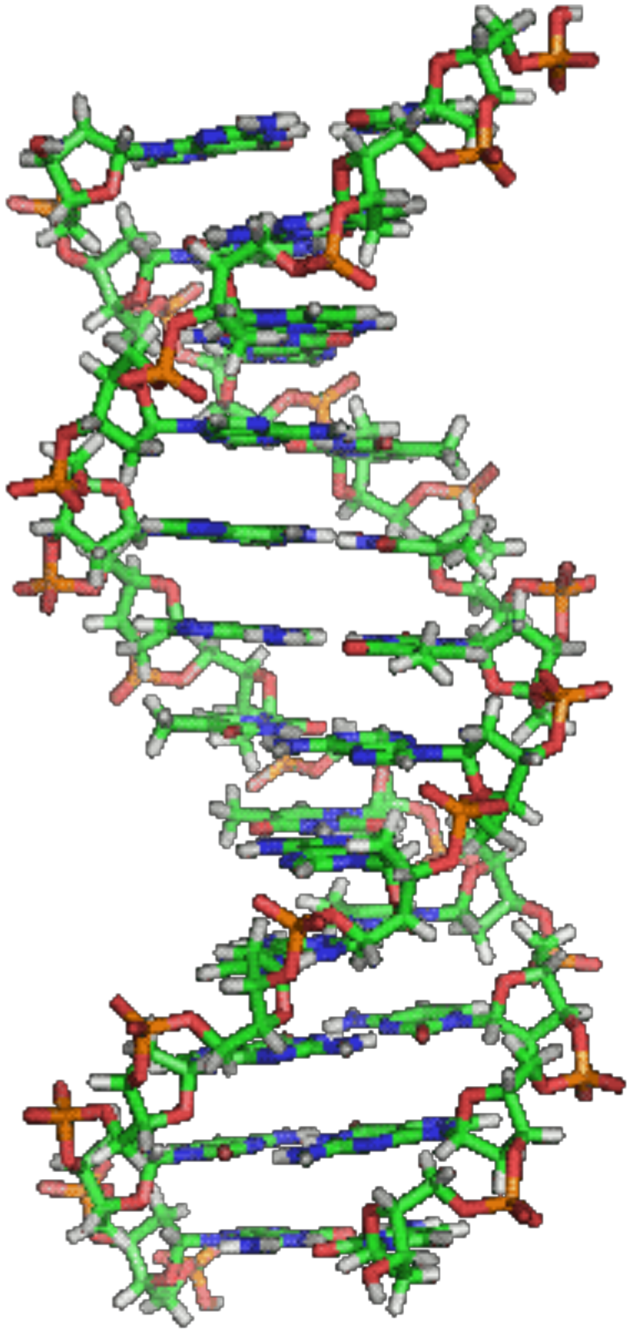
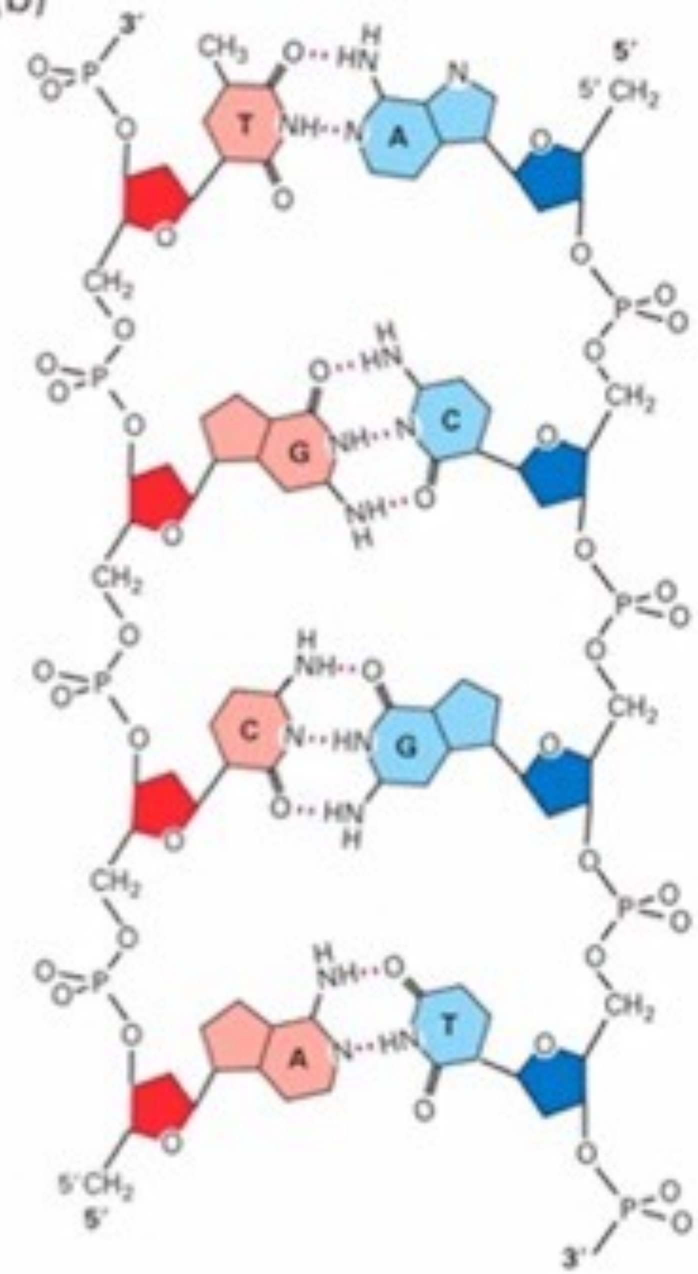


Figure 3.10

Biology: How Life Works



(b)

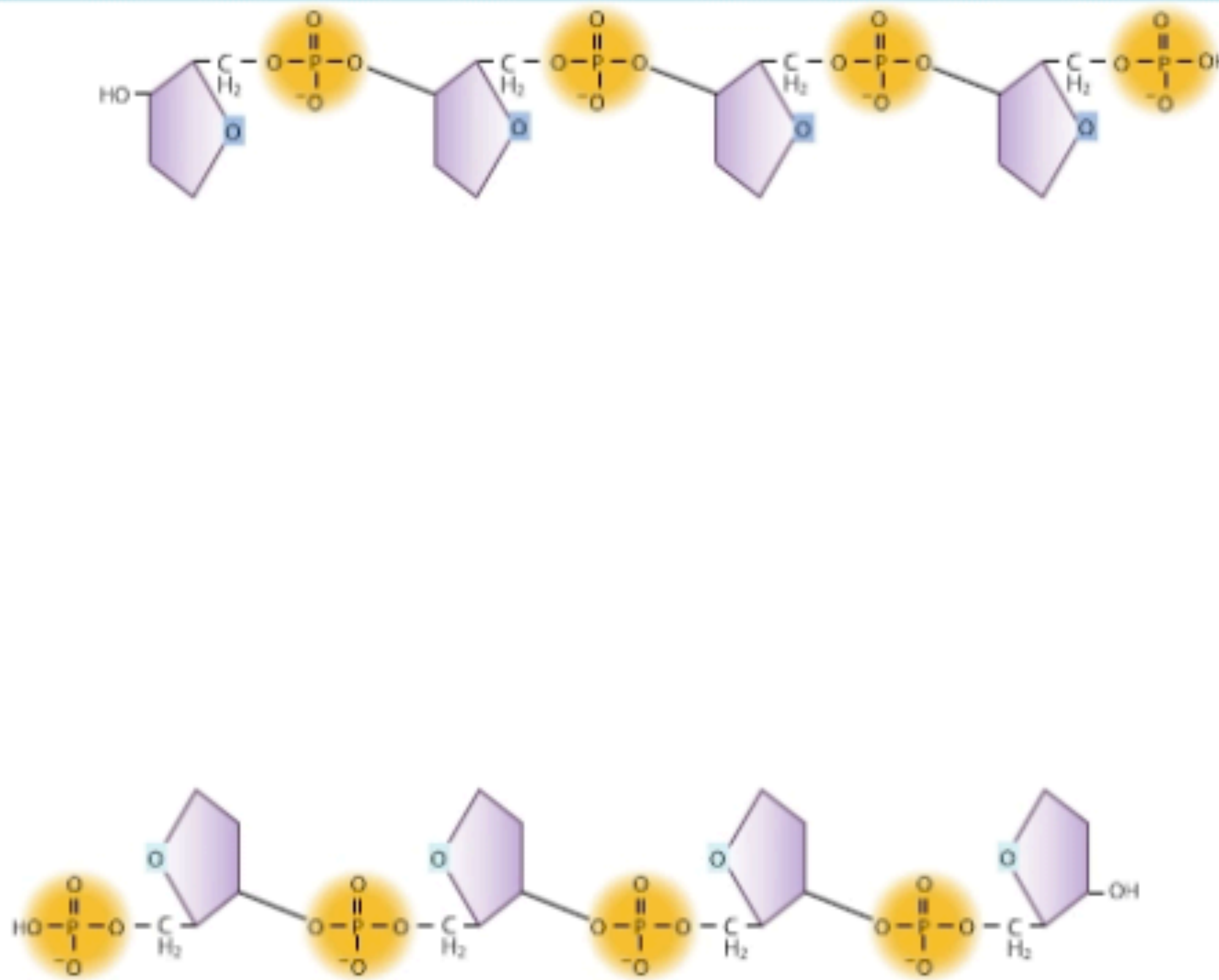


B form DNA

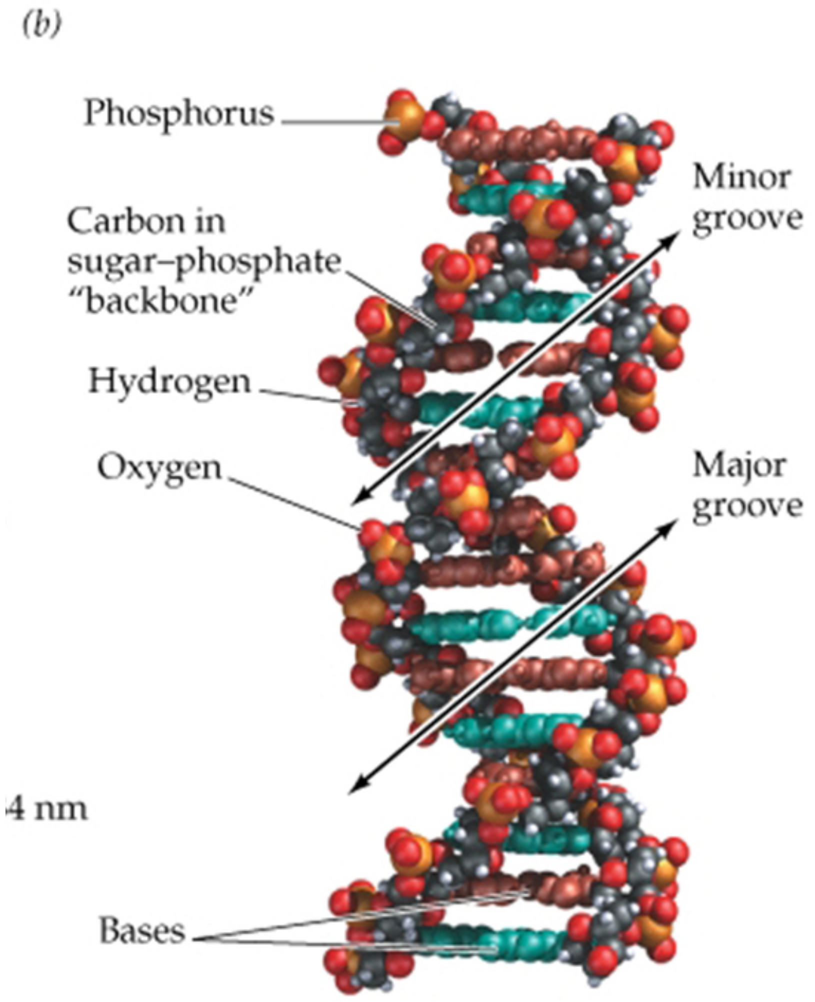
2.0 nM dia (20 Á)
0.36 nM (3.6 Á)
  between bases
~10 bases per turn
antiparallel strands
bases perpendicular
  to axis

Figure 4-3

Base Pairing and Base Stacking

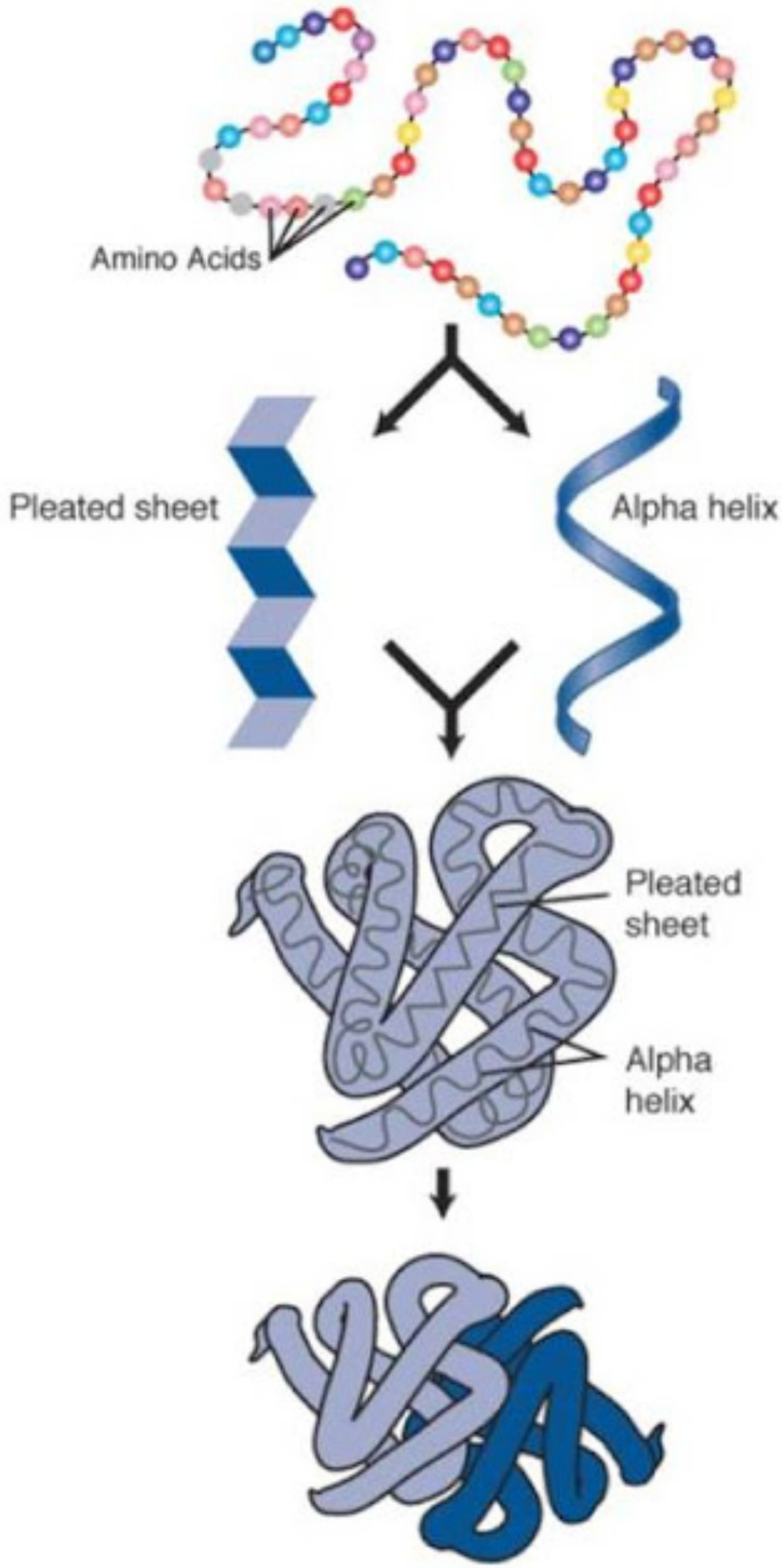


Double-stranded DNA consists of two paired strands that run in opposite directions. The oppositely oriented strands are said to be antiparallel.



As the genetic material of the cell, DNA must perform four important functions:

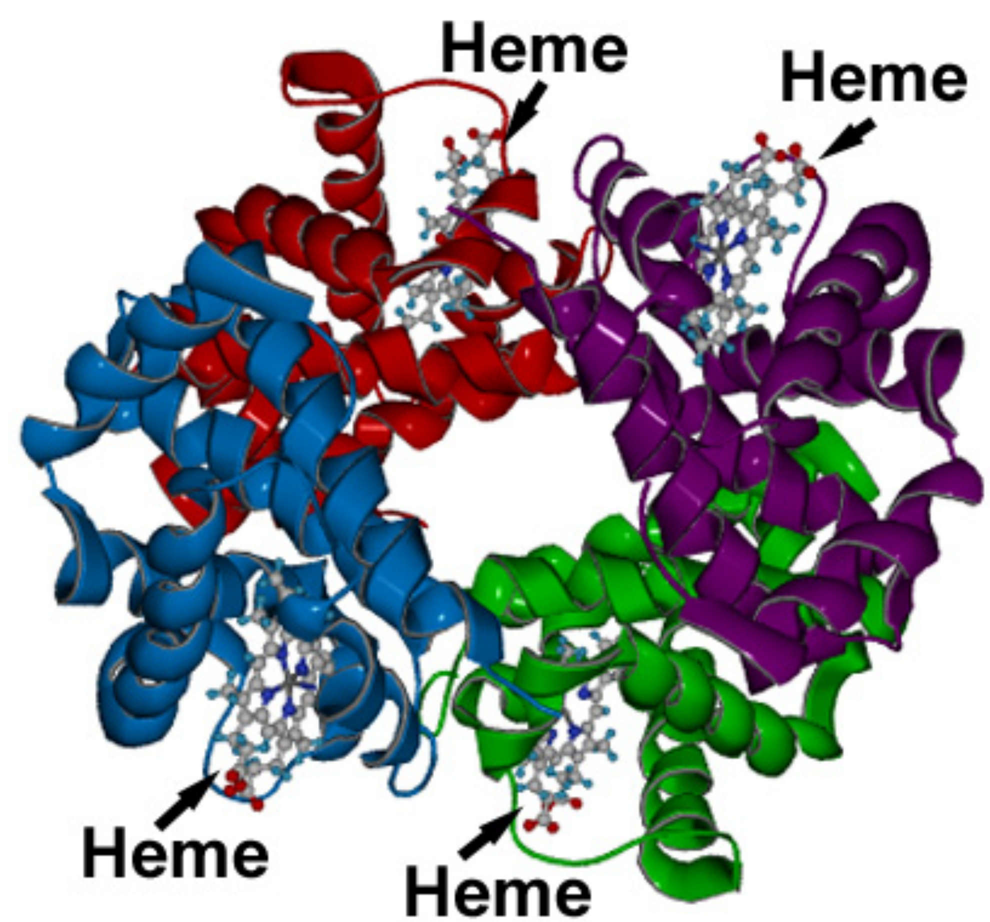
Rubin’s Vase

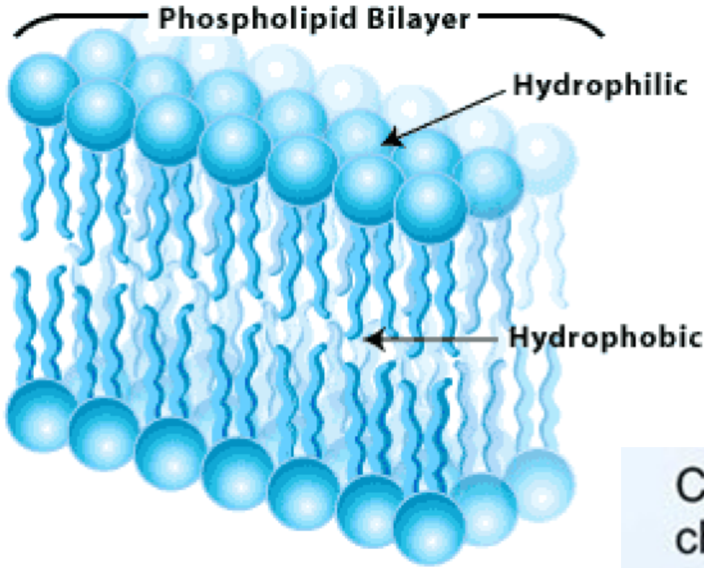


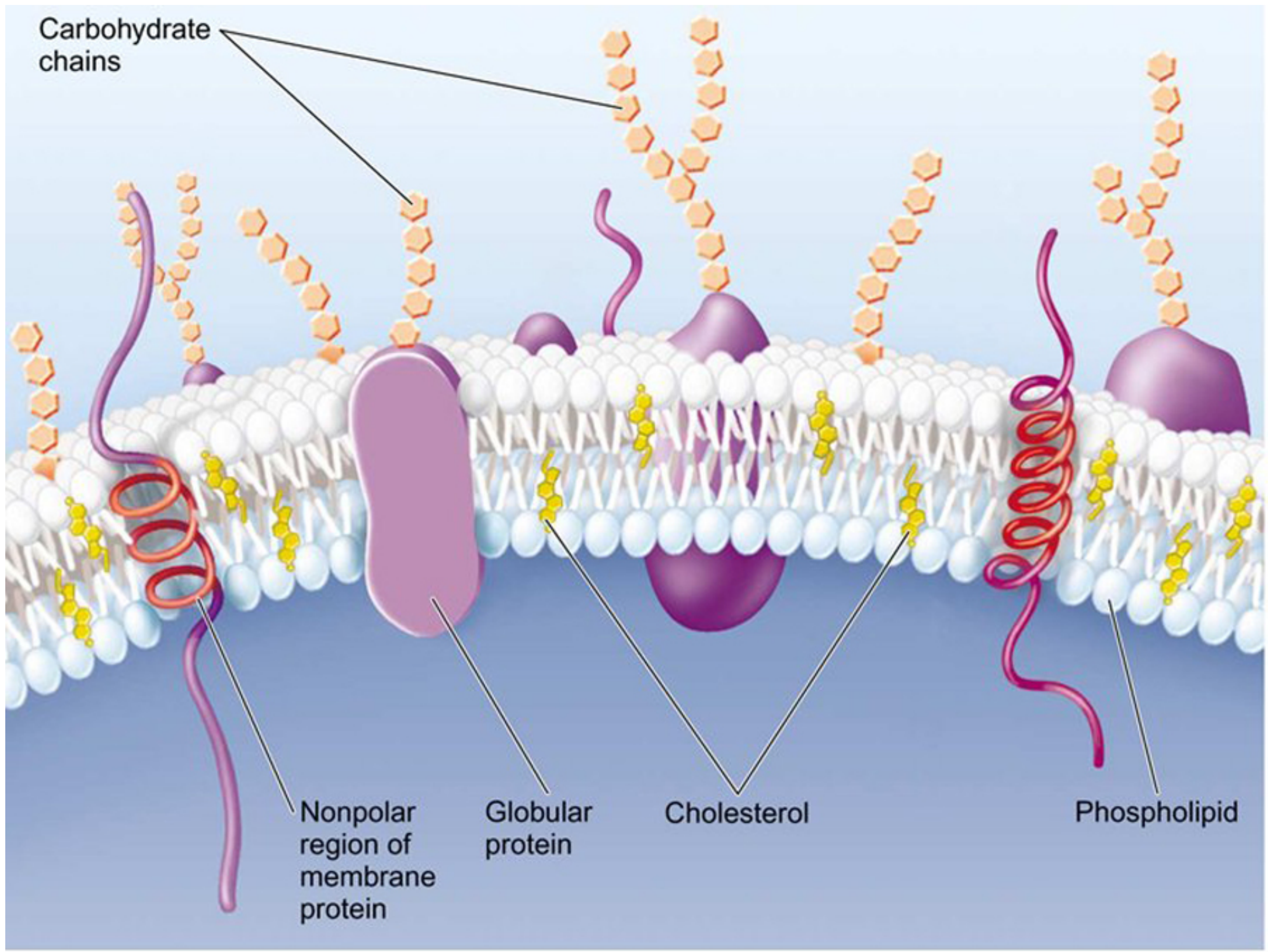
Levels of protein organization

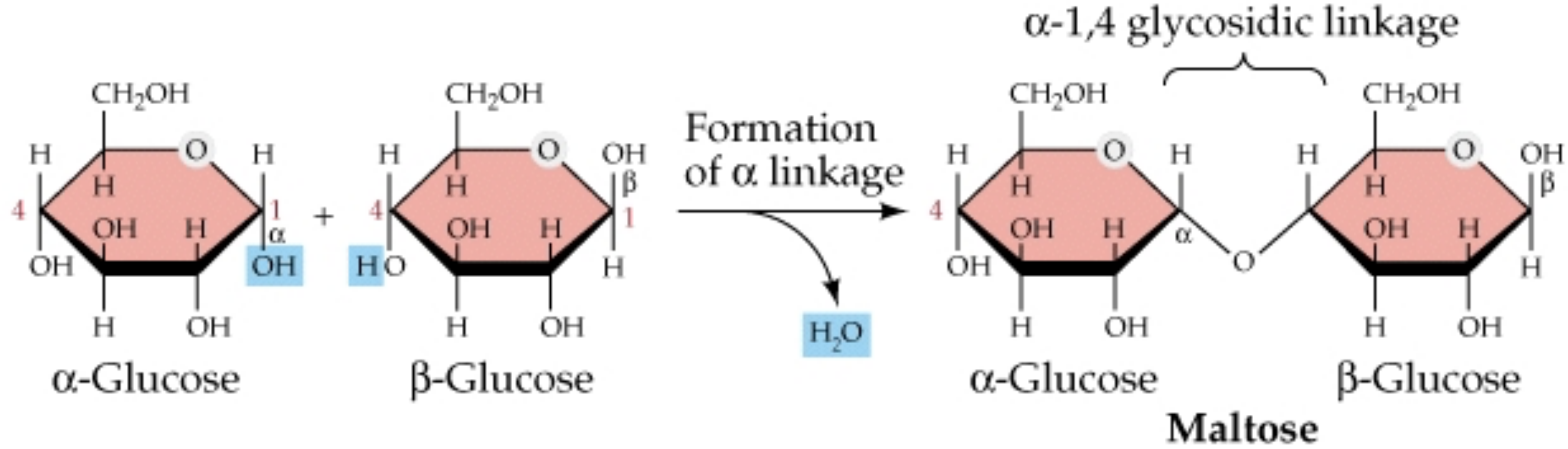
Primary protein structure
is sequence of a chain of amino acids

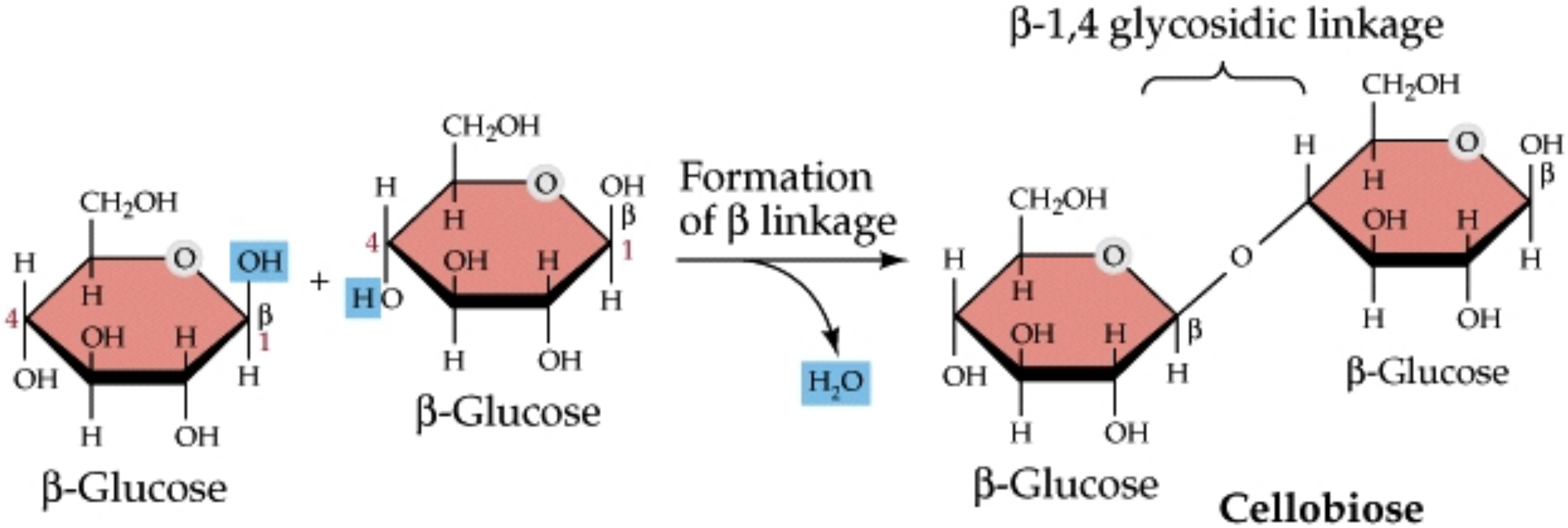
Secondary protein structure
occurs when the sequence of amino acids
are linked by hydrogen bonds




Phospholipid Bilayer
Hydrophilic
Hydrophobic

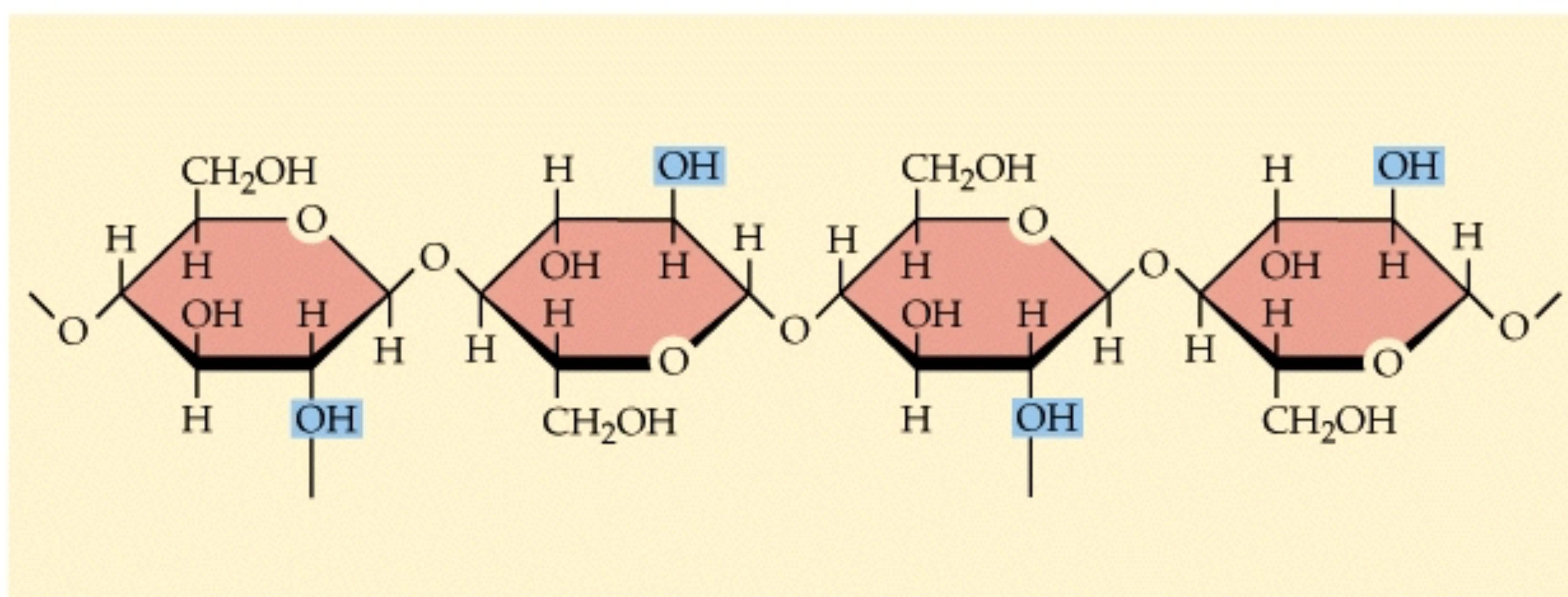

Carbohydrate chains
Nonpolar region of membrane protein
Globular protein
Cholesterol
Phospholipid

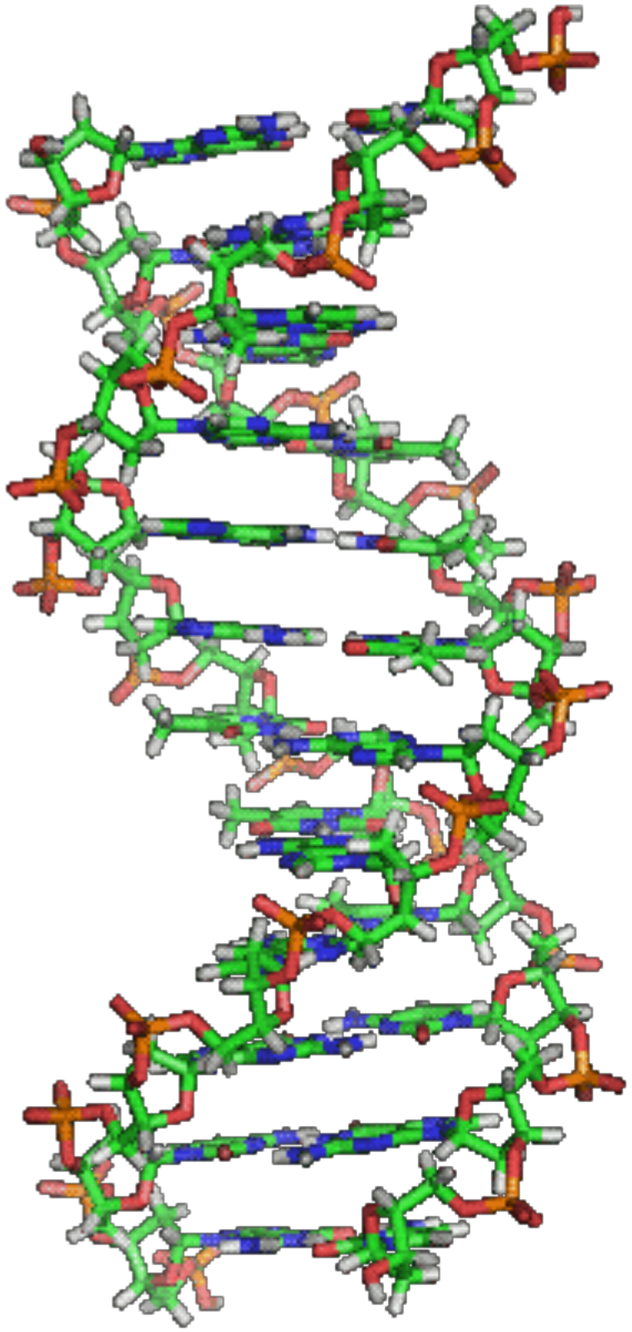




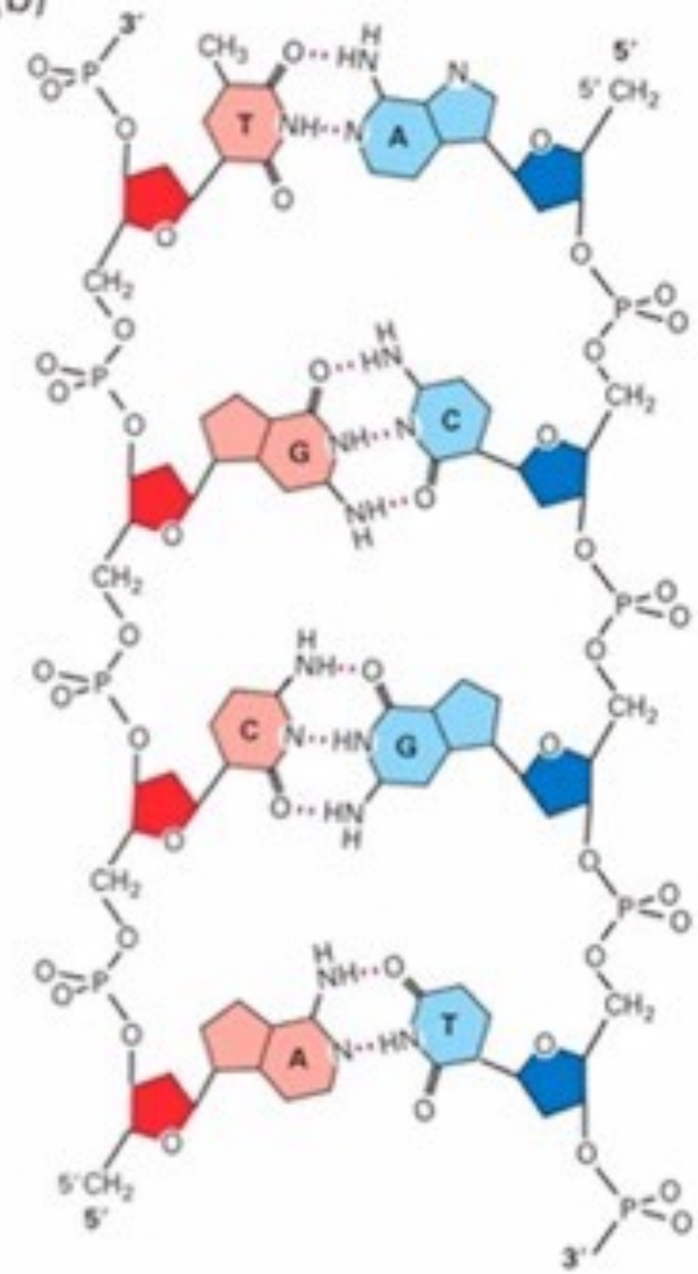
(*a*) **Molecular structure**

Cellulose





(b)



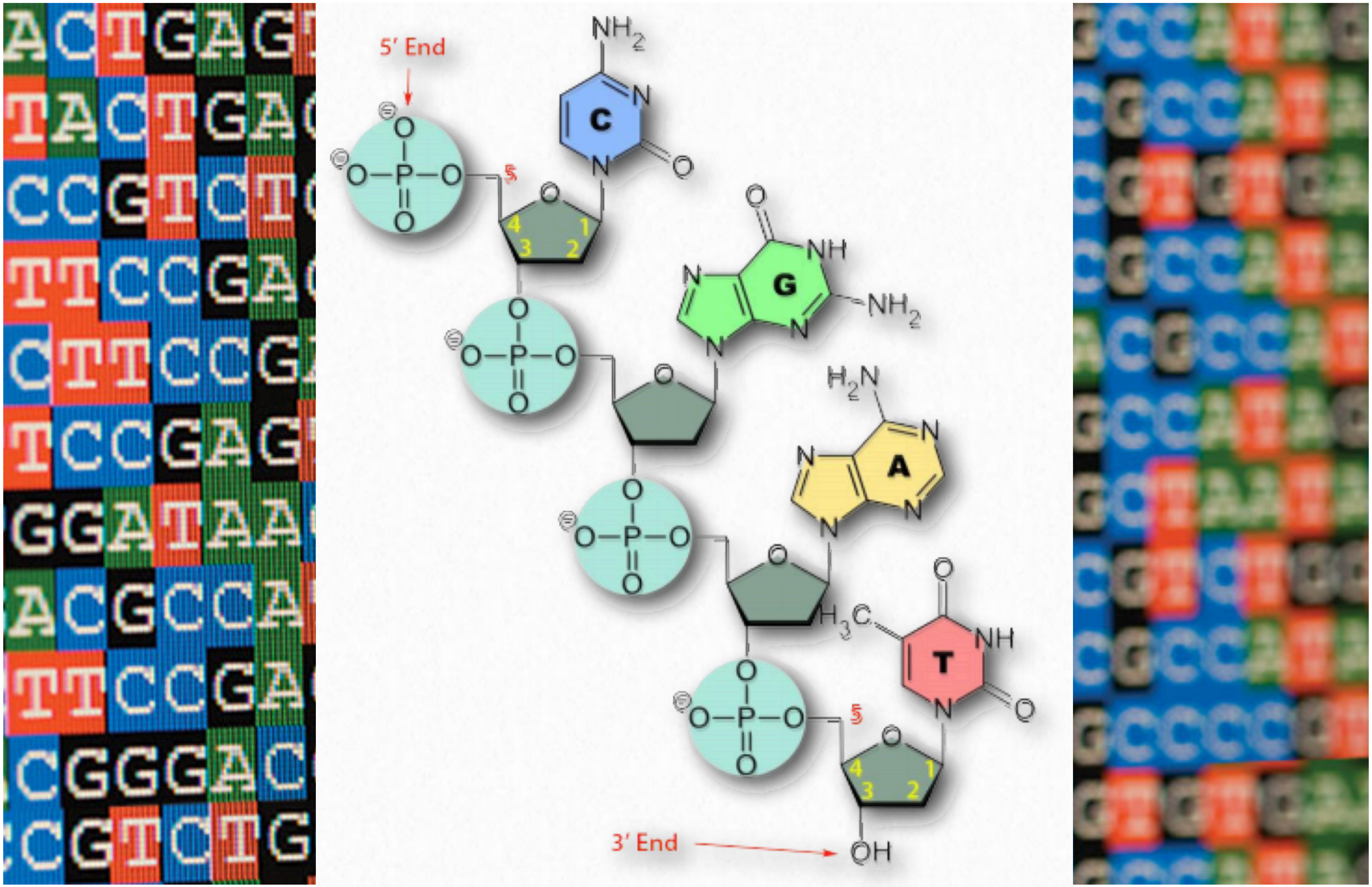
B form DNA

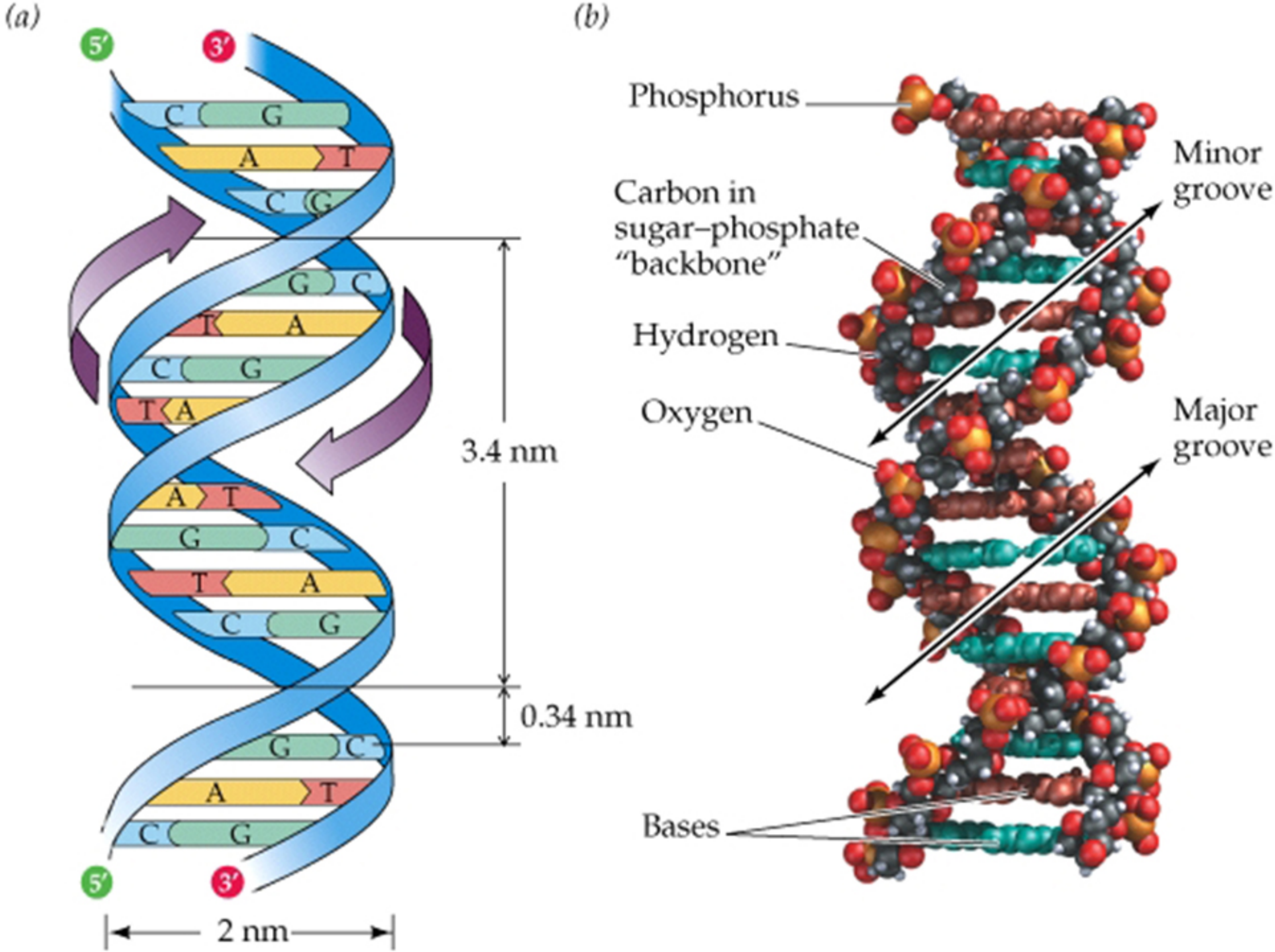
2.0 nM dia (20 Ǻ)
0.36 nM (3.6 Ǻ)
between bases
~10 bases per turn
antiparallel strands
bases perpendicular
to axis

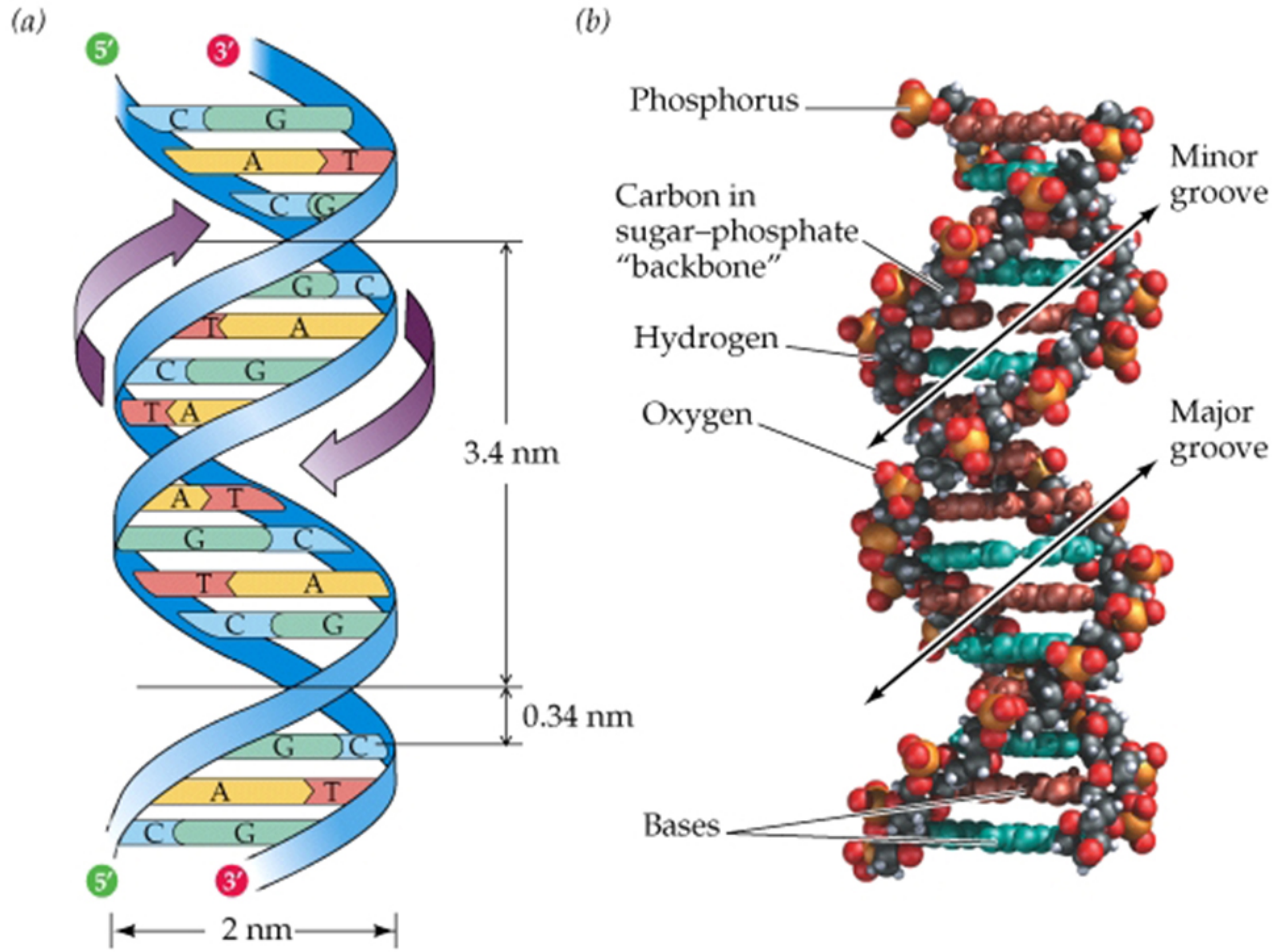
Figure 4-3

Rubin’s Vase illusion


FedEx


5' End
C
G
A
T
3' End


(a)
5′
3′
C
G
A
T
3.4 nm
0.34 nm
5′
3′
2 nm
(b)
Phosphorus
Carbon in sugar–phosphate "backbone"
Hydrogen
Oxygen
Bases
Minor groove
Major groove



As the genetic material of the cell, DNA must perform four important functions:

It must be able to store all of an organism's genetic information.

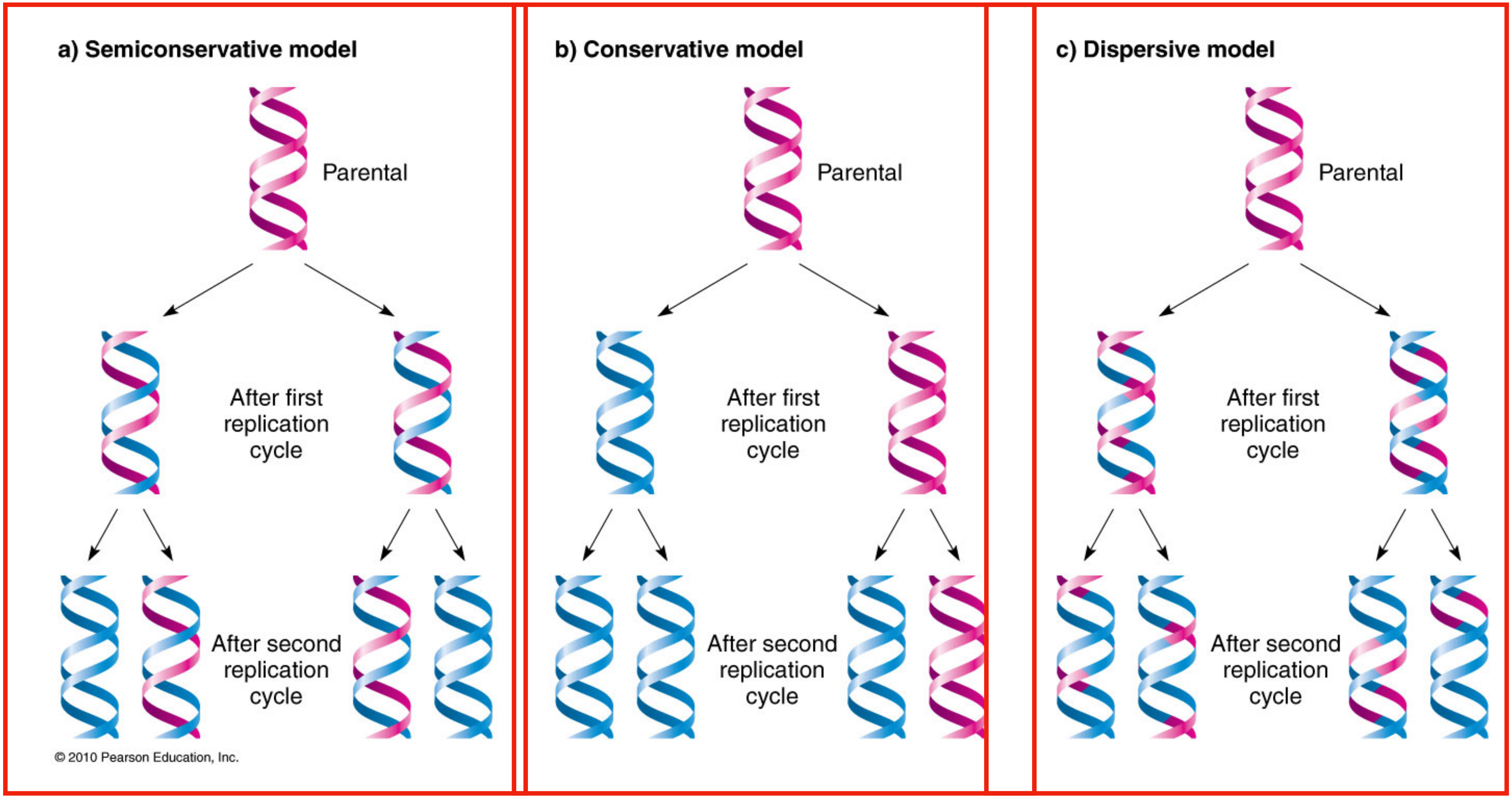
Meselson and Stahl distinguished parental strands of DNA ("old") from newly synthesized strands using two isotopes of nitrogen atoms.

The researchers first grew bacterial cells on medium containing only the heavy ^{15}N form of nitrogen. As the cells grew, ^{15}N was incorporated into the DNA bases, resulting, after several generations, in DNA containing only ^{15}N.

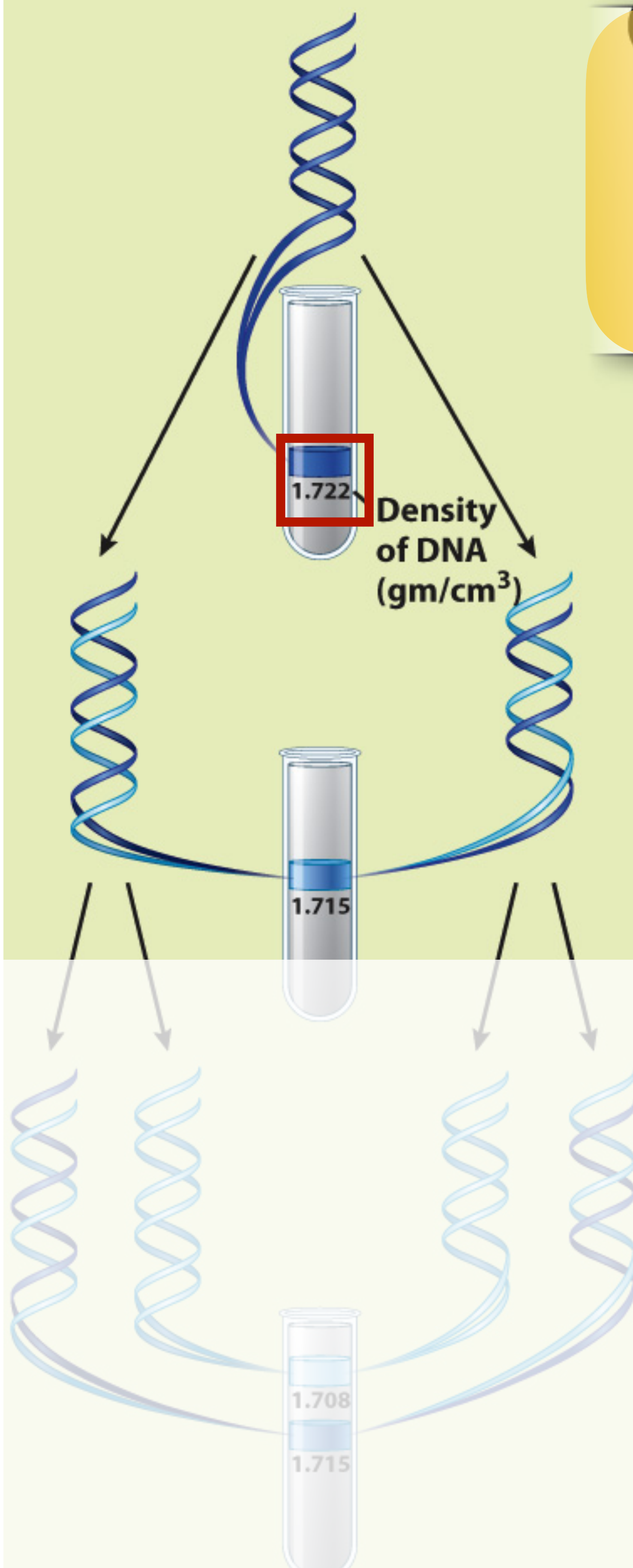
They then transferred the cells into medium containing only light ^{14}N nitrogen.

After one round of replication in this medium, cell replication was halted. While the researchers could not observe the DNA directly they could measure the density of the DNA by spinning it in a high-speed centrifuge in tubes containing a solution of caesium chloride.

3 potential outcomes of Heavy Nitrogen (15N) experiments.



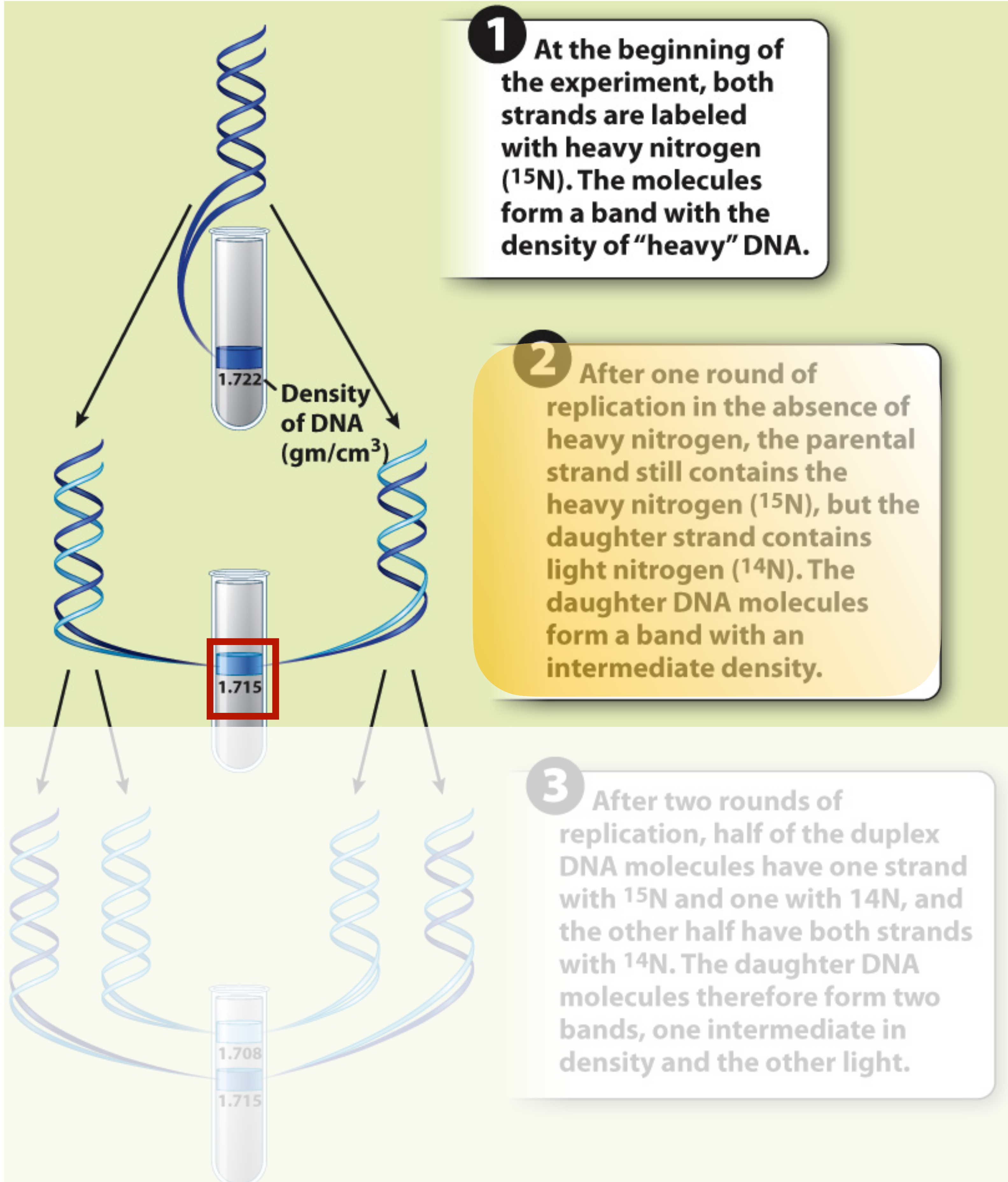

14N
1.708
15N
1.715



1. At the beginning of the experiment, both strands are labeled with heavy nitrogen (^{15}N). The molecules form a band with the density of "heavy" DNA.

2. After one round of replication in the absence of heavy nitrogen, the parental strand still contains the heavy nitrogen (^{15}N), but the daughter strand contains light nitrogen (^{14}N). The daughter DNA molecules form a band with an intermediate density.

3. After two rounds of replication, half of the duplex DNA molecules have one strand with ^{15}N and one with 14N, and the other half have both strands with ^{14}N. The daughter DNA molecules therefore form two bands, one intermediate in density and the other light.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1.722
Density of DNA (gm/cm^3)
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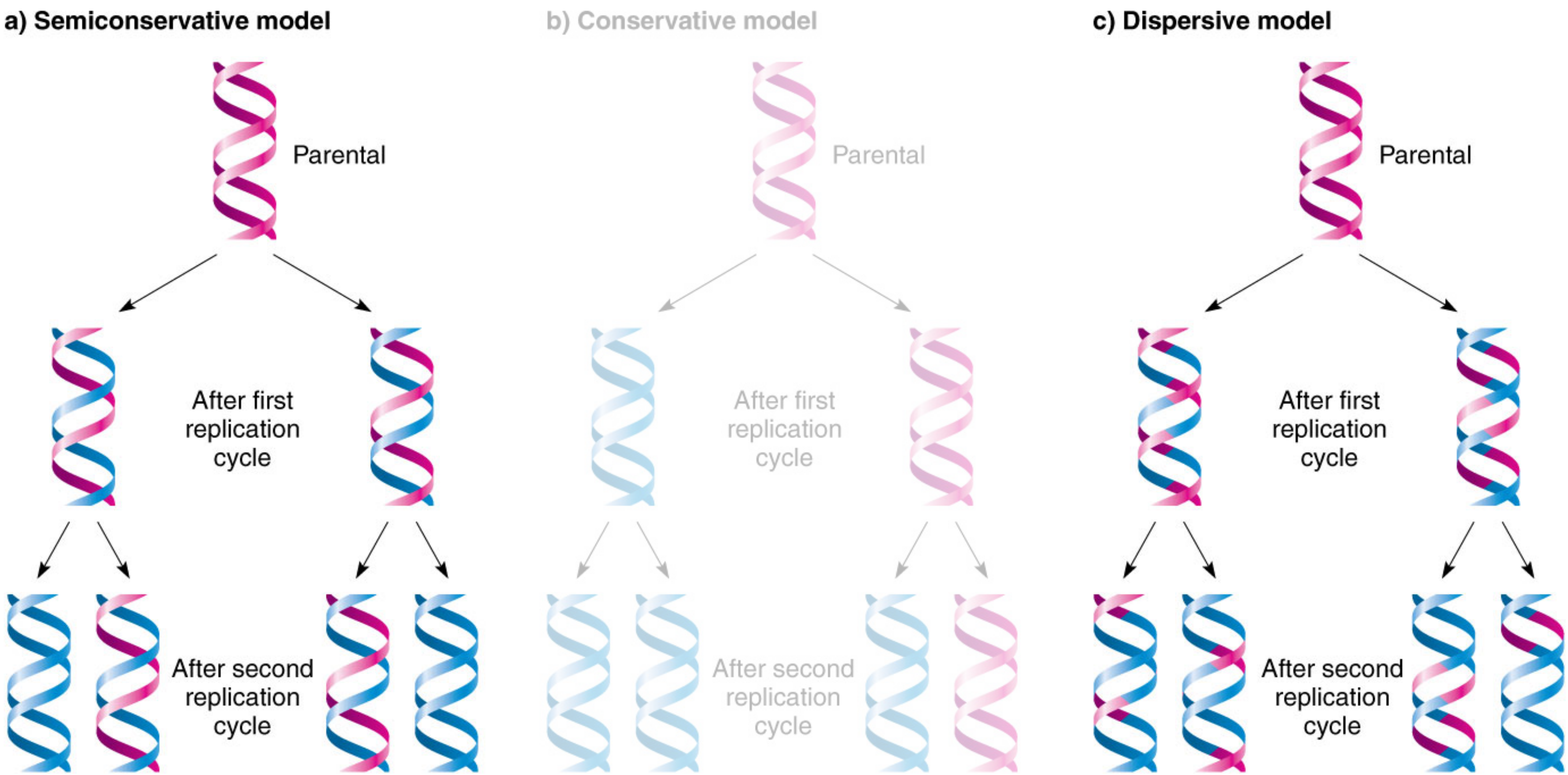
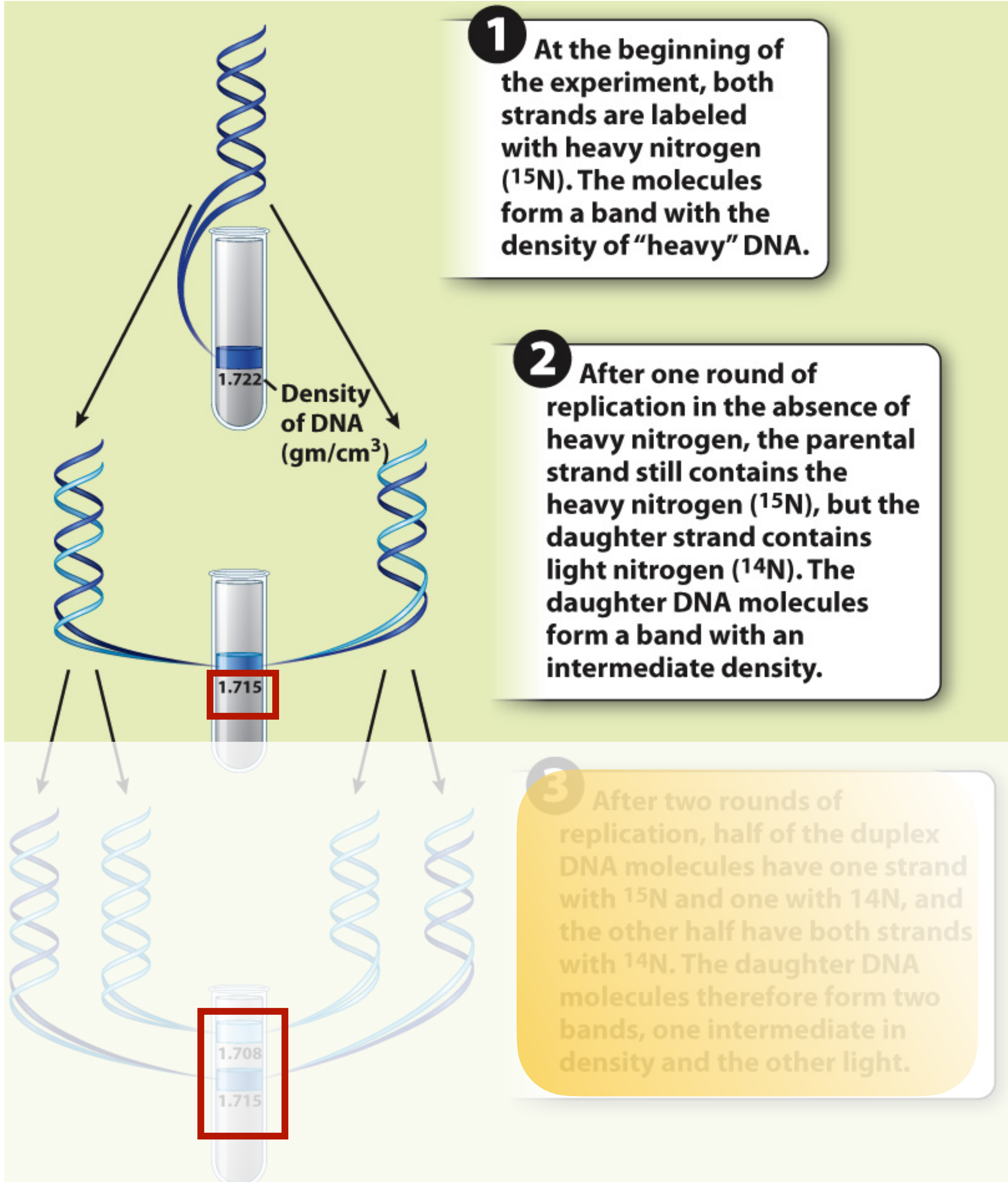
3 potential outcomes of Heavy Nitrogen (15N) experiments.

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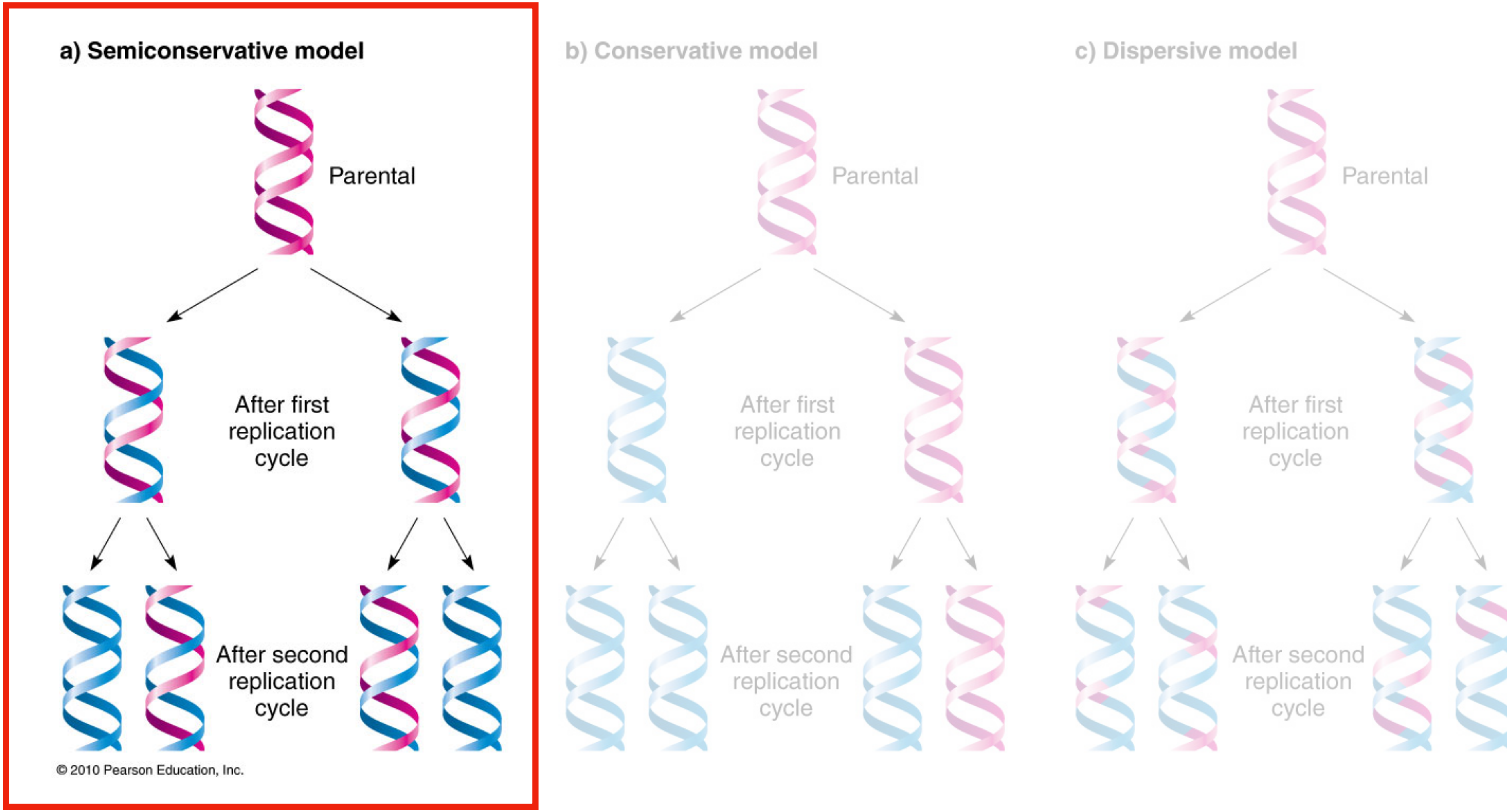
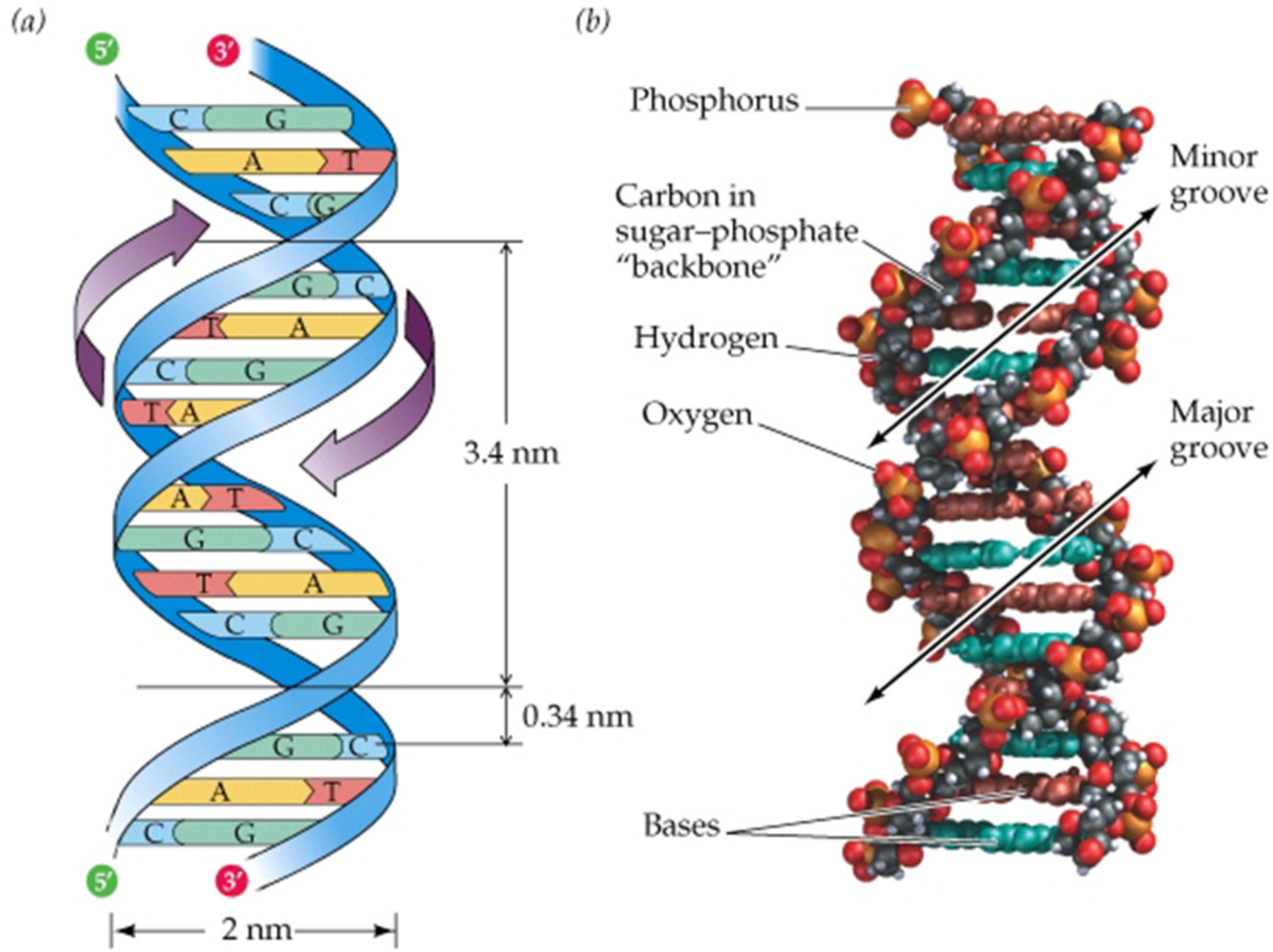


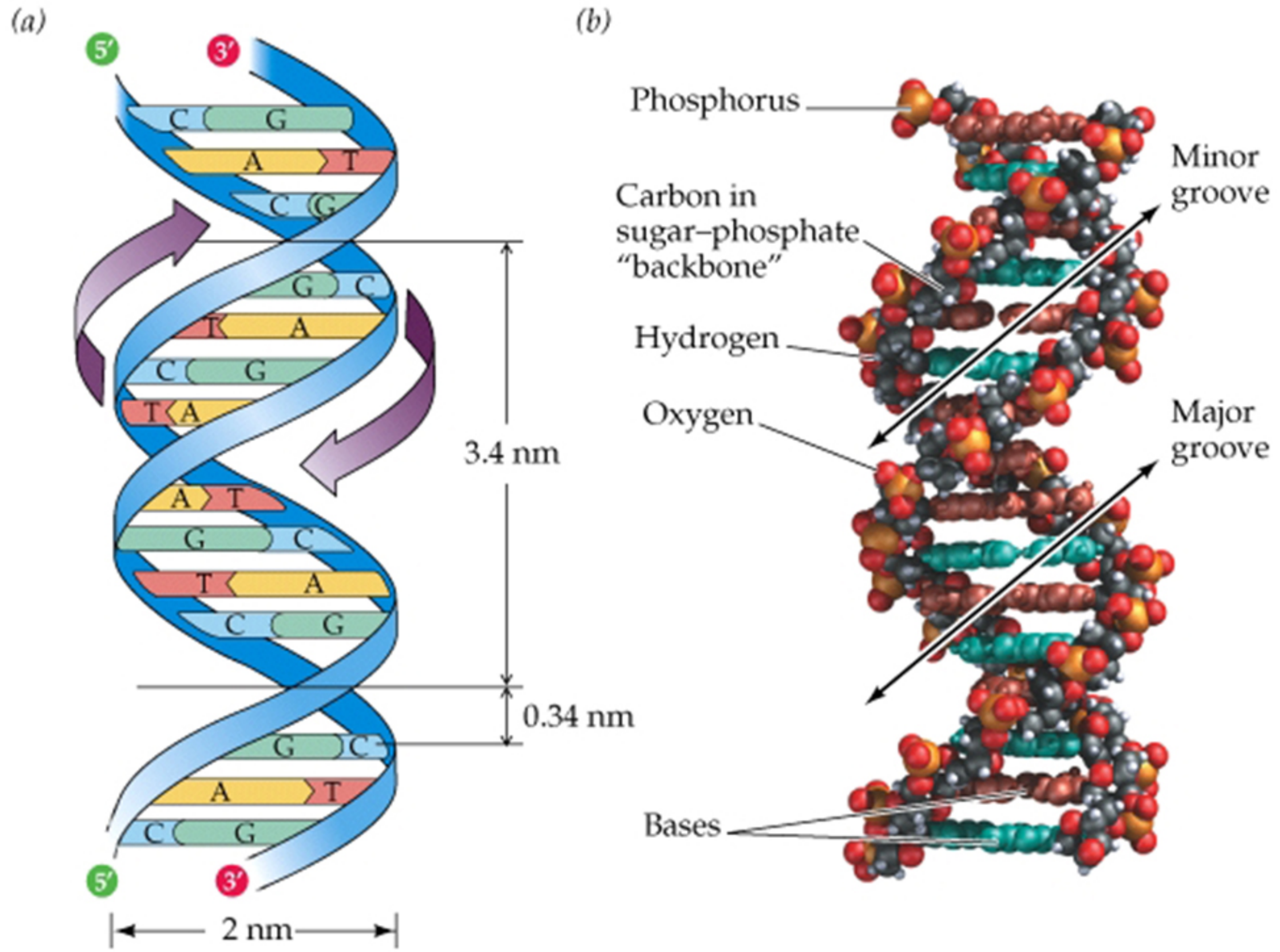


As the genetic material of the cell, DNA must perform four important functions:

It must be able to store all of an organism's genetic information.

It must be susceptible to mutation.

It must be precisely replicated in the cell division cycle.



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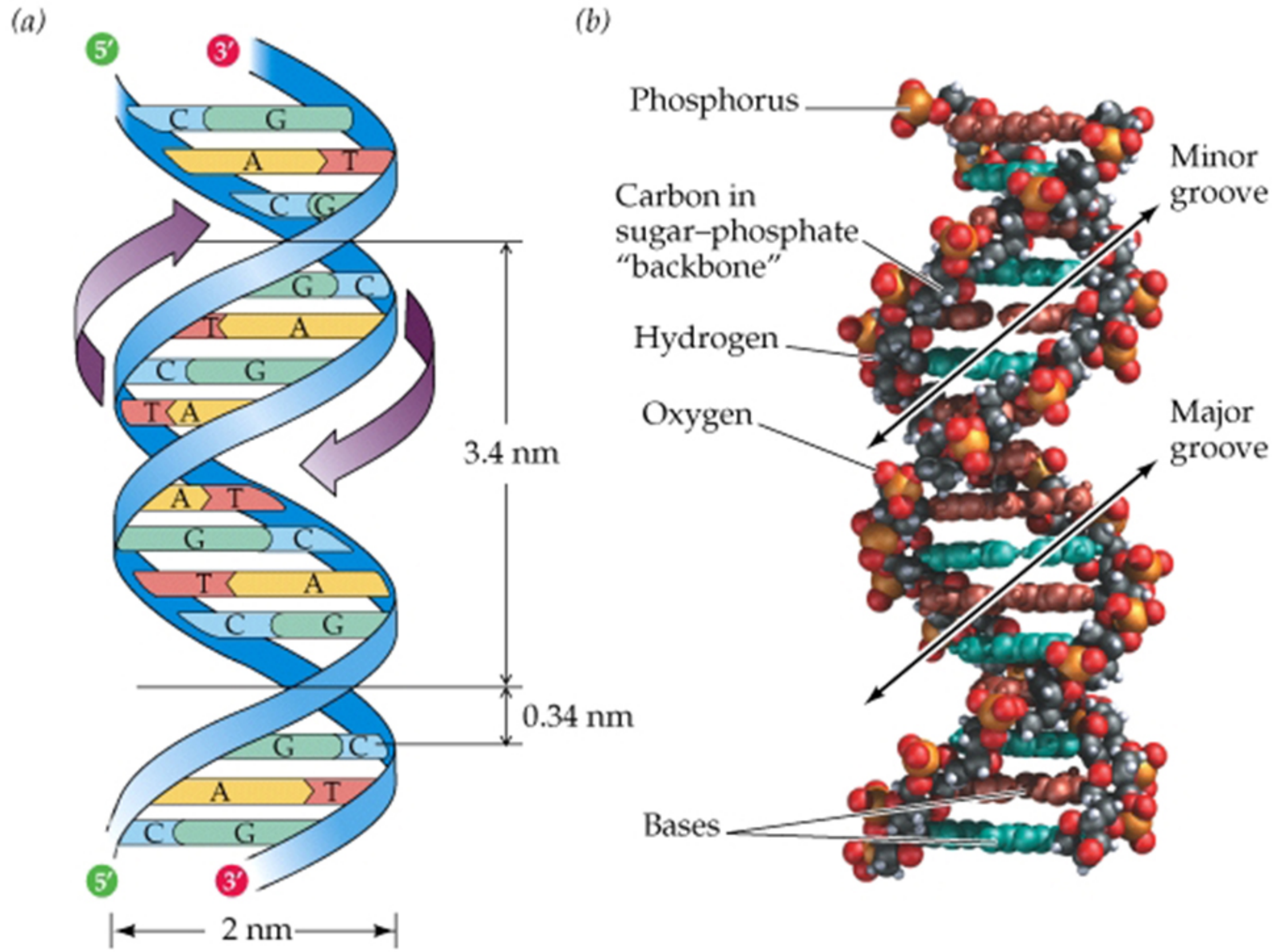
DNA Replication

DNA replication begins with separation of the two paired strands of double-stranded DNA by proteins that unwind the double helix, creating a replication fork.



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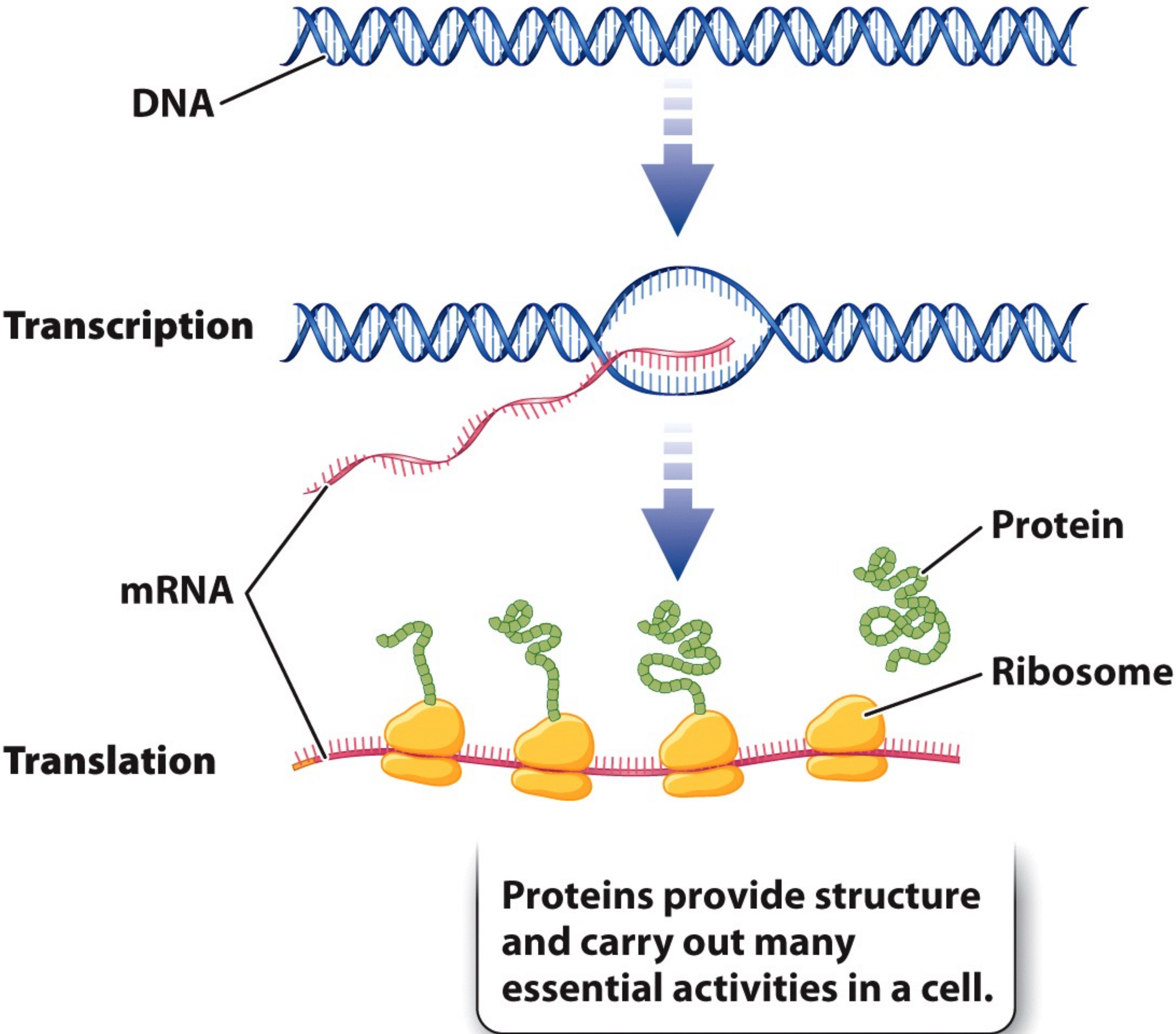
DNA
Transcription
mRNA
Protein
Ribosome
Translation
Proteins provide structure and carry out many essential activities in a cell.