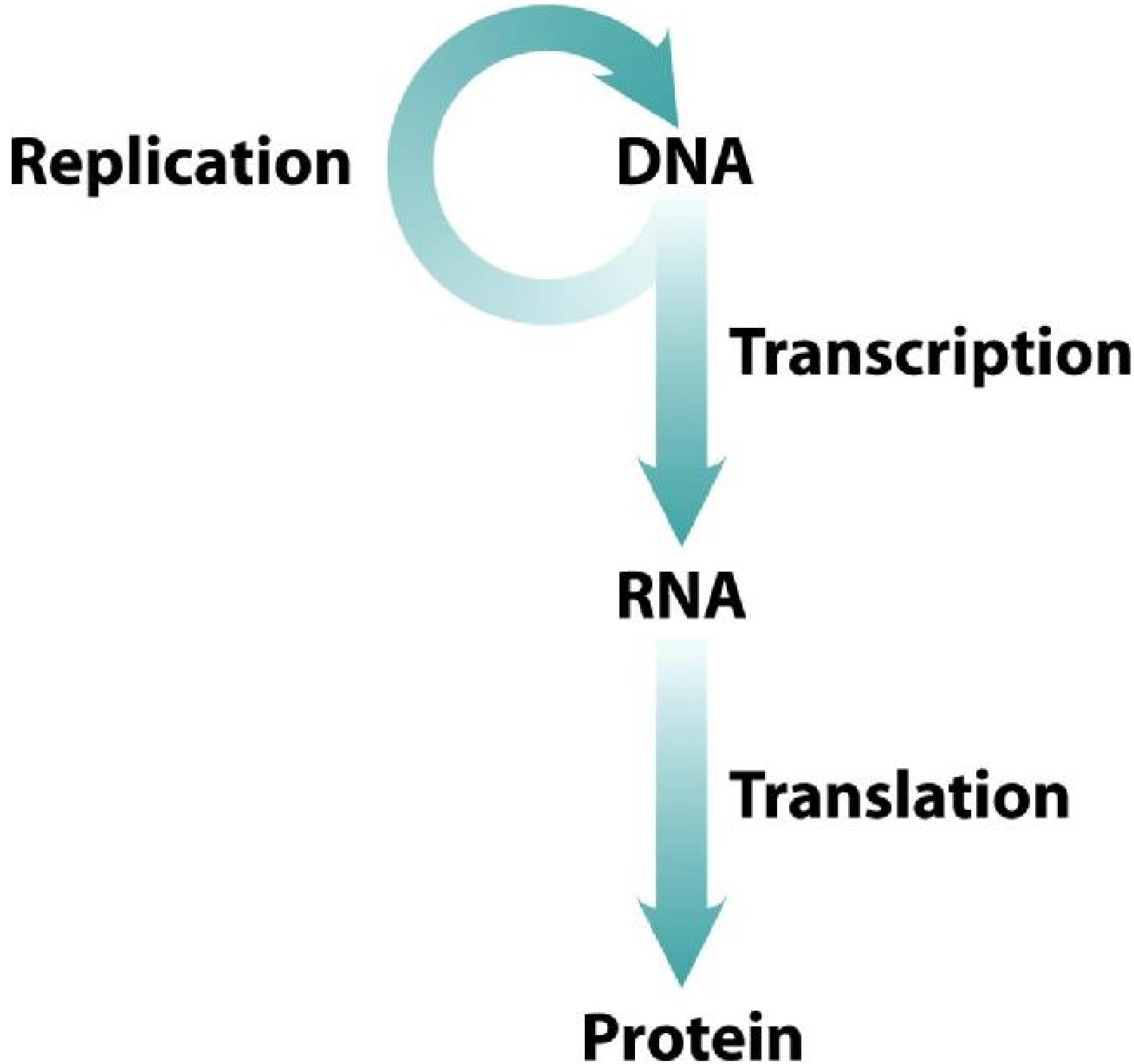

Figure III-1
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T2 bacteriophage DNA

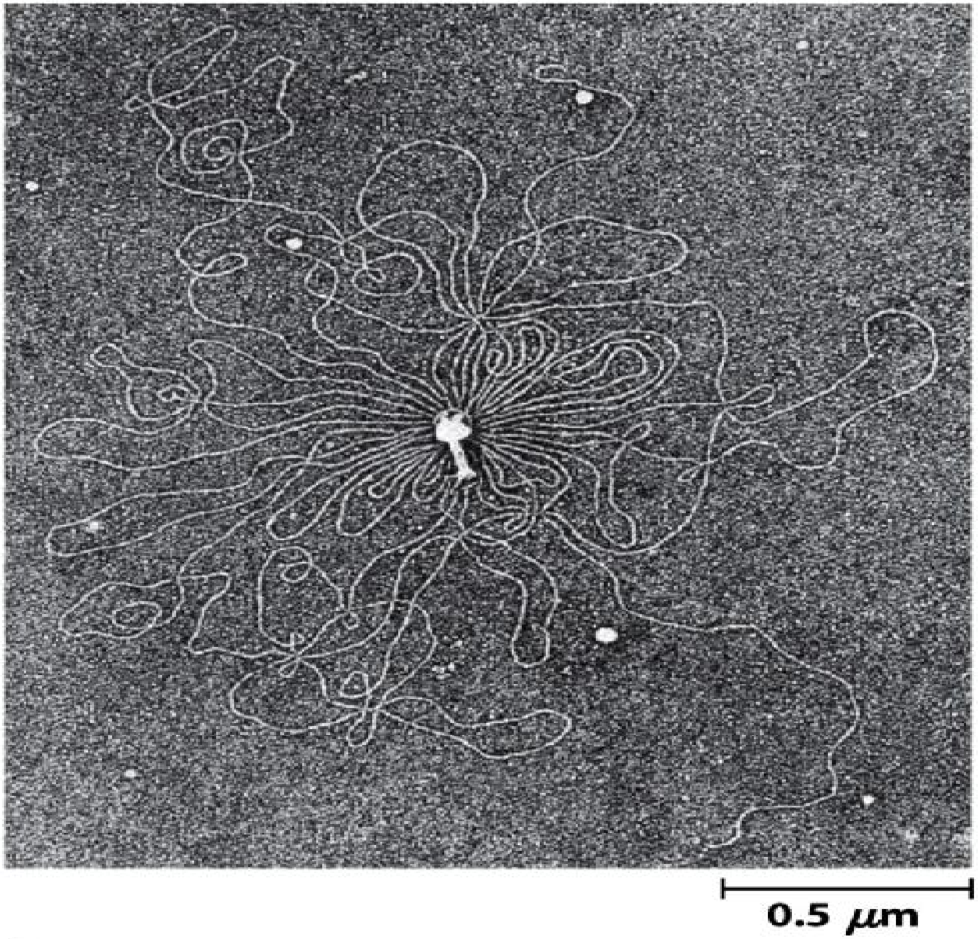

Figure 24-1
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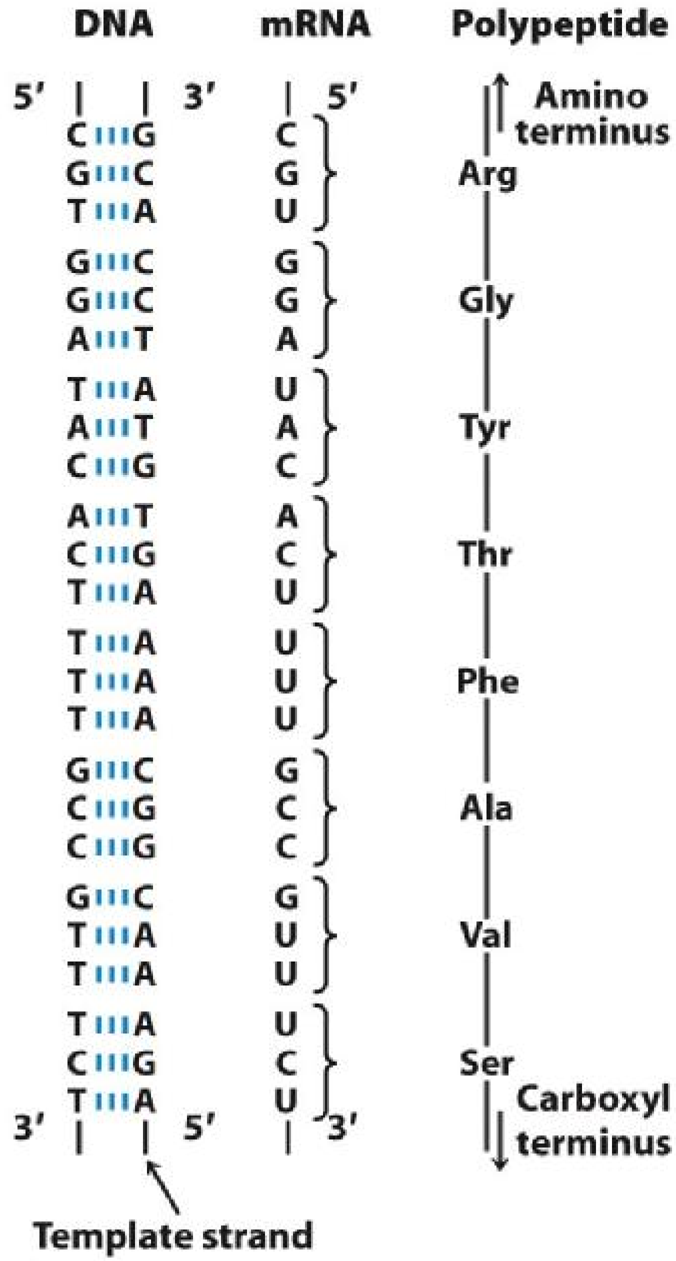

Figure 24-2

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TABLE 24–1	The Sizes of DNA and Viral Particles for Some Bacterial Viruses (Bacteriophages)		
Virus	Size of viral DNA (bp)	Length of viral DNA (nm)	Long dimension of viral particle (nm)
ϕX174	5,386	1,939	25
T7	39,936	14,377	78
λ (lambda)	48,502	17,460	190
T4	168,889	60,800	210

Note: Data on size of DNA are for the replicative form (double-stranded). The contour length is calculated assuming that each base pair occupies a length of 3.4 Å (see Fig. 8–13).

Table 24-1
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length of about 1.7 mm, some 850 times the Iength of the *E coli*, cell

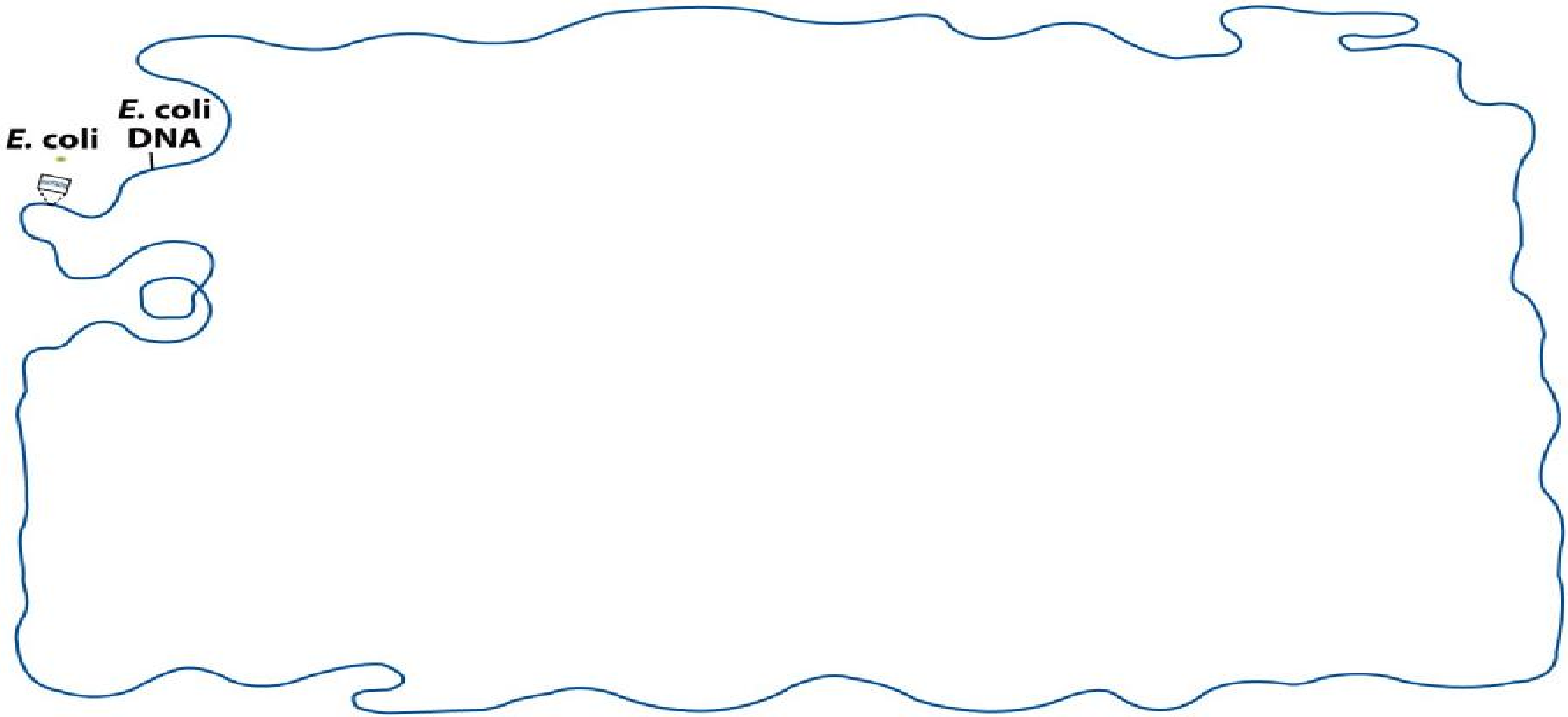

Figure 24-3
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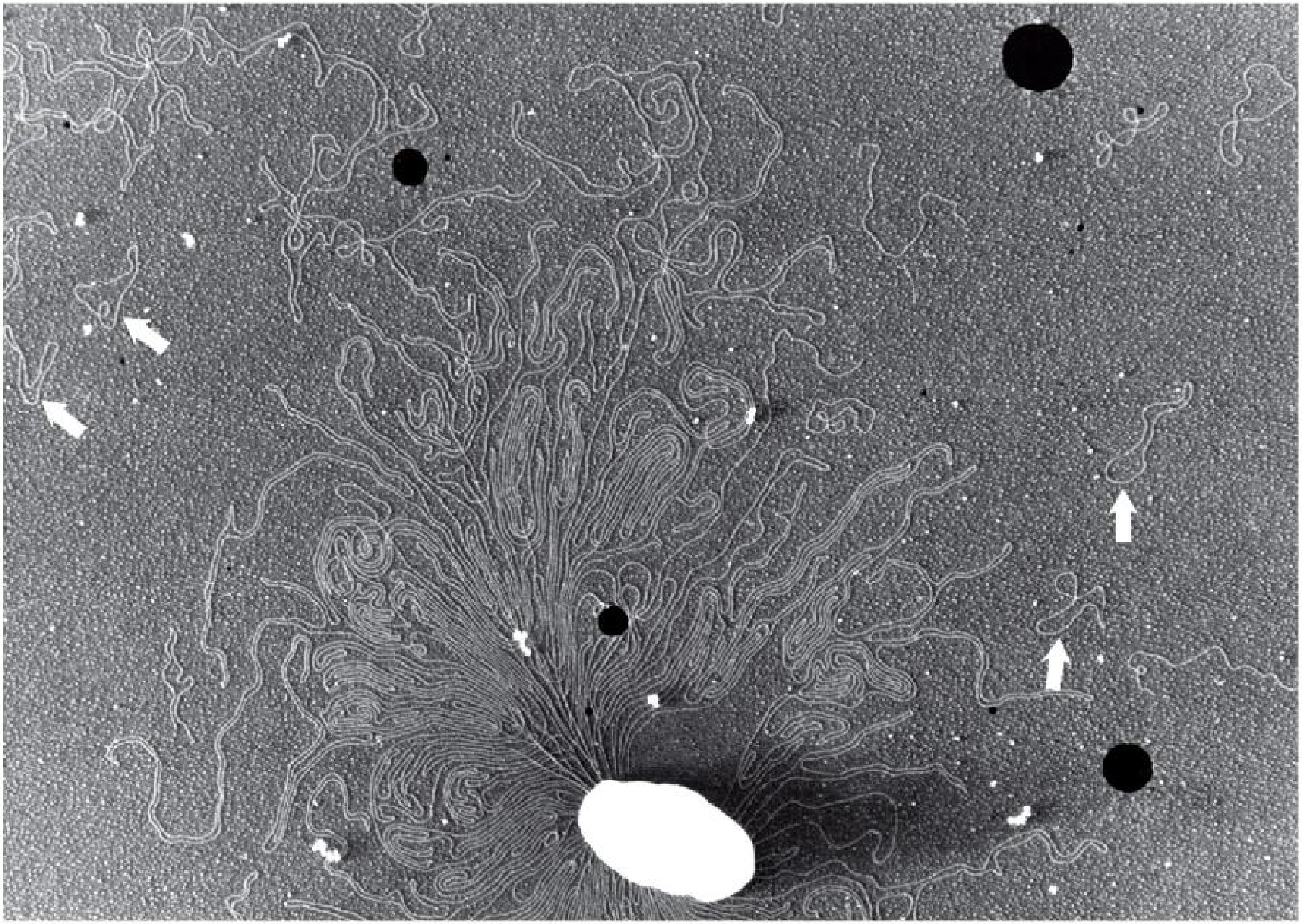

Figure 24-4

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TABLE 24–2 DNA, Gene, and Chromosome Content in Some Genomes

	Total DNA (bp)	Number of chromosomes*	Approximate number of genes
Escherichia coli K12 (bacterium)	4,639,675	1	4,435
Saccharomyces cerevisiae (yeast)	12,080,000	16†	5,860
Caenorhabditis elegans (nematode)	90,269,800	12‡	23,000
Arabidopsis thaliana (plant)	119,186,200	10	33,000
Drosophila melanogaster (fruit fly)	120,367,260	18	20,000
Oryza sativa (rice)	480,000,000	24	57,000
Mus musculus (mouse)	2,634,266,500	40	27,000
Homo sapiens (human)	3,070,128,600	46	29,000

Note: This information is constantly being refined. For the most current information, consult the websites for the individual genome projects.

*The diploid chromosome number is given for all eukaryotes except yeast.

†Haploid chromosome number. Wild yeast strains generally have eight (octoploid) or more sets of these chromosomes.

‡Number for females, with two X chromosomes. Males have an X but no Y, thus 11 chromosomes in all.

Table 24-2

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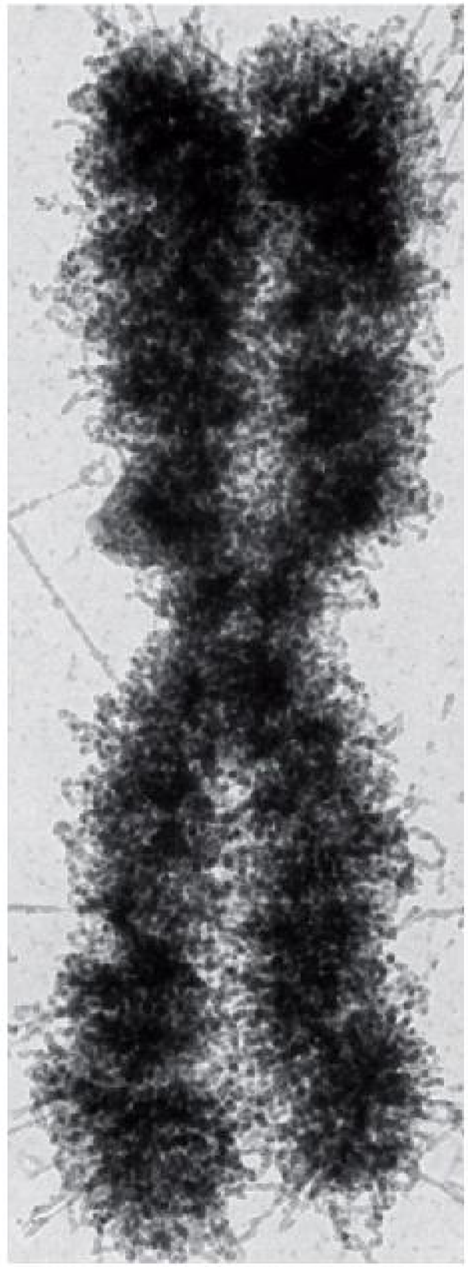

Figure 24-5a
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Figure 24-5b
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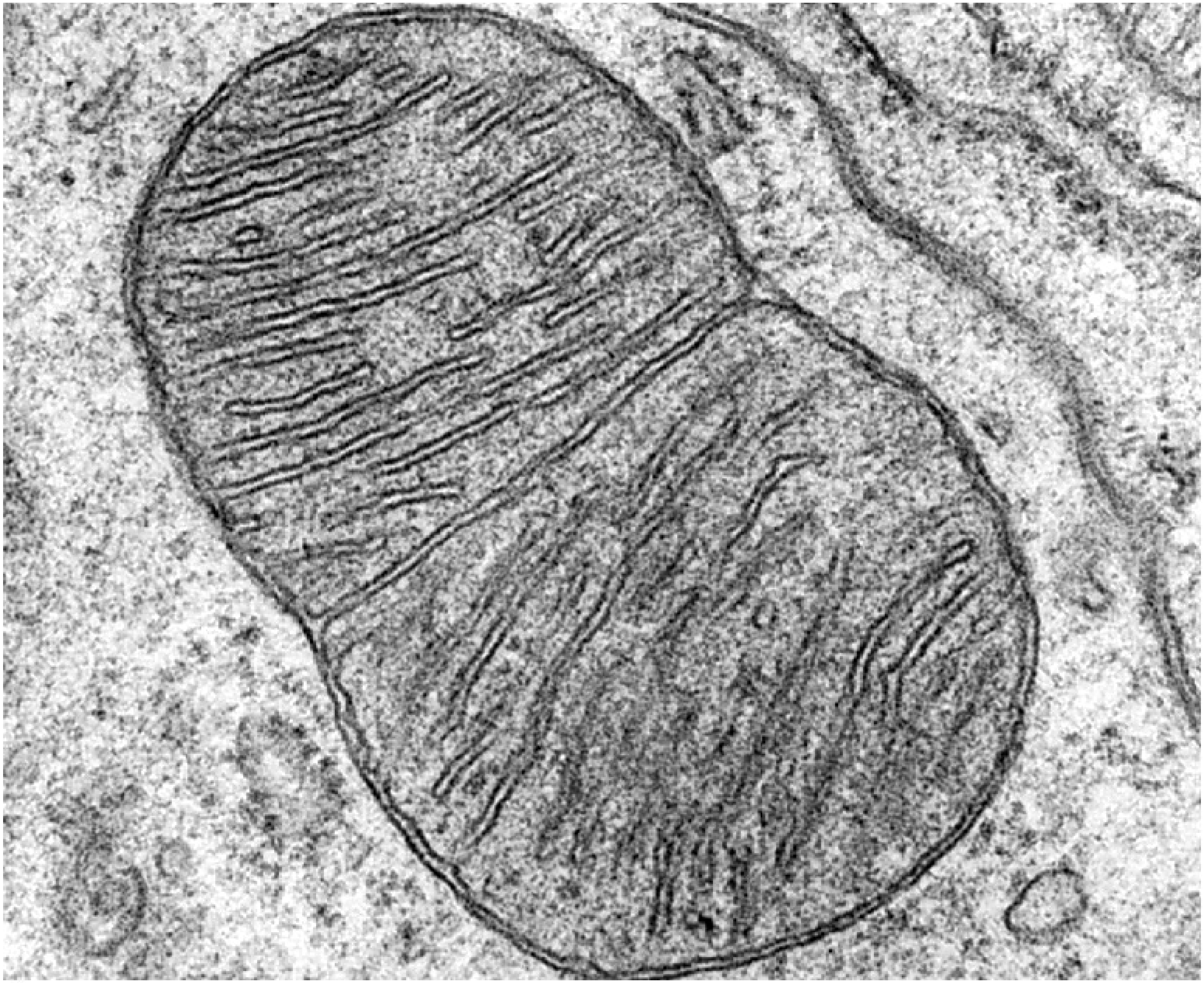

Figure 24-6

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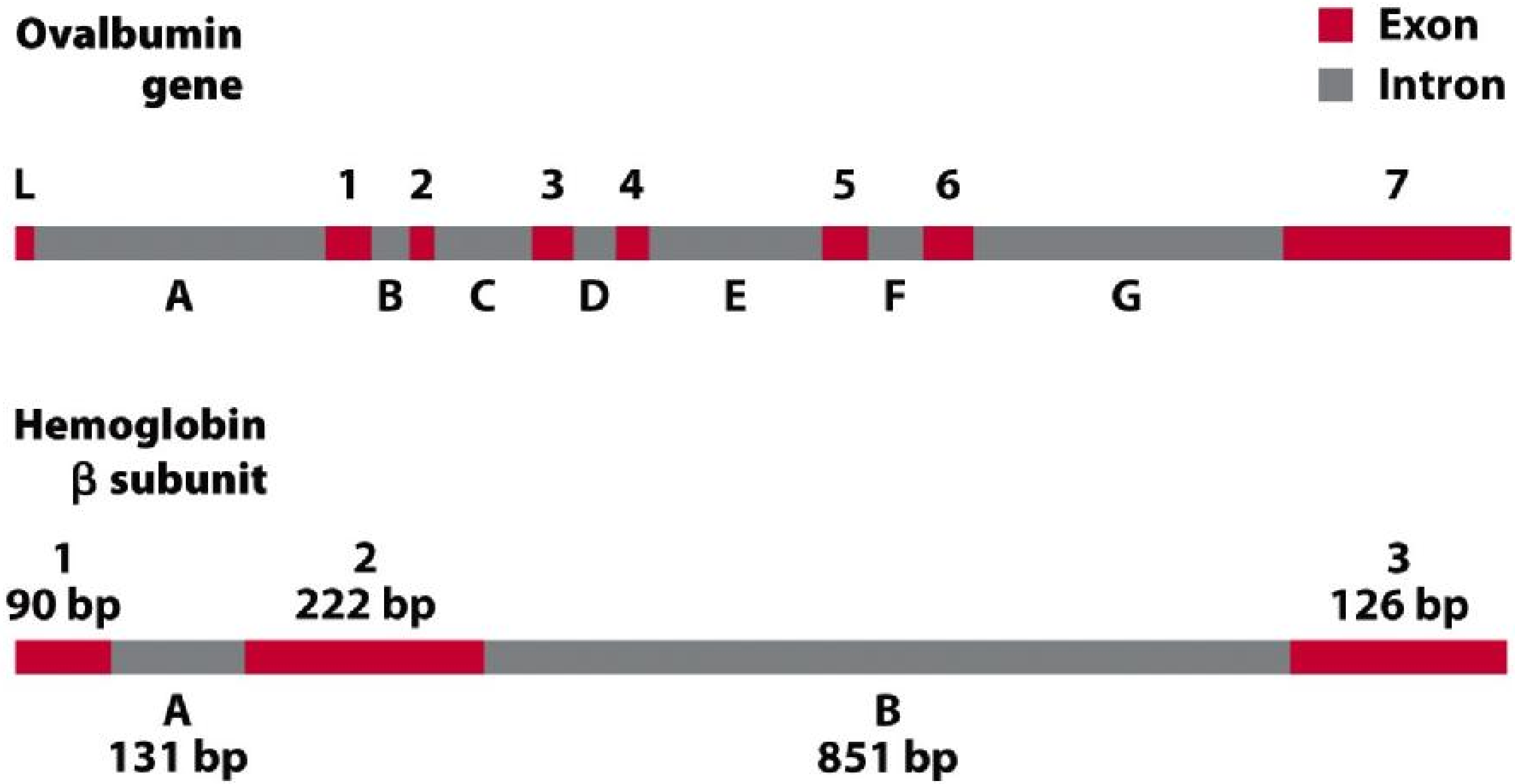

Figure 24-7
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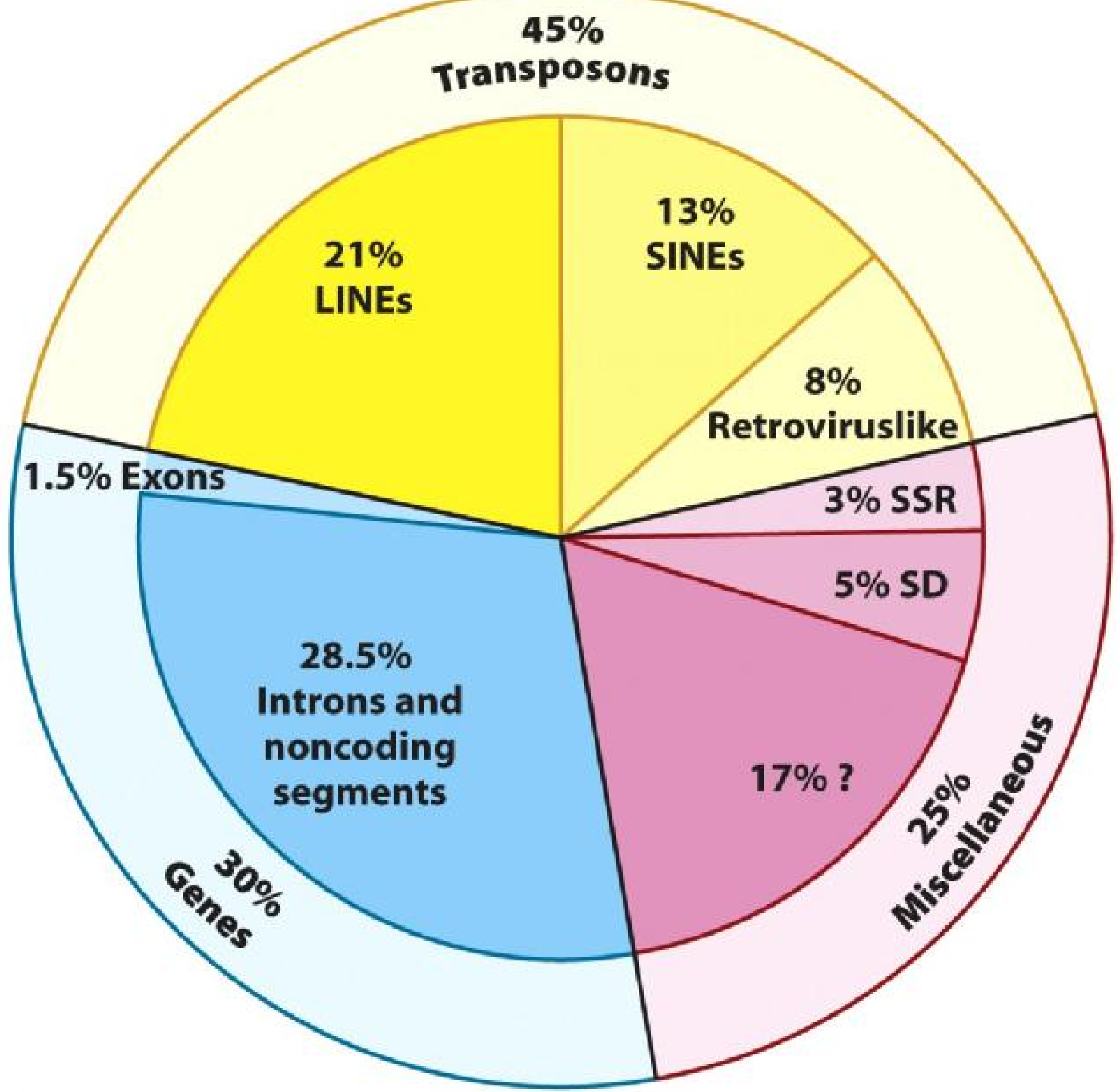

Figure 24-8
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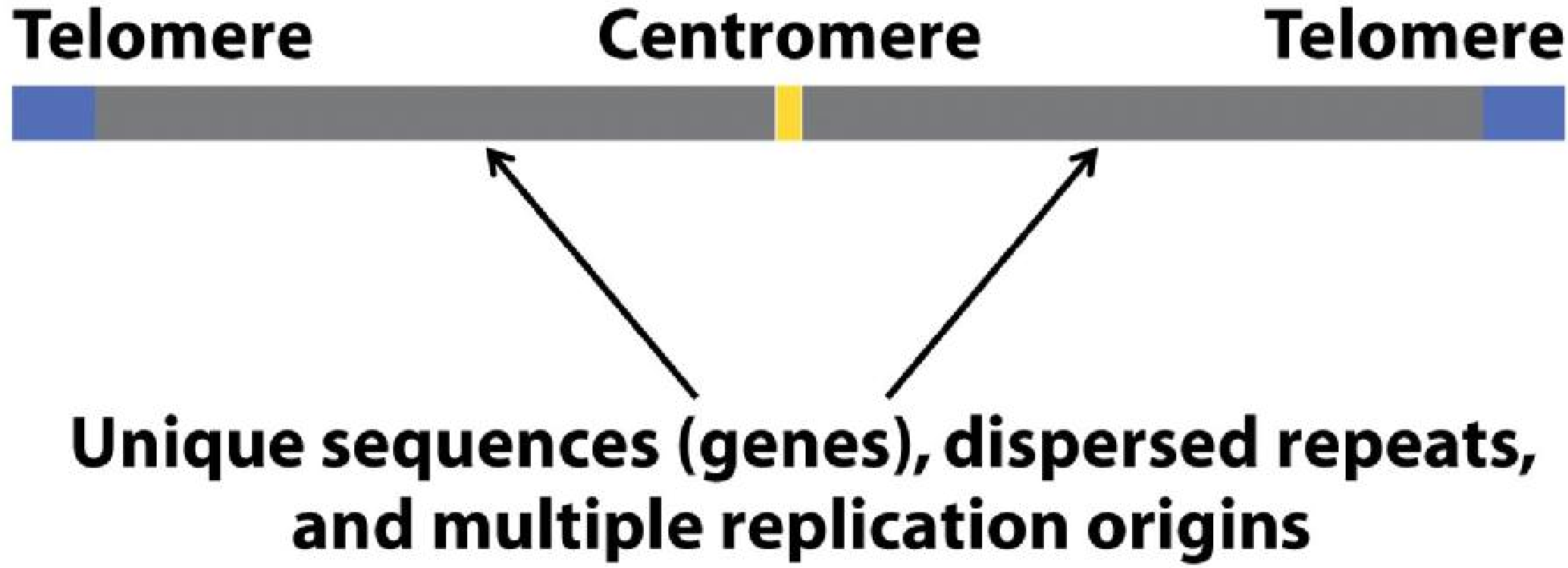

Figure 24-9
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TABLE 24–3 Telomere Sequences

	Telomere repeat sequence
Homo sapiens (human)	$(TTAGGG)_n$
Tetrahymena thermophila (ciliated protozoan)	$(TTGGGG)_n$
Saccharomyces cerevisiae (yeast)	$((TG)_{1-3}(TG)_{2-3})_n$
Arabidopsis thaliana (plant)	$(TTTAGGG)_n$

Table 24-3
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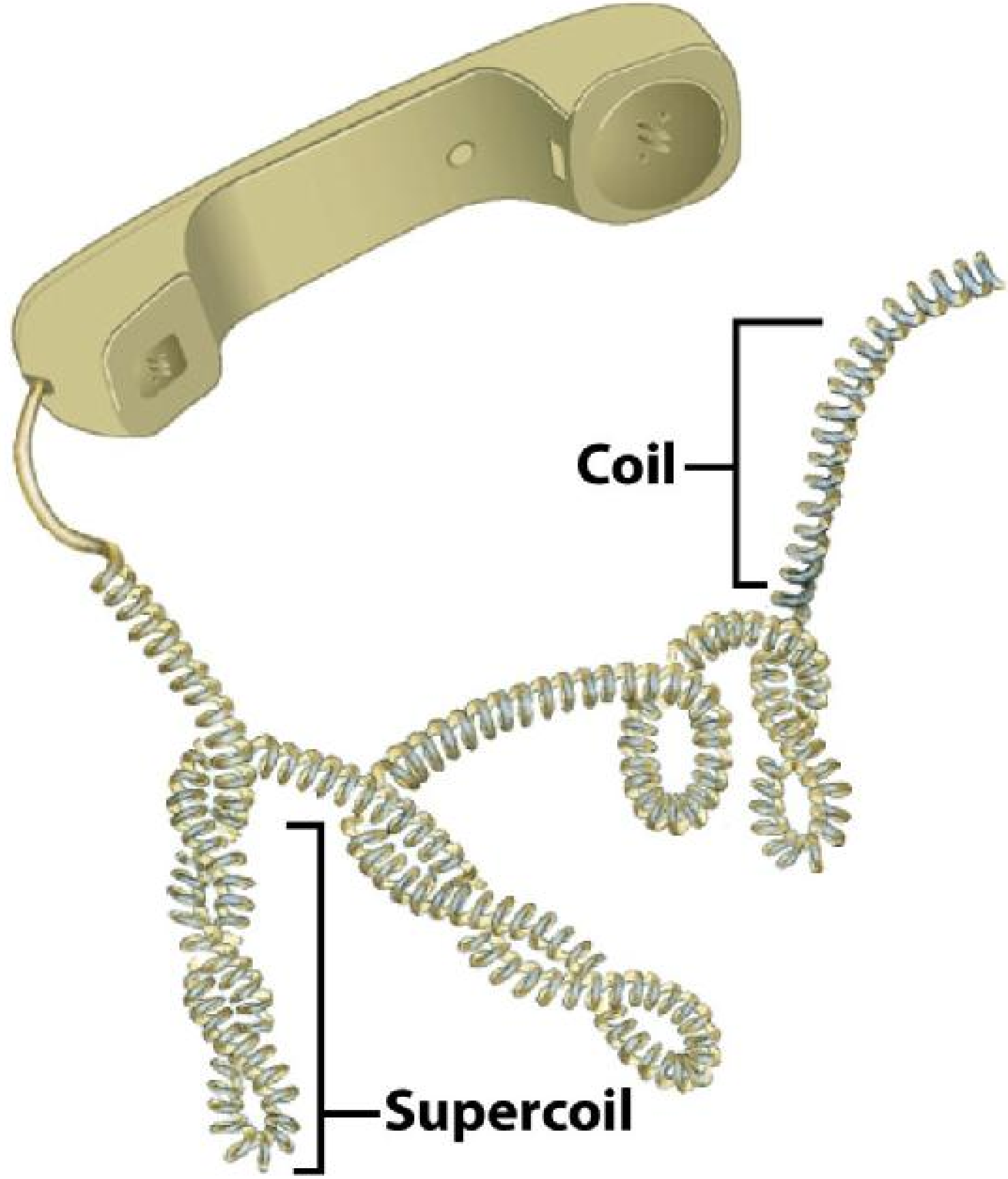

Figure 24-10
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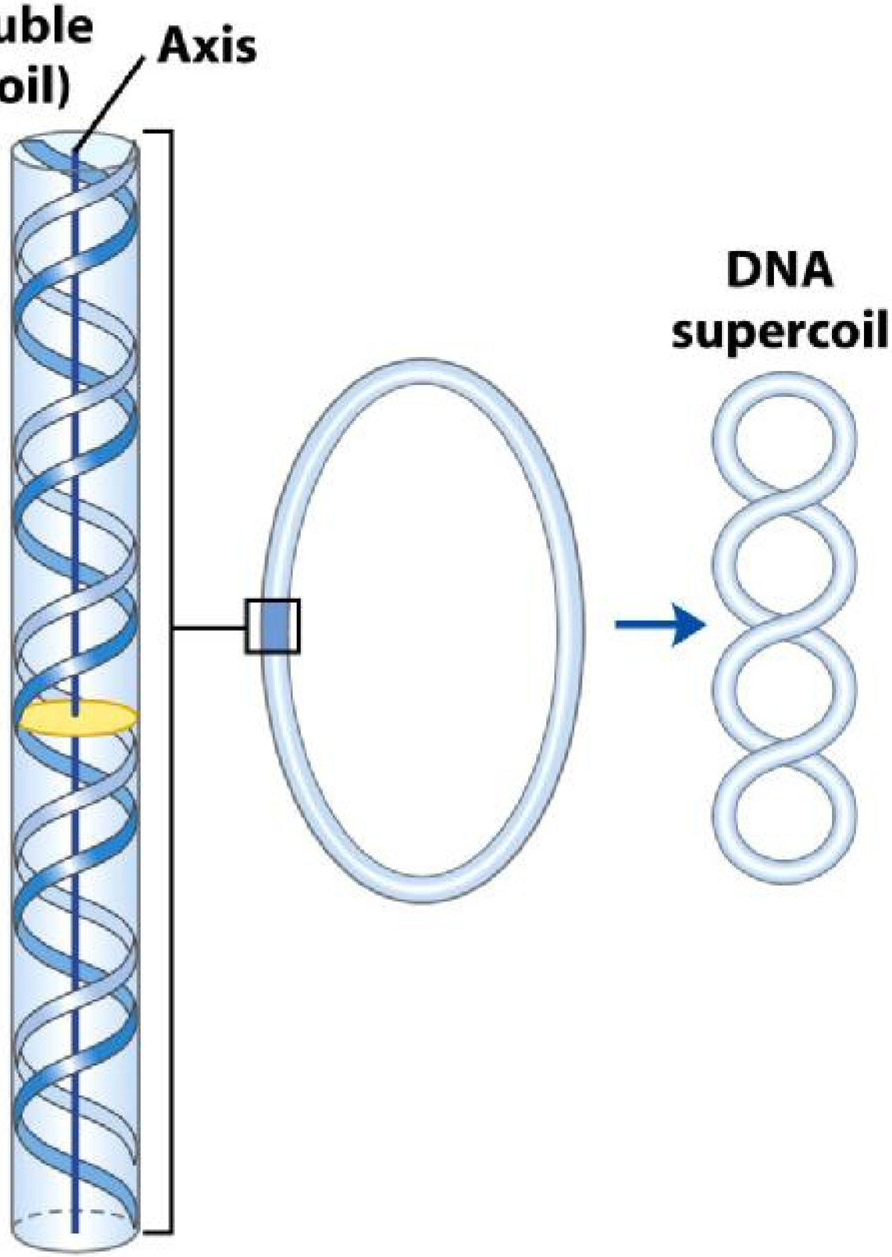

Figure 24-11
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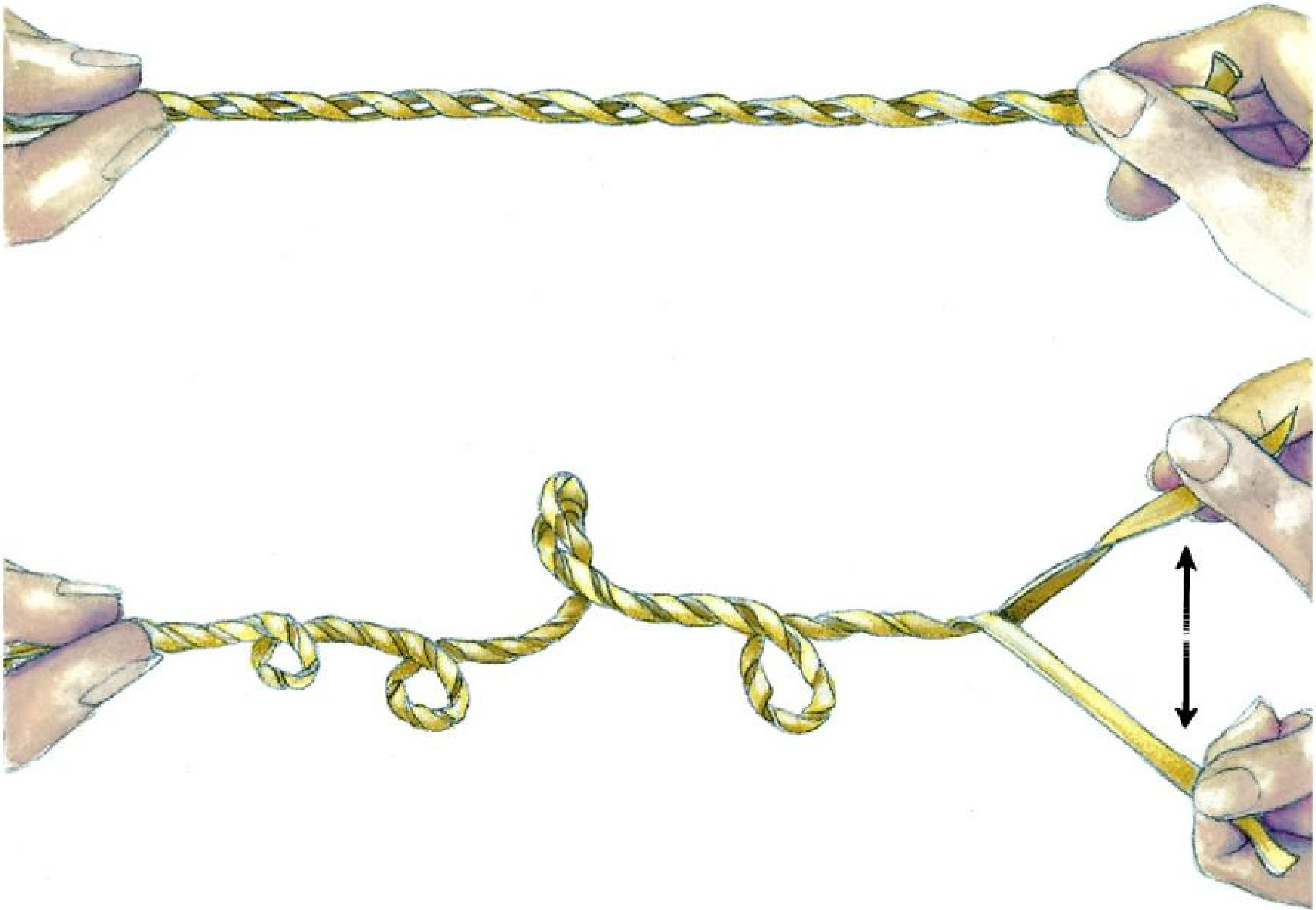

Figure 24-12
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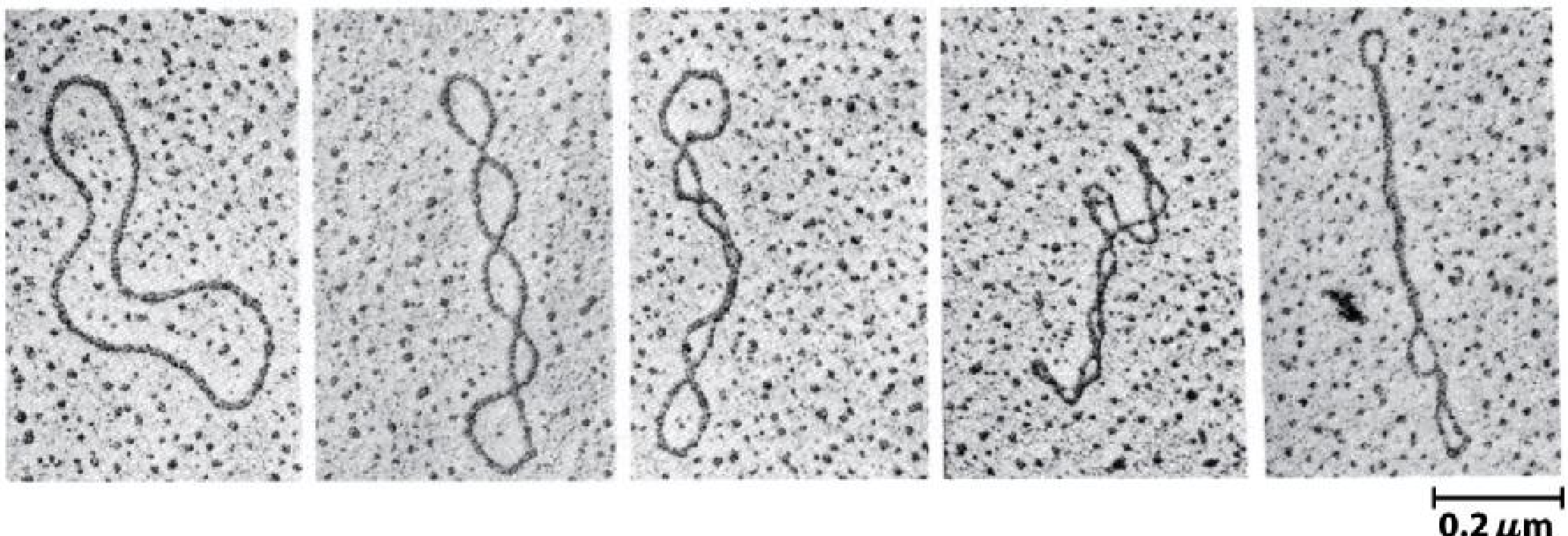

Figure 24-13
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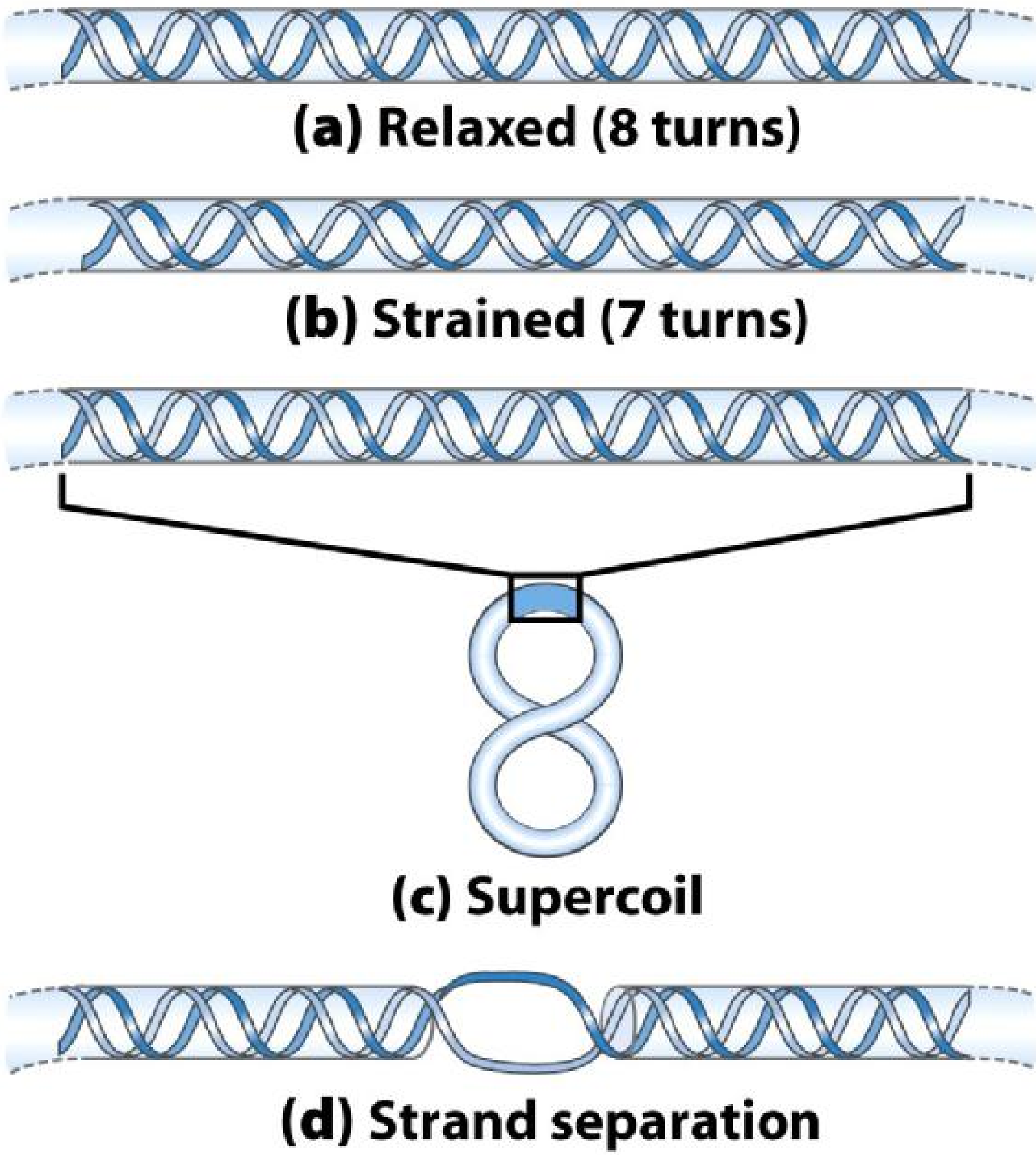

Figure 24-14
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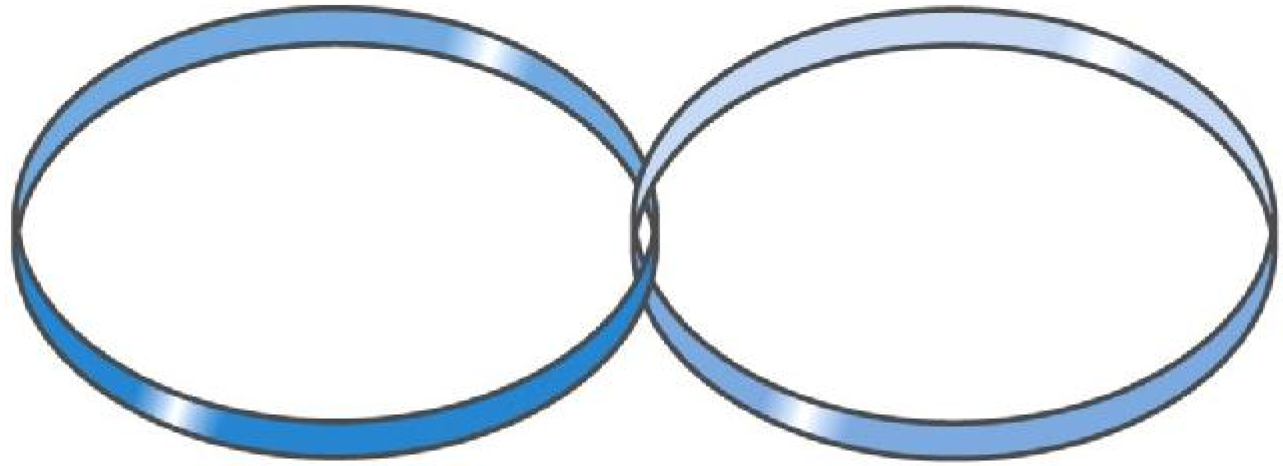
A segment of DNA in a closed-circular molecule, **84 bp long**, in its relaxed form with **8** helical turns (10.5 bp/turn).

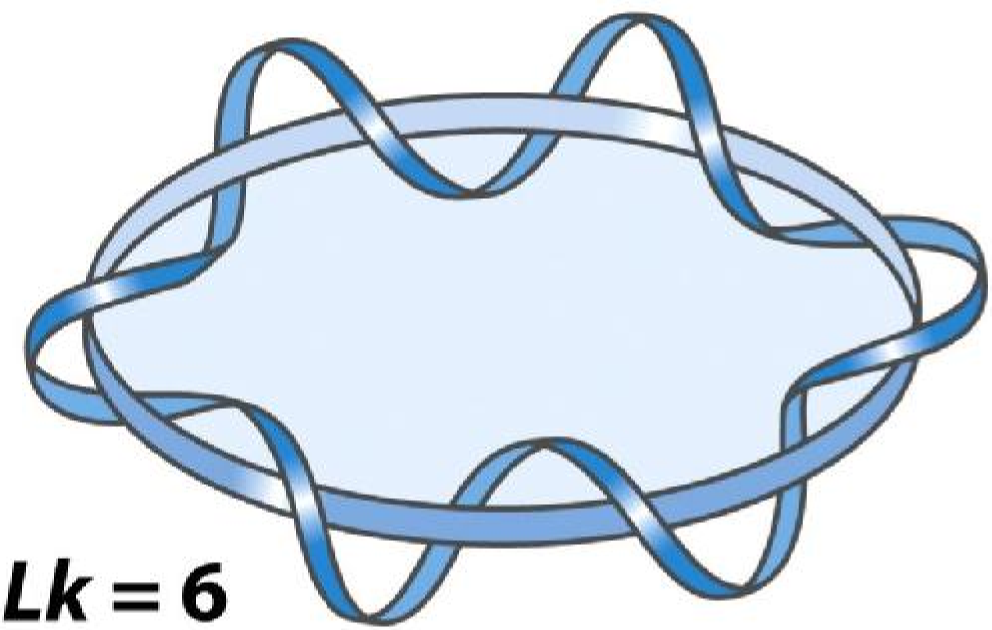
Removal of one turn induces structural strain.
(84 /7) = 12 bp/turn

Topology is the study of the properties of an object that do not change under continuos deformations.
For DNA, **continuos deformations** include conformational changes due to thermal motion or an interaction with proteins or other molecules;
Discontinuous deformations involve DNA strand breakage.

For circular DNA molecules, a topological property is one that is unaffected by deformations of the DNA strands as long as no breaks are introduced. Topological properties are changed only by breakage and rejoining of the backbone of one or both DNA strands.



(a) $Lk = 1$



(b) $Lk = 6$

Figure 24-15
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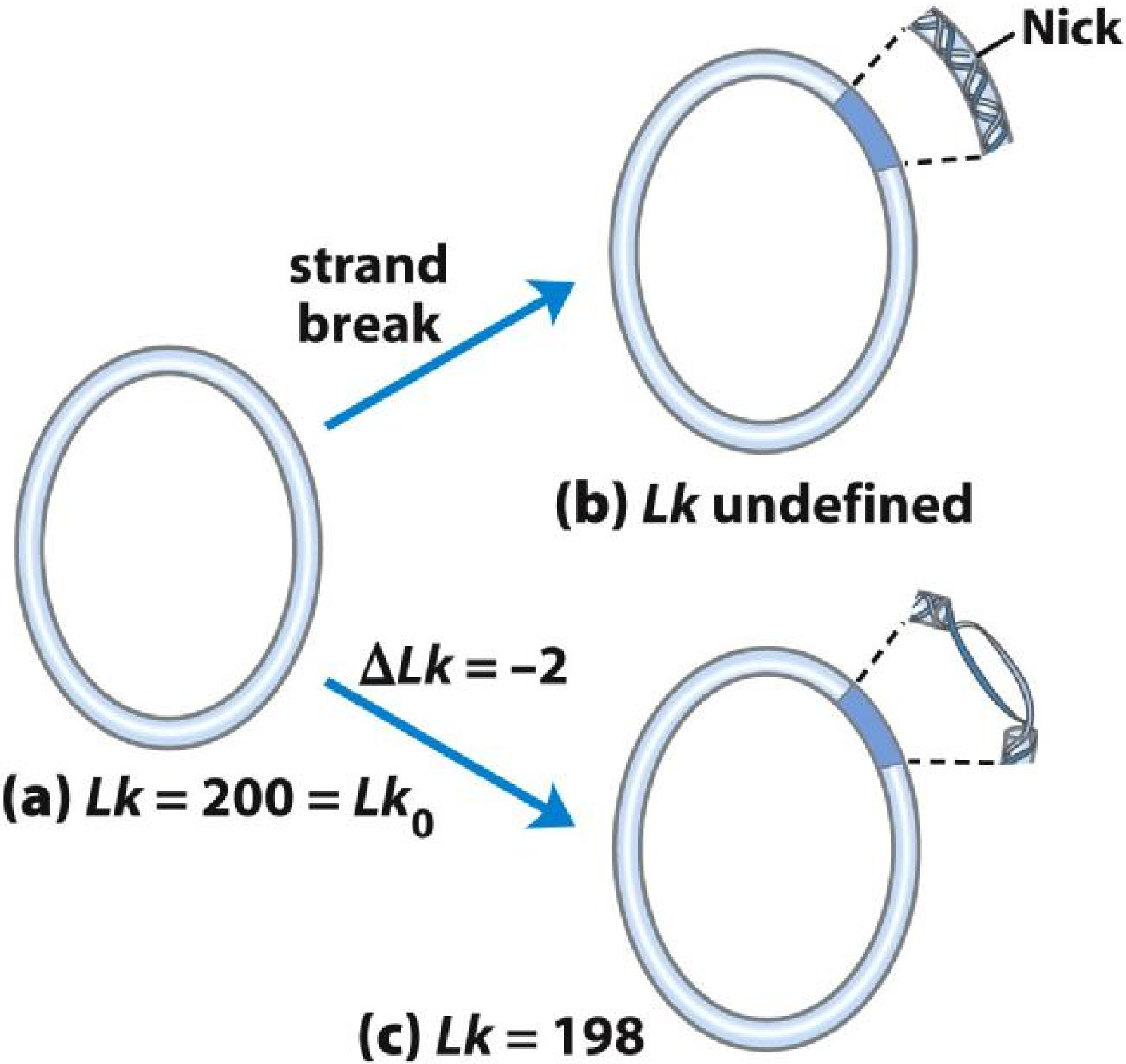

Figure 24-16
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Specific linking difference (σ) or superhelical density, is a measure of the number of turns removed relative to the number present in relaxed DNA

$$\sigma = \frac{\Delta Lk}{Lk_0}$$

σ = -0.01, means that l% of (2 of 200) of the helical turns present in the DNA (in its B form) have been removed.
The degree of underwinding in cellular DNAs generally falls in the range of 5% to 7% that is, σ : -0.05 to -0.07. The negative sign indicates that the change in Iinking number is due to underwinding of the DNA. The supercoiling induced by underwinding is therefore defined as negative supercoiling. Conversely under some conditions D NA can be overwound, resulting in positive supercoiling.

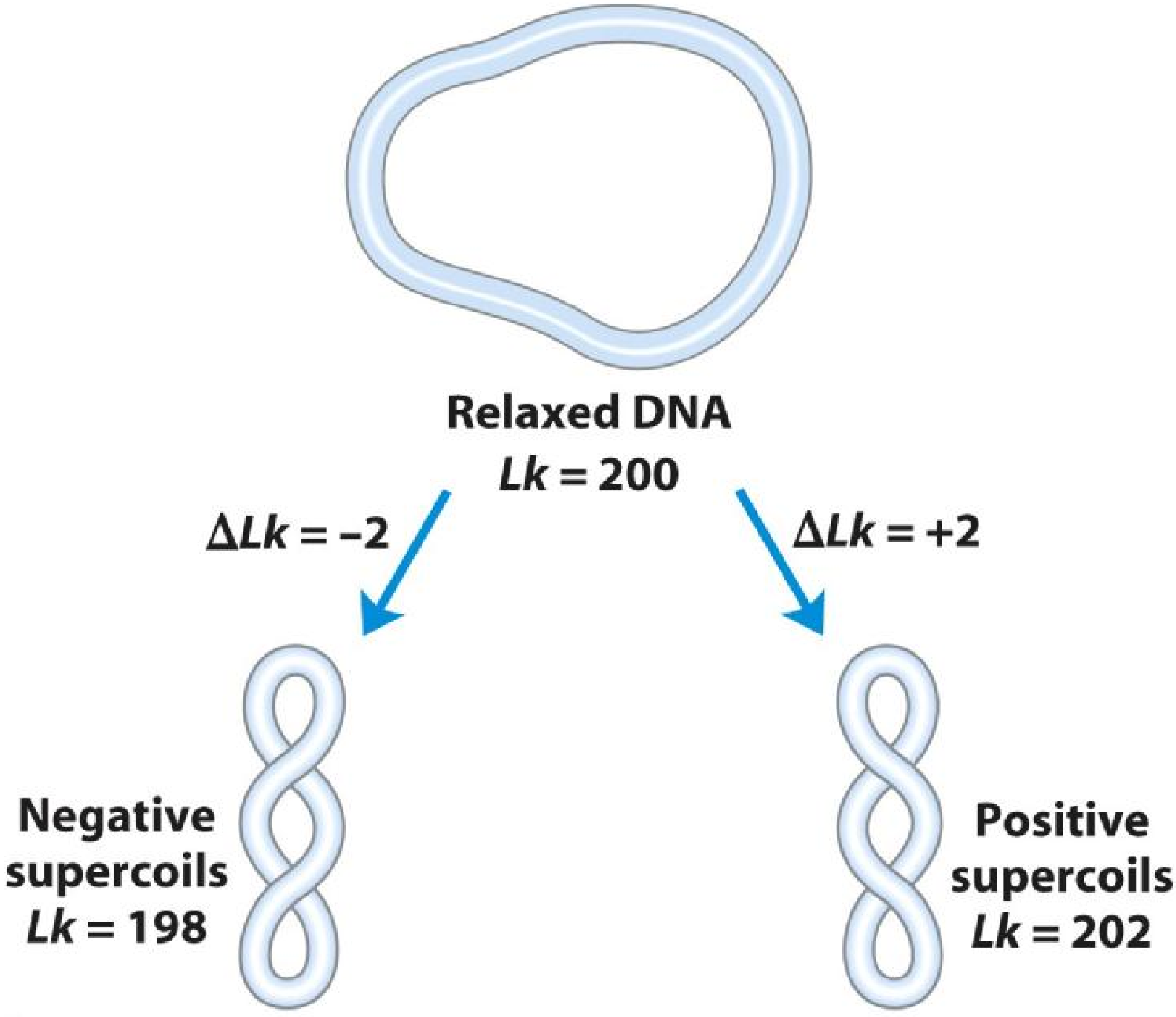

Figure 24-17
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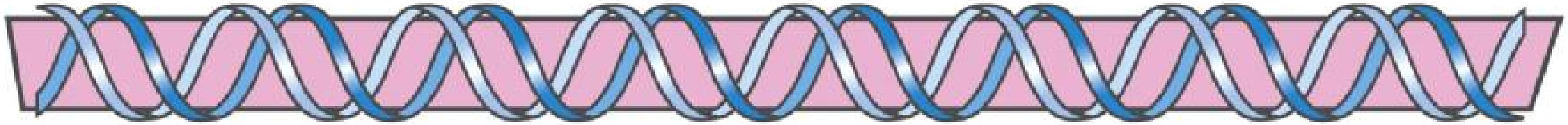
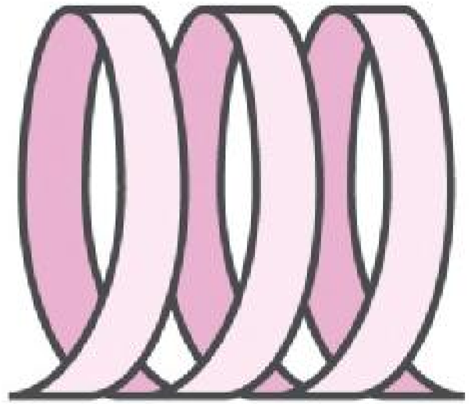


Straight ribbon (relaxed DNA)

Topological changes in linking number are usually accompanied by geometric changes in both writhe and twist.



Large writhe, small change in twist

Zero writhe, large change in twist

Figure 24-18
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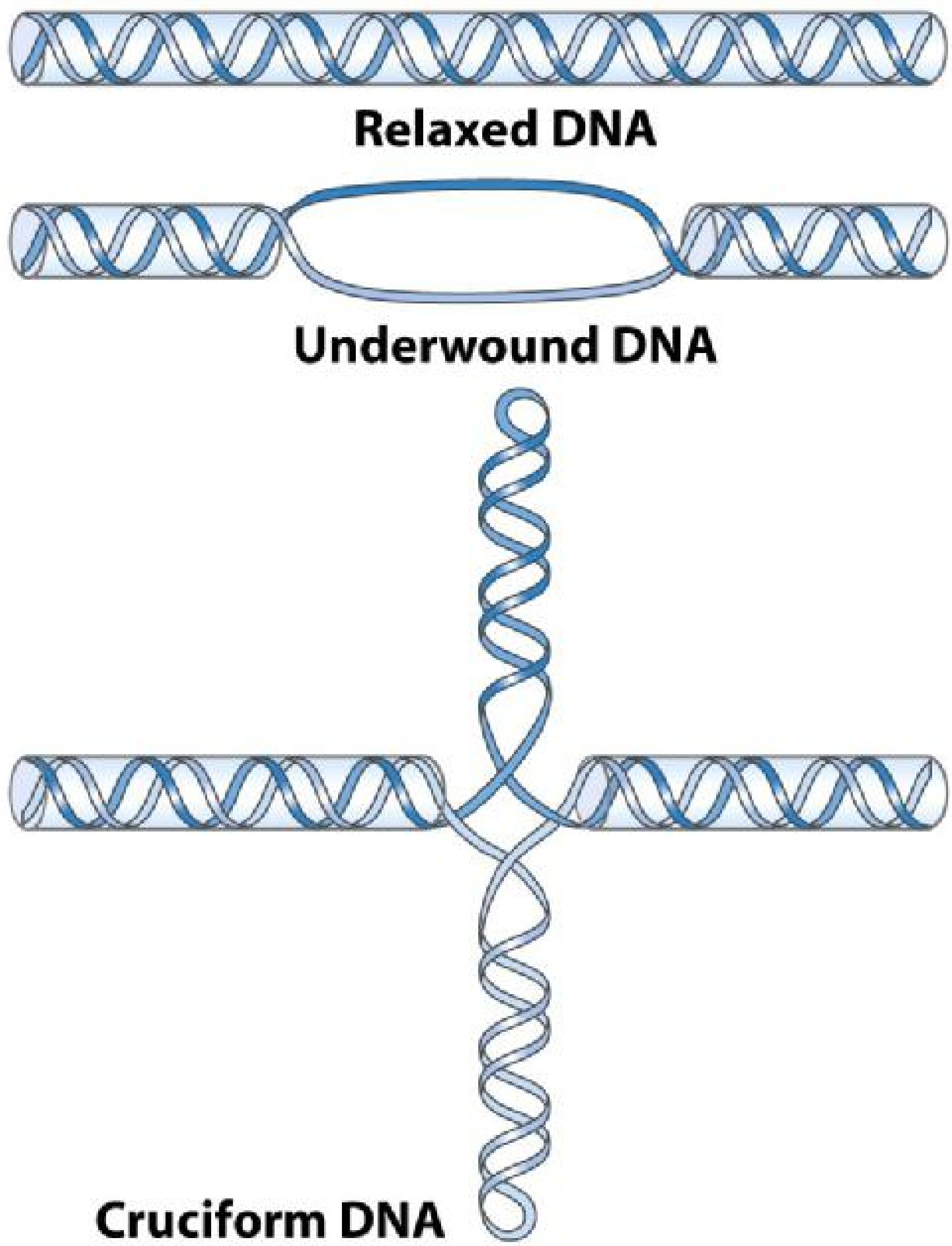

Figure 24-19
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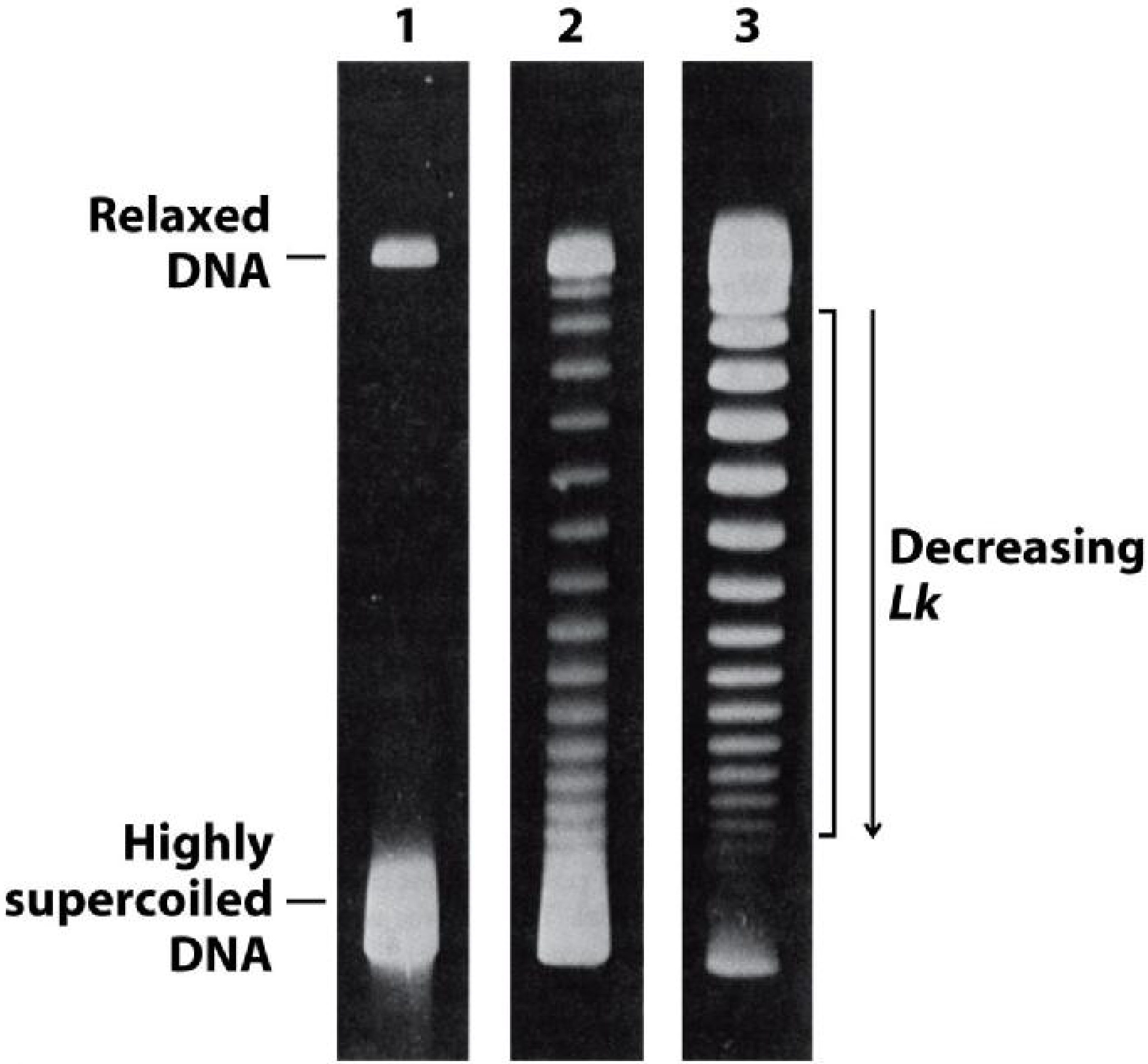

Figure 24-20
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DNA topoisomerases

In *E. coli*:

Type I topoisomerase: Generally relax DNA by removing negative supercoils (increase in Lk)

Topoisomerase I

Topoisomerase III

Type II topoisomerase: Introduce negative supercoils (decrease in Lk); uses ATP

Topoisomerase II (DNA gyrase)

Topoisomerase IV

DNA topoisomerases

In Eukaryotes:

Type I topoisomerase: Generally relax DNA by removing negative supercoils (increase in Lk)

Topoisomerase I

Topoisomerase III

Type II topoisomerase: Introduce negative supercoils (decrease in Lk); uses ATP

Topoisomerase IIα

Topoisomerase IIβ

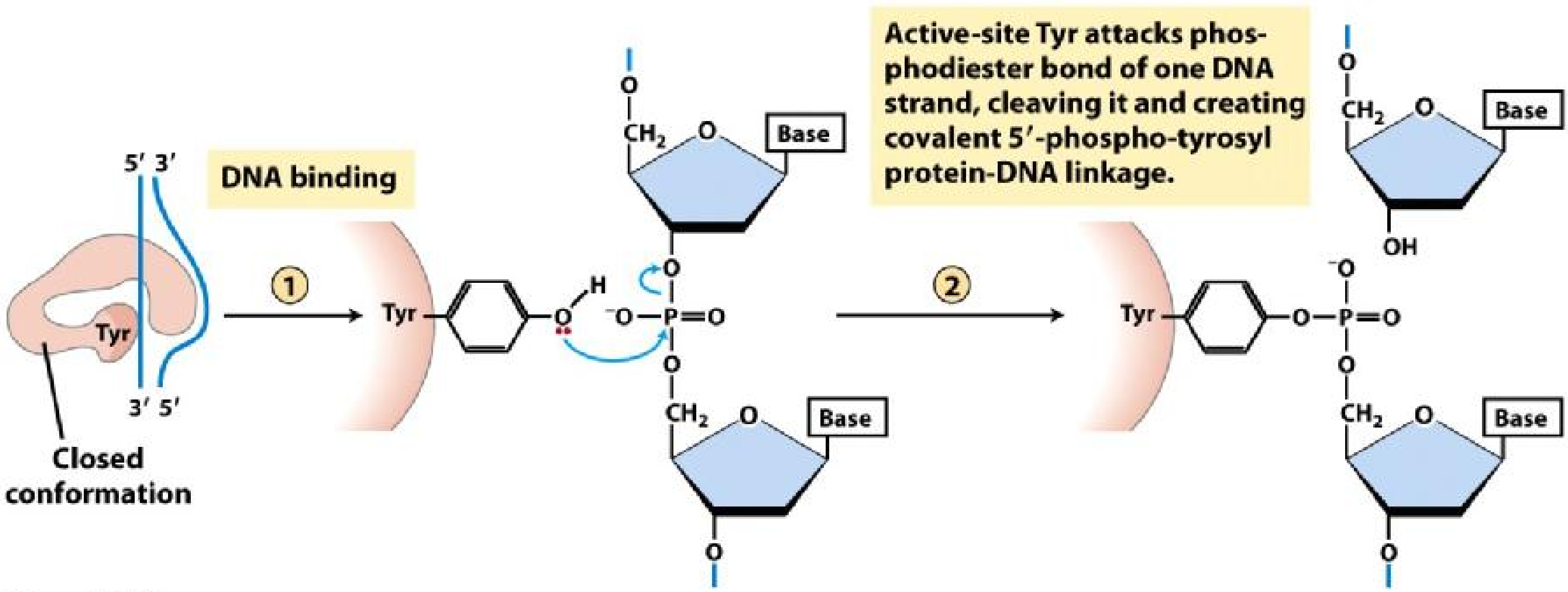

Figure 24-21a
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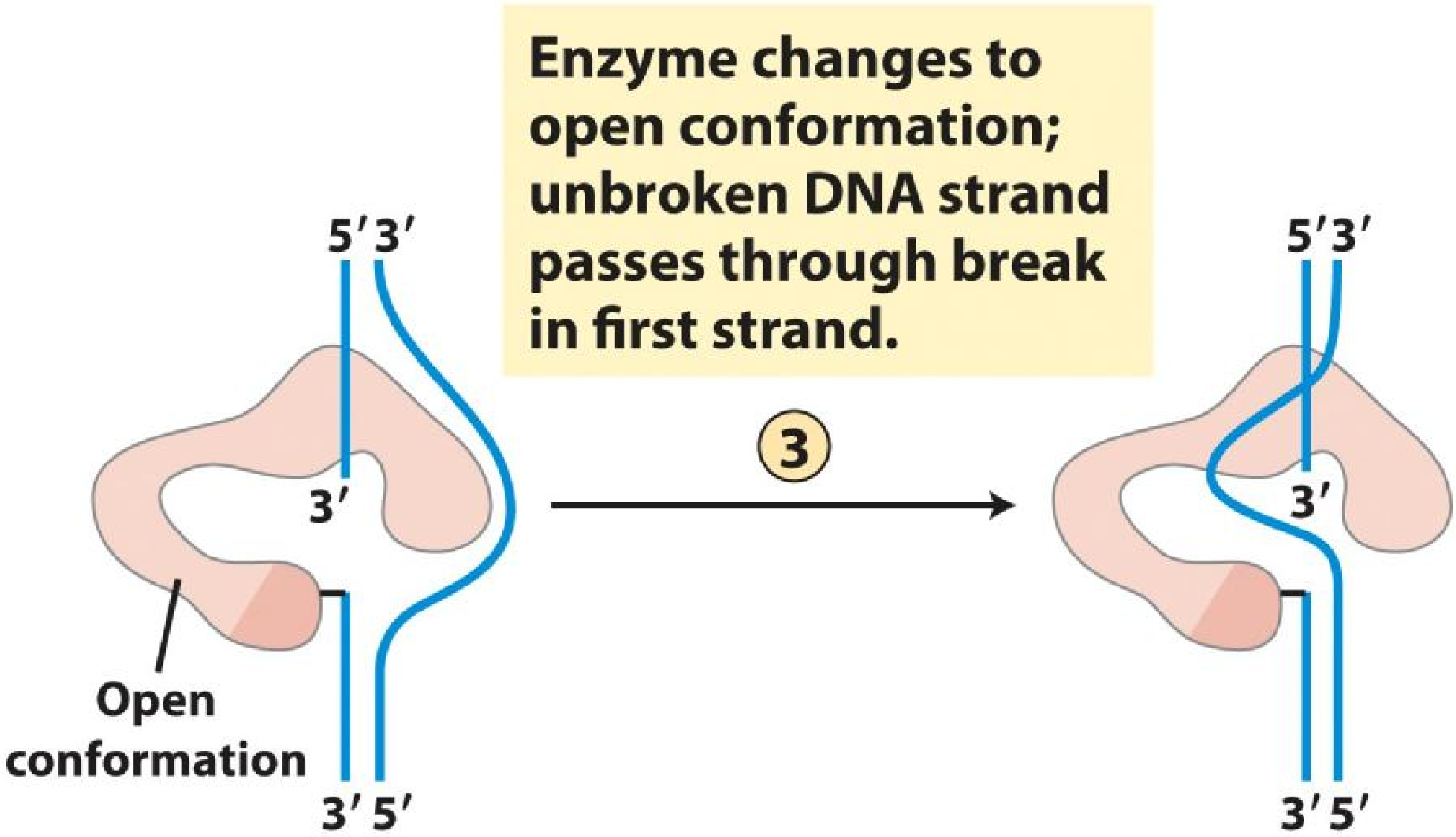

Figure 24-21b

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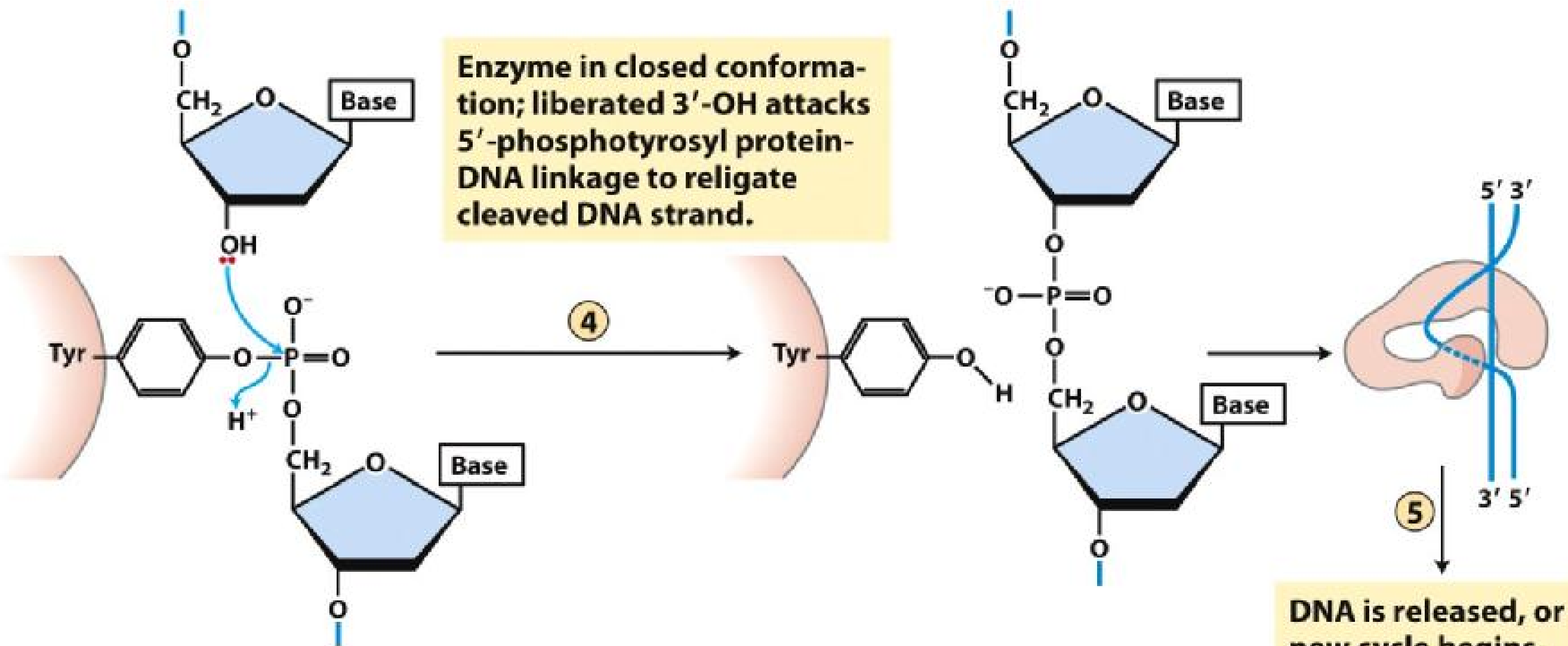

Figure 24-21c
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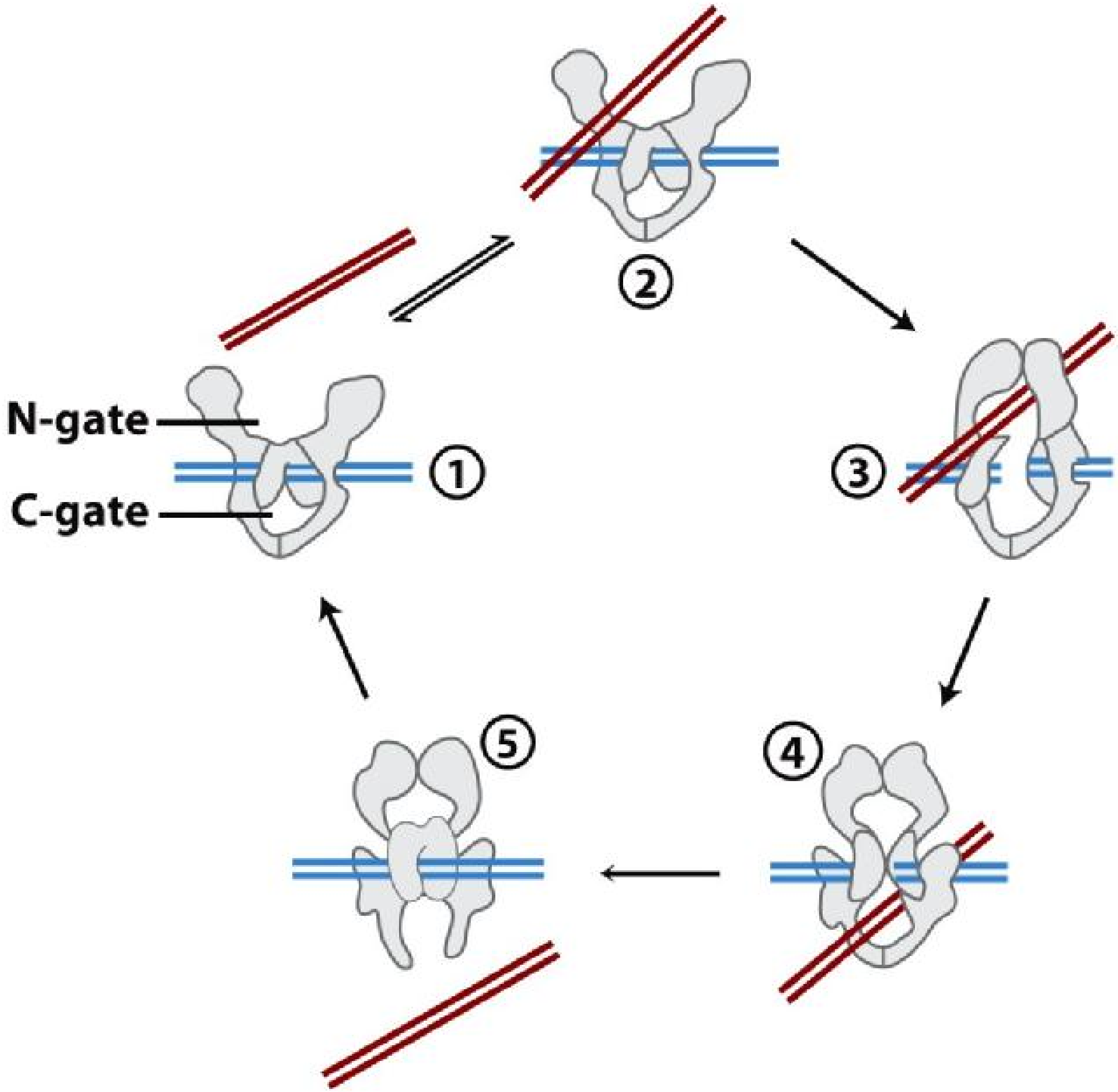

Figure 24-22
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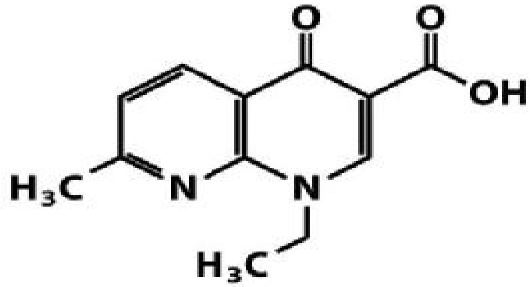
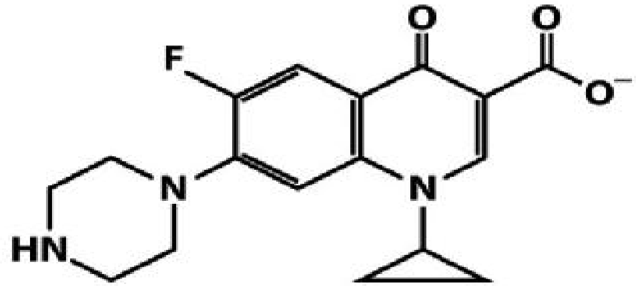
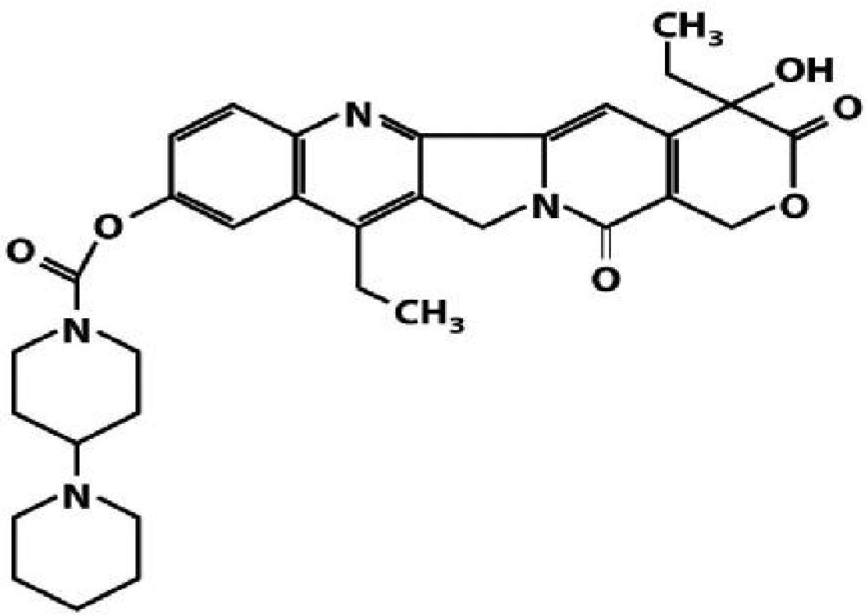
Bacterial topoisomerase inhibitors as antibiotics



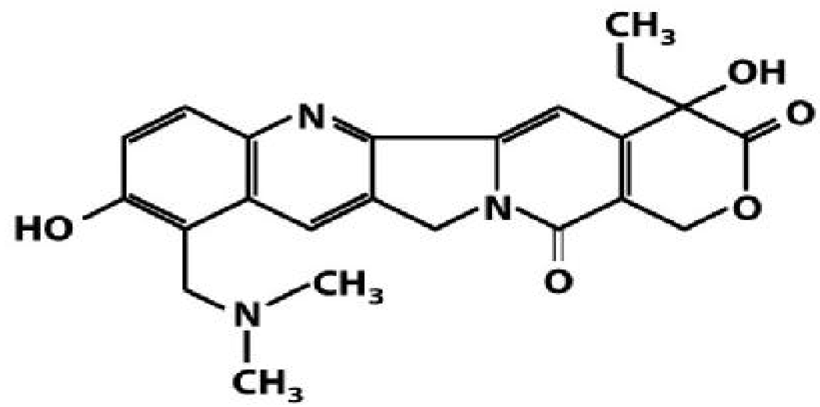
Nalidixic acid



Ciprofloxacin



Irinotecan



Topotecan

Box 24-1 part 1

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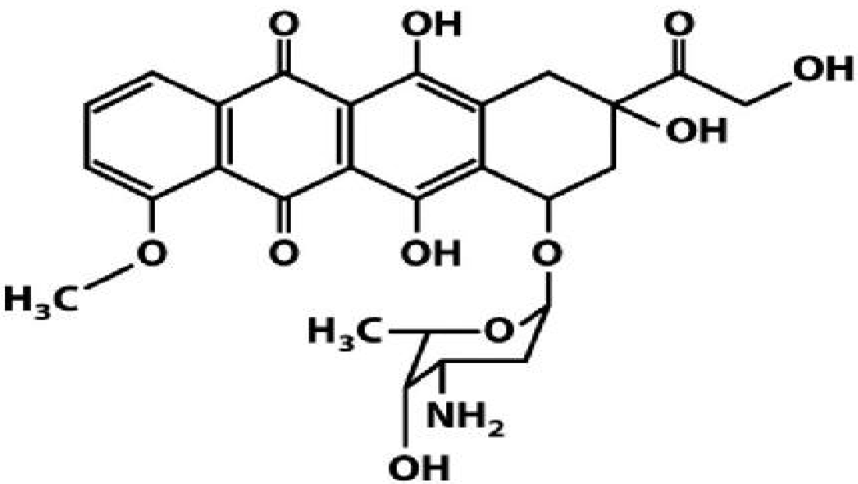
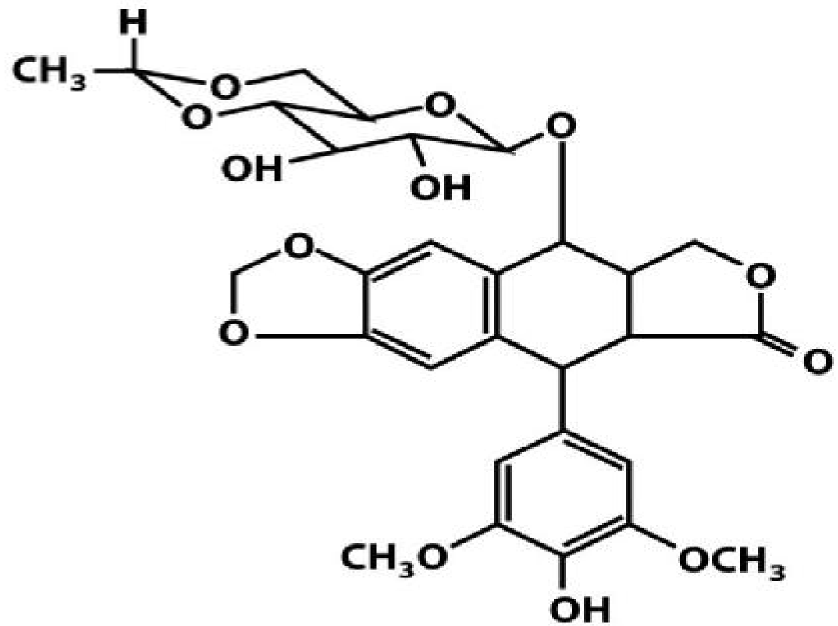
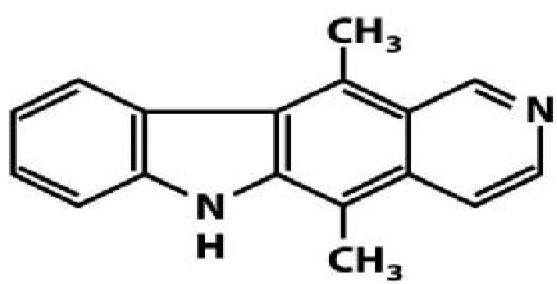
Eukaryotic topoisomerase inhibitors as anticancer drugs



Doxorubicin



Etoposide



Ellipticine

Box 24-1 part 2
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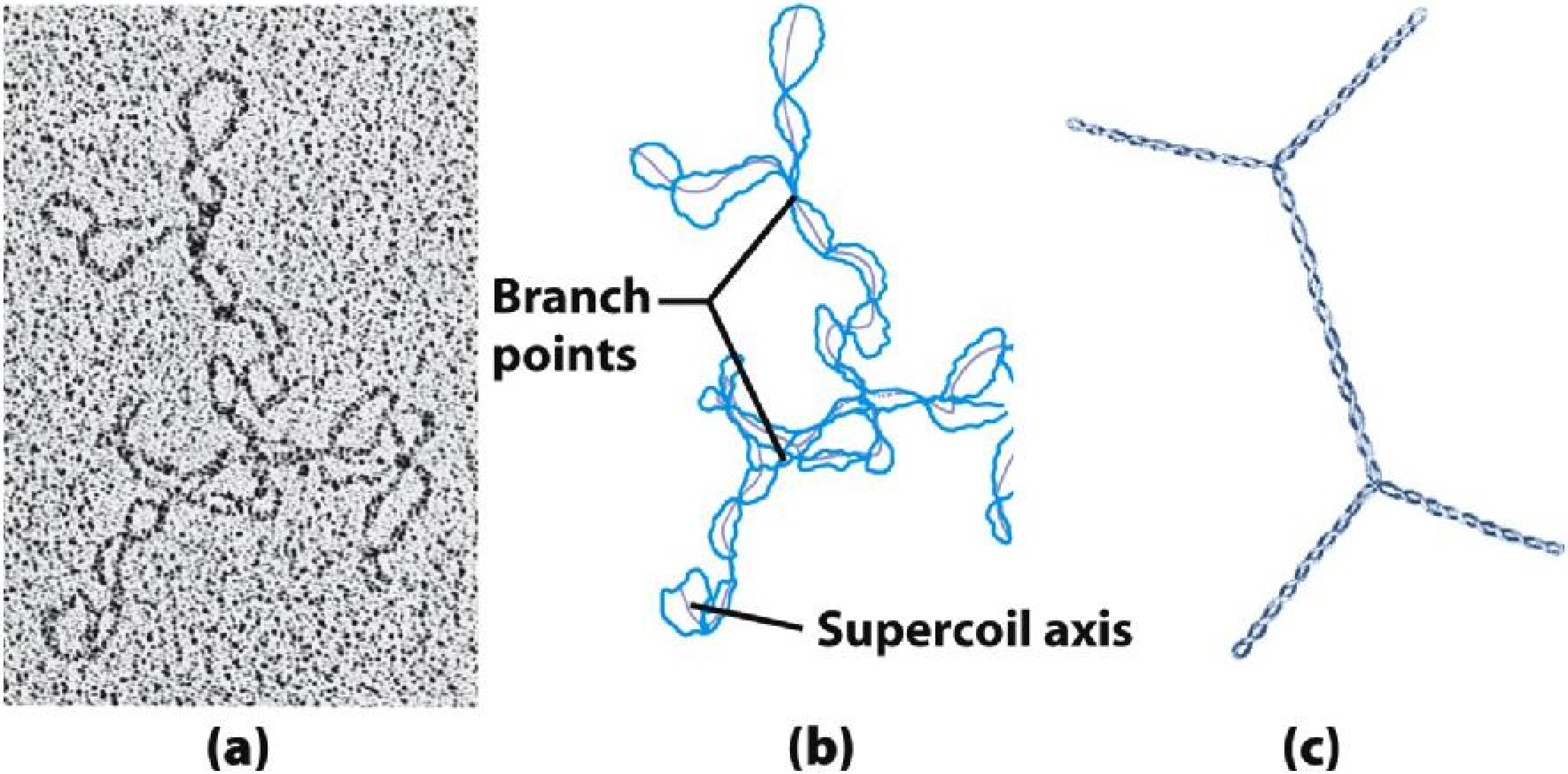

Figure 24-23
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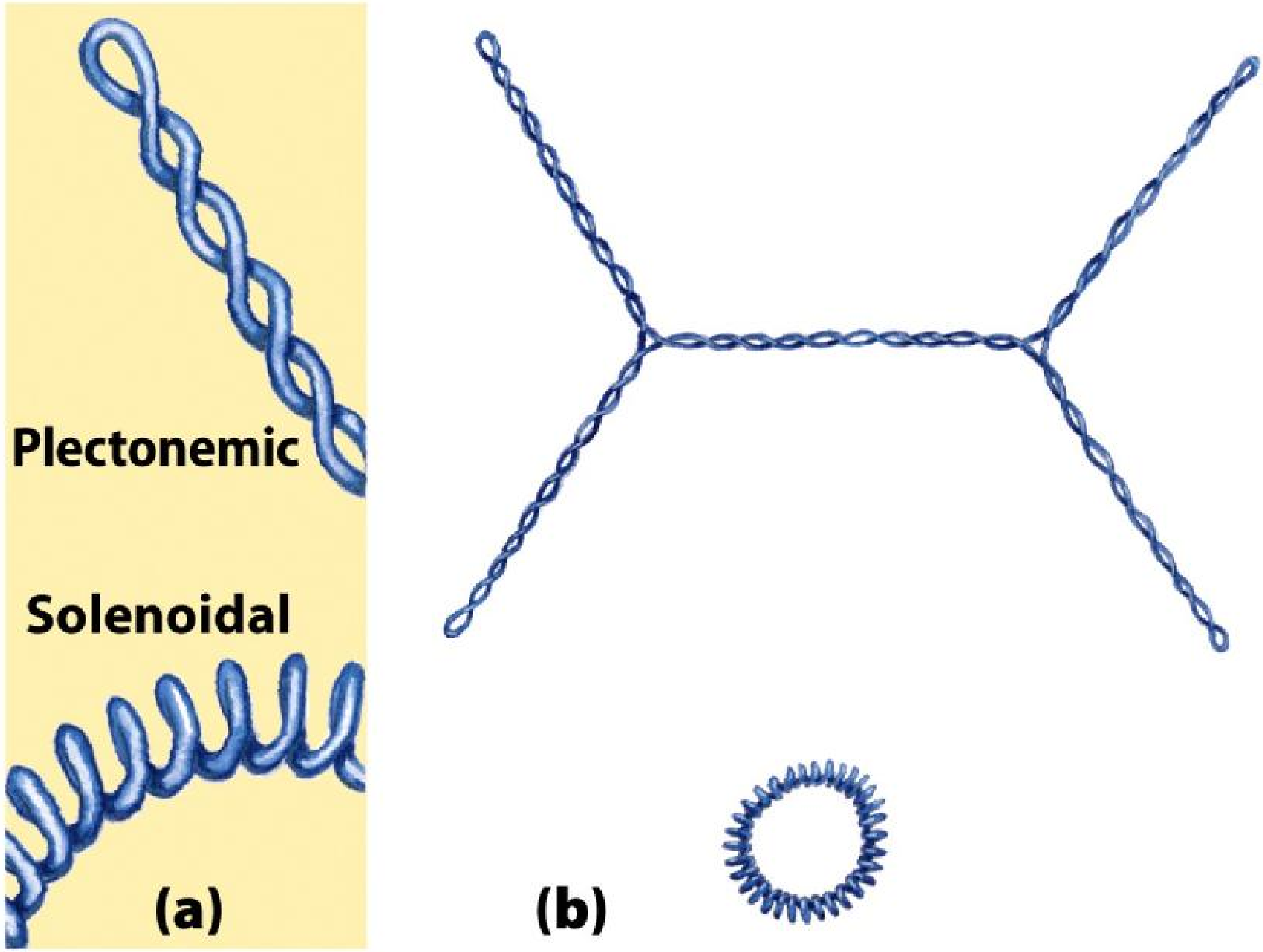

Figure 24-24
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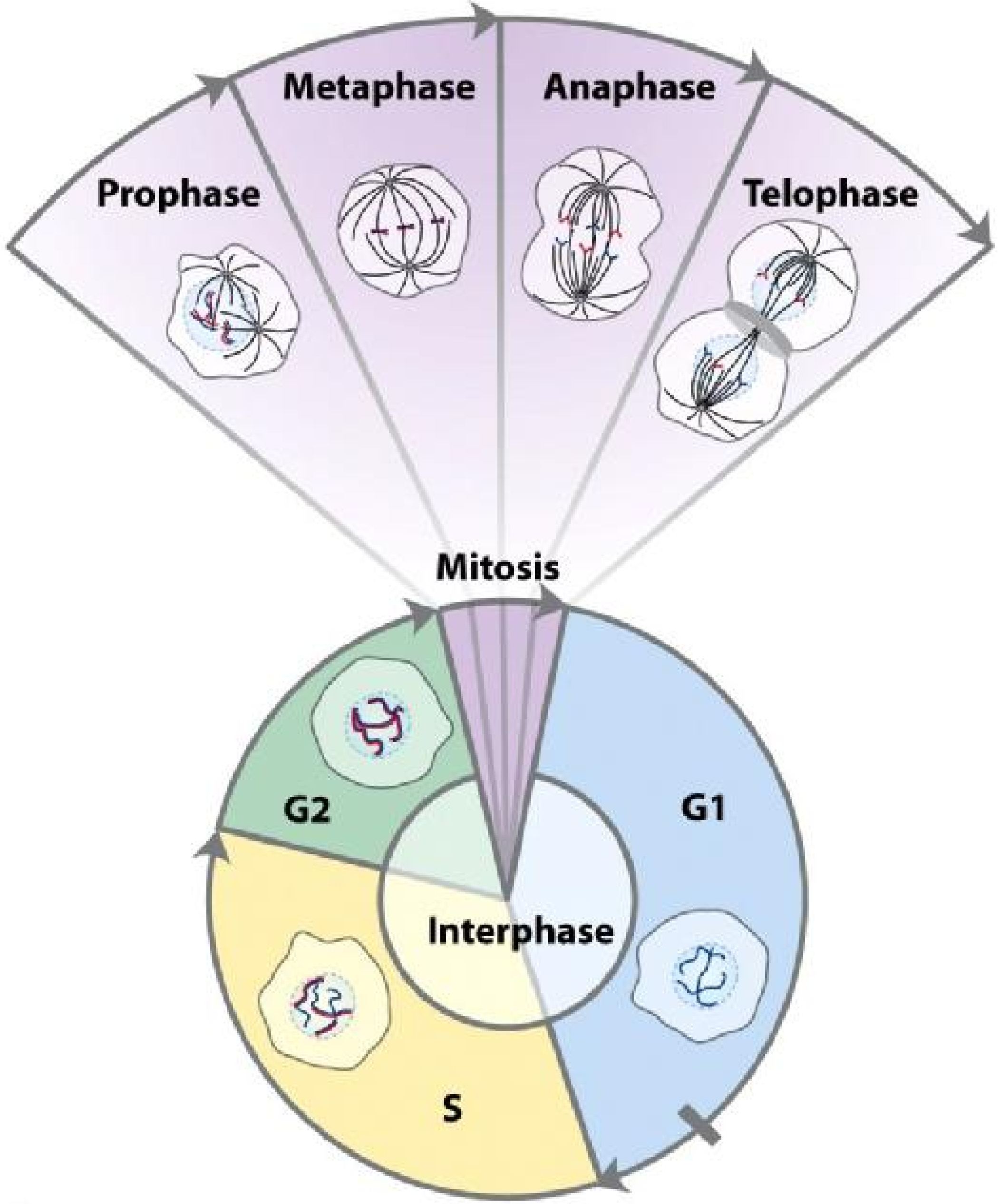

Figure 24-25
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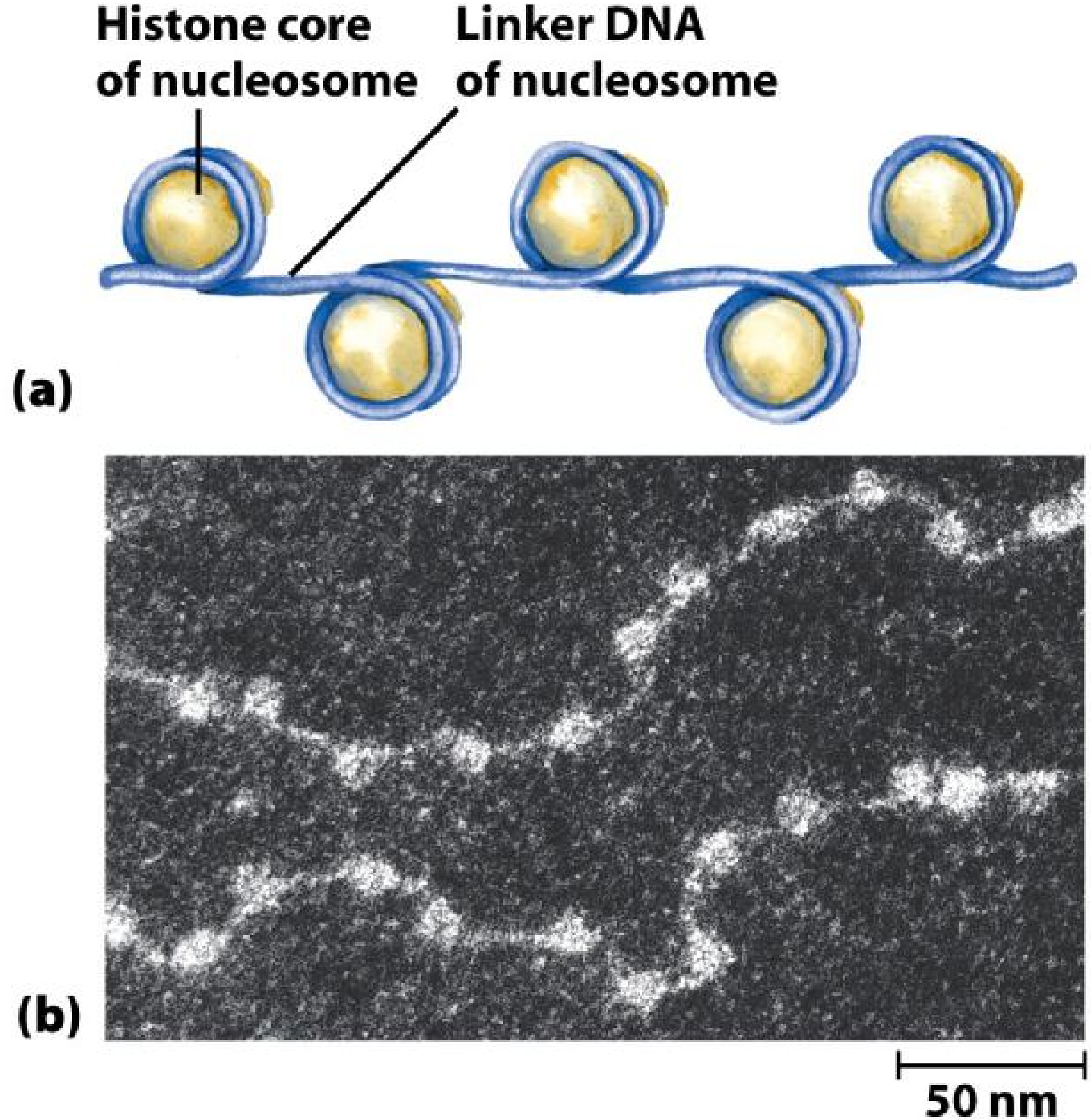

Figure 24-26
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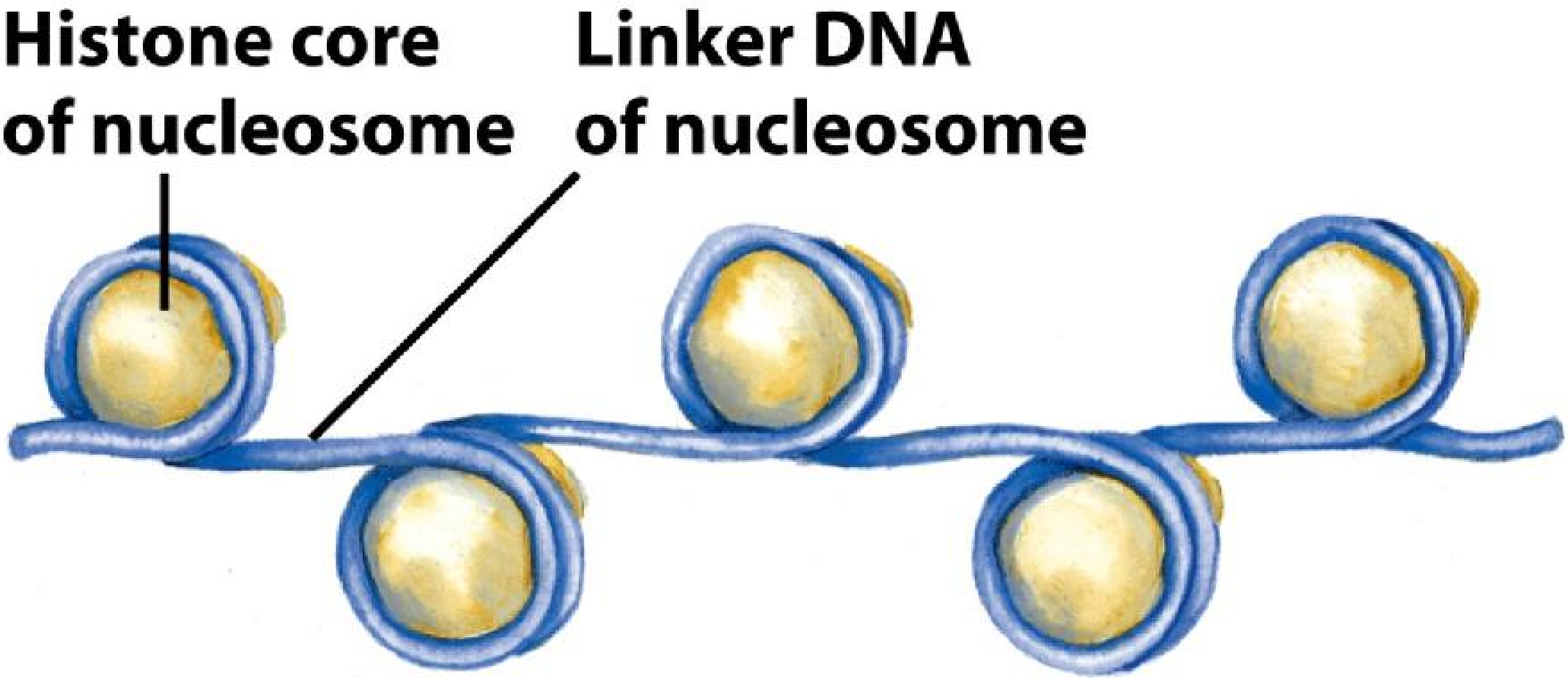

Figure 24-26a
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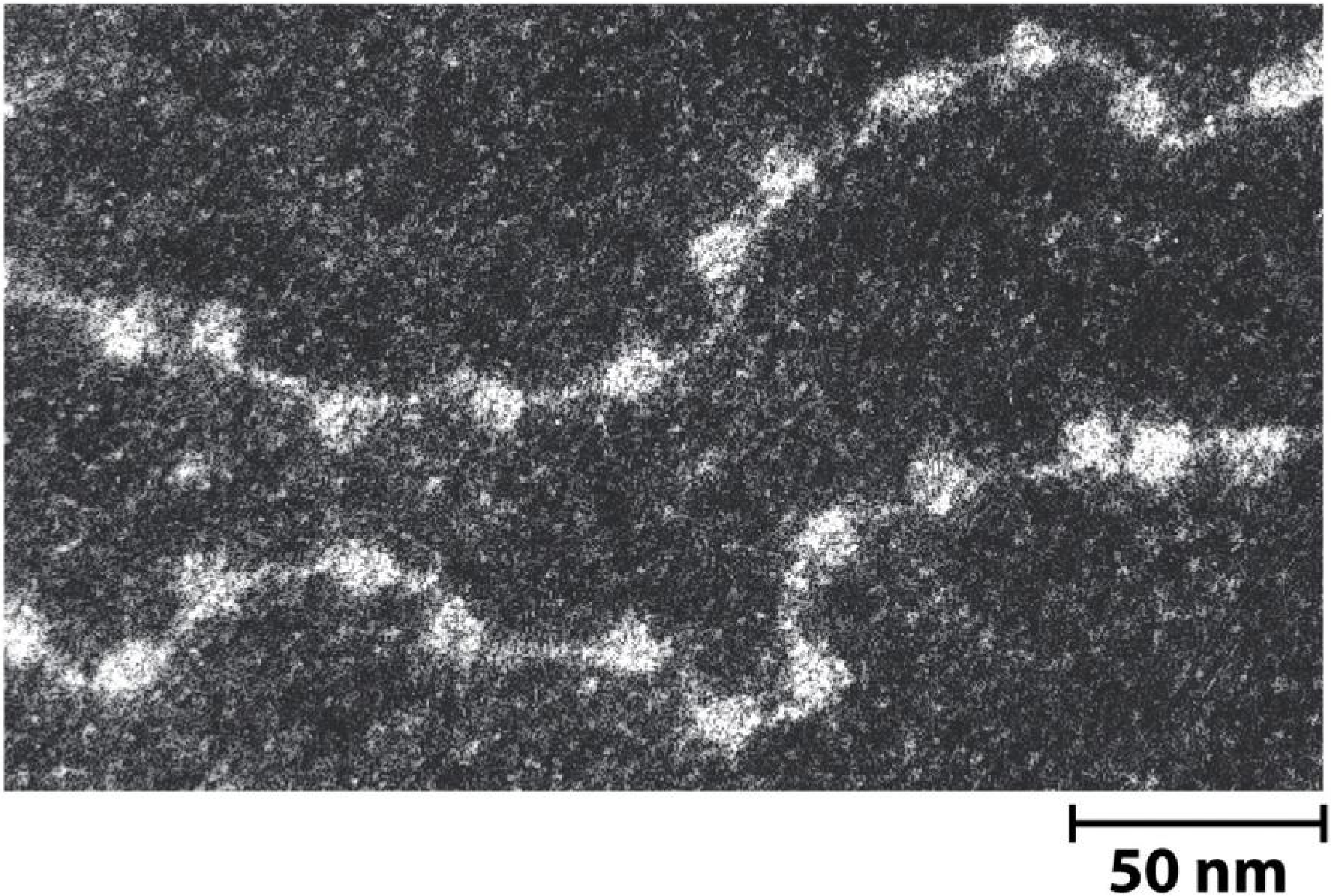

Figure 24-26b
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TABLE 24–4 Types and Properties of Histones

Histone	Molecular weight	Number of amino acid residues	Content of basic amino acids (% of total)	
			Lys	Arg
H1*	21,130	223	29.5	11.3
H2A*	13,960	129	10.9	19.3
H2B*	13,774	125	16.0	16.4
H3	15,273	135	19.6	13.3
H4	11,236	102	10.8	13.7

*The sizes of these histones vary somewhat from species to species. The numbers given here are for bovine histones.

Table 24-4
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Each type of histone is subject to enzymetic modification by
methylation, acetylation, ADP-ribosylation, phosphorylation, glycosylation, sumoylation, or ubiquitination.

Such modifications affect the net electric charge, shape, and other properties of histones, as well as the structural and functional properties of the chromatin, and they play a role in the regulation of transcription.

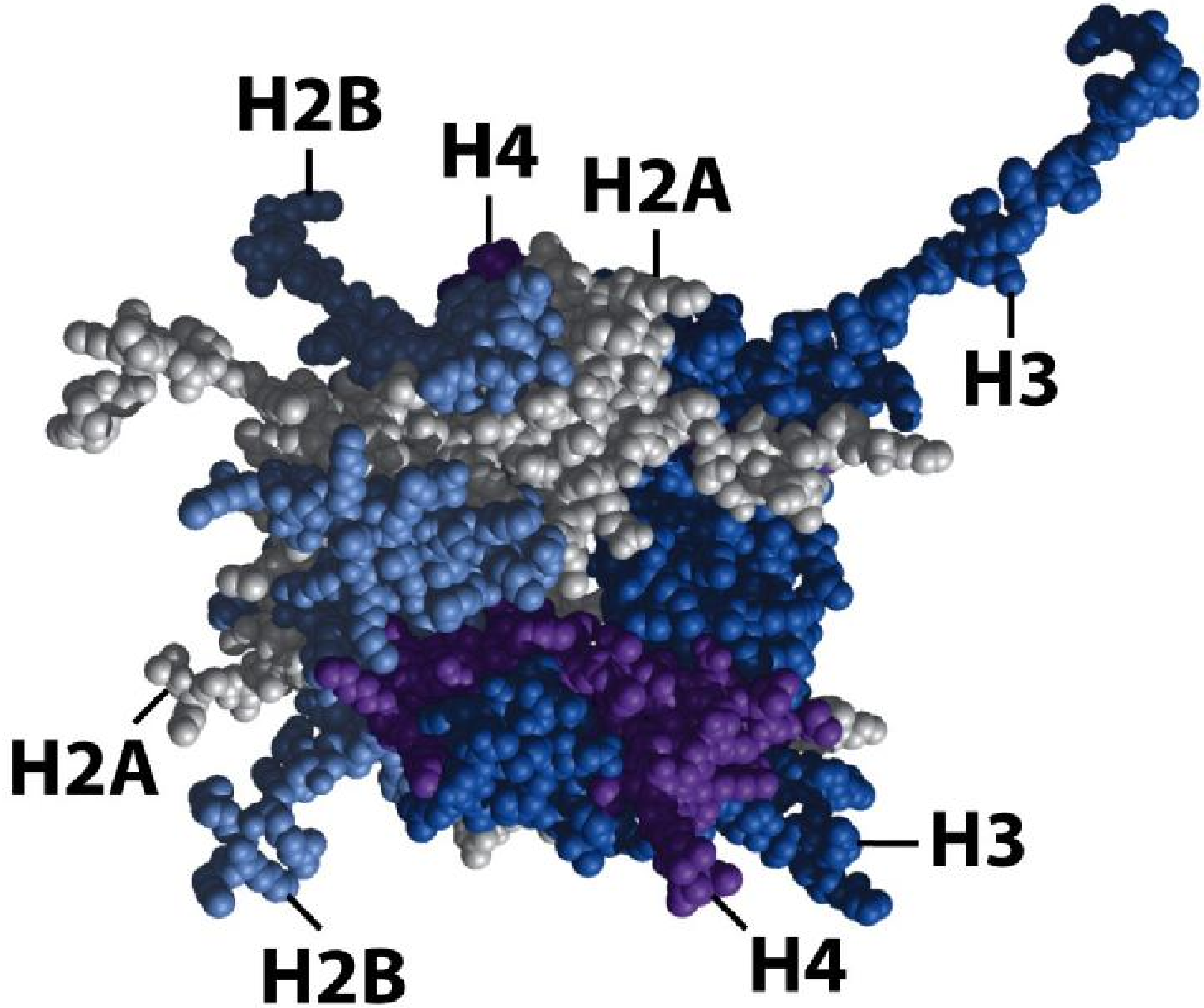

Figure 24-27a
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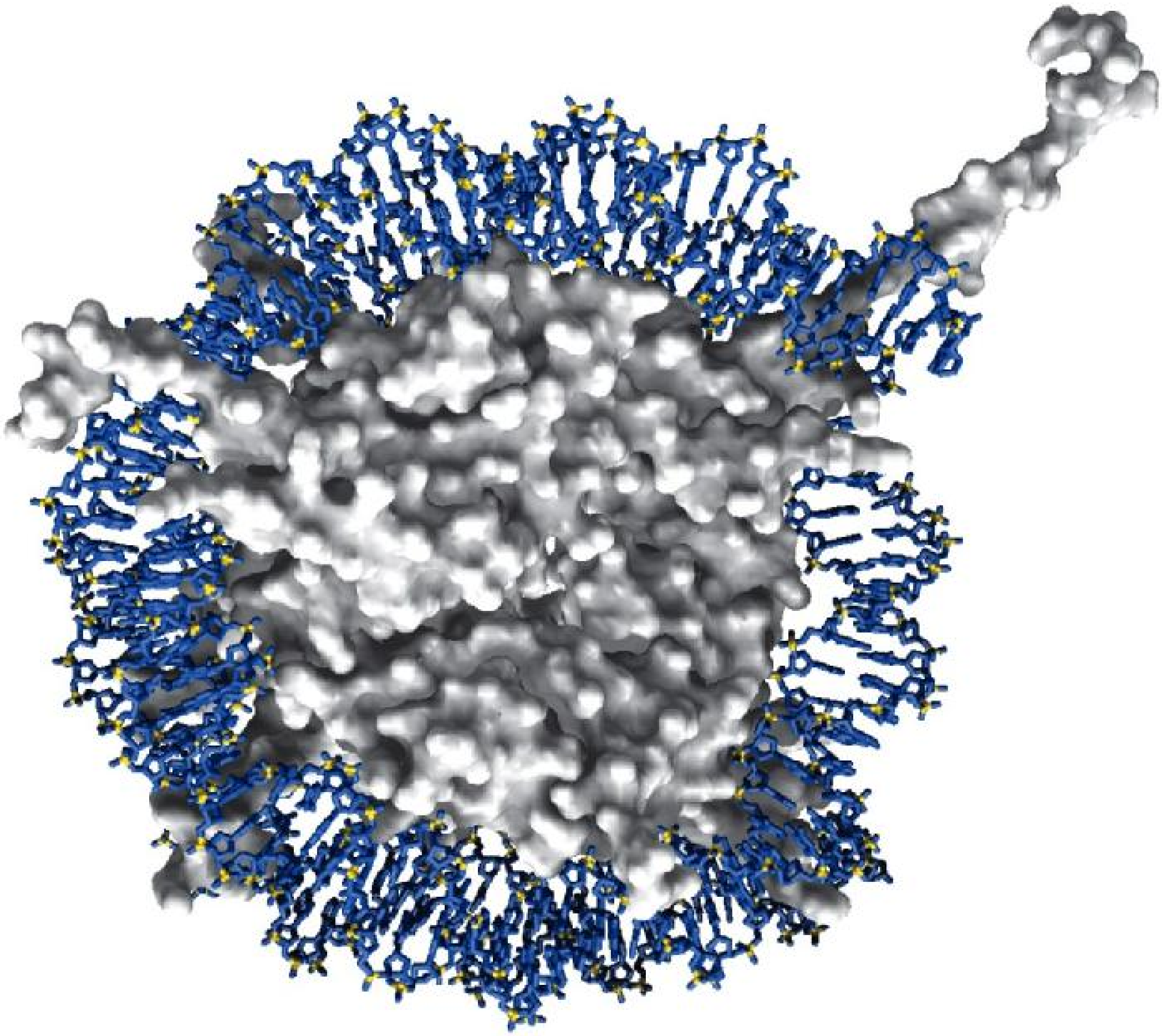

Figure 24-27b
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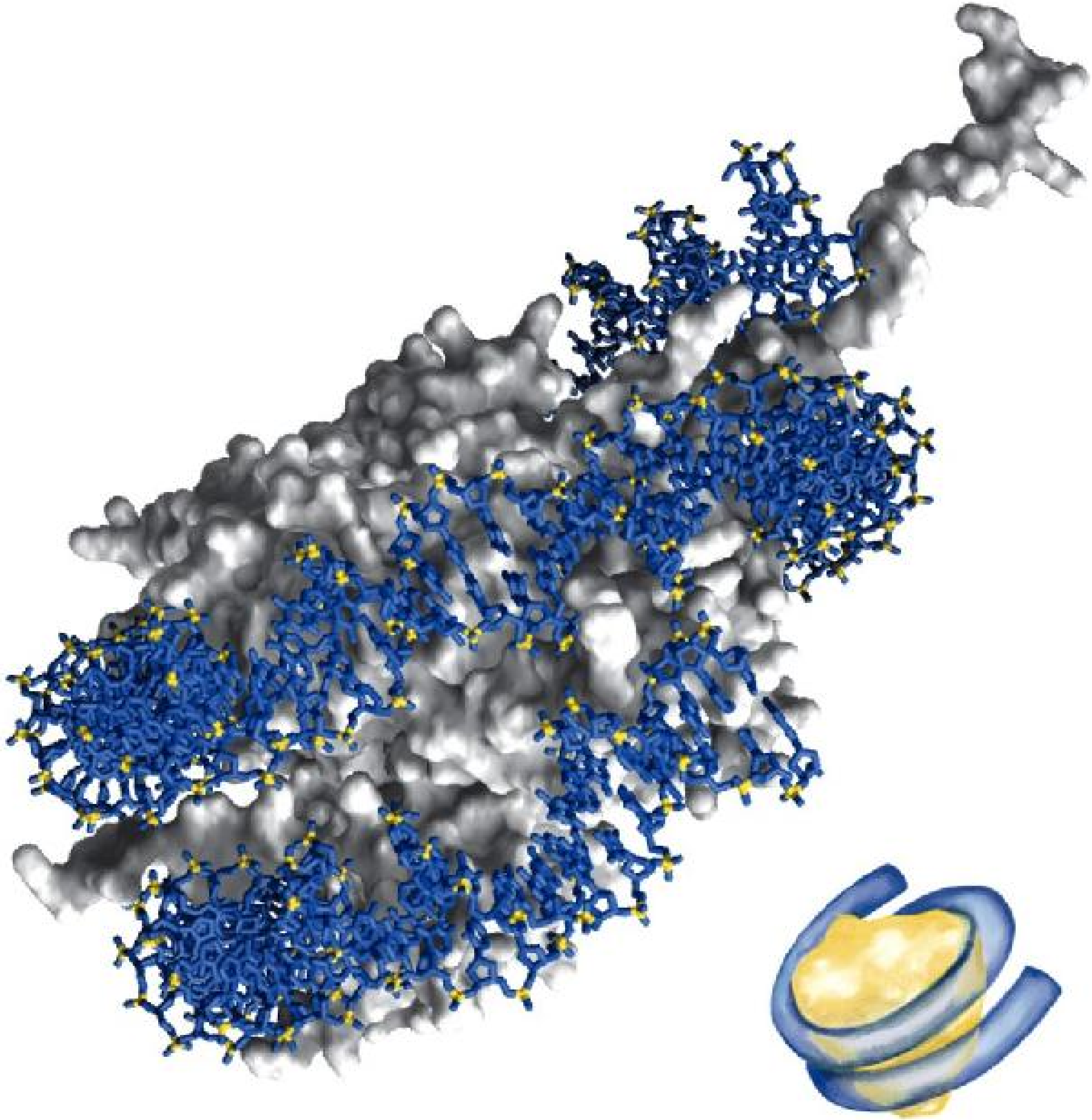

Figure 24-27c

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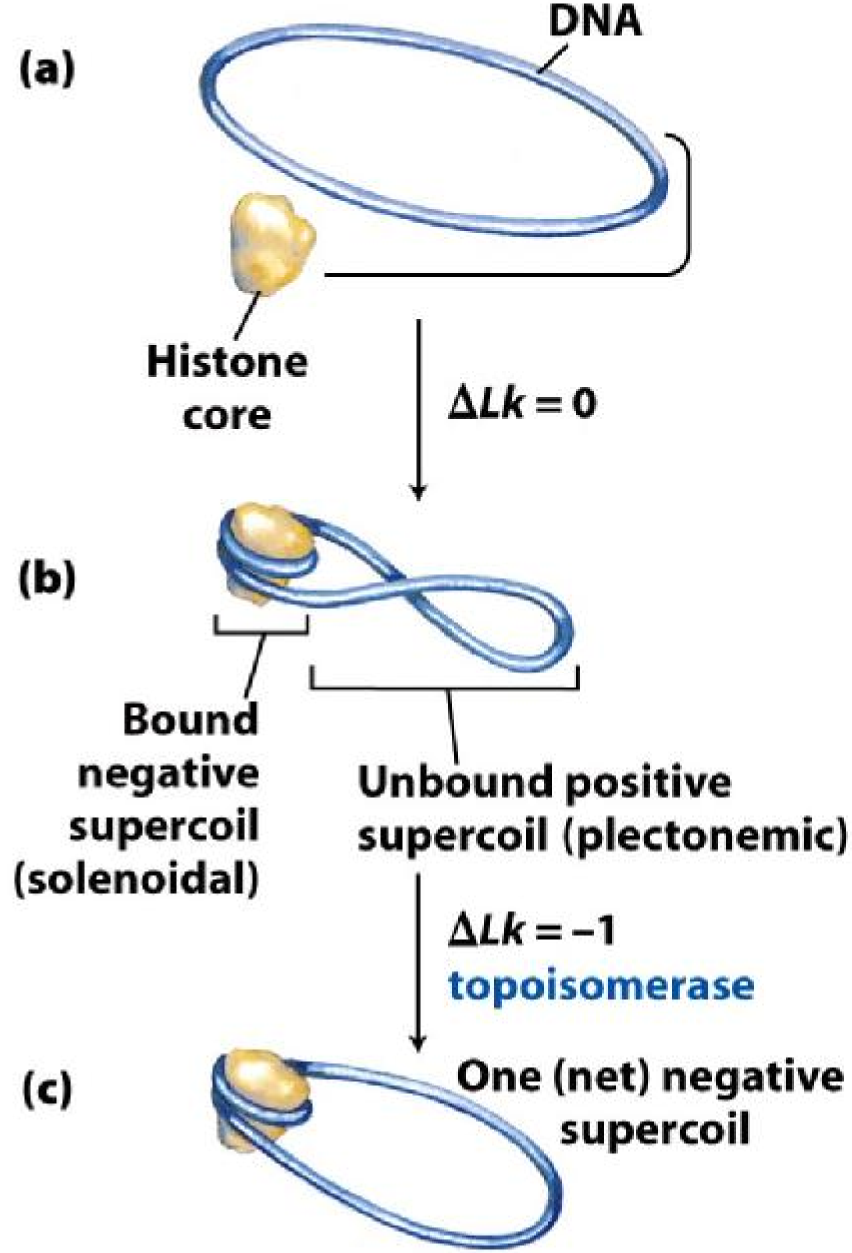

Figure 24-28
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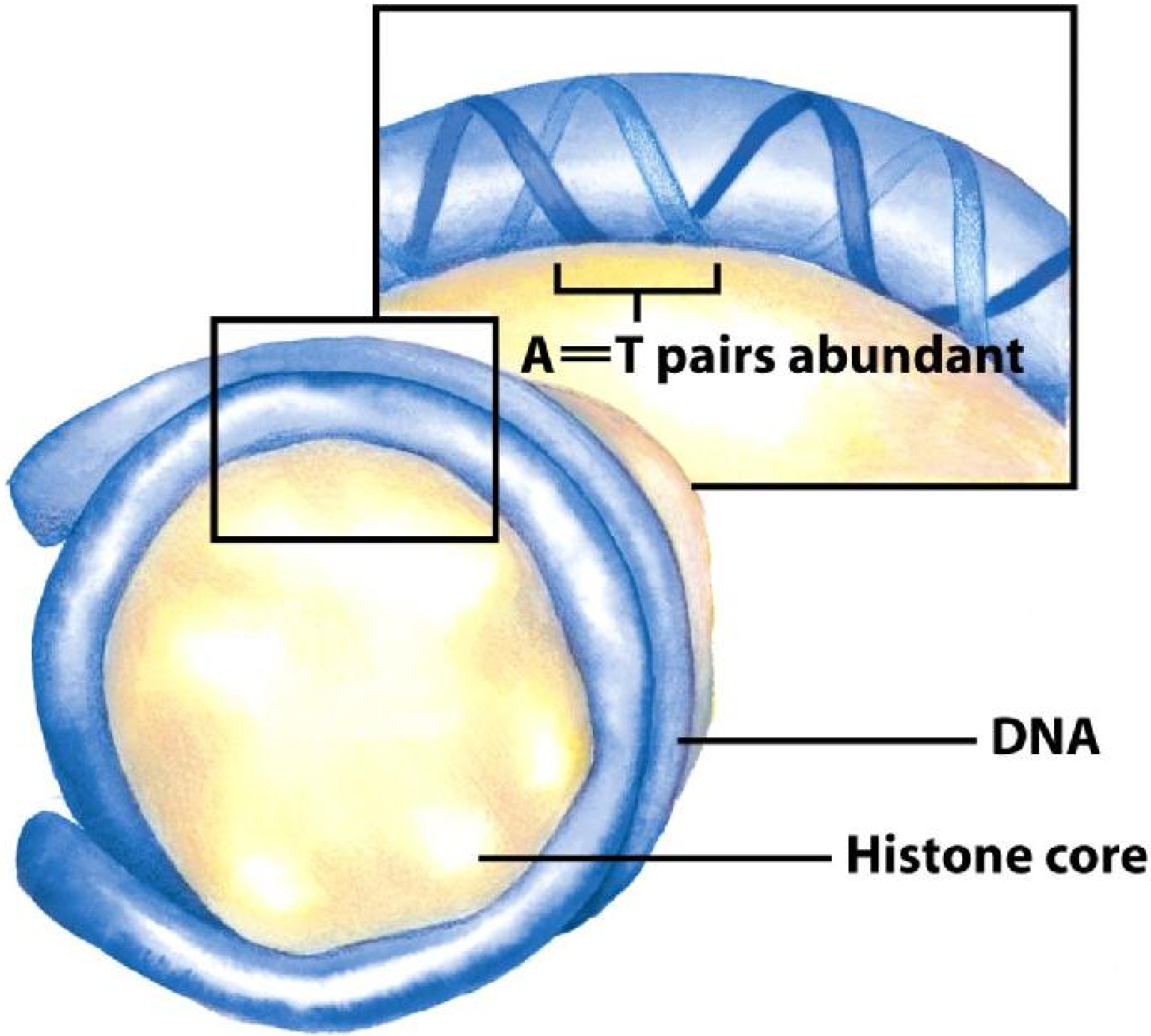

Figure 24-29
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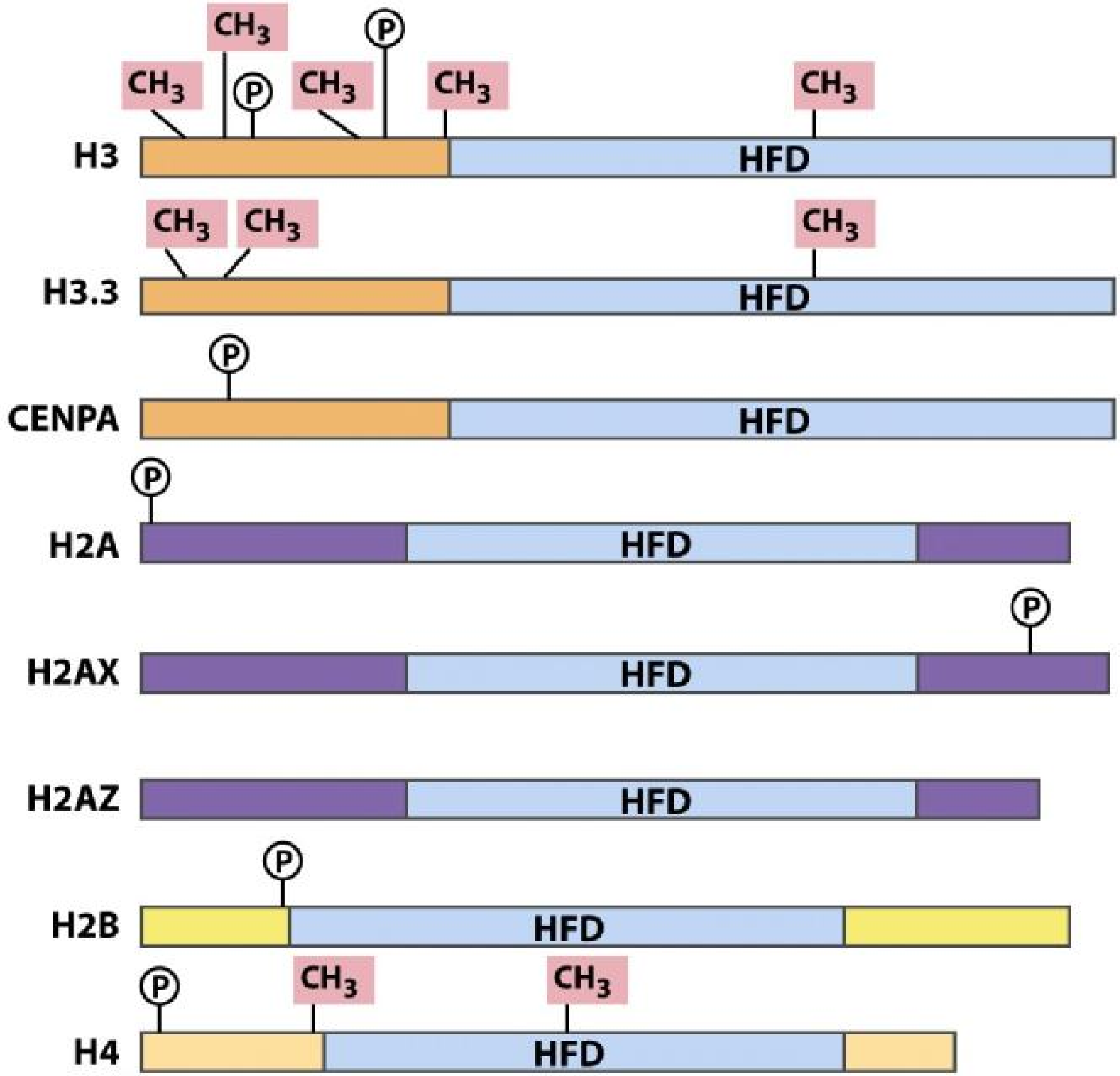

Box 24-2 figure 1

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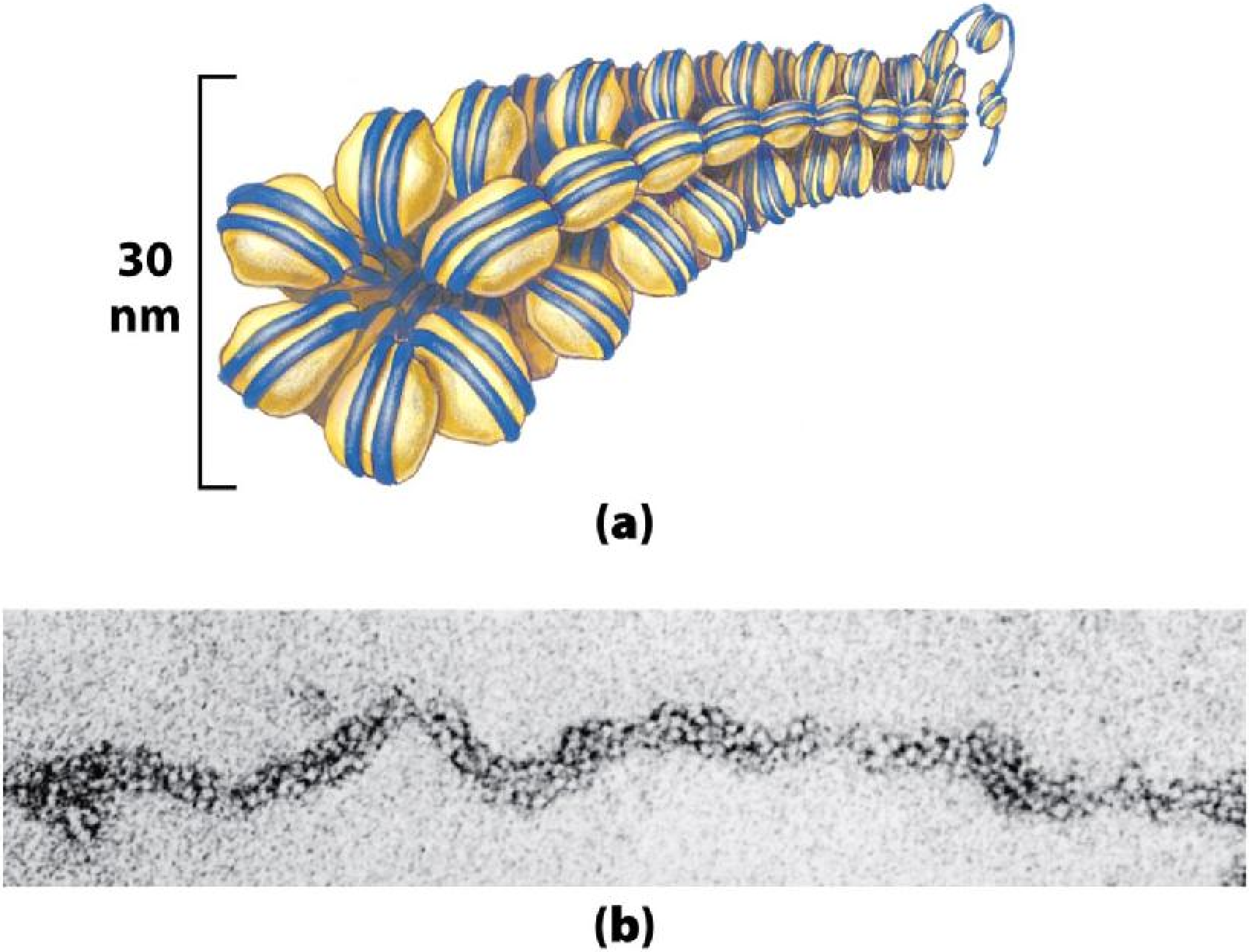

Figure 24-30
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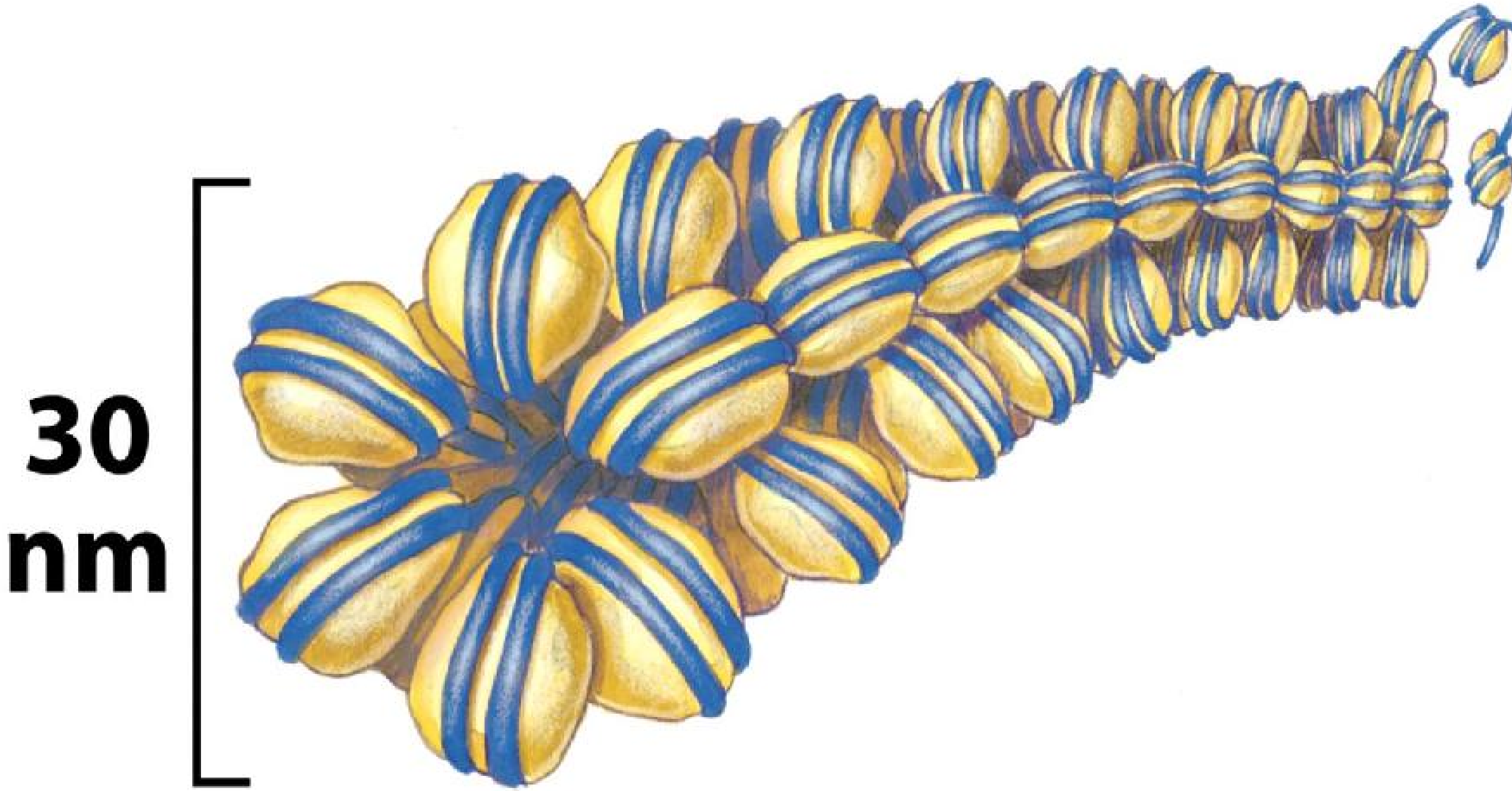

Figure 24-30a
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Figure 24-30b
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Figure 24-31
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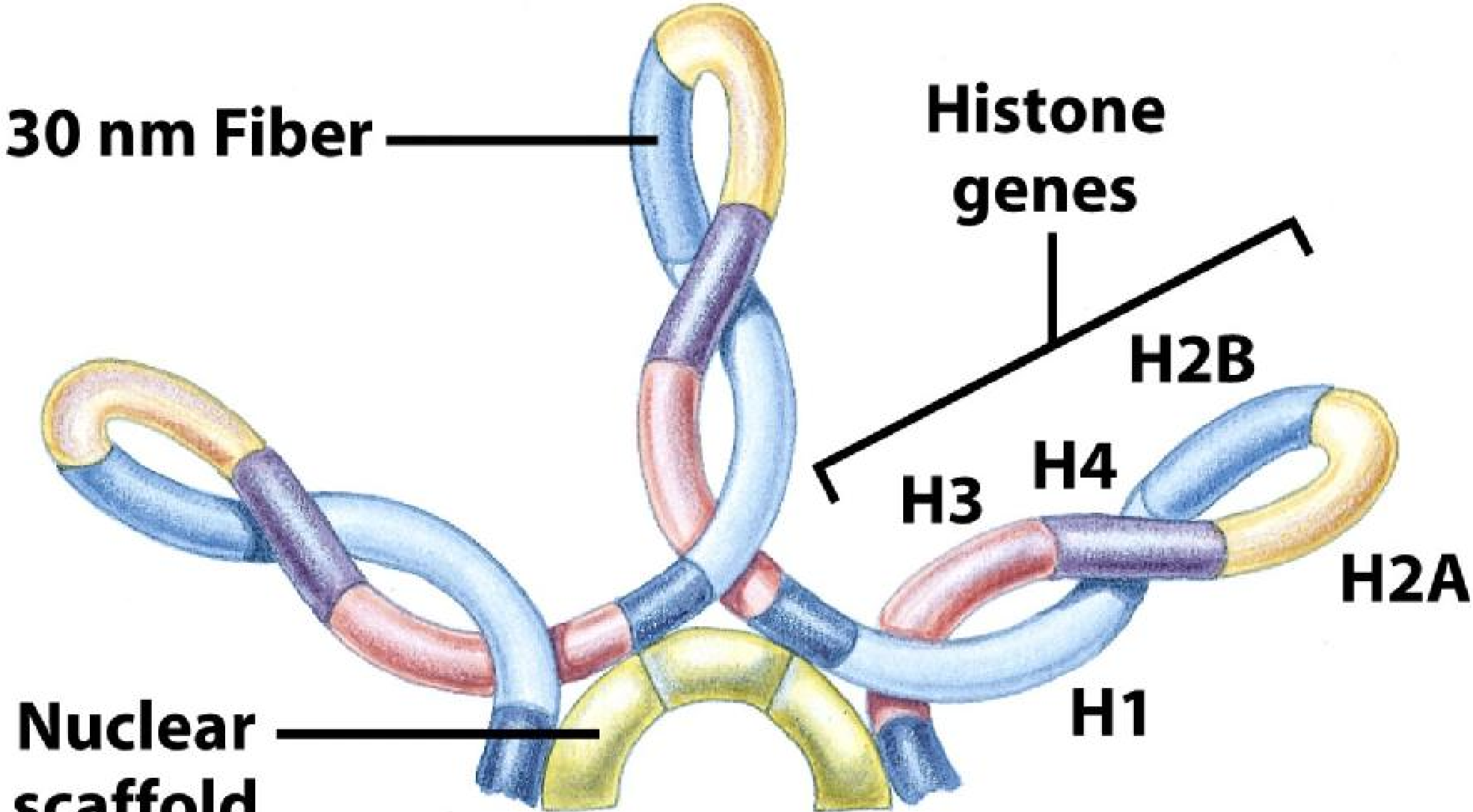

Figure 24-32
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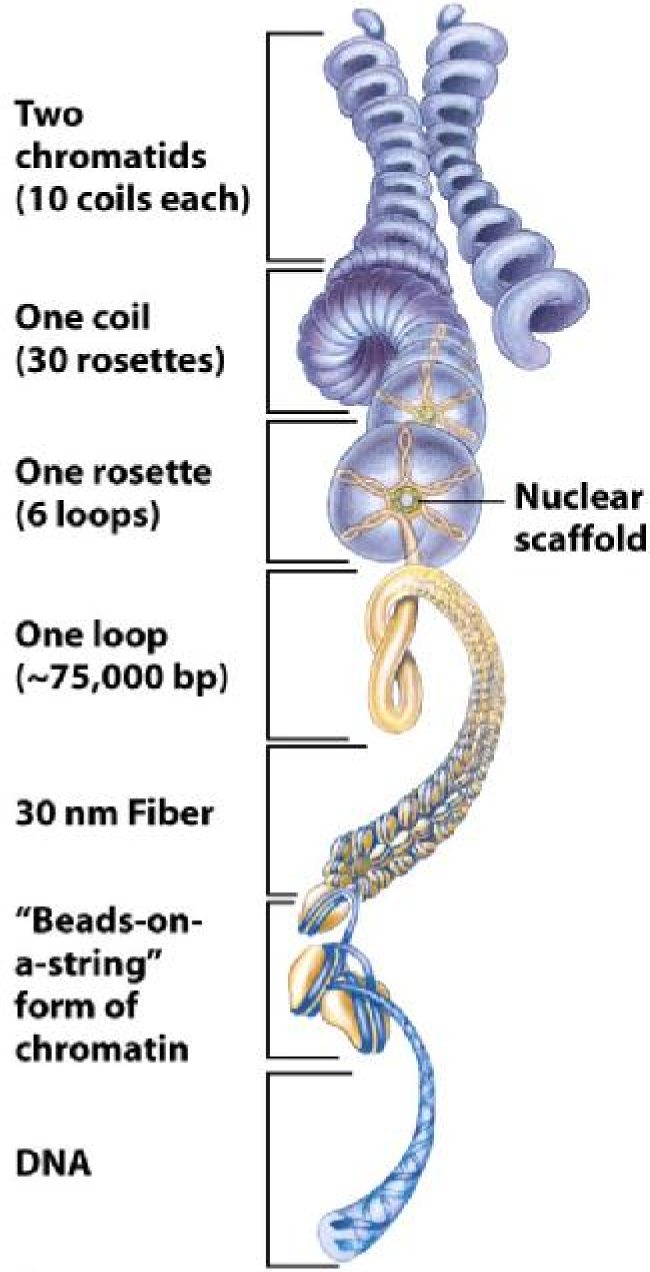

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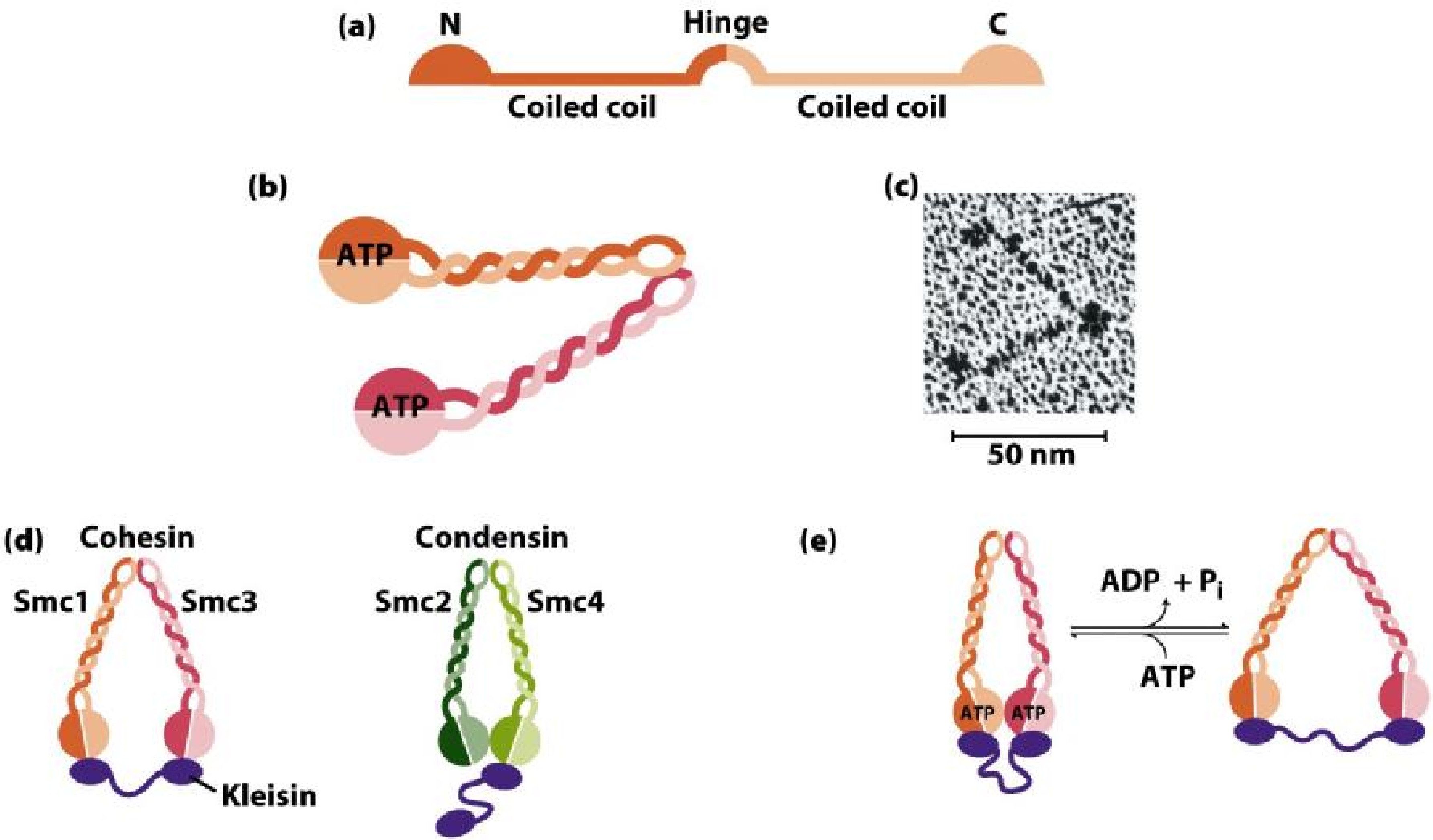

Figure 24-34
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Figure 24-34a
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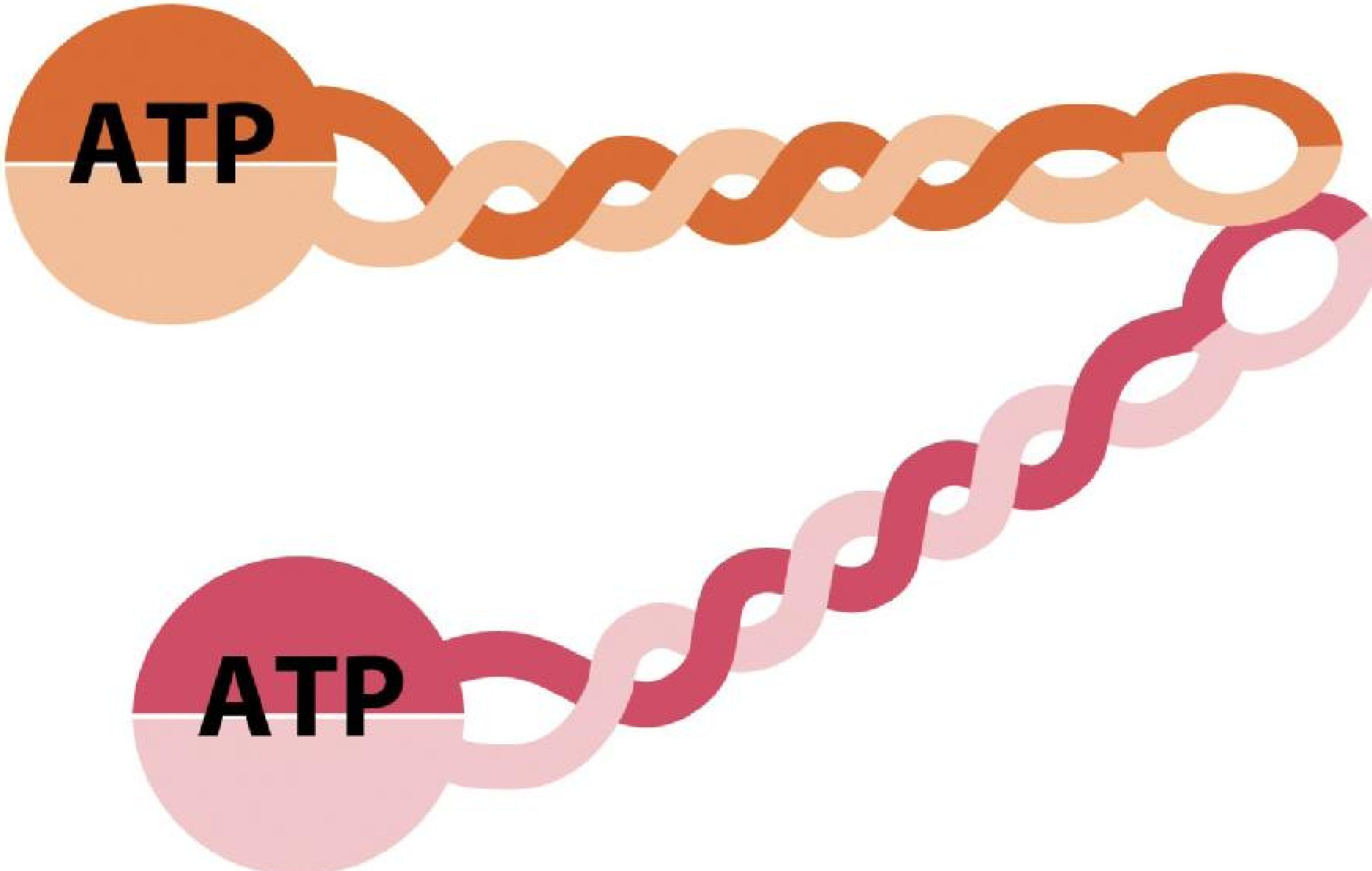

Figure 24-34b
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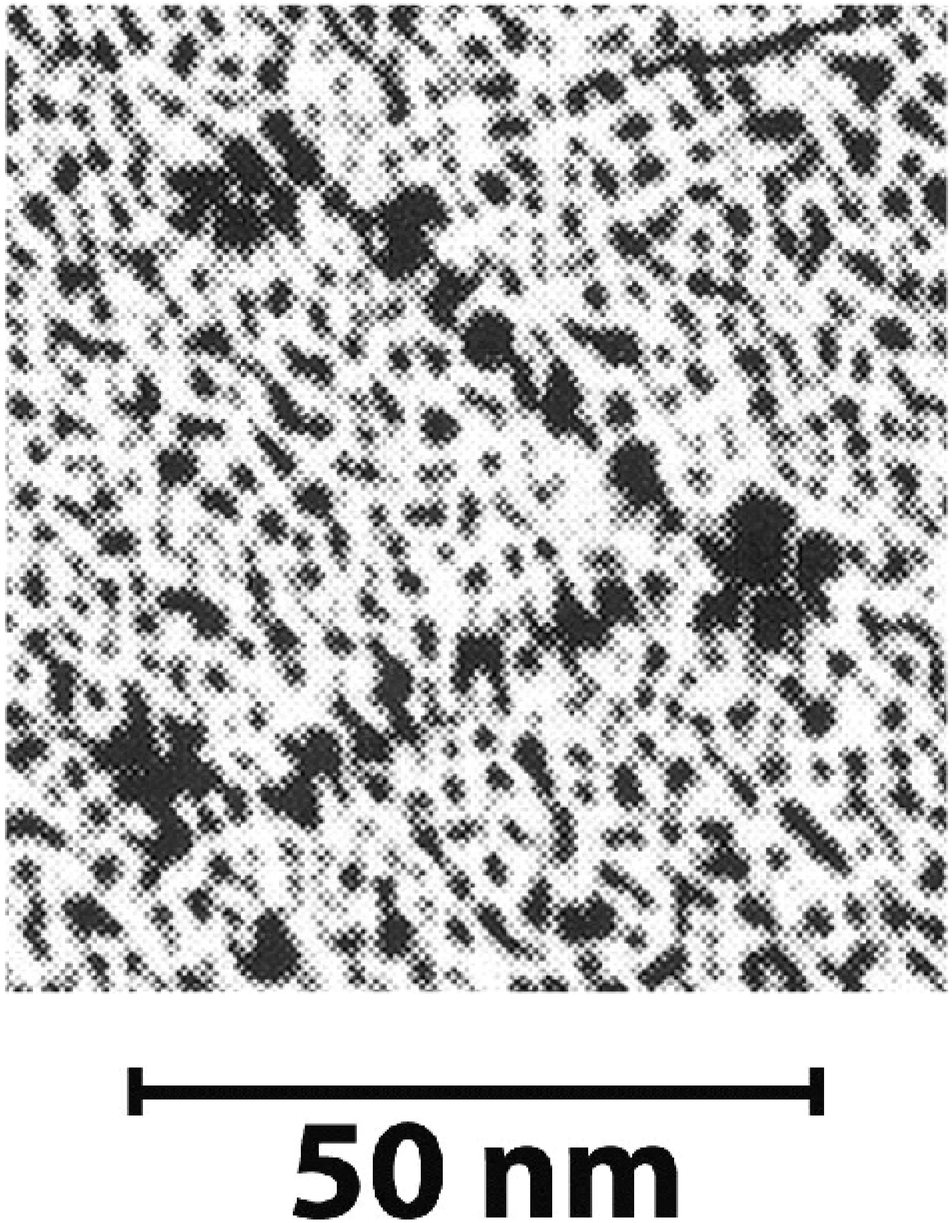

Figure 24-34c
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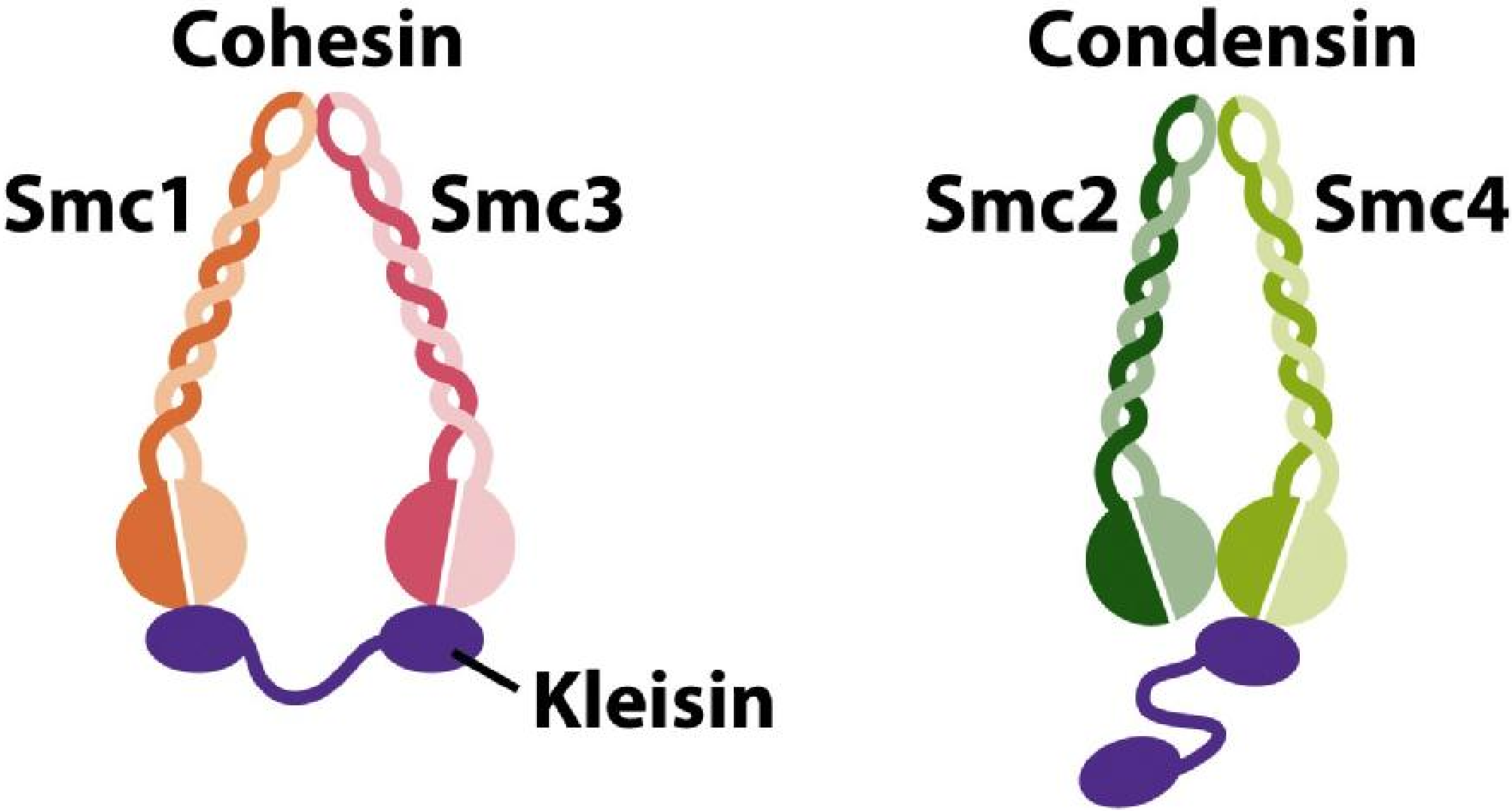

Figure 24-34d
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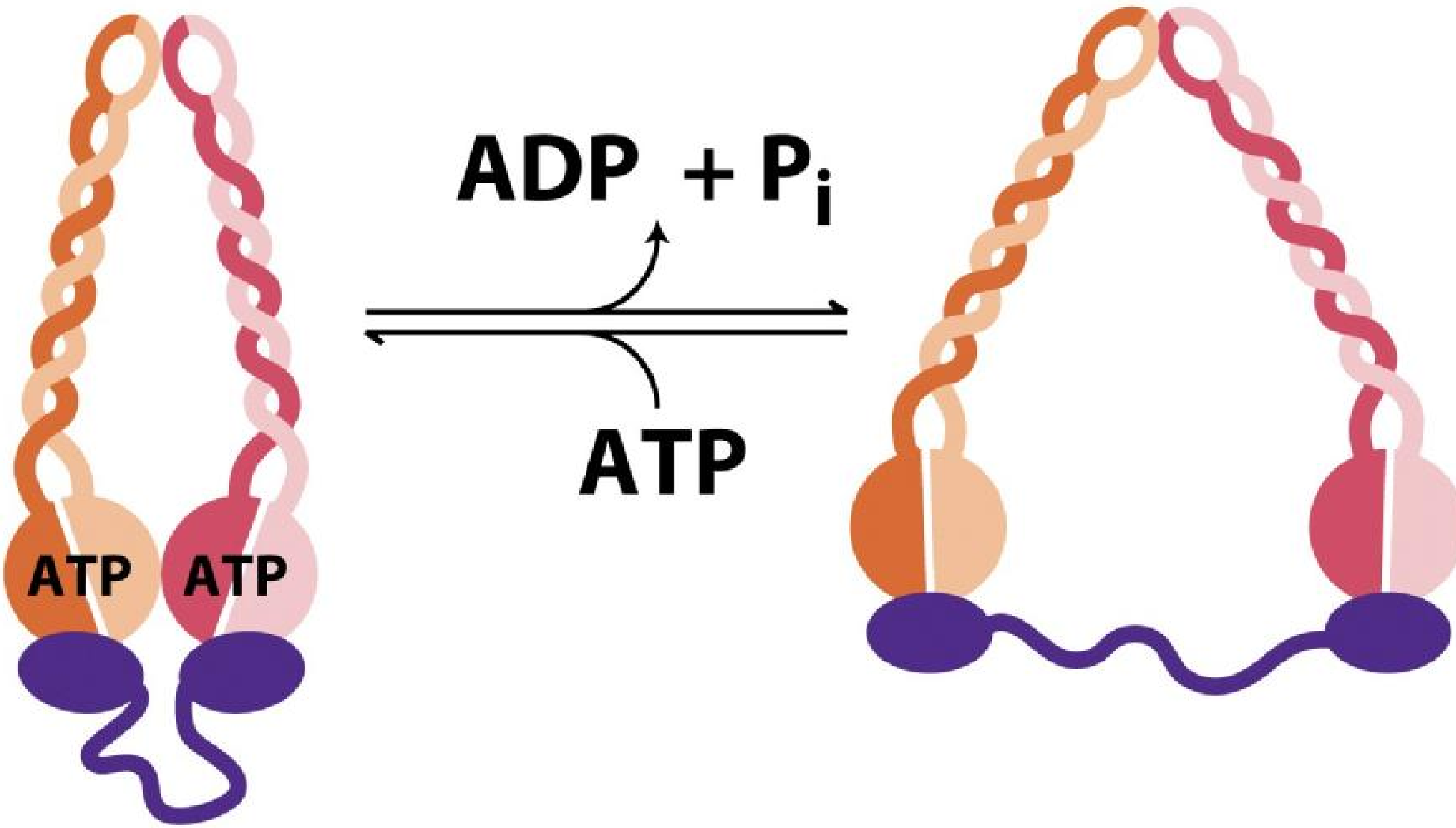

Figure 24-34e
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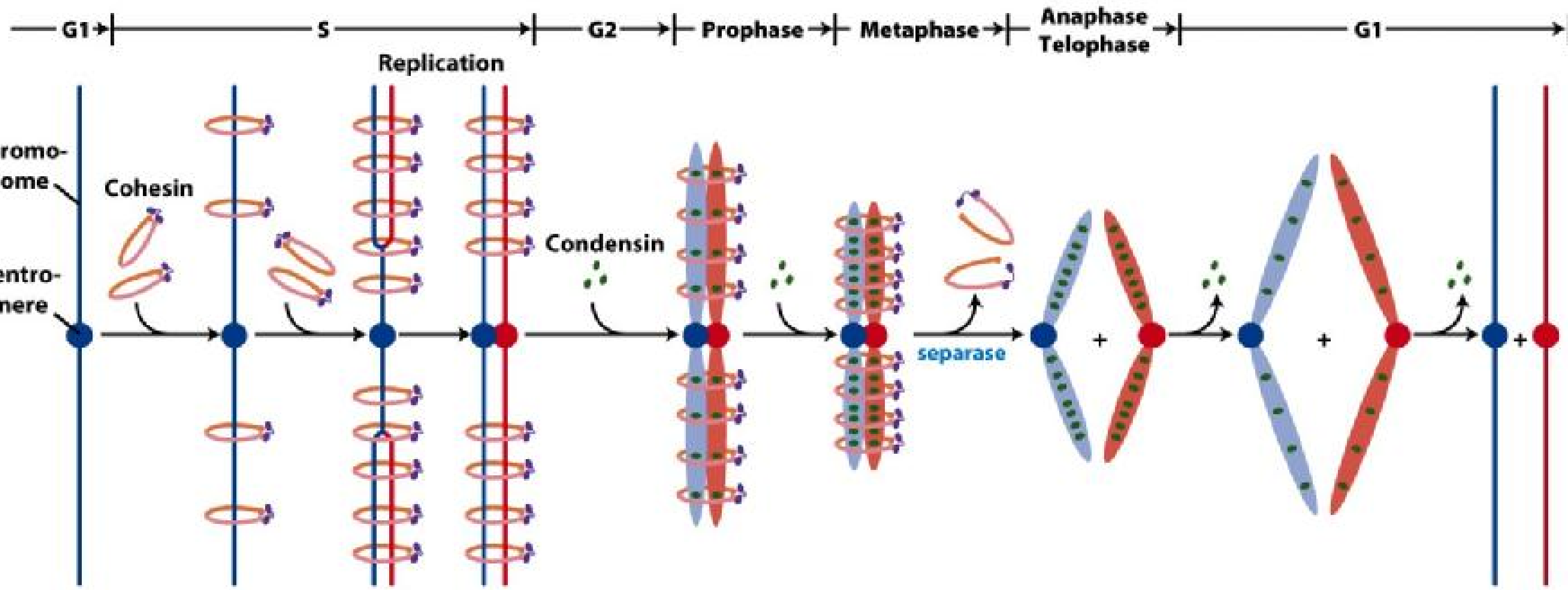

Figure 24-35

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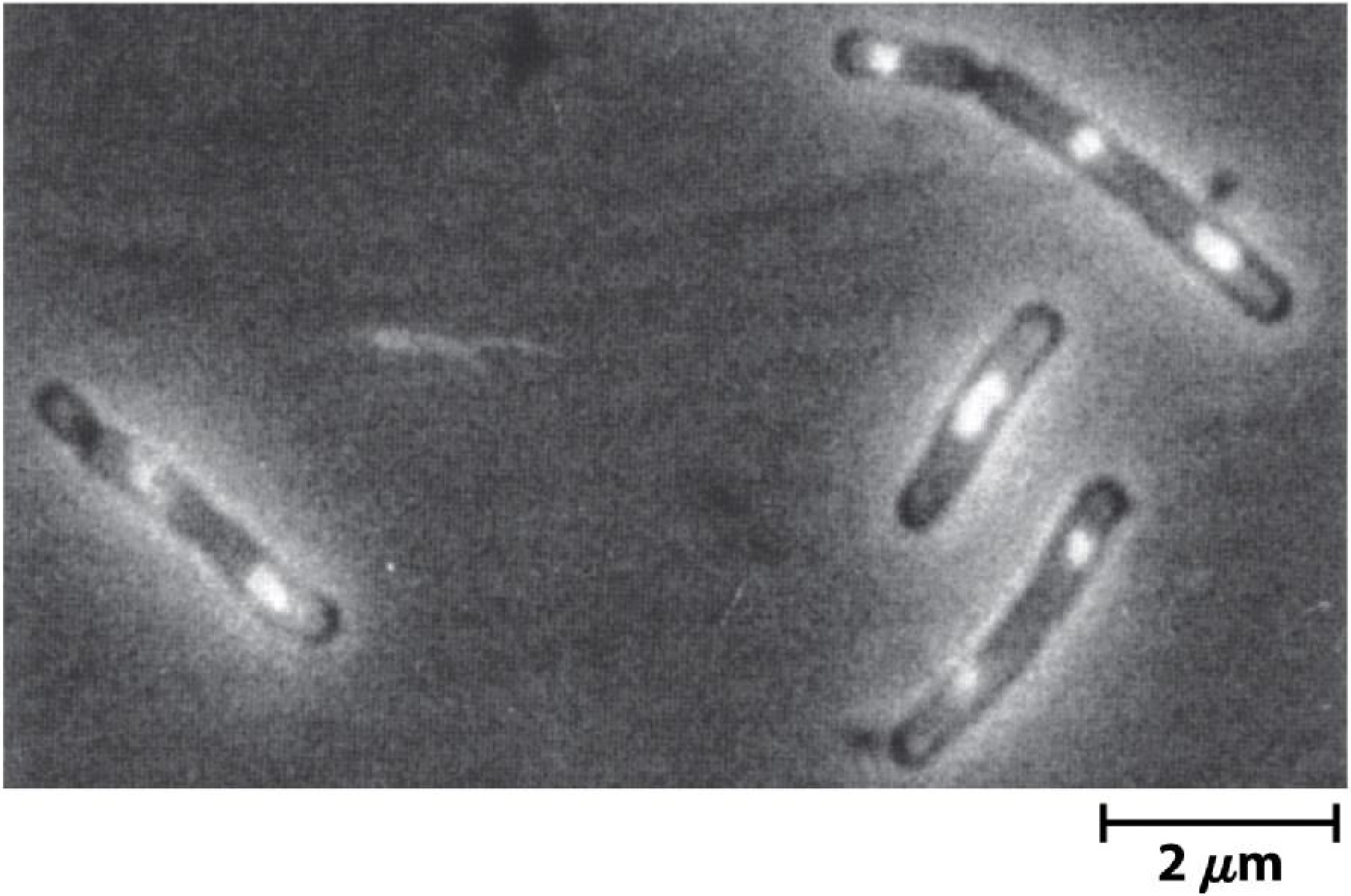

Figure 24-36
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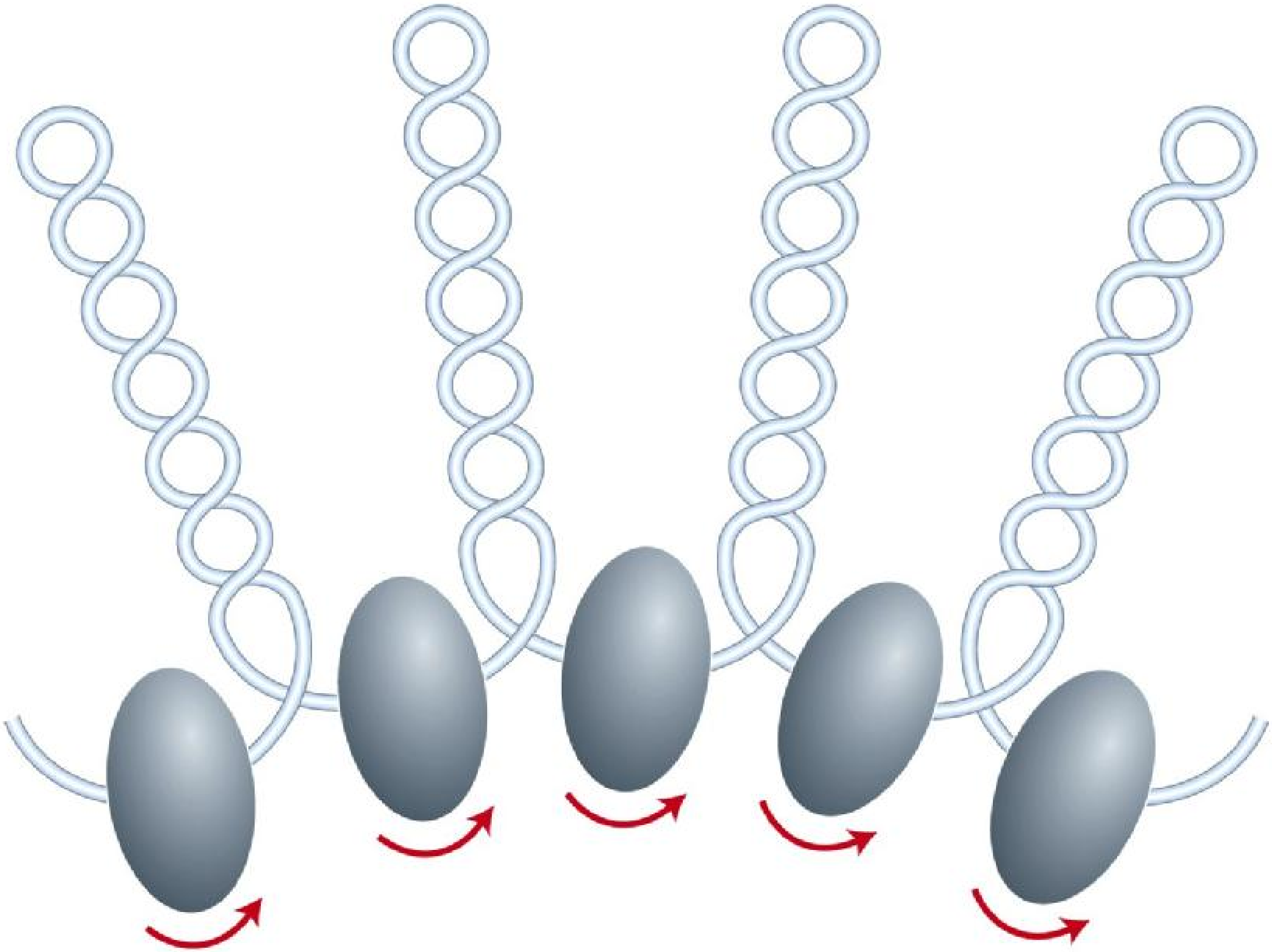

Figure 24-37
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