

Alberts • Johnson • Lewis • Raff • Roberts • Walter

# ***Molecular Biology of the Cell***

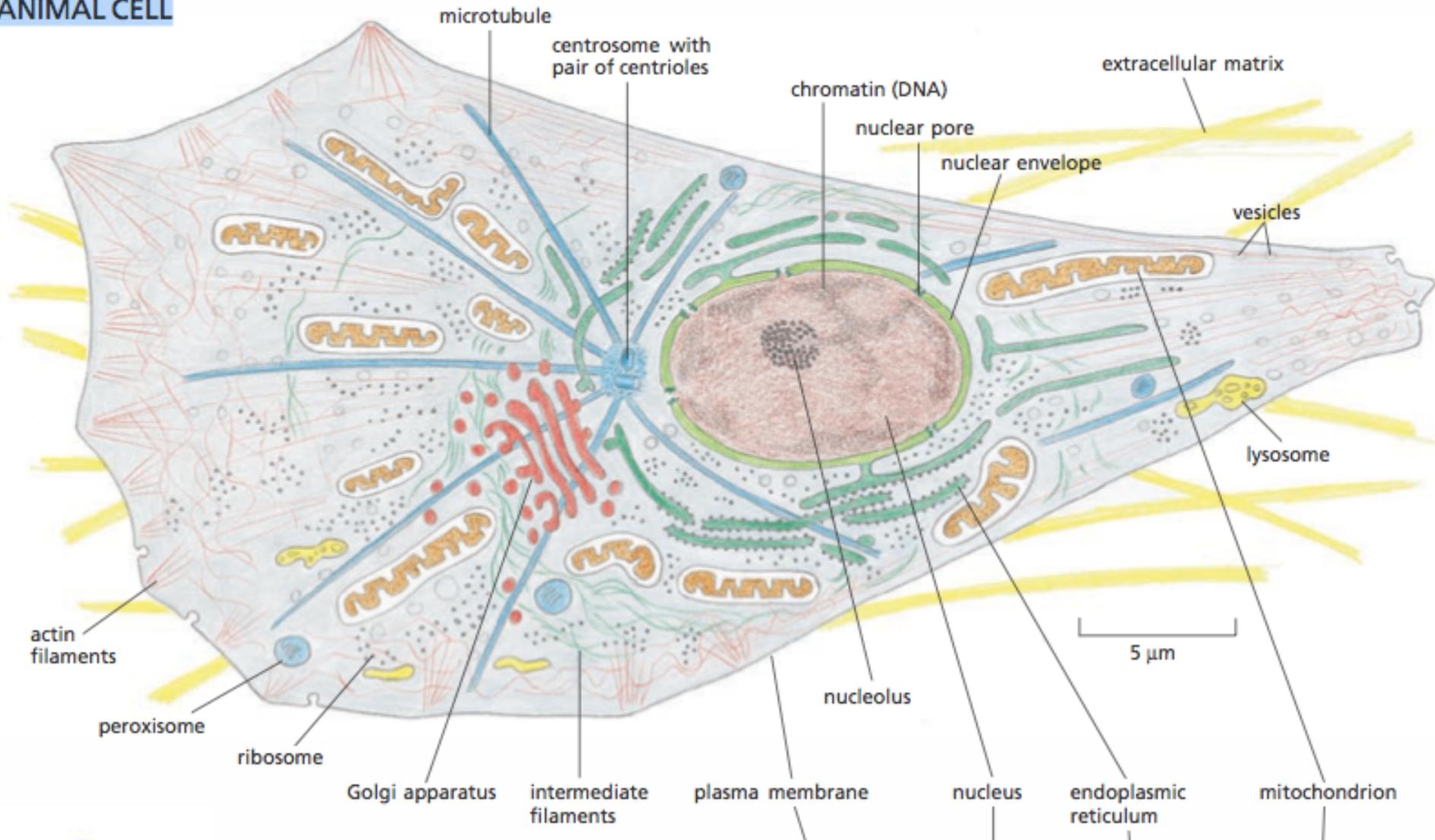
**Fifth Edition**

## **Chapter 4**

**DNA, Chromosomes, and Genomes**

# PANEL 1-2 Cell architecture

## ANIMAL CELL



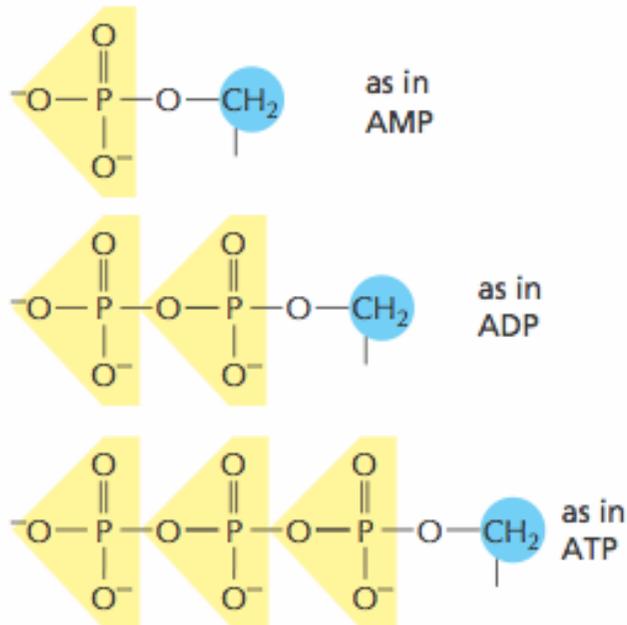
뉴클레오타이드/핵산

염색체

## 뉴클레오타이드는 핵산의 기본단위

### PHOSPHATES

The phosphates are normally joined to the C5 hydroxyl of the ribose or deoxyribose sugar (designated 5'). Mono-, di-, and triphosphates are common.



as in  
AMP

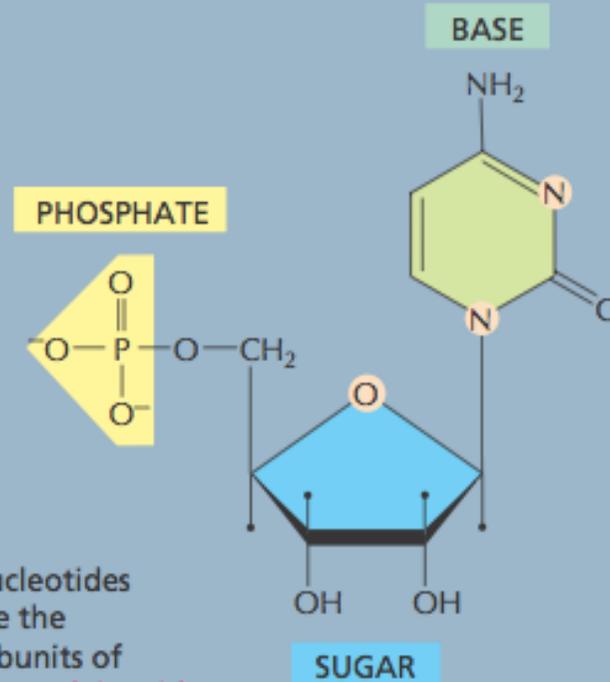
as in  
ADP

as in  
ATP

The phosphate makes a nucleotide negatively charged.

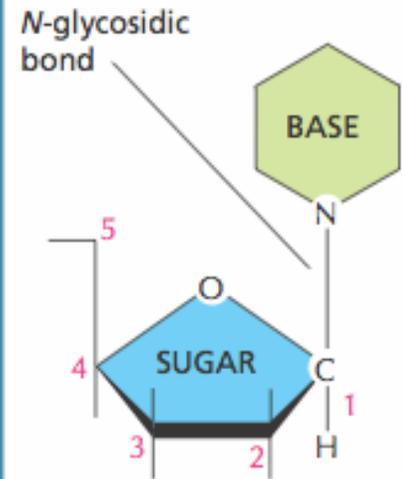
### NUCLEOTIDES

A nucleotide consists of a nitrogen-containing base, a five-carbon sugar, and one or more phosphate groups.



Nucleotides are the subunits of the **nucleic acids**.

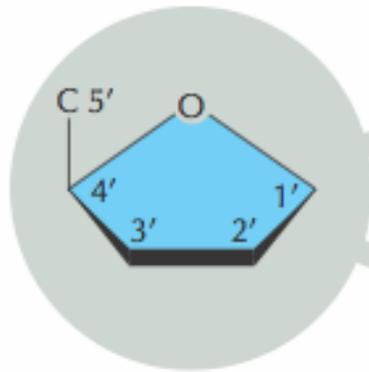
### BASIC SUGAR LINKAGE



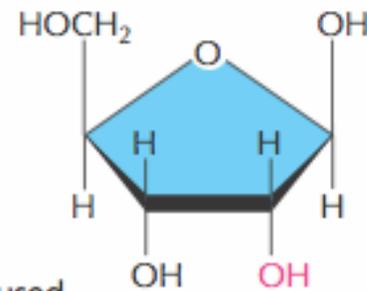
The base is linked to the same carbon (C1) used in sugar-sugar bonds.

## SUGARS

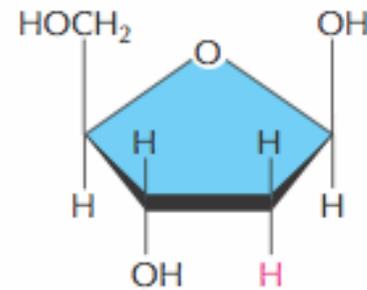
**PENTOSE**  
a five-carbon sugar



two kinds are used



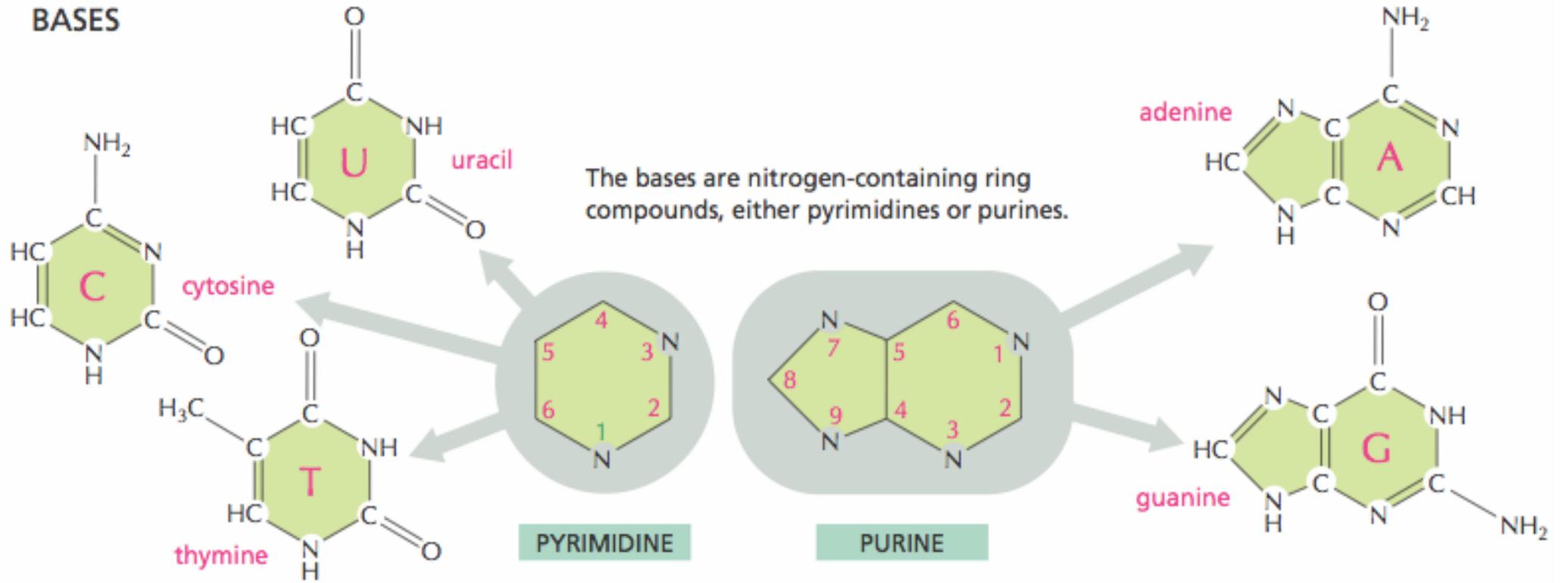
$\beta$ -D-ribose  
used in ribonucleic acid



$\beta$ -D-2-deoxyribose  
used in deoxyribonucleic acid

Each numbered carbon on the sugar of a nucleotide is followed by a prime mark; therefore, one speaks of the "5-prime carbon," etc.

# BASES



# Depurination & Deamination

The *most frequent* chemical reactions.

Create serious *DNA damage* in cells.

- *Depurination*

*Release guanine* as well as *adenine* from DNA (does not break the phosphodiester backbone).

*Spontaneous* reaction:  $10^{12}$  purines will be lost.

## *Deamination*

Converts *cytosine to Uracil*.

*Spontaneous* reaction.

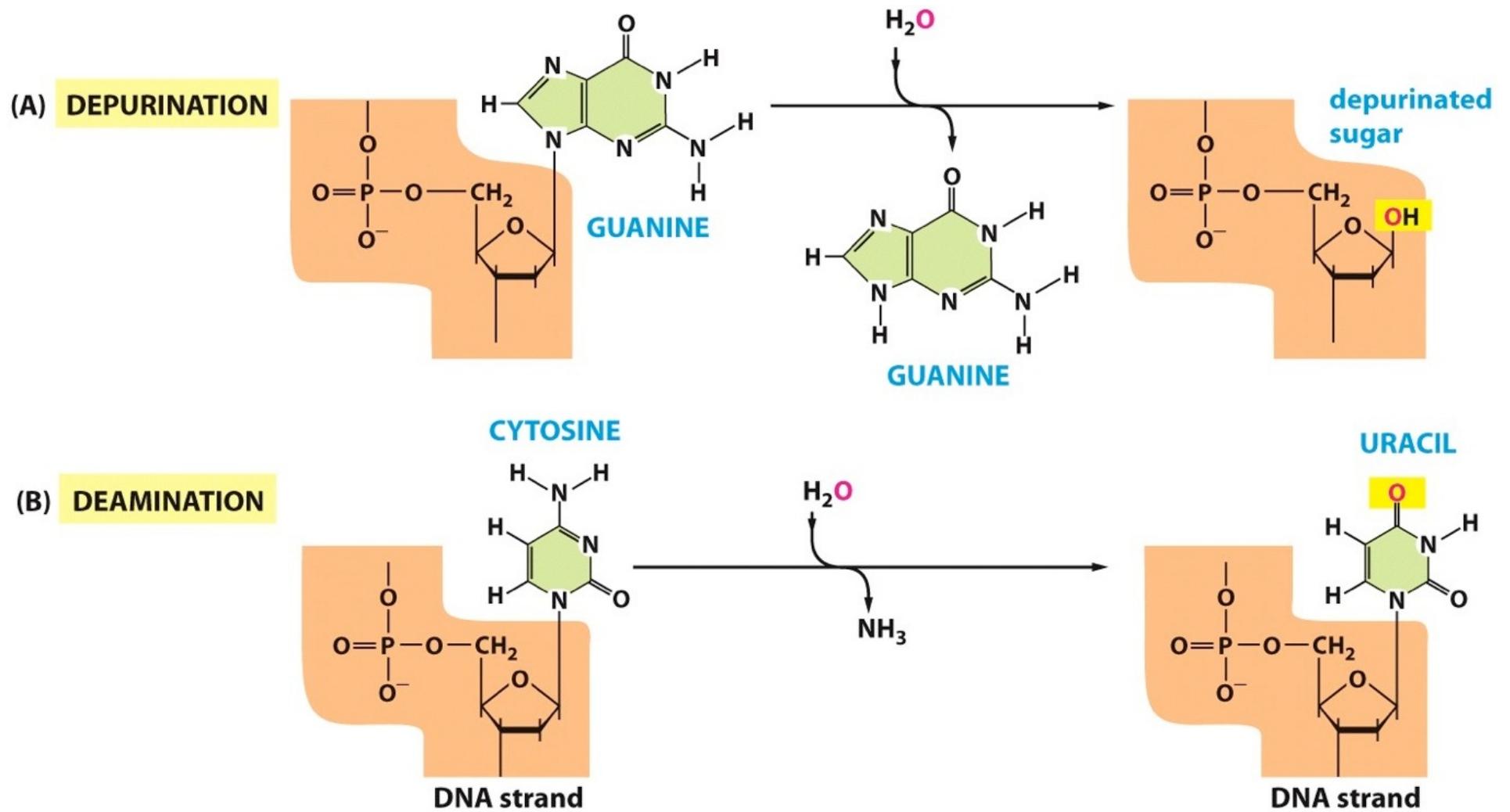


Figure 6-23 Essential Cell Biology 3/e (© Garland Science 2010)

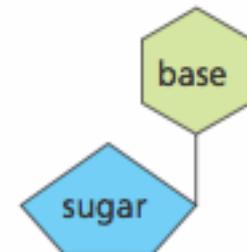
## NOMENCLATURE

The names can be confusing, but the abbreviations are clear.

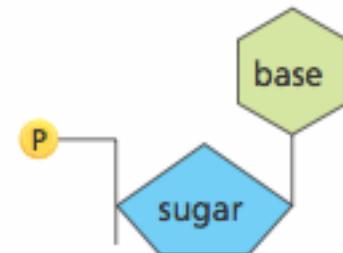
| BASE     | NUCLEOSIDE | ABBR. |
|----------|------------|-------|
| adenine  | adenosine  | A     |
| guanine  | guanosine  | G     |
| cytosine | cytidine   | C     |
| uracil   | uridine    | U     |
| thymine  | thymidine  | T     |

Nucleotides are abbreviated by three capital letters. Some examples follow:

AMP = adenosine monophosphate  
dAMP = deoxyadenosine monophosphate  
UDP = uridine diphosphate  
ATP = adenosine triphosphate



BASE + SUGAR = NUCLEOSIDE

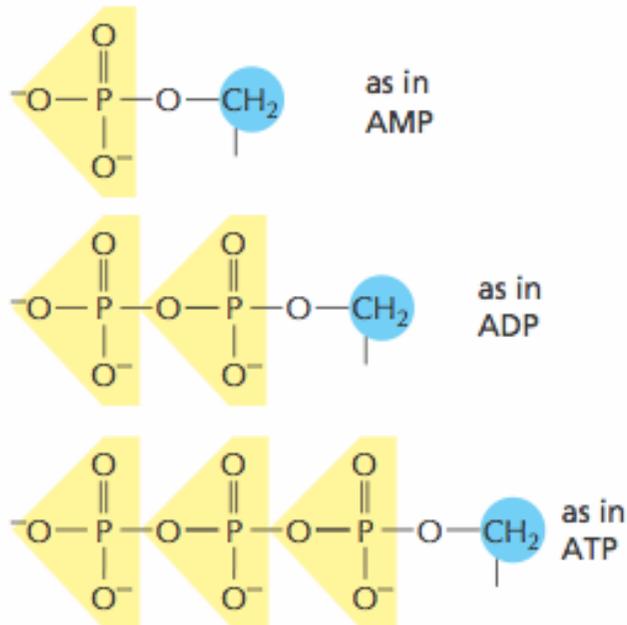


BASE + SUGAR + PHOSPHATE = NUCLEOTIDE

## 뉴클레오타이드는 핵산의 기본단위

### PHOSPHATES

The phosphates are normally joined to the C5 hydroxyl of the ribose or deoxyribose sugar (designated 5'). Mono-, di-, and triphosphates are common.



as in  
AMP

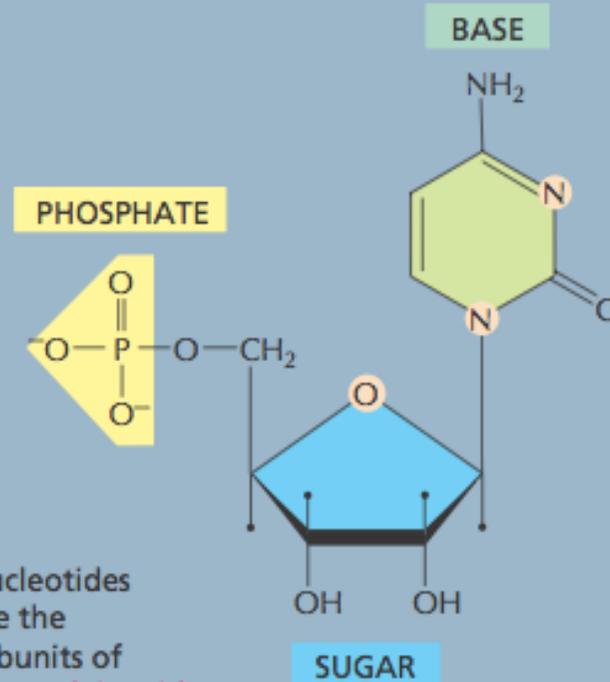
as in  
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The phosphate makes a nucleotide negatively charged.

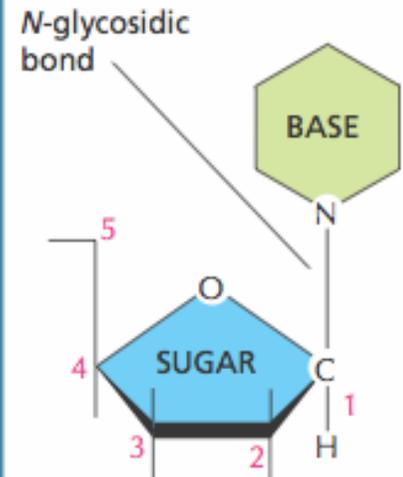
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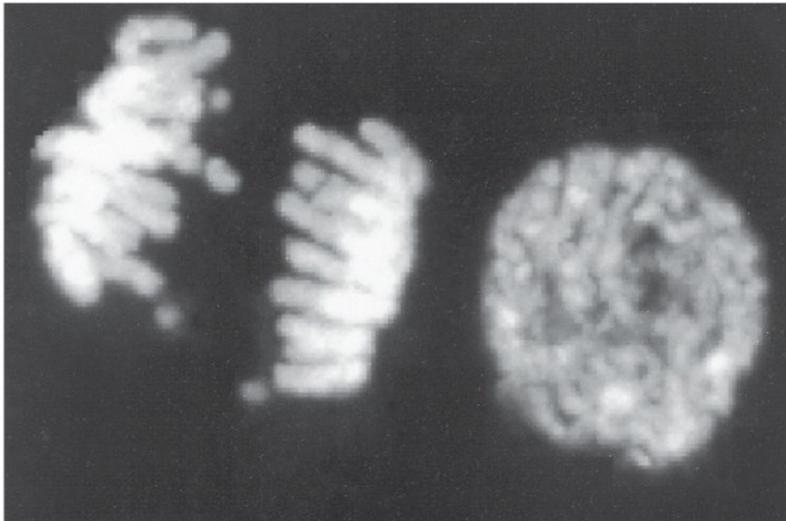


Nucleotides are the subunits of the **nucleic acids**.

### BASIC SUGAR LINKAGE



The base is linked to the same carbon (C1) used in sugar-sugar bonds.



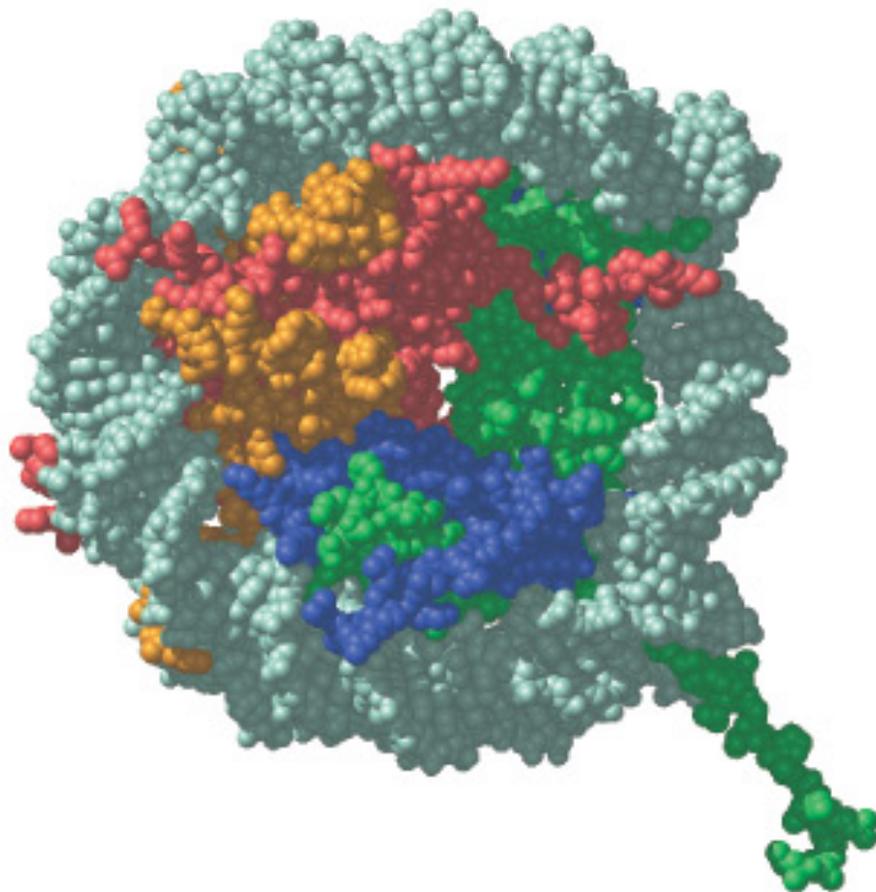
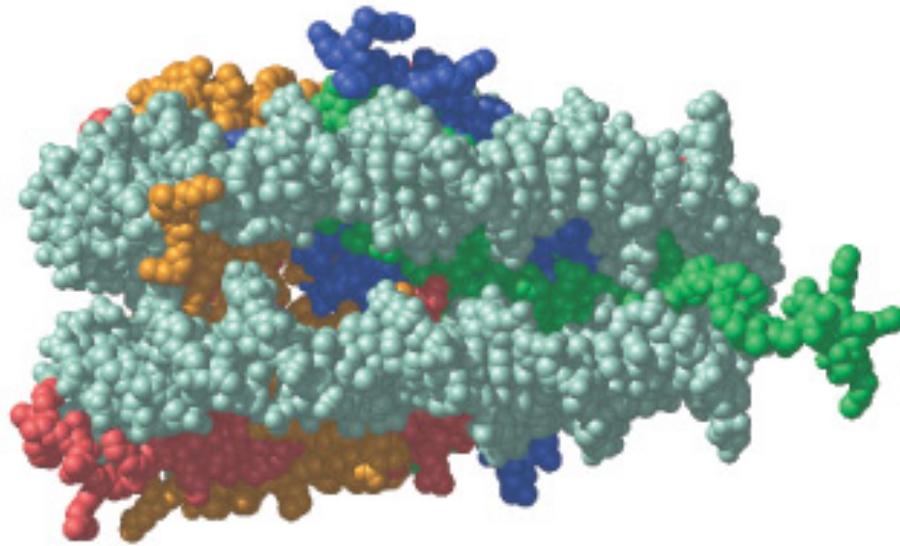
(A) **dividing cell**      **nondividing cell**



(B)   
 10  $\mu\text{m}$

**Chromosomes become visible as cells prepare to divide.**

(A) Two adjacent plant cells. The DNA has been stained with a fluorescent dye (DAPI) that binds to it. The DNA is present in chromosomes, which become visible as distinct structures, as shown on the *left*. The cell on the *right*, which is not dividing, contains the identical chromosomes; they cannot be distinguished as individual chromosomes.



**The nucleosome.** The basic structural unit of all eucaryotic chromosomes is the nucleosome. The DNA double helix (*gray*) is wrapped around a core particle of histone proteins (colored) to create the nucleosome. Nucleosomes are spaced roughly 200 nucleotide pairs apart along the chromosomal DNA.

(Nature 389:251-260, 1997)

- The Structure and Function of DNA
- The Structure of Eucaryotic Chromosomes
- The Regulation of Chromosome Structure

# The Structure and Function of DNA

A DNA molecule consists of *two complementary chains of nucleotides*

## building blocks of DNA

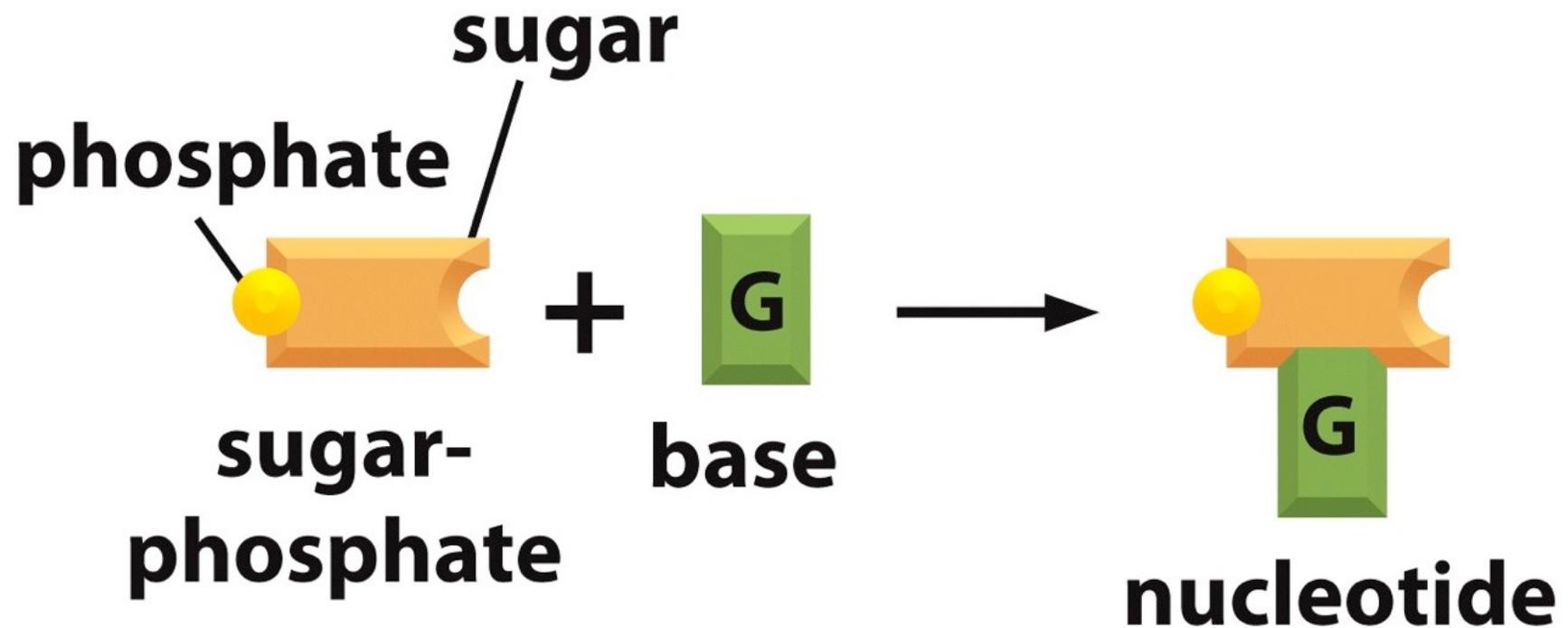
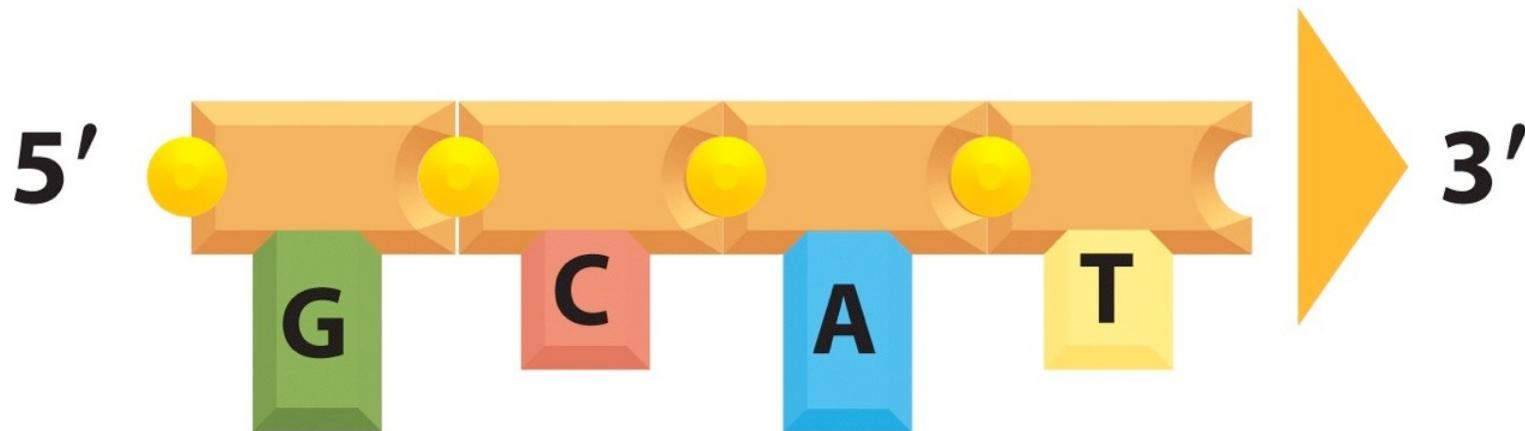


Figure 5-2a Essential Cell Biology 3/e (© Garland Science 2010)

- *Chemical polarity*

DNA is made of *four nucleotide building blocks*

## DNA strand



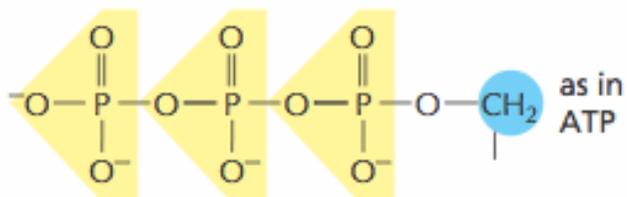
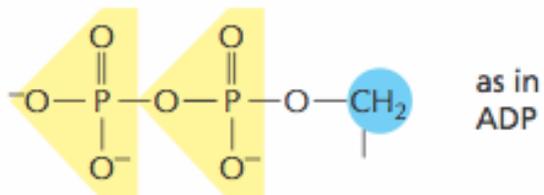
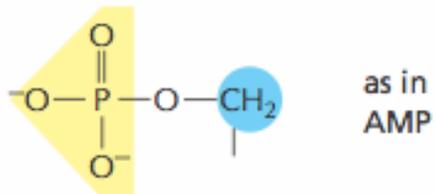
by 'DNA polymerase'

Figure 5-2b Essential Cell Biology 3/e (© Garland Science 2010)

- $3.2 \times 10^9$  (3.2 billion) nt (2 m) over 24 chromosomes

## PHOSPHATES

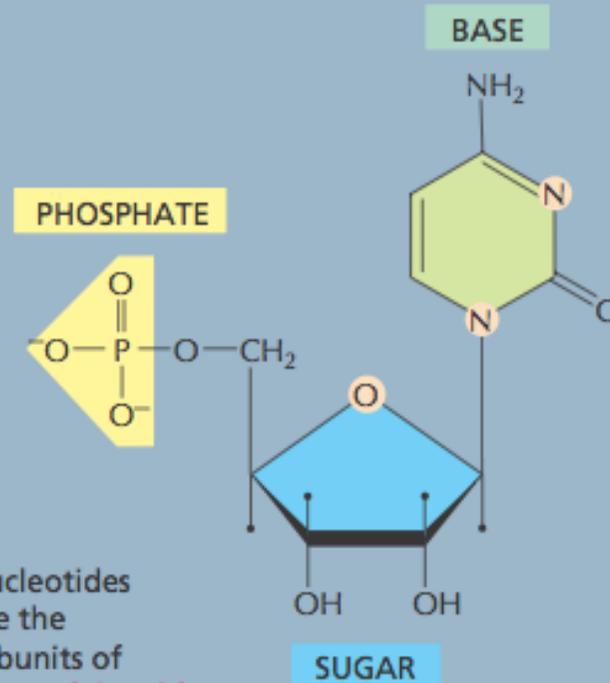
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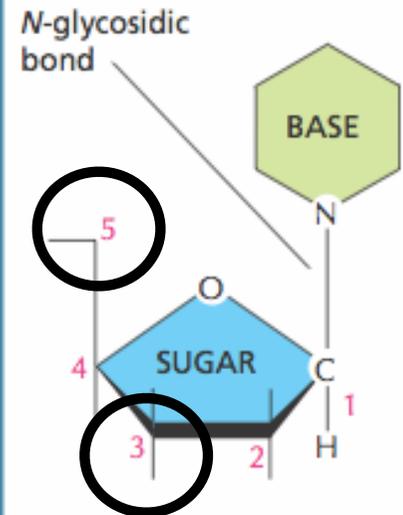
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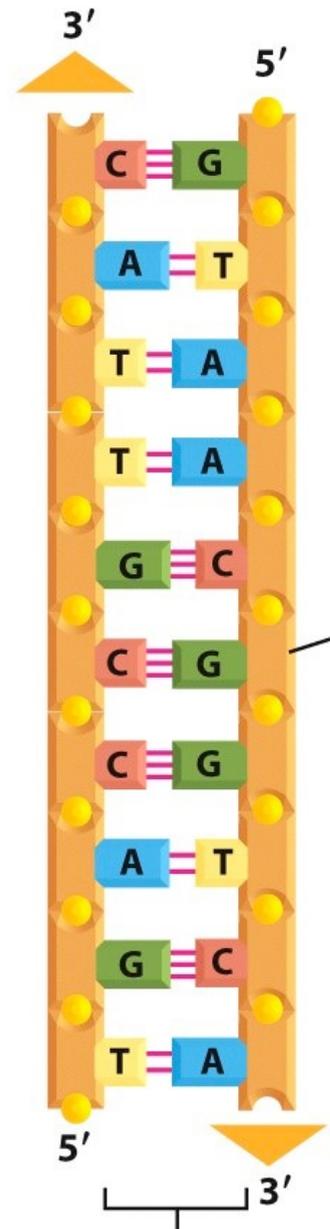


## BASIC SUGAR LINKAGE



The base is linked to the same carbon (C1) used in sugar-sugar bonds.

(C) double-stranded DNA



sugar-phosphate backbone

hydrogen-bonded base pairs

(D) DNA double helix

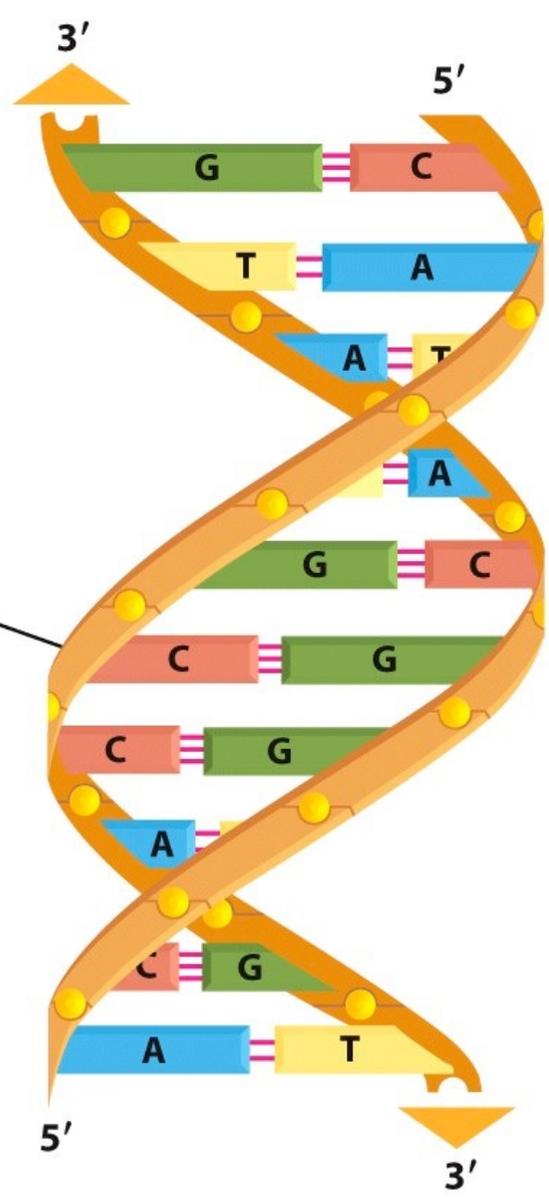
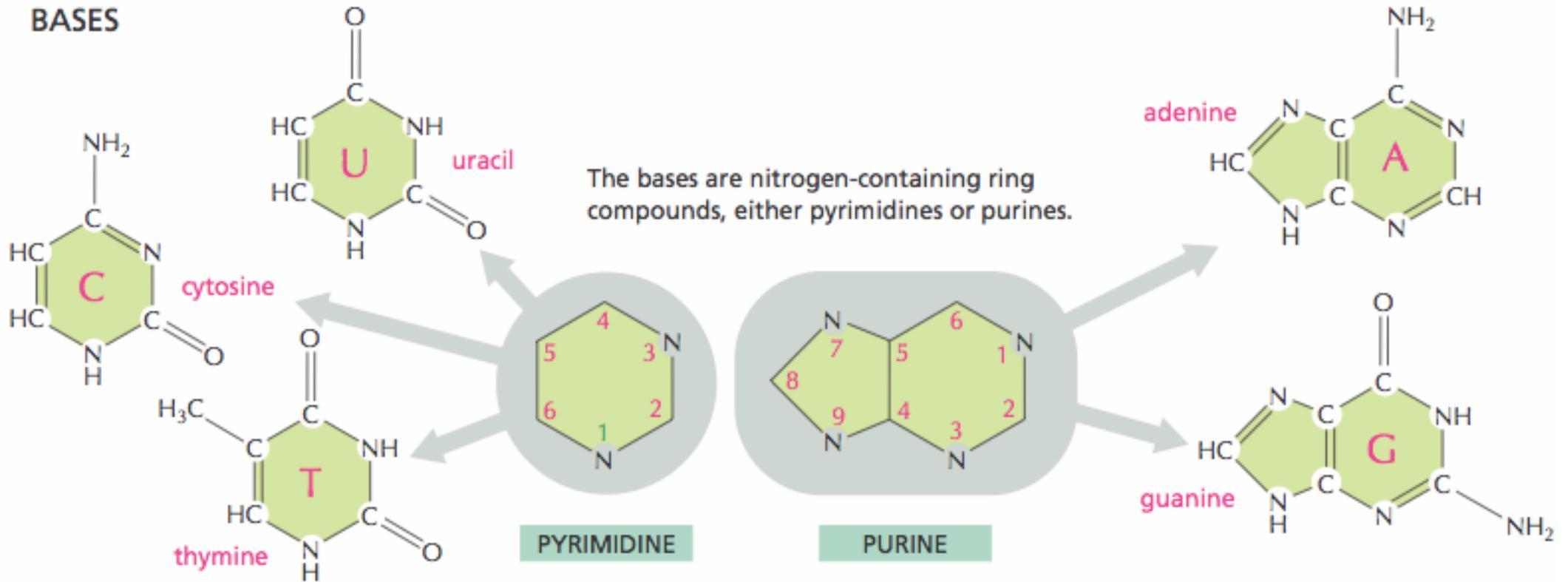
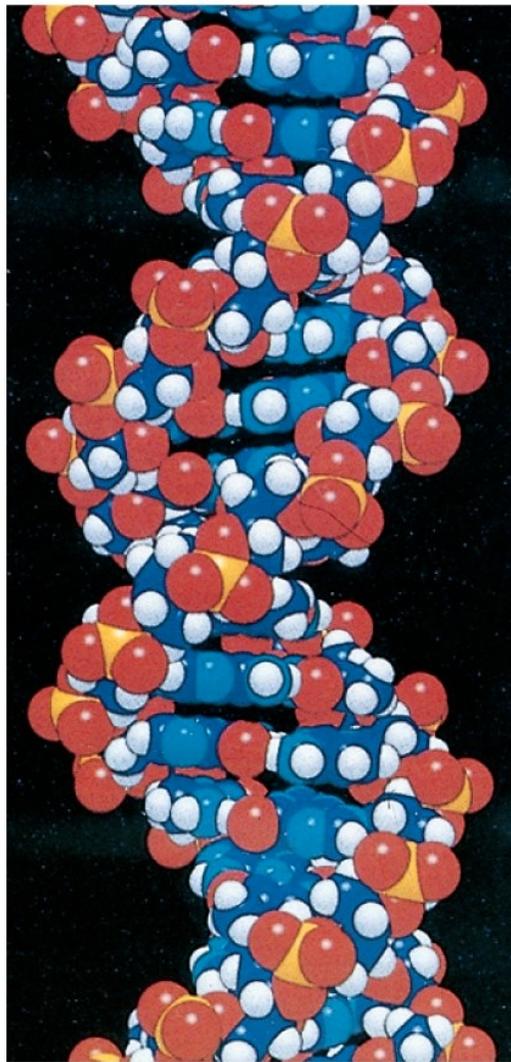


Figure 5-2cd Essential Cell Biology 3/e (© Garland Science 2010)

# BASES



# The DNA double helix has a major and minor groove



minor groove

major groove

The strand *twist around each other* to form a double helix containing 10 base pairs per helical turn.

2 nm

# A DNA molecule

DNA strand (or DNA chain)

The base: **A** (adenine), **C** (cytosine), **G** (guanine), **T** (thymine).

Hydrogen bonds (AT and GC).

The way in which the nucleotide subunits are linked together gives a DNA strand *a chemical polarity*.

- In the *same orientation*.
- Easily *distinguishable*.
- *3' end, 5' end* (3' hydroxyl and 5' phosphate)

**TABLE I****Fidelity Comparison of Thermostable DNA Polymerases Using a *lacIOZ $\alpha$* -Based Fidelity Assay<sup>a</sup>**

| <b>Thermostable DNA polymerase</b>                 | <b>Error rate<sup>b</sup></b> | <b>Percentage (%) of mutated PCR products<sup>c</sup></b> |
|--|-------------------------------|---|
| <i>Pfu</i> DNA polymerase                          | $1.3 \times 10^{-6}$          | 2.6   |
| <i>Taq</i> DNA polymerase                          | $8.0 \times 10^{-6}$          | 16.0  |
| Vent <sub>R</sub> <sup>®</sup> DNA polymerase      | $2.8 \times 10^{-6}$          | 5.6   |
| Deep Vent <sub>R</sub> <sup>®</sup> DNA polymerase | $2.7 \times 10^{-6}$          | 5.4   |
| <i>Tfi</i> DNA polymerase                          | $8.3 \times 10^{-6}$          | 16.6  |
| <i>Tbr</i> DNA polymerase                          | $9.5 \times 10^{-6}$          | 19.0  |
| <i>UITma</i> <sup>™</sup> DNA polymerase           | $55.3 \times 10^{-6}$         | 110.6 <sup>d</sup>  |

<sup>a</sup> Fidelity is measured using a PCR-based forward mutation assay based on the *lacI* target gene.<sup>5</sup>

<sup>b</sup> The error rate equals mutation frequency per base pair per duplication.

<sup>c</sup> The percentage of mutated PCR products after amplification of a 1-kb target sequence for 20 effective cycles.

<sup>d</sup> Some PCR products will exhibit more than one error.

# Complementary base pairs are formed in the DNA double helix

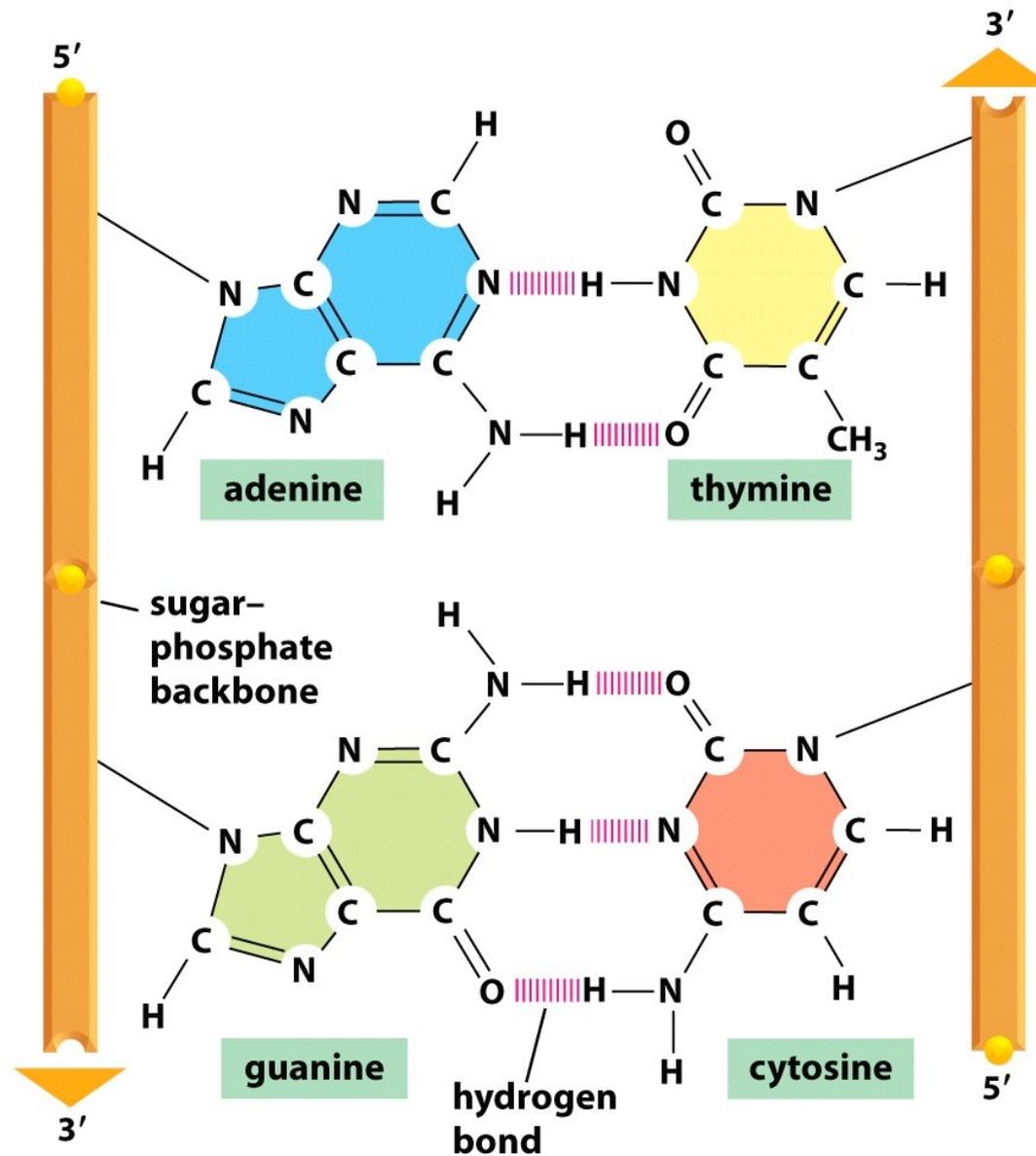


Figure 5-6a Essential Cell Biology 3/e (© Garland Science 2010)

# DNA double helix

## I. Complementary base-pairing

Hydrogen bonds to form *AT and GC* (purine + pyrimidine).

Each base pair is of *similar width, an equal distance* apart along the DNA.

Important for both *copying and repairing the DNA*.

*Antiparallel* (oriented in opposite polarities)

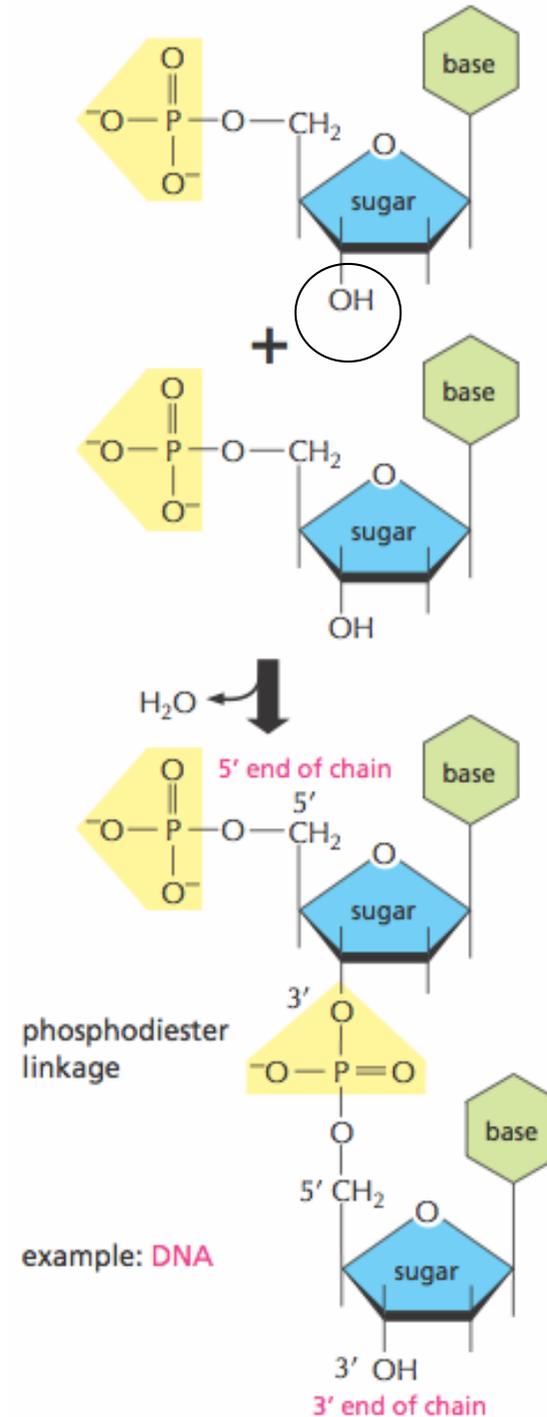
# Primer Melting Temperature:

Primer Melting Temperature ( $T_m$ ) by definition is the temperature at which one half of the DNA duplex will dissociate to become single stranded and indicates the duplex stability. Primers with melting temperatures in the range of 52-58 °C generally produce the best results.

$$T_m = 4(G+C) + 2(A+T)$$

GC 함량이 많아지면  $T_m$  값이 높아짐 (Primer는 보통  $T_m = 50-60$  정도.  
 $T_m$  값이 높아지면 낮은 온도에서도 annealing이 쉽게 됨.

The nucleotides are linked together covalently by *phosphodiester bonds*



The 3' end carries – *OH* group; the 5' end carries a free *phosphate* group

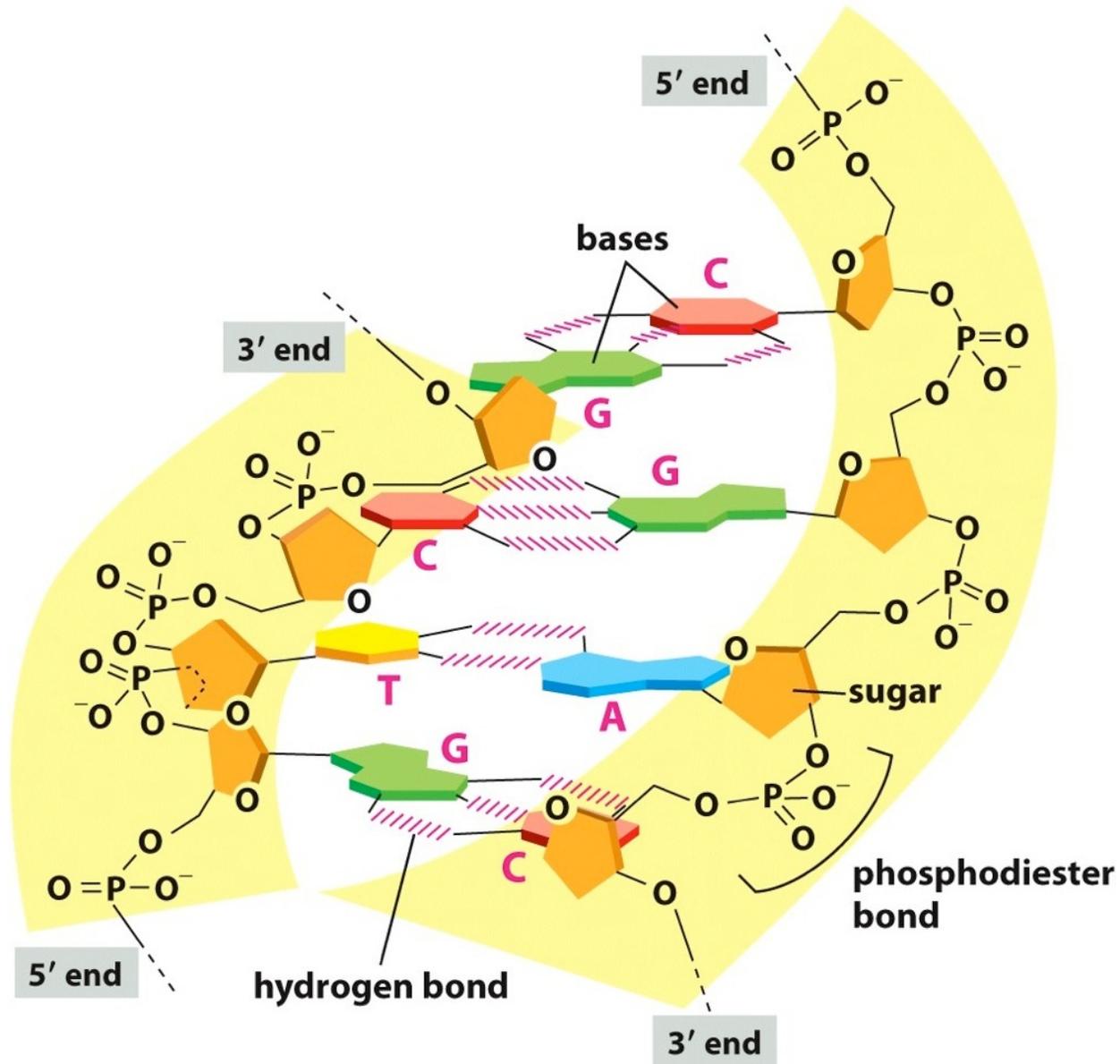


Figure 5-6b Essential Cell Biology 3/e (© Garland Science 2010)

## 2. Held together by base pairing

The nucleotides are linked together covalently by *phosphodiester bonds*

The 3' end carries – *OH group*; the 5' end carries *a free phosphate group*

# Summary

## 1. Complementary base-pairing

- Hydrogen bonds to form *AT and GC* (purine + pyrimidine).
- Each base pair is of *similar width, an equal distance* apart along the DNA.
- Important for both *copying and repairing the DNA*.
- *Antiparallel* (oriented in opposite polarities)

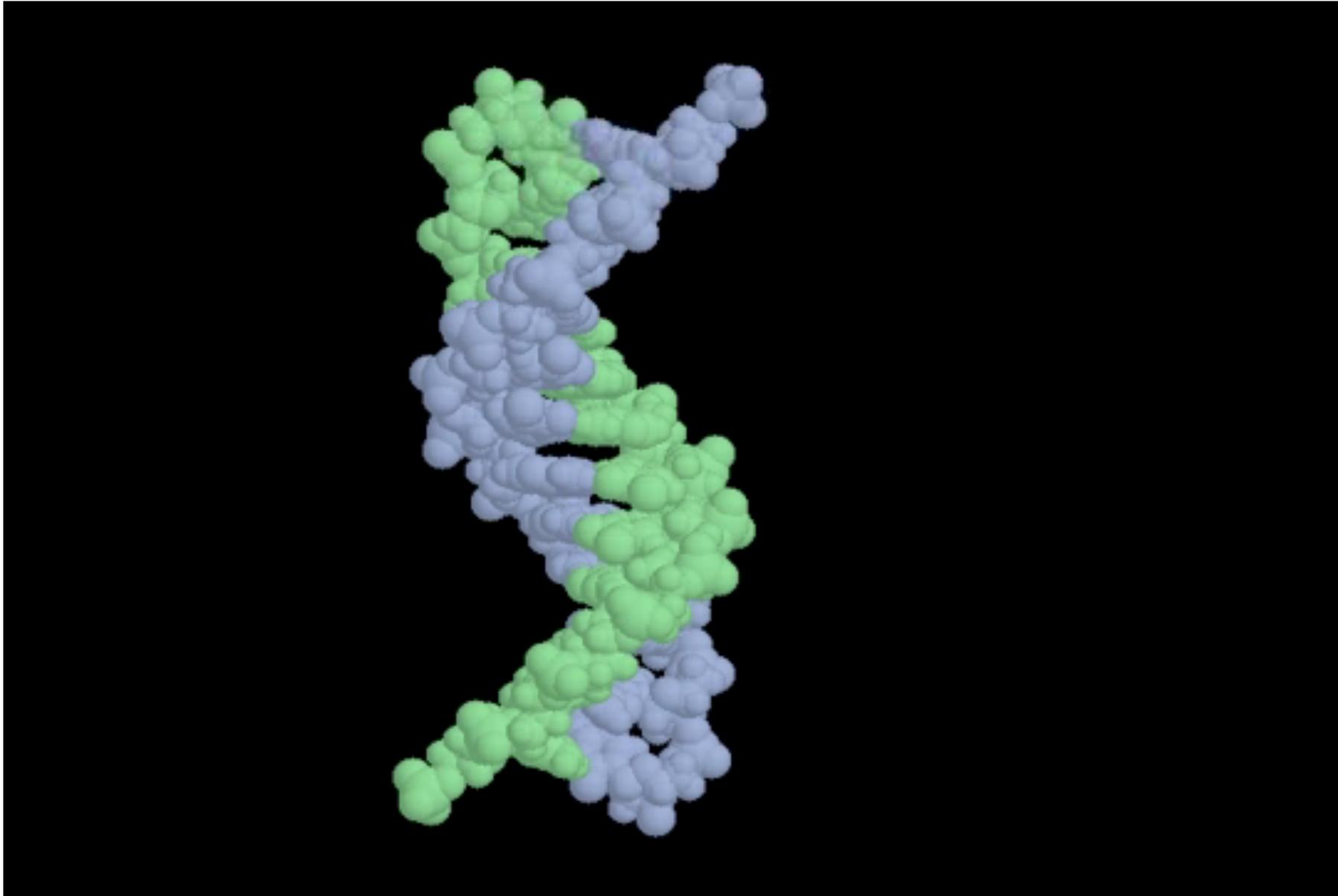
## 2. Held together by base pairing

- The nucleotides are linked together covalently by *phosphodiester bonds*
- The 3' end carries – *OH group*; the 5' end carries *a free phosphate group*.

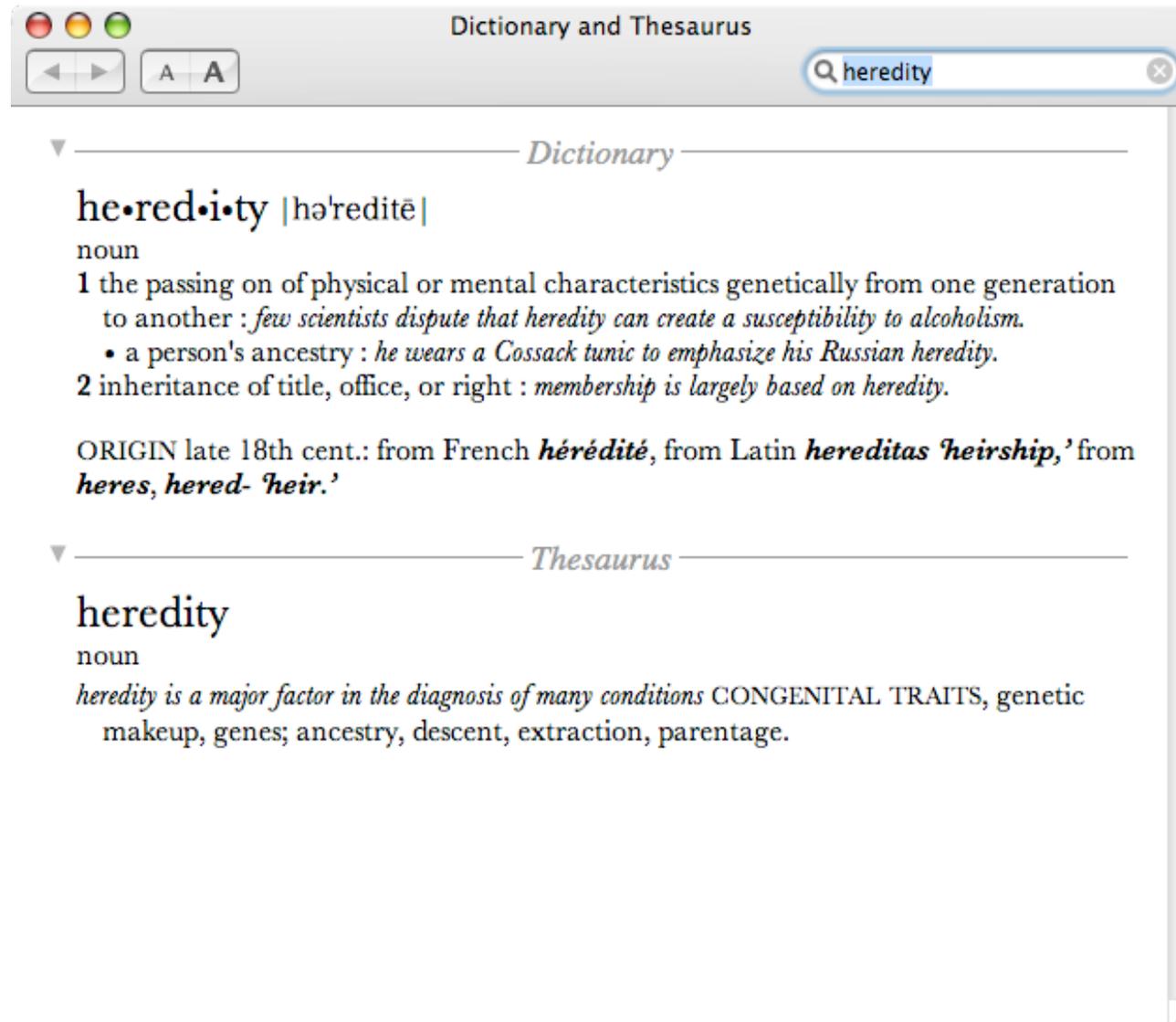
## 3. Major and minor groove

The strand *twist around each other* to form a double helix containing **10** base pairs per helical turn.

# DNA structure



# The structure of DNA provide a mechanism for heredity



Dictionary and Thesaurus

heredity

▼ ————— *Dictionary* —————

**he•red•i•ty** |hə'reditē|  
noun

**1** the passing on of physical or mental characteristics genetically from one generation to another : *few scientists dispute that heredity can create a susceptibility to alcoholism.*

- a person's ancestry : *he wears a Cossack tunic to emphasize his Russian heredity.*

**2** inheritance of title, office, or right : *membership is largely based on heredity.*

ORIGIN late 18th cent.: from French *hérédité*, from Latin *hereditas* 'heirship,' from *heres, hered-* 'heir.'

▼ ————— *Thesaurus* —————

**heredity**  
noun

*heredity is a major factor in the diagnosis of many conditions* CONGENITAL TRAITS, genetic makeup, genes; ancestry, descent, extraction, parentage.

## heredity (유전형질)

How can *the information for specifying an organism* be carried in chemical form?

How is it *accurately copied?* (next chapter)

*Linear messages* come in many forms

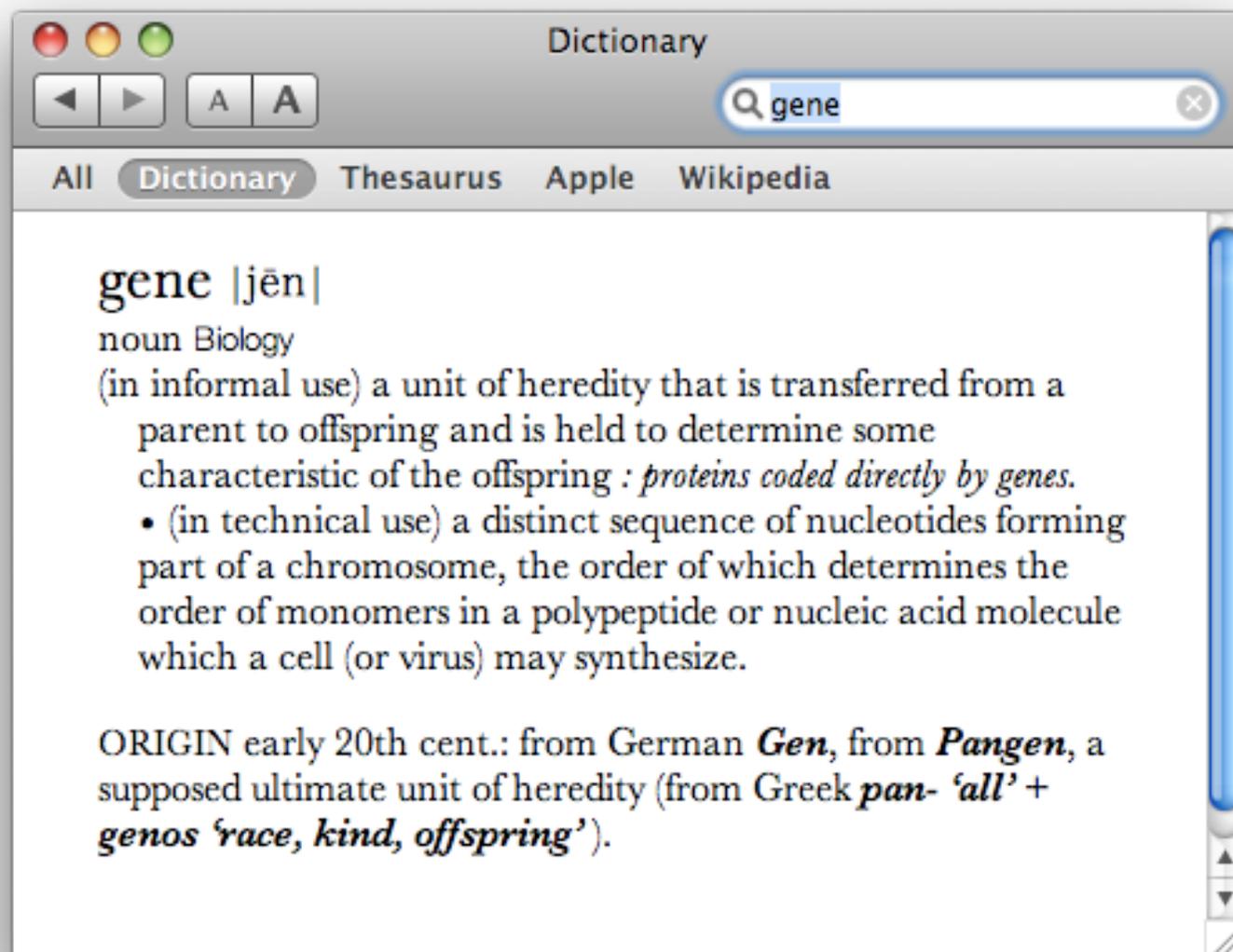
**(A) molecular biology is...**



**(C)** • — • — • • — • •

**(D)** 细胞生物学乐趣无穷

**(E) TTCGAGCGACCTAACCTATAG**



## gene |jēn|

noun Biology

(in informal use) a unit of heredity that is transferred from a parent to offspring and is held to determine some characteristic of the offspring : *proteins coded directly by genes.*

- (in technical use) a distinct sequence of nucleotides forming part of a chromosome, the order of which determines the order of monomers in a polypeptide or nucleic acid molecule which a cell (or virus) may synthesize.

ORIGIN early 20th cent.: from German *Gen*, from *Pangen*, a supposed ultimate unit of heredity (from Greek *pan-* 'all' + *genos* 'race, kind, offspring').

*Genes* contain information to make *proteins*

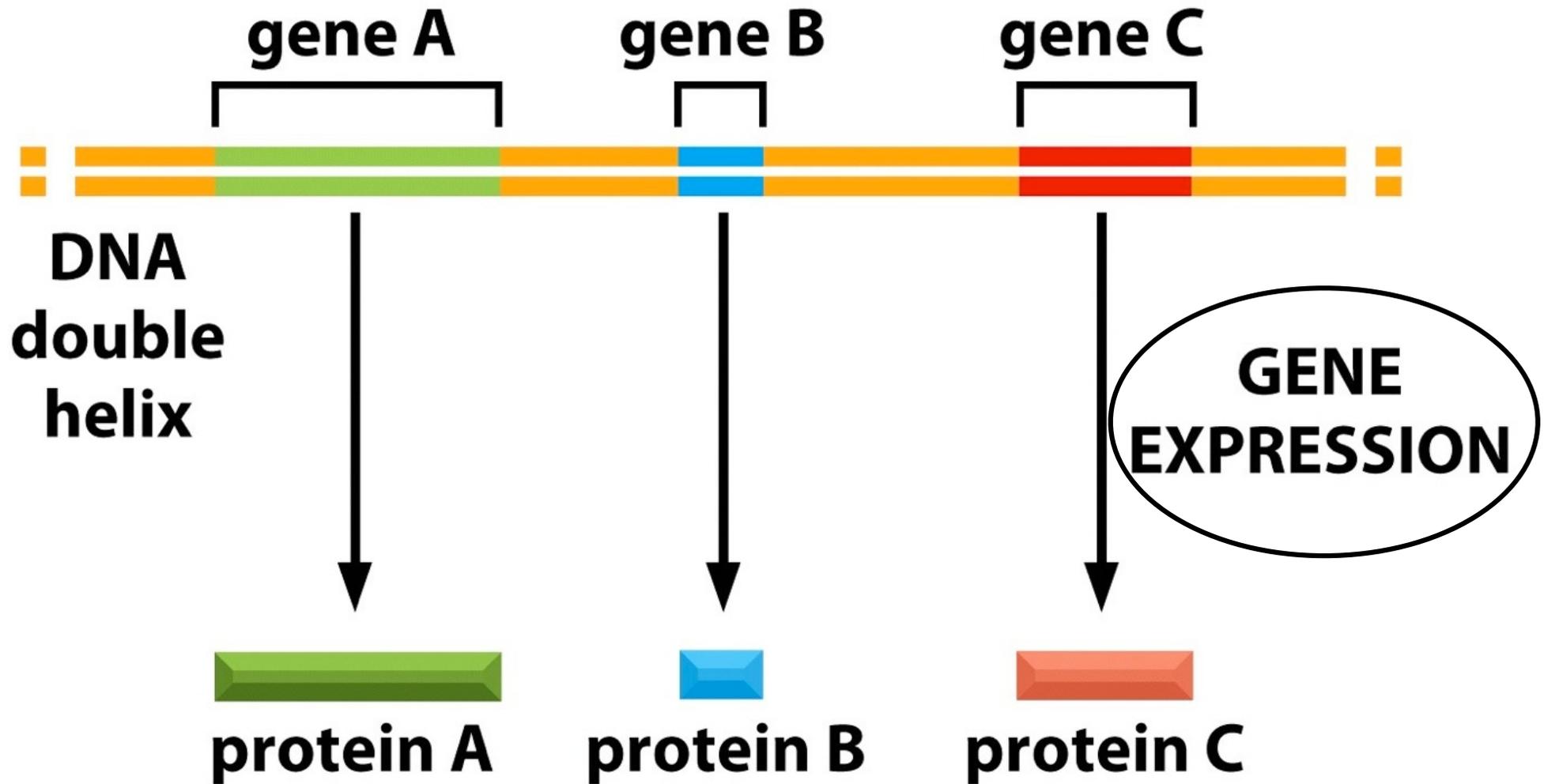


Figure 5-9 Essential Cell Biology 3/e (© Garland Science 2010)

```

CCCTGTGGAGCCACACCCCTAGGGTTGGCCA
ATCTACTCCGAGGAGCAGGGAGGGCAGGAG
CCAGGGCTGGGCATAAAAGTCAGGGCAGAG
CCATCTATPTGCTTACATTTGCTCTGACAC
AACTGTGTTTCACTAGCAACTCAAAACAGACA
CCATGGTGCACCTGACTCCTGAGGAGAAGT
CTGCCGTTACTGCCCTGTGGGGCAAGGTGA
ACGTGGATGAAGTTGGTGGTGAAGCCCTGG
GCAGSTTGGTATCAAGGTTACAAGACAGGT
TTAAGGAGACCAATAGAACTGGGCATGTG
GAGACAGAGAAGACTCTTGGTTTCTGATA
GGCACTGACTCTCTCTGGCTATTGGCTAT
TTTCCACCCTTAGGCTGCTGGTGGTCTAC
CCTTGGACCAGAGGTTCTTTGAGTCCCTT
GGGATCTGTCCACTCCTGATGCTGTATG
GGCAACCCTAAGGTGAAGGCTCATGGCAAG
AAAGTGTCTGGTGGCTTTAGTGATGGCTG
GCTCACTGGACAACCTCAAGGGCACCTTT
GCCACACTGAGTGAAGCTGCACTGTGACAAG
CTGCACGTGGATCCTGAGAACTTCAGGCTG
AGTCTATGGGACCCCTGATGTTTCTTTCC
CCTCTTTTCTATGGTTAAGTTCATGTCAT
AGGAGGGGAGAGTAAACGGTACAGTTT
AGAAATGGAAACAGACGAATGATTGCATCA
GTGTGGAGTCTCAGGATCGTTTAAAGTTT
TTTTATTGCTGTTCATAACAATGTTTTC
TTTTGTTAATTCCTGCTTTCTTTT
CTTCTCCGCAATTTTACTATTACTTAA
TGCCCTAAGATTTGTATACAAAAGGAA
TATCTCTGAGATACATTAAGTAACTTAAA
AAAAACTTTACACAGCTGCTTAGTACATT
ACTATTTGGAATATATGTGTCTTATTGTC
ATAATCATAAATCTCCCTACTTTATTTCTT
TTATTTTAAATGATACATAATCATTATAC
ATAATTAAGGTTAAGTGAATGTTTAA
TATGTGTACACATAATGACCAAAATCAGGGT
AATTTTGCATTTGTAATTTTAAAAAATGCT
TTCTTCTTTAAATACTTTTTTGTTAATC
TTATTTCTAATACTTTCCCTAATCTCTTTC
TTTCAGGGCAATAATGATACAATGATCAT
GCCCTTTGCACCAATCTAAAGAATAACAG
TGATAATTTCTGGGTAAAGCAATAGCAAT
ATTTCTGCATATAAATATTTCTGCATATA
ATTGTAACGTGATGAAGAGGTTTCATATG
CTAATAGCAGCTACAATCCAGCTACCATT
TGCTTTTATTTATGGTGGGATAAGGCTG
GATTATCTGAGTCCAAGCTAGGCCCTTTT
GCTAATCATGTTCTATACCTCTTATCTTCT
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TTTTAAAAATAAAGAAATGATGAGCTGTYC
AAACCTTGGGAAAATACACTATATCTTAAA
CTOCATGAAAGAAGGTGAGGCTGCAACCAG
CTAATGCACATTTGGCAACAGCCCTGATGC
CTATGCTTATTTCACTCCCTCAGAAAAGGAT
TCTGTAGAGGCTTGATTTGCAGGTTAAG
TTTTGCTATGCTGATTTTACATTACTTAT
TGTTTTAGCTGTCTCATGAATGCTTTTTT

```

## Gene sequences can be written and read like any text

- human  $\beta$ -globin gene.
- the sequence (seq) should be read from left to right in successive lines
- the DNA seq highlighted in yellow color show the three regions of the gene that specify the amino seq of the  $\beta$ -globin protein

Figure 4–7. Molecular Biology of the Cell, 4th Edition.



DNA\_1kb\_up\_down : SEQUENCE

Selection: 1001 -> 3100 = 2100

4.100kb

10 20 30 40 50 60 70 80 90 100 110 120

CCGTCACAGCCGCAAAATCGAATTCCTTTGAGCAAAATTTGGGATCAGCAATTTAATGAGTAAATGGATGGATTTTCCTCGTTCAAAATTTGACGGCCGCAAGCATATAAAATCAATAGCT 120  
 AAAGTAAAACCGAGAAGTCAACAATAATCAATATGTTCCCAATTTAGATTGACTACAGCCGACTAGCAACAATAACCGTTTATAGCATATAAGCGCTTATAAATTTCAATATG 240  
 CTCGGGACCTTTTCGGCAATGGTCTGGTAAATCCCTTTGCGCTAGAAATGAACACTAGGTAACAATCACCTTCCTGGAATGAGATTTAGTCATATAGTGTTTTCCTCGAGCTTAAAGT 360  
 ATAGAGGTATATAACAAATTTTGTGTGATCTTTTATGACATTTTGTAAATAAGAAATTAACAACAGTAAATTTGAAAGATTAGTTAAAGTGGTGTATGCGAGCTTTTCCATTTATATAT 480  
 CTGTTAATAGATCAAAATATCCGCTTCGCTGATTAATTAACCCAGAAATAAGGCTAAAAACATAACGCAATATCATCCATGTTGTTAATTTGATTCGTTAAATTTGAAGGTTTGTGG 600  
 GGGCAGGTTACTGCCAATTTTCCCTCTCAAAACATAAAAGCTAGTATGTTGAAATCTTTATGTTTCGGAGCAGTGGCGGCGAGGCACTATCGCTTTAGCAACGCGACCGGTGAAG 720  
 ACGAGGACGCACGGAGGAGTCTCCCGTCGGAGGGCTGTCGCCCGCTCGGCGCTTCAATCCGTACTCAATAATAGCAATGAGCAGTTAAGCGTATTACTGAAAAGTTCAAGAGAA 840  
 GTTTTTTAAAGCTAAGATAATGGGGCTCTTACATTTCCCAACAATATAAGTAAGATTAGATATGGATATGATATATGTTGGTAAATGCGCATGATAATGATATATAAATCTTTTGGCTCC 960  
 ATCAAAAAAAAAAAGTAAGAATTTTGAATAATCAATAAATGACAGCTCAGTTACAAAAGTGAAGTACTTCTAAAATTTGTTTTGGTTACAGGTGGTGGTGGATACATTTGGTTCCACAC 1080  
 TGTGGTAGAGCTAAATTTGAGAATGGATATGACTGTGTTGTTGCTGATAACCTGTGGAATTCACATTTGATGTTCTGAGCCAGGTTAGAGGTTGACCAAGCATCACATTTCCCTCTATGA 1200  
 GGTGATTTGTGTGACCGAAAAGGCTGGAAGGTTTCAAGAATAATAAAATTTGATTCGGTAATTCACCTTGTGGTTTTAAAGGCTGAGGTGAATCTACACAAATCCCGCTGAGATA 1320  
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 TATGATTCCTATCCCGAGAAGAATGTTCCCTTAGGGCTACTAATCCGTATGGTCTACAGAAATACGCCATTGAGAATATCTTGAATGATCTTACAAATAGCGCAAAAAAGTTGGAAGTT 1560  
 TGCATCTTCGGTATTTTAAACCAATTTGGGCGACATCCCTCTGGATTAATGGAGAGATCCCGTAGGTATACCAACAATTTGTTGCCATATATGGCTCAAGTAGCTGTTGGTAGGGC 1680  
 CGAGAAGCTTTACATCTTCGGAGACGATATGATTTCCAGAGATGGTACCCGATCAGGGATATATCCACGTAGTTGATCTACGAAAAGGCTATATTCGAGCCCTGCAATACCTAGAGGC 1800  
 CTACAATGAAAATGAAGTTTGTGCTGAGTGGAACTTGGGTTCCGGTAAAGGTTCTACAGTTTTTGAAGTTTATCATGCAATTCGCAAAAGCTTCTGATTTGATCTTCCATACAAGT 1920  
 TACGGGCGAGAAGCAGGTTGATGTTTGAACCTGACGGCTAAACCAGATAGGGCCAAACCGCAACTGAAATGGCAGCCGAGTTGCAAGCTTCCGCAAGGATTTATGGAATG 2040  
 GACTACTGAGAATCTTTTGGTACCAGTTAAGGGGTGTCGAGGCGAGATTTTCGCTGAAGATATGCGTTATGACGCAAGATTTGACTATTGGTGGCGGCGACCAAGTTTCAAGCCAC 2160  
 GTTGGCAATTTGGGCGCCAGCATTTGTTGACCTGAAAGTGAAGCGGCAATCAGTTGTTCTTGGCTATGAAAATGAGGAGGGTATTTGAAATCTGATAGTGCCTATATAGGGCCACAGAT 2280  
 CGGCAAGTATGCTAATCTGATTTTCGAAAGGTAAGTTTGTATGCAACAAGACTATCAGTTAAACCGTTAATAGCGGCGTTAATGCGAATCATAGTATATCGGTTCTTTCCACAGAAA 2400  
 AAGATTTTGGGACCCATCATTCAAAATCTTCAAGGATGTTTTTACCGCGGAGTACATGCTGATAGATAAGTGAAGGACACCGAATTTCCAGGTGATCTATTTGGTAAACATACAGTA 2520  
 TACTGTGAAGCTTGGCCAAAAAGTTTGGAAATGTTATATAAGGTAATTTGACTGCTGGTGAAGCGACCCAAATAAATTTAAACAATCATAGTTATTTCAATCTGAACAAGCCATATGG 2640  
 AGACATTTGAGGGTACGGAGATTTAGTGGCTTAAAAAATCTGTTGATGTCGACAAAAATGATTTCTCAGGGTAAATCTGCTGATAGAGAAATTTGCTACTTTAACCTACAAA 2760  
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 GTTCAATTCGTACTTTTGTATACCTCAACAATTTGCGAAGCGCTTCAAGTGAAGAAATATAAGGAAAAGTTGTAATATTTATTTGGTATTTCTGTTGTTGAAGTAGAGGGGTAAT 3480  
 TTTTCCCTTTATTTGTTGATCACTTTAAATTTGCTTTGCCCTCCTTTTGGAAAGCTATACCTCGGAGCAGTGTGAGCGAAGGCTCATAGATATATTTCTGTGATTTCCCTTAA 3600  
 CCCCCAAAATAAGGGAAGGTTCCAAAAAGCTCGGACAACTGTTGACCGTGTCCGAAAGGACTGGCTATACAGTGTTCACAAAATAGCCAAAGTGAATAATGTTGATGTTGTTGAG 3720  
 TTAGTTTGGCTAGCAAGATATAAAGGAGGCTGGAAATATTTATGGGCTATATTTAGGAGACATCAACATGATAAAAAAAGCAAGTGAATTTCCCTCAAAATGACTTTCAAGAA 3840  
 TTTGATTTTCTAGCAATTTCCATAGAGCTTACAACTCAACCGATTTAGTTTCTCCACACAGAGCTTAAAGACCTTGGTTAGGTTCAACAGGCTGCTTCAAGGCTTGG 3960  
 ACAGCTCAATGATGATCAAAATGCTATCTATGTCCTGGTAAACAAAAGAGCTACTGGTAACCTAAACCAAGATATGAATCAACGTATATTTTCCCAATGATATGCTGGCTTAGG 4080  
 CTCGATCAACCTATTTTACC 4100

TGA: Stop codon

# GallO gene (2,100 bp)

- Promoter
- ORF (open reading frame)
- 3'-UTR

|                        |        |
|------------------------|--------|
| Length (a.a.)          | 699    |
| Molecular Weight (Da)  | 78,195 |
| Isoelectric Point (pI) | 5.84   |

Orf Search

1 MTAQLQSEST SKIVLVTGGA GYIGSHTVVE LIENGYDCVV ADNLSNSTYD  
 51 SVARLEVLTK HHIPFYEDVL CDRKGLEKVF KEYKIDSVIH FAGLKAVGES  
 101 TQIPLRYHYN NILGTVVLL LMQQYNVSKF VFSSSATVYG DATRFPNMIP  
 151 IPEECPLGPT NPYGHTKYAI ENILNDLYNS DKKSWKFAIL RYFNPIGAHP  
 201 SGLIGEDPLG IPNLLPYMA QVAVGRREKL YIFGDDYDSR DGTPIRDYIH  
 251 VVDLAKGHIA ALQYLEAYNE NEGLCREWNL GSGKGSTVFE VYHAFCKASG  
 301 IDLPYKVTGR RAGDVLNLT A KPDRAKRELK WQTELQVEDS CKDLWKWTE  
 351 NPFQYQLRGV EARFSAEDMR YDARFVTIGA GTRFQATFAN LGASIVDLKV  
 401 NGQSVVLLGYE NEEGYLNPDS AYIGATIGRY ANRISKGLFS LCNKDYQLTV  
 451 NNGVNIHSS IGSFHRKRF L GPIIQNSPKD VFTAEMYKLD NEKDTEFFGD  
 501 LLVTIQYTVN VAQKSLEMYV KGLTAGEAT PINLTNHSYF NLNKPYGDTI  
 551 EGTEIMVRSK KSVDDVKNMI PTGNIVDREI ATFNSTKPTV LGPKNPQFDC  
 601 CFVVDENAKP SQINTLNNEL TLIVKAFHPD SNITLEVELST EPTYQFYTG  
 651 FLSAGYEARQ GFAIEPGRYI DAINQENWKD CVTLKNGETY GSKIVYRFS\*

Calculator

700

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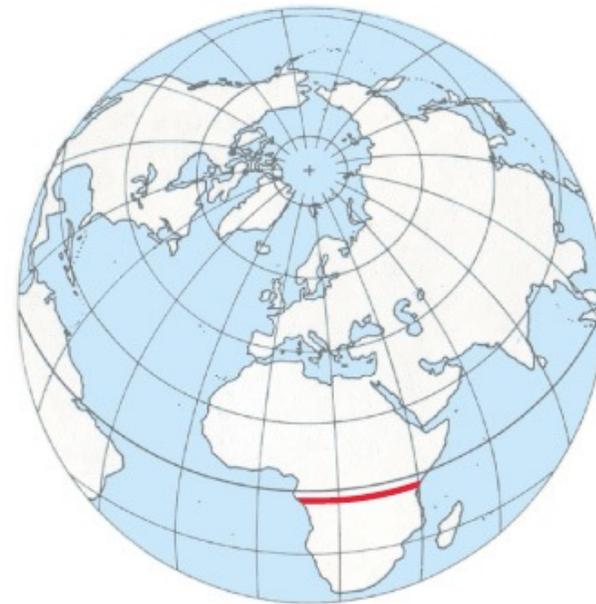
Clear

# The Structure of Eucaryotic Chromosomes

Human genome :  $3.2 \times 10^9$  nt over 24 chromosomes.  
Human 32억개의 Nucleotide 쌍으로 구성 ( $3.2 \times 10^9$  nt)  
 $3.2 \times 10^9$  mm =  $3.2 \times 10^8$  cm =  $3.2 \times 10^6$  m =  $3.2 \times 10^3$  km  
(만일 mm단위로 그린다면 Africa를 횡단할 수 있는 길이)



(A)



(B)

Figure 4-16. Molecular Biology of the Cell, 4th Edition.

Fig. Scale of the human genome

If each nucleotide pair is drawn as 1 mm as in (A), then the human genome would extend 3,200 km, far enough to stretch across the center of Africa (B).

# 101년

|   |   |   |   |
|---|---|---|---|
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|---|-----------------|----------------------|
| ☆ | 53,333,333.3333 | 3200000000 ÷ 60      |
| ☆ | 888,888.888889  | 53,333,333.3333 ÷ 60 |
| ☆ | 37,037.037037   | 888,888.888889 ÷ 24  |
| ☆ | 101.471334348   | 37,037.037037 ÷ 365  |

5천3백 분

8십8만 시간

3만7천 일

101년

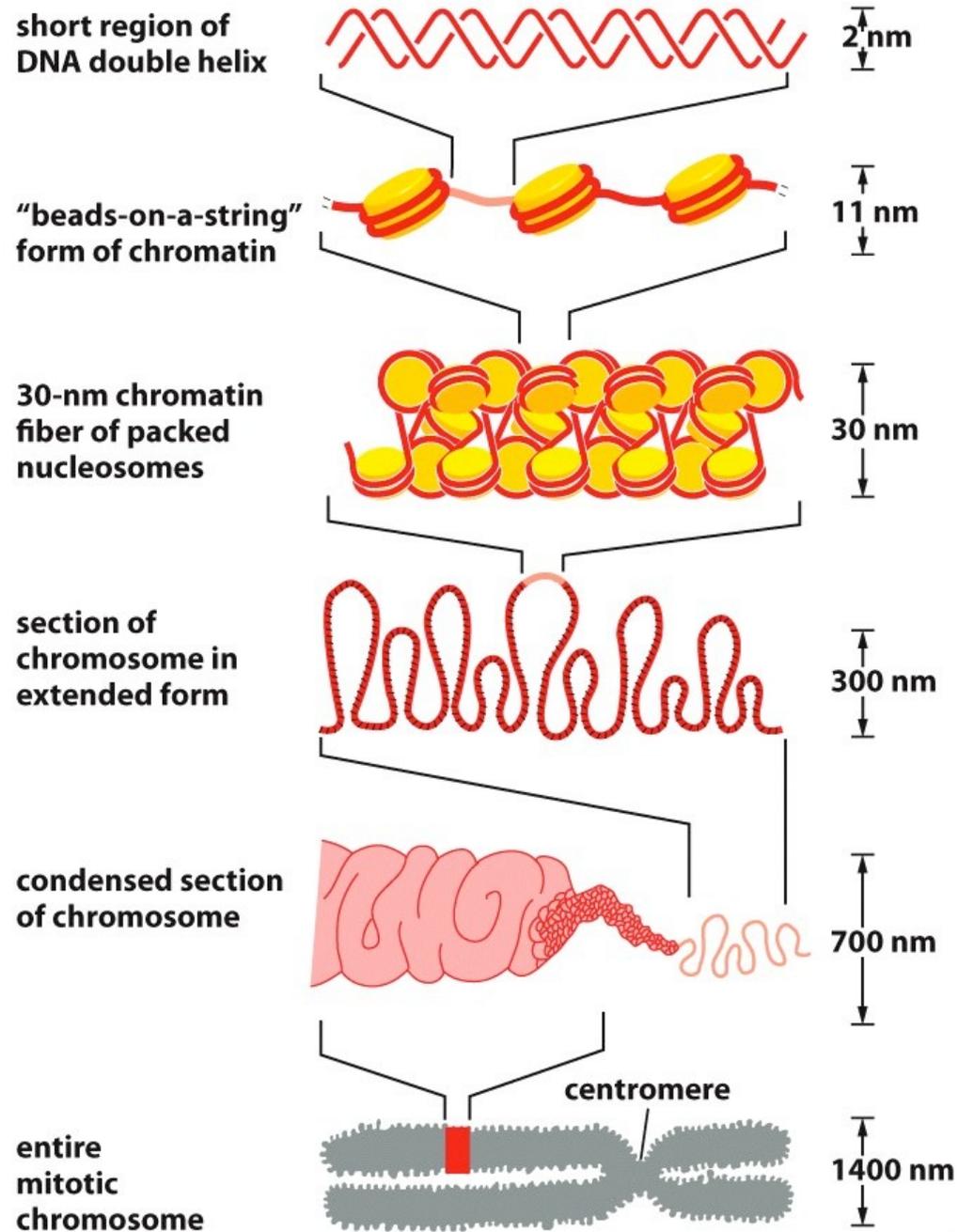
# Backgrounds

Each human cell contains about *2 m of DNA*; yet the cell *nucleus* is only *5 to 8  $\mu\text{m}$*  in diameter (the equivalent of trying to fold 40 km of extremely fine thread into a tennis ball).

In eukaryotic cells, enormously long double-stranded DNA molecules are *packaged into chromosomes*.

The complex task of packing DNA is accomplished by *specialized* *proteins* that bind to and fold the DNA.

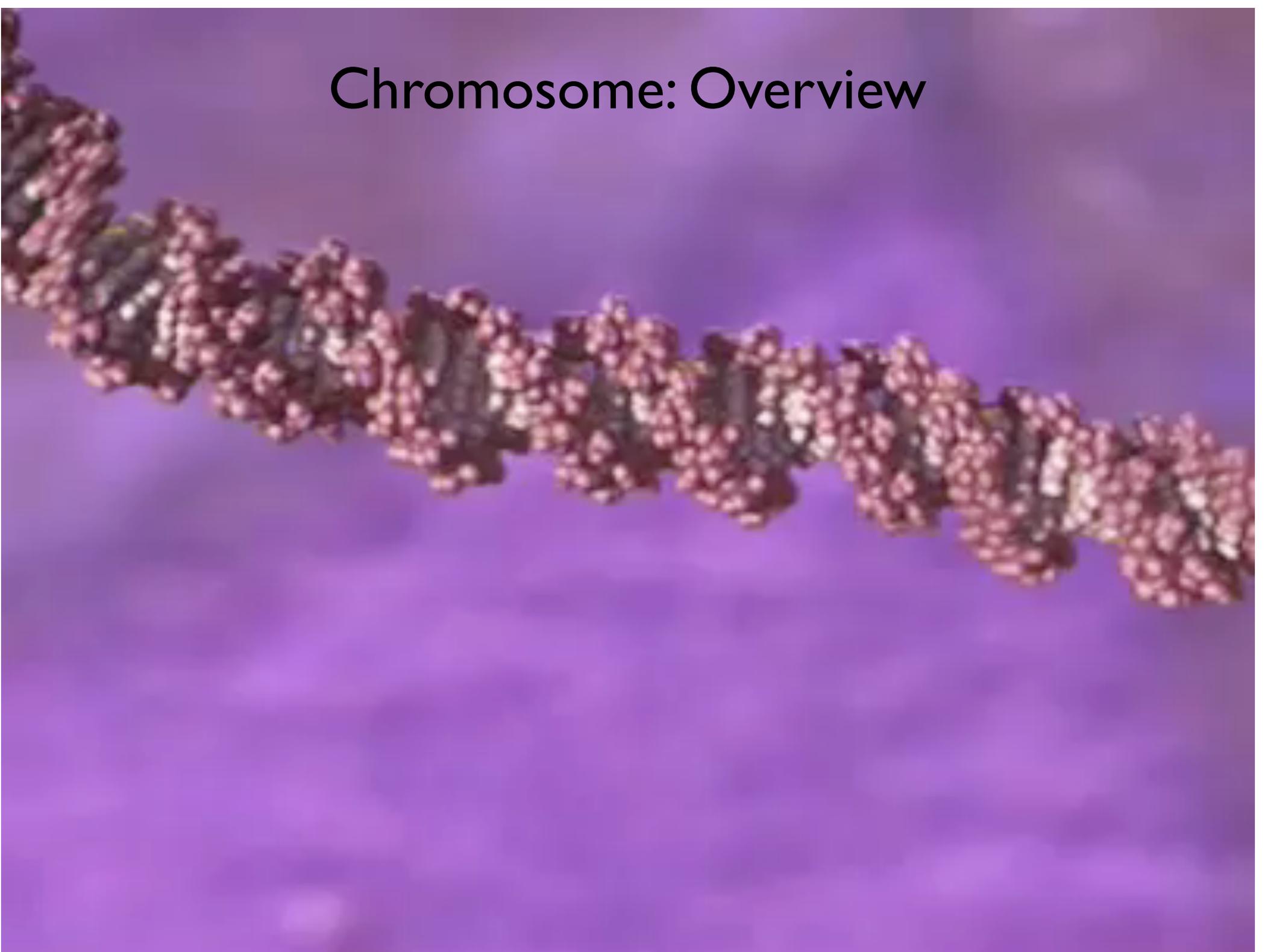
Amazingly, the DNA is compacted in a way that allows it to *remain accessible to* all of the enzymes and other proteins that *replicate it, repair it, and direct the expression of its gens*.



**NET RESULT: EACH DNA MOLECULE HAS BEEN PACKAGED INTO A MITOTIC CHROMOSOME THAT IS 10,000-FOLD SHORTER THAN ITS EXTENDED LENGTH**

Figure 5-25 Essential Cell Biology 3/e (© Garland Science 2010)

# Chromosome: Overview



# Eucaryotic DNA is *packed into multiple chromosomes*

**Chromosomes:** The human genome contains about  $3.2 \times 10^9$  (3.2 billion) nucleotides distributed over 24 chromosomes.

**Chromatin:** Each chromatin consists of a single, enormously long linear DNA molecules associated with proteins that fold and pack the fine thread of DNA into a more compact structure. Also associated with proteins in gene expression, DNA replication, and DNA repair.

**Homologous chromosomes** (상동염색체, 22쌍) Two copies of each chromosome, one inherited from the mother and one from the father.

**Sex chromosomes** (성염색체, 1쌍): X and Y chromosome.

- *DNA hybridization*: the technique uses a set of DNA molecules coupled to fluorescent molecules to “paint” each chromosome a different color.
- *Human karyotype*: a display of the full set of **46** human chromosomes.

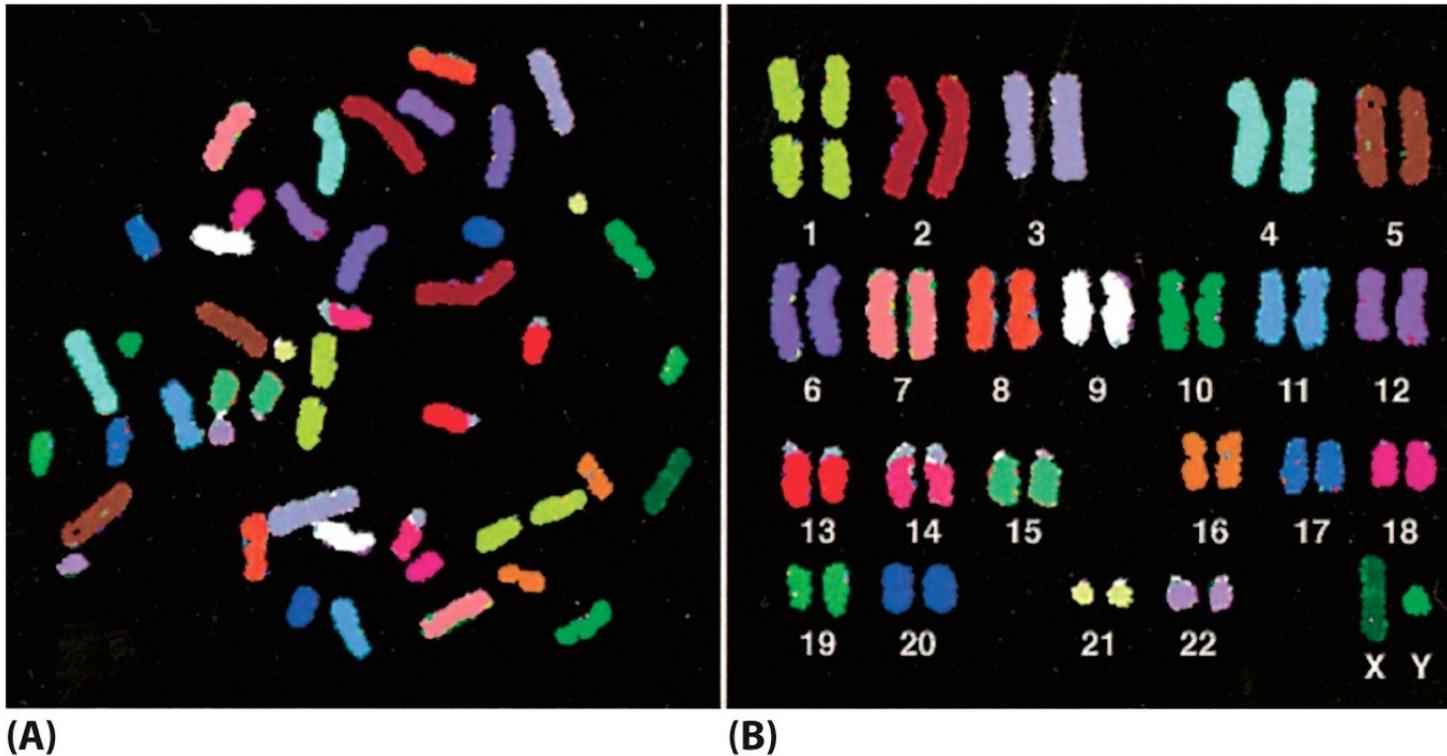
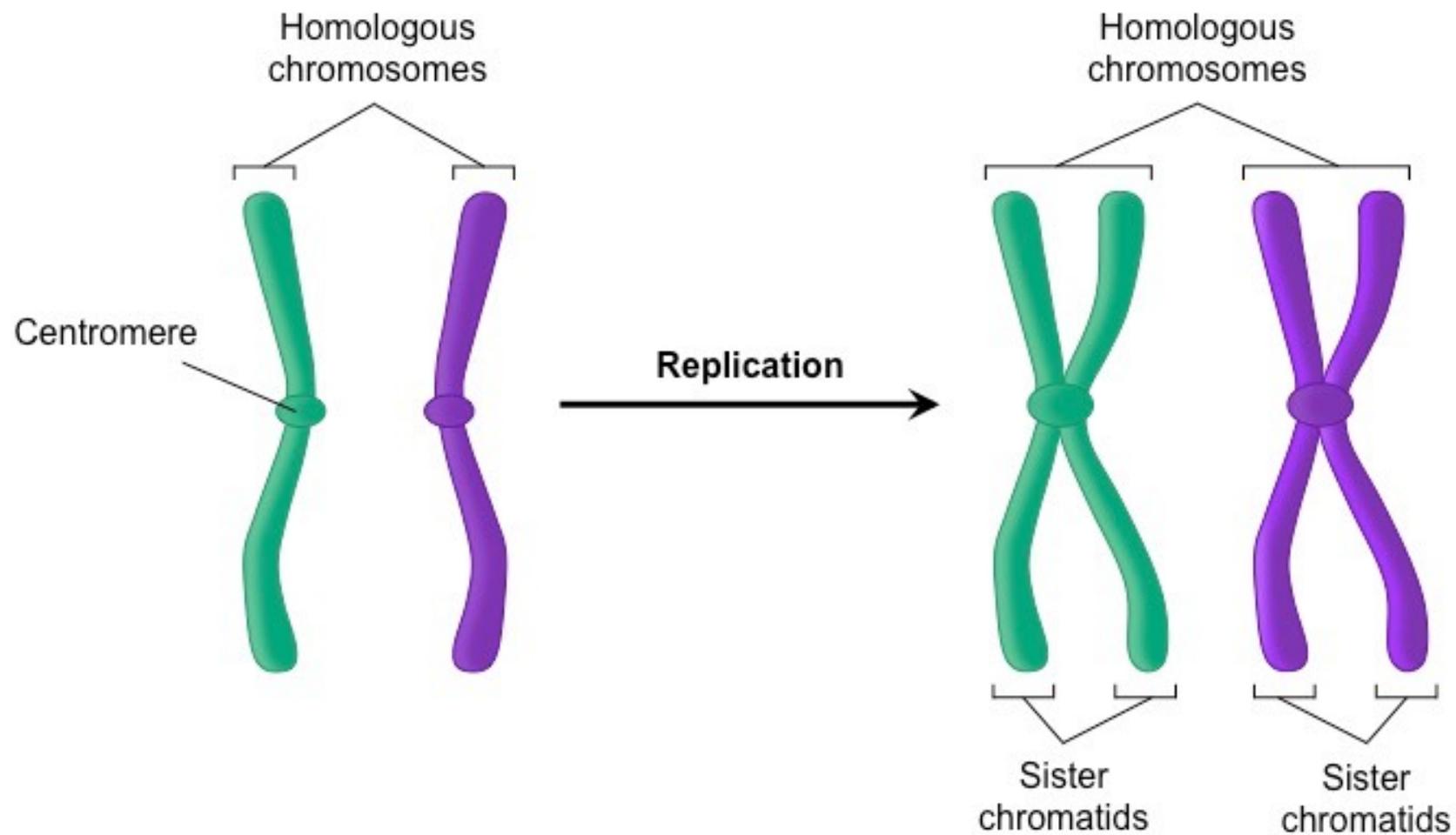
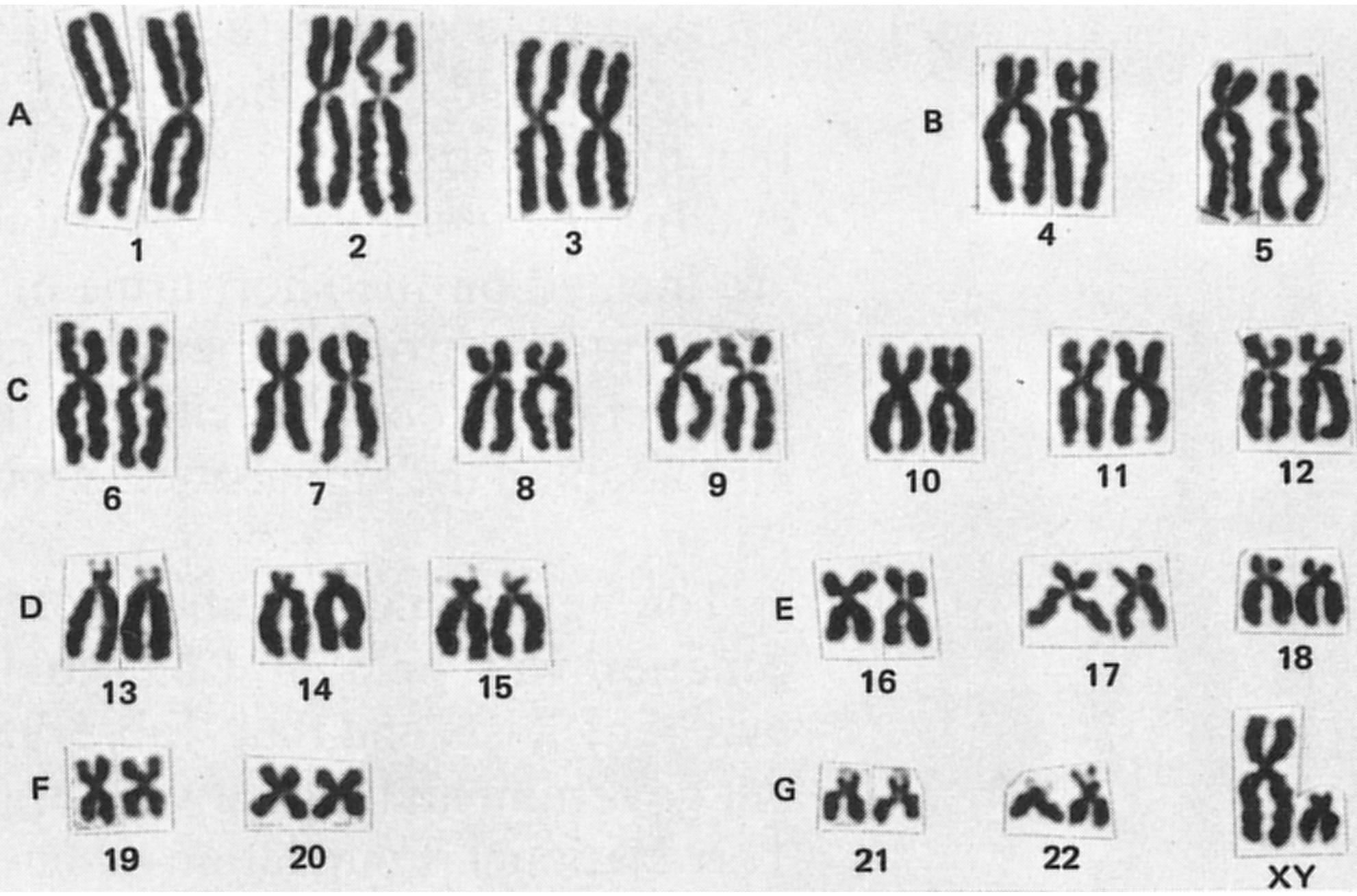
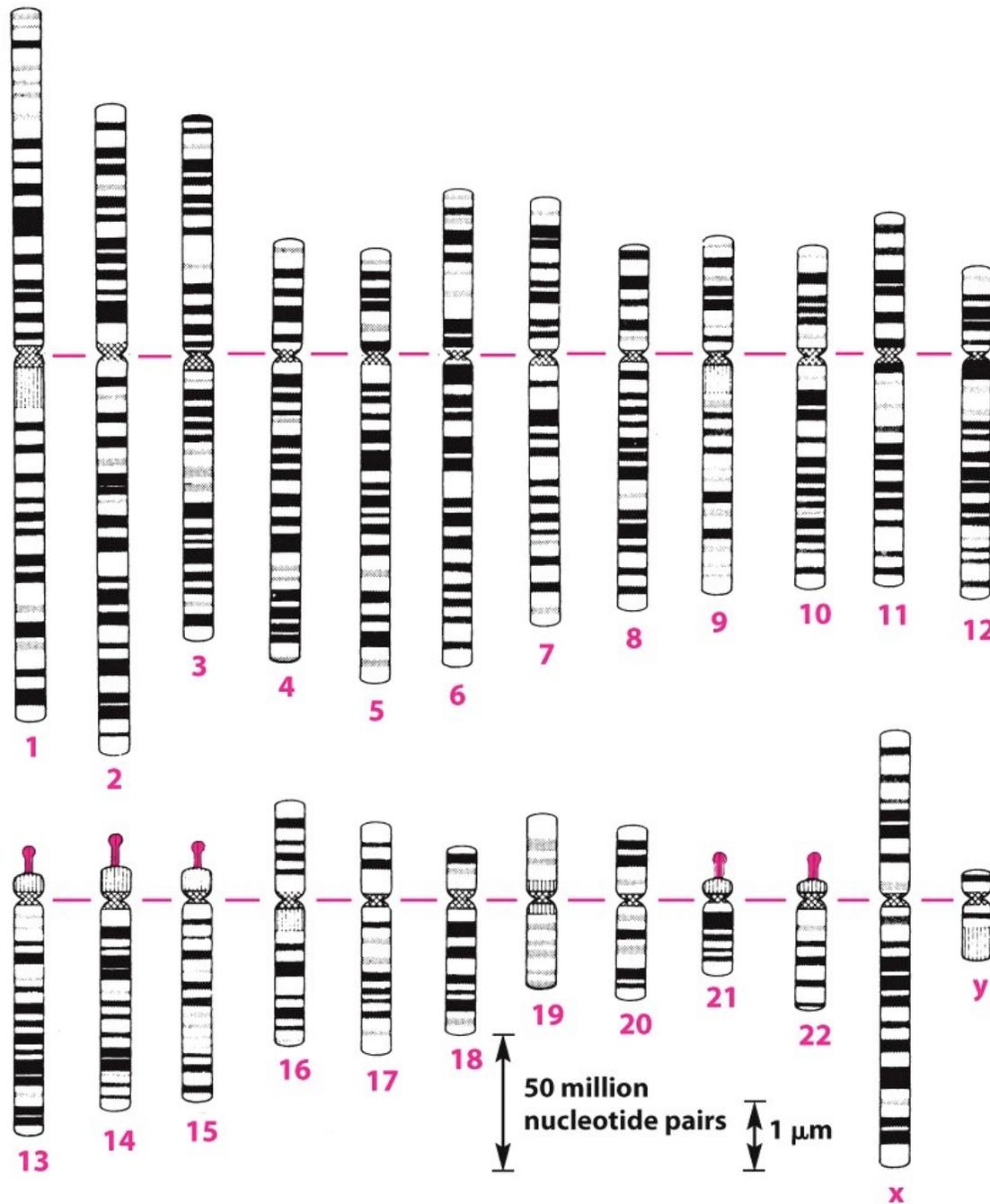


Figure 5-10 Essential Cell Biology 3/e (© Garland Science 2010)







Unique banding patterns allow the identification of each human chromosome

- To stain the chromosomes with dyes that bind to certain types of DNA sequences.
- These dyes mainly distinguish between DNA that is rich in A-T nucleotide pairs and DNA that is G-C rich, and they produce a striking and reliable pattern of bands along each chromosome.
- *Giemsa stain*: produce dark bands in AT rich region.
- Giemsa stain is named after German chemist and bacteriologist Gustav Giemsa.
- Giemsa's solution is a mixture of methylene blue, eosin, and Azure B.

Figure 5-11 Essential Cell Biology 3/e (© Garland Science 2010)

## Abnormal chromosomes are associated with some inherited genetic defects

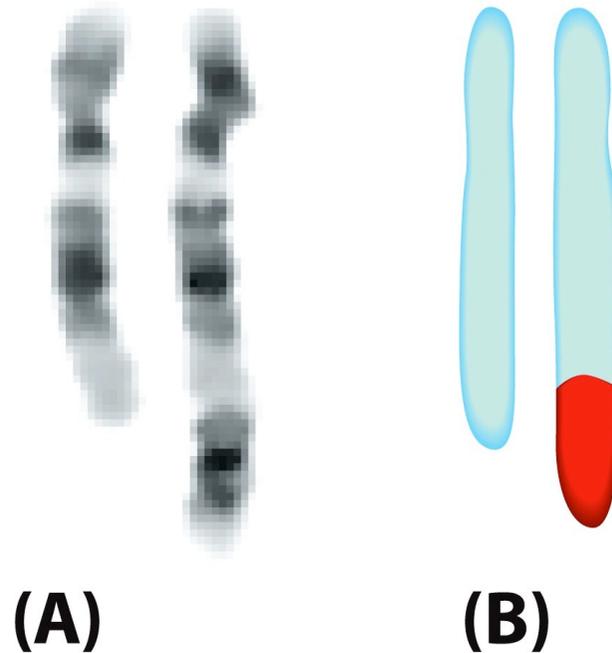


Figure 5-12 Essential Cell Biology 3/e (© Garland Science 2010)

(A) Inherited ataxia (운동실조). The patient has one normal Chromosome 12 (left) and one aberrant chromosome 12  
(B) Chromosome 4 DNA “painted” red and the parts corresponding to Chromosome 12 DNA painted blue.

# Chromosomes contain *long strings of genes*

The most important function of chromosomes is *to carry genes (the functional units of heredity)*

**Gene:** a segment of DNA that contains the instructions for *making a particular protein.*

(cf, Some genes produce an *RNA* molecules)

# Genes are arranged along the chromosomes

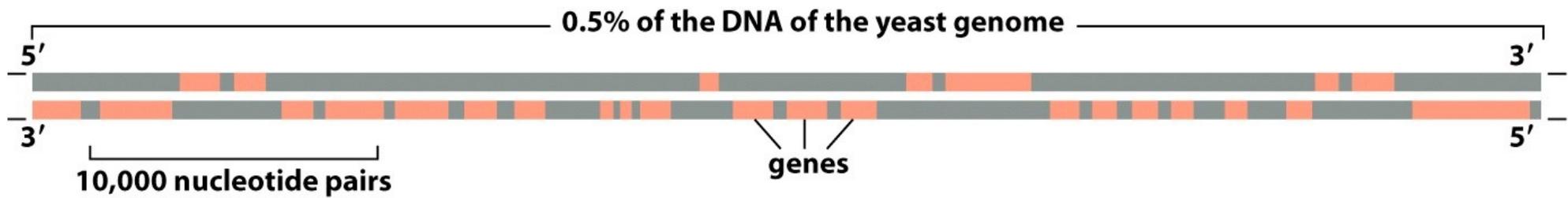


Figure 5-13 Essential Cell Biology 3/e (© Garland Science 2010)

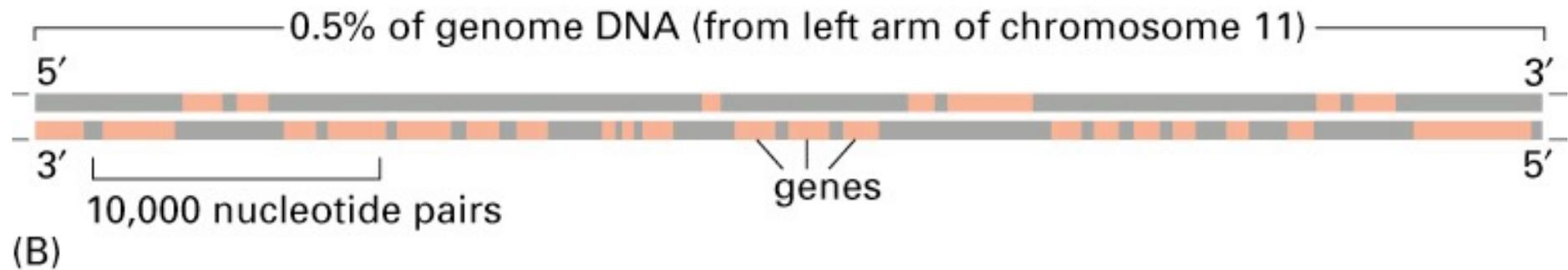
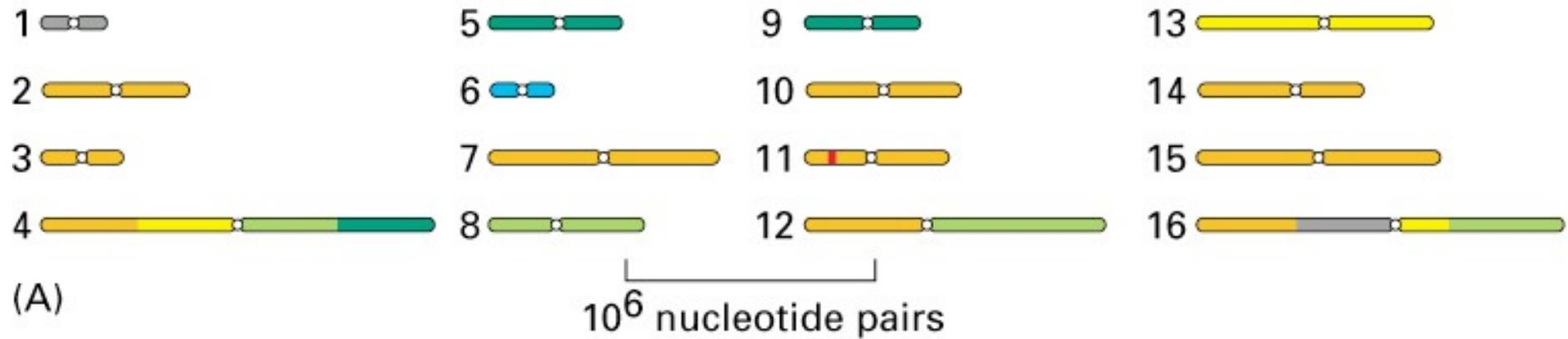


Figure 4–13. Molecular Biology of the Cell, 4th Edition.

Fig. The genome of *S. cerevisiae* (budding yeast)  
 (A) The genome : 16 chromosomes  
 (B) A small region of chromosome 11

# The nucleotide sequence of the human genome shows how our genes are arranged

The *conserved regions* include both functionally important exons and regulatory DNA sequences.

The *nonconserved regions* represent DNA whose sequence unlikely to be critical for function.

Roughly 5% of the human genome consists of "multi-species conserved sequences".

Only about one- third of these sequences code for proteins.

(A) human chromosome 22— $48 \times 10^6$  nucleotide pairs of DNA

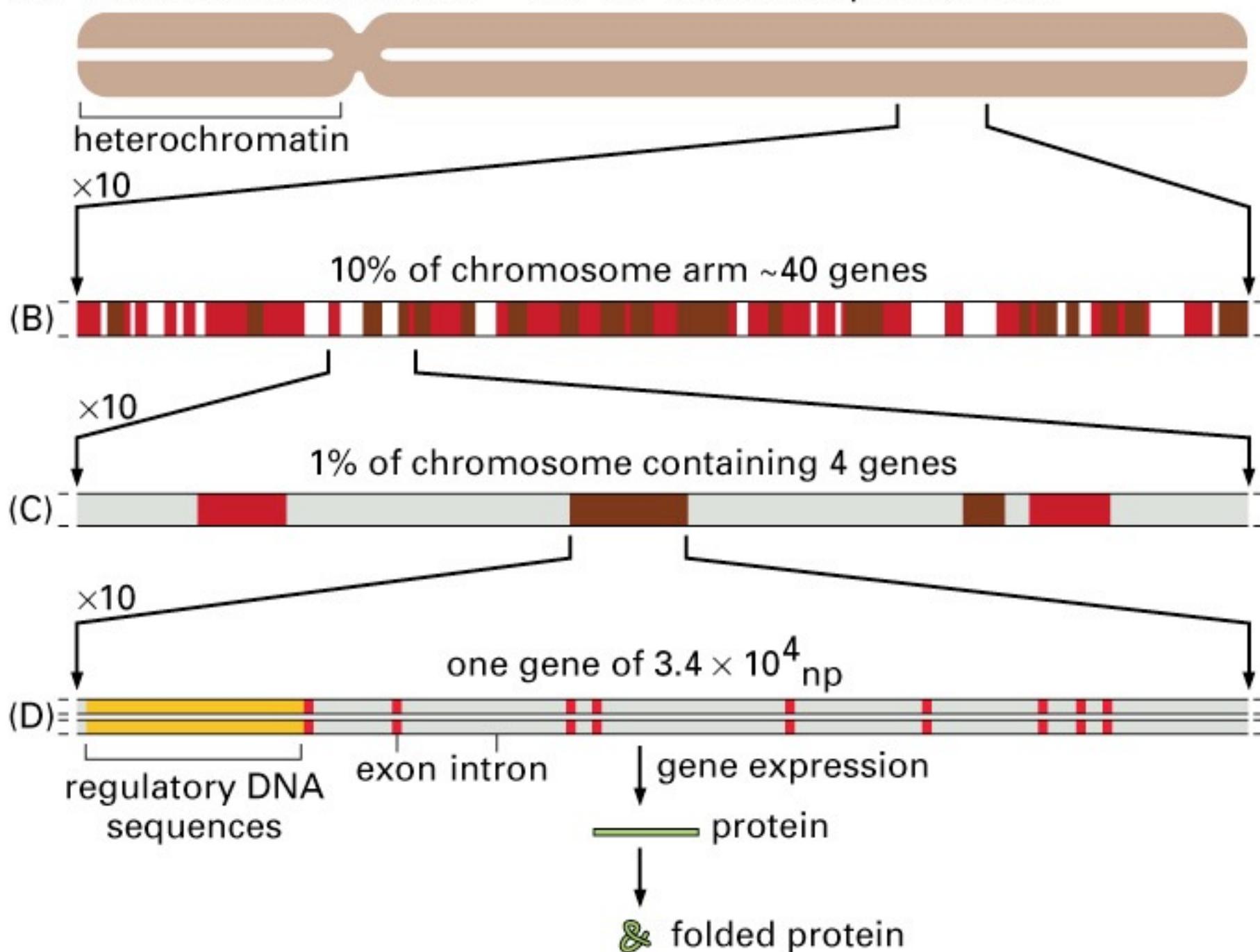


Figure 4-15. Molecular Biology of the Cell, 4th Edition.

**Table 4–1 Some Vital Statistics for the Human Genome**

|  | HUMAN GENOME                        |
|--|-------------------------------------|
| DNA length   | $3.2 \times 10^9$ nucleotide pairs* |
| Number of genes  | approximately 25,000                |
| Largest gene   | $2.4 \times 10^6$ nucleotide pairs  |
| Mean gene size   | 27,000 nucleotide pairs             |
| Smallest number of exons per gene                              | 1                                   |
| Largest number of exons per gene                               | 178                                 |
| Mean number of exons per gene                                  | 10.4                                |
| Largest exon size  | 17,106 nucleotide pairs             |
| Mean exon size   | 145 nucleotide pairs                |
| Number of pseudogenes**  | more than 20,000                    |
| Percentage of DNA sequence in exons (protein coding sequences) | 1.5%                                |
| Percentage of DNA in other highly conserved sequences***       | 3.5%                                |
| Percentage of DNA in high-copy repetitive elements             | approximately 50%                   |

\* The sequence of 2.85 billion nucleotides is known precisely (error rate of only about one in 100,000 nucleotides). The remaining DNA primarily consists of short highly repeated sequences that are tandemly repeated, with repeat numbers differing from one individual to the next.

\*\* A pseudogene is a nucleotide sequence of DNA closely resembling that of a functional gene, but containing numerous mutations that prevent its proper expression. Most pseudogenes arise from the duplication of a functional gene followed by the accumulation of damaging mutations in one copy.

\*\*\* Preserved functional regions; these include DNA encoding 5' and 3' UTRs (untranslated regions), structural and functional RNAs, and conserved protein-binding sites on the DNA.

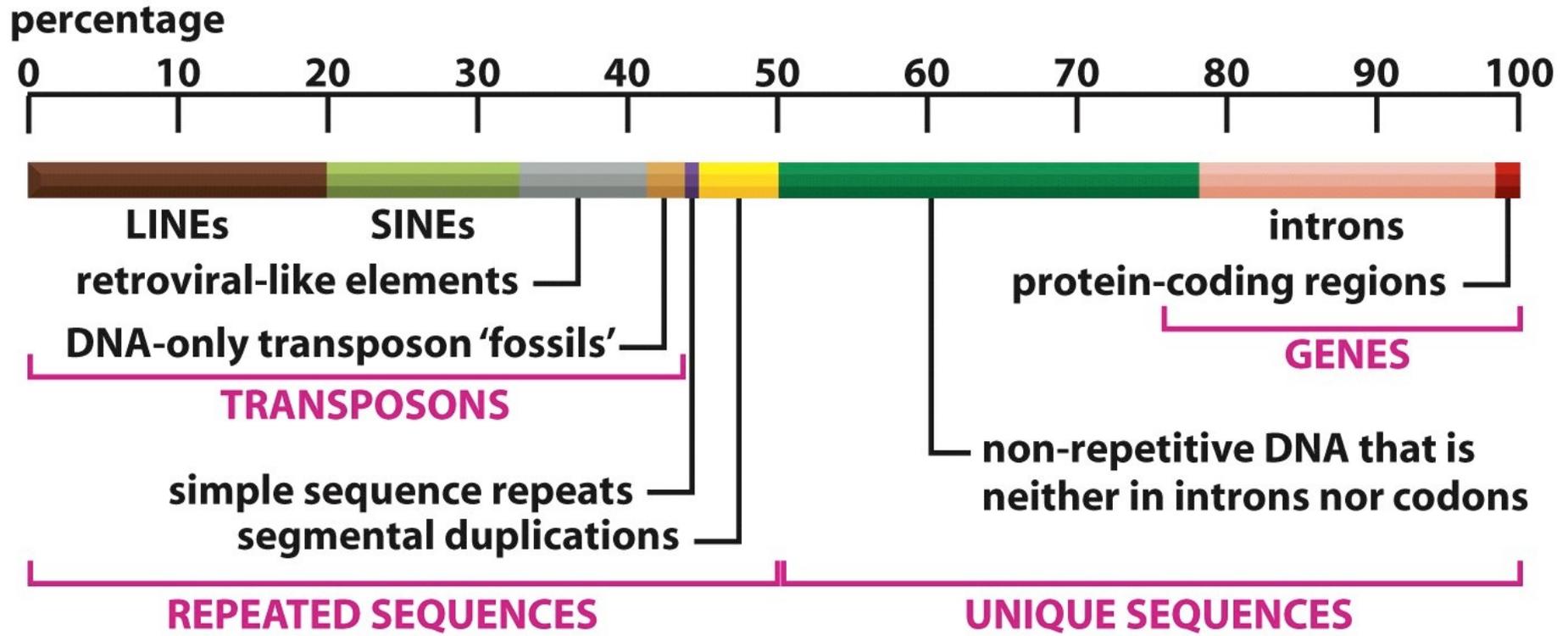


Figure 4-17 Molecular Biology of the Cell 5/e (© Garland Science 2008)

This unexpected discovery has led scientists to conclude that we *understand much less about the cell biology of vertebrates* than we had previously imagined.

Certainly, there are *enormous opportunities for new discoveries*, and we should expect *many surprises ahead*.

**'Junk DNA'**: a large excess of interspersed DNA, the majority of which does not seem to carry critical information.

may be crucial for the *long-term evolution*.

this extra DNA is highly *conserved among related species*.

In general, the *more complex* an organism is, *the larger* its genome.

But, not always true.

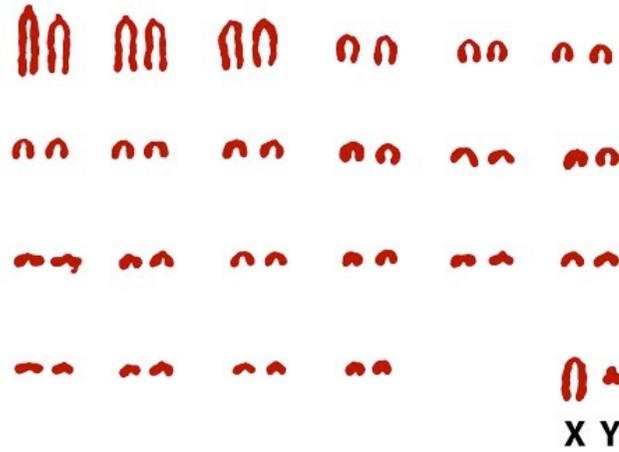
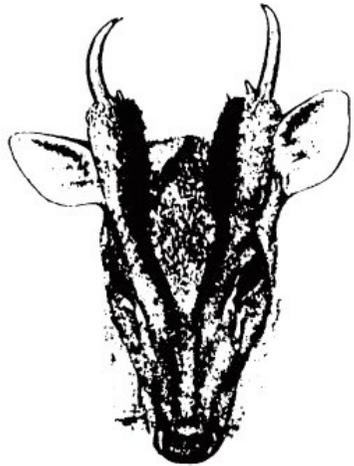
e.g., closely related species (see fig. 5-14).

*No simple relationship* between gene number, chromosome number, and the total size.

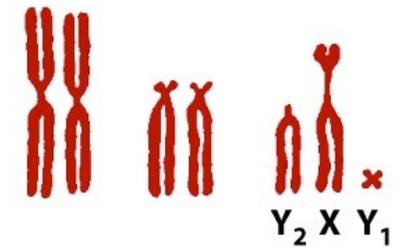
e.g., Human vs (*S. cerevisiae* / plant / amoeba).

22 pairs + XY

2 pairs + XYY



Chinese muntjac



Indian muntjac

Figure 5-14 Essential Cell Biology 3/e (© Garland Science 2010)



중국 문자크(동남아시아 원산의 작은 사슴)

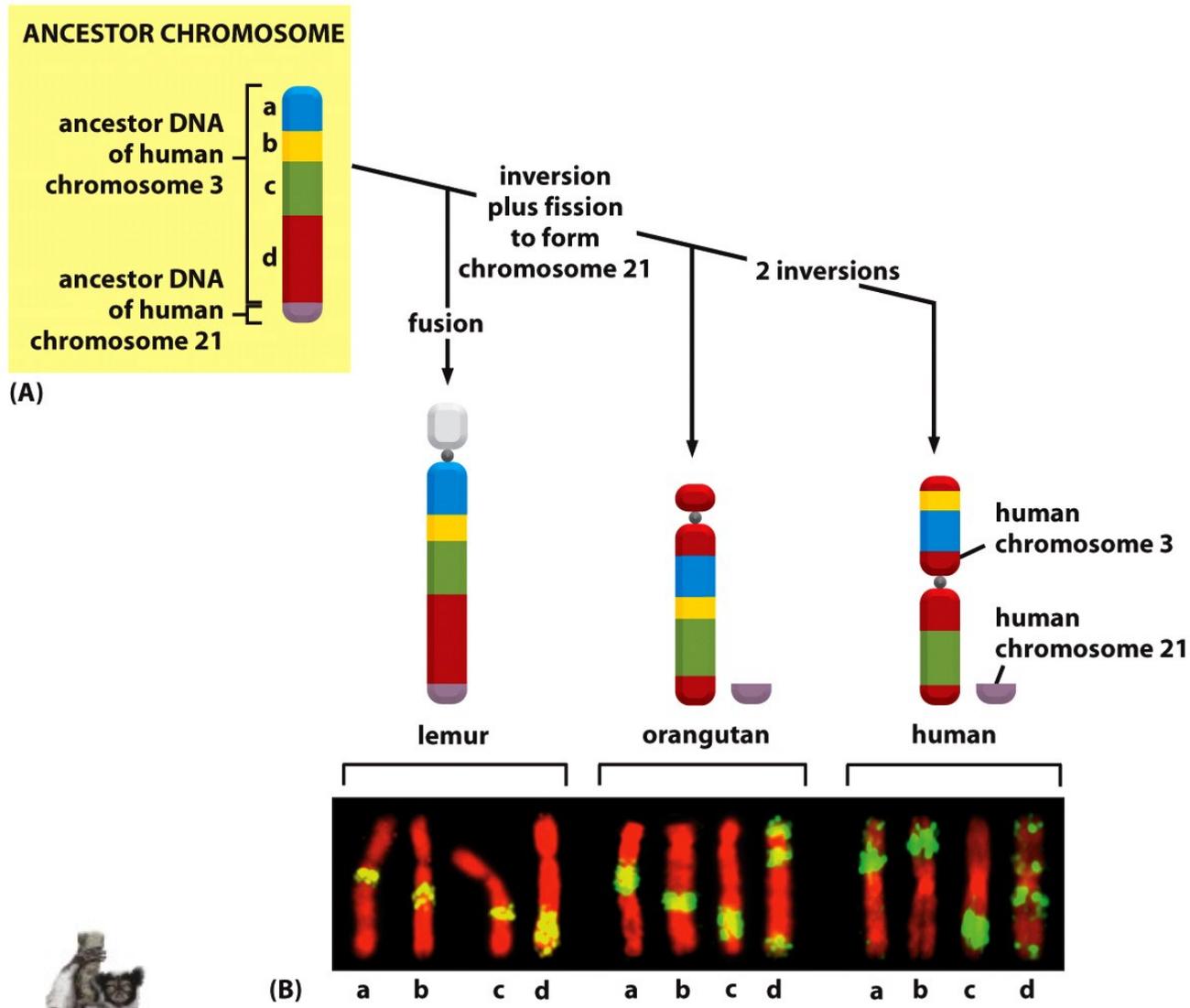


인도 문자크(동남아시아 원산의 작은 사슴)

# Genome comparisons reveal evolutionarily conserved DNA sequences

Major obstacle in interpreting the nucleotide sequences of human chromosome

1. Much of the sequence is probably *unimportant*.
2. Coding regions in *short* segments (ave about 145 nt pairs).
3. Where a gene begins and ends?
4. Exactly *how many exons* a gene spans?



**Figure 4–18 A proposed evolutionary history of human chromosome 3 and its relatives in other mammals.** (A) The order of chromosome 3 segments hypothesized to be present on a chromosome of a mammalian ancestor is shown (yellow box). The minimum changes in this ancestral chromosome necessary to account for the appearance of each of the three modern chromosomes are indicated. (The present-day chromosomes of humans and African apes are identical at this resolution.) The *small circles* depicted in the modern chromosomes represent the positions of centromeres. **A fission and inversion that leads to a change in chromosome organization is thought to occur once every  $5\text{--}10 \times 10^6$  years in mammals.** (B) Some of the chromosome painting experiments that led to the diagram in (A). Each image shows the chromosome most closely related to human chromosome 3, painted *green* by hybridization with different segments of DNA, lettered a, b, c, and d along the *bottom* of the figure. These letters correspond to the colored segments of the diagrams in (A), as indicated on the ancestral chromosome. (From S. Müller et al., *Proc. Natl Acad. Sci. U.S.A.* 97:206–211, 2000. With permission from National Academy of Sciences.)



**lemur** 미국·영국 [li:mə(r)]  
 [명사] (마다가스카르산) 여우원숭이

Comparative studies have revealed not only that humans and other mammals *share most of the same genes*, but also that large blocks of our genomes contain these genes in the *same order*, a feature called *conserved synteny*.

As a result, large blocks of our chromosomes can be recognized in other species. This allows the chromosome painting technique to be used to reconstruct the *recent evolutionary history of human chromosomes*.

synteny 미국·영국 sɪntəni

명사 (유전) 신터니 ((복수의 유전자가 동일 염색체 위에 있는 일))

Chromosomes exist *in different states* throughout the life of a cell

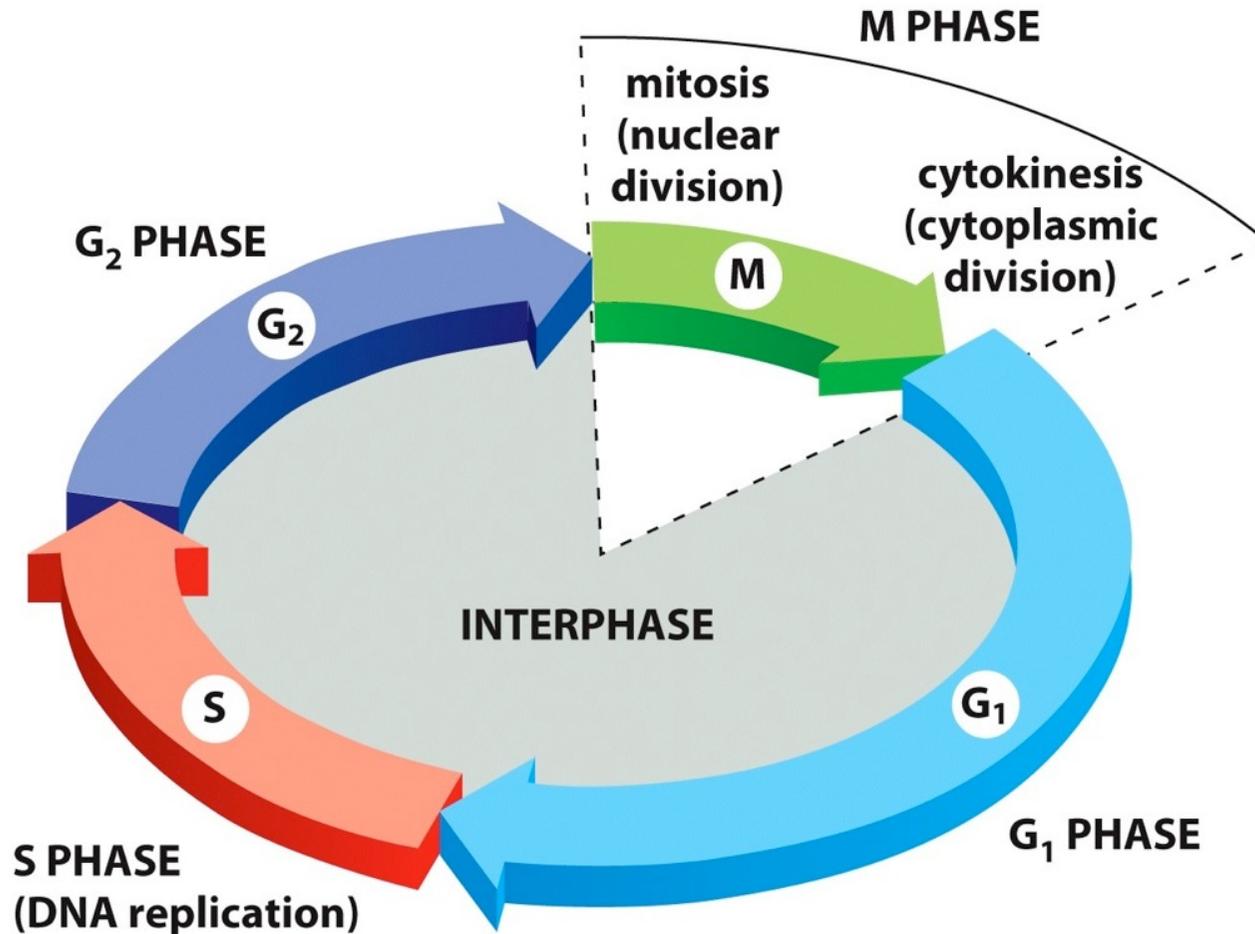


Figure 18-2 Essential Cell Biology 3/e (© Garland Science 2010)

**Cell cycle:** Cell growth and division (when the replication and segregation of chromosomes occurs).

## **Interphase:**

*Interphase Chromosomes*

Extended as *long, thin, tangled thread of DNA*.

Not be easily distinguished.

**Mitosis:** Chromosomes are distributed to the two daughter nuclei.

*Mitotic chromosomes*

*More and more compact structure* (highly condensed).

- *Most easily visualized.*

# Mitotic chromosome is highly compact

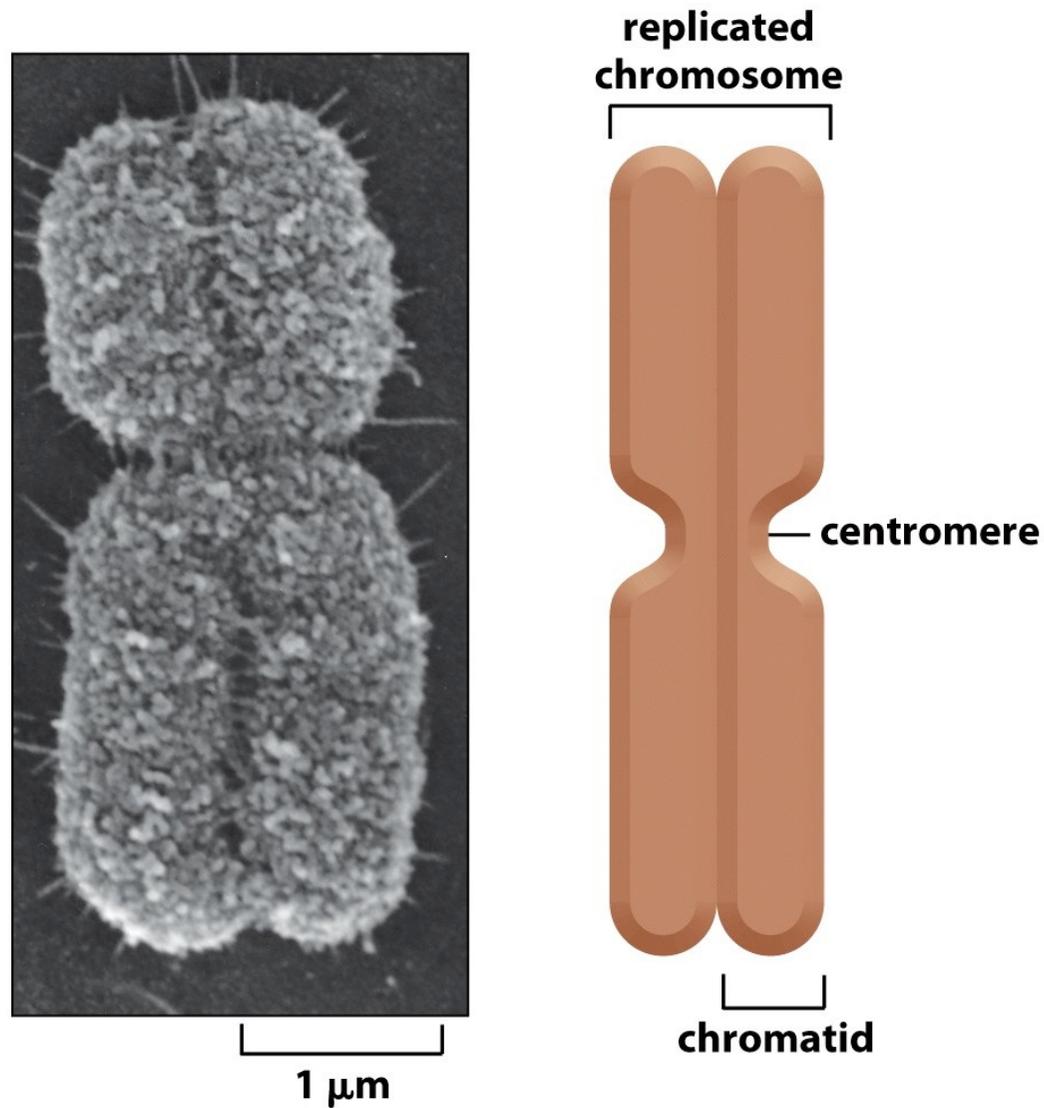


Figure 5-17 Essential Cell Biology 3/e (© Garland Science 2010)

# Replication and segregation of chromosomes occur through the cell cycle

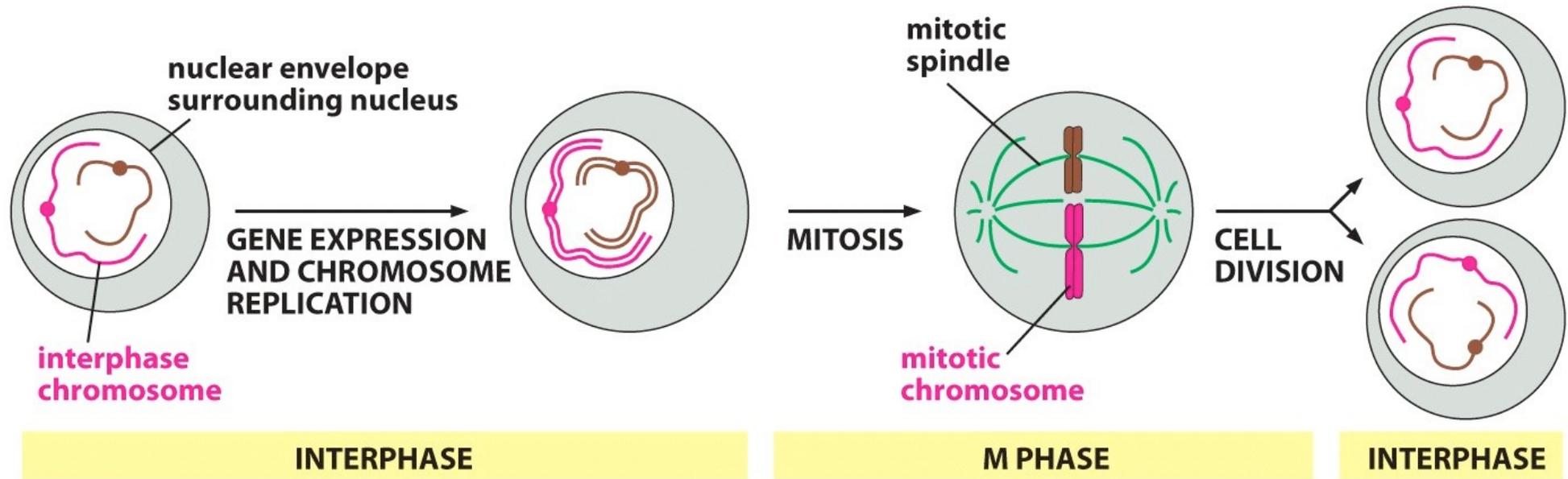


Figure 5-15 Essential Cell Biology 3/e (© Garland Science 2010)

*Interphase*, when chromosomes are duplicated

*Mitosis*, when chromosomes are distributed to the two daughter nuclei

The duration of the cell cycle varies greatly from one cell type to another

**TABLE 18-1 SOME EUCARYOTIC CELL-CYCLE TIMES**

| <b>CELL TYPE</b>                             | <b>CELL-CYCLE TIMES</b> |
|--|-------------------------|
| <b>Early frog embryo cells</b>               | <b>30 minutes</b>       |
| <b>Yeast cells</b>                           | <b>1.5–3 hours</b>      |
| <b>Mammalian intestinal epithelial cells</b> | <b>~12 hours</b>        |
| <b>Mammalian fibroblasts in culture</b>      | <b>~20 hours</b>        |
| <b>Human liver cells</b>                     | <b>~1 year</b>          |

Table 18-1 Essential Cell Biology 3/e (© Garland Science 2010)

# Three DNA sequence elements are needed to produce a eucaryotic chromosome

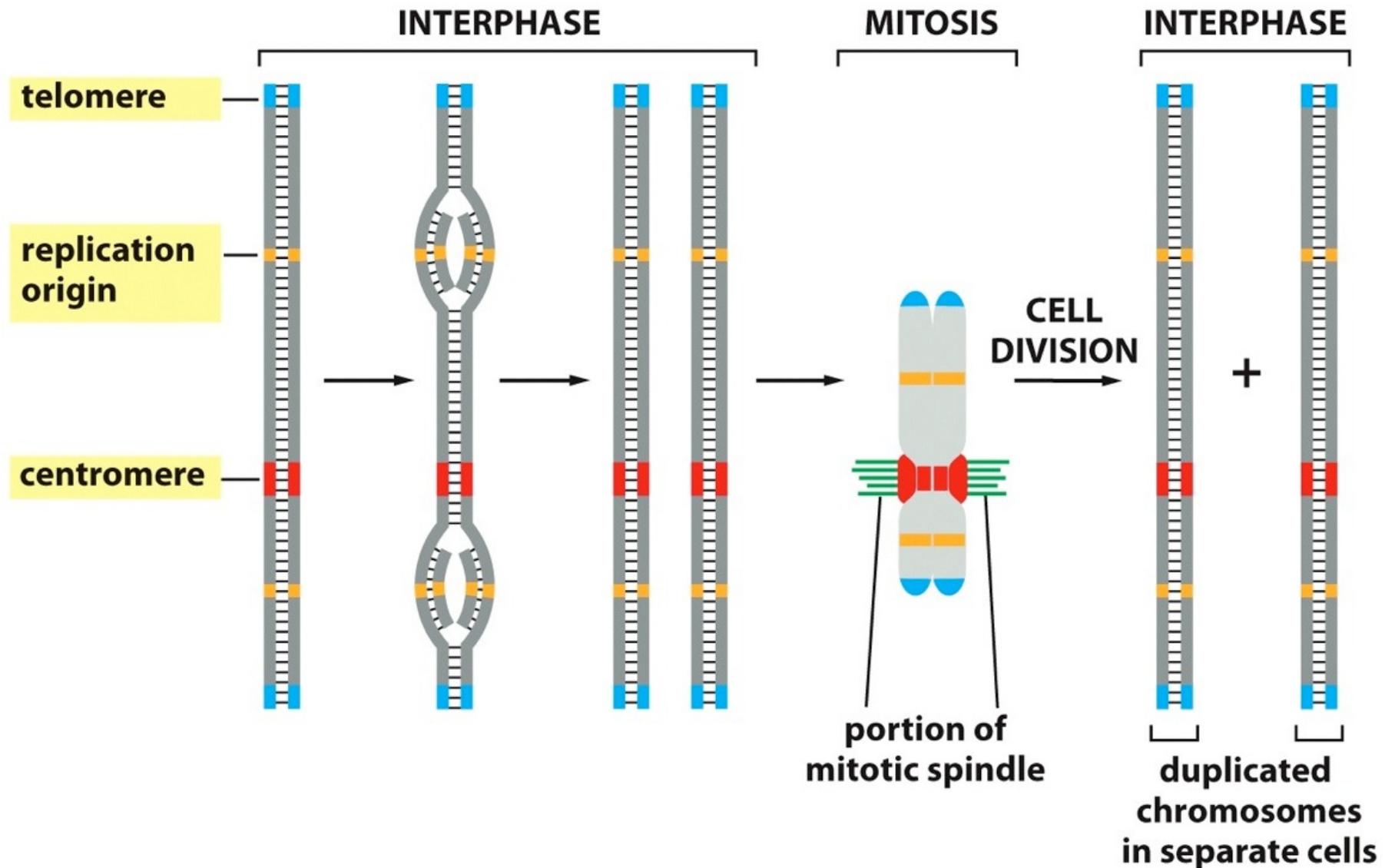


Figure 5-16 Essential Cell Biology 3/e (© Garland Science 2010)

## **Replication origin**

*Duplication* of the DNA begins.

*Many* replication origins to be replicated *rapidly*.

## **Telomeres**

Found at each of the *two ends* of a chromosome.

*Repeated* nucleotide sequences (***GGGGTTA*** repeats in human) that enable the ends of chromosomes to be replicated.

*Protect* the end of the chromosome from being mistaken by the cell as a broken DNA molecule in need of repair.

## **Centromere**

Allows one copy of each duplicated chromosome to be *apportioned* to each daughter cell.

# *Interphase chromosomes are organized within the nucleus*

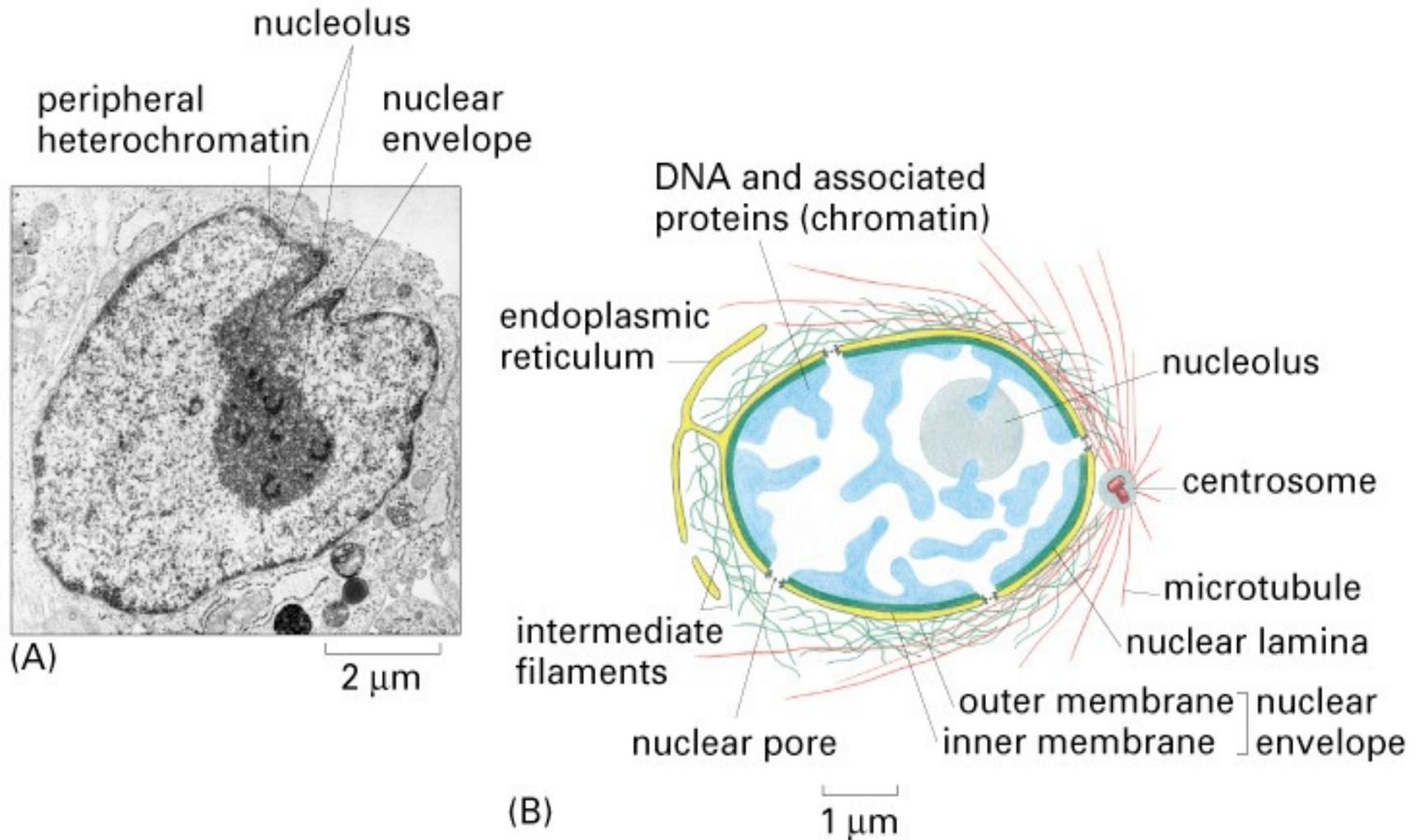


Figure 5-19 Essential Cell Biology, 2/e. (© 2004 Garland Science)

***Nuclear envelop***: formed by *two concentric membranes*; *punctuated* at intervals by nuclear pores.

***Nuclear pores***: *actively transport* selected molecules to and from the cytosol.

***Nuclear lamina***: *a network of protein filaments* that forms a thin layer underlying and the inner membrane.

## ***Nucleolus***

***The most obvious*** example of chromosome organization in the interphase nucleus.

Parts of the different chromosomes carrying genes for *ribosomal RNA* cluster together.

“...Not being mixed with each other like spaghetti in a bowl...”

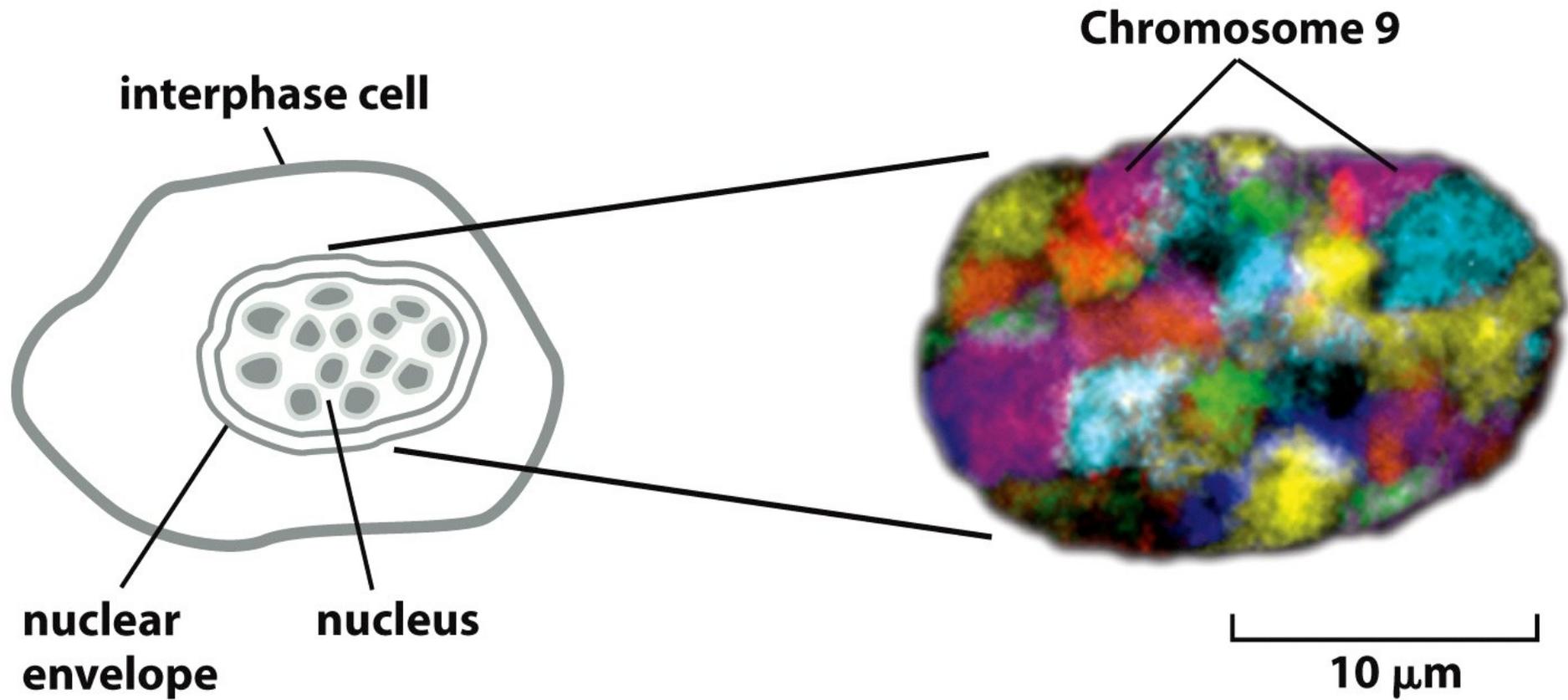
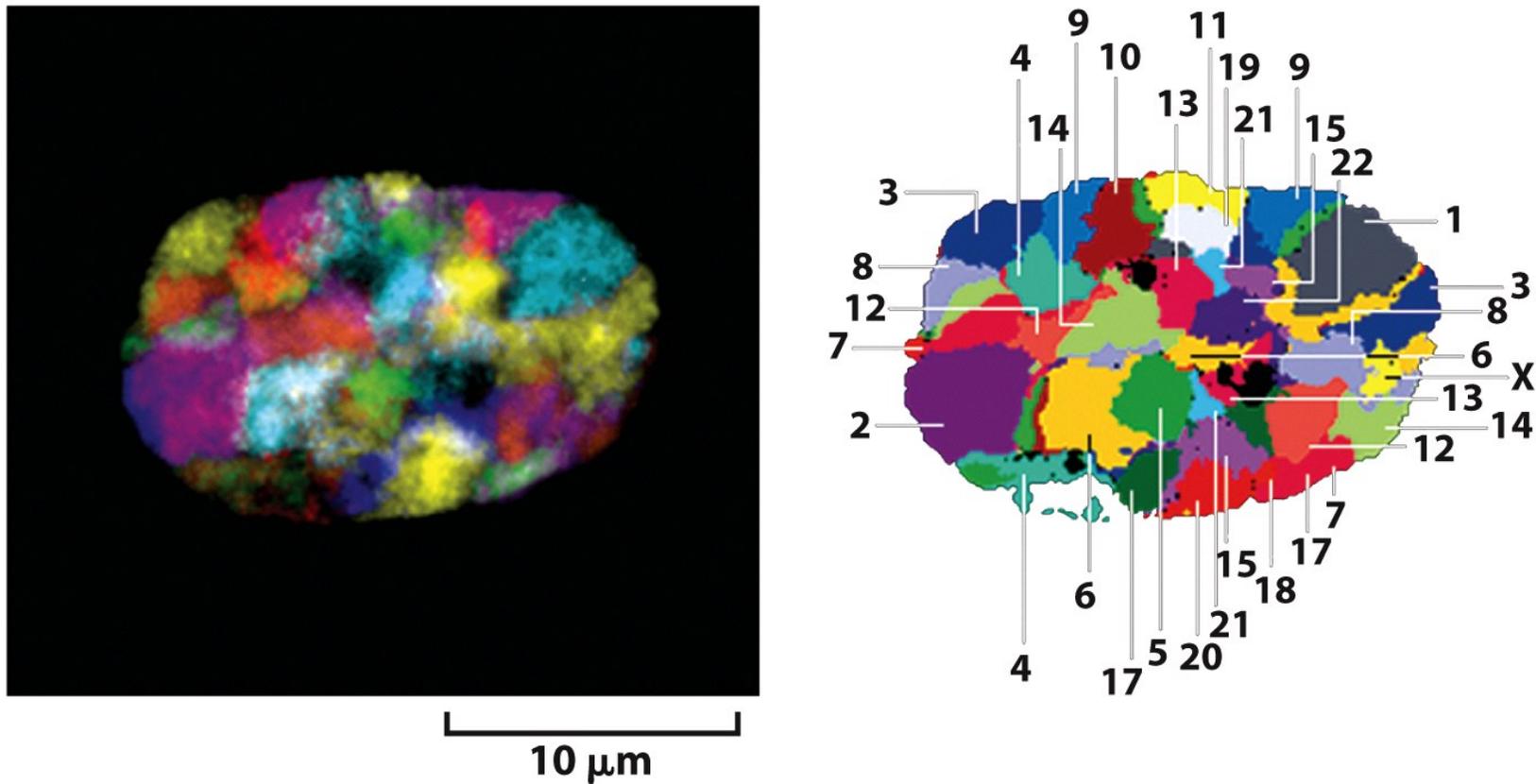


Figure 5-18 Essential Cell Biology 3/e (© Garland Science 2010)



**Figure 4–63** Simultaneous visualization of the chromosome territories for all of the human chromosomes in a single interphase nucleus. A FISH analysis using a different mixture of fluorochromes for marking the DNA of each chromosome, detected with seven color channels in a fluorescence microscope, allows each chromosome to be distinguished in three-dimensional reconstructions. Below the micrograph, each chromosome is identified in a schematic of the actual image. Note that the two homologous chromosomes (e.g., the two copies of chromosome 9), are not in general co-located. (From M.R. Speicher and N.P. Carter, *Nat. Rev. Genet.* 6:782–792, 2005. With permission from Macmillan Publishers Ltd.)

***Nuclear envelop***: formed by *two concentric membranes*; *punctuated* at intervals by nuclear pores.

***Nuclear pores***: *actively transport* selected molecules to and from the cytosol.

***Nuclear lamina***: *a network of protein filaments* that forms a thin layer underlying and the inner membrane.

## ***Nucleolus***

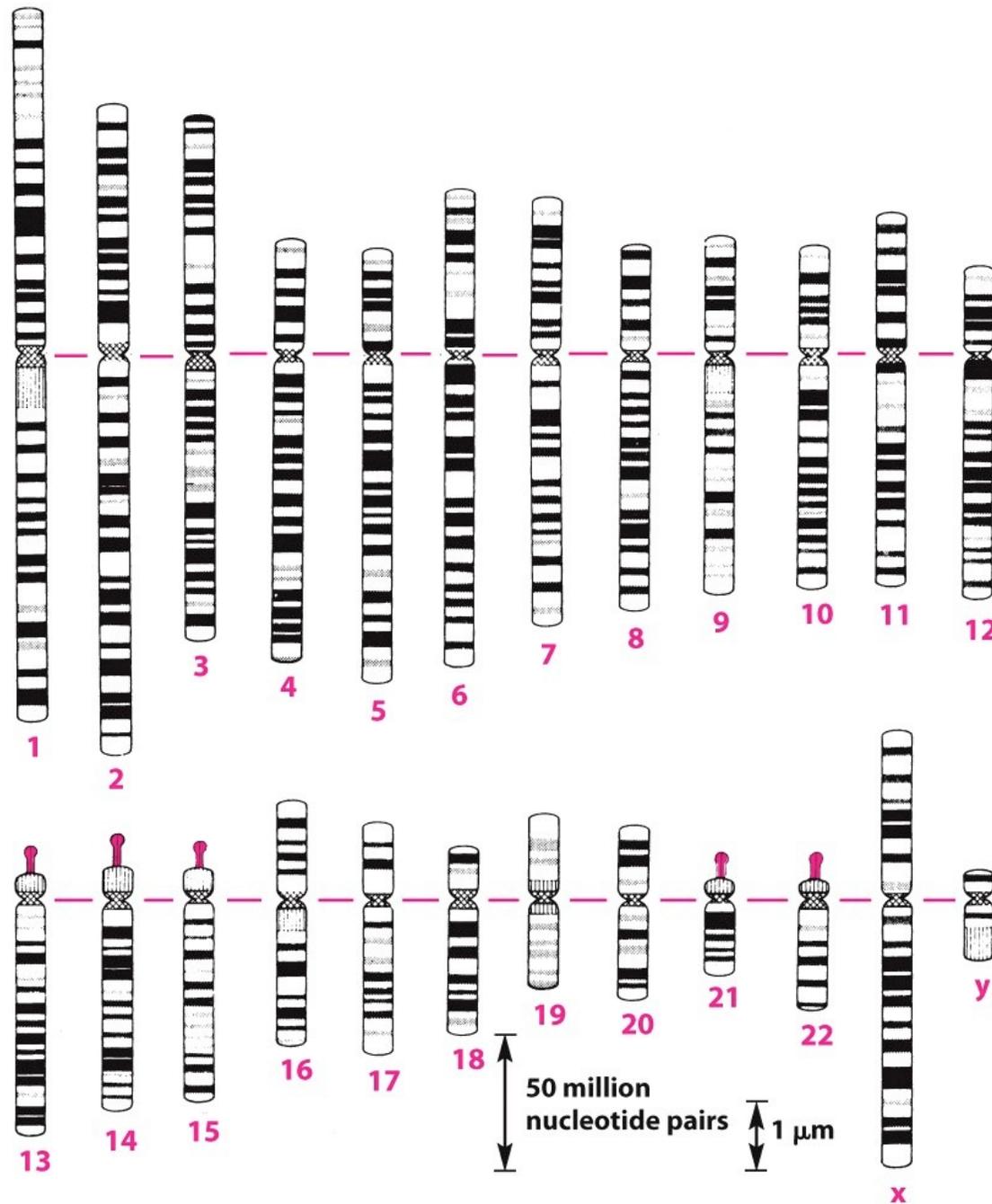
***The most obvious*** example of chromosome organization in the interphase nucleus.

Parts of the different chromosomes carrying genes for *ribosomal RNA* cluster together.

# Chromatin Can Move to Specific Sites Within the Nucleus to Alter Gene Expression

*The heterochromatic regions* of a chromosome are often closely associated with *the nuclear lamina*, regardless of the chromosome examined.

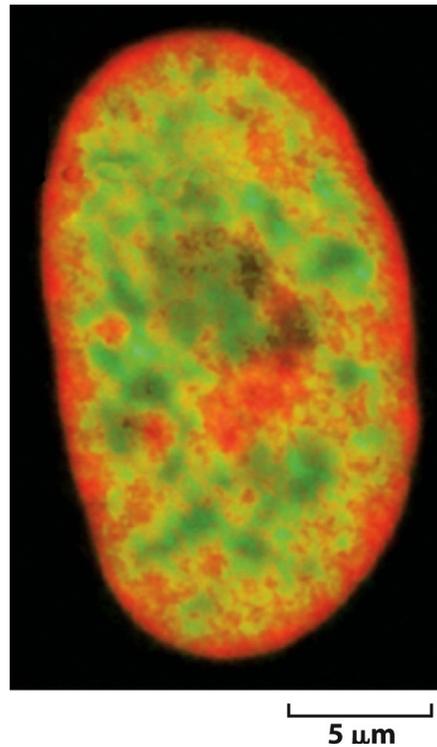
Different average positions for *active and inactive genes*.



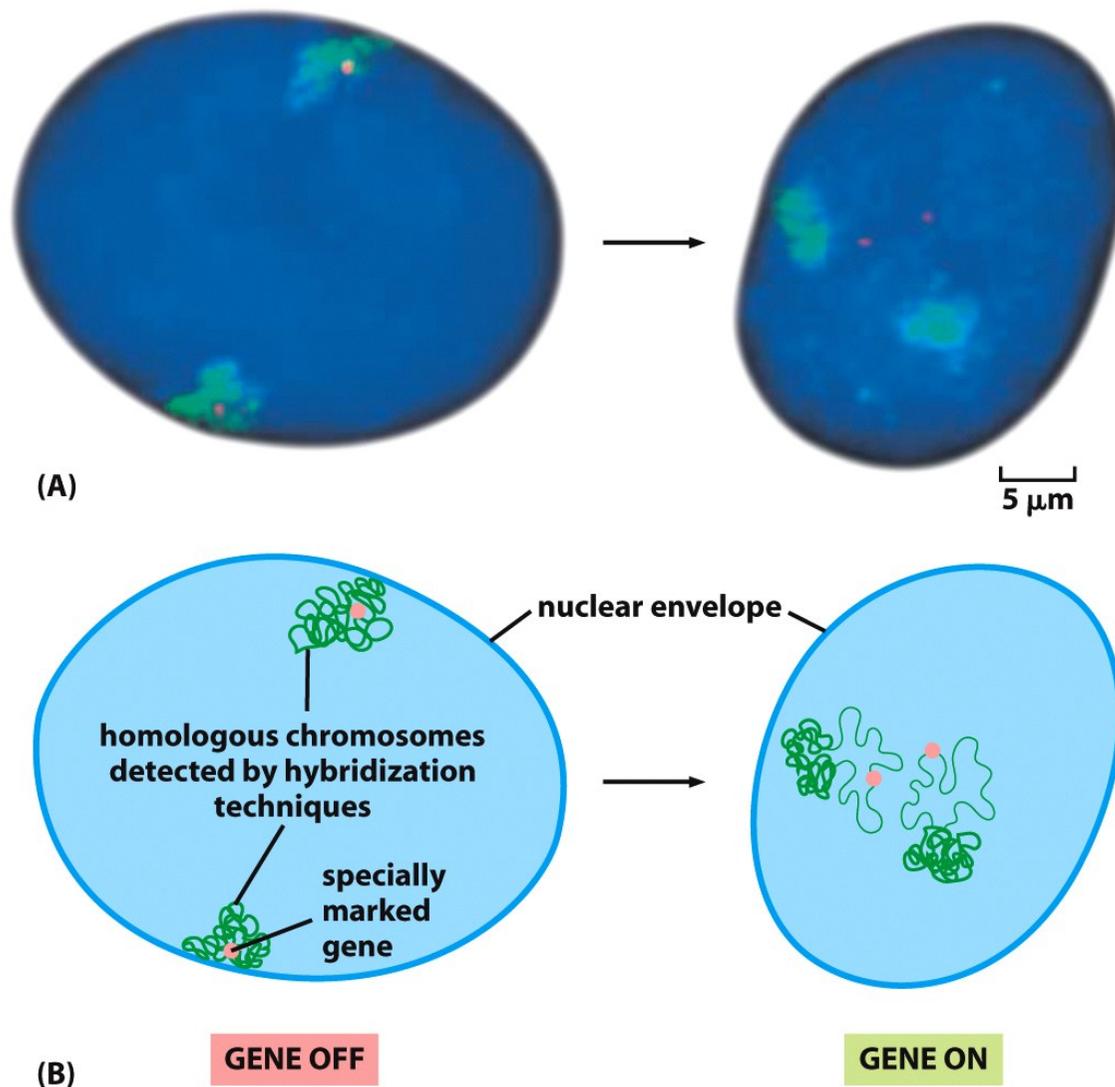
Unique banding patterns allow the identification of each human chromosome

- To stain the chromosomes with dyes that bind to certain types of DNA sequences.
- These dyes mainly distinguish between DNA that is rich in A-T nucleotide pairs and DNA that is G-C rich, and they produce a striking and reliable pattern of bands along each chromosome.
- *Giemsa stain*: produce dark bands in AT rich region.
- Giemsa stain is named after German chemist and bacteriologist Gustav Giemsa.
- Giemsa's solution is a mixture of methylene blue, eosin, and Azure B.

Figure 5-11 Essential Cell Biology 3/e (© Garland Science 2010)



**Figure 4–64** The distribution of gene-rich regions of the human genome in an interphase nucleus. Gene-rich regions have been visualized with a fluorescent probe that hybridizes to the Alu interspersed repeat, which is present in more than a million copies in the human genome (see Figure 5–75). For unknown reasons, these sequences cluster in chromosomal regions rich in genes. In this representation, regions enriched for the Alu sequence are *green*, regions depleted for these sequences are *red*, while the average regions are *yellow*. The gene-rich regions are seen to be depleted in the DNA near the nuclear envelope. (From A. Bolzer et al., *PLoS Biol.* 3:826–842, 2005. With permission from Public Library of Science.)



**Figure 4–65 An effect of high levels of gene expression on the intranuclear location of chromatin.** (A) Fluorescence micrographs of human nuclei showing how the position of a gene changes when it becomes highly transcribed. The region of the chromosome adjacent to the gene (*red*) is seen to leave its chromosomal territory (*green*) only when it is highly active. (B) Schematic representation of a large loop of chromatin that expands when the gene is on, and contracts when the gene is off. Other genes that are less actively expressed can be shown by the same methods to remain inside their chromosomal territory when transcribed. (From J.R. Chubb and W.A. Bickmore, *Cell* 112:403–406, 2003. With permission from Elsevier.)

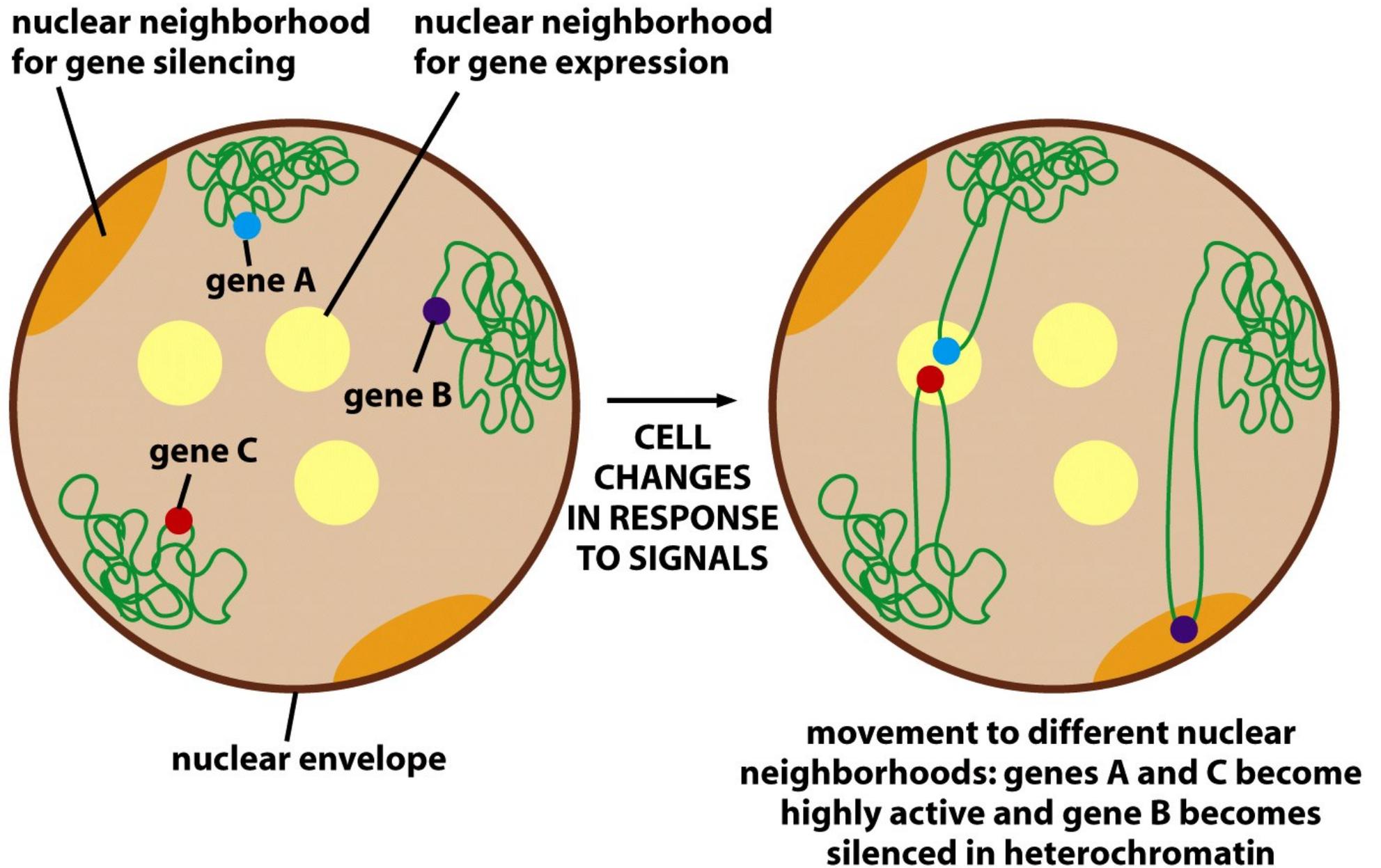


Figure 4-66 *Molecular Biology of the Cell* (© Garland Science 2008)

*The position of a gene* in the interior of the nucleus *changes* when it becomes highly expressed.

Thus, *a region* that becomes very *actively transcribed* is often found to extend out of its chromosome territory, as if *in an extended loop*.

*The initiation of transcription*, the first step in gene expression, requires the assembly of *over 100 proteins*, and it makes sense that this would *occur most rapidly in regions* of the nucleus particularly rich in these proteins.

The DNA in chromosomes is *highly condensed*

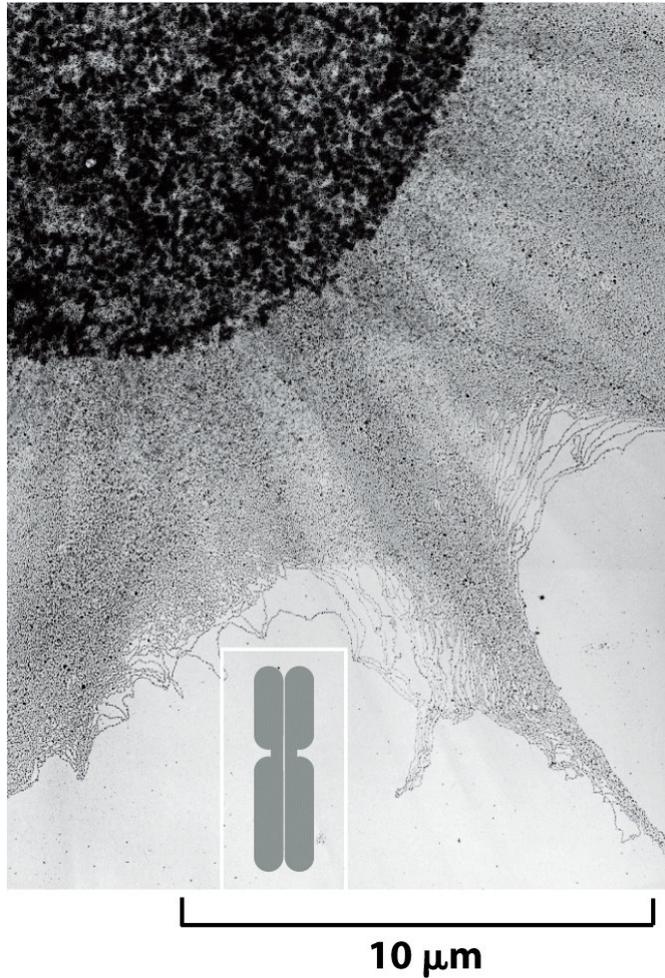


Figure 5-20 Essential Cell Biology 3/e (© Garland Science 2010)

- ***The interphase chromosomes***

*Longer* and *finer* than mitotic chromosomes

Nonetheless *organized* in various ways.

tends to *occupy a particular region*.

do *not* become extensively *entangled*.

specific regions of chromosomes are *attached to sites* on the nuclear envelop or the nuclear lamina.

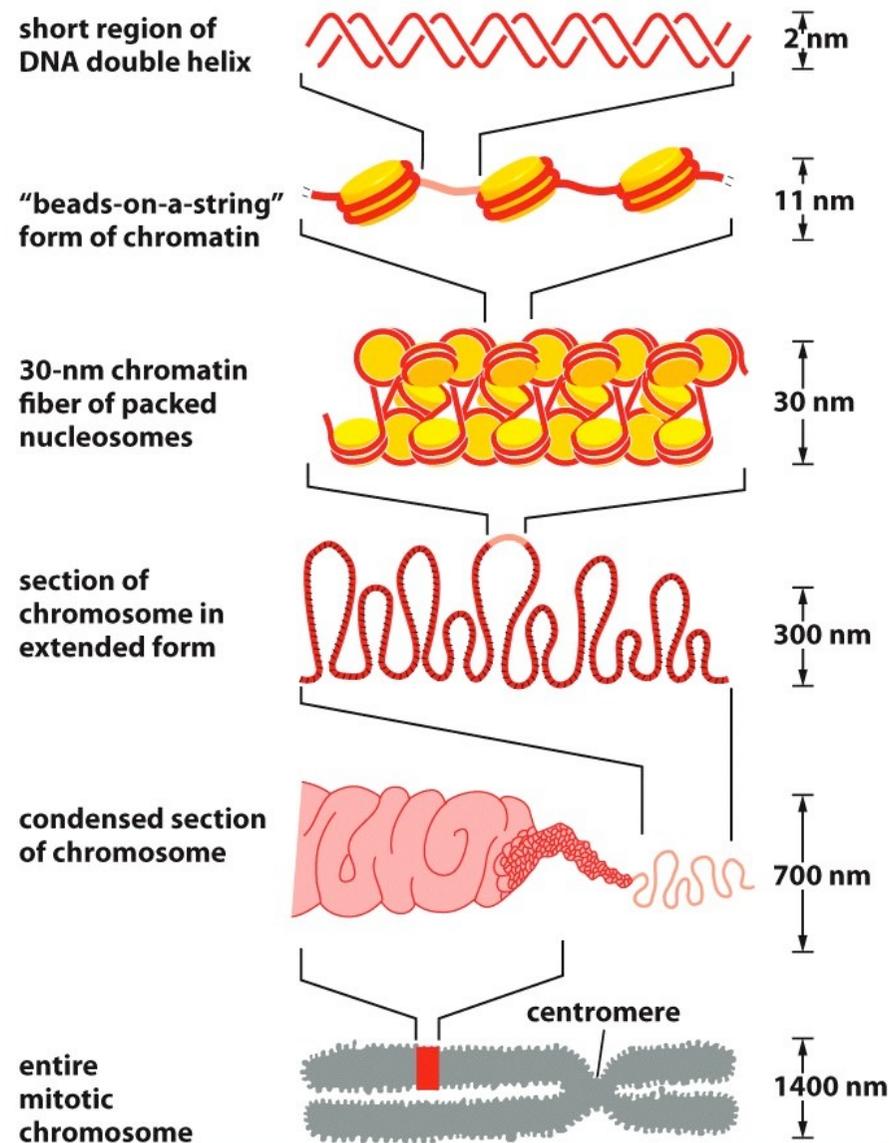
All eucaryotic cells package *DNA tightly into chromosomes.*

Chromosome structure is dynamic.

Not only do chromosomes condense and relax in concert with the cell cycle,

but different regions of the interphase chromosome must unpack to allow cells to access specific DNA sequence for replication, repair, or gene expression.

# Chromosomes packing occurs on *multiple levels*



**NET RESULT: EACH DNA MOLECULE HAS BEEN PACKAGED INTO A MITOTIC CHROMOSOME THAT IS 10,000-FOLD SHORTER THAN ITS EXTENDED LENGTH**

Figure 5-25 Essential Cell Biology 3/e (© Garland Science 2010)

# Controlling the double helix

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NATURE | VOL 421 | 23 JANUARY 2003 | www.nature.com/nature

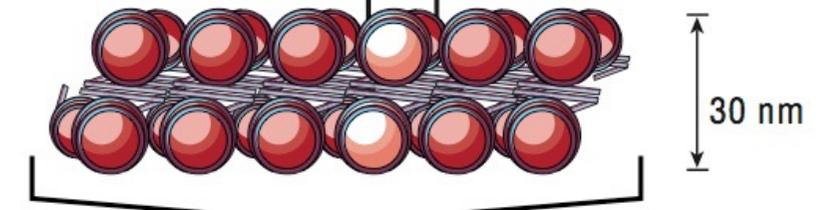
Short region of DNA double helix



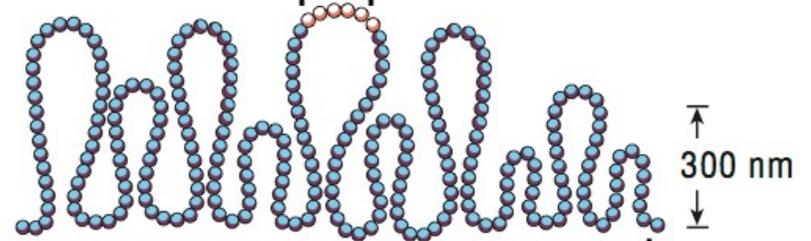
"Beads on a string" form of chromatin



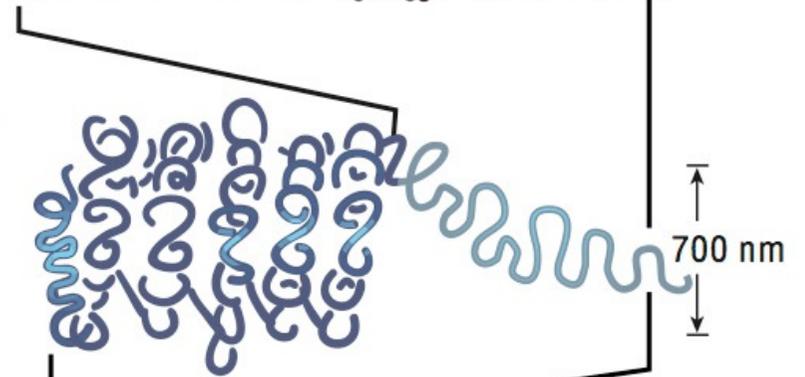
30-nm chromatin fibre of packed nucleosomes



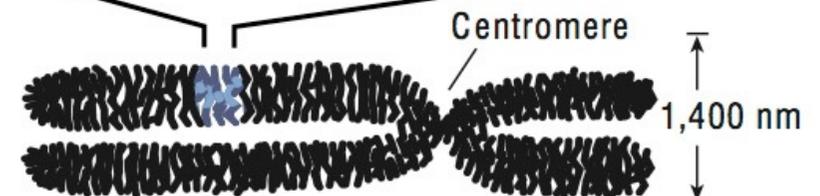
Section of chromosome in an extended form



Condensed section of chromosome



Entire mitotic chromosome



## DNA double helix

- “*beads-on-a-string*” form of chromatin
- *30-nm chromatin fiber*
- Chromosome *in extended form*
- *Condensed* section of chromosome
- Entire mitotic chromosome

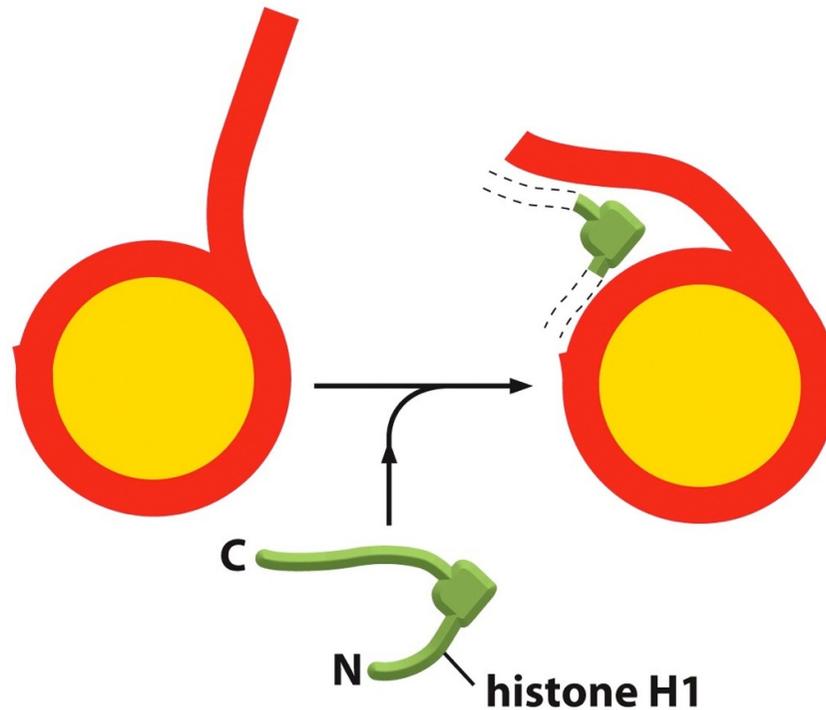


Figure 5-24 Essential Cell Biology 3/e (© Garland Science 2010)

## Histone H1

Histone H1 is one of the five **main histone protein families** which are components of chromatin in eukaryotic cells. Though **highly conserved**, it is nevertheless **the most variable histone** in sequence across species.

H1 is involved with **the packing** of the "beads on a string" sub-structures into a **high order structure**, whose details have not yet been solved

[https://en.wikipedia.org/wiki/Histone\\_H1](https://en.wikipedia.org/wiki/Histone_H1)

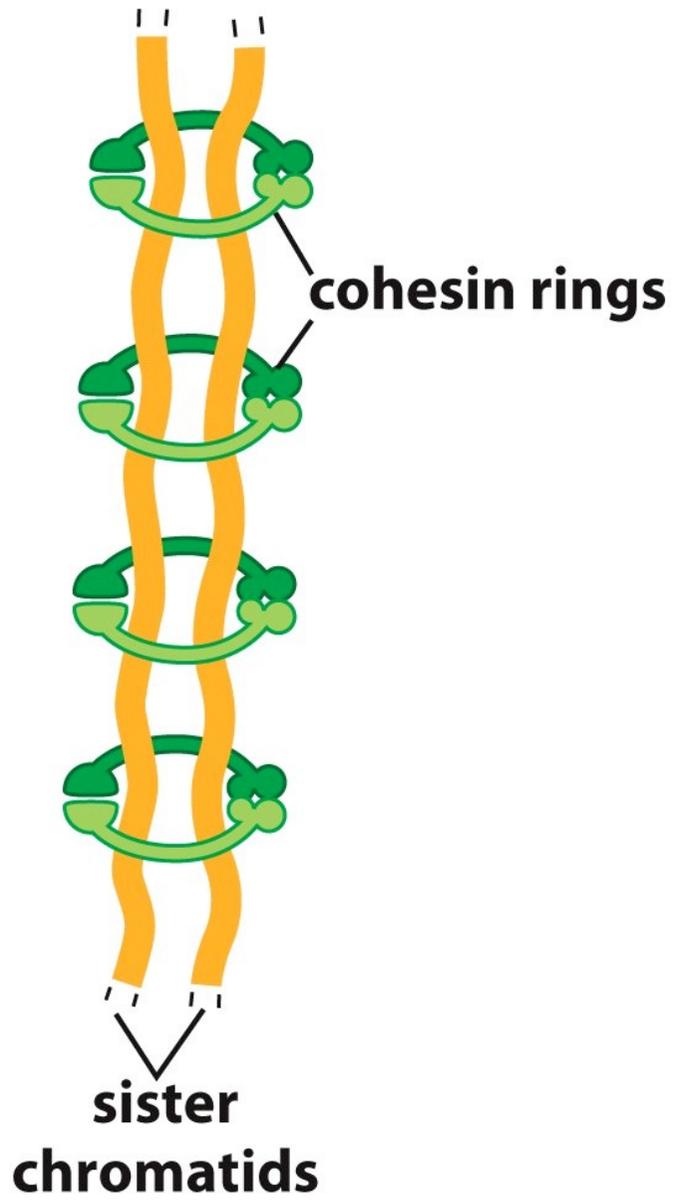


Figure 18-15 Essential Cell Biology 3/e (© Garland Science 2010)

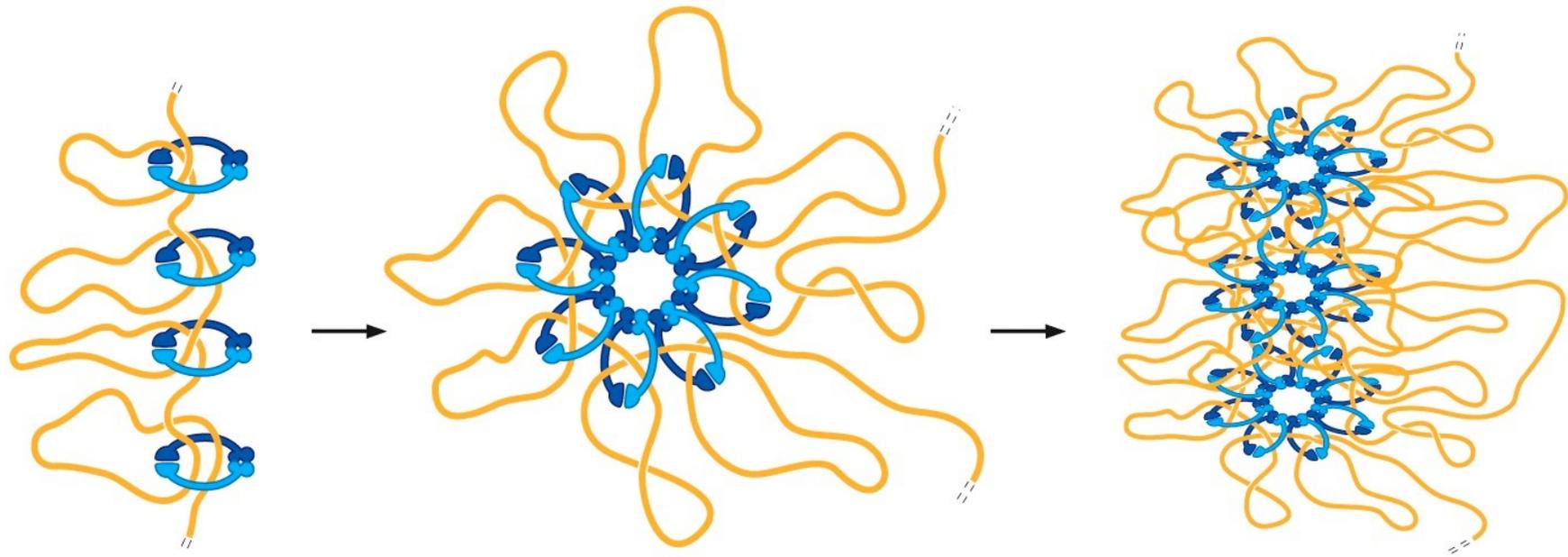


Figure 18-19a Essential Cell Biology 3/e (© Garland Science 2010)

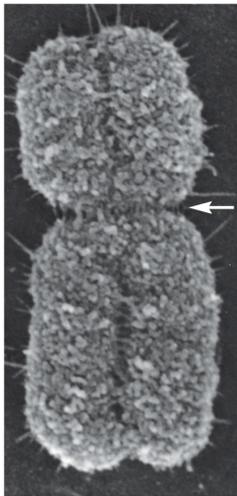
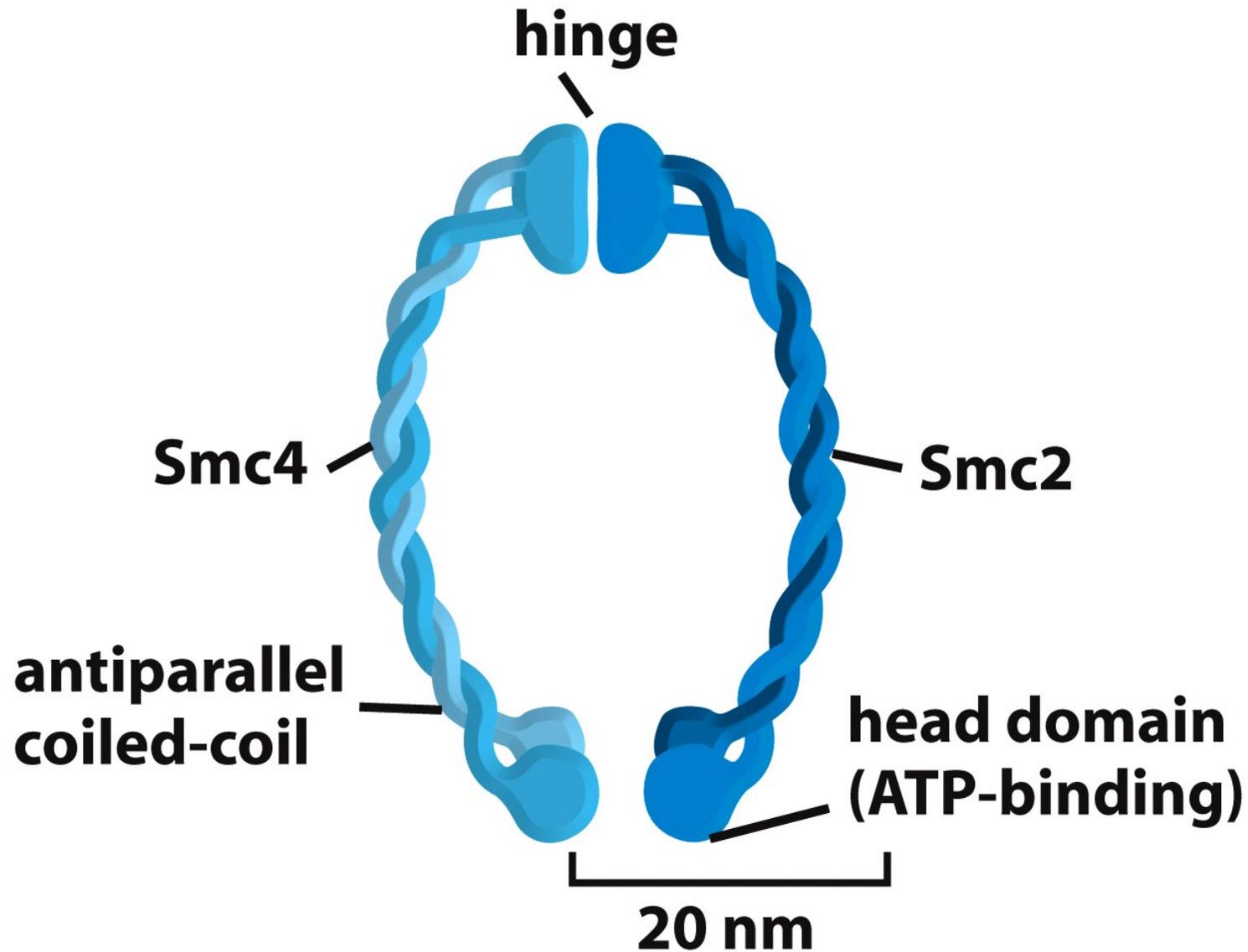
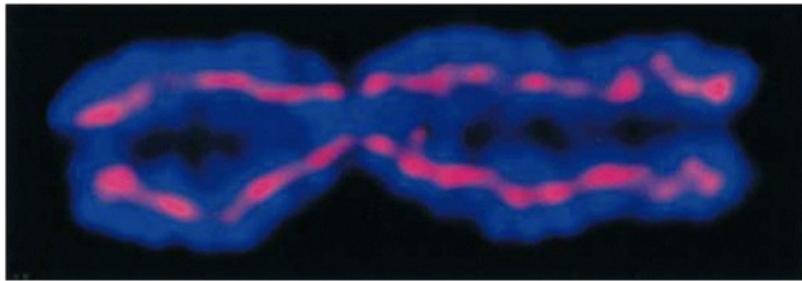


Figure 18-19b Essential Cell Biology 3/e (© Garland Science 2010)

‘Condensins help to coil the mitotic chromatids into, smaller, **more compact** structures that can be more easily segregated during mitosis.’

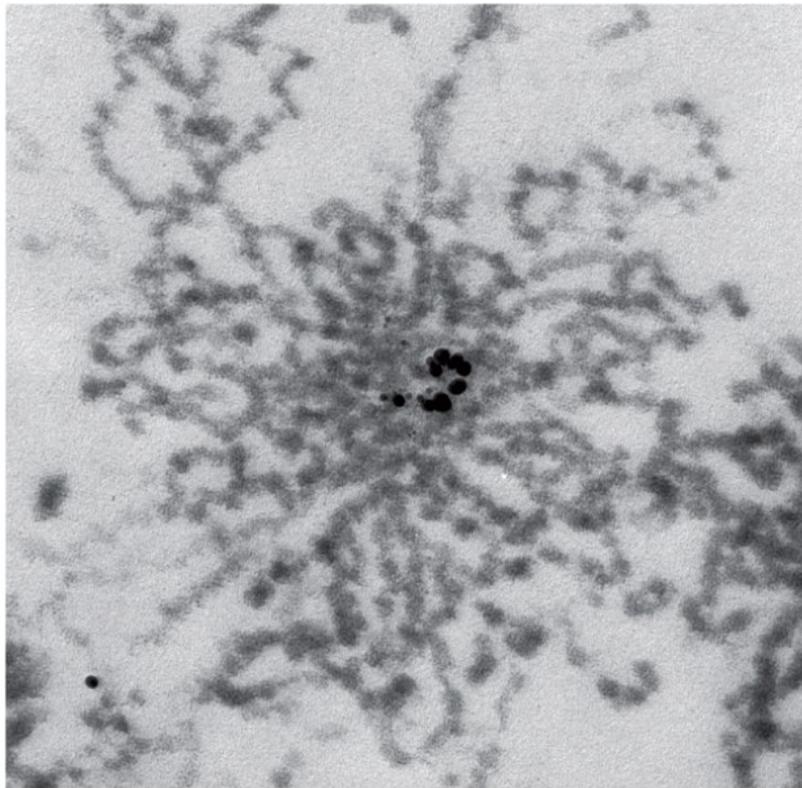


The structure of a SMC dimer. The long central region of this protein is an antiparallel coiled-coil with a flexible hinge in its middle.



(A)

1  $\mu\text{m}$



(B)

0.5  $\mu\text{m}$

**Figure 4-74 The location of condensin in condensed mitotic chromosomes.** (A) Fluorescence micrograph of a human chromosome at mitosis, stained with an antibody that localizes condensin. In chromosomes that are this highly condensed, the condensin is seen to be concentrated in punctate structures along the chromosome axis. Similar experiments show a similar location for DNA topoisomerase II, an enzyme that makes reversible double-strand breaks in DNA that allow one DNA double helix to pass through another (see Figure 5-23). (B) Immunogold electron microscopy reveals localization of condensin (*black dots*). Here a chromatid is seen in cross section, with the chromosome axis perpendicular to the plane of the paper. (A, from K. Maeshima and U.K. Laemmli, *Dev. Cell* 4:467-480, 2003. With permission from Elsevier. B, courtesy of U.K. Laemmli, from K. Maeshima, M. Eltsov and U.K. Laemmli, *Chromosoma* 114:365-375, 2005. With permission from Springer.)

Chromatin in the living cell rarely adopts the extended beads-on-a-string form. Instead, the nucleosomes are further packed to generate a more compact structure, the *30-nm fiber*.

## 1) Histone H1

- *5th histone; Linker histone*.

Pull the nucleosomes together into a regular repeating array into 30-nm fiber.

## Mitotic chromosome

30-nm fiber is folded into a series of loops.

Further condensed to produce the interphase chromosome.

Undergo at least one more level of packing for the mitotic chromosome.

## 2) Condensin

# Nucleosomes are the basic units of chromatin structure

- (A) Chromatin from an interphase nucleus as a thread 30 nm thick
- (B) Chromatin experimentally *unpacked* to show the nucleosomes.

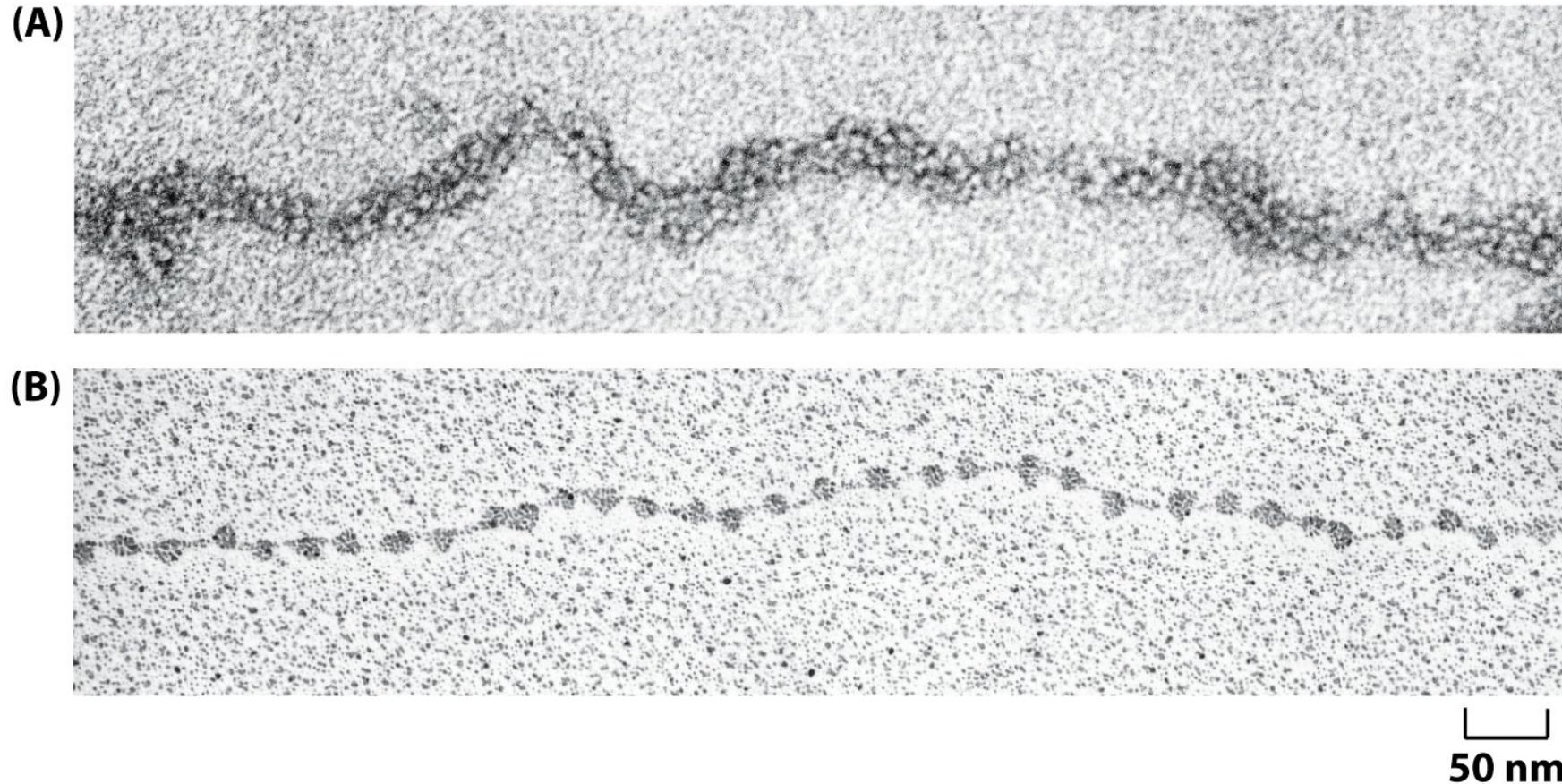


Figure 5-21 Essential Cell Biology 3/e (© Garland Science 2010)

The *proteins* that bind to the DNA

*Histones*

*Nonhistone chromosomal proteins*

- *Histones*

*Enormous quantities:* 60 million molecules / cell.

*Equal mass* to that of DNA itself.

## *Chromatin*

The complex of both classes of *proteins + nuclear DNA*.

Exist in the form of *fiber* with a 30 nm diameter.

## *Nucleosome*

Consists of *DNA wound around a core histones*.

*“beads on a string”*

# Nucleosomes contain DNA + Histones

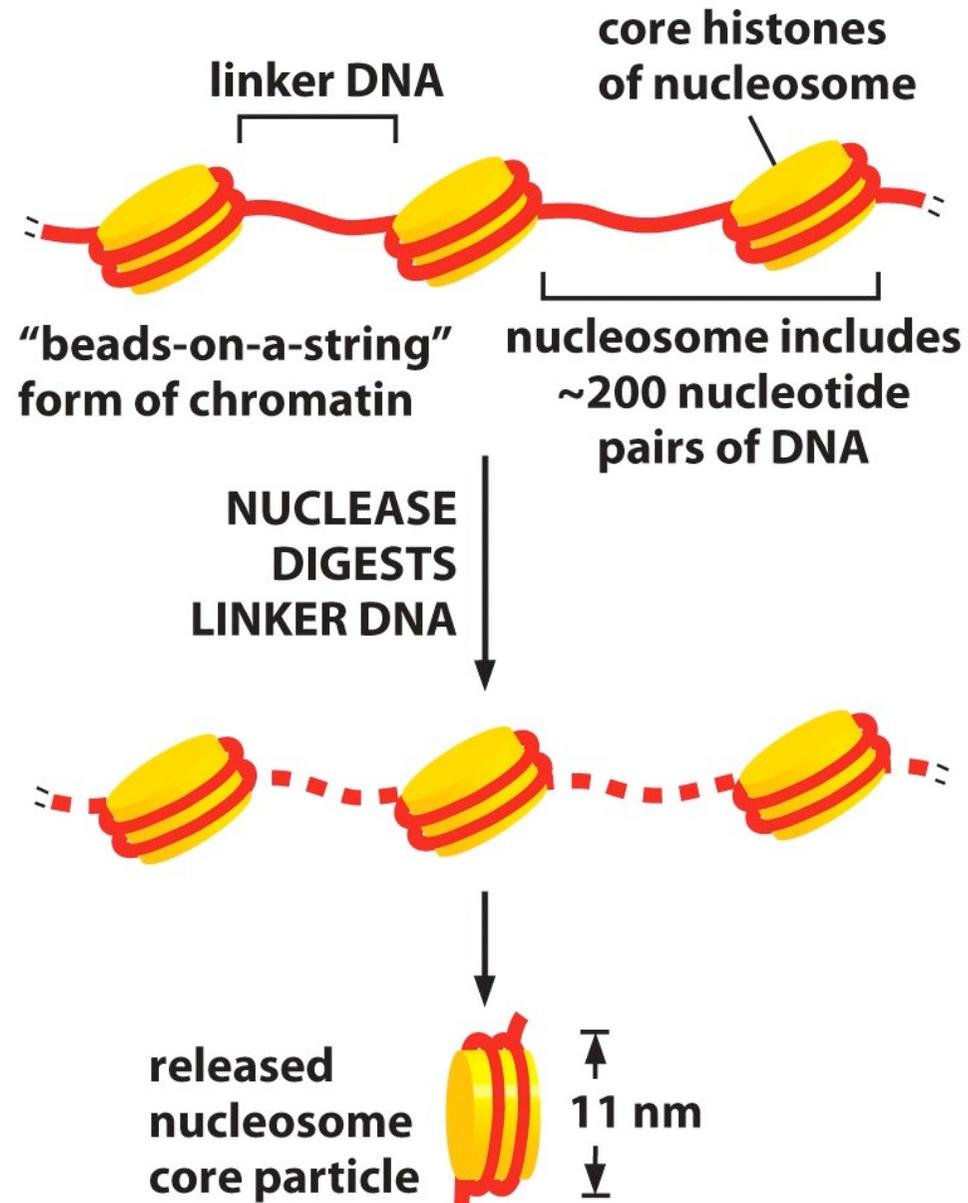


Figure 5-22 part 1 of 2 Essential Cell Biology 3/e (© Garland Science 2010)

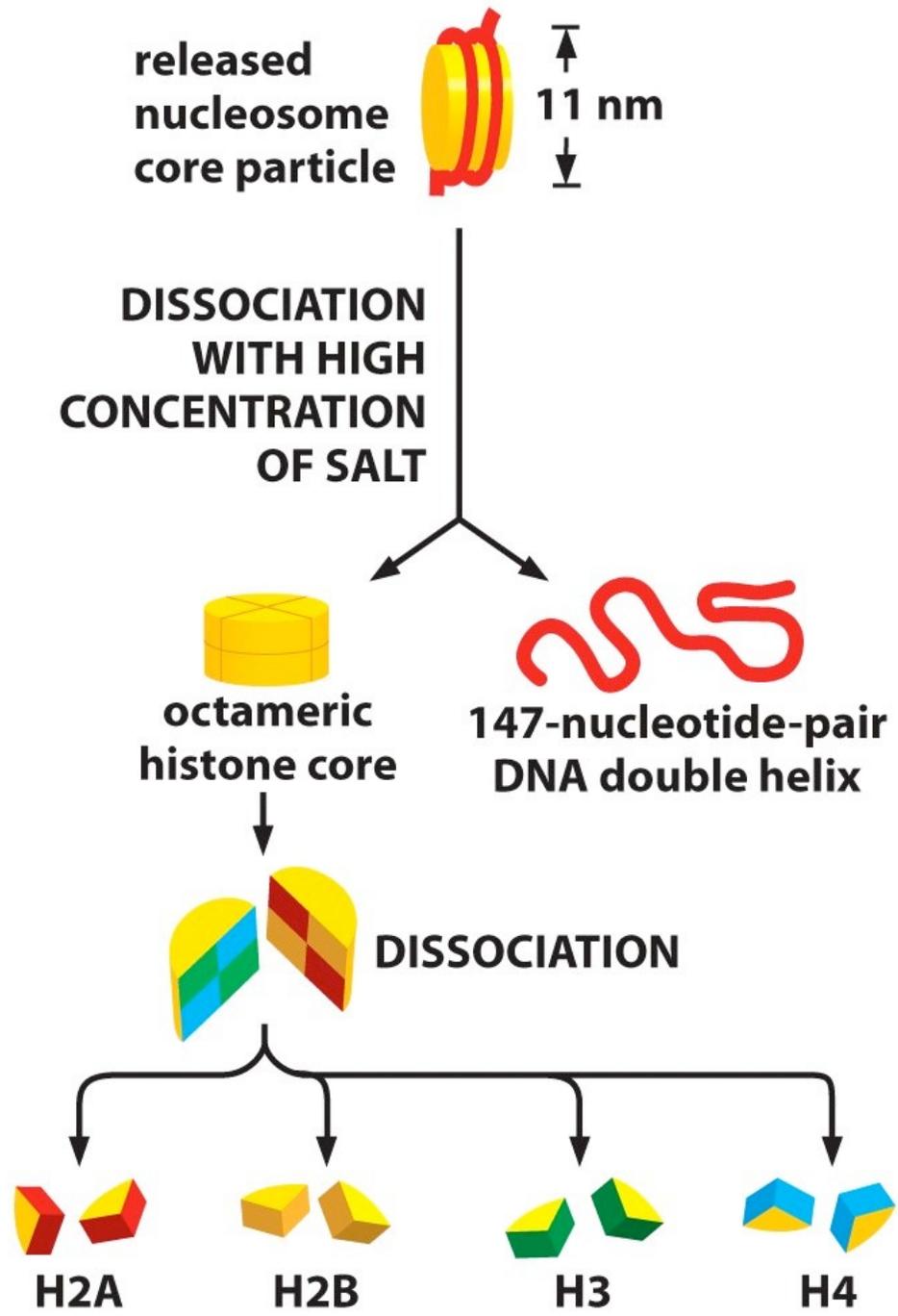


Figure 5-22 part 2 of 2 Essential Cell Biology 3/e (© Garland Science 2010)

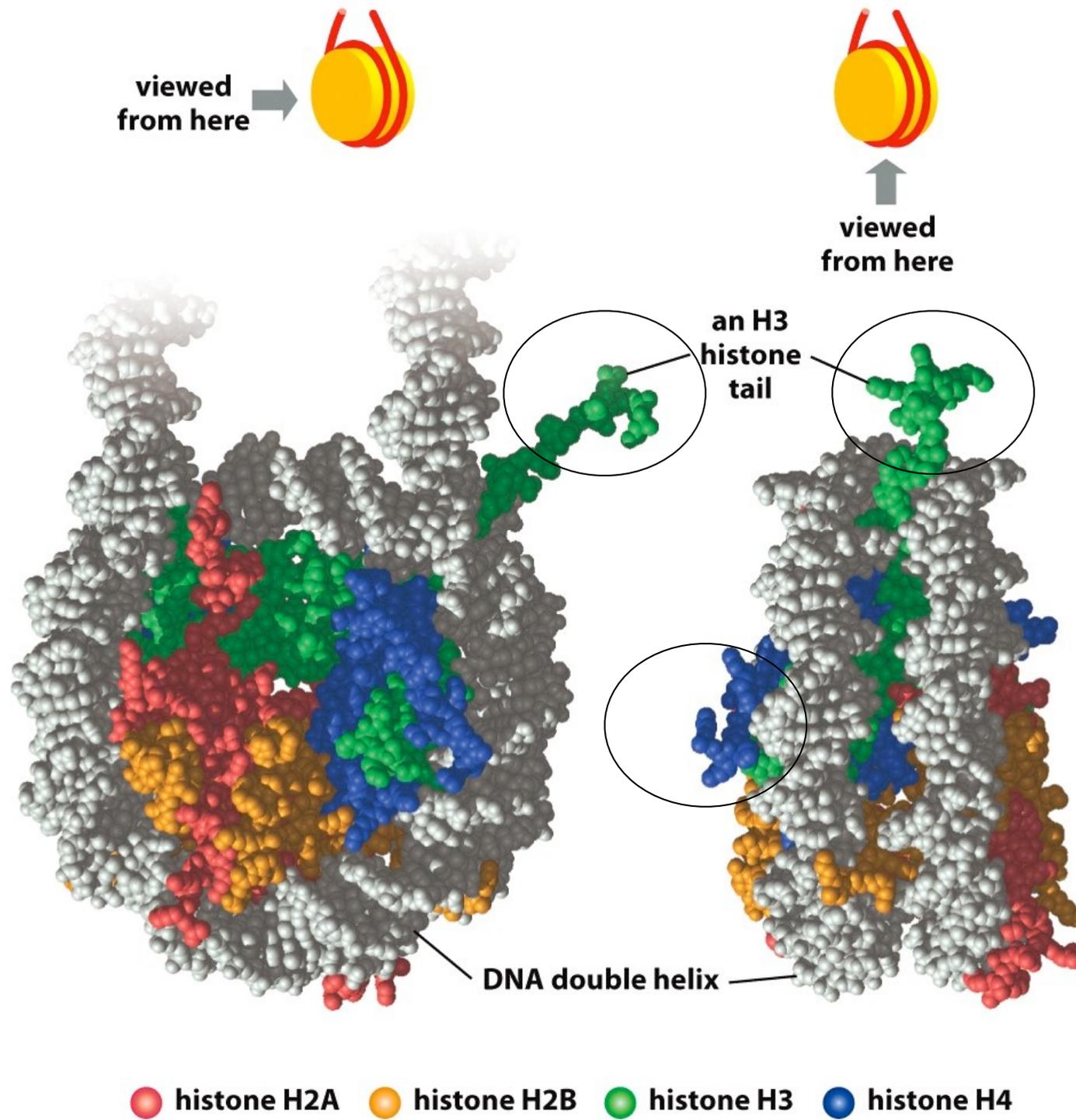


Figure 5-23 Essential Cell Biology 3/e (© Garland Science 2010)



# The structure of *nucleosome*

Isolation of nucleosome : 'nuclease'.

An individual 'nucleosome core particle'

Eight histone proteins (H2Ax2, H2Bx2, H3x2, and H4x2) and double-stranded DNA.

DNA is **147 nt** pairs long, winds around the histone octamer.

High resolution structure of the nucleosome

Solved in **1997** in atomic detail.

Disc-shaped histone complex around which the DNA is *tightly wrapped*, making **1.7 turns in a left-handed coil**.

Linker DNA

DNA between nucleosomes : **~ 80 nt**.

Meaning...

Converts a DNA molecule into a chromatin thread ~ 1/3 of its initial length.

*First level of DNA packing.*

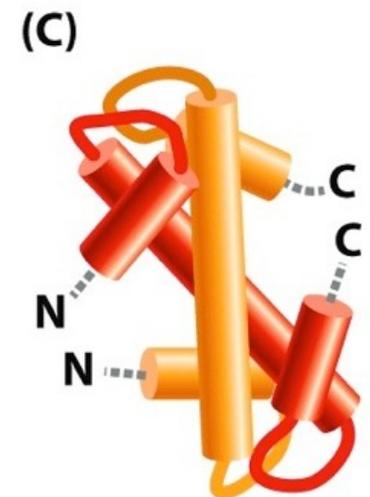
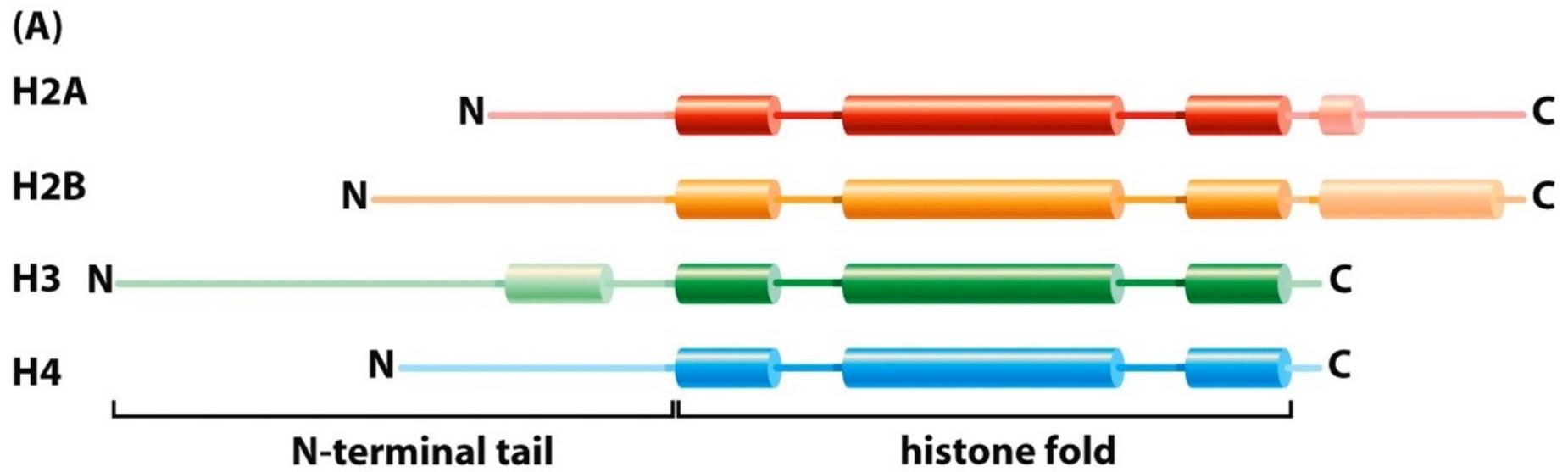


Figure 4-25 Molecular Biology of the Cell 5/e (© Garland Science 2008)



# Histones

*Small proteins* (H2A, H2B, H3, H4 and H1)

Contain positively charged amino acids (K or R).

*Bind tightly* to the negatively charged DNA.

Histone N-terminal tail

Several types of covalent modification (*epigenetically inherited*)

*Control* many aspects of chromatin structure and gene expression (acetylation; methylation; phosphorylation; ubiquitination).

Highly conserved of all known eukaryotic proteins.

*Extreme evolutionary conservation* (e.g. peas and cows).

Vital role in *controlling eucaryotic chromosome structure*.

Also found in *archaea*.

# The Regulation of Chromosome Structure

*Changes in nucleosome structure allow access to DNA*

Two ways to adjust the *local structure* of their chromatin *rapidly*

1. *Chromatin Remodeling Complexes*

2. *Chemical Modifications of the Histones*

# Dynamic Nucleosome

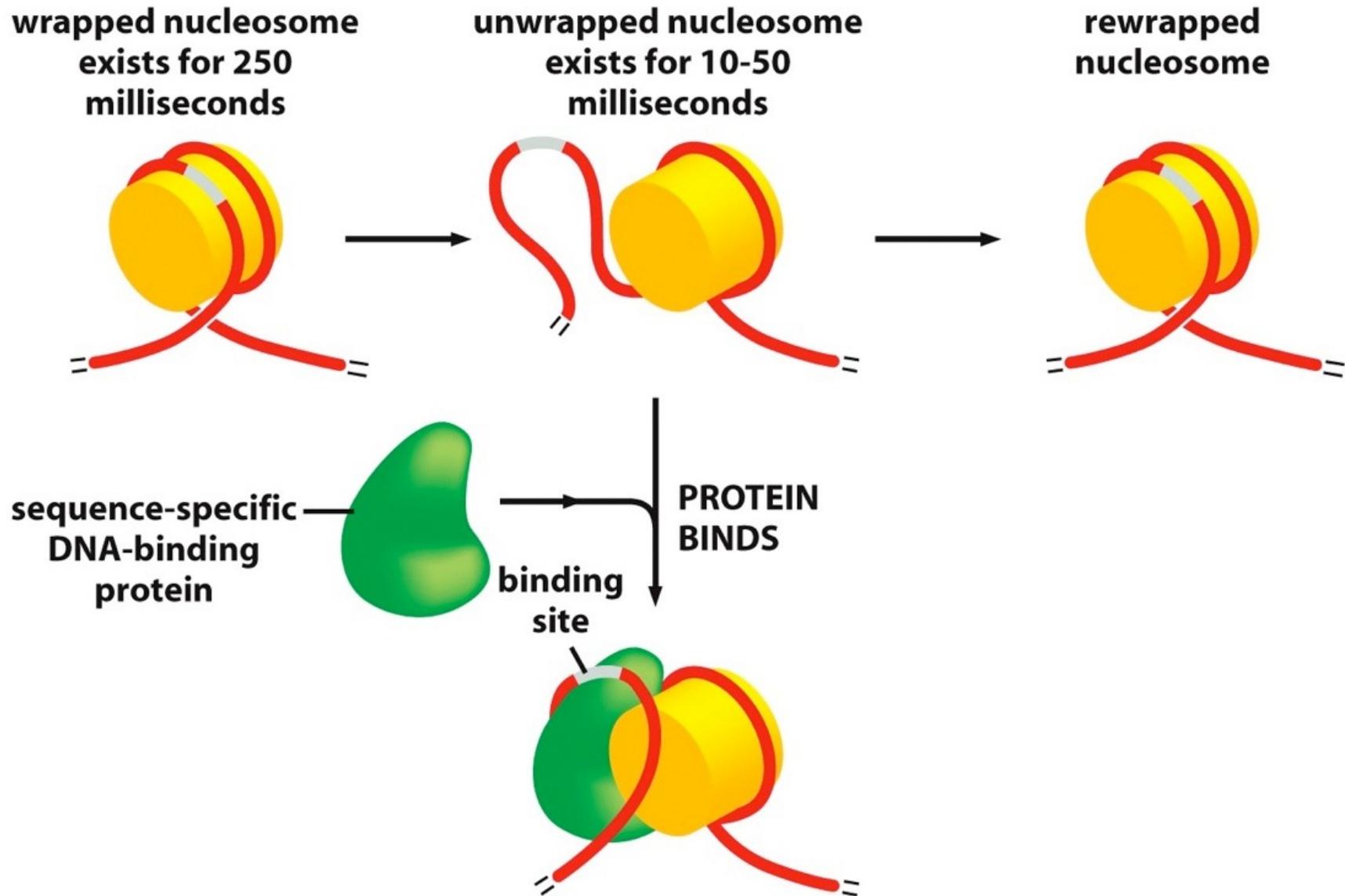


Figure 4-28 Molecular Biology of the Cell 5/e (© Garland Science 2008)

# I. Chromatin Remodeling Complexes

ATP-dependent  
chromatin remodeling  
complex

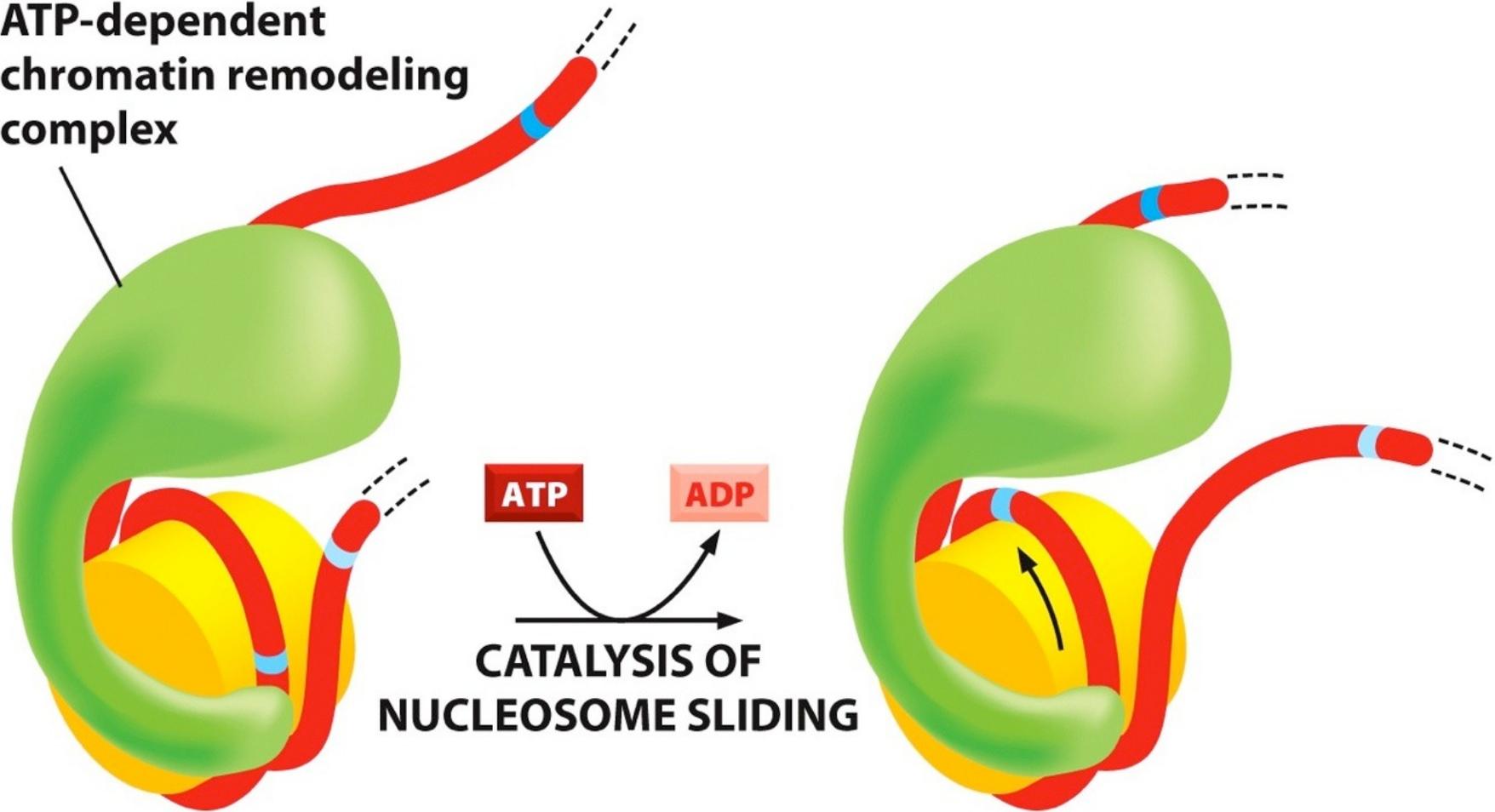


Figure 5-27a Essential Cell Biology 3/e (© Garland Science 2010)

*adjustment; sliding; movement; altering*

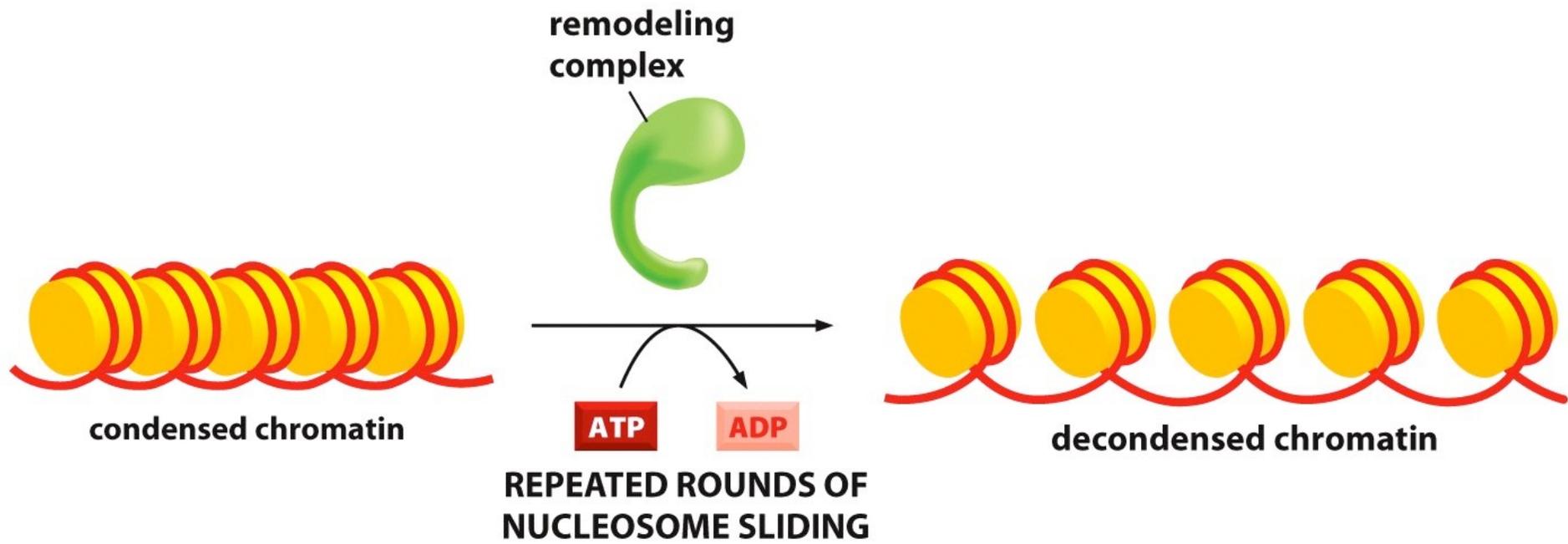


Figure 5-27b Essential Cell Biology 3/e (© Garland Science 2010)

# Nucleosome removal and histone exchange

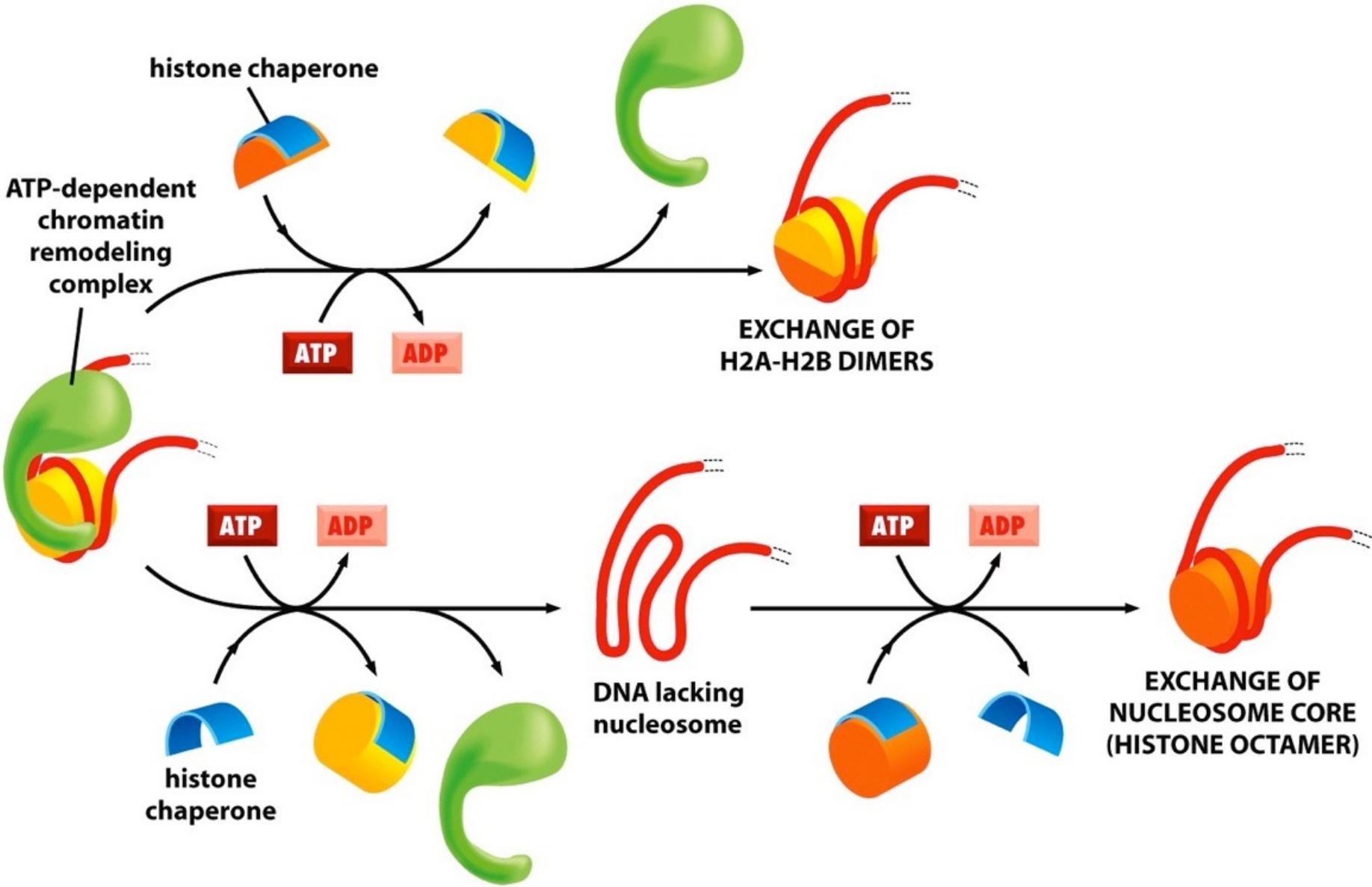


Figure 4-30 Molecular Biology of the Cell 5/e (© Garland Science 2008)

# I. Chromatin Remodeling Complexes

*Protein complex*

Use the *ATP hydrolysis* to change the position of the DNA (*adjustment; sliding; movement; altering*)

*Loosen* the nucleosomal DNA by *pushing* it along the histone core.

Make DNA *more accessible* to other proteins.

*Inactivated* during mitosis.

Other types of *sliding* can also condense the chromatin in a particular region.

In addition, they catalyze *nucleosome removal* and *histone exchange*.

Alberts • Johnson • Lewis • Raff • Roberts • Walter

# ***Molecular Biology of the Cell***

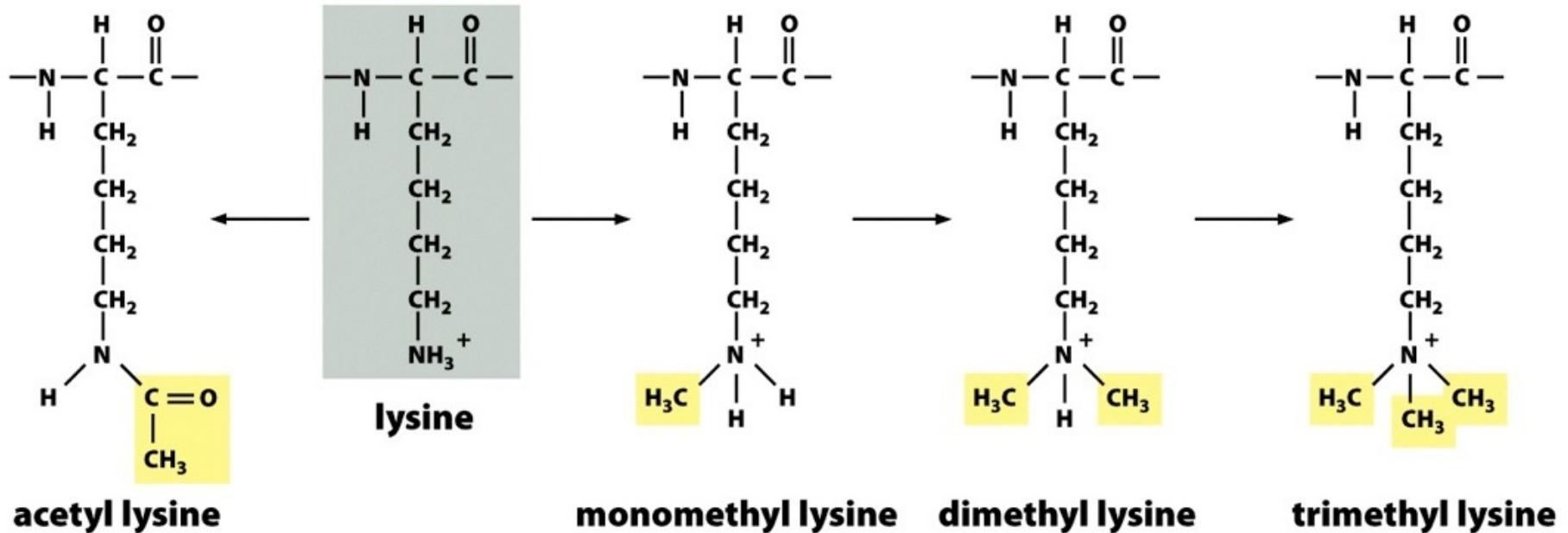
**Fifth Edition**

## **Chapter 4**

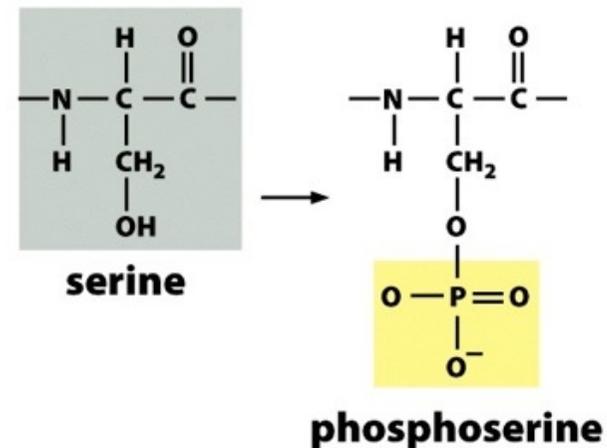
**DNA, Chromosomes, and Genomes**

## 2. Chemical Modifications of the Histones

### (A) LYSINE ACETYLATION AND METHYLATION ARE COMPETING REACTIONS



### (B) SERINE PHOSPHORYLATION



# The covalent modification of core histone tails

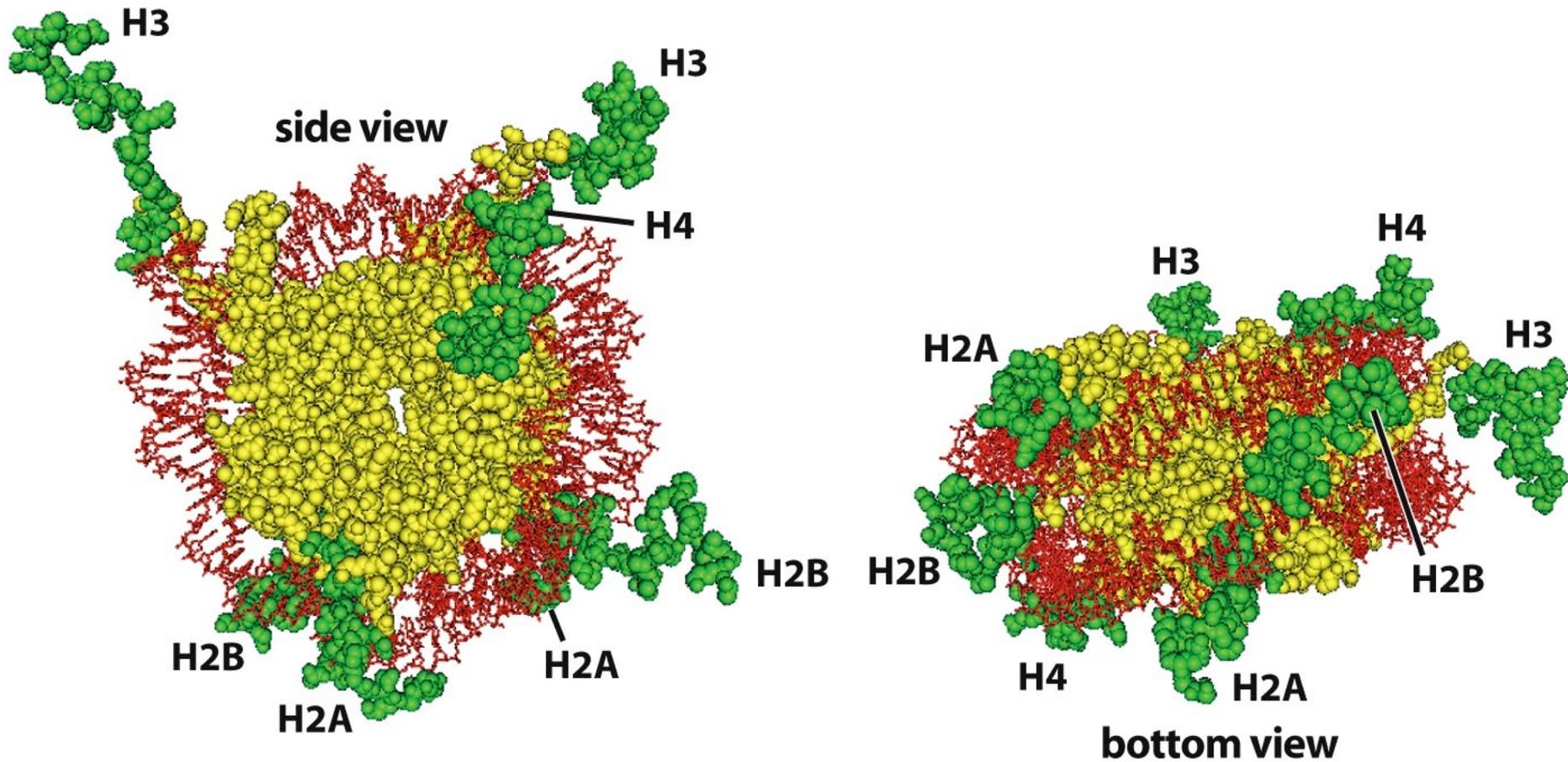


Figure 4-39a Molecular Biology of the Cell 5/e (© Garland Science 2008)

# A map of histone modifications on the surface of the nucleosome core particle

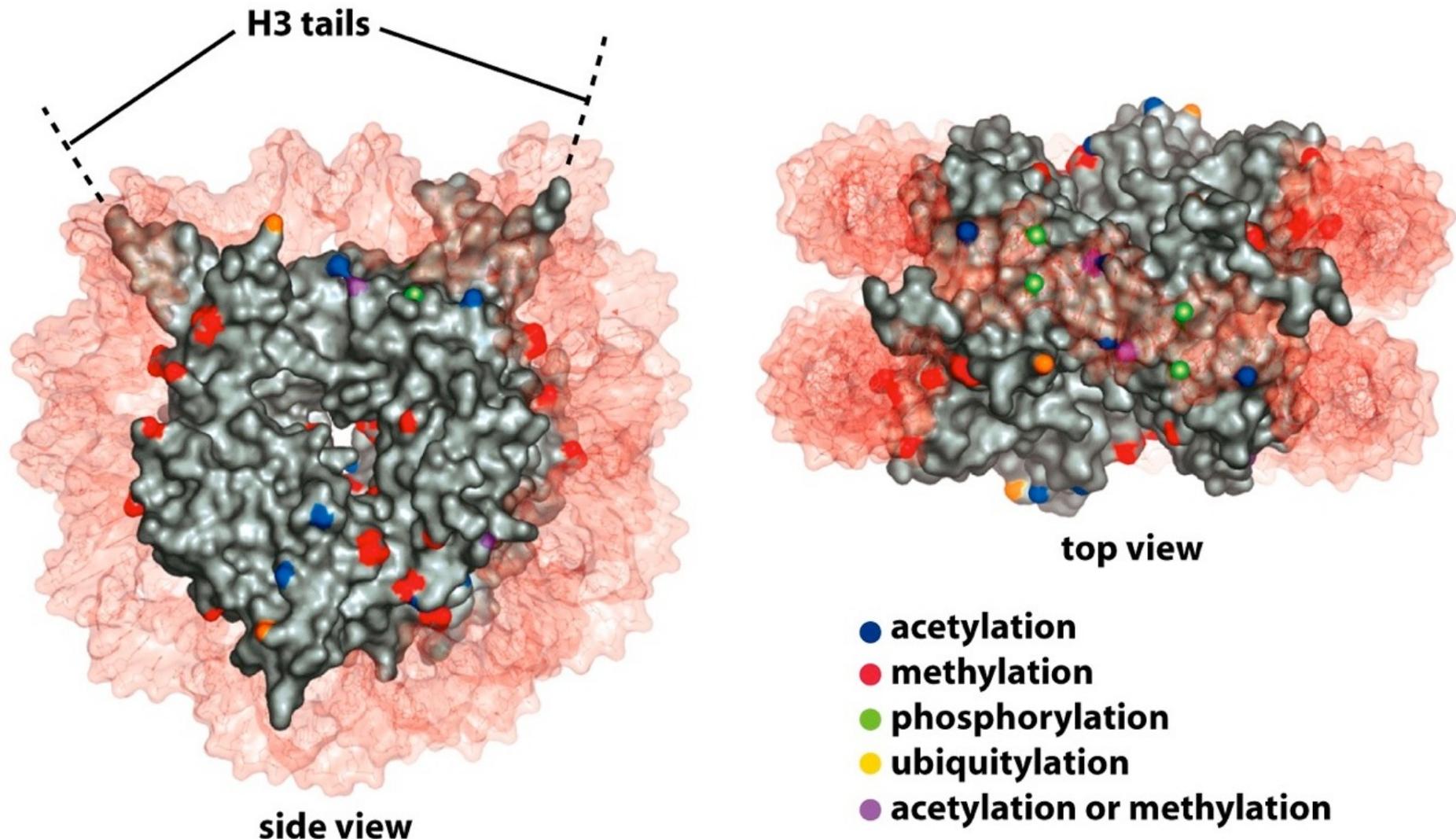


Figure 4-40 Molecular Biology of the Cell 5/e (© Garland Science 2008)

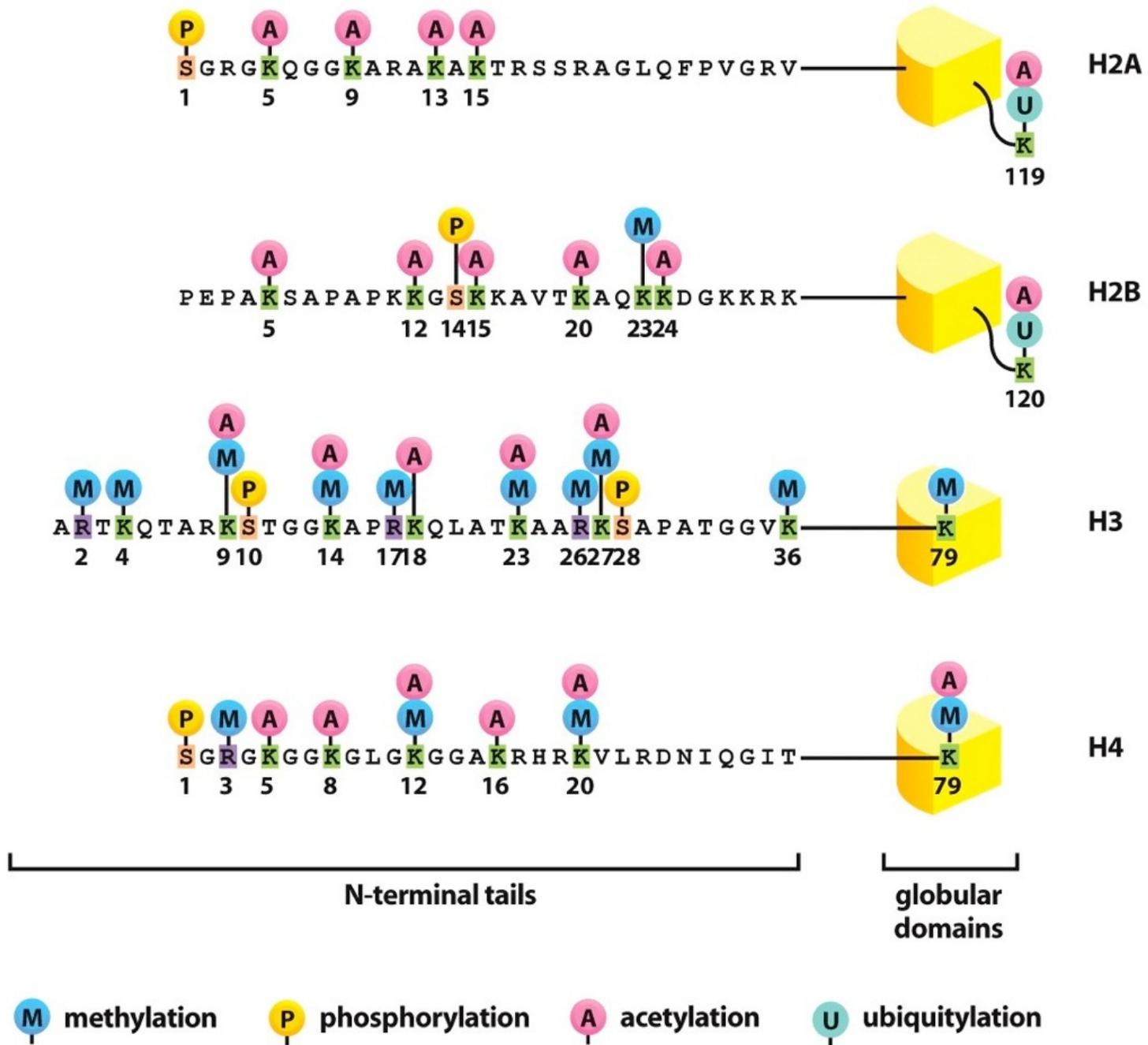


Figure 4-39b Molecular Biology of the Cell 5/e (© Garland Science 2008)

# Some specific meanings of the histone code

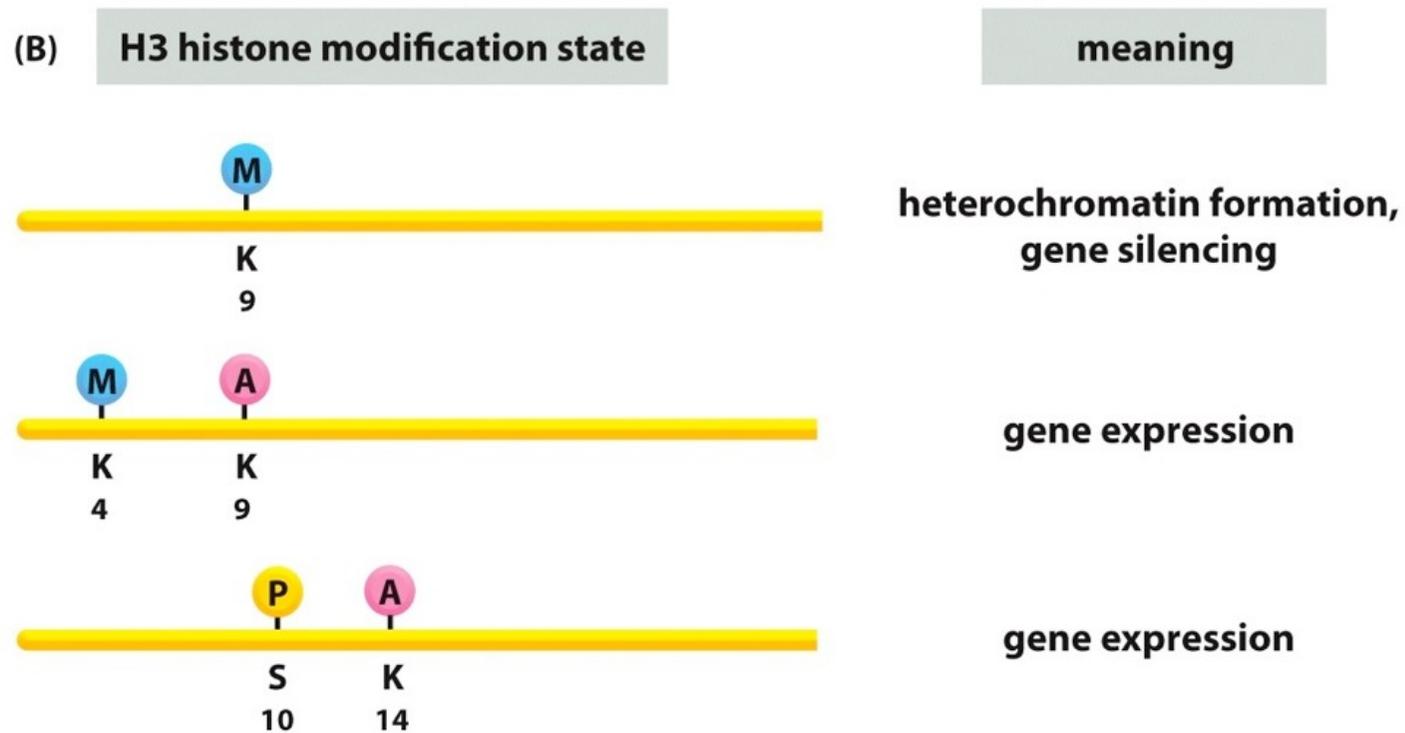
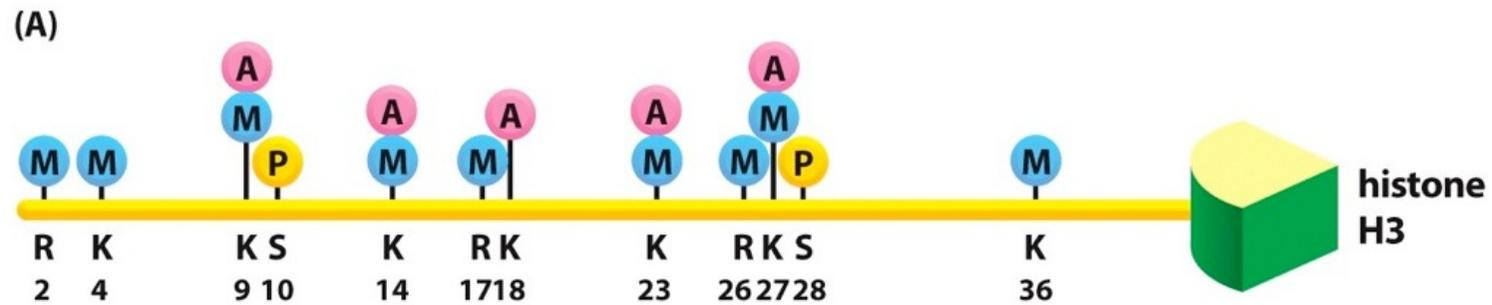


Figure 5-28 Essential Cell Biology 3/e (© Garland Science 2010)

# Chemical Modifications of the Histones

*Tails* of all four of the core histones.

*Covalent modifications* (ac, ph, me, or ub).

Affect the ability of the *histone tails to bind specific proteins* and therefore *recruit* them to particular stretches of chromatin.

*Different patterns* attract *different proteins*.

*Specific combinations* have *different meanings* for the cell.

*Further (de)condensation* of chromatin.

*The enzymes that modify histone tails are tightly regulated.*

*The histone-modifying enzymes **work in concert with (Team work)** the chromatin-remodeling complexes to (de)condense stretches of chromatin.*

결론: *Rapidly change local chromatin structure* according to the needs of the cell.

# Heterochromatin

How is the formation of heterochromatin *induced*?

*A particular set* of histone tail modifications (ex. H3K9me, Fig. 5-28B).

H3K9me attracts a set of *heterochromatin-specific proteins*.

These specific proteins then *induce the same H3K9me* in adjacent nucleosomes.

## Conclusion

*A spreading wave of condensed chromatin.*

In this manner, *an extended region of heterochromatin* is established along the DNA.

# Example #1

## Position effect *Variiegation*

(see Figure legend 5-29, p190)

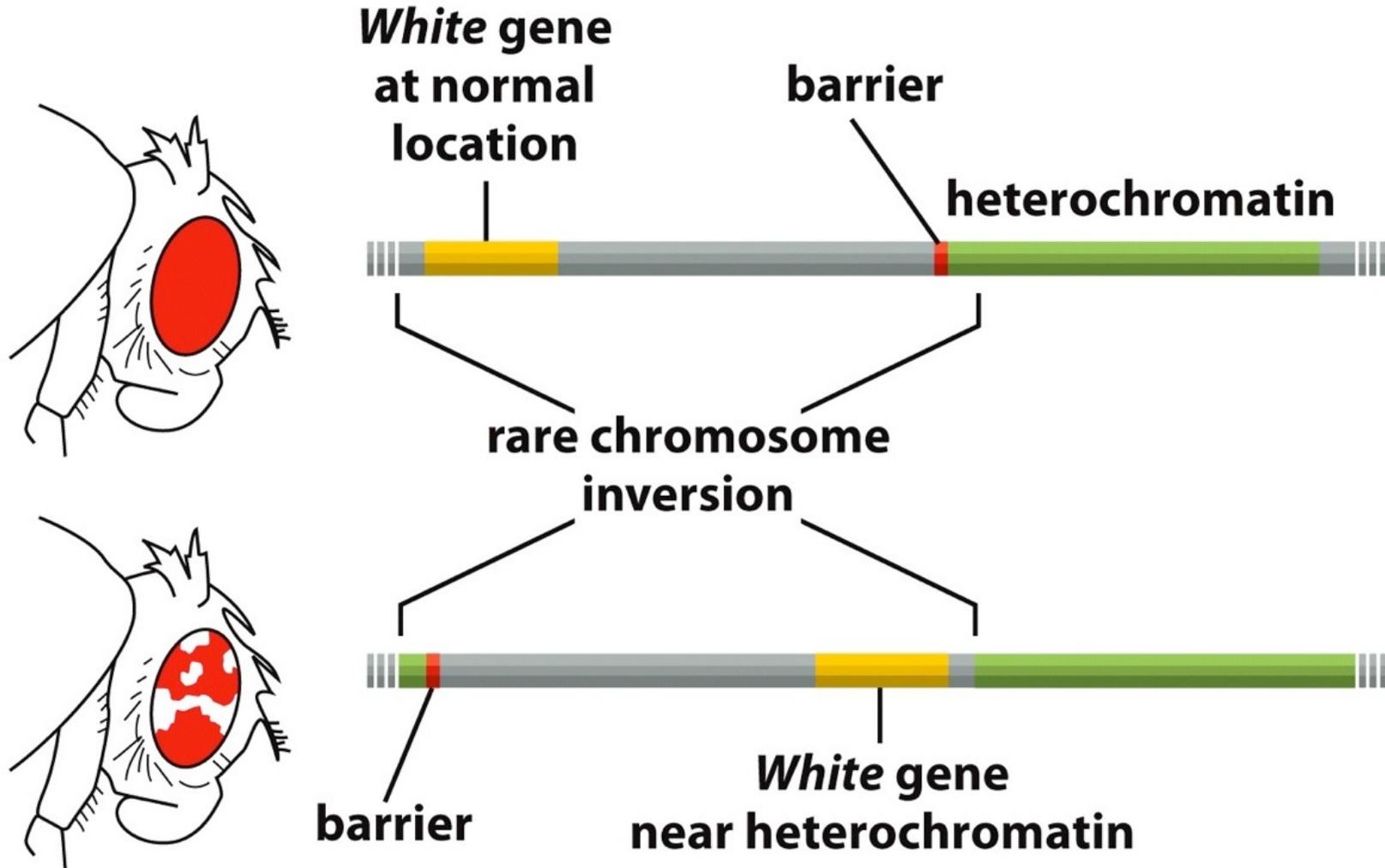


Figure 5-29 Essential Cell Biology 3/e (© Garland Science 2010)

## I. *Position Effect Variegation*

The activity of a gene depends on its *position* along a chromosome (Fig. 5-29).

Genes that do become packaged into heterochromatin usually *become resistant to being expressed* because heterochromatin is unusually compact.

## Example #2

*Inappropriate packing* of genes in heterochromatin can cause *disease*.

$\beta$ -globin is situated next to heterochromatin.

If, DNA is deleted, the region of heterochromatin is spreads, the the gene is poorly expressed.

A severe form of *anemia*.

# Example #3

## X chromosome inactivation

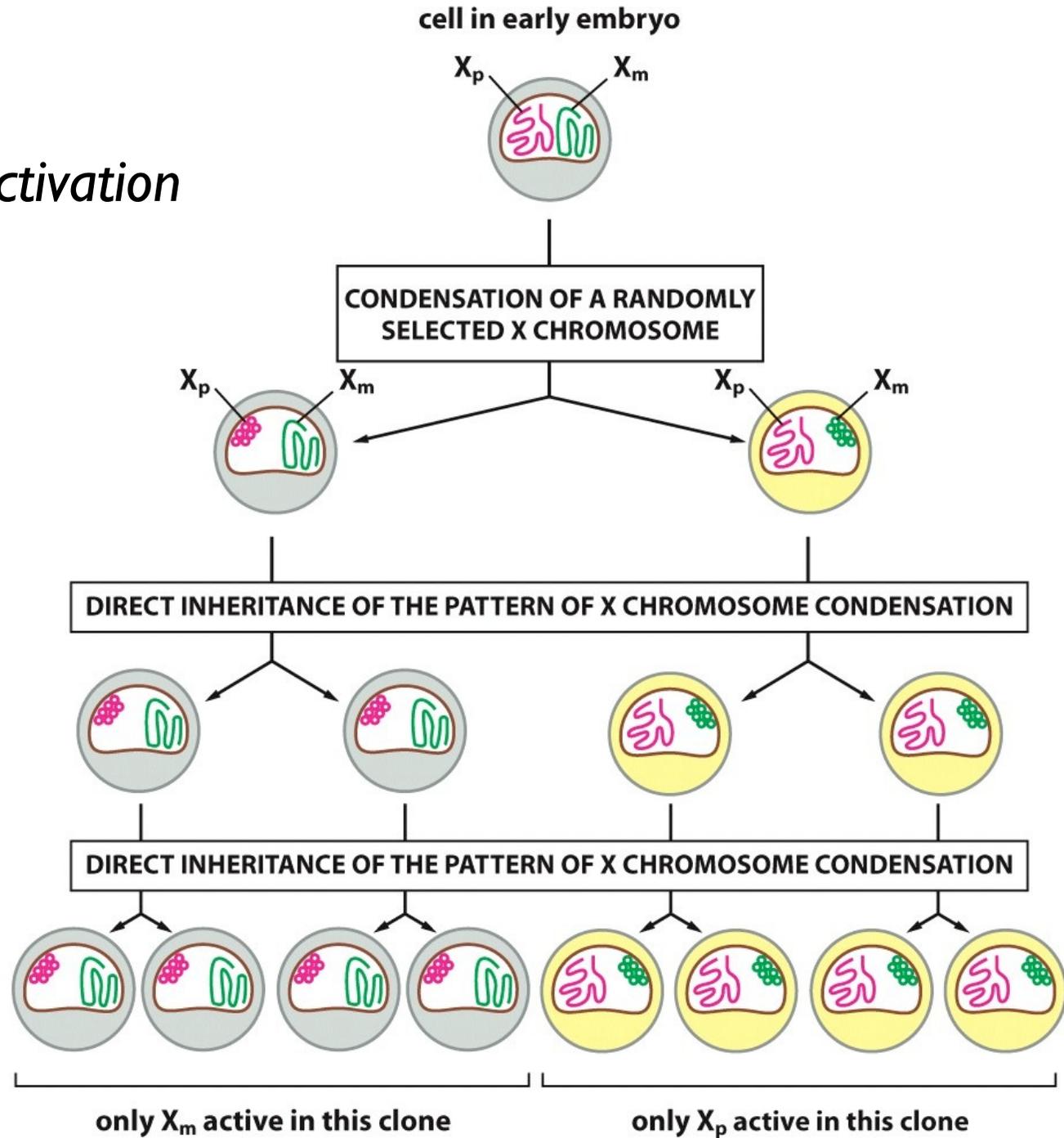


Figure 5-30 Essential Cell Biology 3/e (© Garland Science 2010)

### 3. *X chromosome inactivation*

The *interphase X chromosomes* of female mammals.

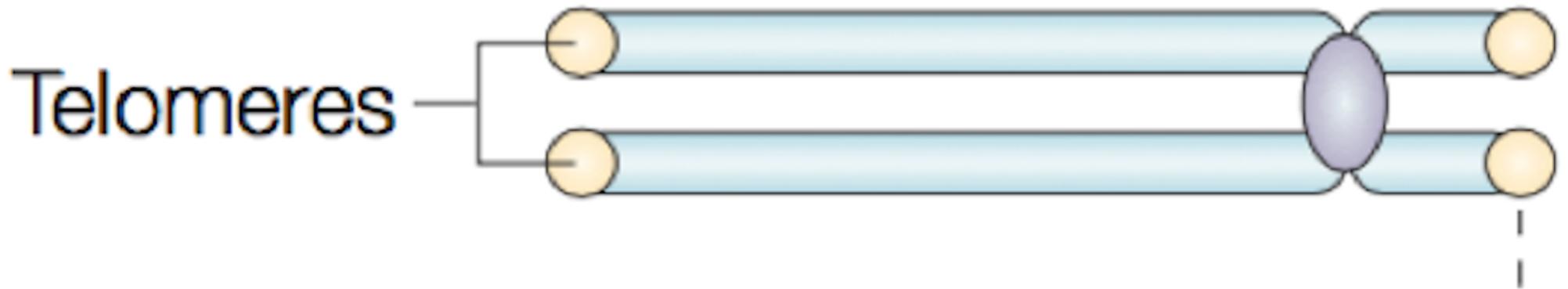
*A double dose* of X-chromosome products would be *lethal*.

*One* of the two X chromosomes in each cell is *permanently inactivated*.

*Completely inactivated* by heterochromatin formation *in early embryo* (see fig 5-28).

Inactive state of X-chromosome is *inherited*.

# Telomeres Have a Special Form of Heterochromatin

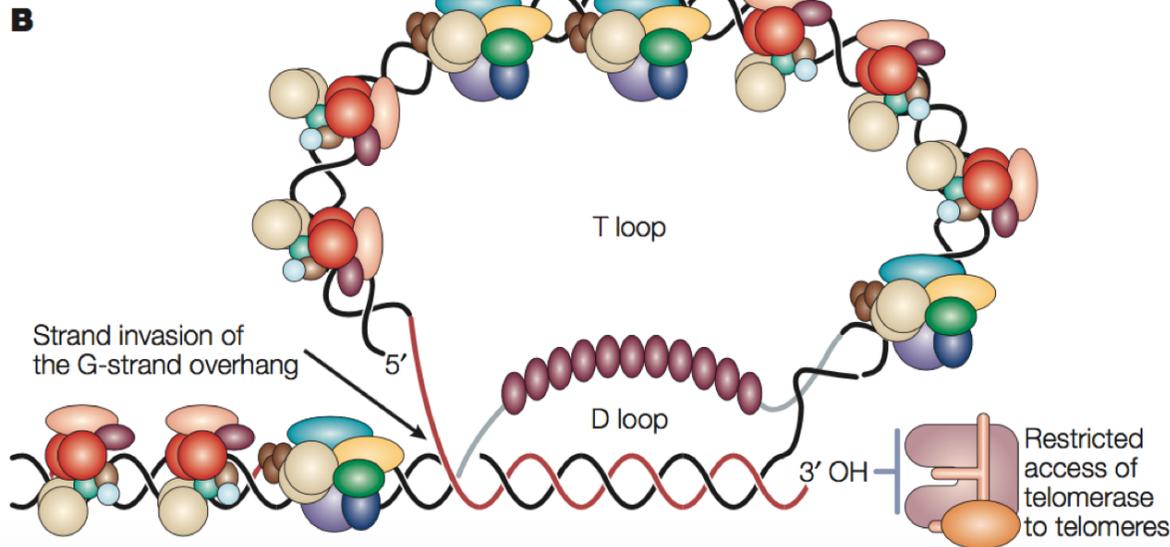
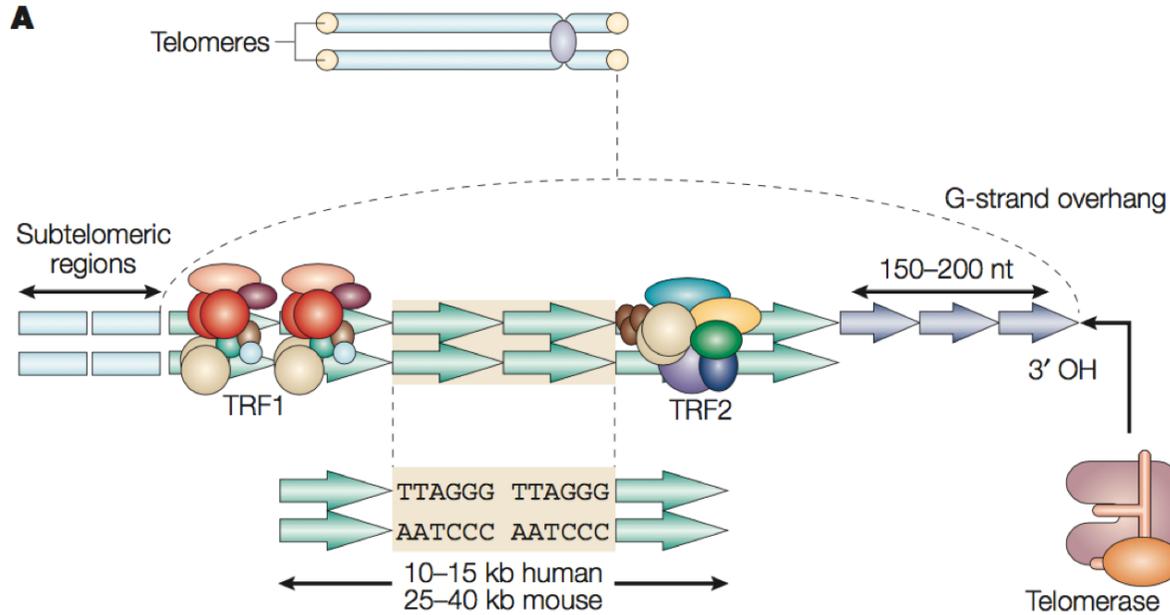


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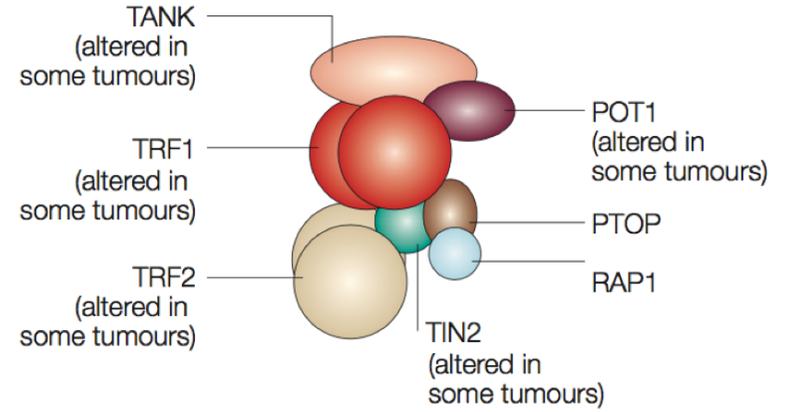
TELOMERES AND HUMAN DISEASE:  
AGEING, CANCER AND BEYOND

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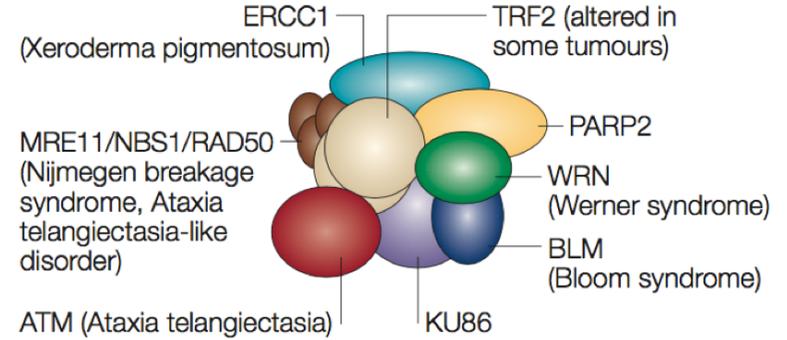
*Maria A. Blasco*



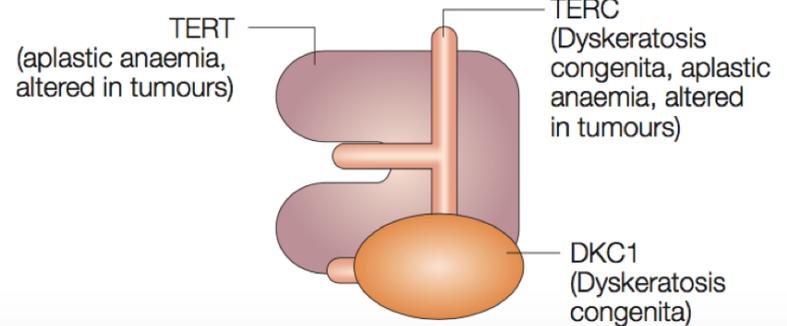
**Ca TRF1 complex**



**Cb TRF2 complex**



**Cc Telomerase**



# Telomeres Have a Special Form of Heterochromatin

Heterochromatin involves an additional level of folding and requires many proteins in addition to histones.

Silent information regulator (Sir) proteins induce the silencing of genes located near telomeres.

A telomere-bound Sir protein complex that recognizes underacetylated N-terminal tails of selected histones.

Sir2 is a highly conserved histone deacetylase (HDAC).

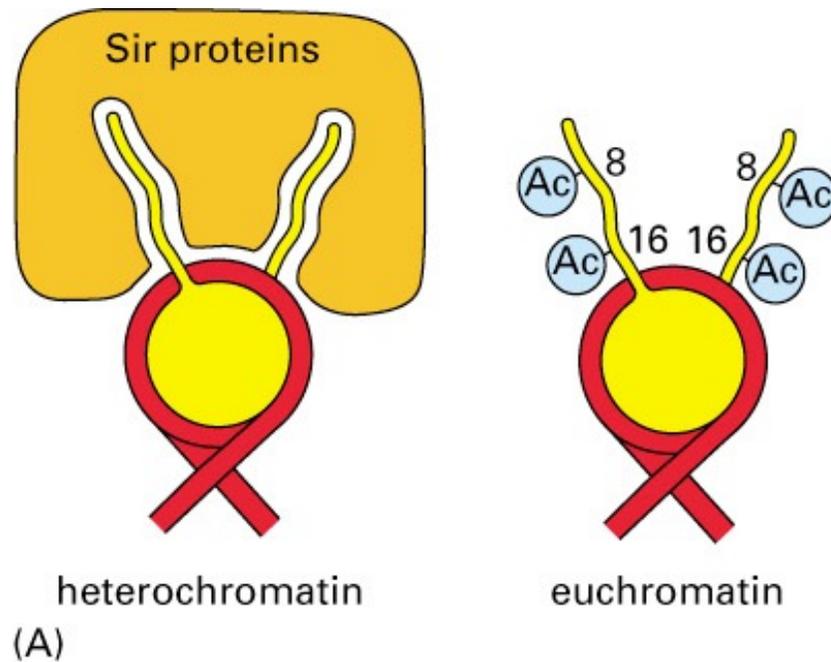
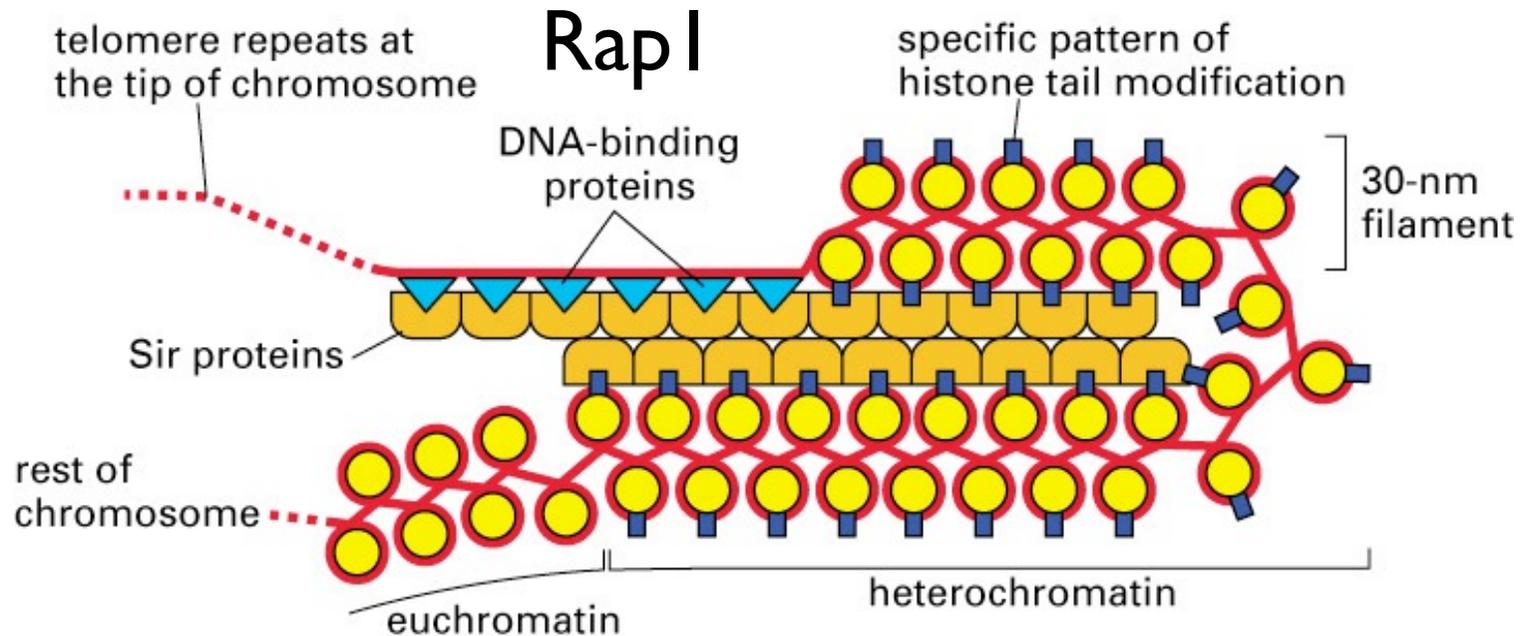


Figure 4-47 part 1 of 2. Molecular Biology of the Cell, 4th Edition.

- Heterochromatin is generally underacetylated.
- Underacetylated tails of histone H4 are proposed to interact with a complex of Sir proteins, thus stabilizing the association of these proteins with nucleosomes.



(B)

Figure 4-47 part 2 of 2. Molecular Biology of the Cell, 4th Edition.

Specialized DNA-binding proteins (blue triangles) recognize DNA sequences near the ends of chromosomes and attract the Sir proteins (Sir2). This then leads to the cooperative spreading of the Sir protein complex down the chromosome.