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NINTH EDITION

**HOLE'S
ESSENTIALS**

SHIER, BUTLER, LEWIS

of Human Anatomy and Physiology

Chapter 4

Image Slides

COLOR ART AND PHOTOS

Fig. 4.01

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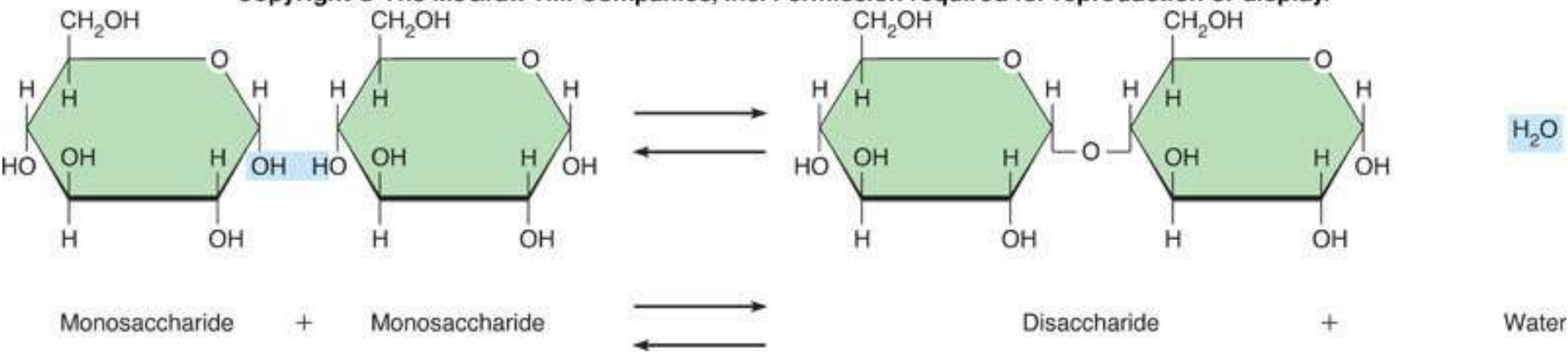


Fig. 4.02

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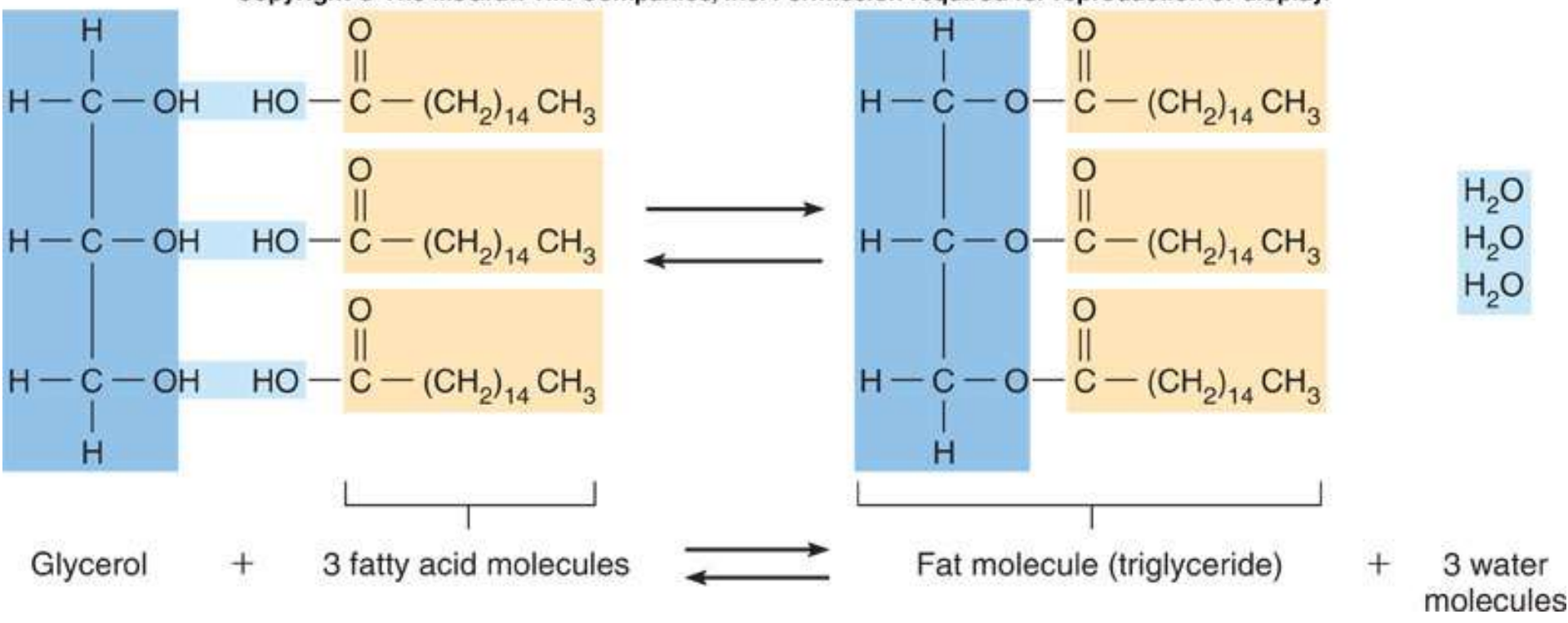


Fig. 4.03

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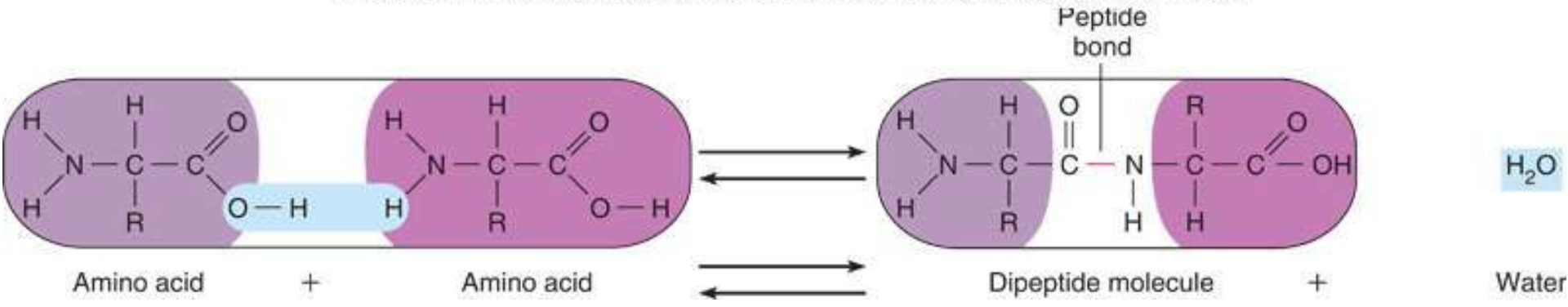


Fig. 4.04

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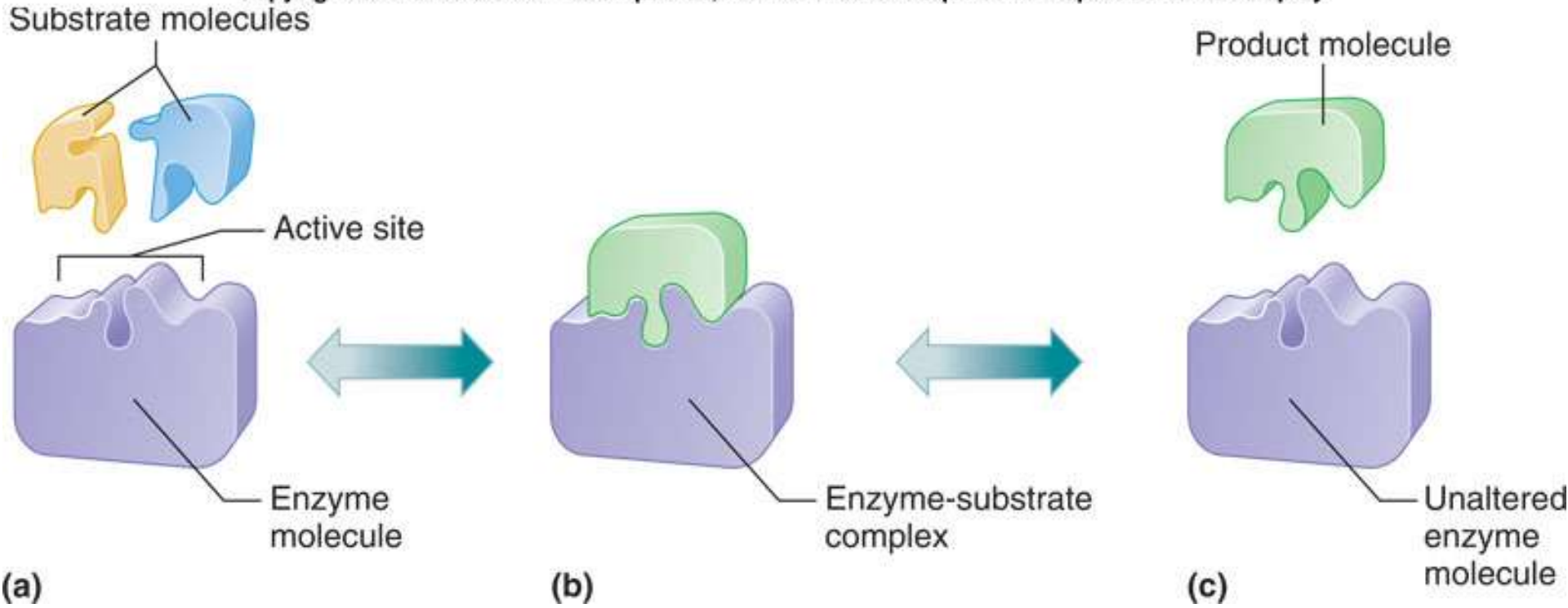
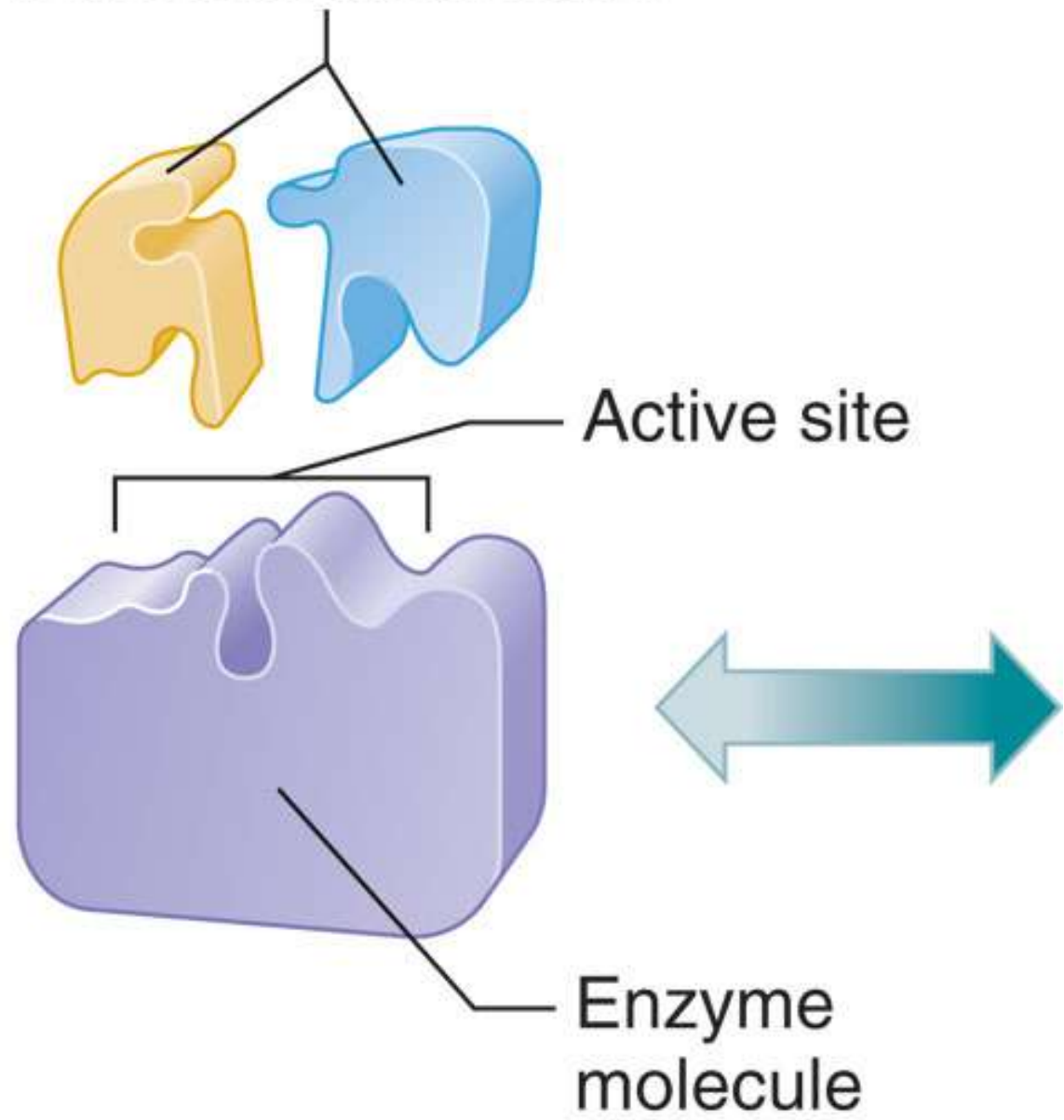


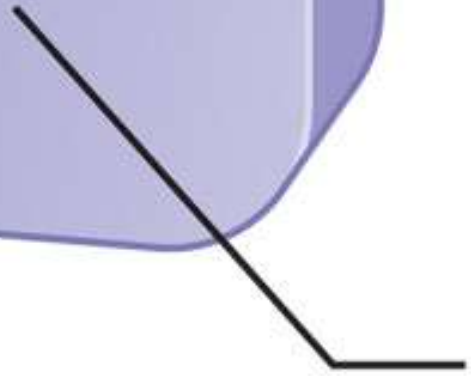
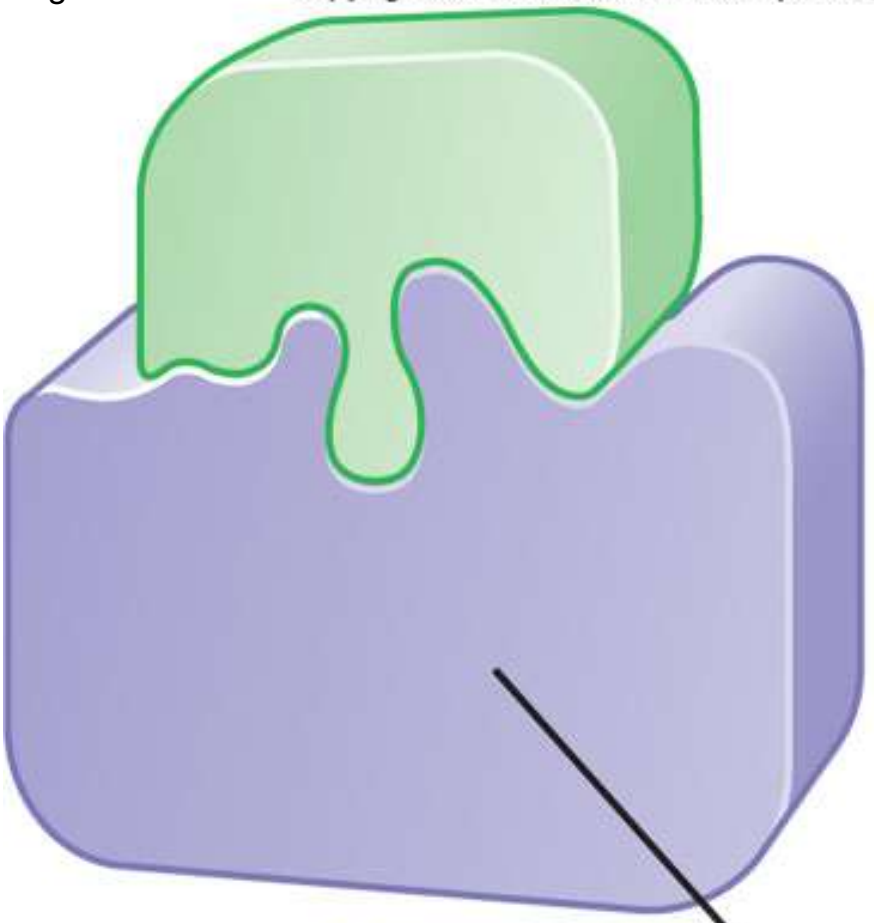
Fig. 4.04a

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Substrate molecules



(a)



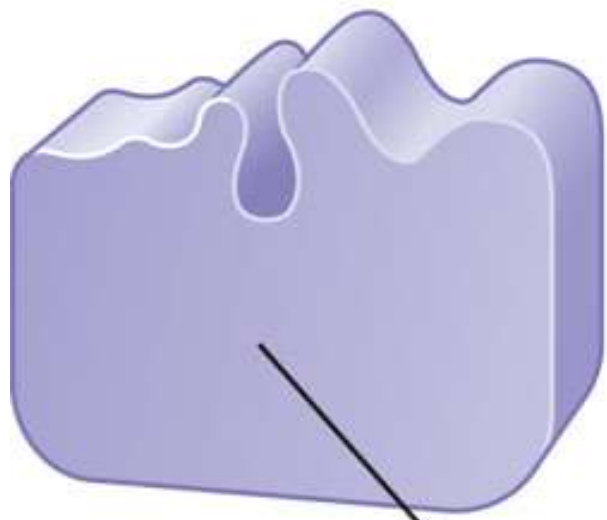
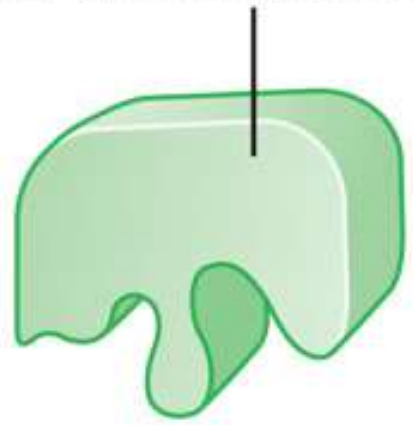
Enzyme-substrate complex

(b)

Fig. 4.04c

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Product molecule



Unaltered
enzyme
molecule

(c)

Glycolysis

- 1 The 6-carbon sugar glucose is broken down in the cytosol into two 3-carbon pyruvic acid molecules with a net gain of 2 ATP and the release of high-energy electrons.

Citric Acid Cycle

- 2 The 3-carbon pyruvic acids generated by glycolysis enter the mitochondria. Each loses a carbon (generating CO_2) and is combined with a coenzyme to form a 2-carbon acetyl coenzyme A (acetyl CoA). More high-energy electrons are released.

- 3 Each acetyl CoA combines with a 4-carbon oxaloacetic acid to form the 6-carbon citric acid, for which the cycle is named. For each citric acid, a series of reactions removes 2 carbons (generating 2 CO_2 's), synthesizes 1 ATP, and releases more high-energy electrons. The figure shows 2 ATP, resulting directly from 2 turns of the cycle per glucose molecule that enters glycolysis.

Electron Transport Chain

- 4 The high-energy electrons still contain most of the chemical energy of the original glucose molecule. Special carrier molecules bring the high-energy electrons to a series of enzymes that convert much of the remaining energy to more ATP molecules. The other products are heat and water. The requirement of oxygen in this last step is why the overall process is called aerobic respiration.

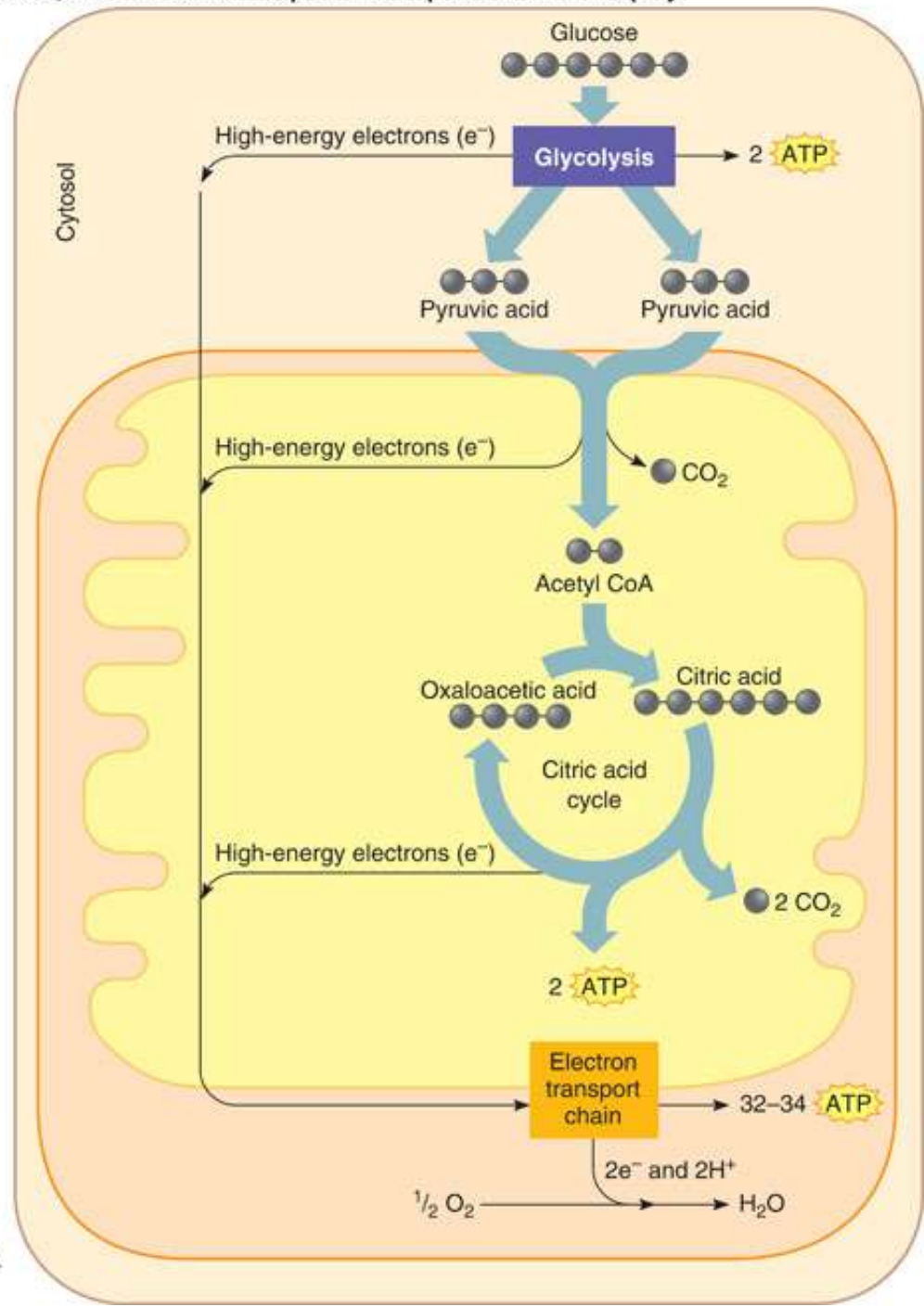


Fig. 4.06

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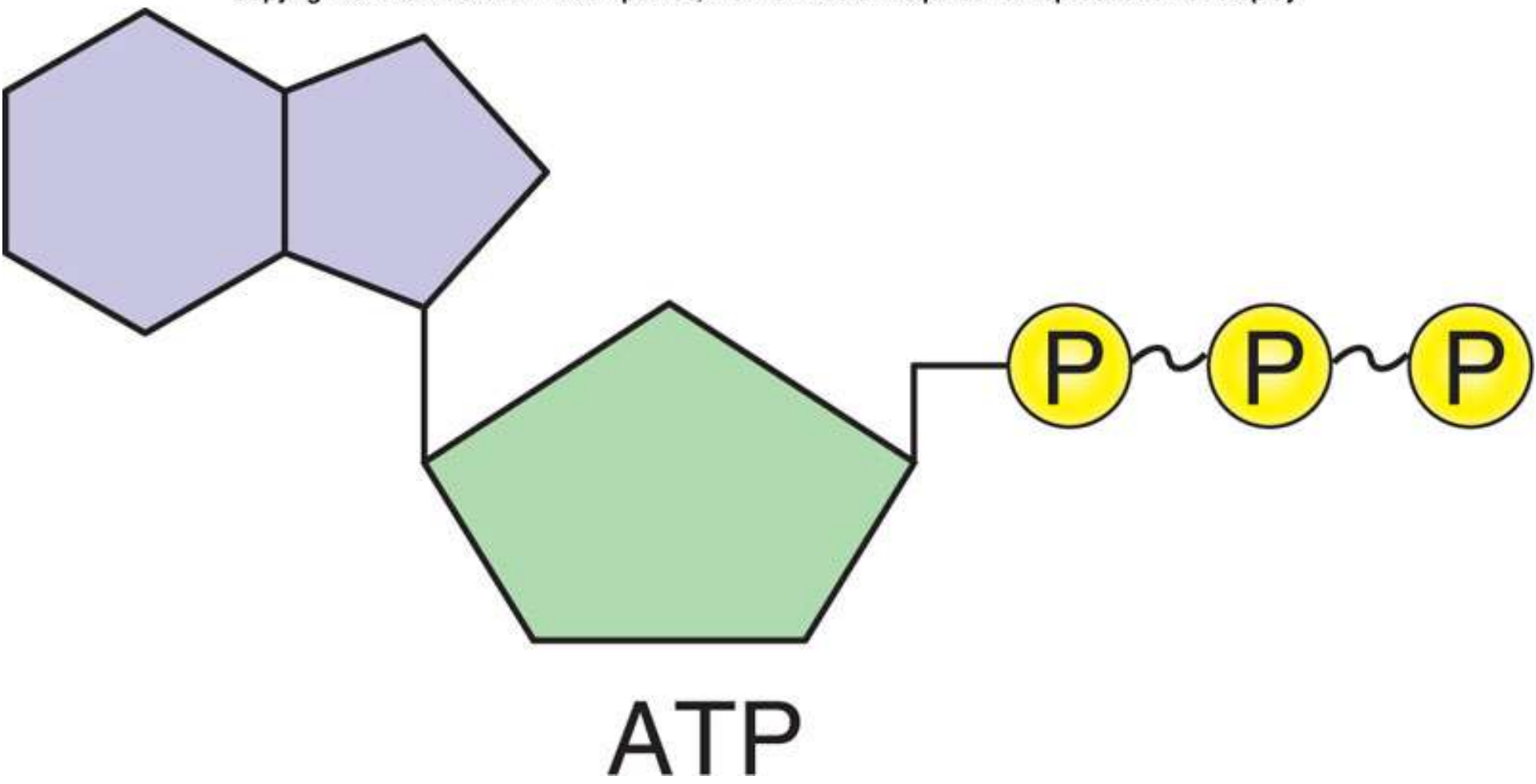


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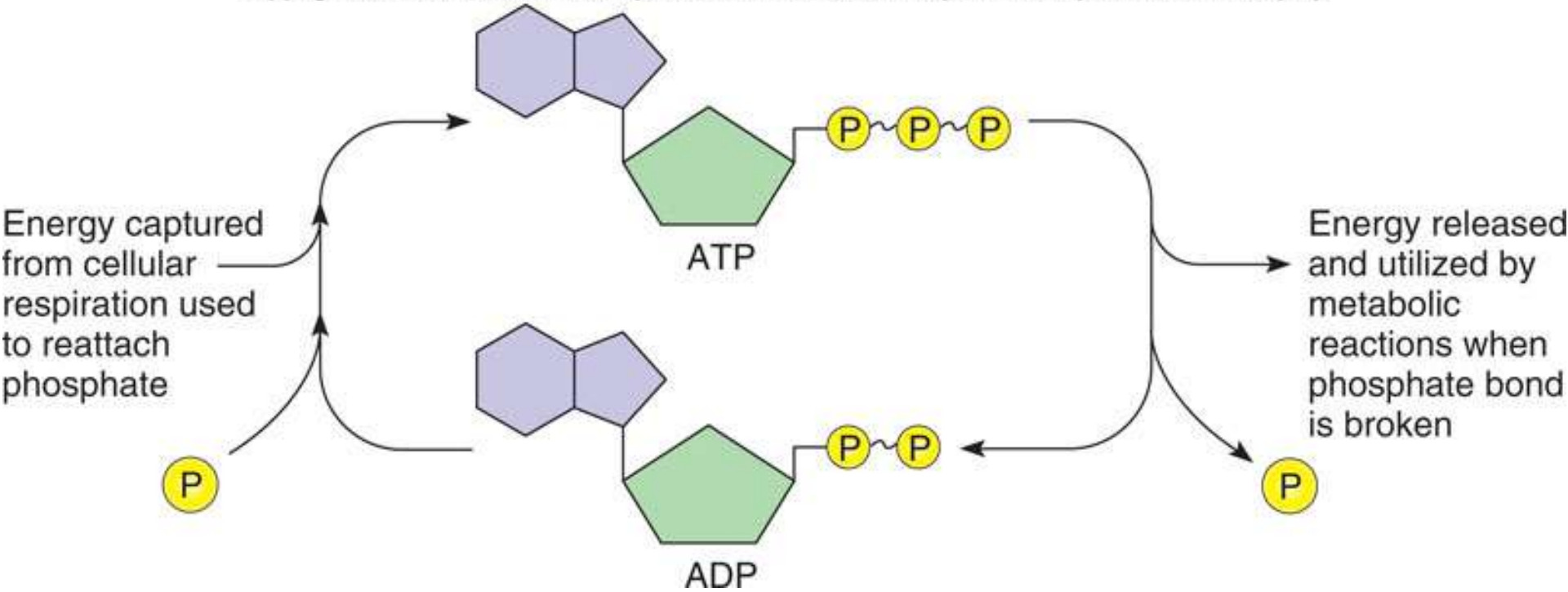


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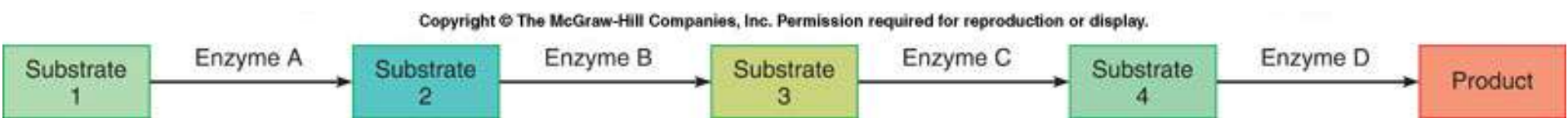


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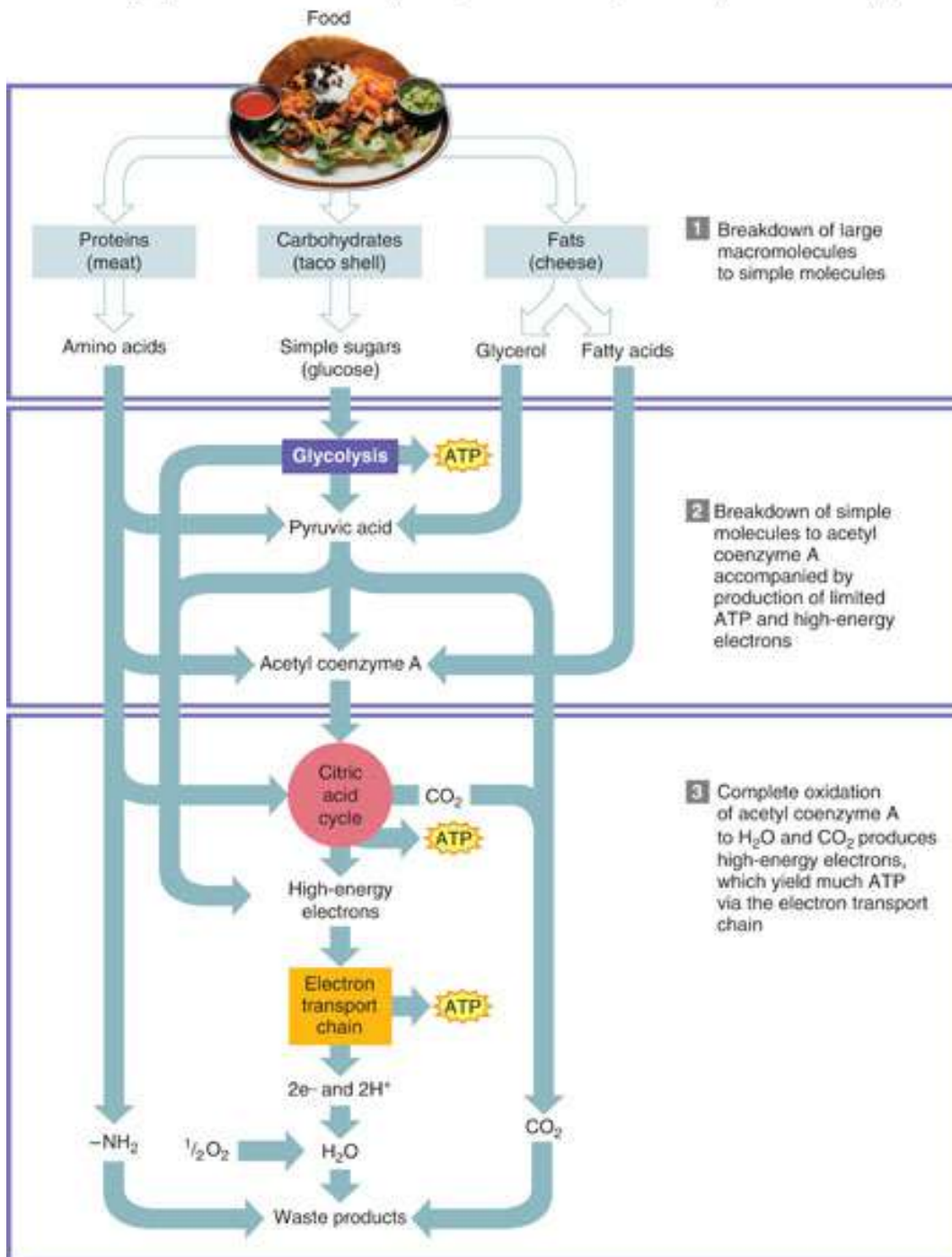


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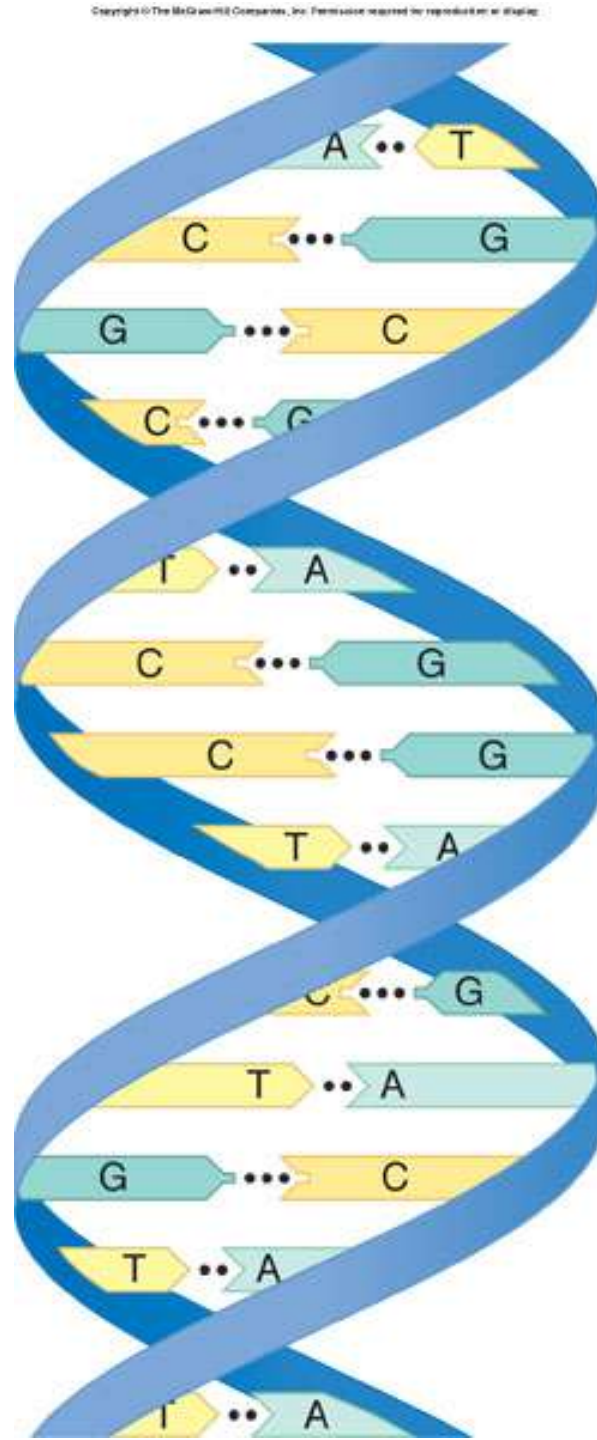


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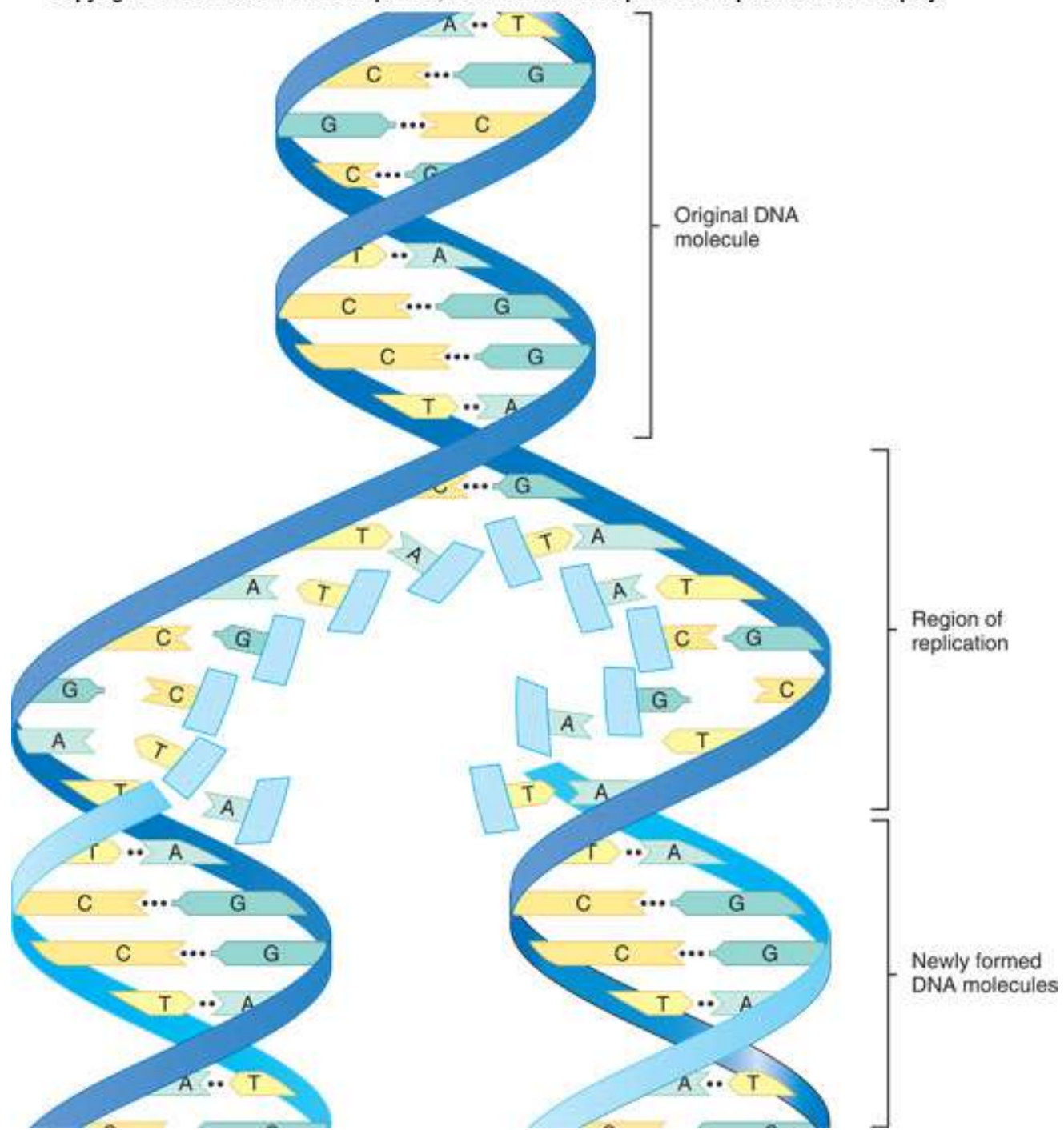


Fig. 4.12

DNA

RNA

Direction of "reading" code
↑

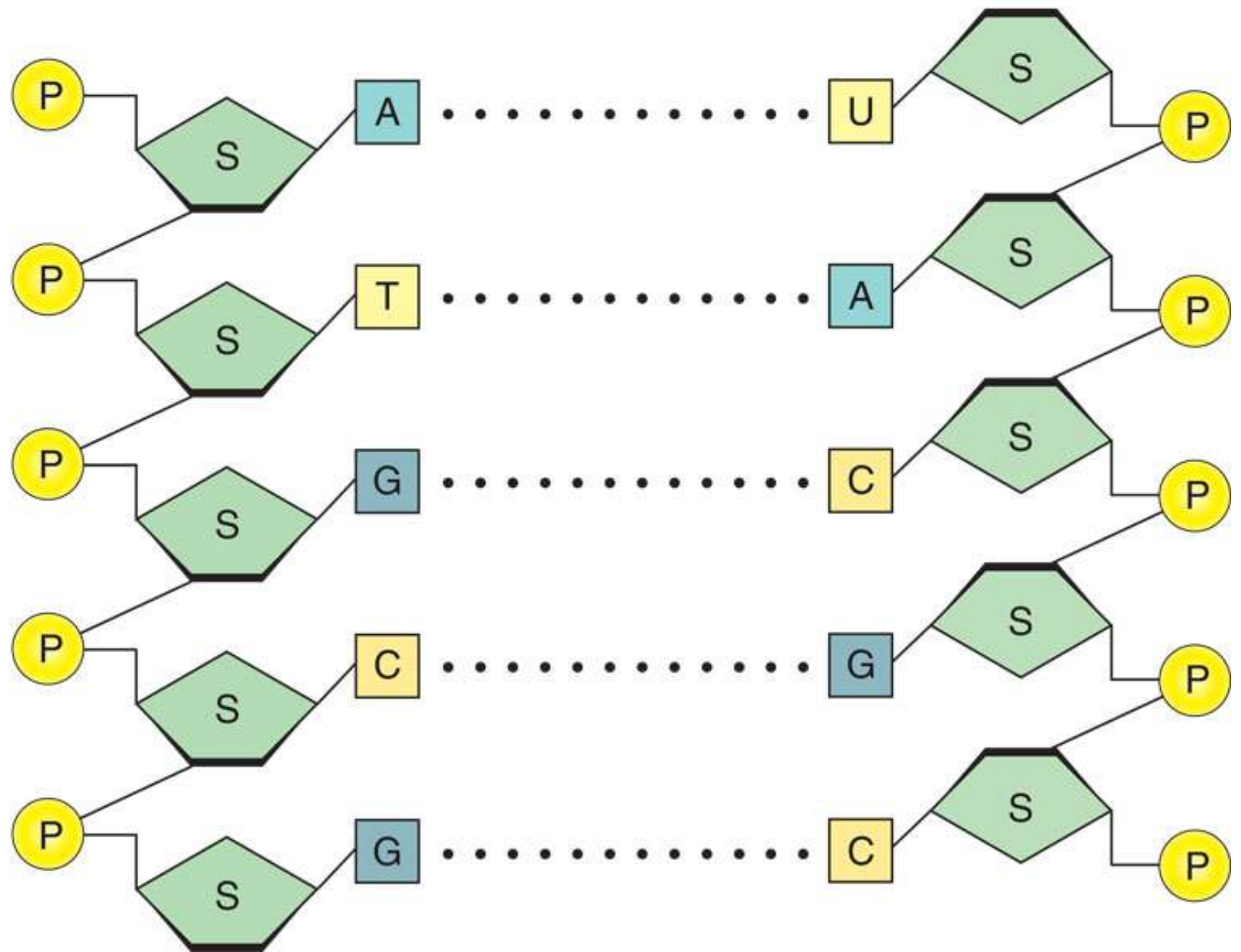


Fig. 4.13

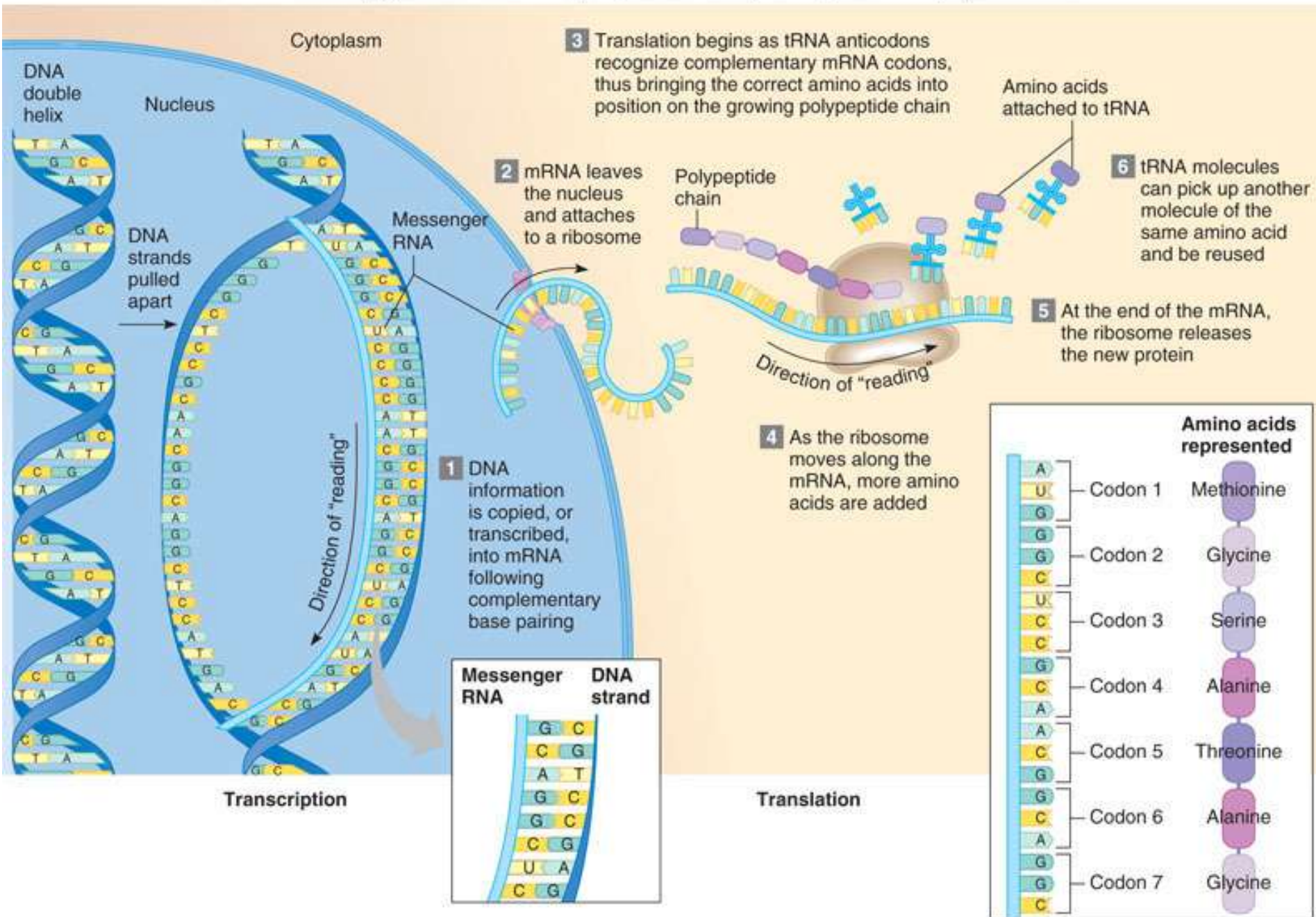


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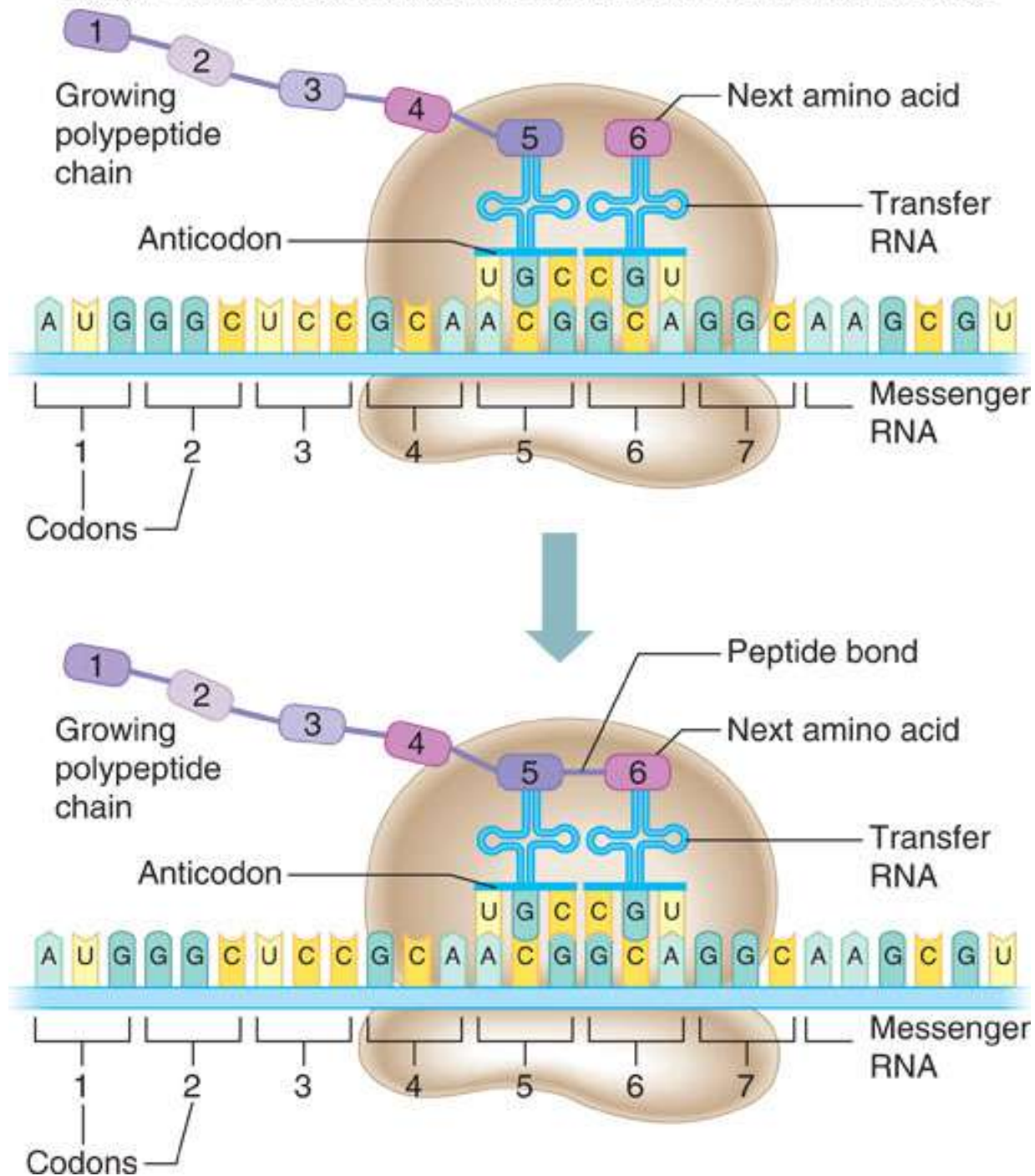


Fig. 4.14b

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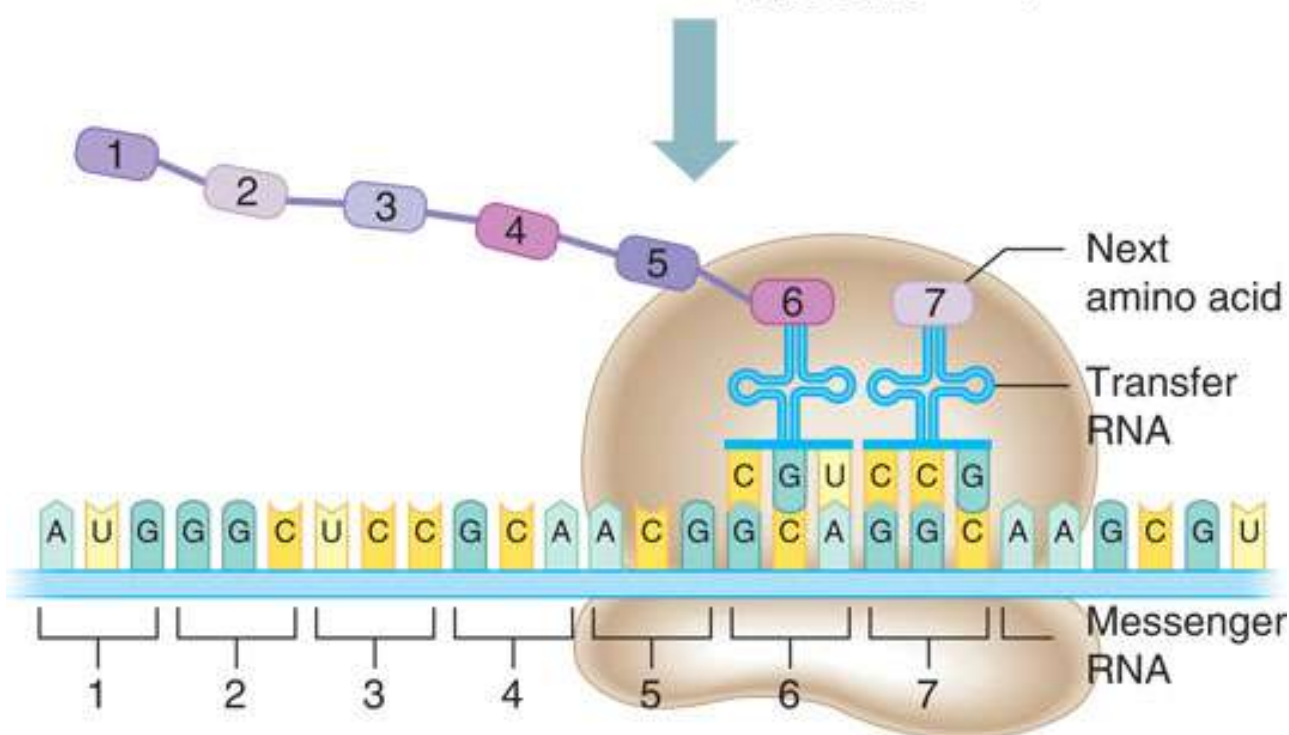
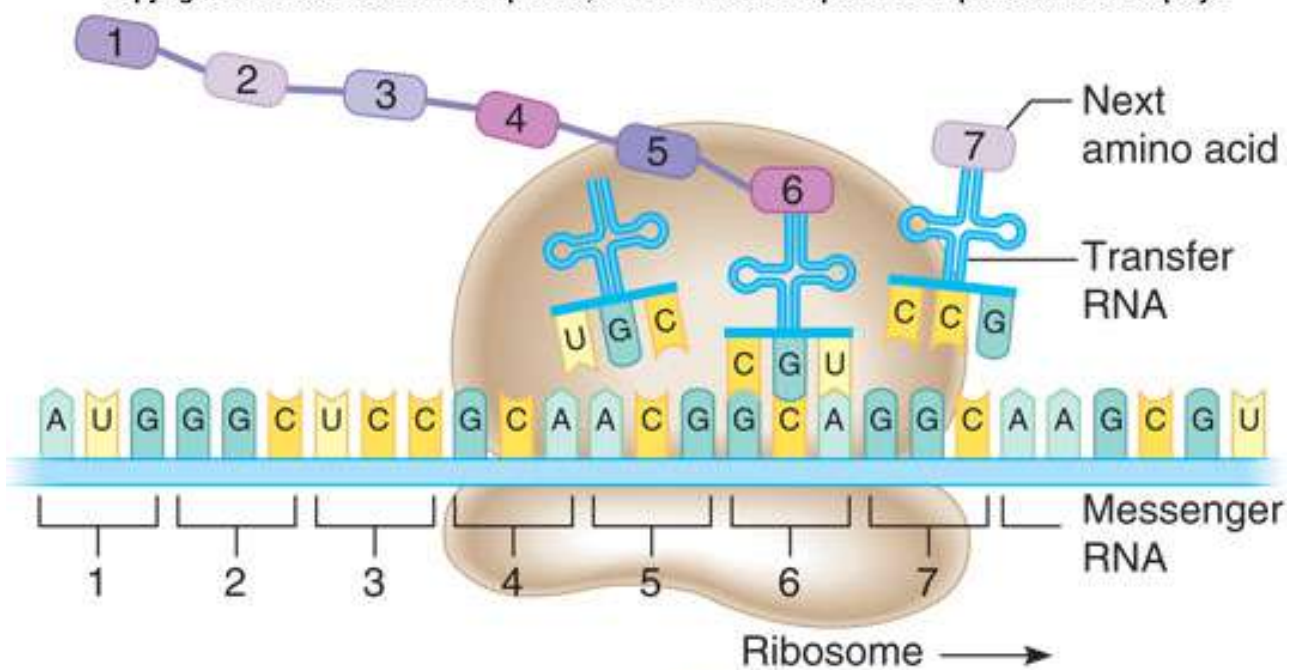


Fig. f4.a

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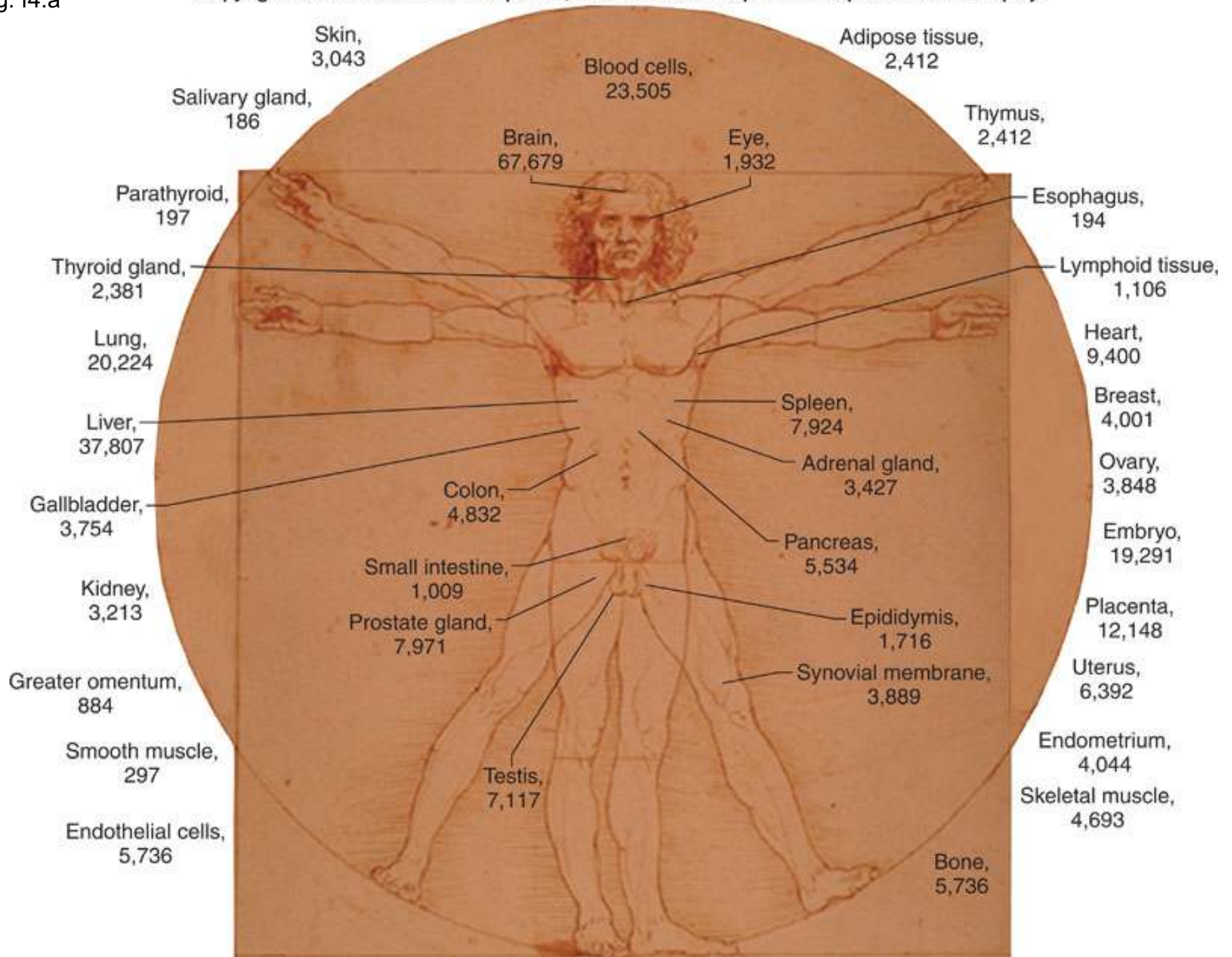


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COLOR
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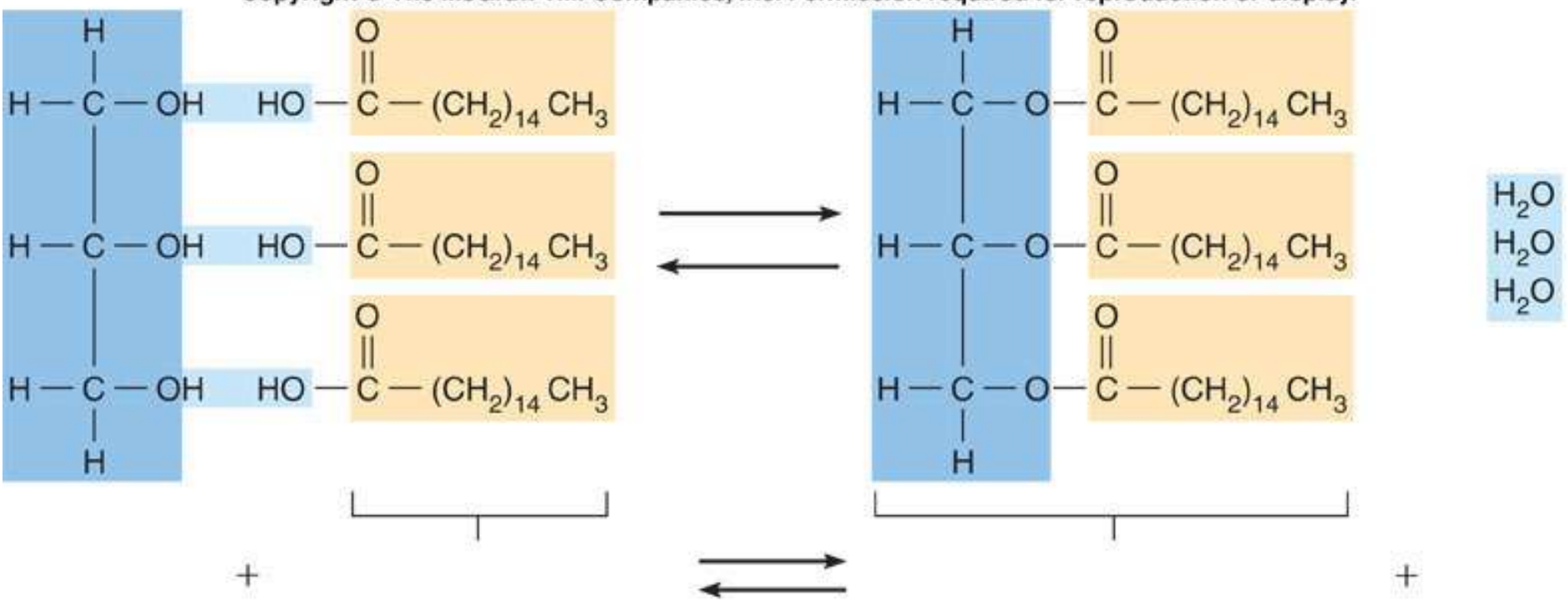


Fig. 4.03

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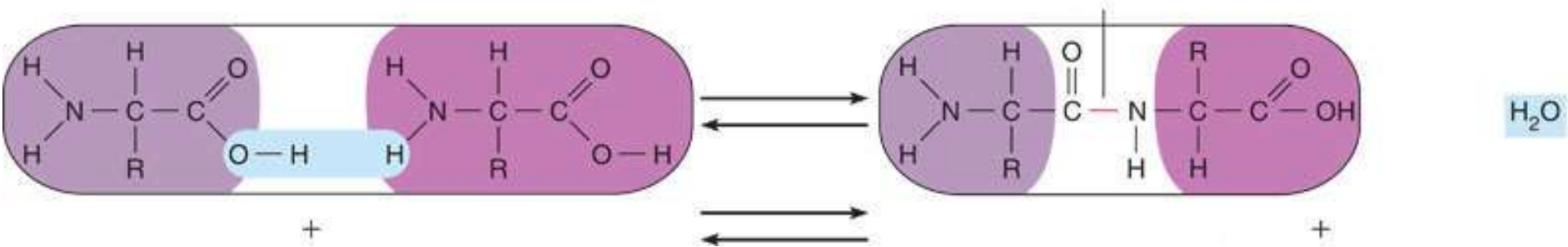


Fig. 4.04

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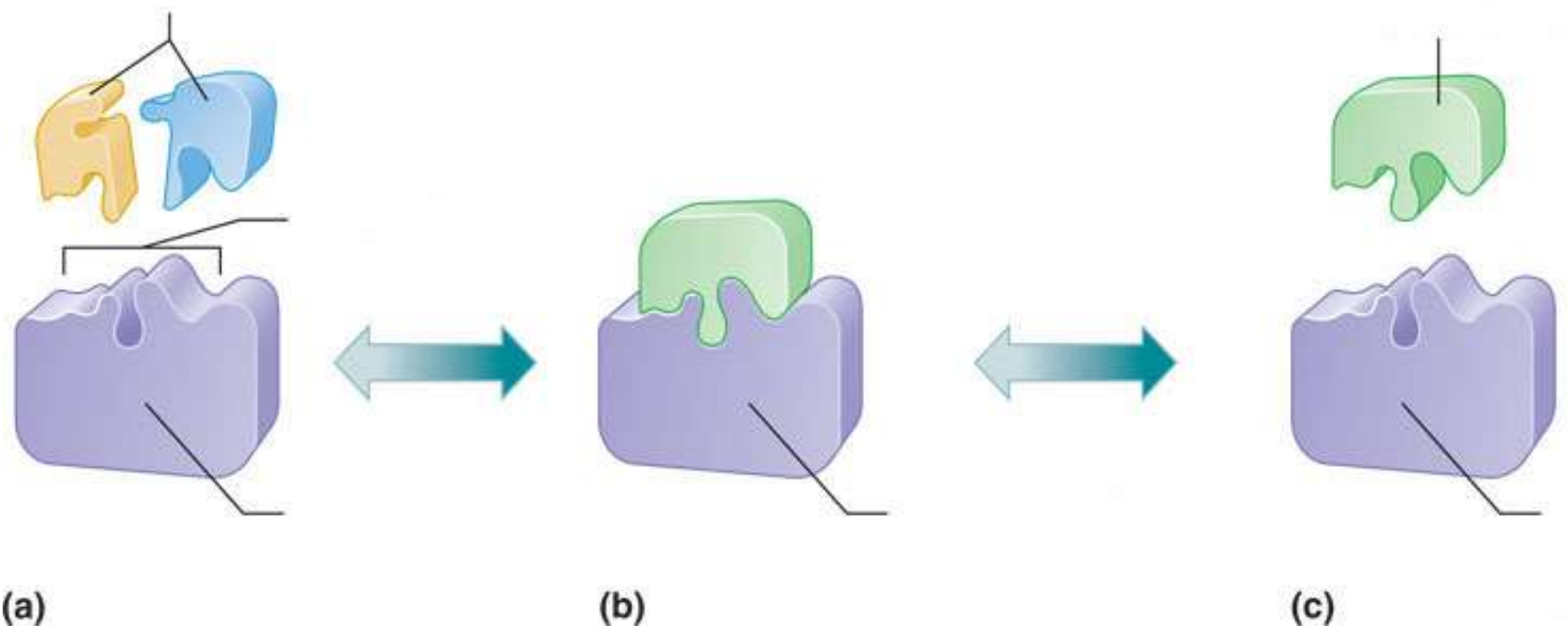
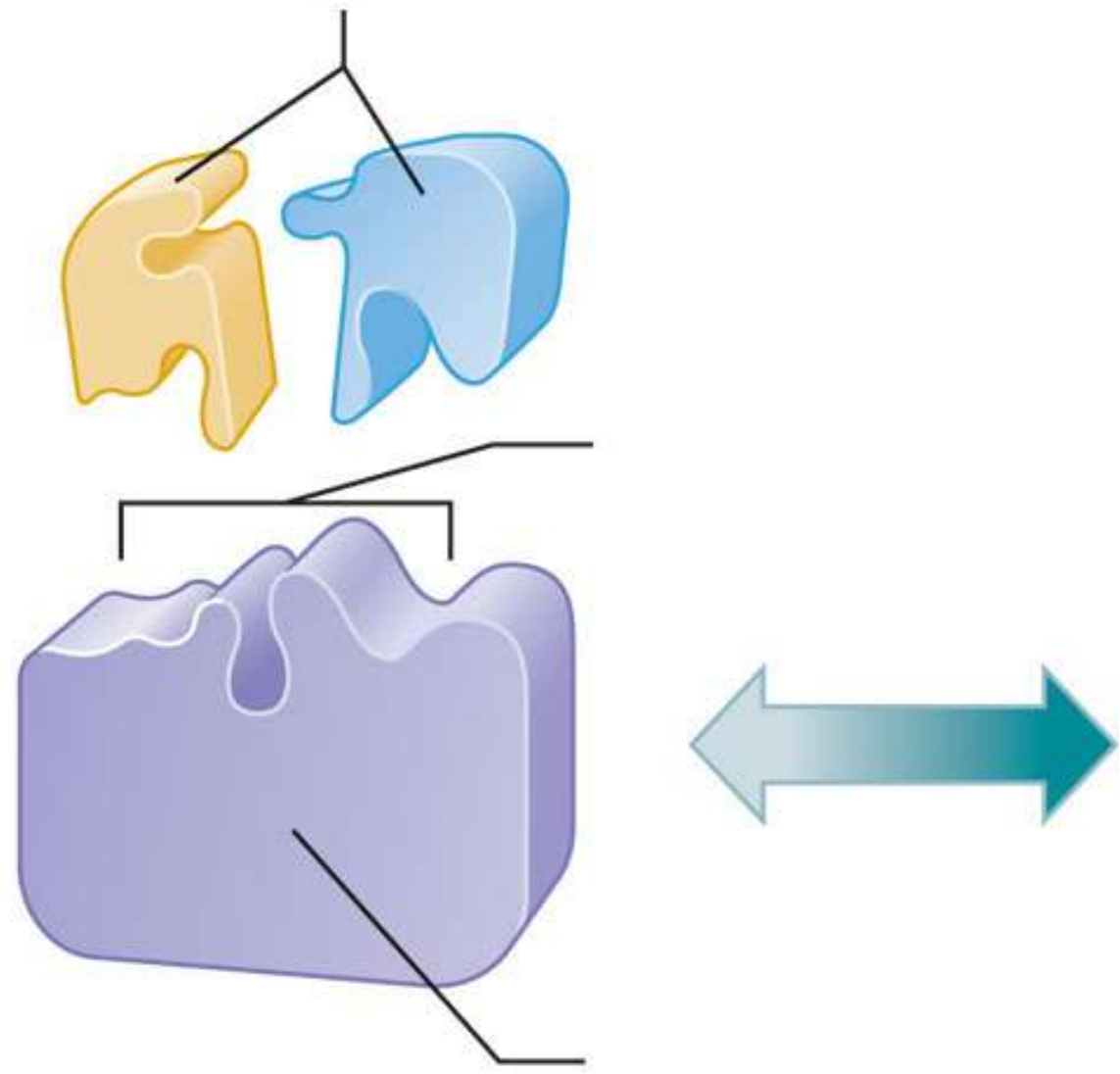


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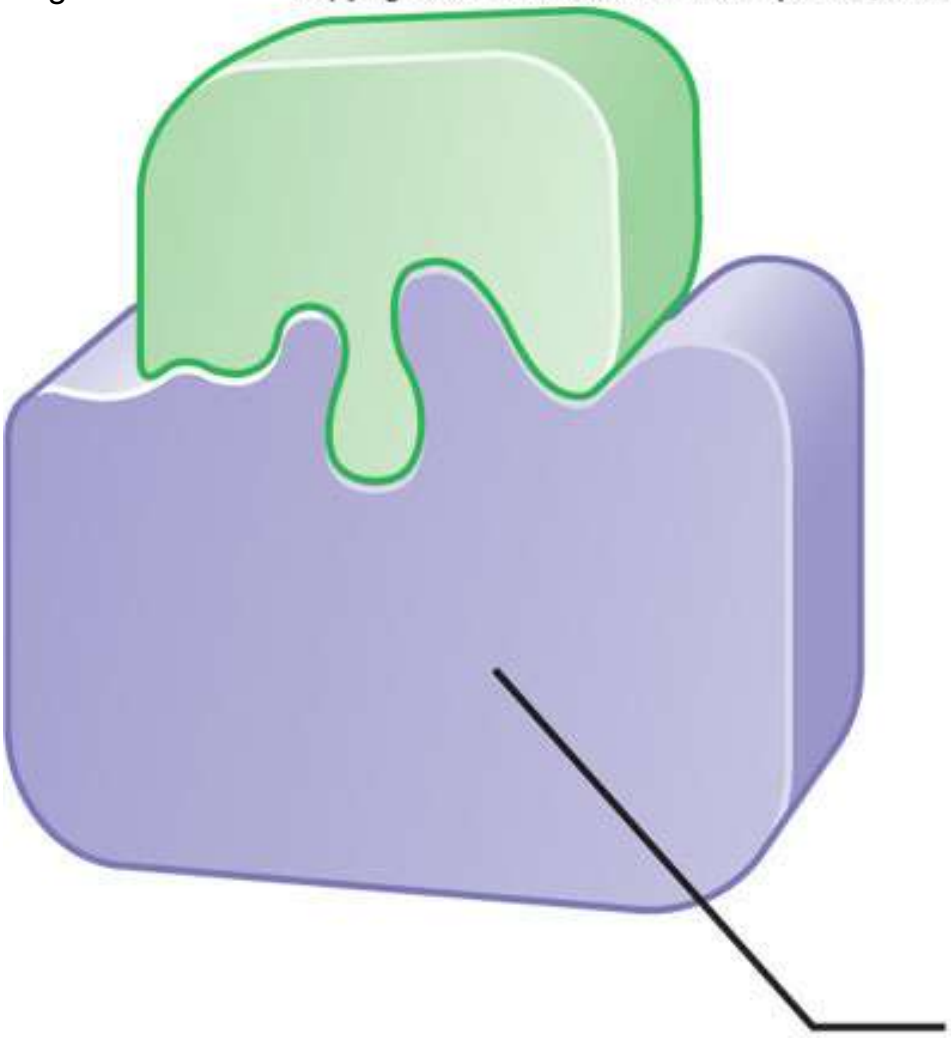
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(a)

Fig. 4.04b

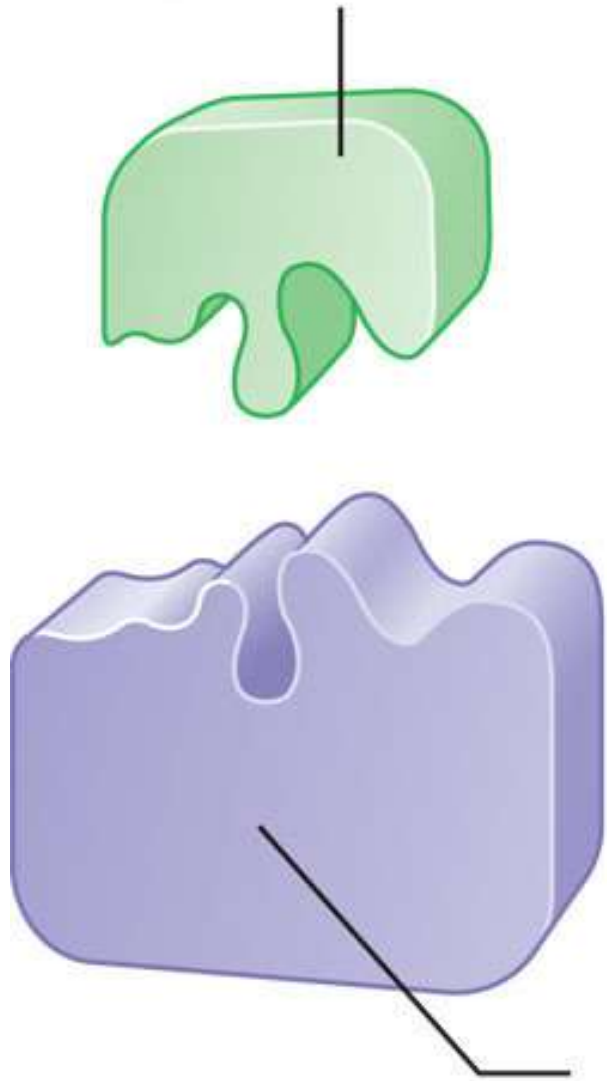
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(b)

Fig. 4.04c

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(c)

Fig. 4.11

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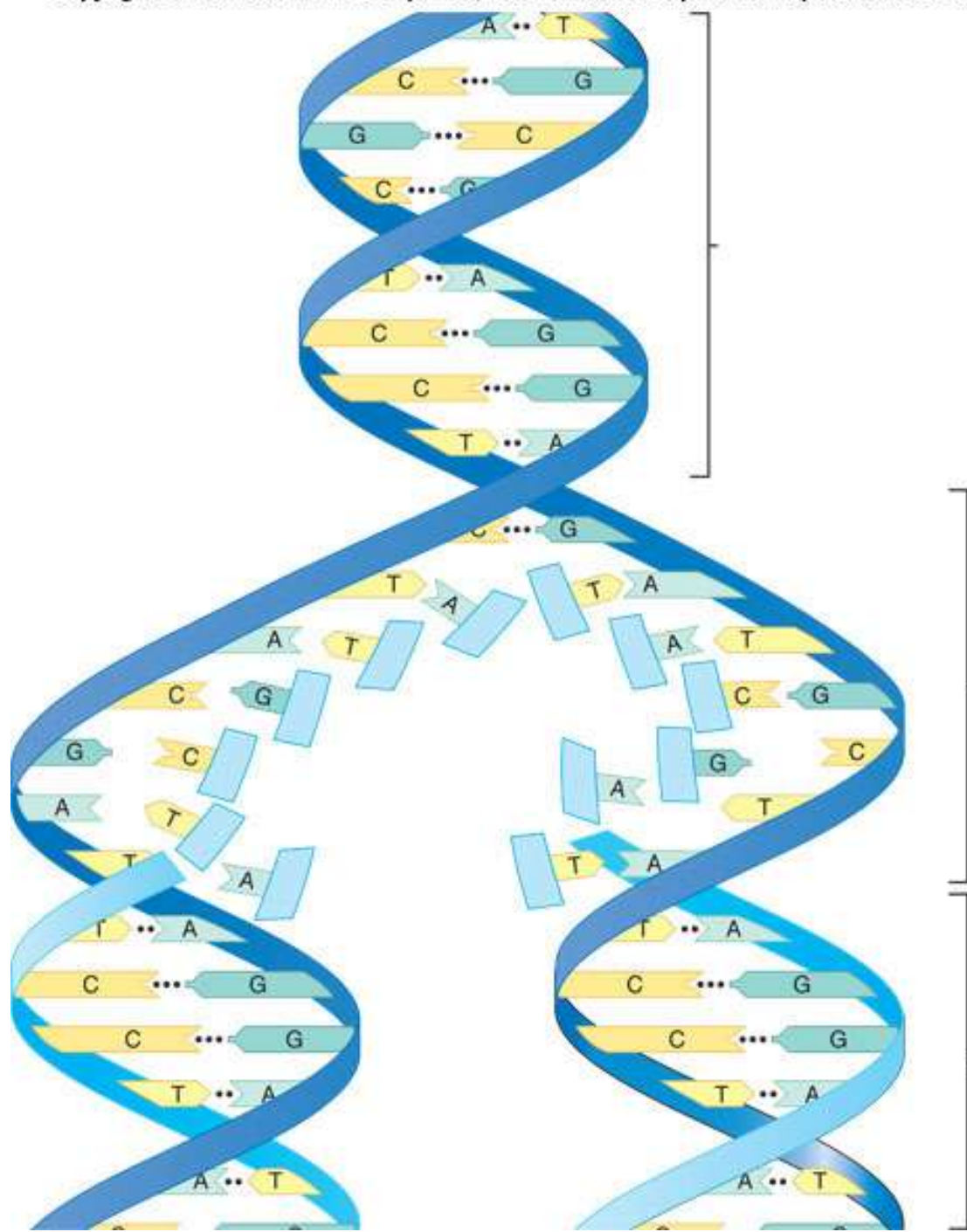


Fig. 4.13

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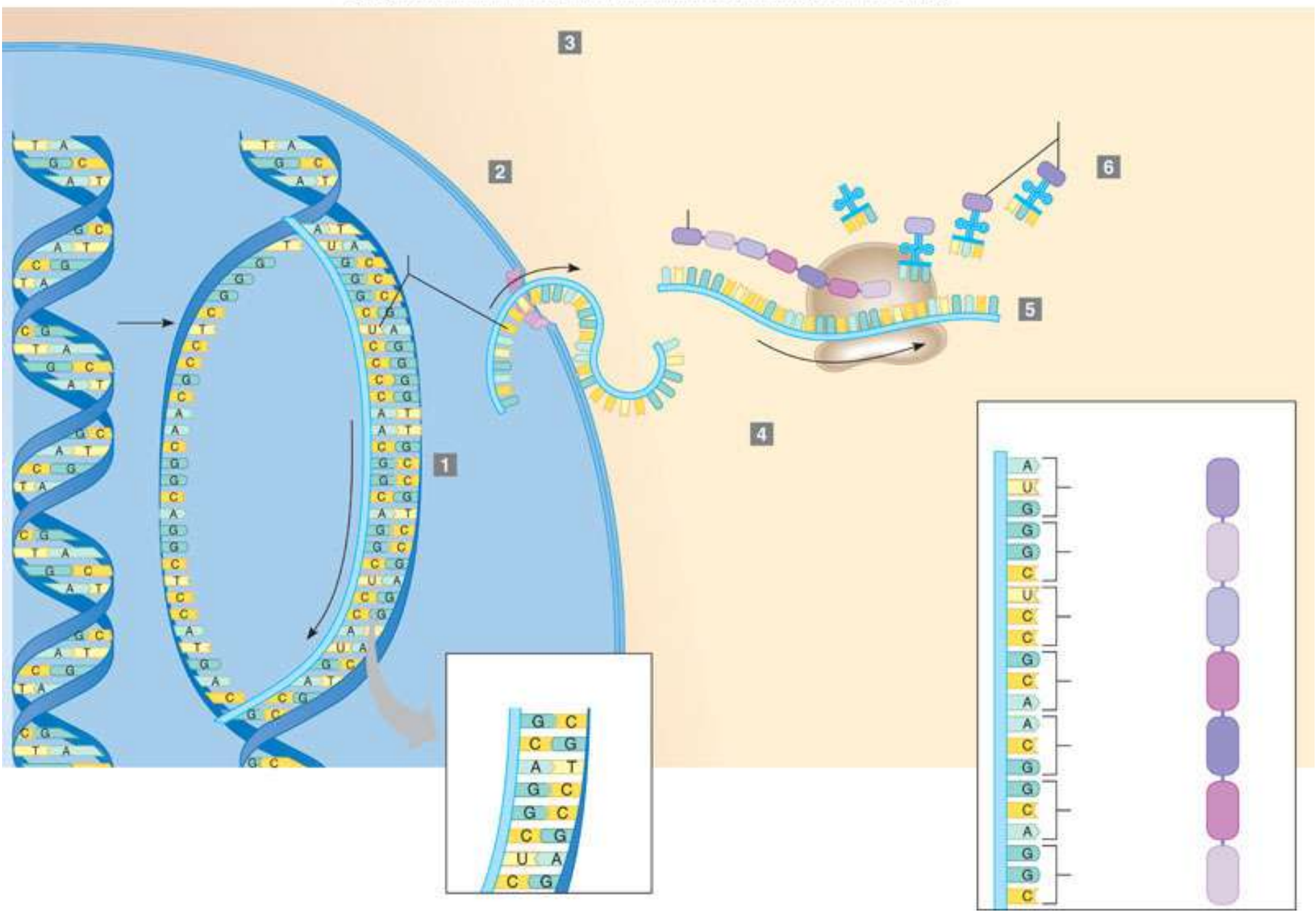


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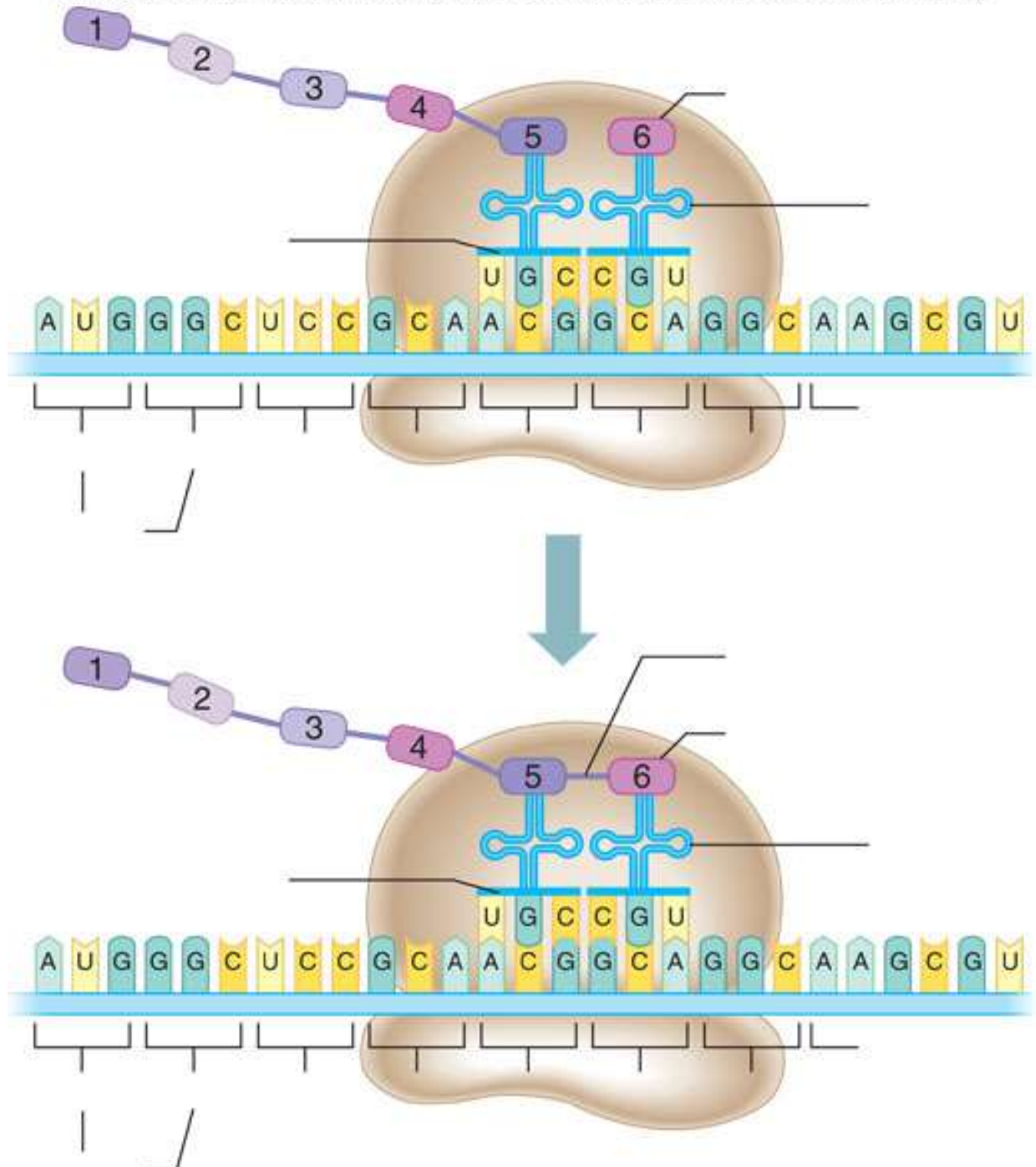


Fig. 4.14b

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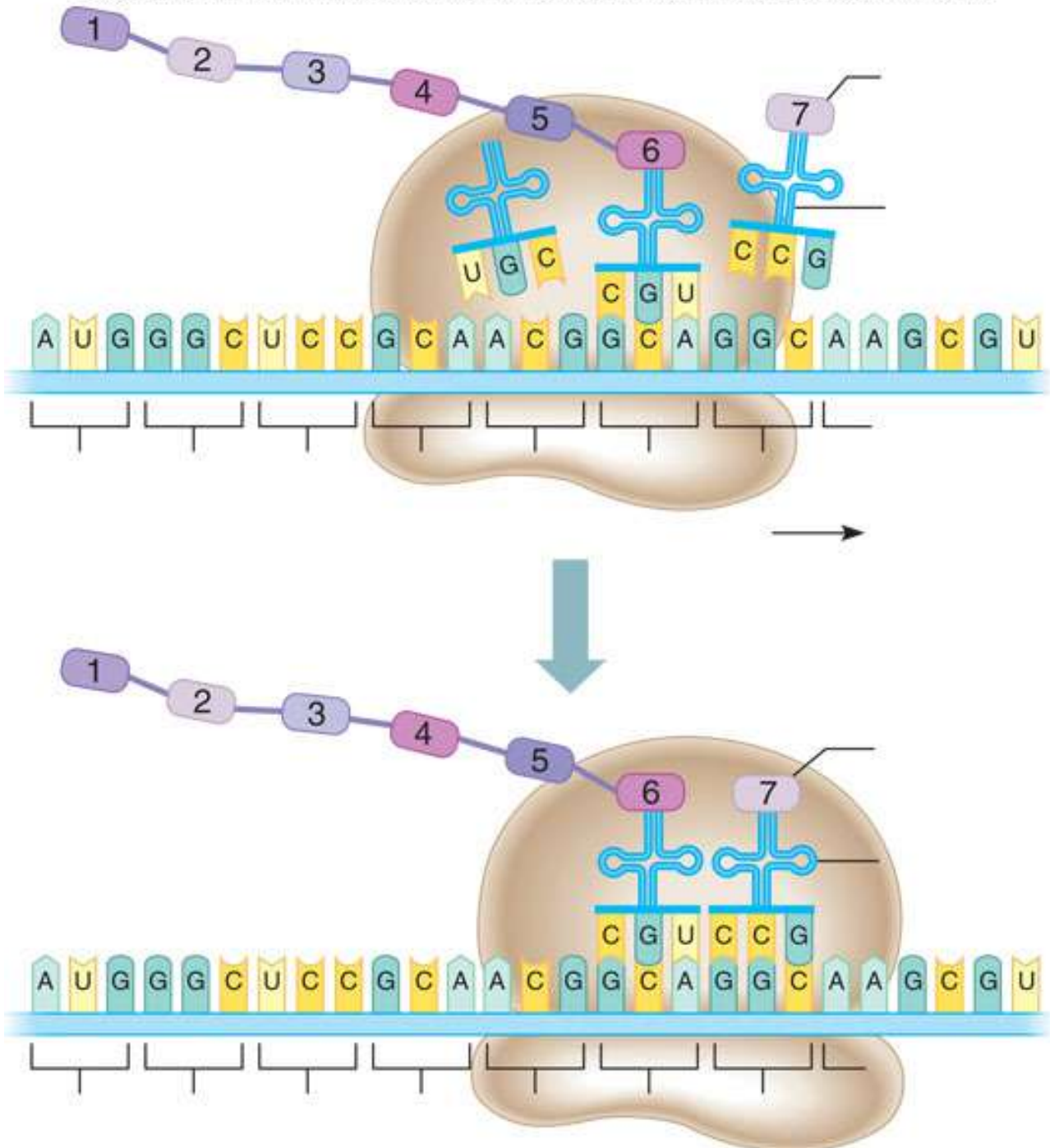


Fig. f4.a

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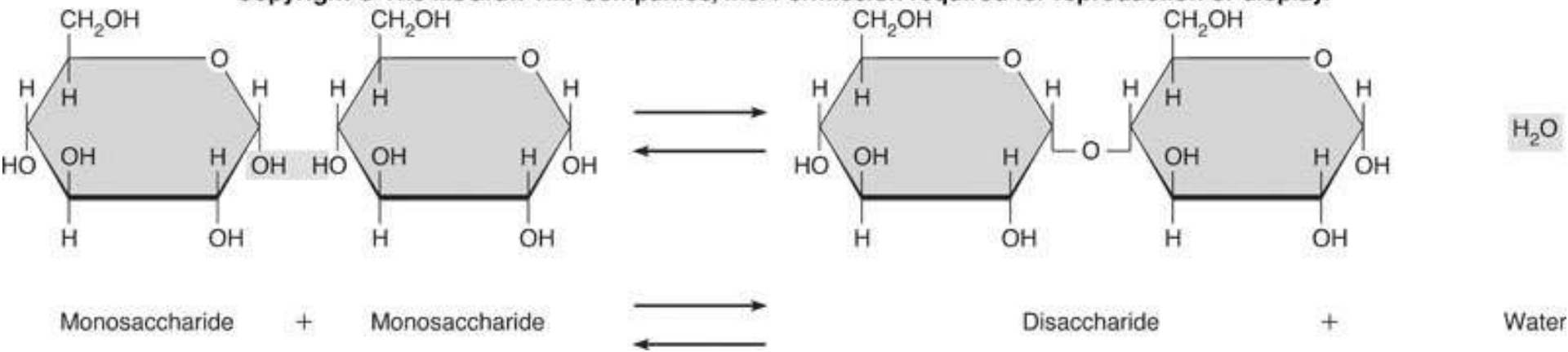


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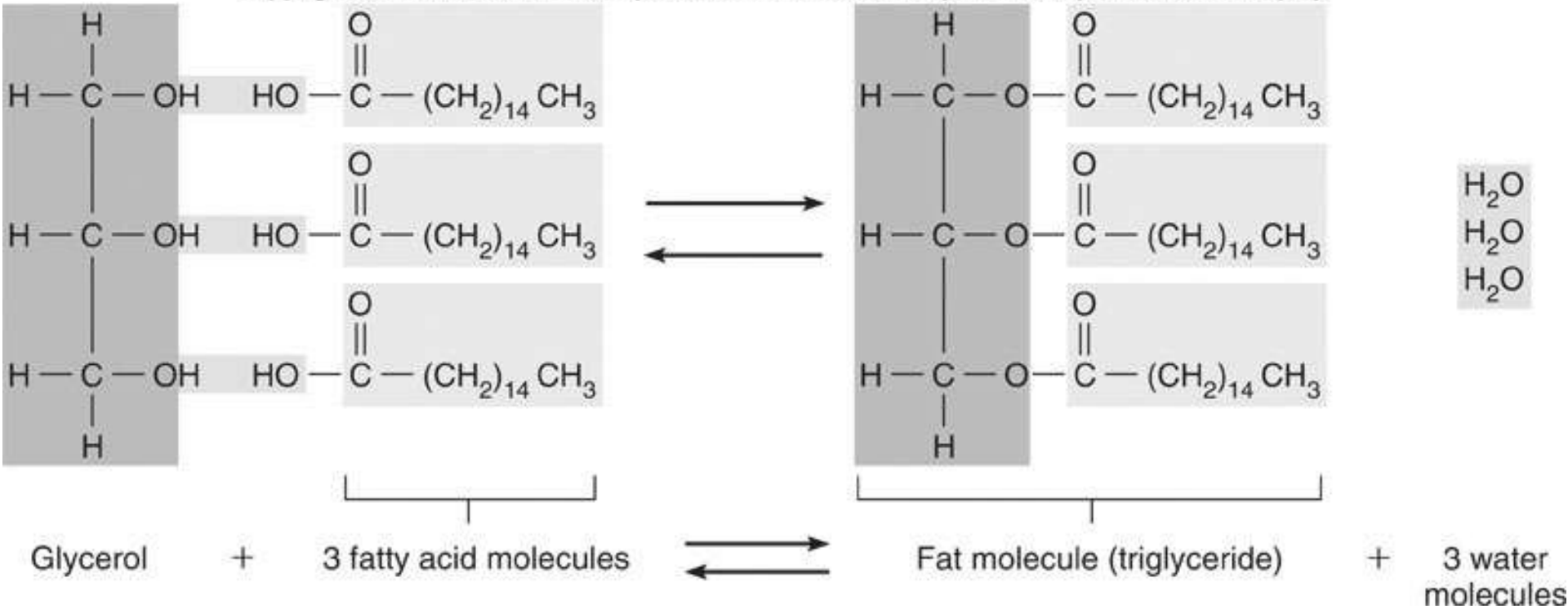


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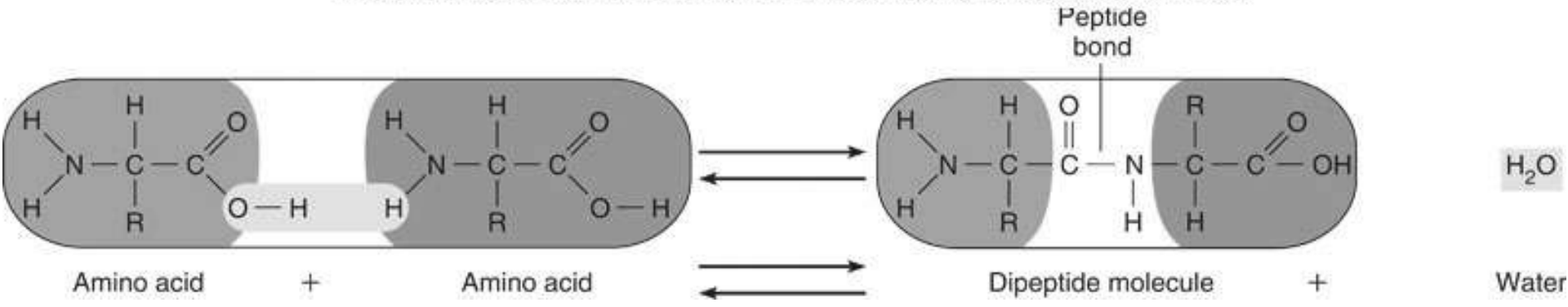


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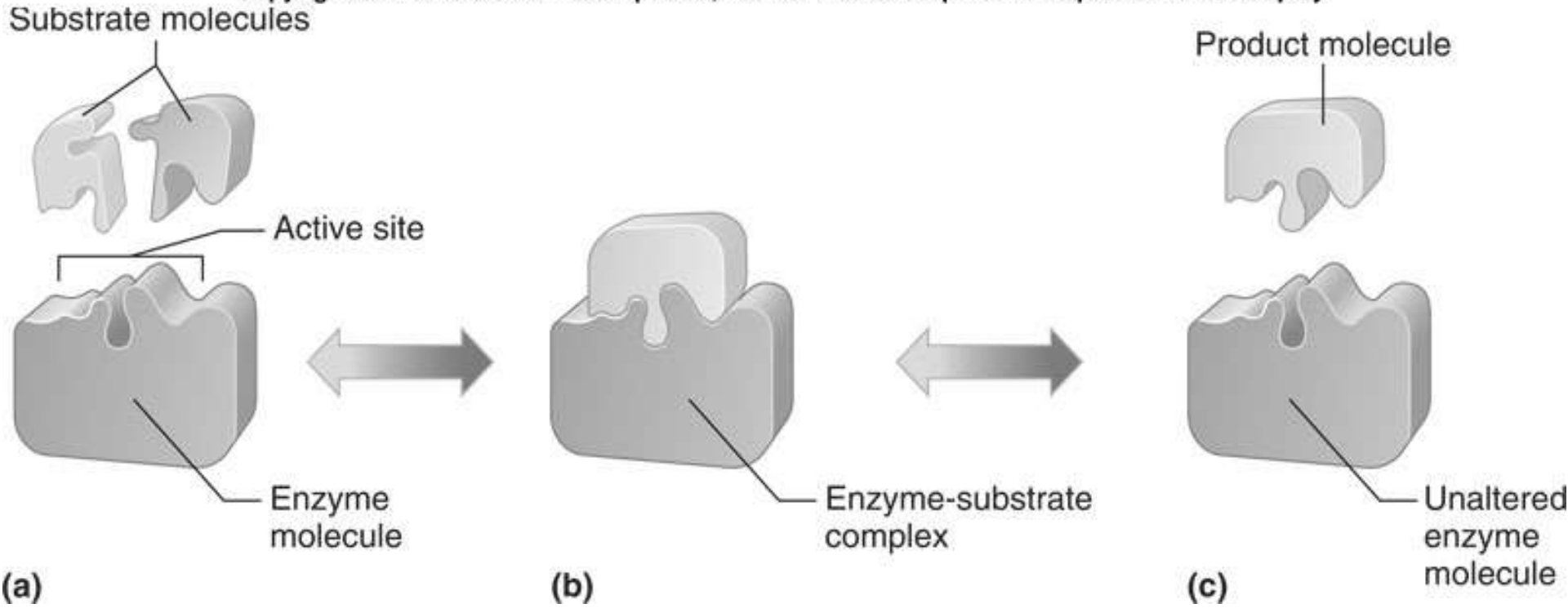
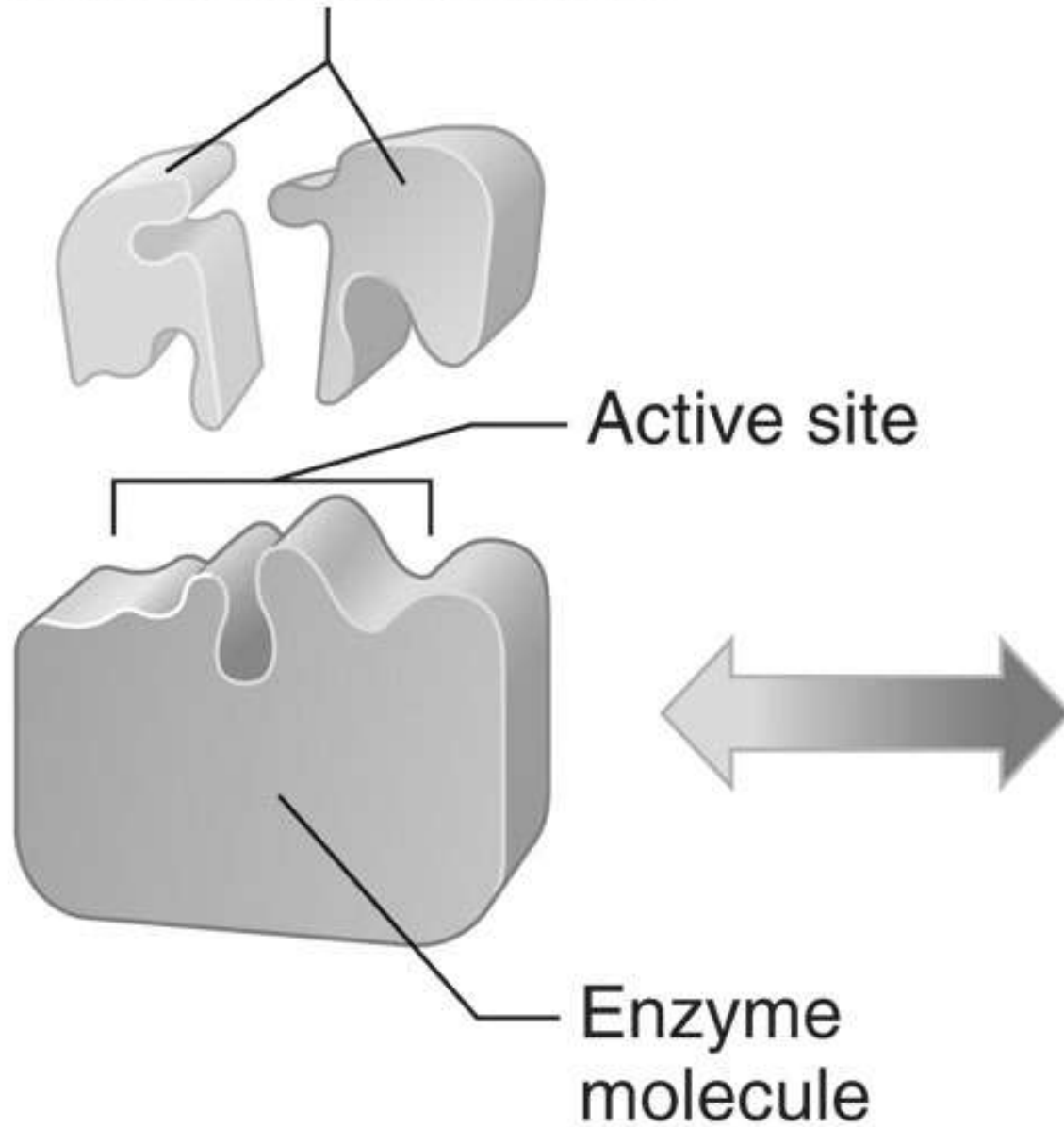


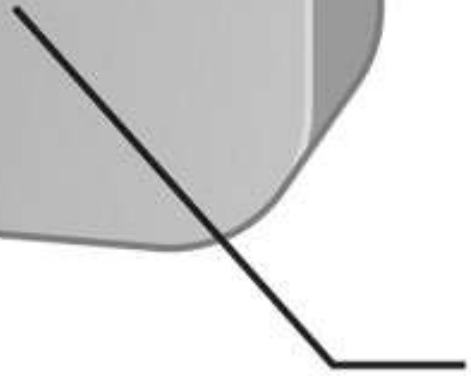
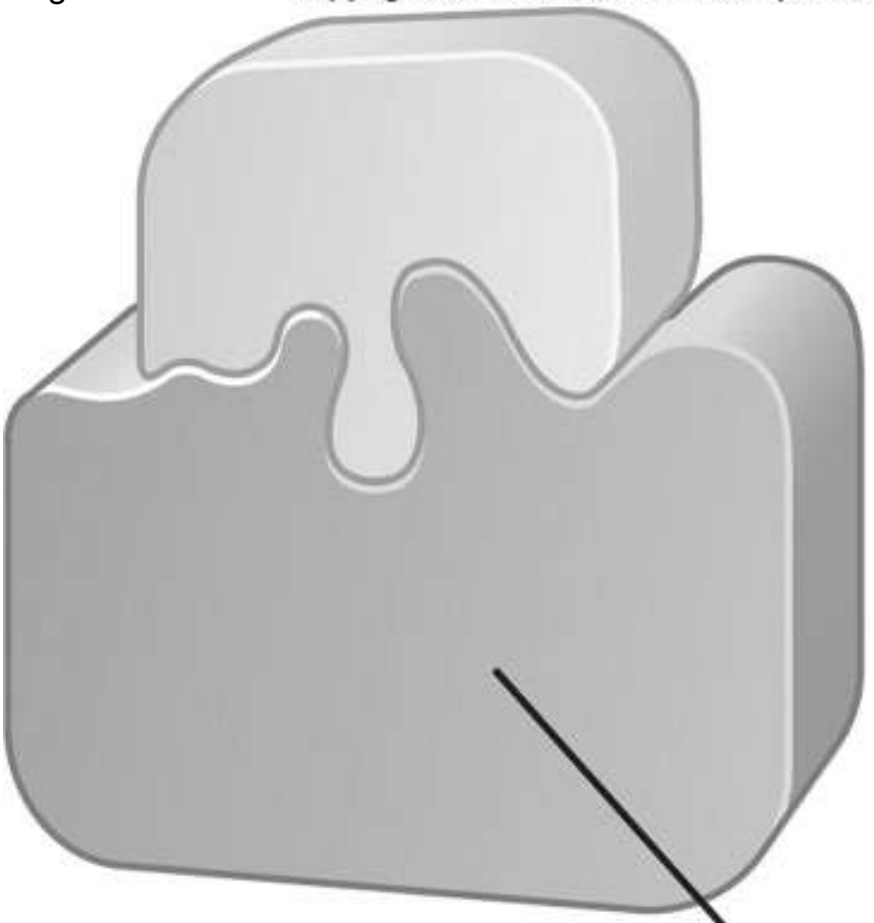
Fig. 4.04a

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Substrate molecules



(a)



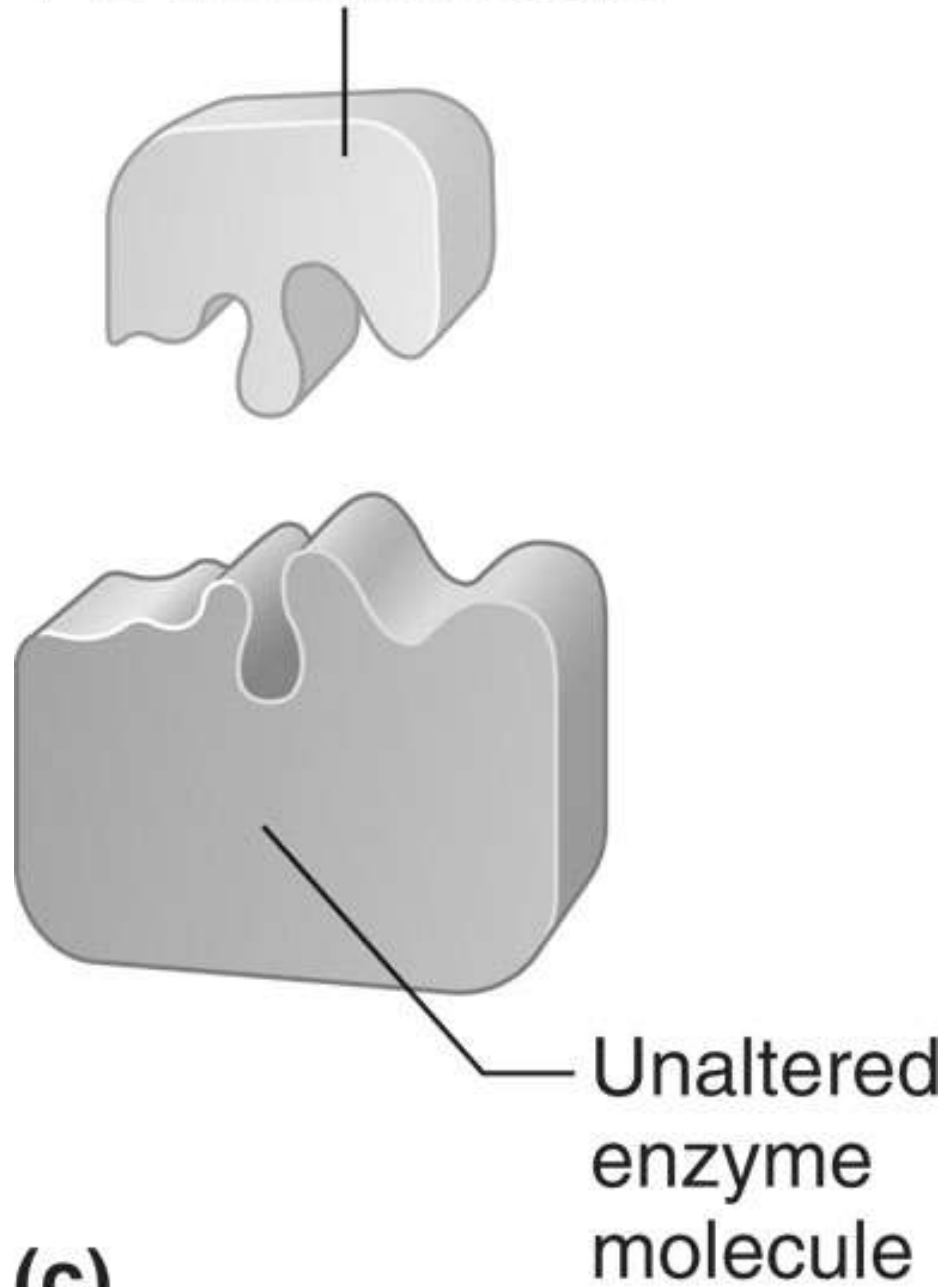
Enzyme-substrate
complex

(b)

Fig. 4.04c

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Product molecule



Glycolysis

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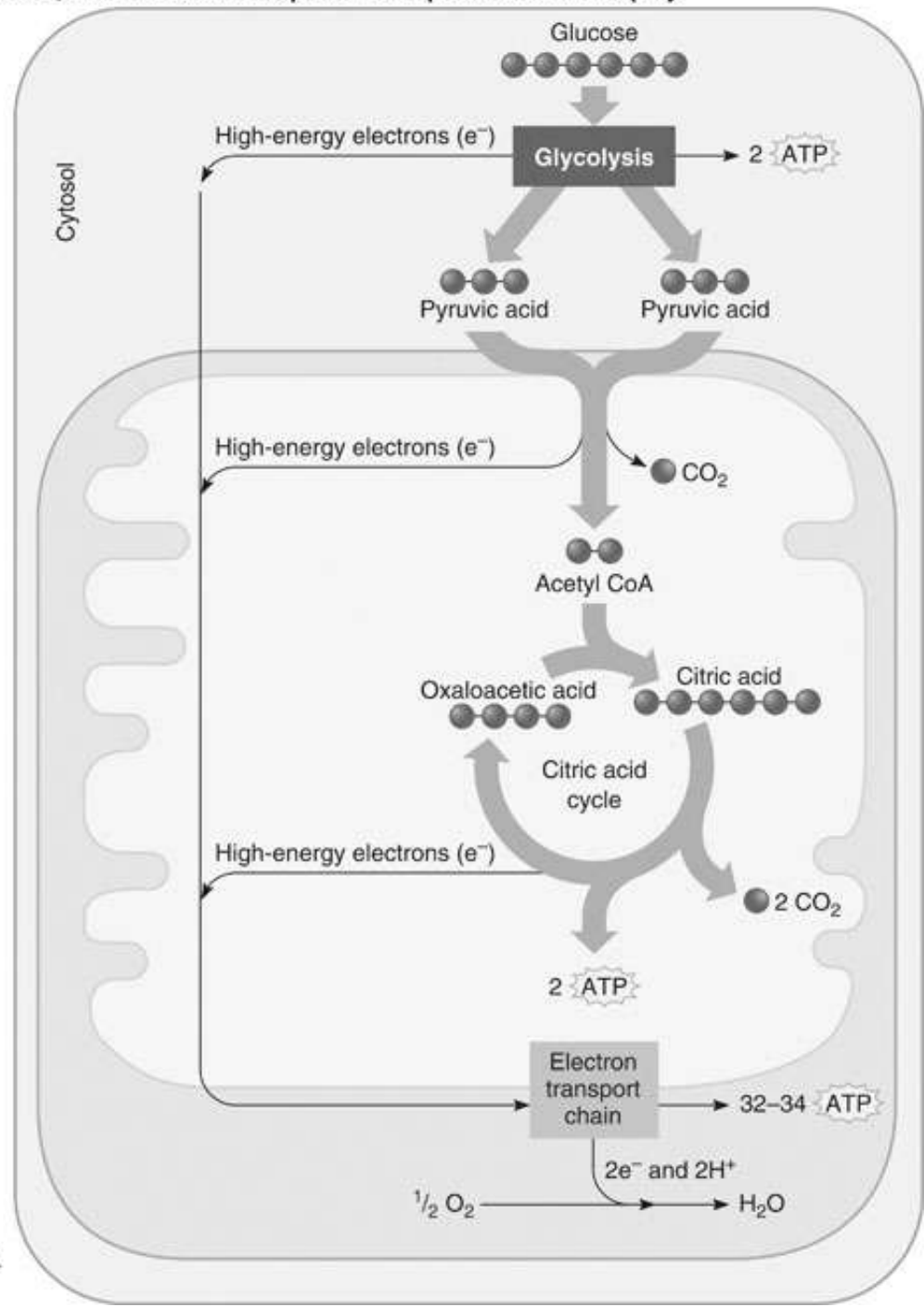


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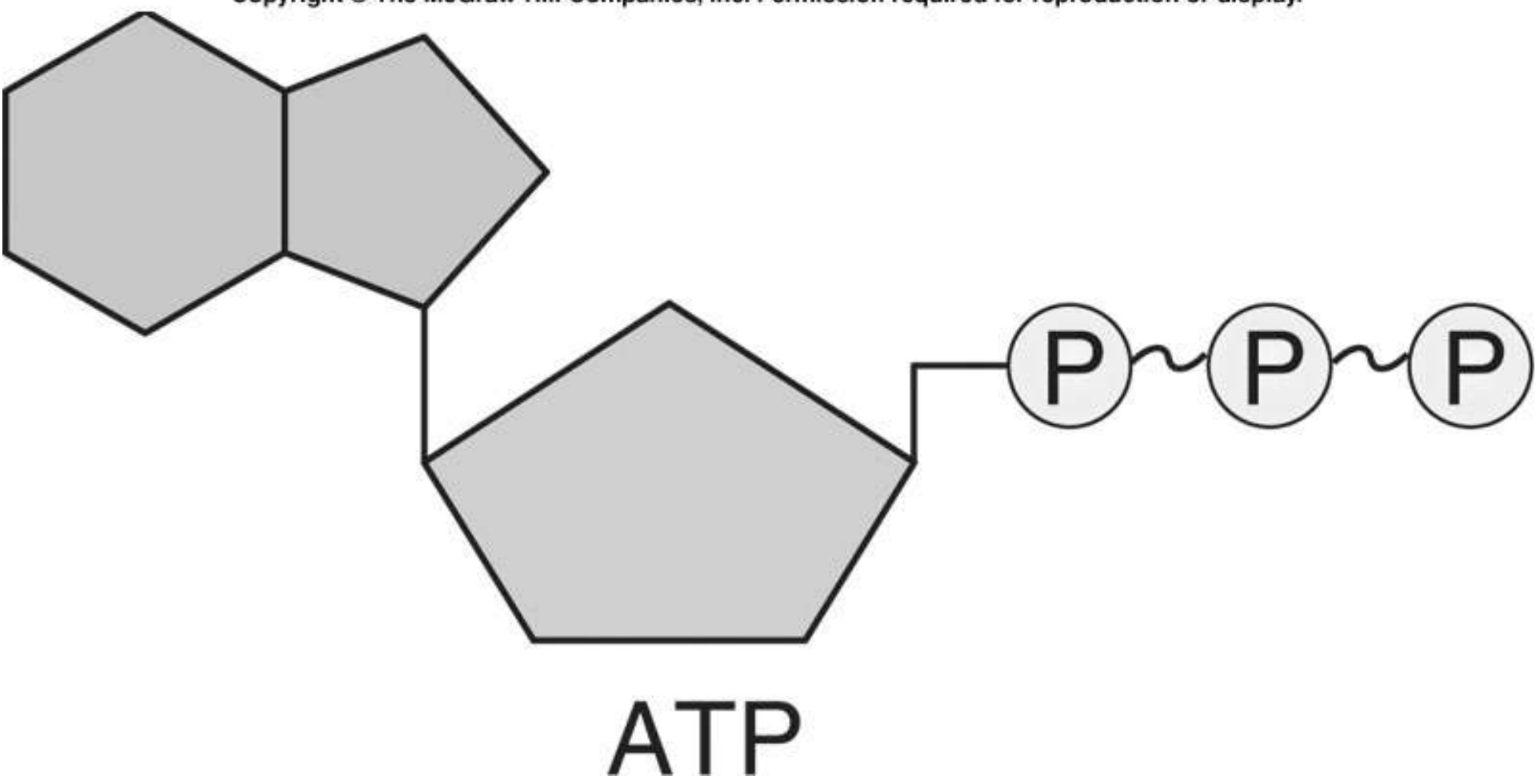


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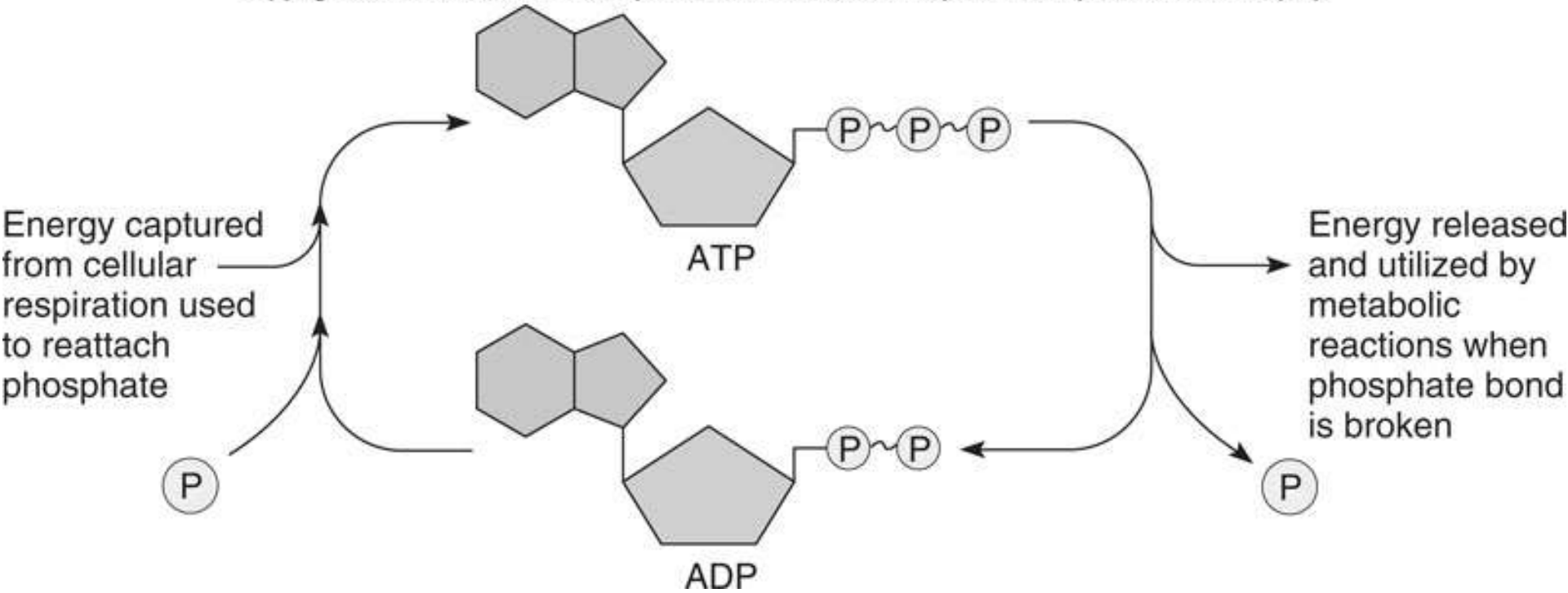


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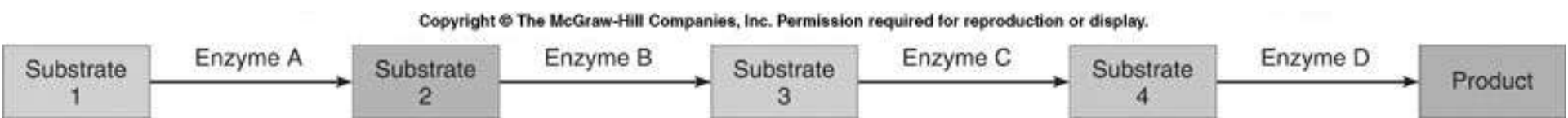


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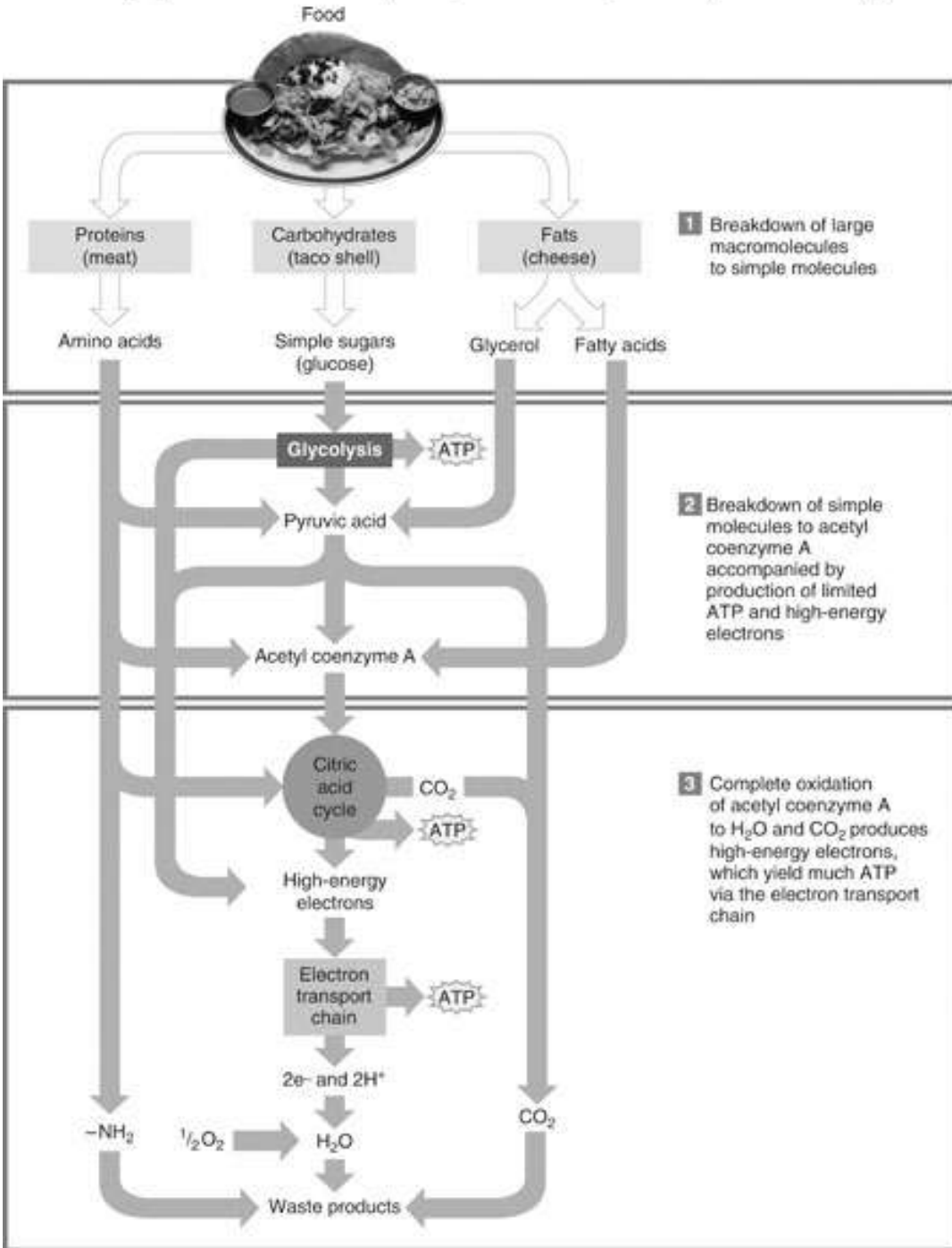


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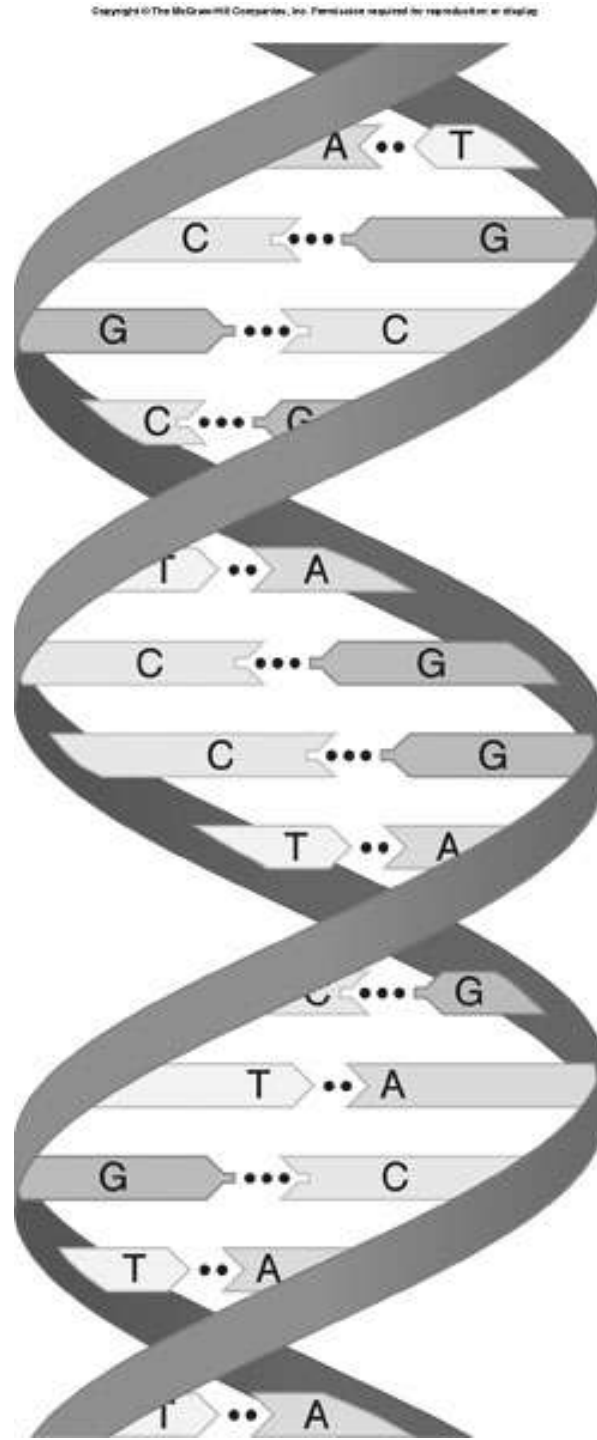


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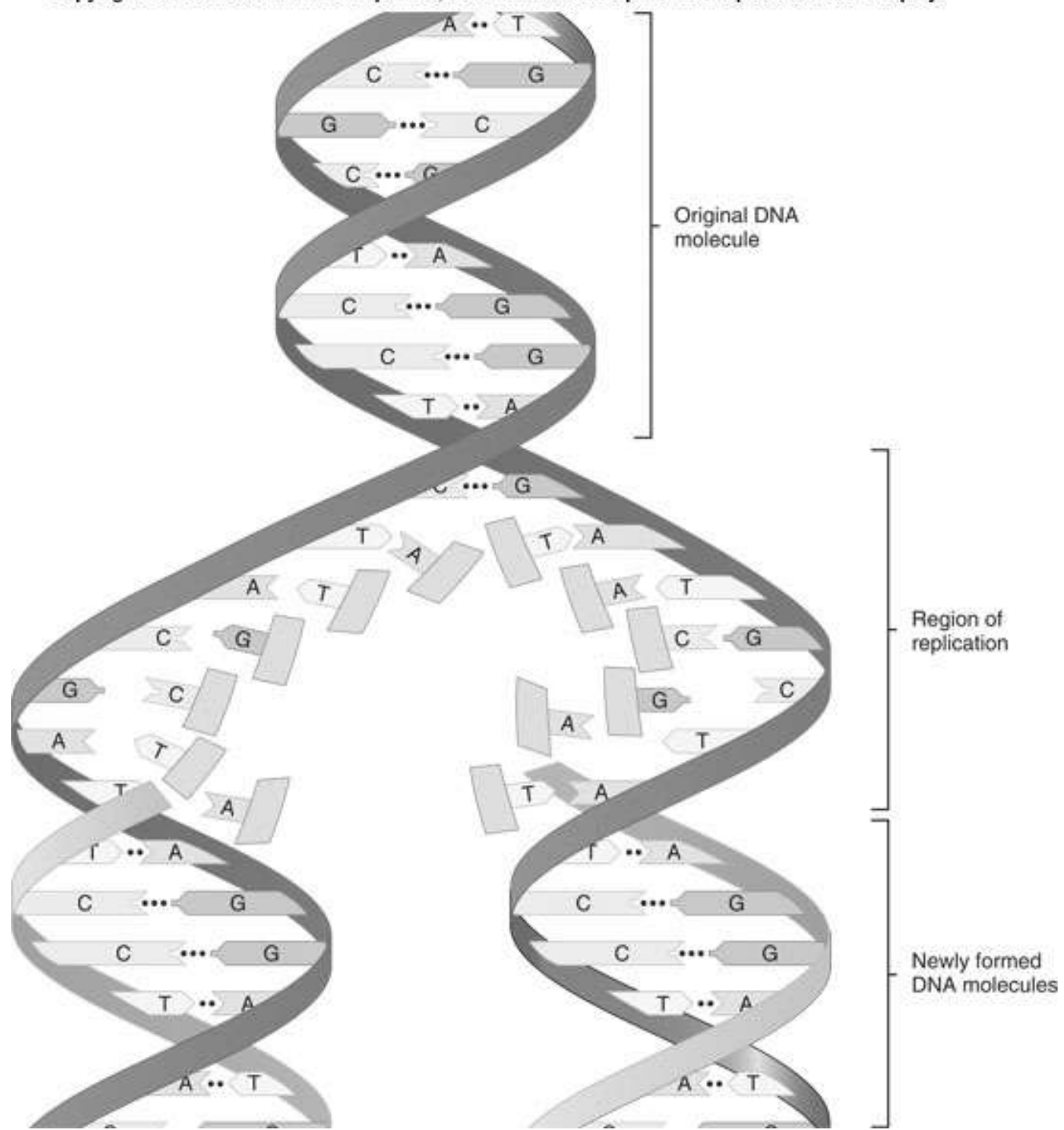


Fig. 4.12

DNA

RNA

Direction of "reading" code
↑

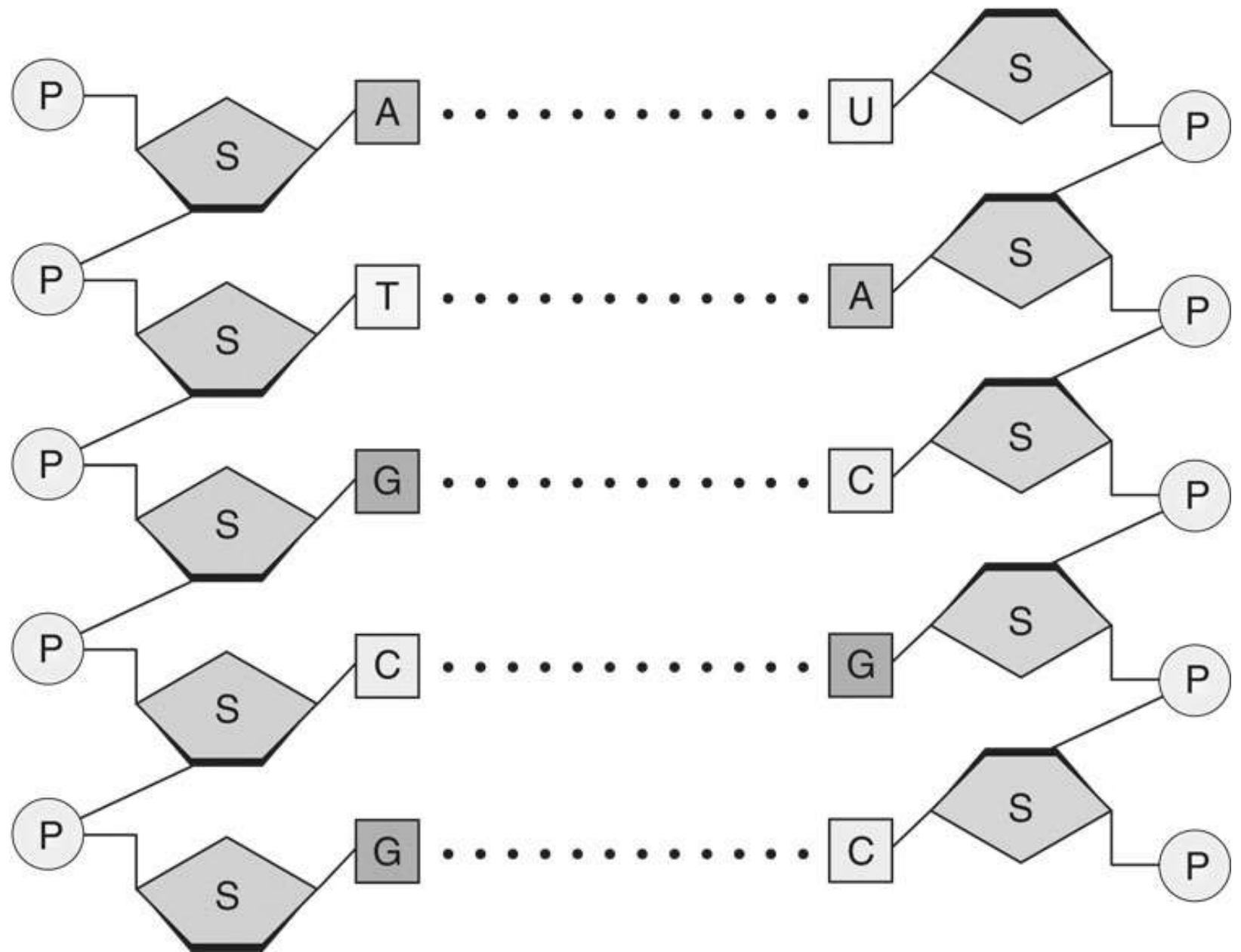


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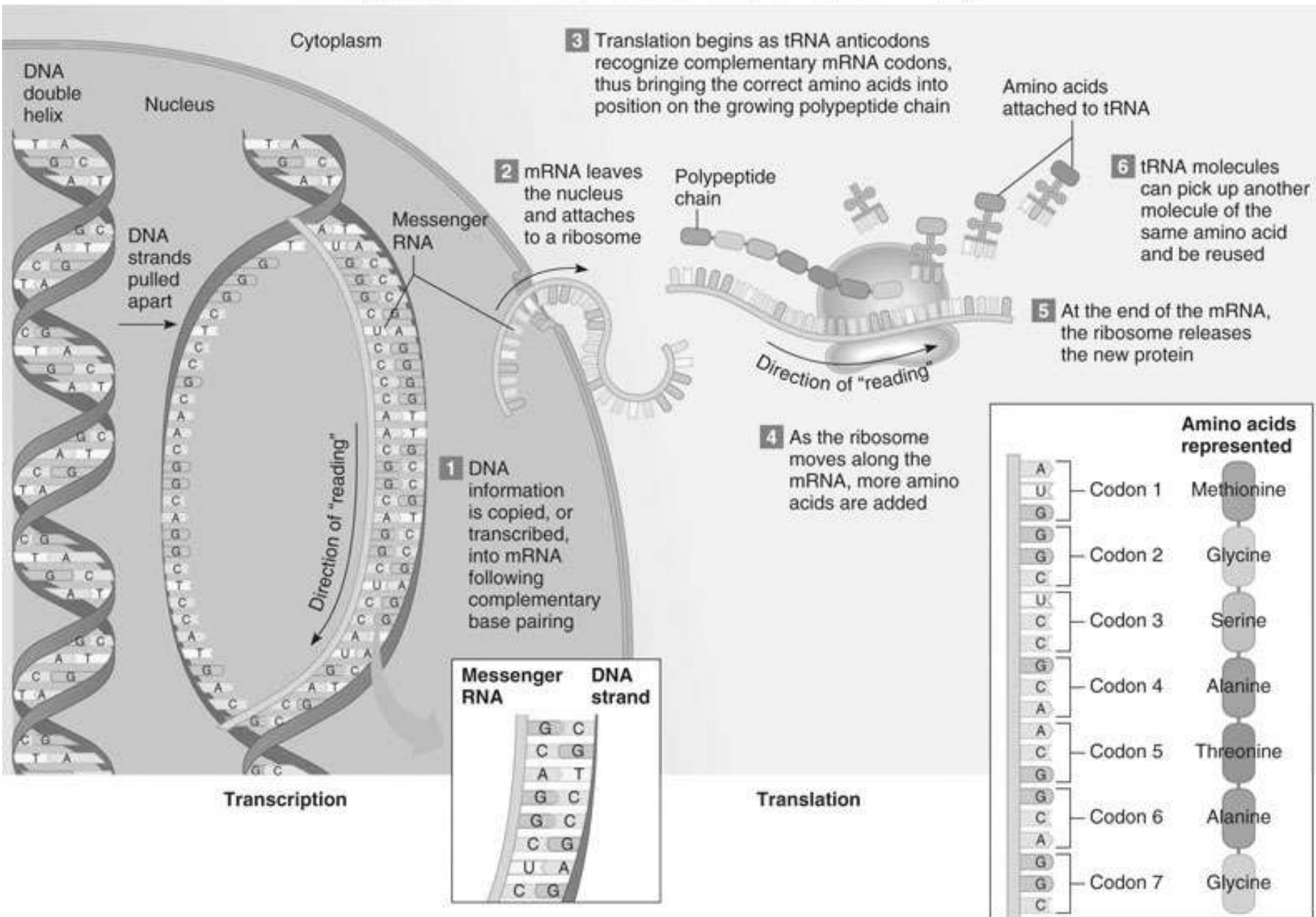


Fig. 4.14a

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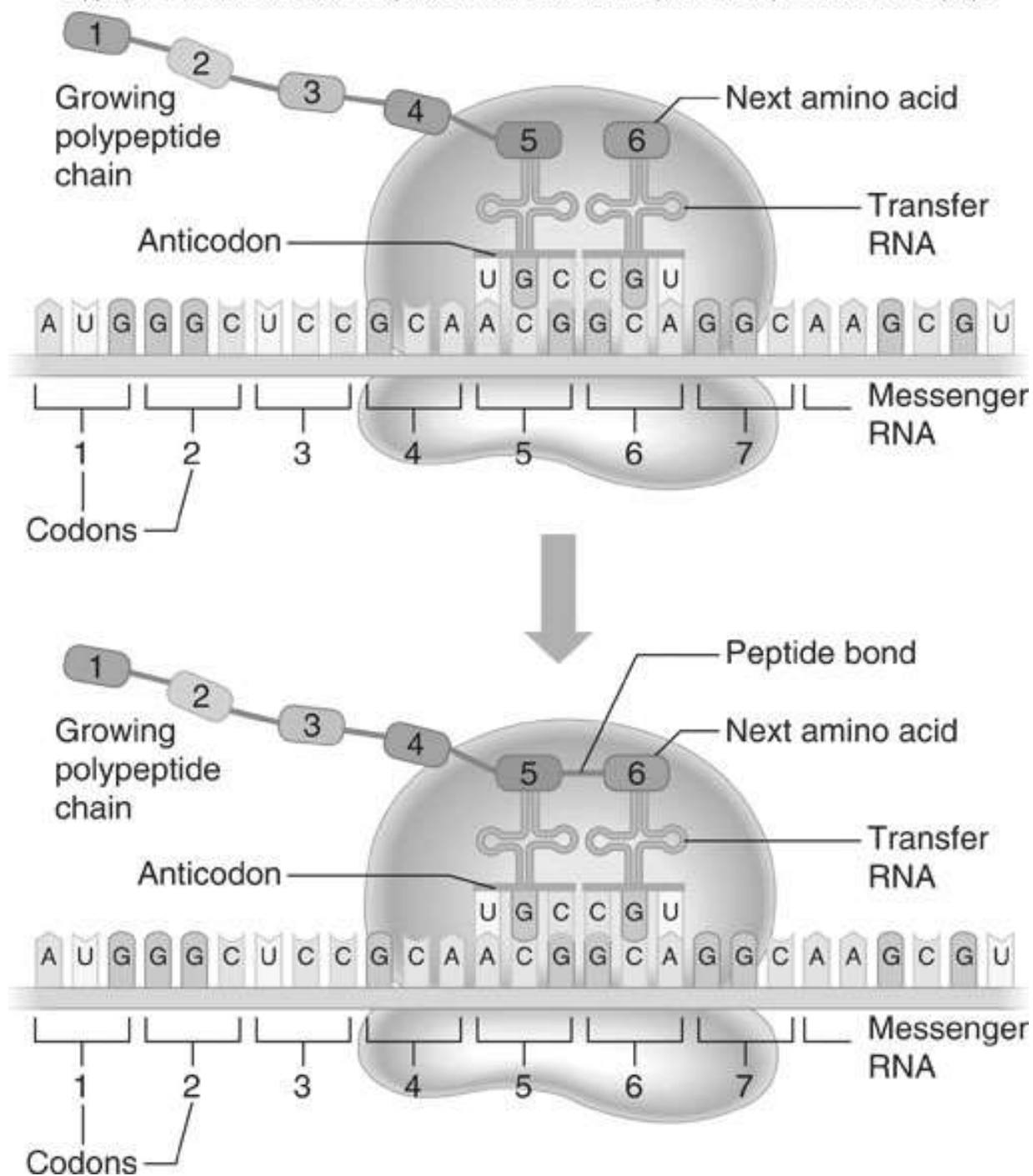


Fig. 4.14b

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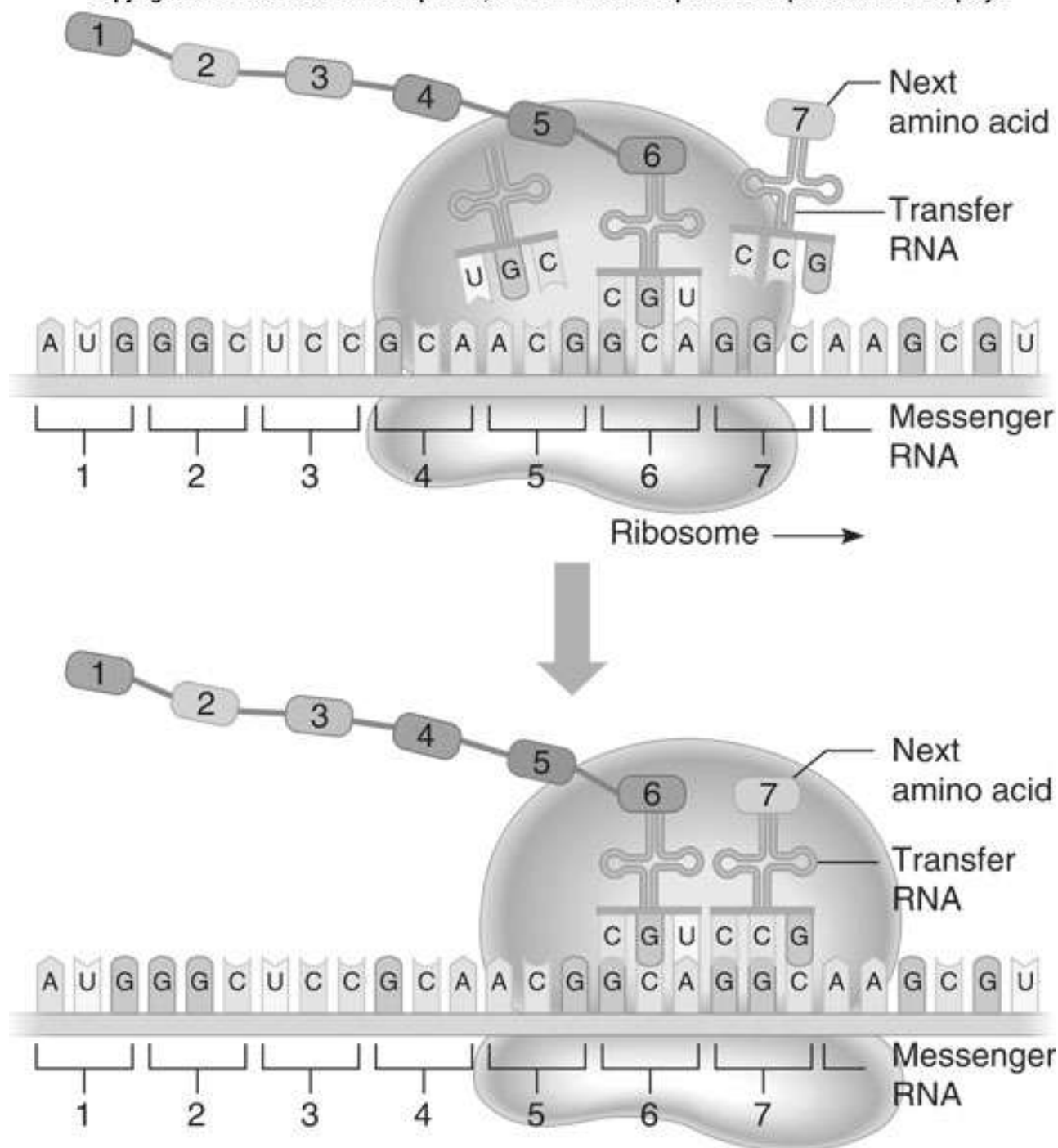
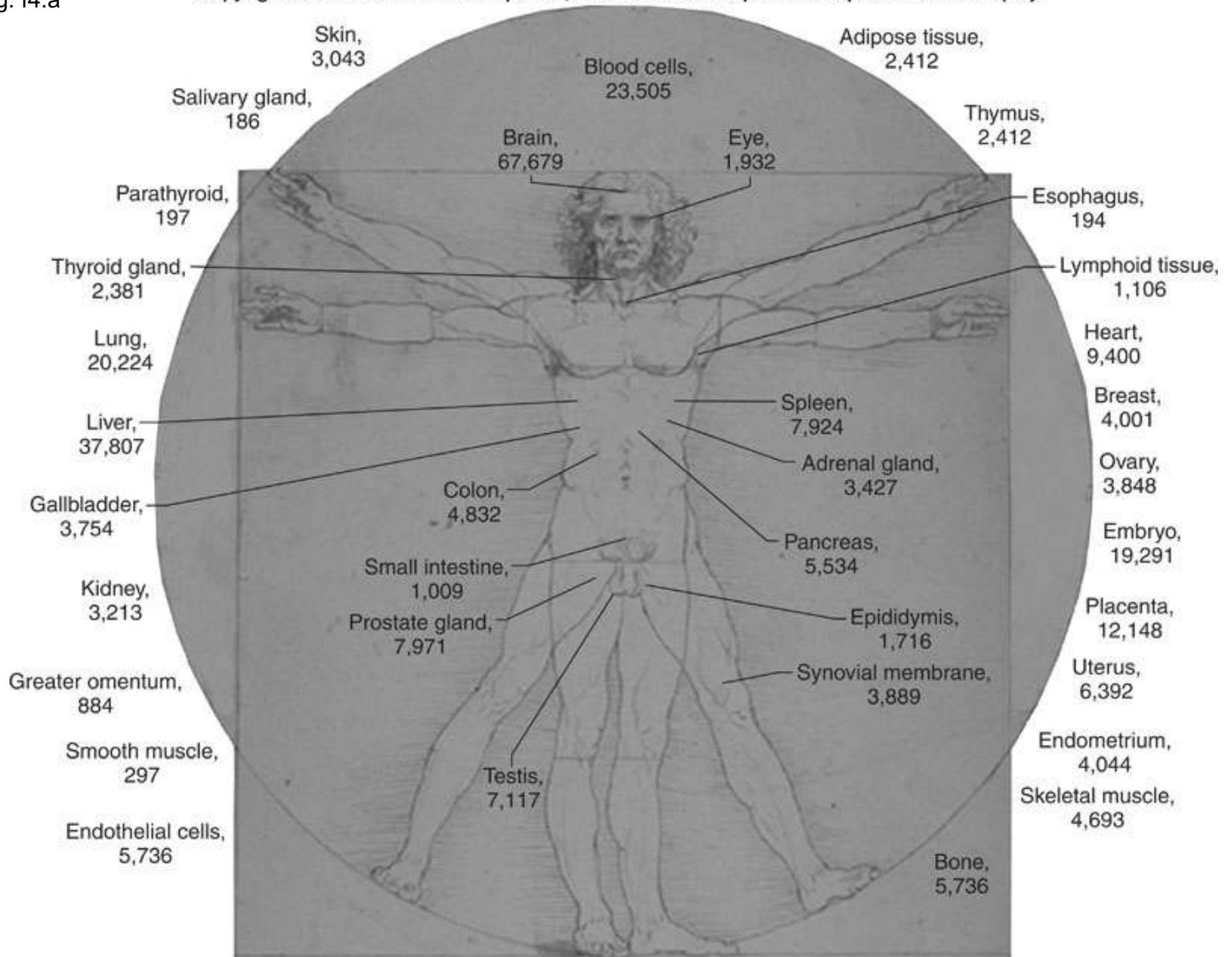


Fig. f4.a

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**GRAYSCALE
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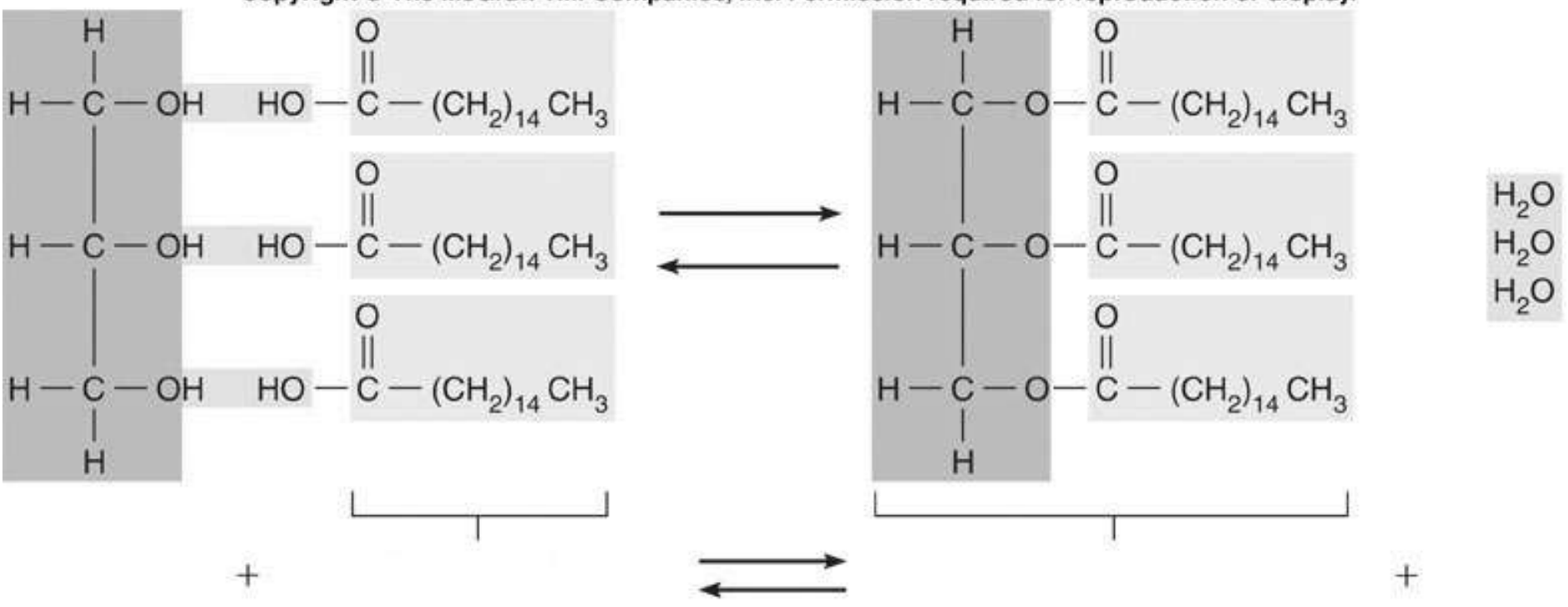


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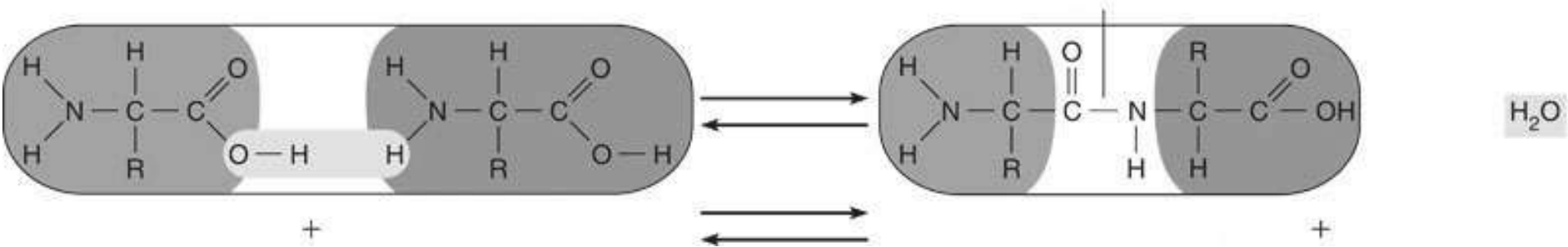


Fig. 4.04

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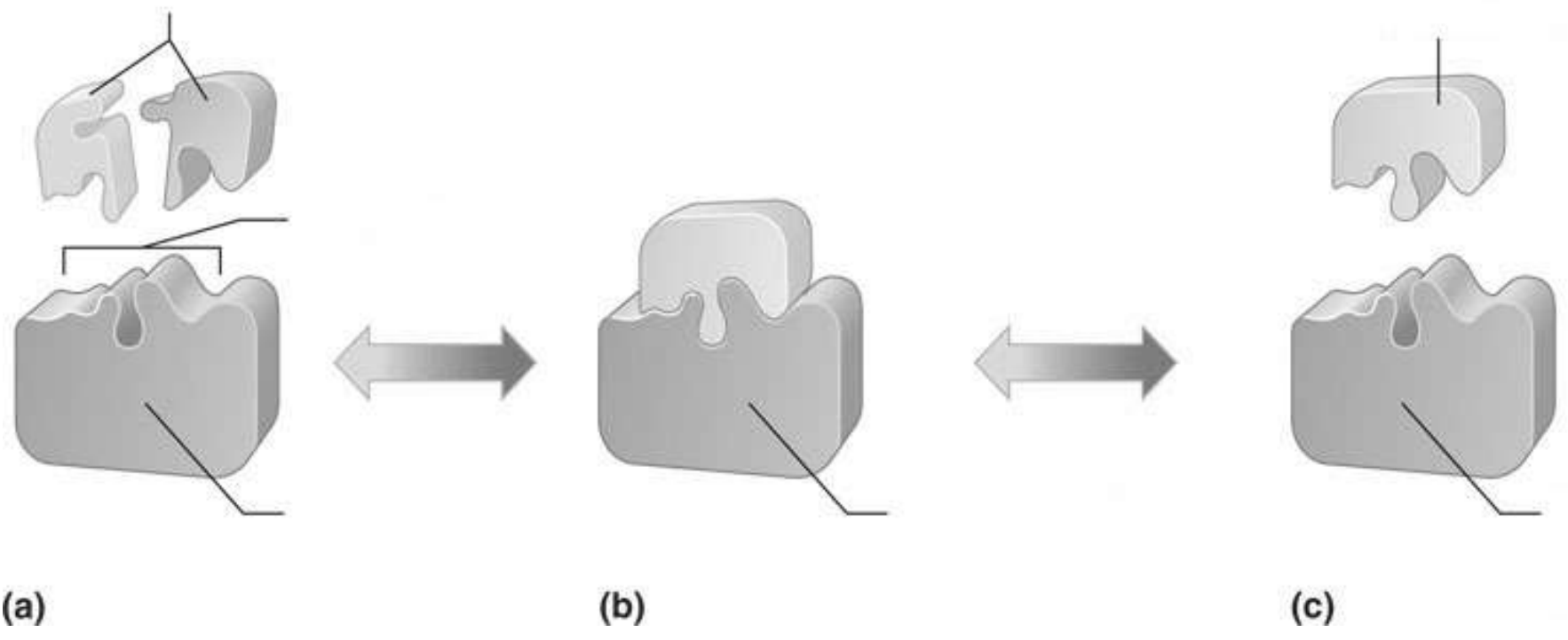
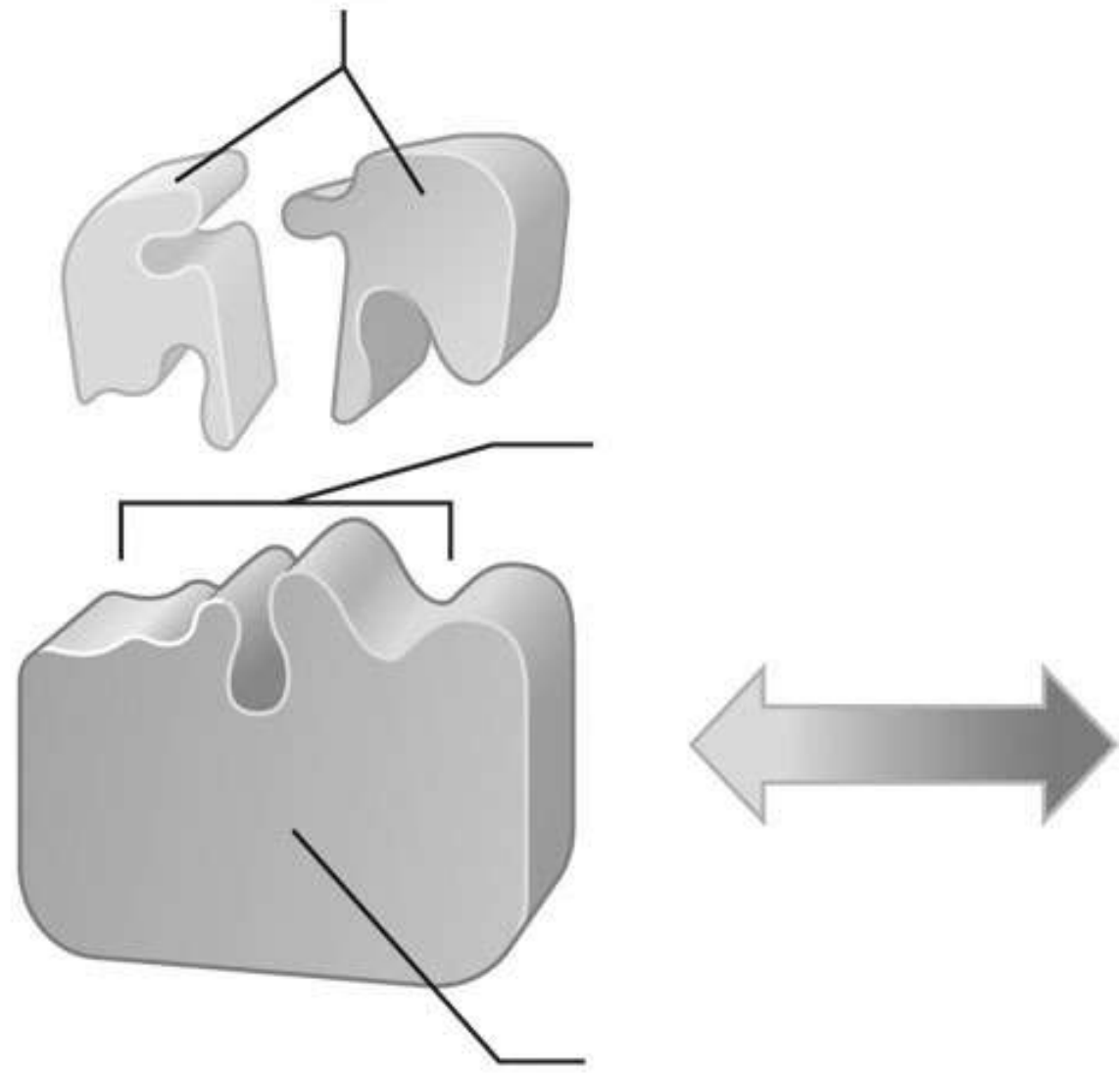
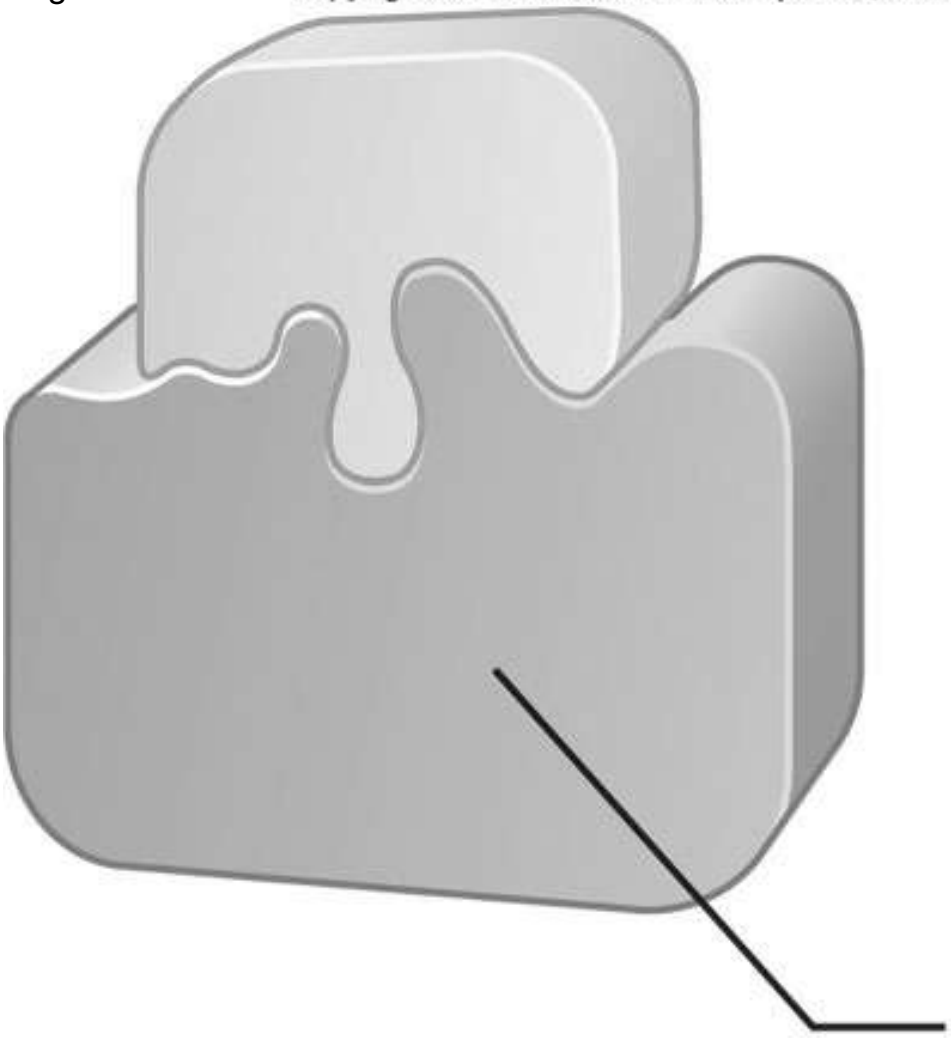


Fig. 4.04a



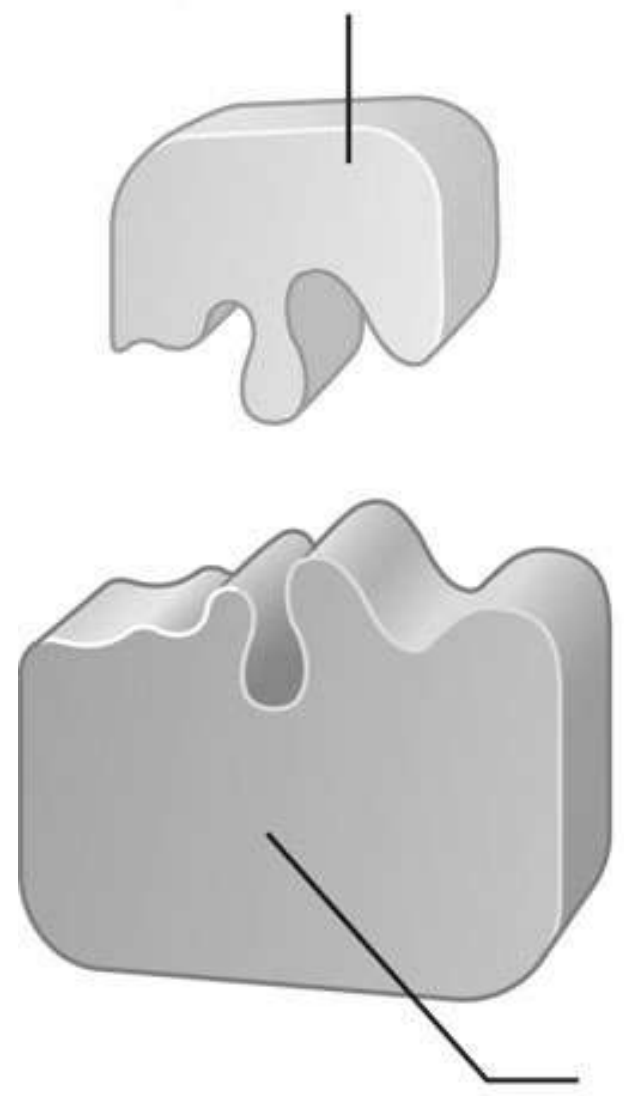
(a)



(b)

Fig. 4.04c

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(c)

Fig. 4.11

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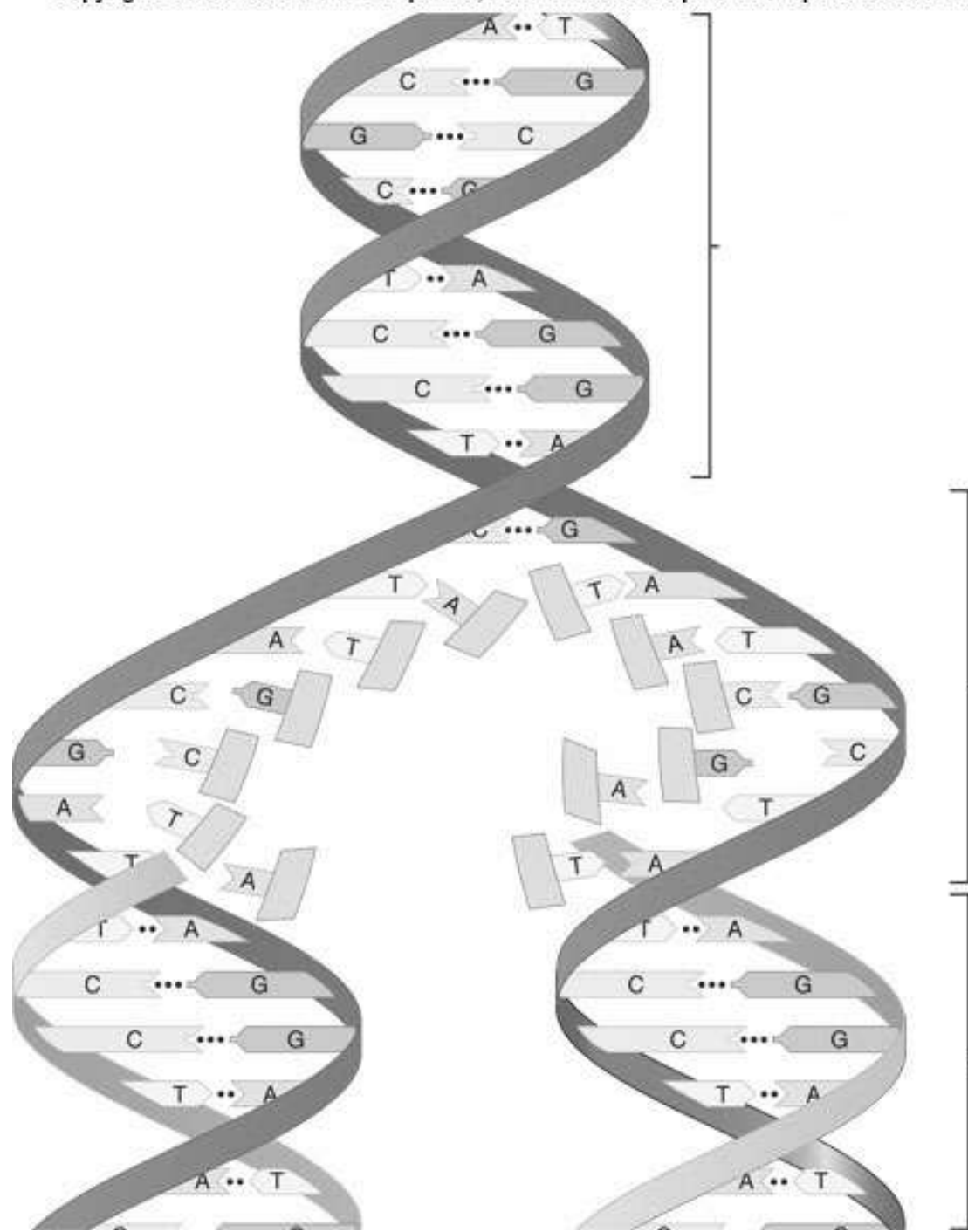


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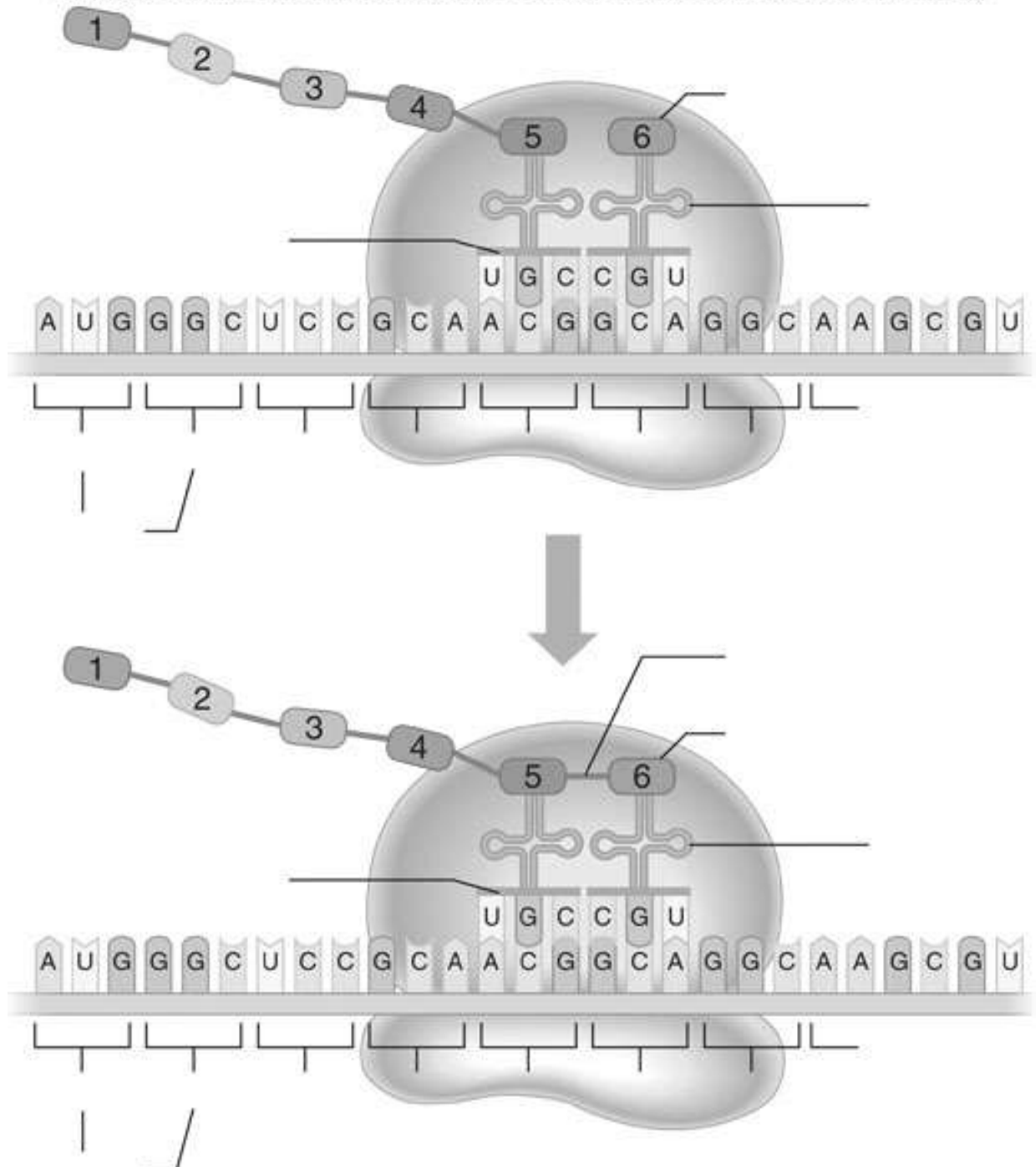


Fig. 4.14b

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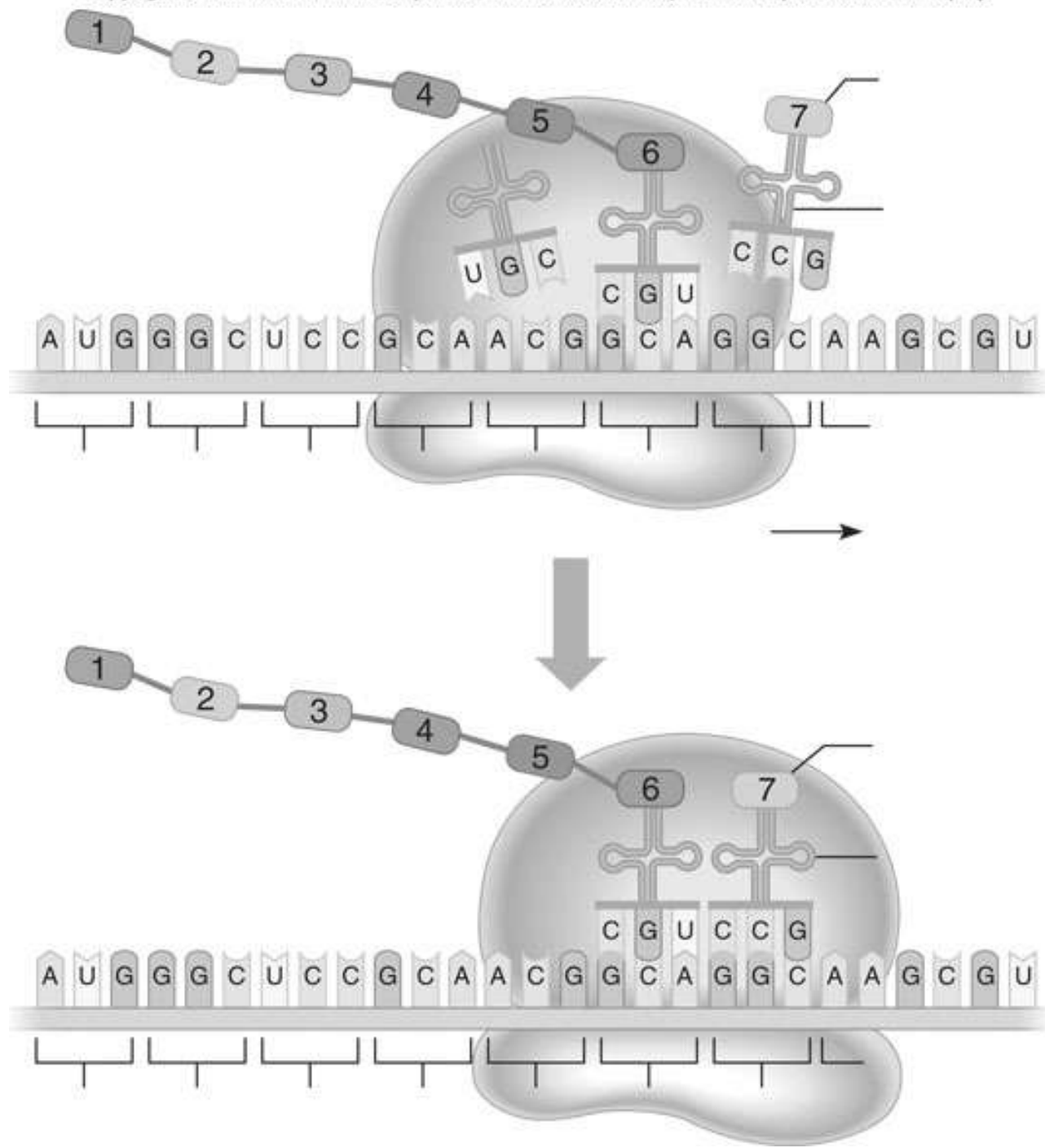
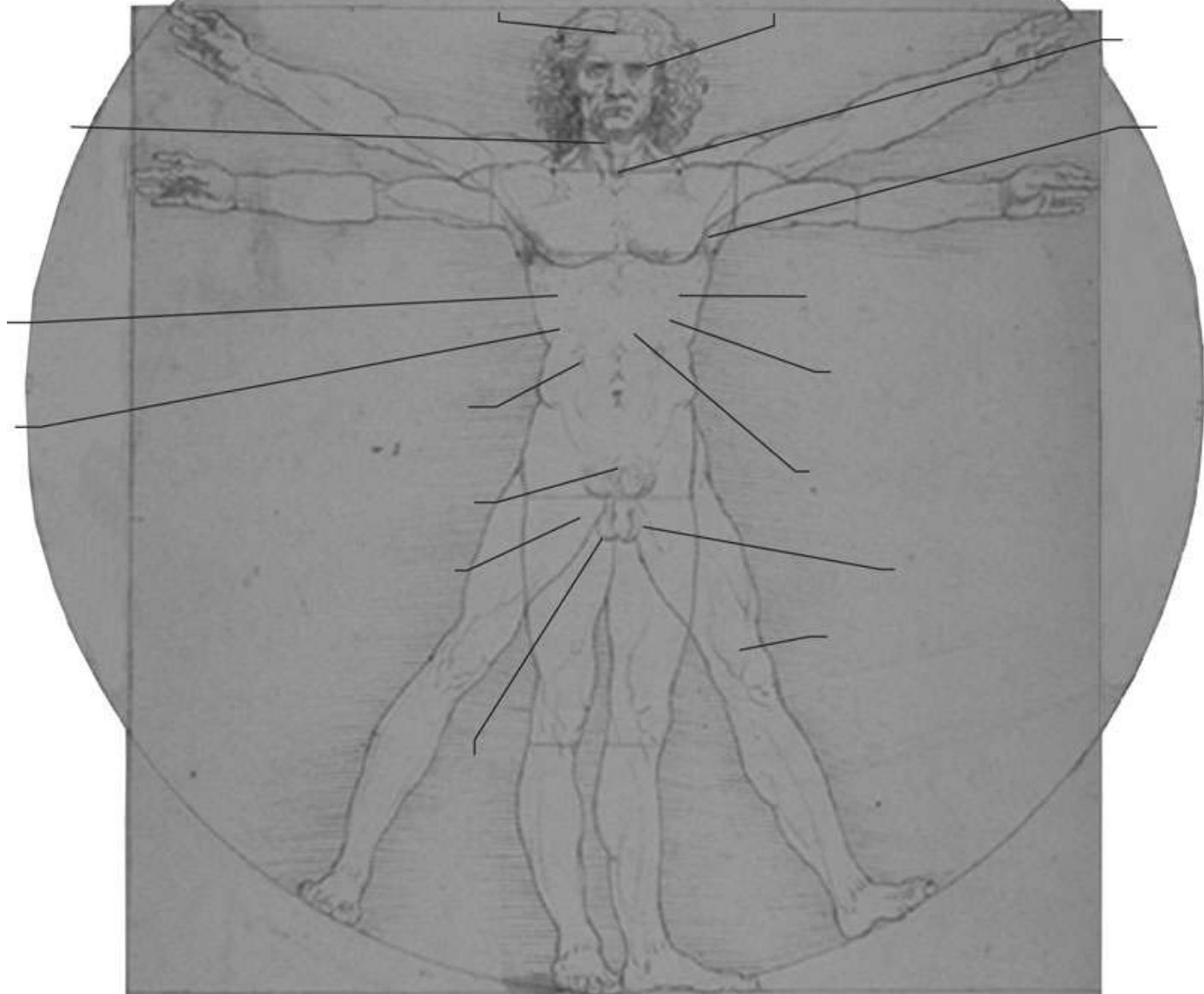


Fig. f4.a

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TABLES

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TABLE 4.1 CODONS (MRNA THREE-BASE SEQUENCES)

		Second Letter							
		U	C	A	G				
First Letter	U	UUU } UUC }	UCU } UCC } UCA } UCG }	UAU } UAC } UAA } UAG }	UGU } UGC } UGA } UGG }	U C A G			
		phenylalanine (phe)					serine (ser)	tyrosine (tyr)	cysteine (cys)
		leucine (leu)					STOP	STOP	STOP
									tryptophan (trp)
	C	CUU } CUC } CUA } CUG }	CCU } CCC } CCA } CCG }	CAU } CAC } CAA } CAG }	CGU } CGC } CGA } CGG }	U C A G			
		leucine (leu)					proline (pro)	histidine (his)	arginine (arg)
								glutamine (gln)	
	A	AUU } AUC } AUA } AUG }	ACU } ACC } ACA } ACG }	AAU } AAC } AAA } AAG }	AGU } AGC } AGA } AGG }	U C A G			
		isoleucine (ile)					threonine (thr)	asparagine (asn)	serine (ser)
		START methionine (met)						lysine (lys)	arginine (arg)
	G	GUU } GUC } GUA } GUG }	GCU } GCC } GCA } GCG }	GAU } GAC } GAA } GAG }	GGU } GGC } GGA } GGG }	U C A G			
		valine (val)					alanine (ala)	aspartic acid (asp)	glycine (gly)
								glutamic acid (glu)	

Third Letter

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TABLE 4.2 A COMPARISON OF DNA AND RNA MOLECULES

	DNA	RNA
Main location	Part of chromosomes in nucleus	In the cytoplasm
5-carbon sugar	Deoxyribose	Ribose
Basic molecular structure	Double-stranded	Single-stranded
Nitrogenous bases included	Adenine, thymine, cytosine, guanine	Adenine, uracil, cytosine, guanine
Major functions	Contains genetic code for protein synthesis; replicates prior to cell division	mRNA carries transcribed DNA information to cytoplasm and acts as template for synthesis of protein molecules; tRNA carries amino acids to mRNA

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TABLE 4.3 PROTEIN SYNTHESIS

TRANSCRIPTION (OCCURS IN THE NUCLEUS)

1. RNA polymerase associates with the base sequence of one strand of a gene.
2. Other enzymes unwind the DNA molecule, exposing a portion of the gene.
3. RNA polymerase moves along the exposed gene and polymerizes an mRNA molecule, whose nucleotides are complementary to those of the gene strand.
4. When the RNA polymerase reaches the end of the gene, the newly formed mRNA molecule is released.
5. The mRNA molecule passes through a pore in the nuclear envelope and enters the cytoplasm.

TRANSLATION (OCCURS IN THE CYTOPLASM)

1. A ribosome binds to the mRNA molecule near the codon at the beginning of the messenger strand.
2. A tRNA molecule with the complementary anticodon associates with the ribosome, and the amino acid it carries becomes part of the chain.
3. This process repeats for each codon in the mRNA sequence as the ribosome moves along the mRNA's length.
4. Enzymes associated with the ribosome catalyze peptide bonds, forming a chain of amino acids.
5. As the chain of amino acids grows, it folds into the unique shape of a functional protein molecule.
6. The completed protein molecule is released. The mRNA molecule, ribosome, and tRNA molecules can function repeatedly to synthesize other protein molecules.