CAMPBELL BIOLOGY IN FOCUS

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18

Genomes and Their Evolution

Lecture Presentations by
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SECOND EDITION

Overview: Reading Leaves from the Tree of Life

- Complete genome sequences exist for a human, chimpanzee, *E. coli*, and numerous other prokaryotes, as well as corn, fruit fly, house mouse, orangutan, and others
- Comparisons of genomes among organisms provide information about the evolutionary history of genes and taxonomic groups

- **Genomics** is the study of whole sets of genes and their interactions
- **Bioinformatics** is the application of computational methods to the storage and analysis of biological data

Figure 18.1

Concept 18.1: The Human Genome Project fostered development of faster, less expensive sequencing techniques

- The **Human Genome Project** officially began in 1990, and the sequencing was largely completed by 2003
- Even with automation, the sequencing of all 3 billion base pairs in a haploid set presented a formidable challenge
- A major thrust of the Human Genome Project was the development of technology for faster sequencing

- The **whole-genome shotgun approach** was developed by J. Craig Venter and colleagues
- This approach starts with cloning and sequencing random DNA fragments
- Powerful computer programs are used to assemble the resulting short overlapping sequences into a single continuous sequence

Figure 18.2-s1

1 **Cut the DNA into overlapping fragments short enough for sequencing.**

2 **Clone the fragments in plasmid or other vectors.**

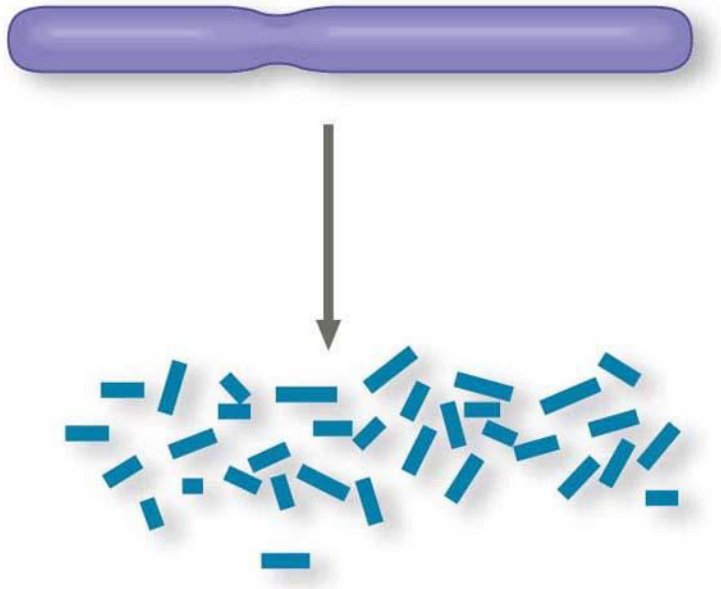


Figure 18.2-s2

1. Cut the DNA into overlapping fragments short enough for sequencing.

2. Clone the fragments in plasmid or other vectors.

3. Sequence each fragment.

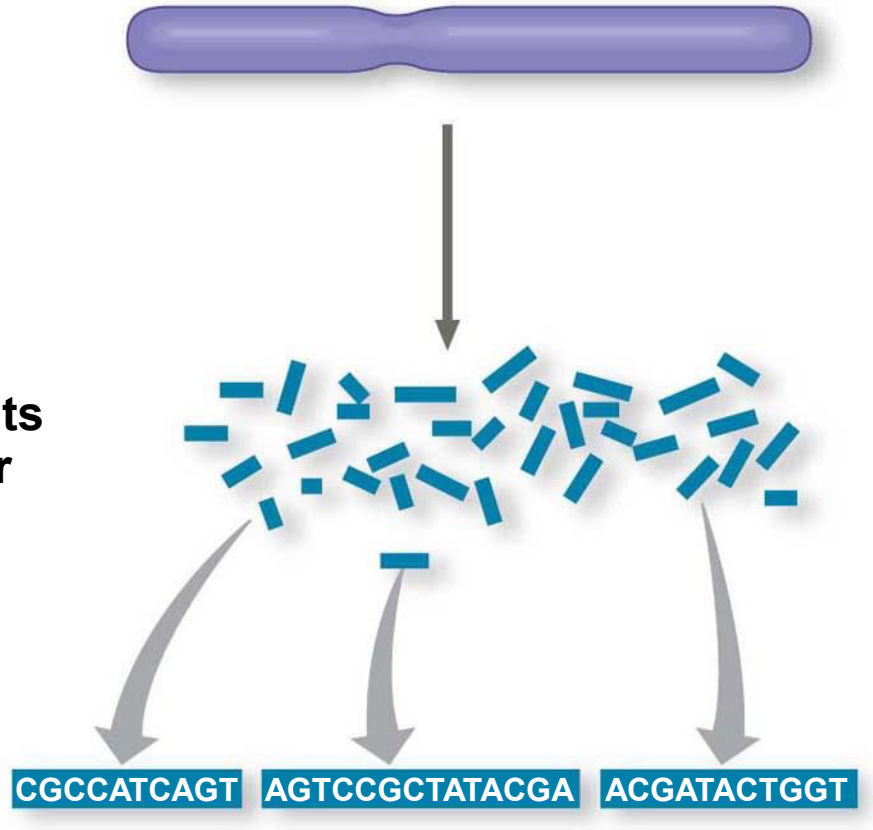
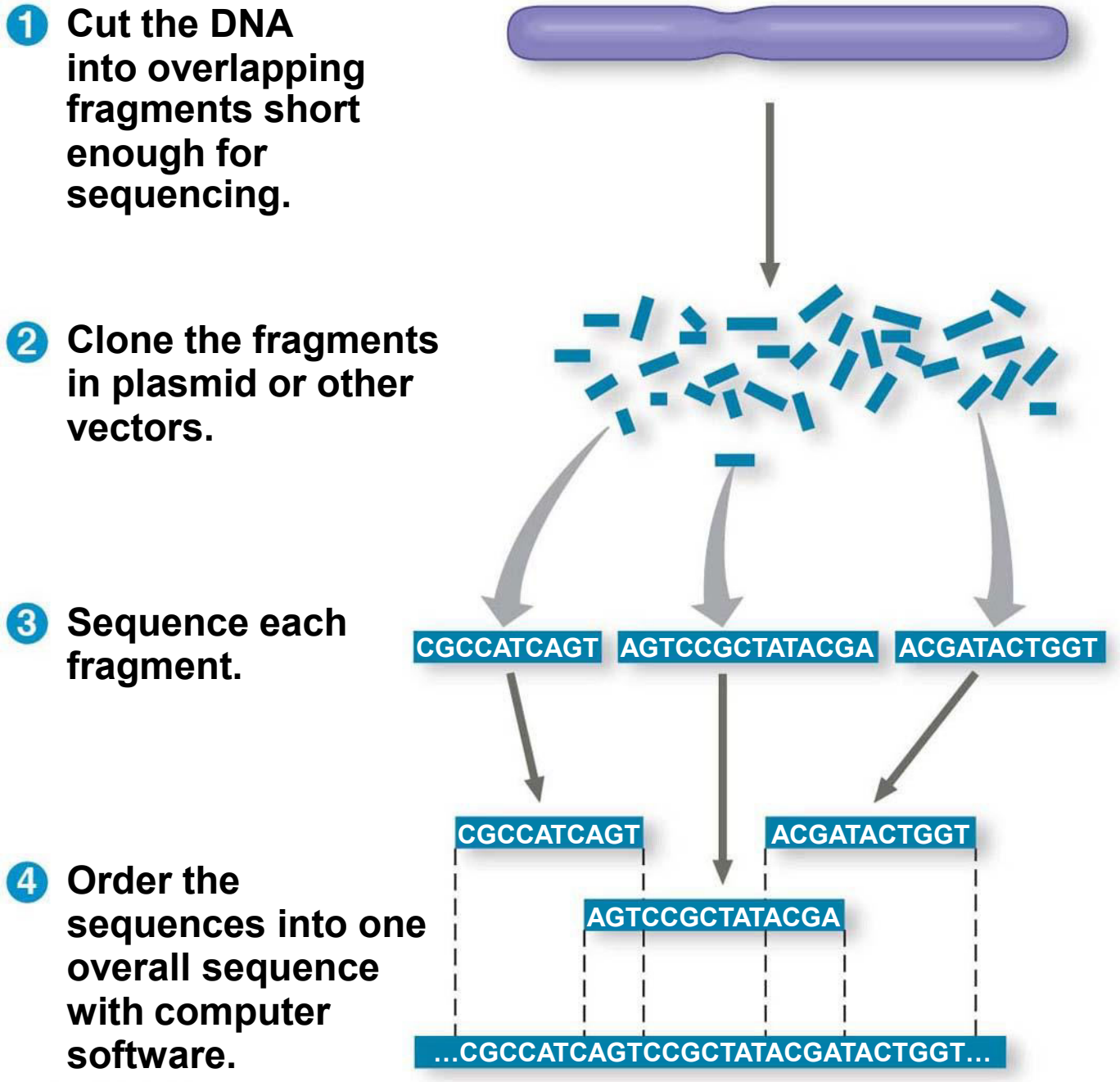


Figure 18.2-s3



- The whole-genome shotgun approach is widely used today
- Newer sequencing techniques, called sequencing by synthesis, have resulted in massive increases in speed and decreases in cost of sequencing entire genomes
- These sensitive techniques allow direct sequencing of fragments without a cloning step

- The new sequencing techniques have facilitated an approach called **metagenomics**
- In this approach, DNA from a group of species in an environmental sample is collected and sequenced
- Computer software sorts out the partial sequences and assembles them into their specific genomes

Concept 18.2: Scientists use bioinformatics to analyze genomes and their functions

- The Human Genome Project established databases and refined analytical software to make data available on the Internet
- This has accelerated progress in DNA sequence analysis

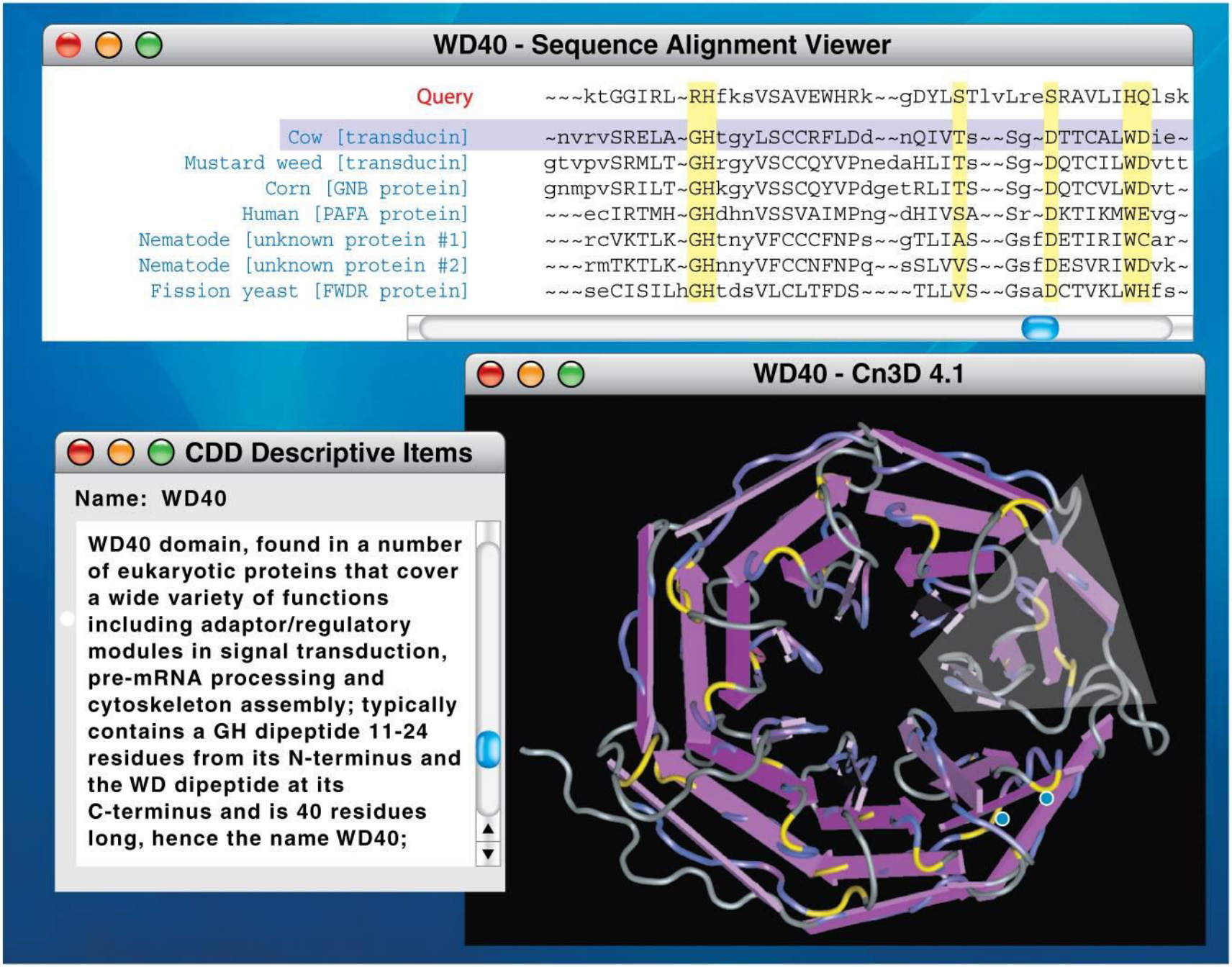
Centralized Resources for Analyzing Genome Sequences

- Bioinformatics resources are provided by a number of sources
  - National Library of Medicine and the National Institutes of Health (NIH) created the National Center for Biotechnology Information (NCBI)
  - European Molecular Biology Laboratory
  - DNA Data Bank of Japan
  - BGI in Shenzhen, China

- GenBank, the NCBI database of sequences, doubles its data approximately every 18 months
- Software is available that allows online visitors to search GenBank for matches to
  - A specific DNA sequence
  - A predicted protein sequence
  - Common stretches of amino acids in a protein and a three-dimensional model of the domain

- Sequences of DNA or proteins can be diagrammed as an evolutionary tree based on sequence relationships
- The Protein Data Bank contains all three-dimensional protein structures that have been determined
- This vast array of resources can be used by researchers anywhere in the world, free of charge

Figure 18.3



Understanding the Functions of Protein-Coding Genes

- DNA sequence may vary more than the protein sequence does
- Scientists interested in proteins often compare the predicted amino acid sequence of a protein with that of other proteins
- Protein function can be deduced from sequence similarity or a combination of biochemical and functional studies

Understanding Genes and Gene Expression at the Systems Level

- Genomics is a rich source of insights into questions about gene organization, regulation of expression, growth and development, and evolution
- A project called ENCODE (Encyclopedia of DNA Elements) has yielded a wealth of information about protein-coding genes, genes for noncoding RNA, and sequences that regulate DNA replication, gene expression, and chromatin modification

Systems Biology

- **Proteomics** is the systematic study of the full protein sets (**proteomes**) expressed by cells
- We must study when and where proteins are produced in an organism in order to understand the function of cells and organisms
- **Systems biology** aims to model the dynamic behavior of whole biological systems based on the study of interactions among the system's parts

Application of Systems Biology to Medicine

- A systems biology approach has several medical applications
  - The Cancer Genome Atlas project (completed in 2010) attempted to identify all the common mutations in three types of cancer by comparing gene sequences and expression in cancer versus normal cells
  - This was so fruitful that it will be extended to ten other common cancers
  - Silicon and glass “chips” have been produced that hold a microarray of most known human genes

- Analyzing which genes are over- or underexpressed in cancers may allow physicians to tailor treatment to particular patients and the specifics of their cancers
- Ultimately, medical records may include an individual's DNA sequence
- The use of such sequences for personalized medicine has great potential

Figure 18.4

Concept 18.3: Genomes vary in size, number of genes, and gene density

- To date, the sequences of thousands of genomes have been completed
- Tens of thousands of genomes are in progress or considered permanent drafts
- 550 metagenomes are also in progress

Genome Size

- Genomes of most bacteria and archaea range from 1 to 6 million base pairs (Mb); genomes of eukaryotes are usually larger
- Most plants and animals have genomes greater than 100 Mb; humans have 3,000 Mb
- Within each domain there is no systematic relationship between genome size and phenotype

Table 18.1

Table 18.1 Genome Sizes and Estimated Numbers of Genes*

Organism	Haploid Genome Size (Mb)†	Number of Genes	Genes per Mb†
Bacteria			
Haemophilus influenzae	1.8	1,700	940
Escherichia coli	4.6	4,400	950
Archaea			
Archaeoglobus fulgidus	2.2	2,500	1,130
Methanosarcina barkeri	4.8	3,600	750
Eukaryotes			
Saccharomyces cerevisiae (yeast, a fungus)	12	6,300	525
Caenorhabditis elegans (nematode)	100	20,100	200
Arabidopsis thaliana (mustard family plant)	120	27,000	225
Drosophila melanogaster (fruit fly)	165	14,000	85
Oryza sativa (rice)	430	42,000	95
Zea mays (corn)	2,300	32,000	14
Ailuropoda melanoleuca (giant panda)	2,400	21,000	9
Homo sapiens (human)	3,000	<21,000	7
Paris japonica (Japanese canopy plant)	149,000	ND‡	ND‡

*Some values given here are likely to be revised as genome analysis continues.
†Mb = million base pairs. ‡ND = not determined.

Table 18.1-1

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Table 18.1-2

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Number of Genes

- Free-living bacteria and archaea have 1,500 to 7,500 genes
- Unicellular fungi have about 5,000 genes
- Multicellular eukaryotes can have up to at least 40,000 genes

- Number of genes is not correlated to genome size
- For example, it is estimated that the nematode *C. elegans* has 100 Mb and 20,100 genes, while *Drosophila* has 165 Mb and about 14,000 genes
- Vertebrate genomes can produce more than one polypeptide per gene because of alternative splicing of RNA transcripts

Gene Density and Noncoding DNA

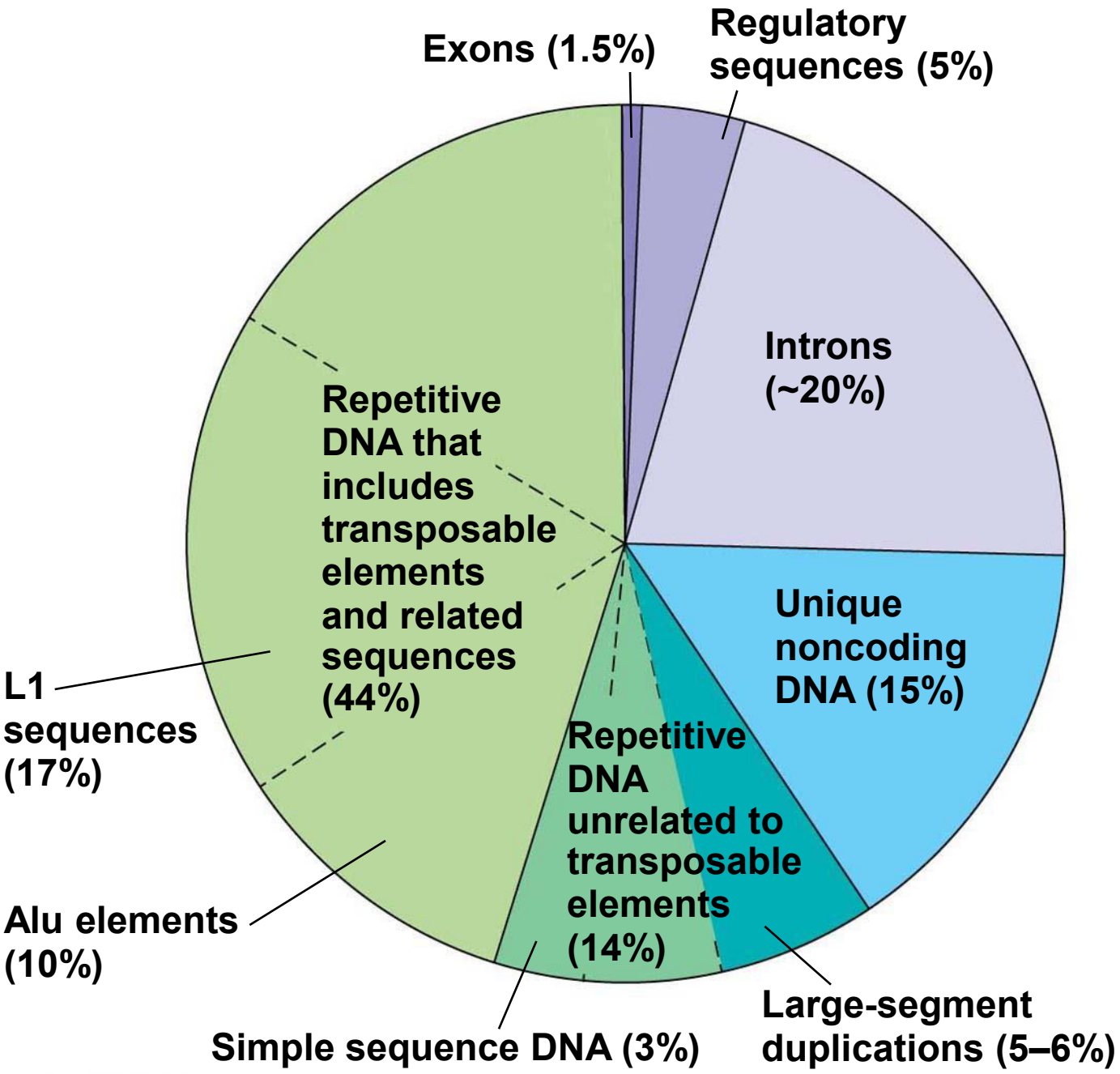
- Humans and other mammals have the lowest gene density, or number of genes, in a given length of DNA
- Multicellular eukaryotes have many introns within genes and noncoding DNA between genes

Concept 18.4: Multicellular eukaryotes have much noncoding DNA and many multigene families

- The bulk of most eukaryotic genomes encodes neither proteins nor functional RNAs
- Sequencing of the human genome reveals that 98.5% does not code for proteins, rRNAs, or tRNAs
- About a quarter of the human genome codes for introns and gene-related regulatory sequences

- The DNA between functional genes includes
  - Unique noncoding sequence such as gene fragments
  - **Pseudogenes**, former genes that have accumulated mutations and are now nonfunctional
  - **Repetitive DNA**, present in multiple copies in the genome
- Some noncoding sequences are identical in humans, rats, and mice, strongly suggesting that these sequences have important functions

Figure 18.5



Transposable Elements and Related Sequences

- Both prokaryotes and eukaryotes have stretches of DNA that can move from one location to another within the genome, called **transposable elements**
- The movement of these transposable genetic elements is called transposition
- About 75% of repetitive DNA is made up of transposable elements and sequences related to them

- The first evidence for mobile DNA segments came from geneticist Barbara McClintock's breeding experiments with Indian corn
- McClintock identified changes in the color of corn kernels that made sense only if some genetic elements move from other genome locations into the genes for kernel color
- McClintock won the Nobel Prize for her pioneering research

Figure 18.6

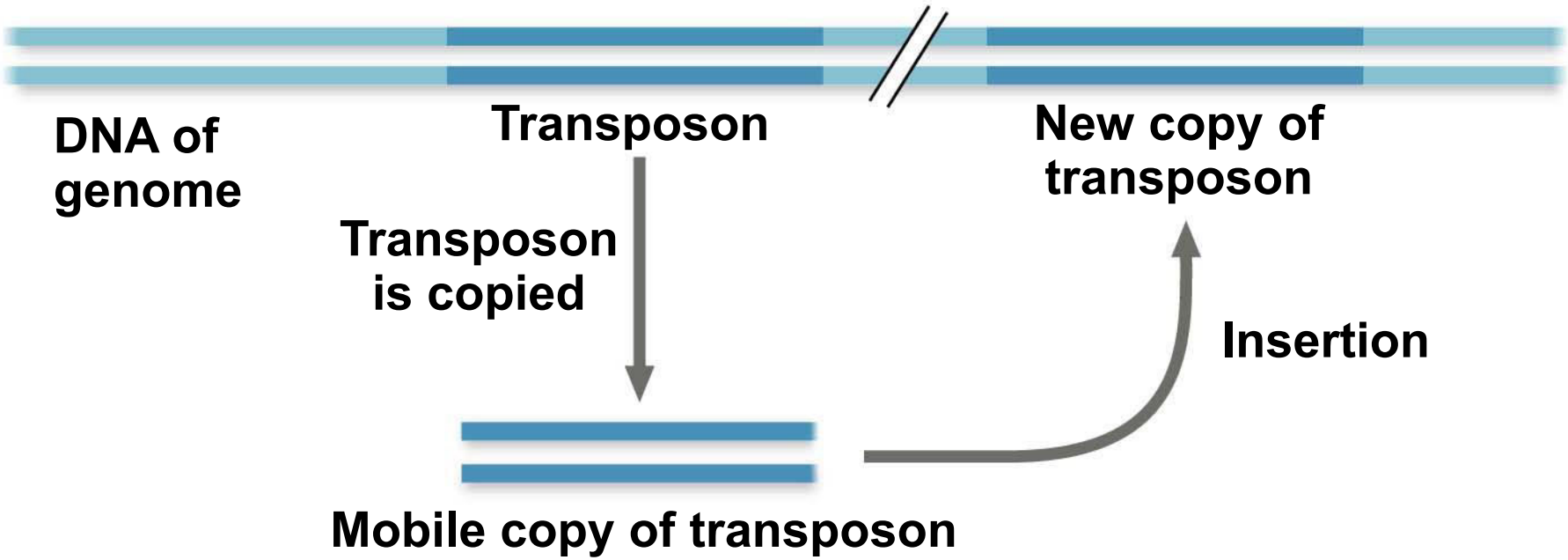
Figure 18.6-1

Figure 18.6-2

Movement of Transposons and Retrotransposons

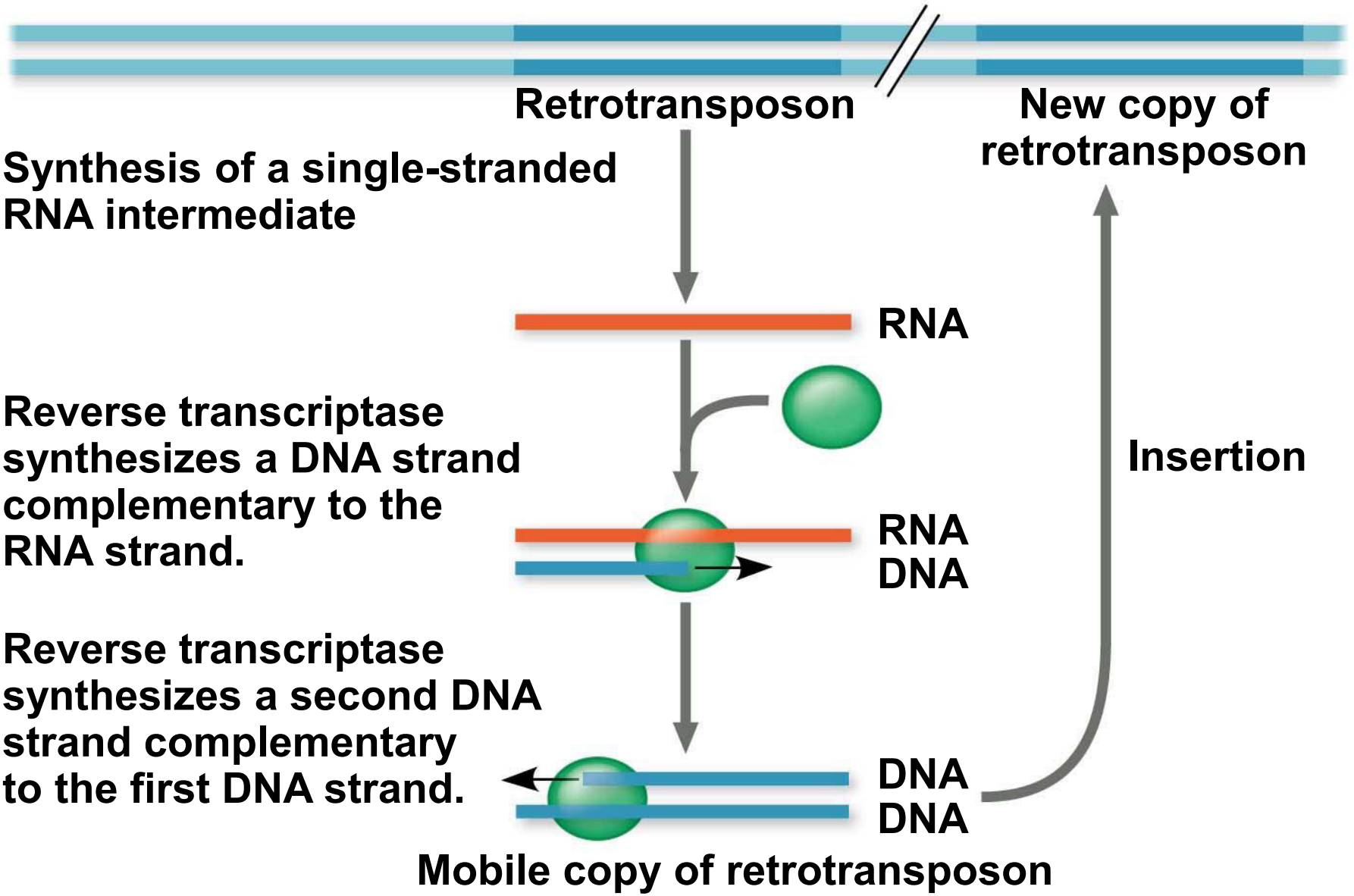
- Eukaryotic transposable elements are of two types, transposons and retrotransposons
- **Transposons** move by a “cut and paste” method or by a “copy and paste” method that leaves a copy behind
- Transposons require an enzyme, called transposase, to move

Figure 18.7



- **Retrotransposons** move by means of an RNA intermediate and always leave a copy behind
- The RNA intermediate must be converted back to DNA by reverse transcriptase, an enzyme encoded by the retrotransposon
- Retroviruses may have evolved from retrotransposons

Figure 18.8



Sequences Related to Transposable Elements

- Multiple copies of transposable elements and related sequences are scattered throughout eukaryotic genomes
- In primates, a large portion of transposable element–related DNA consists of a family of similar sequences called *Alu elements*
- Many *Alu* elements are transcribed into RNA molecules; however, their function, if any, is unknown

- The human genome also contains many sequences of a type of retrotransposon called *LINE-1* (*L1*)
- *L1* sequences have a low rate of transposition and may help regulate gene expression

Other Repetitive DNA, Including Simple Sequence DNA

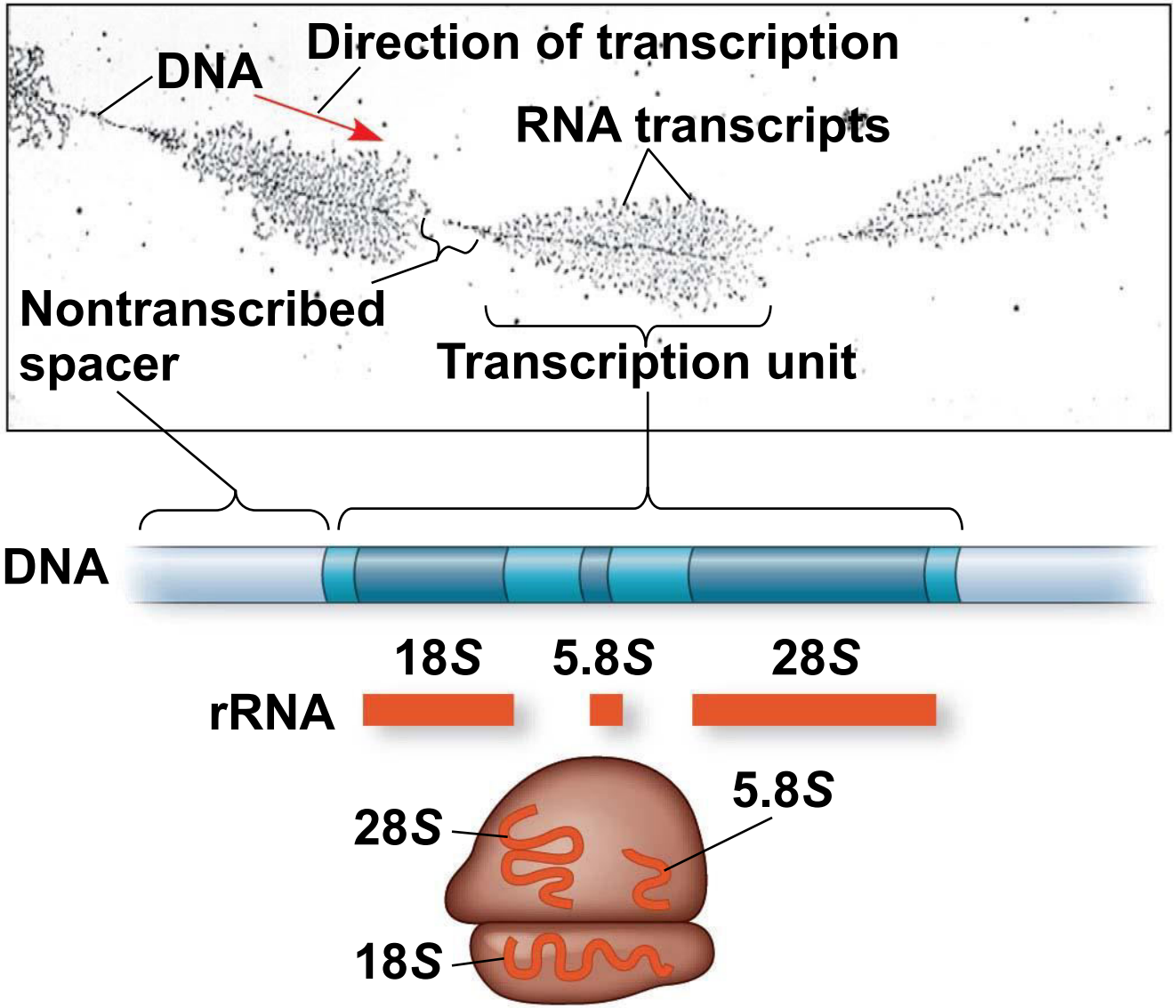
- About 14% of the human genome consists of repetitive DNA resulting from errors during replication or recombination
- About a third of this consists of duplication of long sequences of DNA from one location to another
- In contrast, **simple sequence DNA** contains many copies of tandemly repeated short sequences

- A series of repeating units of two to five nucleotides is called a **short tandem repeat** (**STR**)
- The repeat number for STRs can vary among sites (within a genome) or individuals
- STR diversity can be used to identify a unique set of genetic markers for each individual, his or her **genetic profile**
- Forensic scientists can use STR analysis on DNA samples to identify victims of crime or natural disasters

Genes and Multigene Families

- Many eukaryotic genes are present in one copy per haploid set of chromosomes
- The rest occur in **multigene families**, collections of identical or very similar genes
- Some multigene families consist of identical DNA sequences, usually clustered tandemly, such as those that code for rRNA products

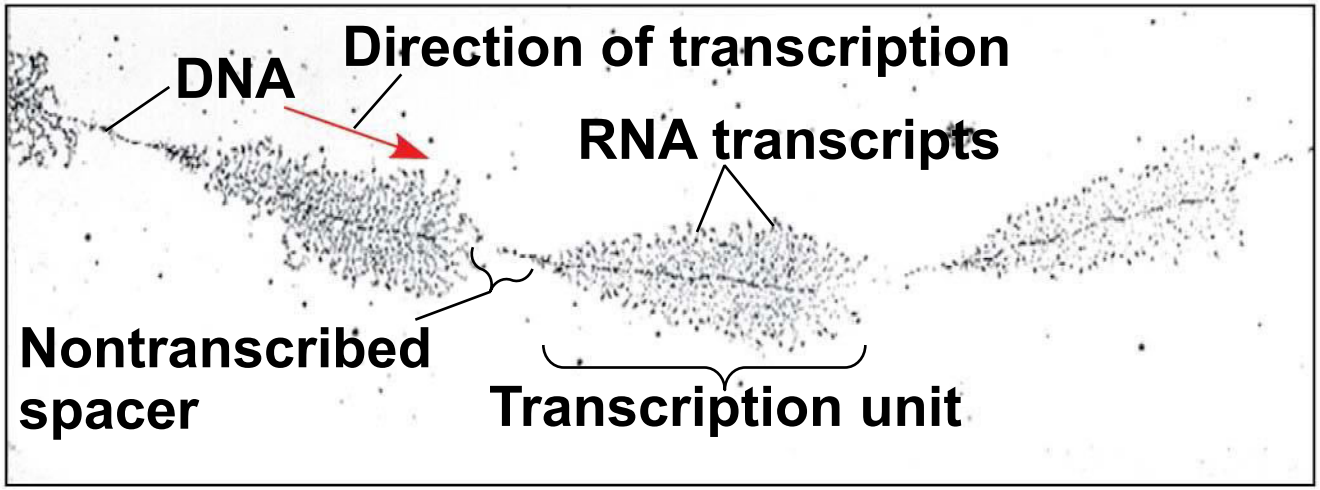
Figure 18.9-1



(a) Part of the ribosomal RNA gene family

- The classic examples of multigene families of nonidentical genes are two related families of genes that encode globins
- α-globins and β-globins are polypeptides of hemoglobin and are coded by genes on different human chromosomes and are expressed at different times in development

Figure 18.9-2



Concept 18.5: Duplication, rearrangement, and mutation of DNA contribute to genome evolution

- The basis of change at the genomic level is mutation, which underlies much of genome evolution
- The earliest forms of life likely had the minimal number of genes necessary for survival and reproduction
- The size of genomes has increased over evolutionary time, with the extra genetic material providing raw material for gene diversification

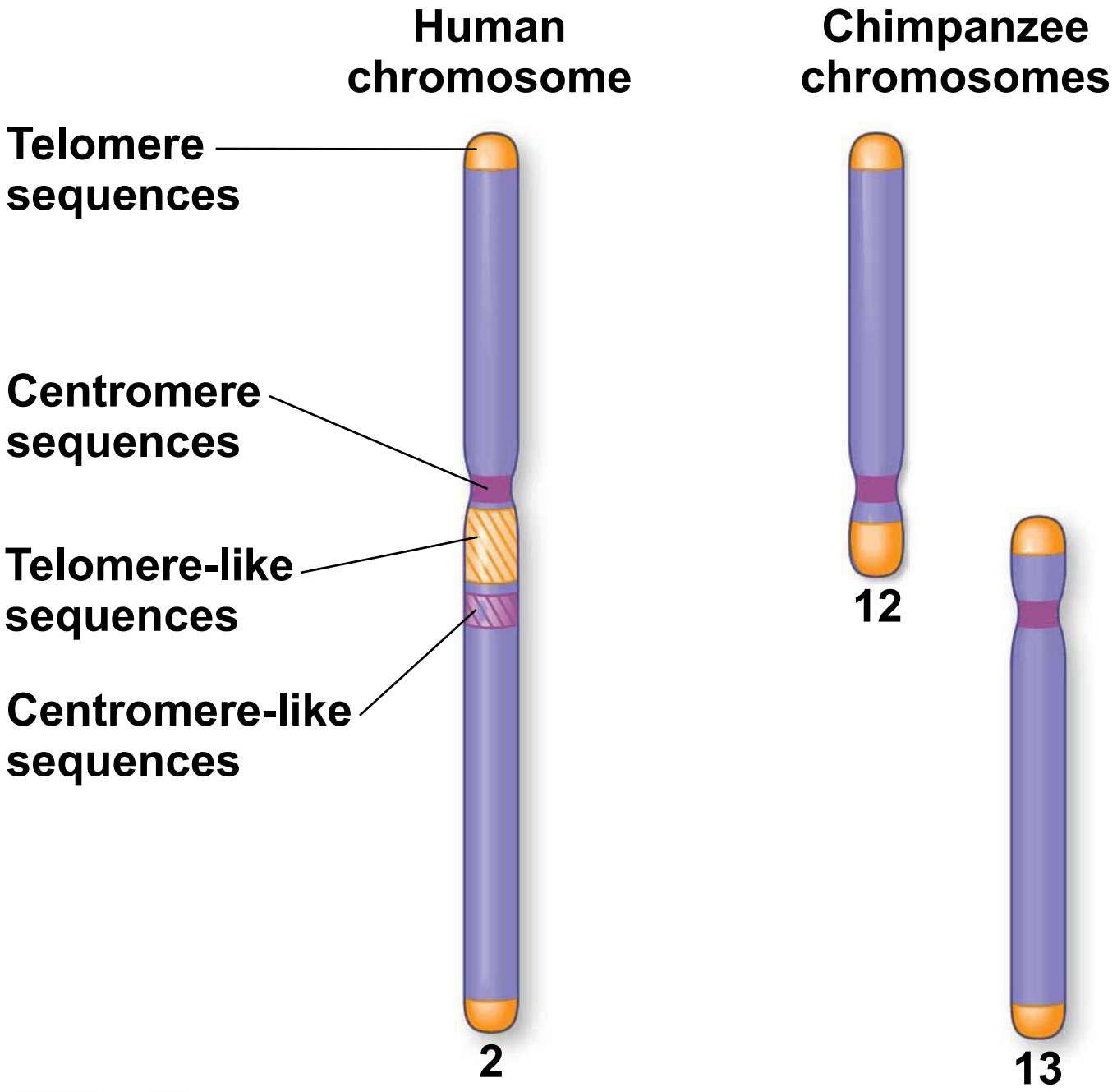
Duplication of Entire Chromosome Sets

- Accidents in meiosis can lead to one or more extra sets of chromosomes, a condition known as polyploidy
- The genes in one or more of the extra sets can diverge by accumulating mutations
- These variations may persist if the organism carrying them survives and reproduces
- Polyploidy is rare in animals but relatively common in plants, especially flowering plants

Alterations of Chromosome Structure

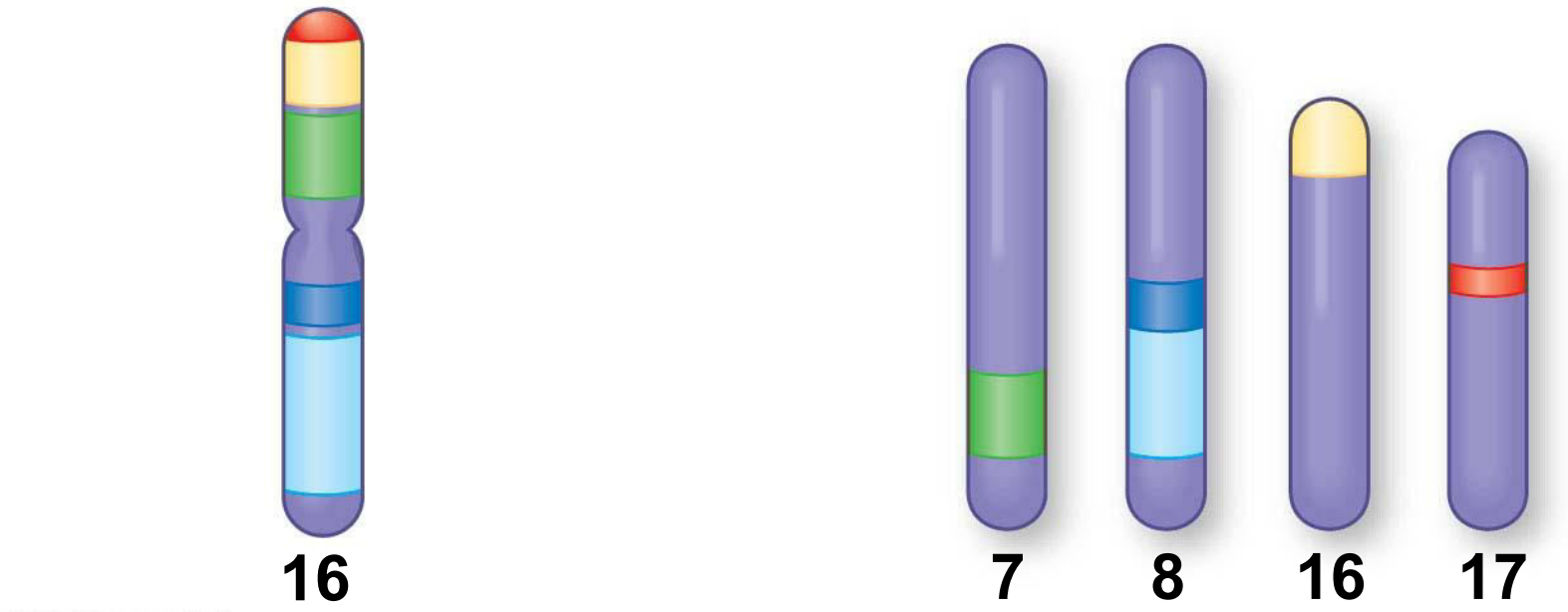
- Humans have 23 pairs of chromosomes, while chimpanzees have 24 pairs
- Following the divergence of humans and chimpanzees from a common ancestor, two ancestral chromosomes fused in the human line

Figure 18.10



- Researchers have compared the DNA sequences of human chromosomes with those of the mouse
- Large blocks of genes from human chromosome 16 can be found on four mouse chromosomes
- This indicates that these blocks of genes have stayed together during evolution of mouse and human lineages

Figure 18.11

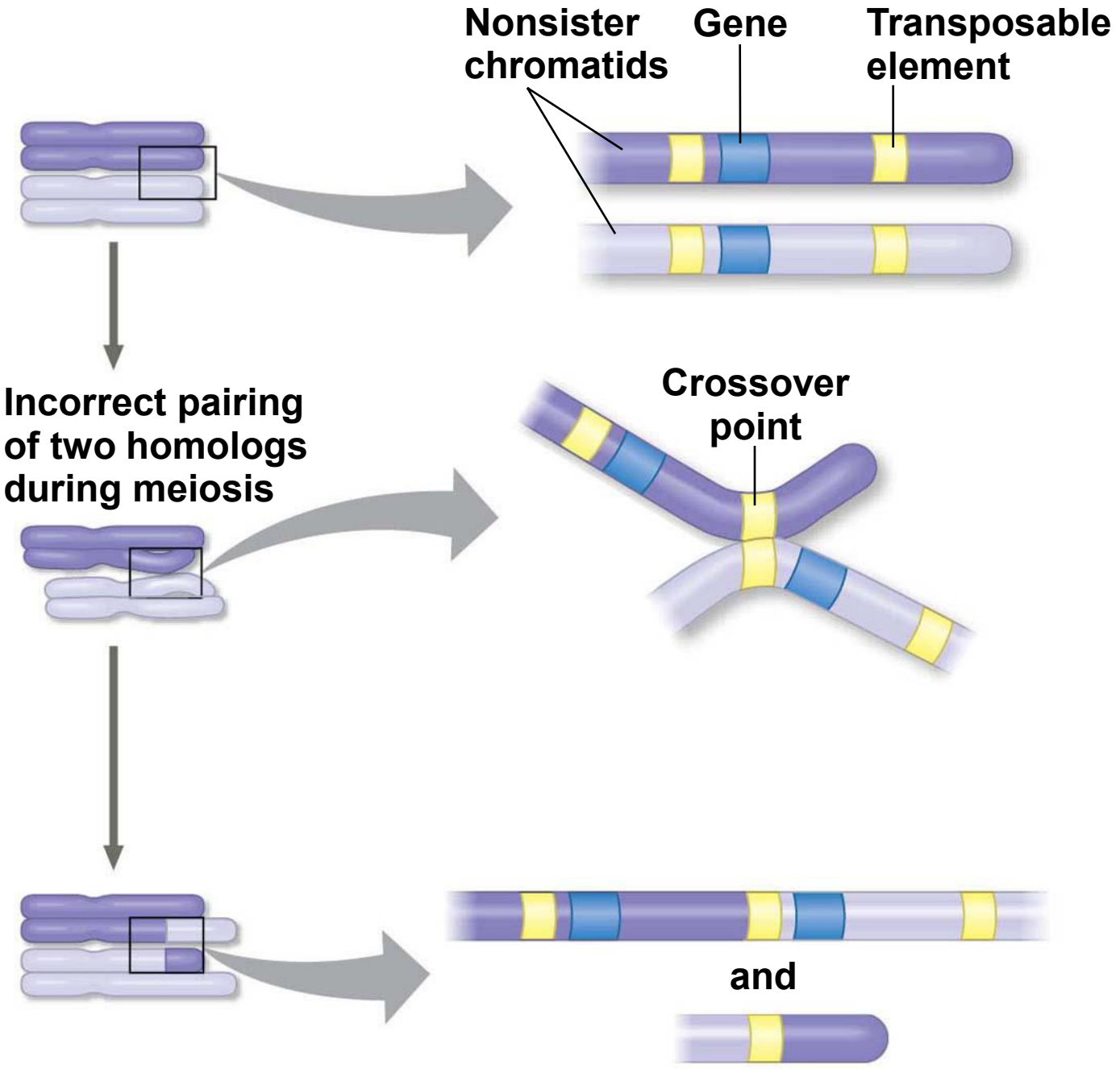


- Duplications and inversions result from mistakes during meiotic recombination
- The rate of duplications and inversions seems to have accelerated about 100 million years ago
- This coincides with the time that large dinosaurs went extinct and mammals diversified

Duplication and Divergence of Gene-Sized Regions of DNA

- Unequal crossing over during prophase I of meiosis can result in one chromosome with a deletion and another with a duplication of a particular region
- Transposable elements can provide sites for crossover between nonsister chromatids
- Slippage can occur during DNA replication so that a part of the template region is either skipped or used twice by the replication machinery

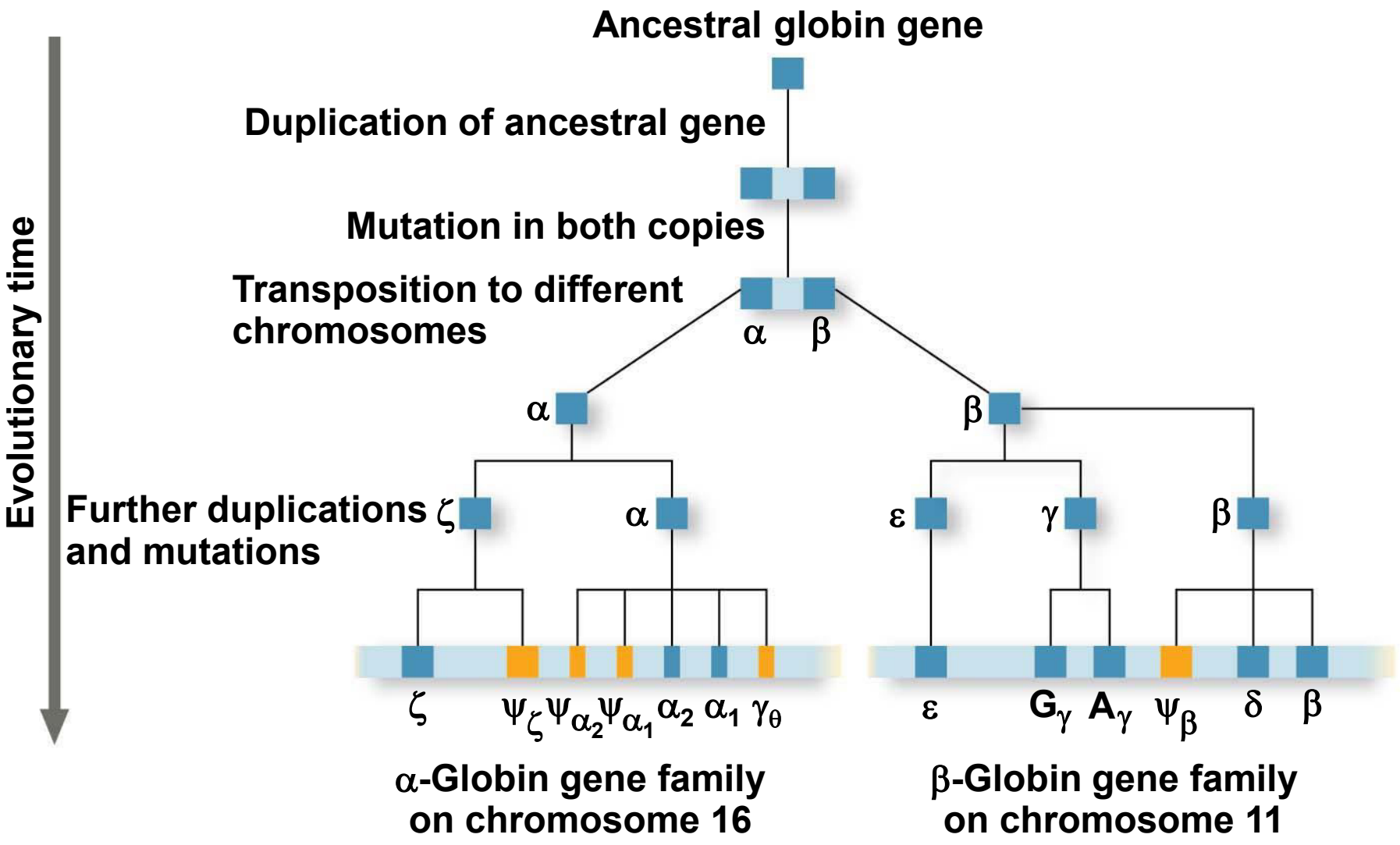
Figure 18.12



Evolution of Genes with Related Functions: The Human Globin Genes

- The genes encoding the various globin proteins evolved from one common ancestral globin gene, which duplicated and diverged about 450–500 million years ago
- After the duplication events, differences between the genes in the globin family arose from the accumulation of mutations

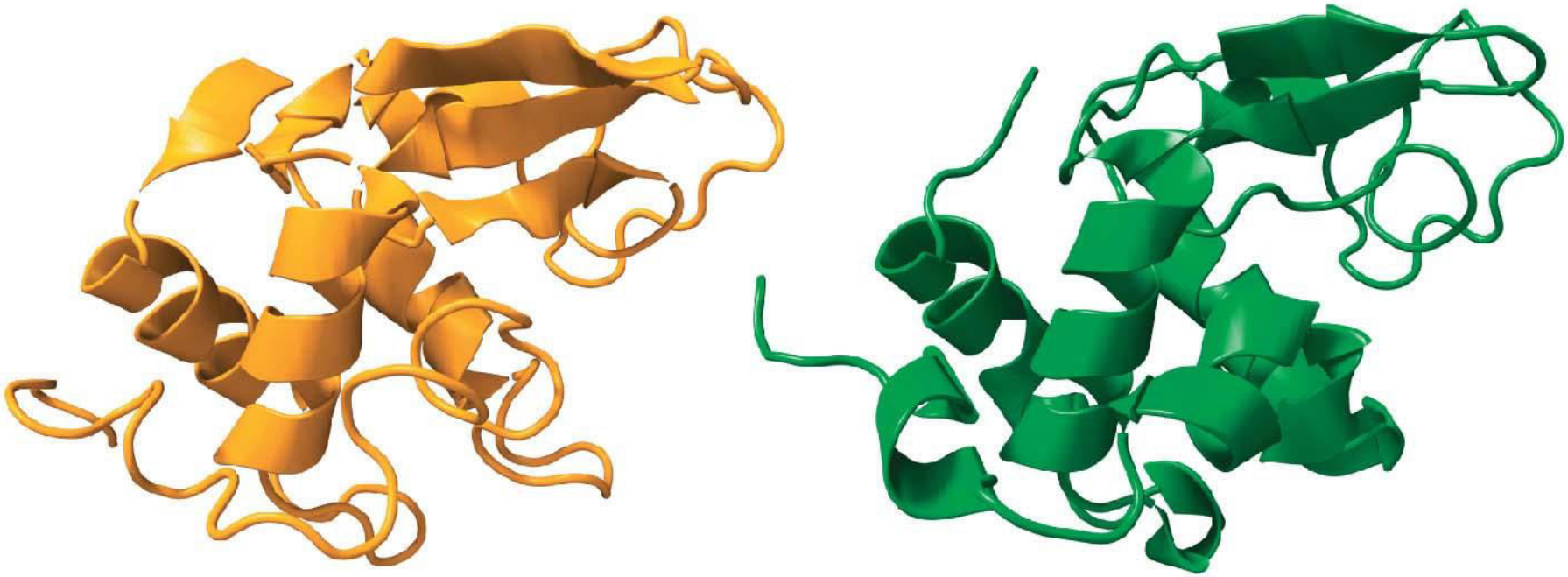
Figure 18.13



Evolution of Genes with Novel Functions

- One copy of a duplicated gene can undergo alterations that lead to a completely new function for the protein product
- The lysozyme and α-lactalbumin genes are good examples
- Lysozyme is an enzyme that helps protect animals against bacterial infection
- α-lactalbumin is a nonenzymatic protein that plays a role in milk production in mammals

Figure 18.UN01



Lysozyme

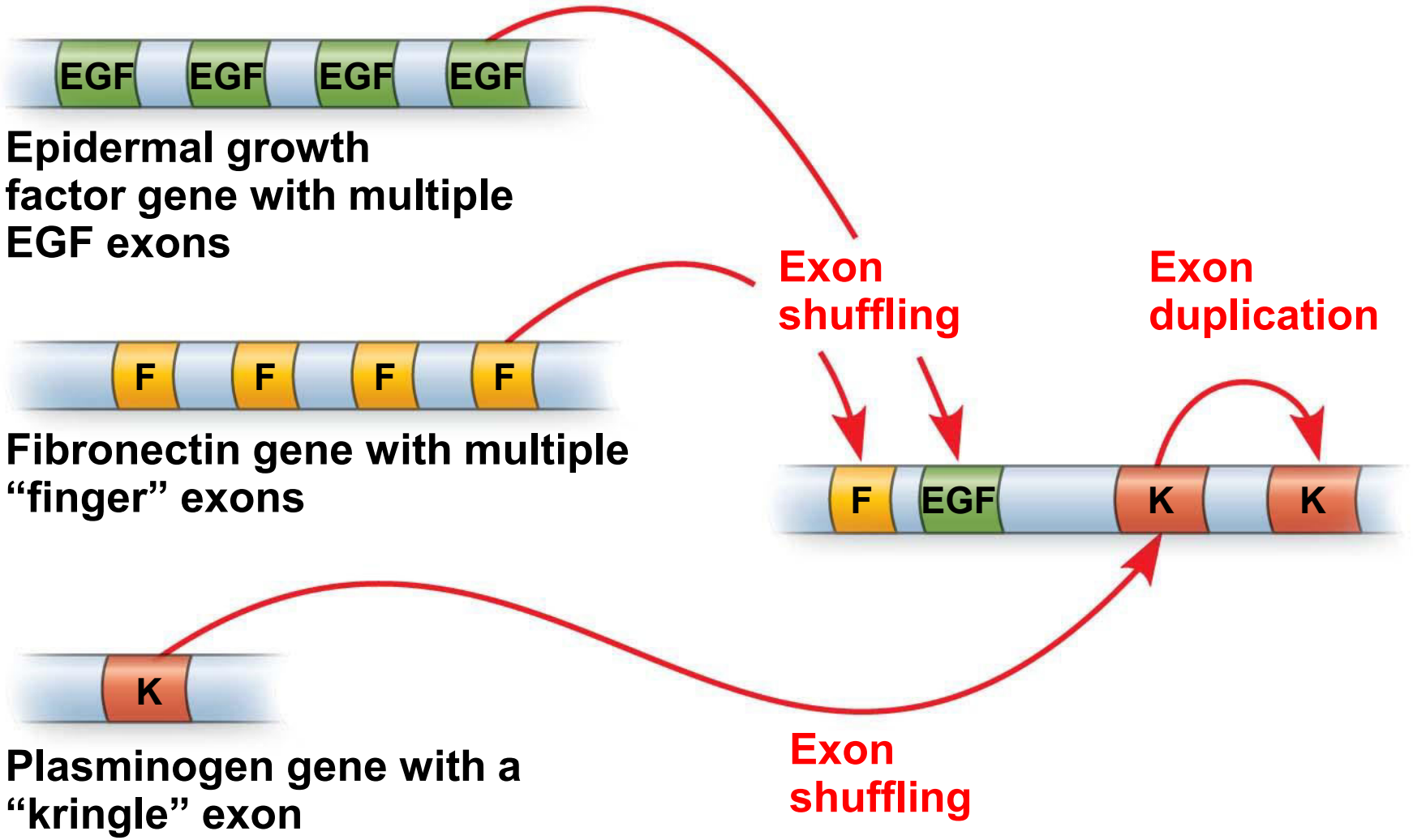
α–lactalbumin

Rearrangements of Parts of Genes: Exon Duplication and Exon Shuffling

- Proteins often consist of discrete structural and functional regions called **domains**, often encoded by different exons
- Errors in meiosis can result in an exon being duplicated on one chromosome and deleted from the homologous chromosome

- Quite a few protein-coding genes have multiple copies of related exons, which presumably arose by duplication and divergence
- Exon shuffling is the occasional mixing and matching of different exons within a gene or between two different genes
- This process could lead to new proteins with novel combinations of functions

Figure 18.14



How Transposable Elements Contribute to Genome Evolution

- Multiple copies of similar transposable elements may facilitate recombination, or crossing over, between different chromosomes
- Insertion of transposable elements within a protein-coding sequence may block protein production
- Insertion of transposable elements within a regulatory sequence may increase or decrease protein production

- Transposable elements may carry a gene or groups of genes to a new position
- In a similar process, an exon from one gene could be inserted into another by a mechanism similar to exon shuffling
- These sorts of changes are usually detrimental but may on occasion prove advantageous to an organism

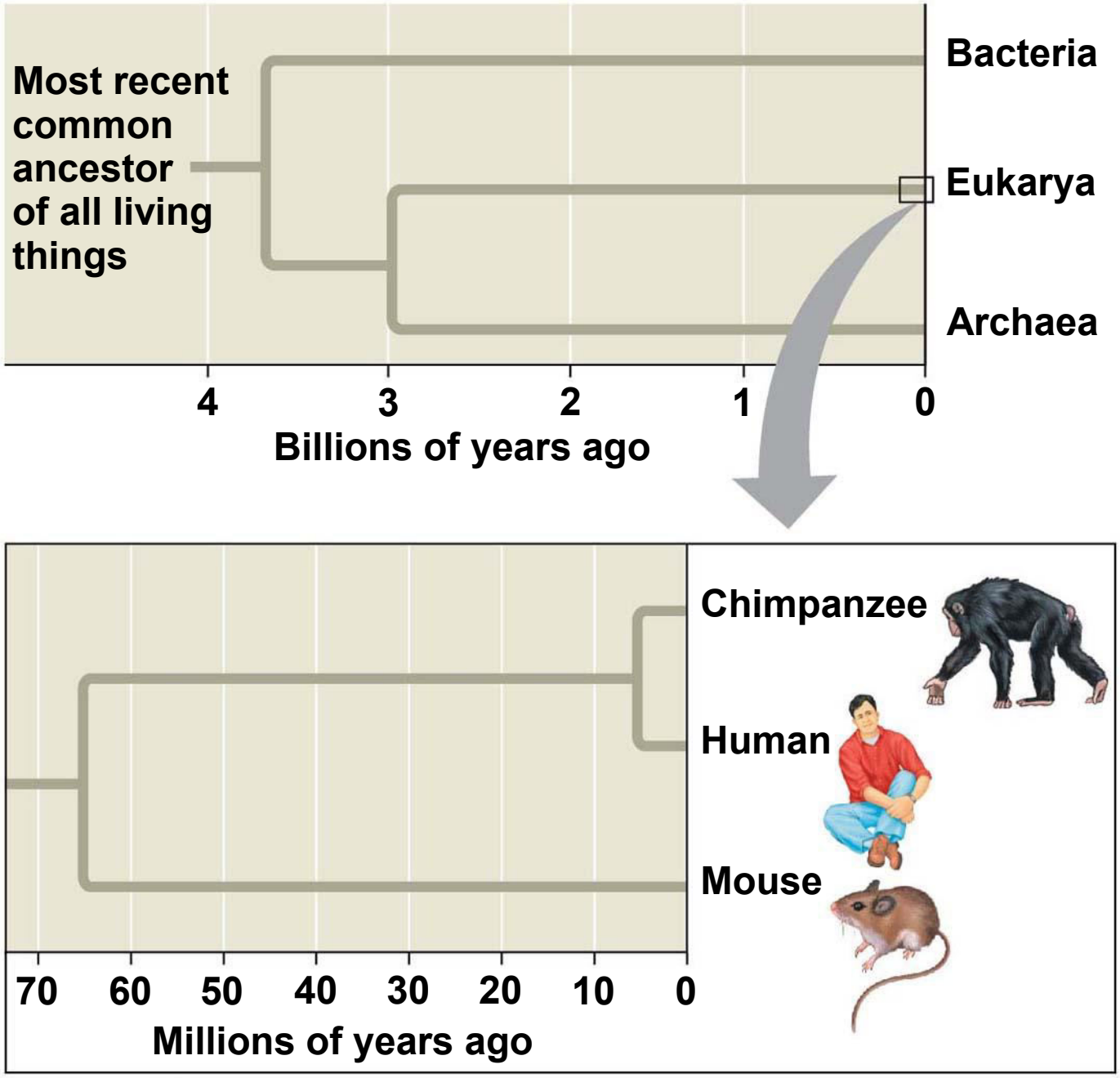
Concept 18.6: Comparing genome sequences provides clues to evolution and development

- Genome sequencing and data collection have advanced rapidly in the last 25 years
- Comparative studies of genomes
  - Reveal much about the evolutionary history of life
  - Help clarify mechanisms that generated the great diversity of present-day life-forms

Comparing Genomes

- Genome comparisons of closely related species help us understand recent evolutionary events
- Genome comparisons of distantly related species help us understand ancient evolutionary events
- Evolutionary relationships among species can be represented by a tree-shaped diagram

Figure 18.15



Comparing Distantly Related Species

- Highly conserved genes have remained similar over time
- These help clarify relationships among species that diverged from each other long ago
- Bacteria, archaea, and eukaryotes diverged from each other between 2 and 4 billion years ago
- Comparative genomic studies confirm the relevance of research on model organisms to our understanding of biology in general and human biology in particular

Comparing Closely Related Species

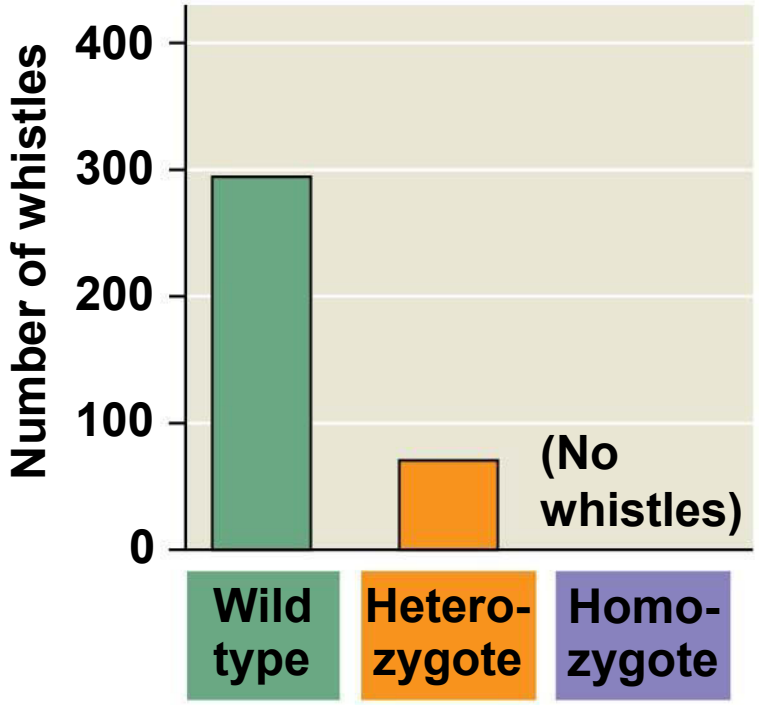
- The genomes of two closely related species are likely to be organized similarly
- Particular genetic differences between the two species can be easily correlated with phenotypic differences between them

- Human and chimpanzee genomes differ by 1.2% at single base pairs and by 2.7% because of insertions and deletions
- Several genes are evolving faster in humans than in chimpanzees
- These include genes involved in defense against malaria and tuberculosis and in regulation of brain size
- Genes that seem to be evolving fastest code for transcription factors

- The *FOXP2* gene is a transcription factor whose product turns on genes involved in vocalization in vertebrates
- When the *FOXP2* gene is disrupted in mice, they fail to vocalize normally

Figure 18.16

(a)



(b)

Figure 18.16-1

(a)

- Genomic comparisons have been made between humans (*Homo sapiens*) and Neanderthals (*Homo neanderthalensis*)
- Some groups of humans and Neanderthals co-existed and interbred for a period of time
- The Neanderthal *FOXP2* gene encodes a protein identical to that of humans, suggesting that they were capable of speech

Comparing Genomes Within a Species

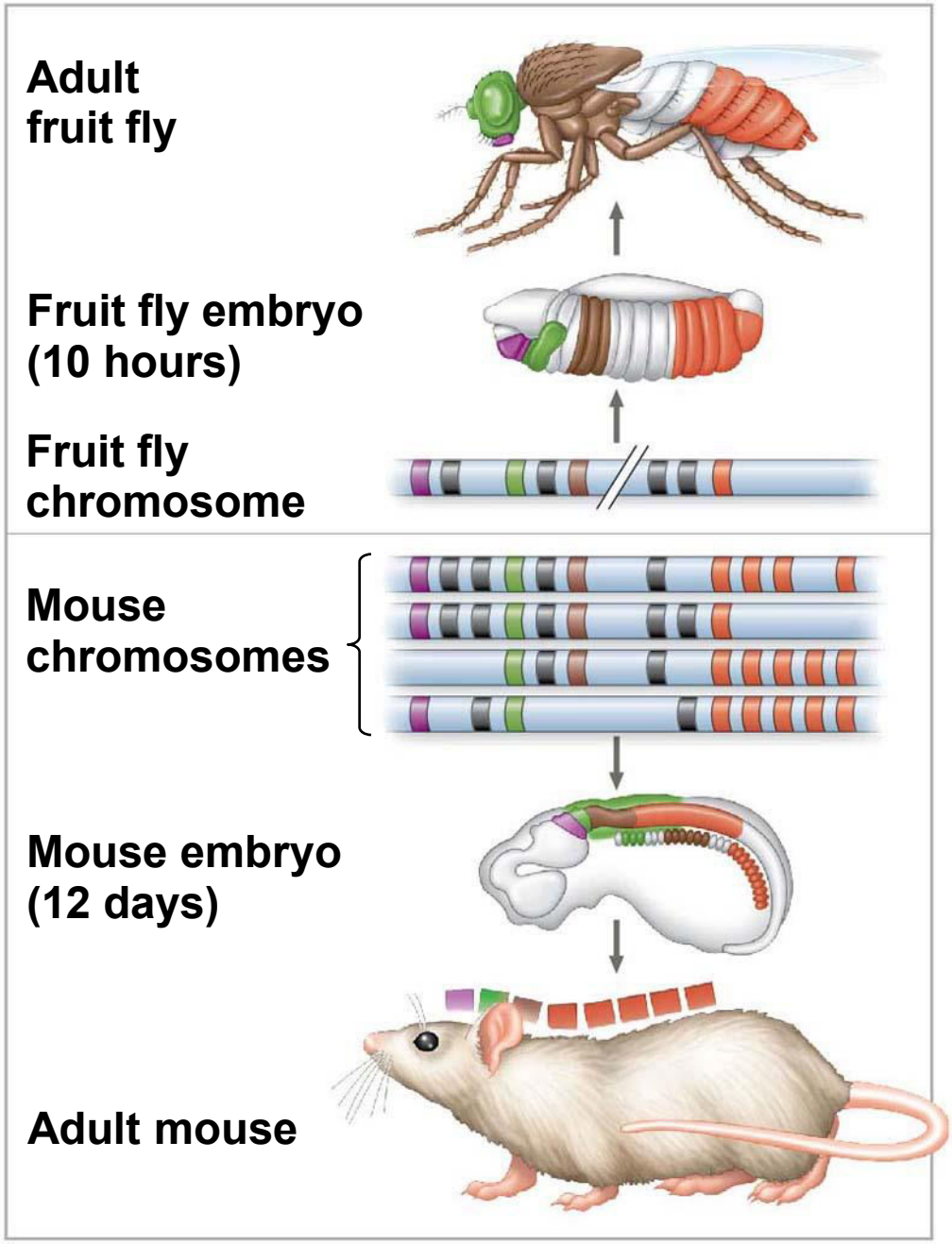
- As a species, humans have only existed for about 200,000 years and have low within-species genetic variation
- Most of the variation within humans is due to **single nucleotide polymorphisms** (**SNPs**)
- There are also inversions, deletions, and duplications and a large number of copy-number variants (CNVs)
- These variations are useful for studying human evolution and human health

Widespread Conservation of Developmental Genes Among Animals

- Evolutionary developmental biology, or **evo-devo**, compares the developmental processes of different multicellular organisms
- Genomic information shows that minor differences in gene sequence or regulation can result in striking differences in form

- Molecular analysis of the homeotic genes in *Drosophila* has shown that they all include a sequence called a **homeobox**
- An identical or very similar nucleotide sequence has been discovered in the homeotic genes of both vertebrates and invertebrates
- The vertebrate genes homologous to homeotic genes of flies have kept the same chromosomal arrangement

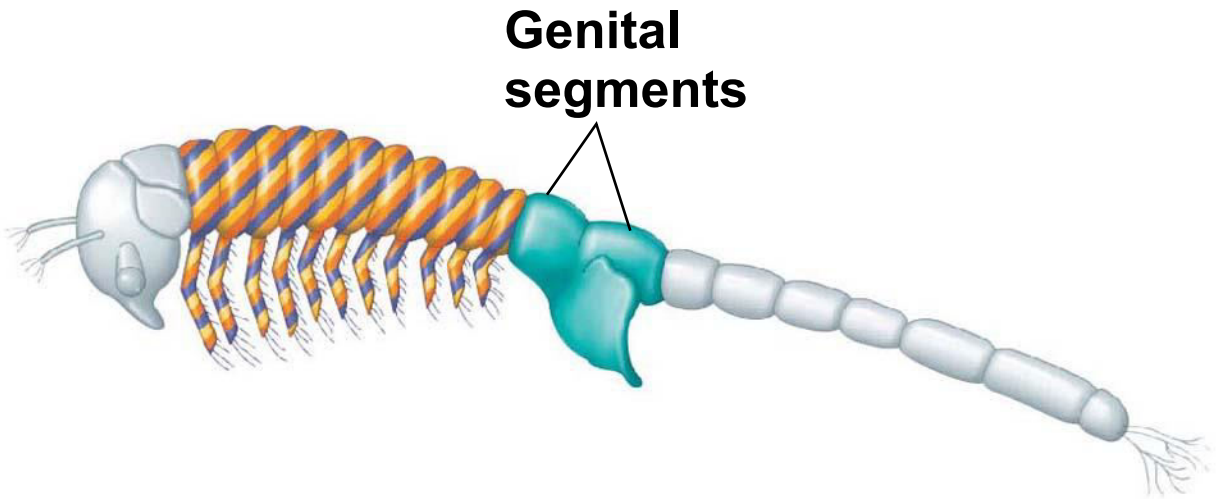
Figure 18.17



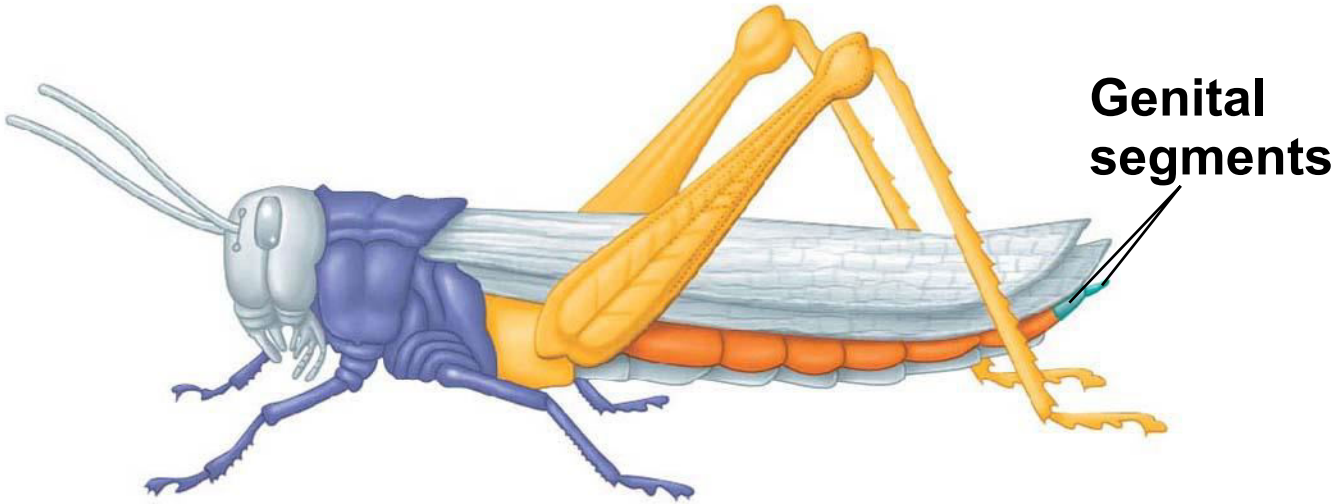
- Related homeobox sequences have been found in regulatory genes of yeasts and plants
- The homeodomain is the part of the protein that binds to DNA when the protein functions as a transcriptional regulator
- The more variable domains in the protein recognize particular DNA sequences and specify which genes are regulated by the protein

- Sometimes small changes in regulatory sequences of certain genes lead to major changes in body form
- For example, variation in *Hox* gene expression controls variation in leg-bearing segments of crustaceans and insects

Figure 18.18

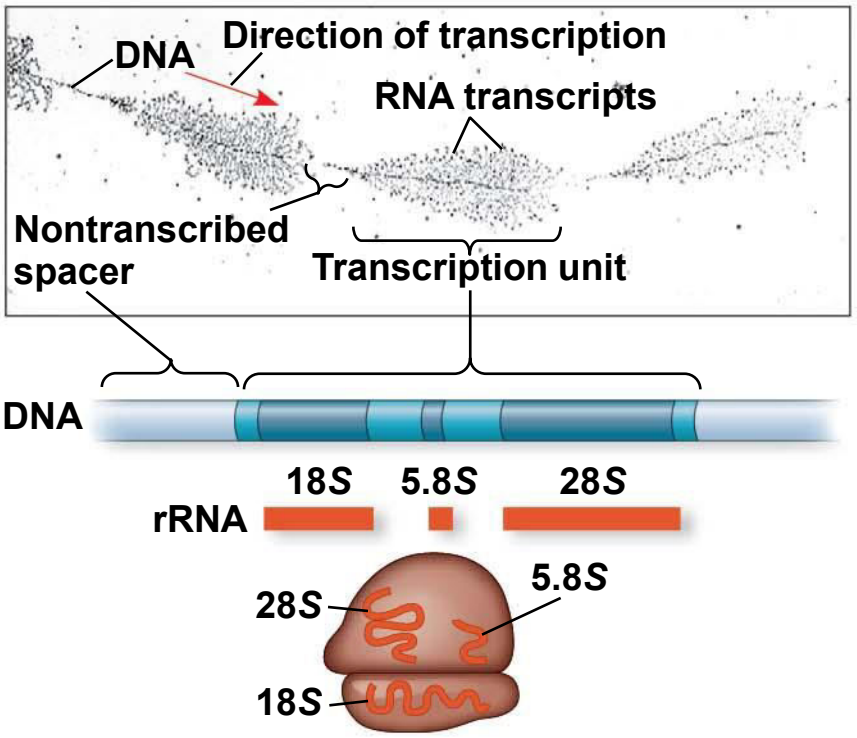


(a) Expression of four *Hox* genes in the brine shrimp *Artemia*

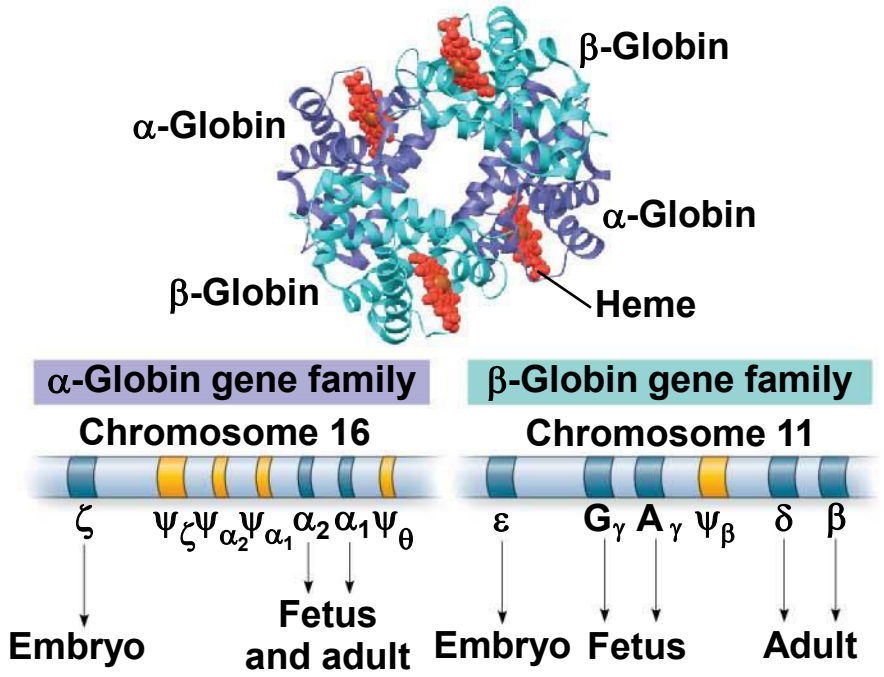


(b) Expression of the grasshopper versions of the same four *Hox* genes

Figure 18.9

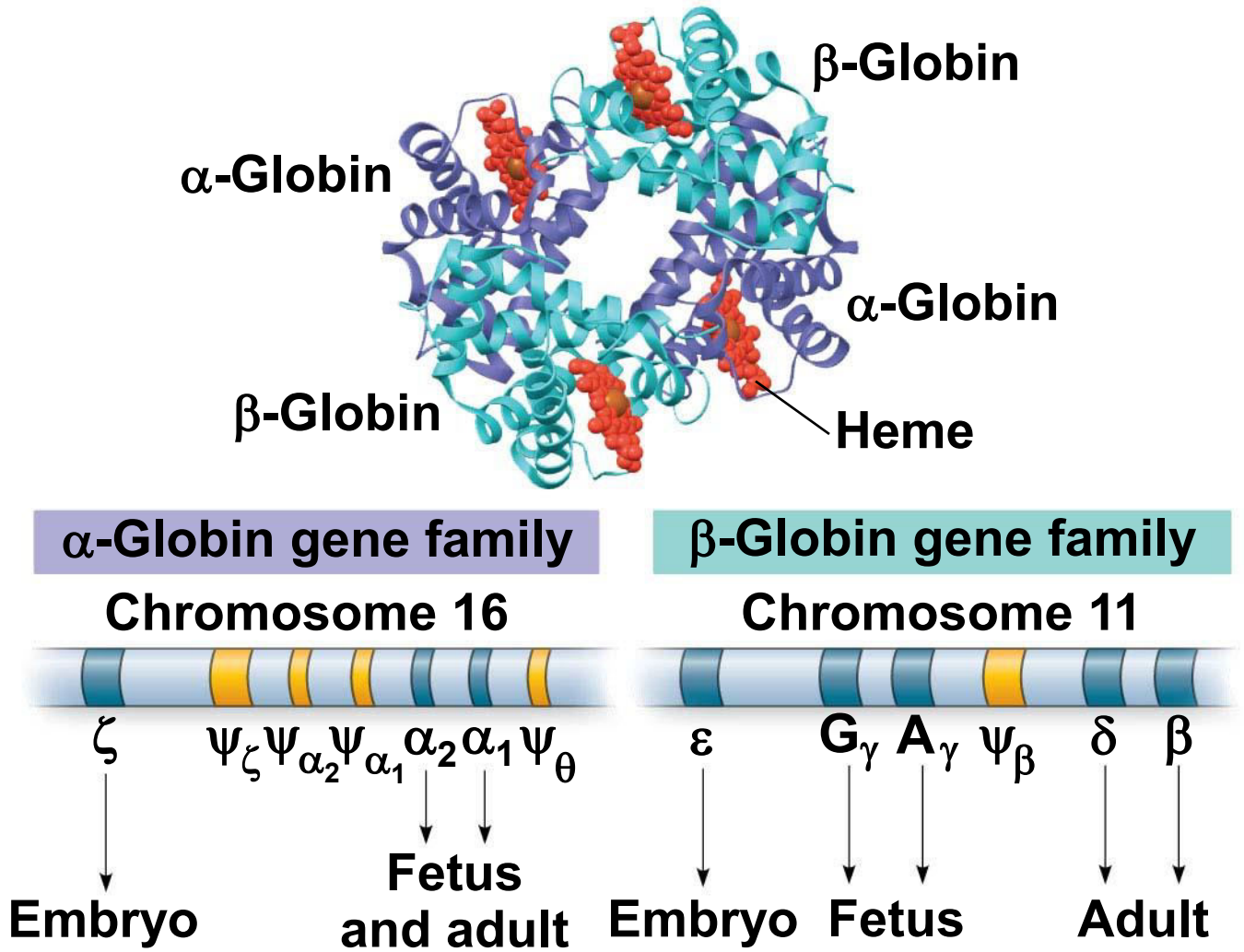


(a) Part of the ribosomal RNA gene family



(b) The human α-globin and β-globin gene families

Figure 18.9-3



(b) The human α-globin and β-globin gene families

Figure 18.UN02-1

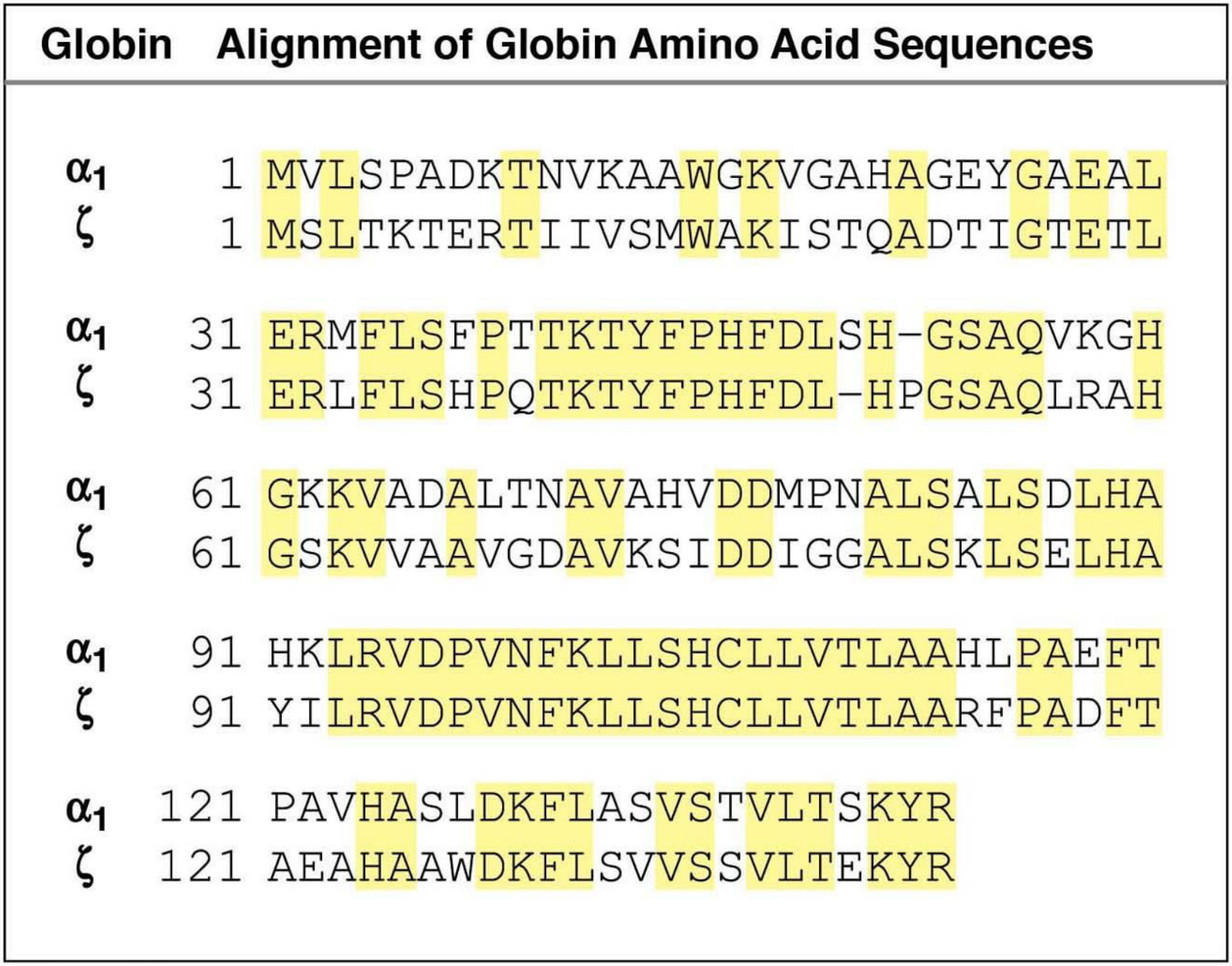


Figure 18.UN02-2

Amino Acid Identity Table									
		α Family			β Family				
		α_1 (alpha 1)	α_2 (alpha 2)	ζ (zeta)	β (beta)	δ (delta)	ϵ (epsilon)	A_γ (gamma A)	G_γ (gamma G)
α Family	α_1	-----	100	60	45	44	39	42	42
	α_2		-----	60	45	44	39	42	42
	ζ			-----	38	40	41	41	41
β Family	β				-----	93	76	73	73
	δ					-----	73	71	72
	ϵ						-----	80	80
	A_γ							-----	99
	G_γ								-----

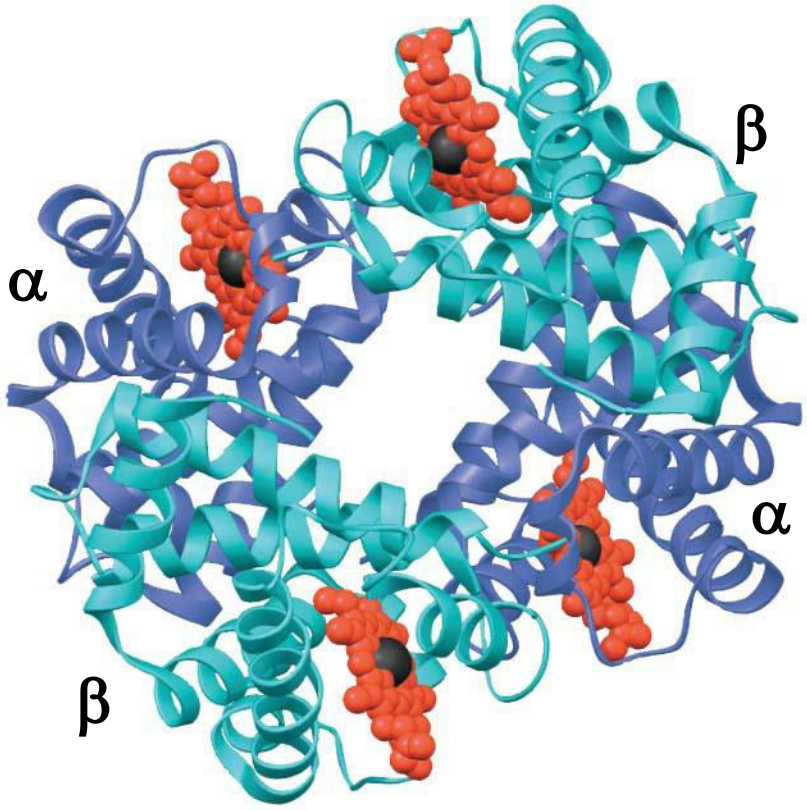
Figure 18.UN02-2a

Amino Acid Identity Table				
α Family				
		α_1 (alpha 1)	α_2 (alpha 2)	ζ (zeta)
α Family	α_1	-----	100	60
	α_2		-----	60
	ζ			-----
β Family	β			
	δ			
	ϵ			
	A_γ			
	G_γ			

Figure 18.UN02-2b

Amino Acid Identity Table						
β Family						
		β (beta)	δ (delta)	ϵ (epsilon)	A_γ (gamma A)	G_γ (gamma G)
α Family	α_1	45	44	39	42	42
	α_2	45	44	39	42	42
	ζ	38	40	41	41	41
β Family	β	-----	93	76	73	73
	δ		-----	73	71	72
	ϵ			-----	80	80
	A_γ				-----	99
	G_γ					-----

Figure 18.UN02-3

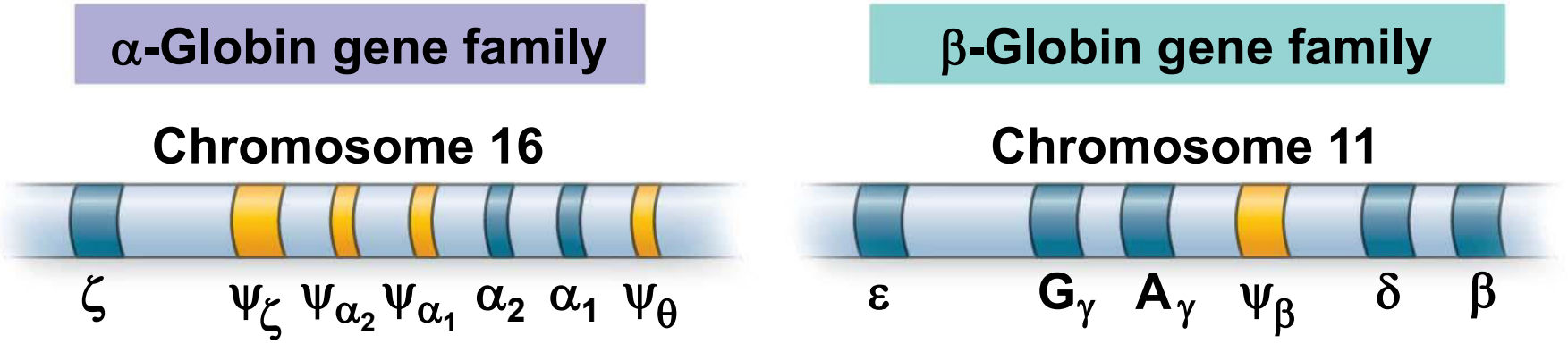


▲ **Hemoglobin**

Figure 18.UN03

	Bacteria	Archaea	Eukarya
Genome size	Most are 1–6 Mb		Most are 10–4,000 Mb, but a few are much larger
Number of genes	1,500–7,500		5,000–40,000
Gene density	Higher than in eukaryotes		Lower than in prokaryotes (Within eukaryotes, lower density is correlated with larger genomes.)
Introns	None in protein-coding genes	Present in some genes	Present in most genes of multicellular eukaryotes, but only in some genes of unicellular eukaryotes
Other noncoding DNA	Very little		Can exist in large amounts; generally more repetitive noncoding DNA in multicellular eukaryotes

Figure 18.UN04



CAMPBELL BIOLOGY IN FOCUS

URRY • CAIN • WASSERMAN • MINORSKY • REECE

17 Viruses

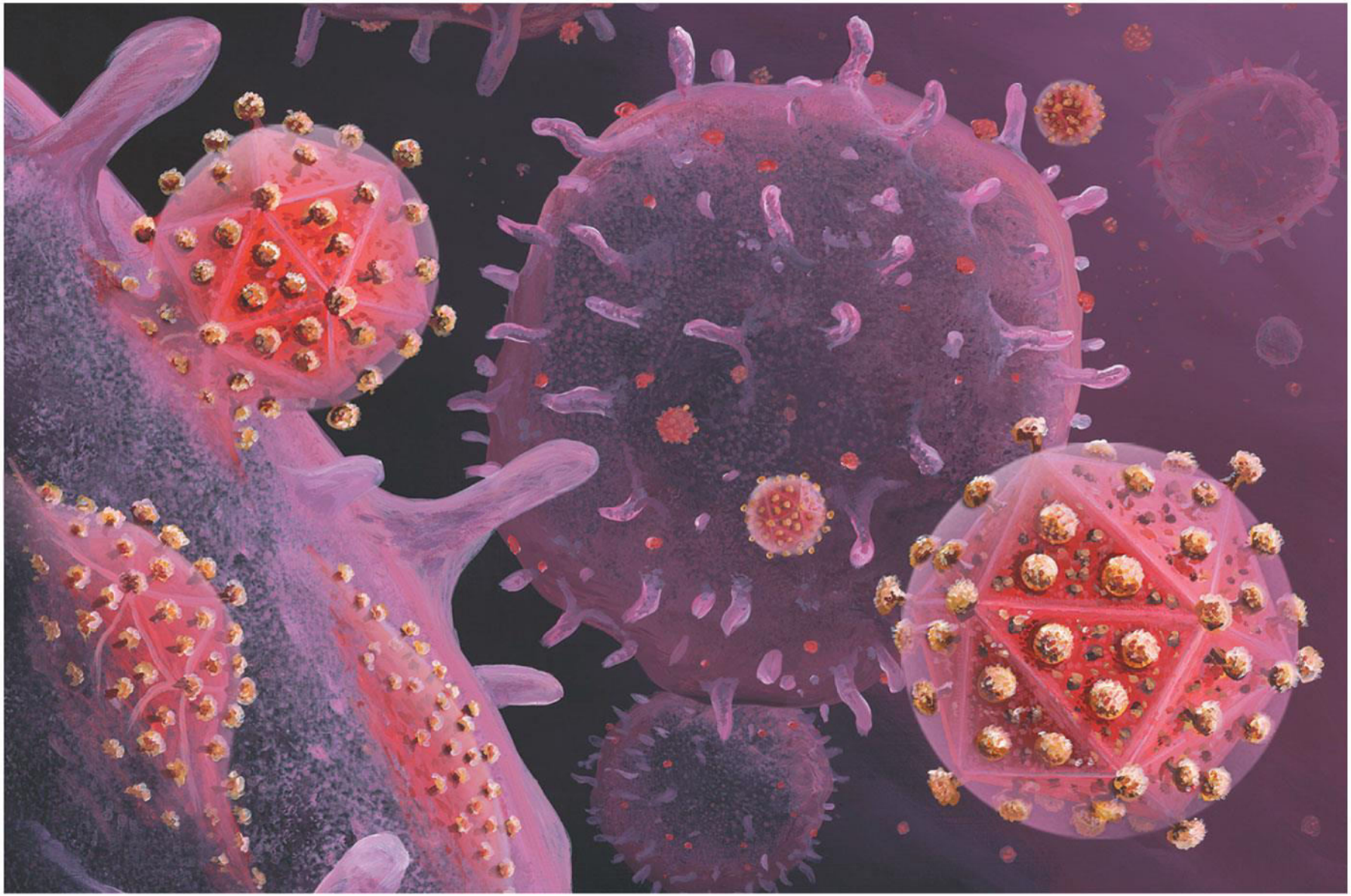
Lecture Presentations by
Kathleen Fitzpatrick and
Nicole Tunbridge,
Simon Fraser University

SECOND EDITION

Overview: A Borrowed Life

- A **virus** is an infectious particle consisting of little more than genes packaged into a protein coat
- Viruses lead “a kind of borrowed life,” existing in a shady area between life-forms and chemicals

Figure 17.1



Concept 17.1: A virus consists of a nucleic acid surrounded by a protein coat

- Even the largest known virus is barely visible under the light microscope
- Some viruses can be crystalized
- Viruses are not cells but are a nucleic acid enclosed in a protein coat

Viral Genomes

- Viral genomes may consist of either
  - Double- or single-stranded DNA, or
  - Double- or single-stranded RNA
- Depending on its type of nucleic acid, a virus is called a DNA virus or an RNA virus

Capsids and Envelopes

- A **capsid** is the protein shell that encloses the viral genome
- Capsids are built from protein subunits called *capsomeres*
- A capsid can have various structures

Figure 17.2

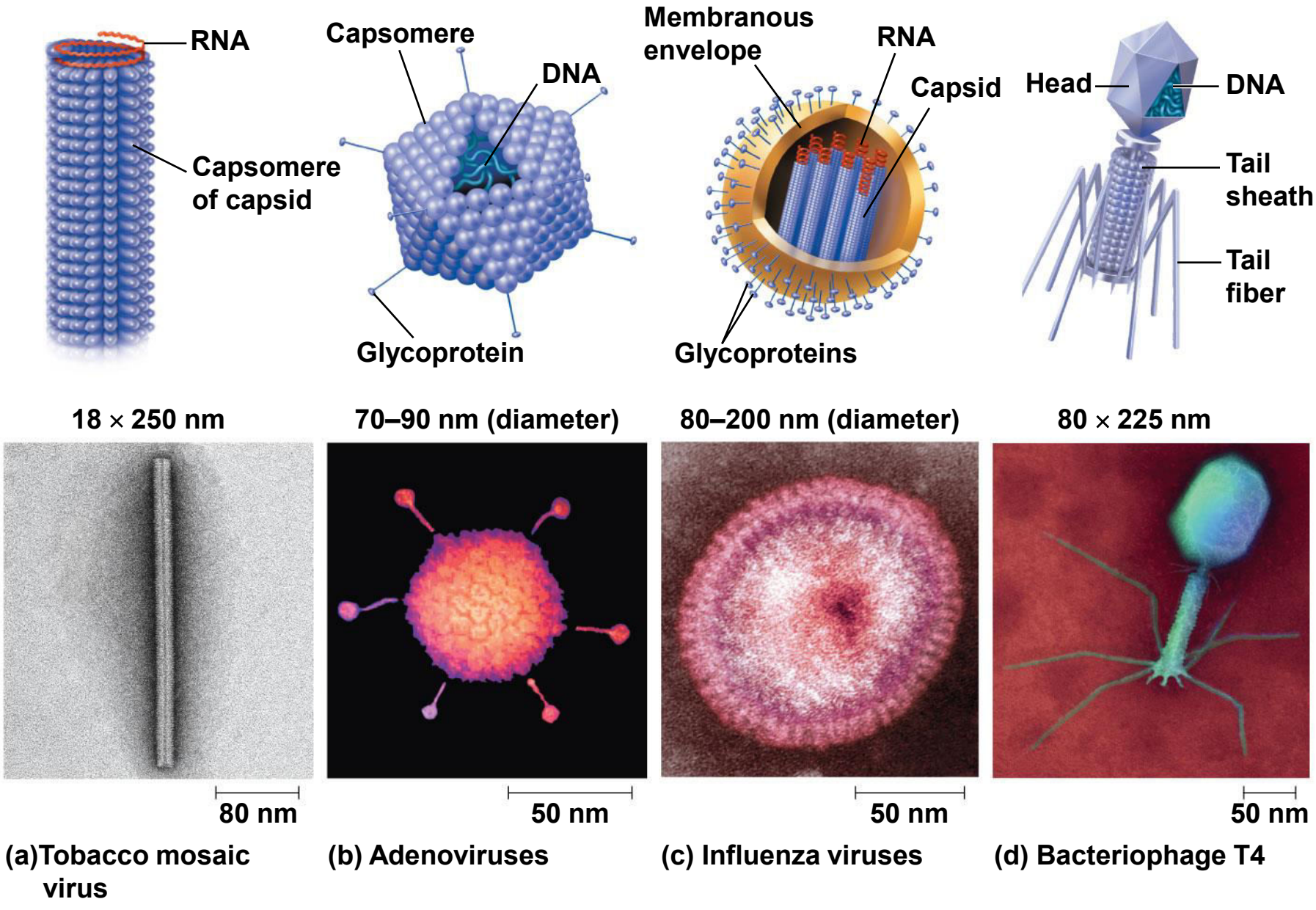


Figure 17.2-1

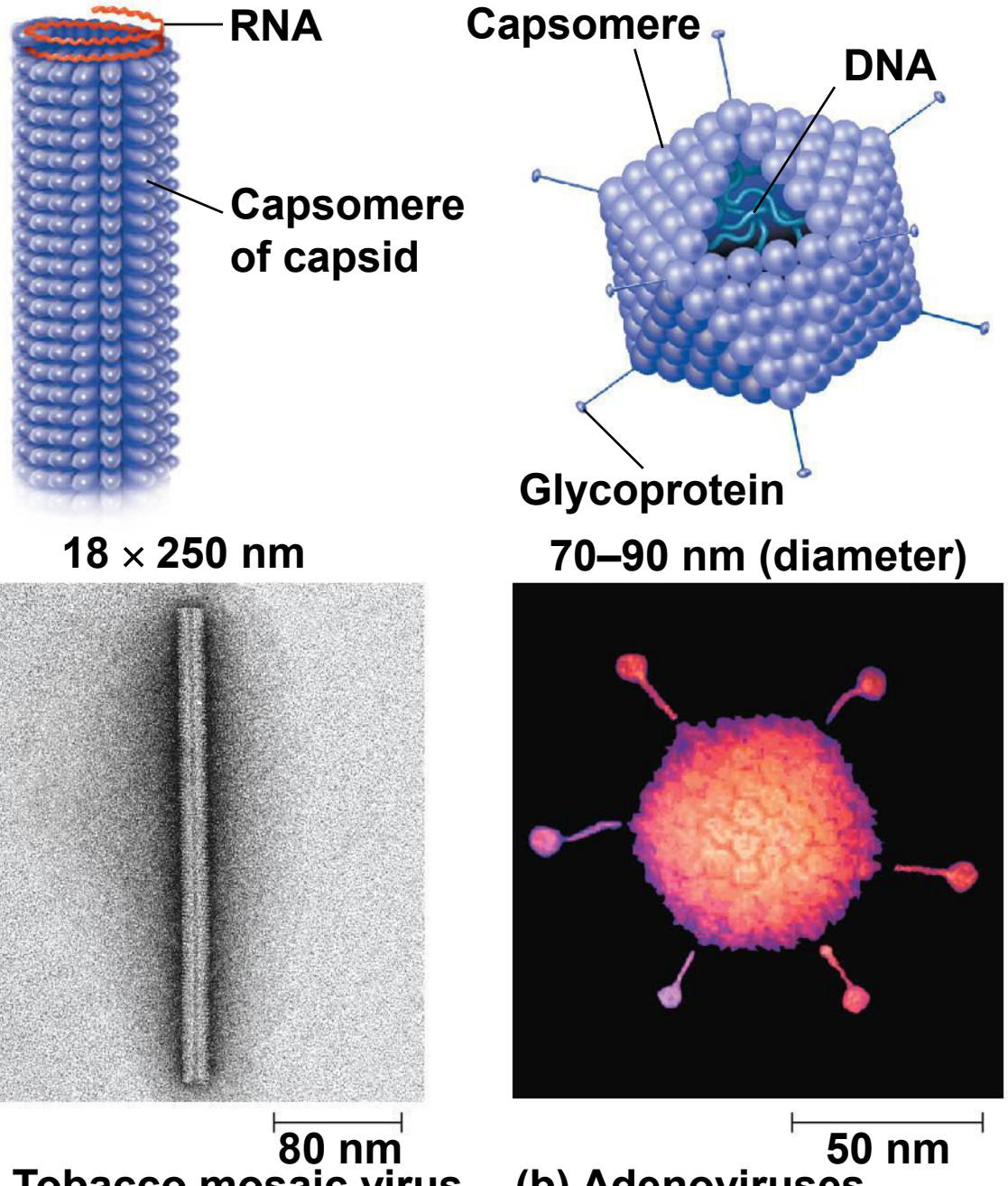
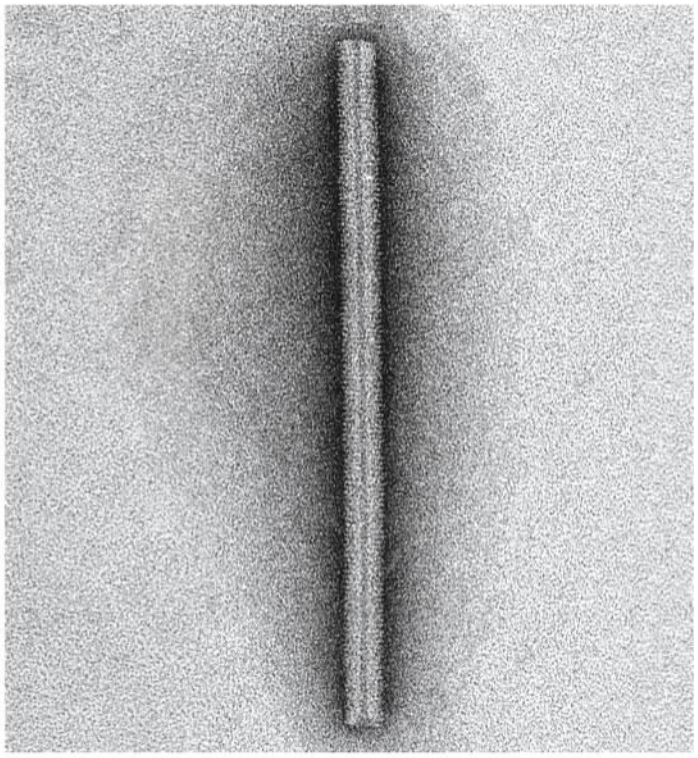
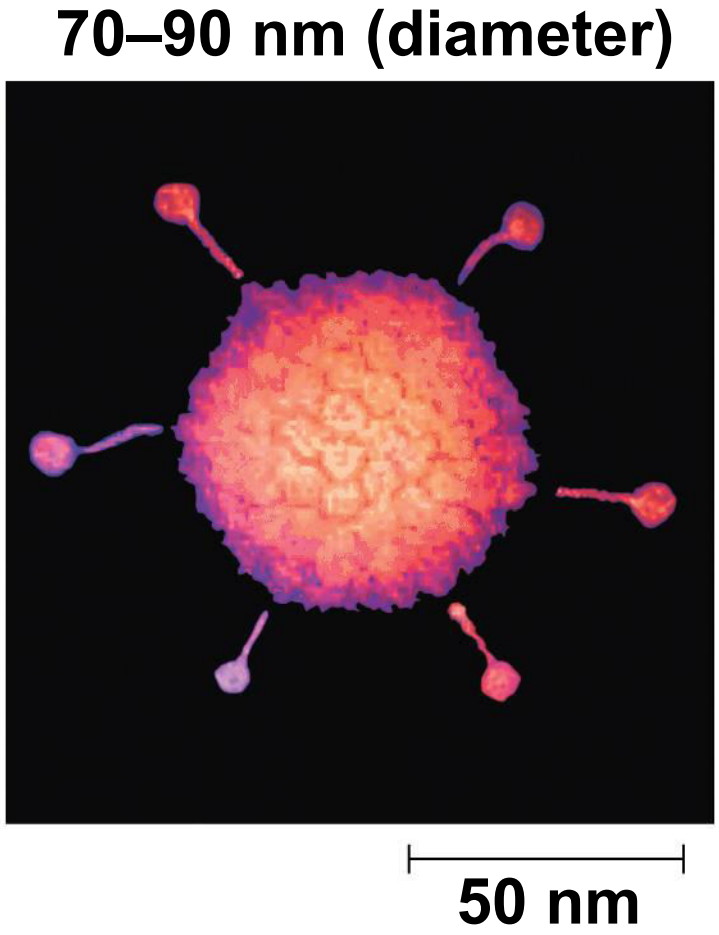


Figure 17.2-1a



(a) Tobacco mosaic virus

Figure 17.2-1b



(b) Adenoviruses

Figure 17.2-2

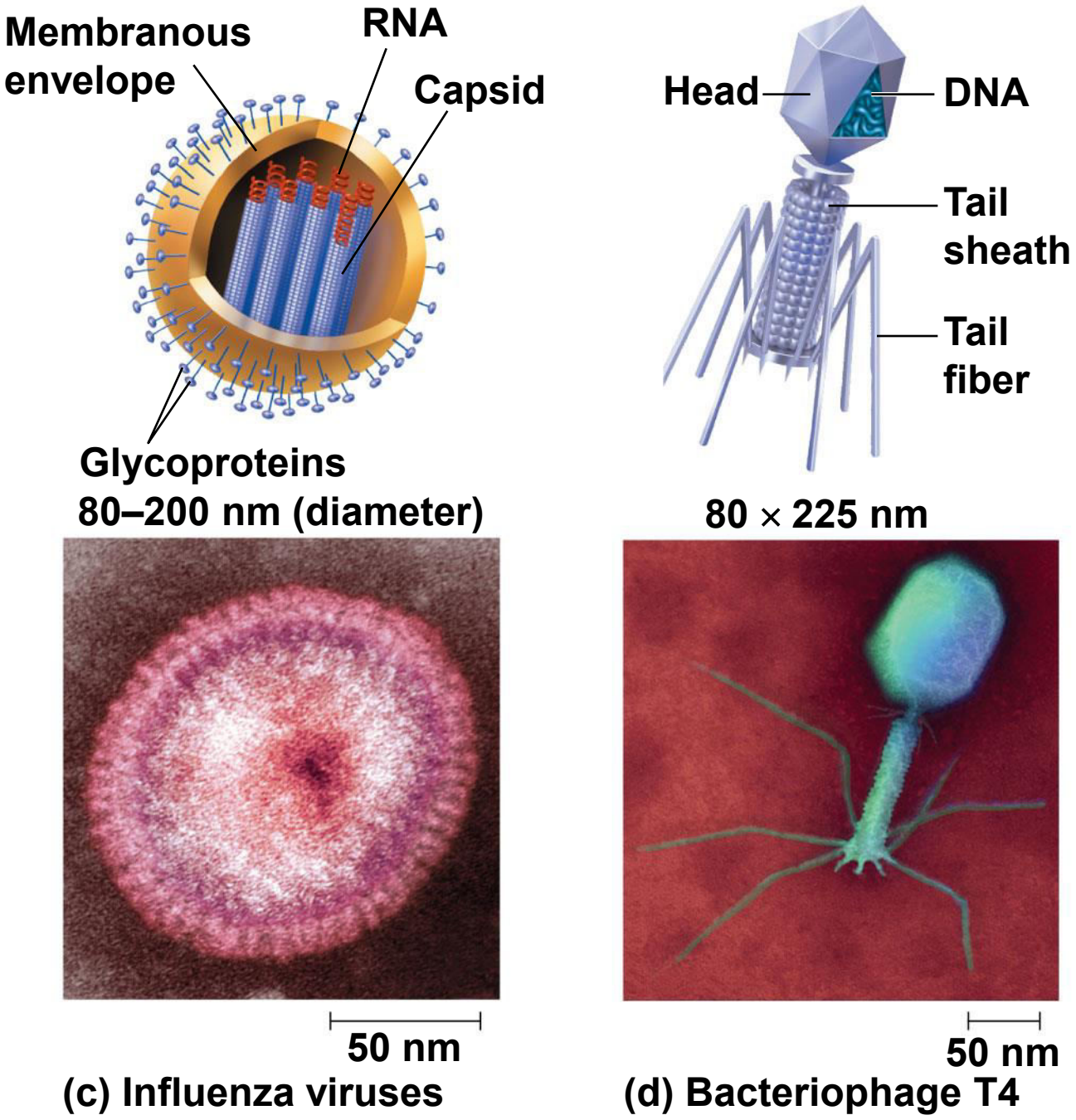
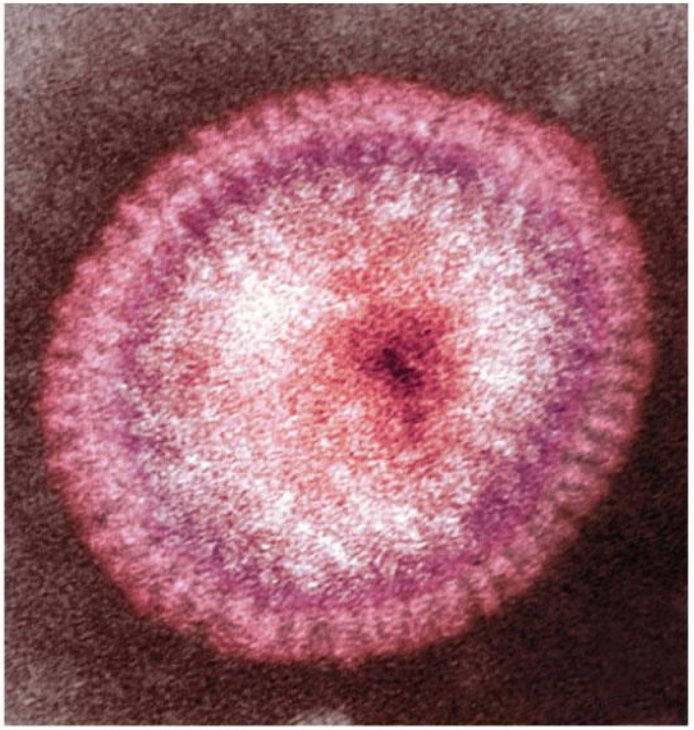


Figure 17.2-2a

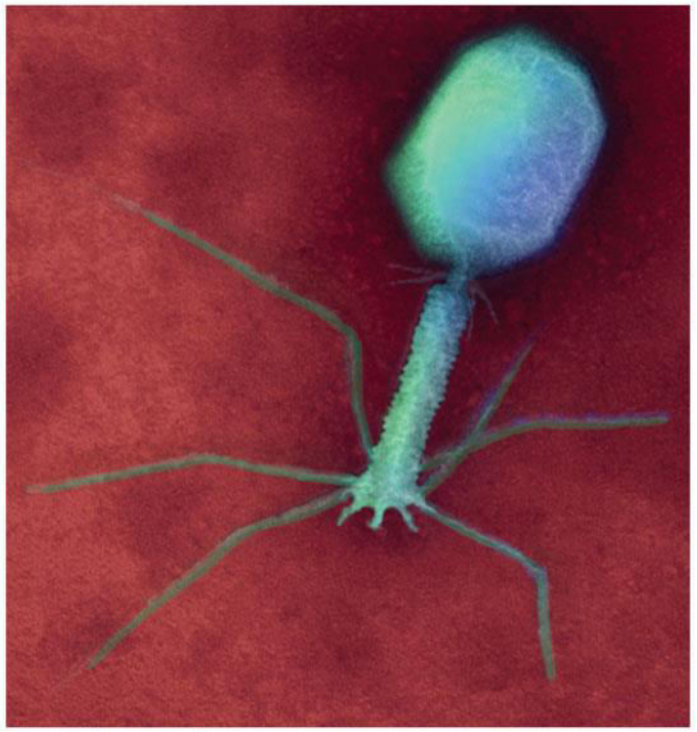
80–200 nm (diameter)



50 nm

(c) Influenza viruses

Figure 17.2-2b



(d) Bacteriophage T4

- Some viruses have membranous envelopes that help them infect hosts
- These **viral envelopes** are derived from the host cell's membrane and contain a combination of viral and host cell molecules

- **Bacteriophages**, also called **phages**, are viruses that infect bacteria
- They have the most complex capsids found among viruses
- Phages have an elongated capsid head that encloses their DNA
- A protein tail piece attaches the phage to the host and injects the phage DNA inside

Concept 17.2: Viruses replicate only in host cells

- Viruses are obligate intracellular parasites, because they can replicate only within a host cell
- Each virus has a **host range**, a limited number of host cells that it can infect

General Features of Viral Replicative Cycles

- Once a viral genome has entered a cell, the cell begins to manufacture viral proteins
- The virus makes use of host enzymes, ribosomes, tRNAs, amino acids, ATP, and other molecules
- Viral nucleic acid molecules and capsomeres spontaneously self-assemble into new viruses
- These exit from the host cell, usually damaging or destroying it

Replicative Cycles of Phages

- Phages are the best understood of all viruses
- Phages have two reproductive mechanisms: the lytic cycle and the lysogenic cycle

The Lytic Cycle

- The **lytic cycle** is a phage replicative cycle that culminates in the death of the host cell
- The lytic cycle produces new phages and lyses (breaks open) the host's cell wall, releasing the progeny viruses
- A phage that reproduces only by the lytic cycle is called a **virulent phage**

Figure 17.4-s1

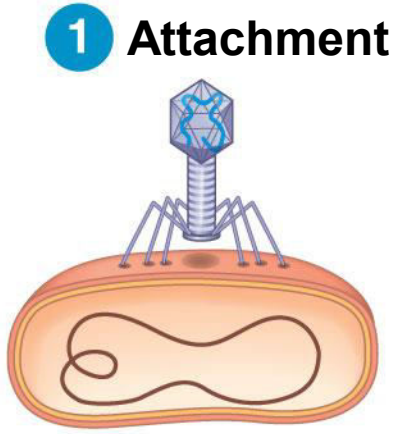


Figure 17.4-s2

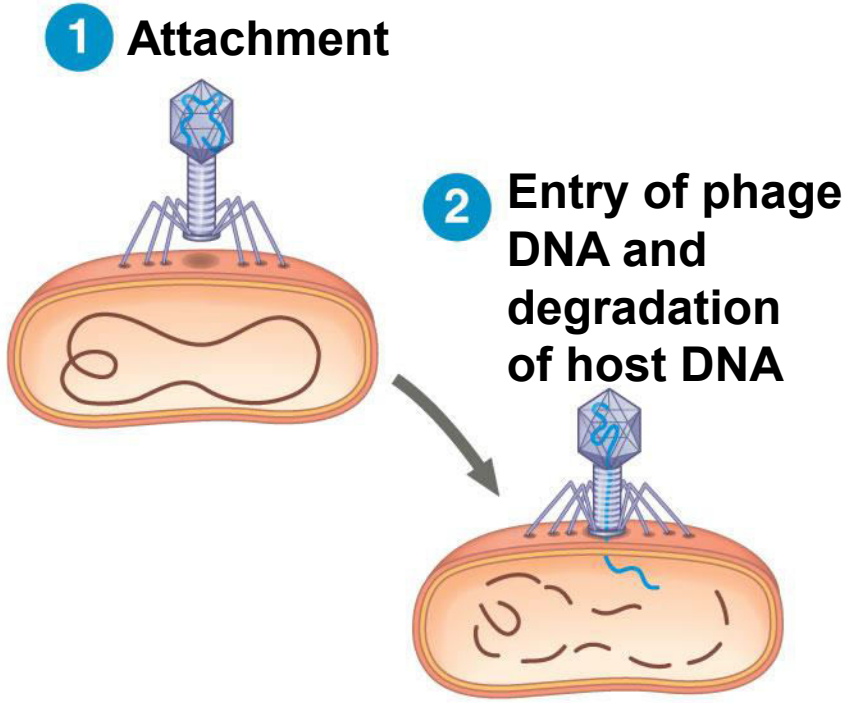


Figure 17.4-s3

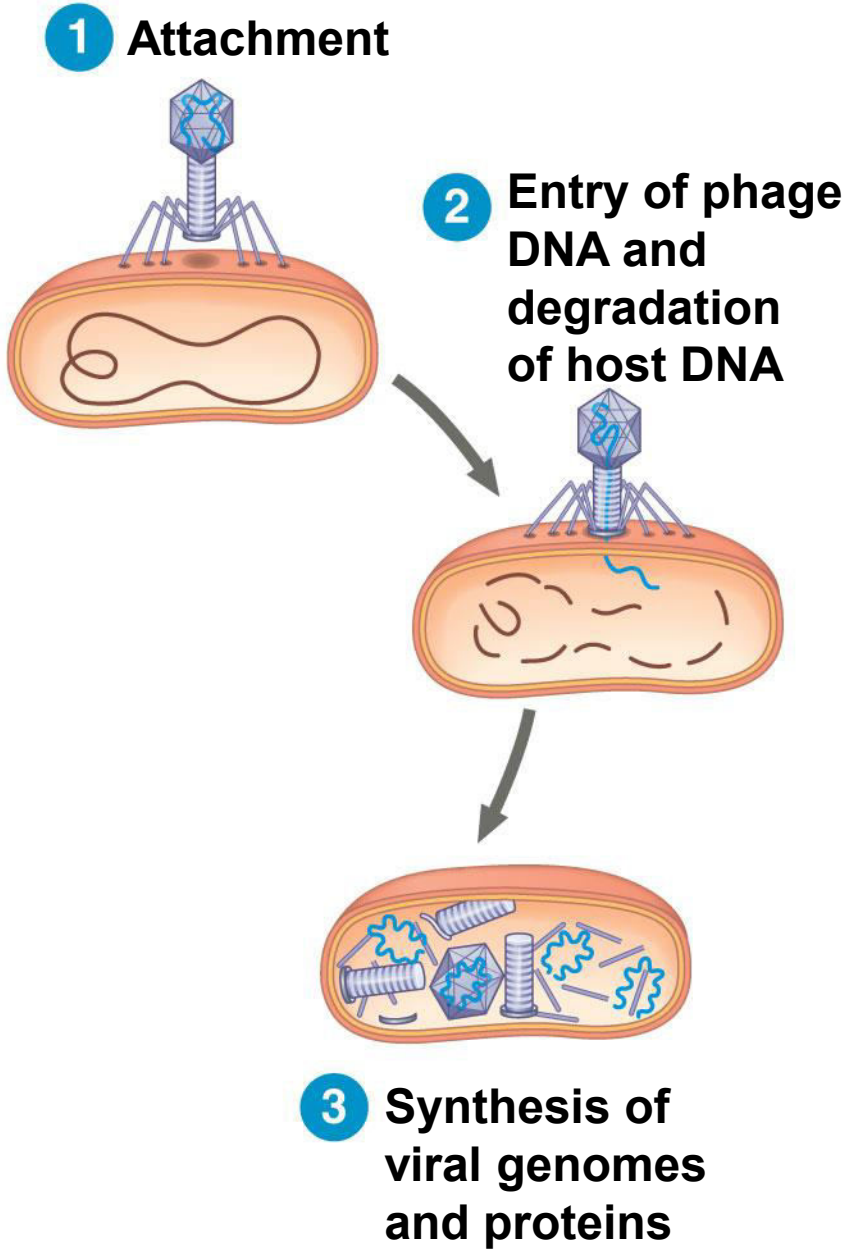


Figure 17.4-s4

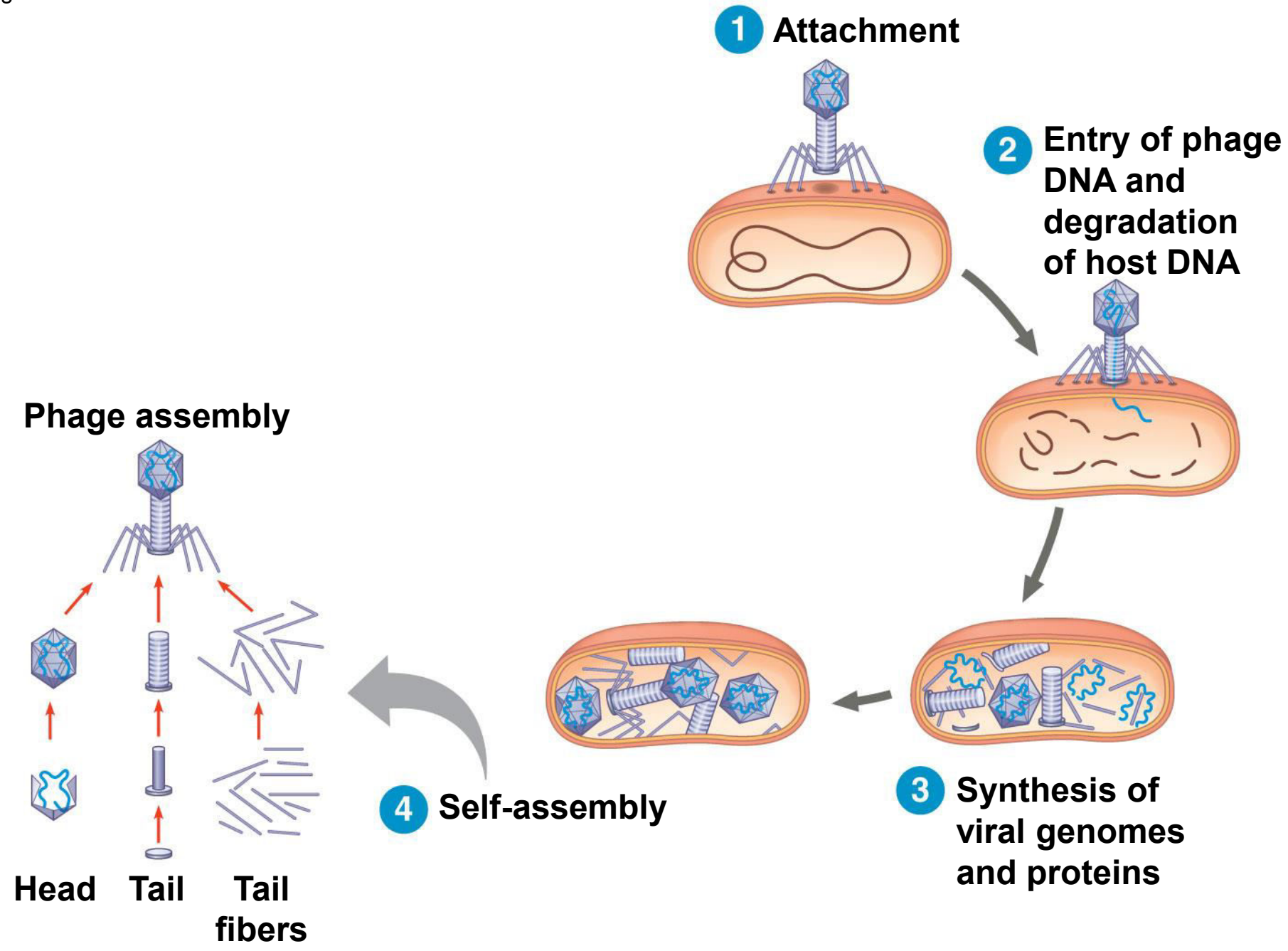
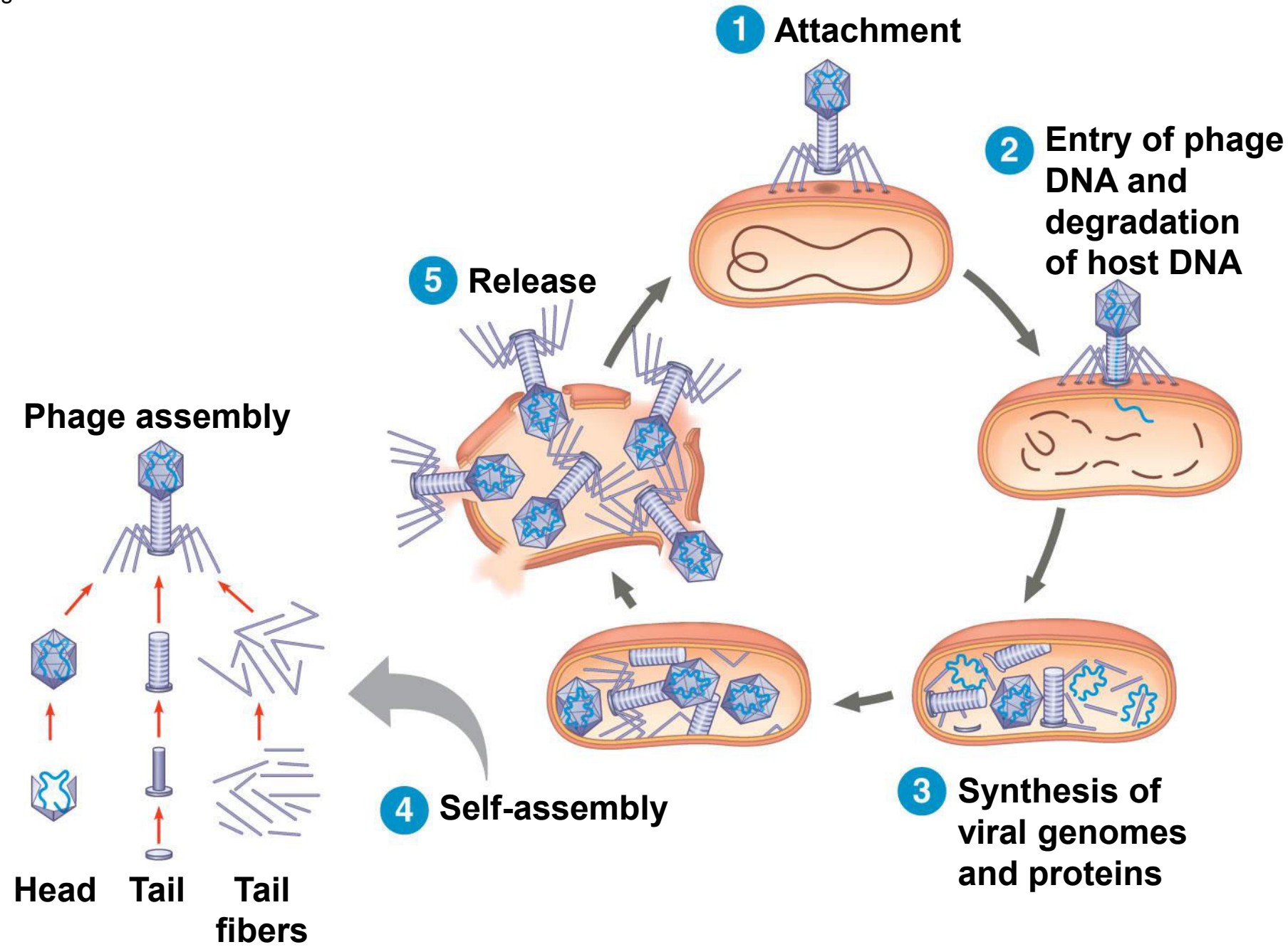


Figure 17.4-s5



The Lysogenic Cycle

- The **lysogenic cycle** replicates the phage genome without destroying the host
- Phages that use both the lytic and lysogenic cycles are called **temperate phages**
- The viral DNA molecule is incorporated into the host cell's chromosome
- This integrated viral DNA is known as a **prophage**

- Every time the host divides, it copies the phage DNA and passes the copies to daughter cells
- A single infected cell can give rise to a large population of bacteria carrying the virus in prophage form
- An environmental signal can trigger the virus genome to exit the bacterial chromosome and switch to the lytic mode

Figure 17.5

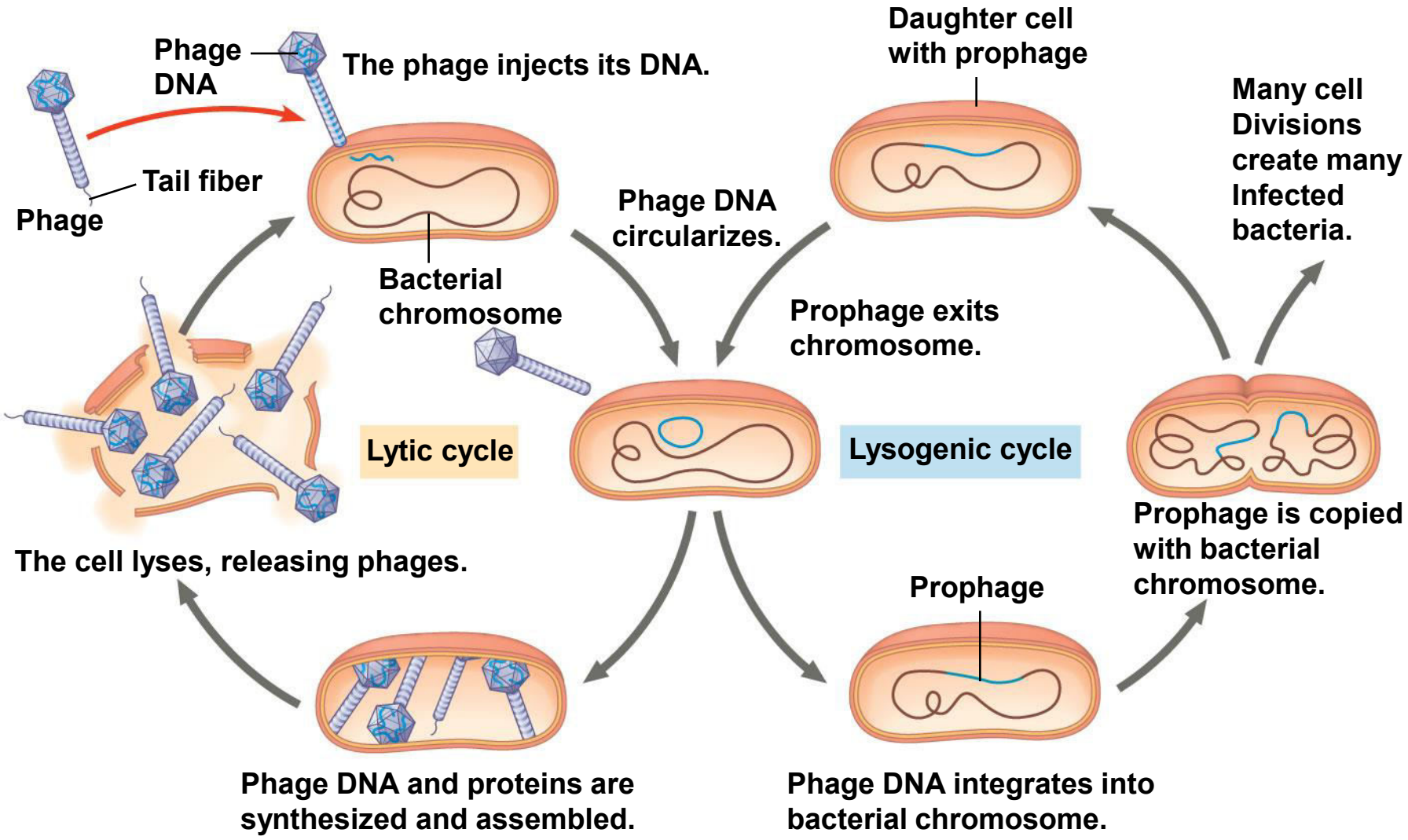


Figure 17.5-1

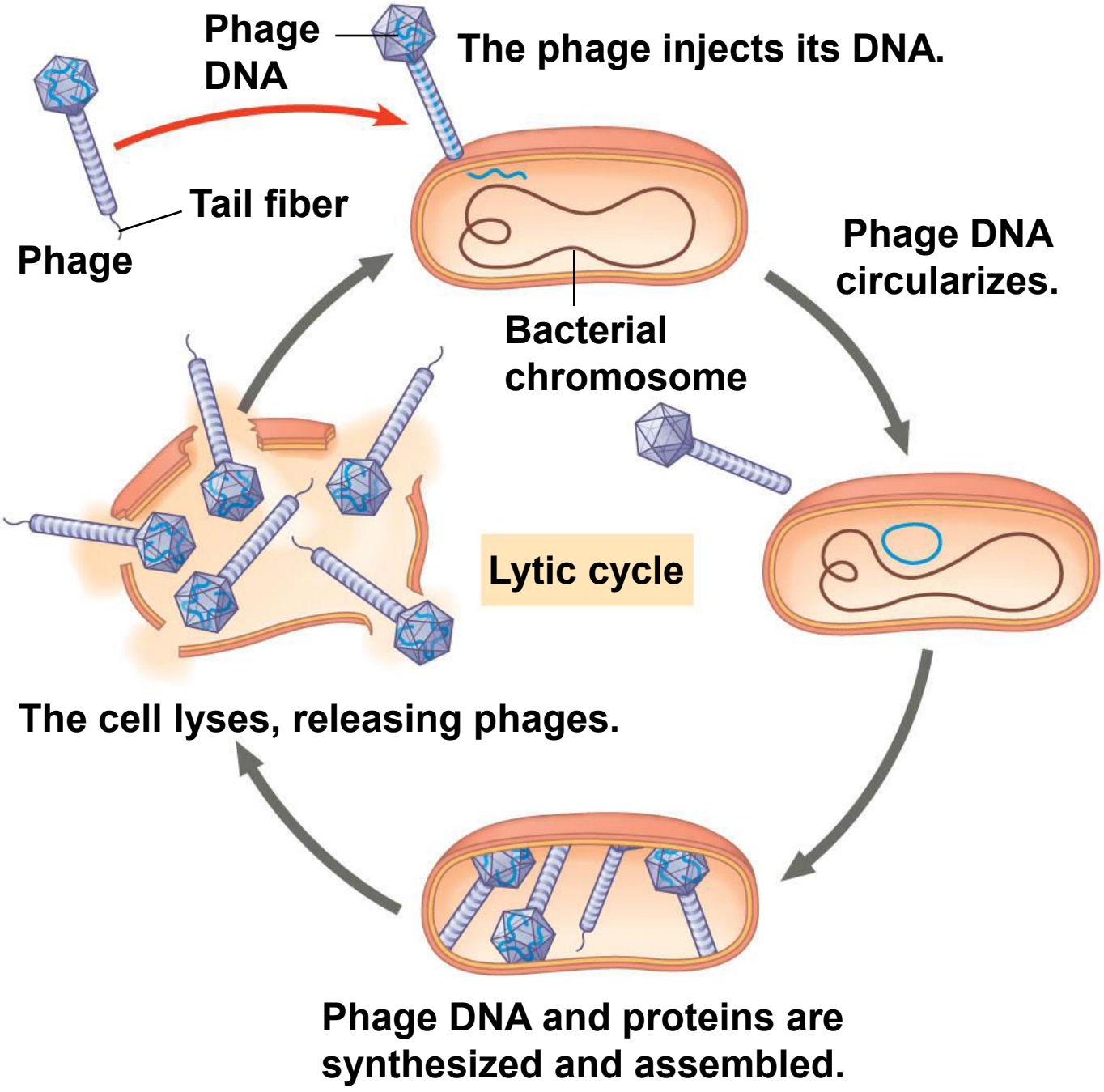
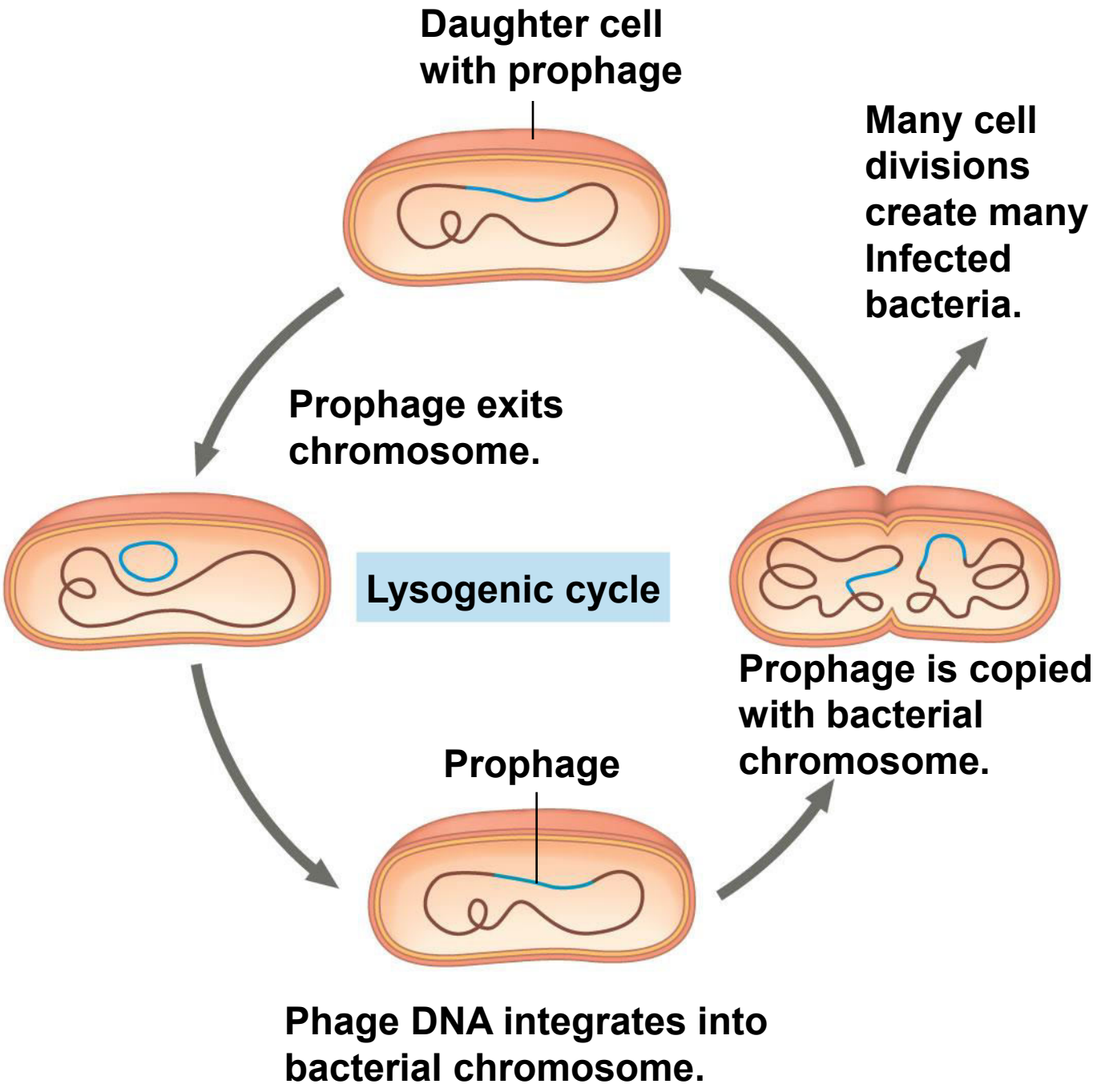


Figure 17.5-2



Bacterial Defenses Against Phages

- Natural selection favors mutant bacteria with surface proteins that are not recognized by a particular phage
- Phage DNA is often identified as foreign and cut up by **restriction enzymes**
- The bacterium's own DNA is methylated in a way that prevents attack by its own restriction enzymes

- The CRISPR-Cas system consists of clustered regularly interspaced short palindromic repeats and nuclease enzymes called Cas, CRISPR-associated proteins
- When a phage infects a bacterium with this system, the phage DNA is integrated between two repeat sequences
- If the cell survives the infection, any further attempt at infection of this cell or its offspring triggers transcription of the CRISPR region

- Transcription of the CRISPR region leads to the resulting RNA being bound by Cas proteins
- The RNA is used to target the corresponding DNA, which is then cut and degraded
- In this way, the bacterial cell and its offspring are protected against further infection by the same type of phage

Figure 17.6

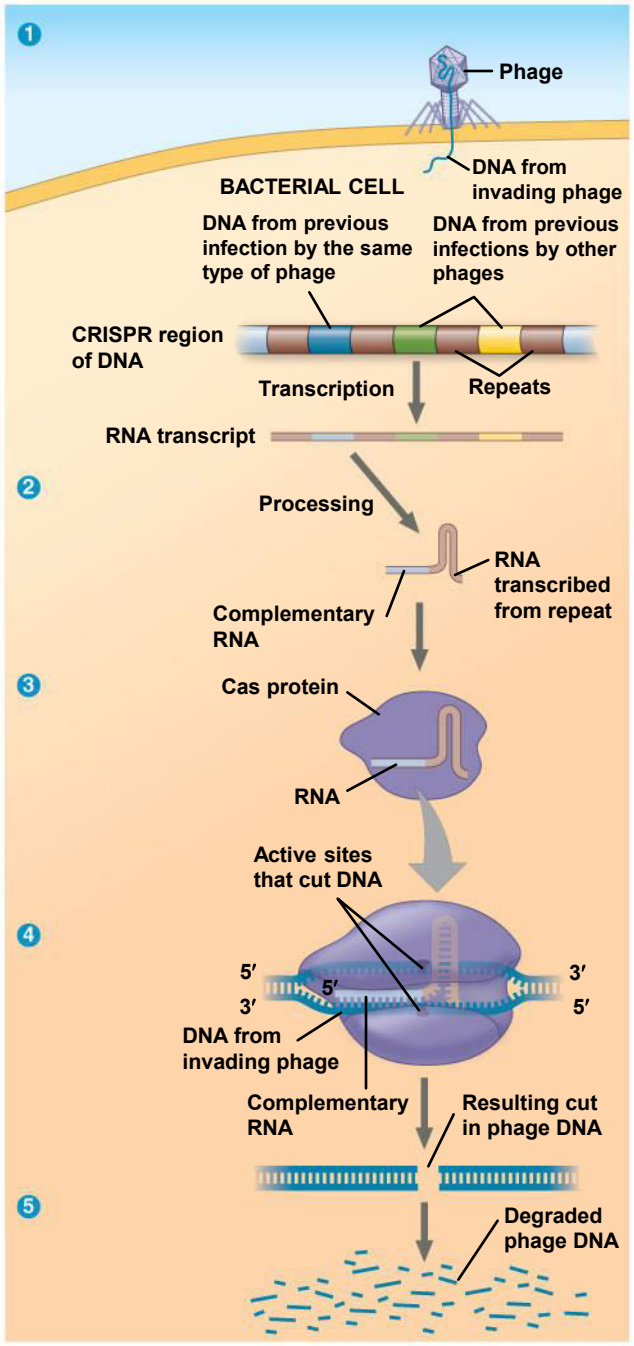


Figure 17.6-1

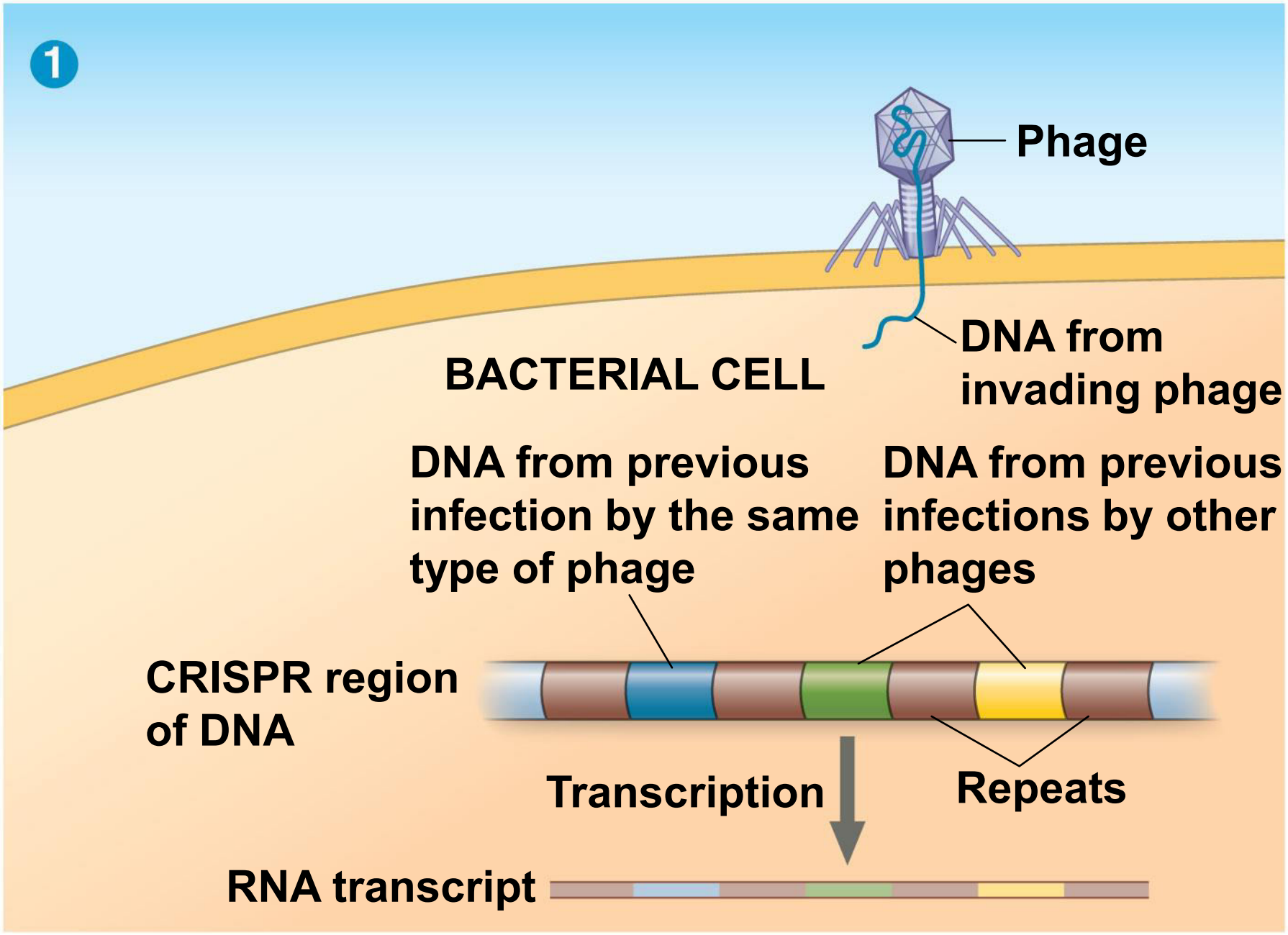


Figure 17.6-2

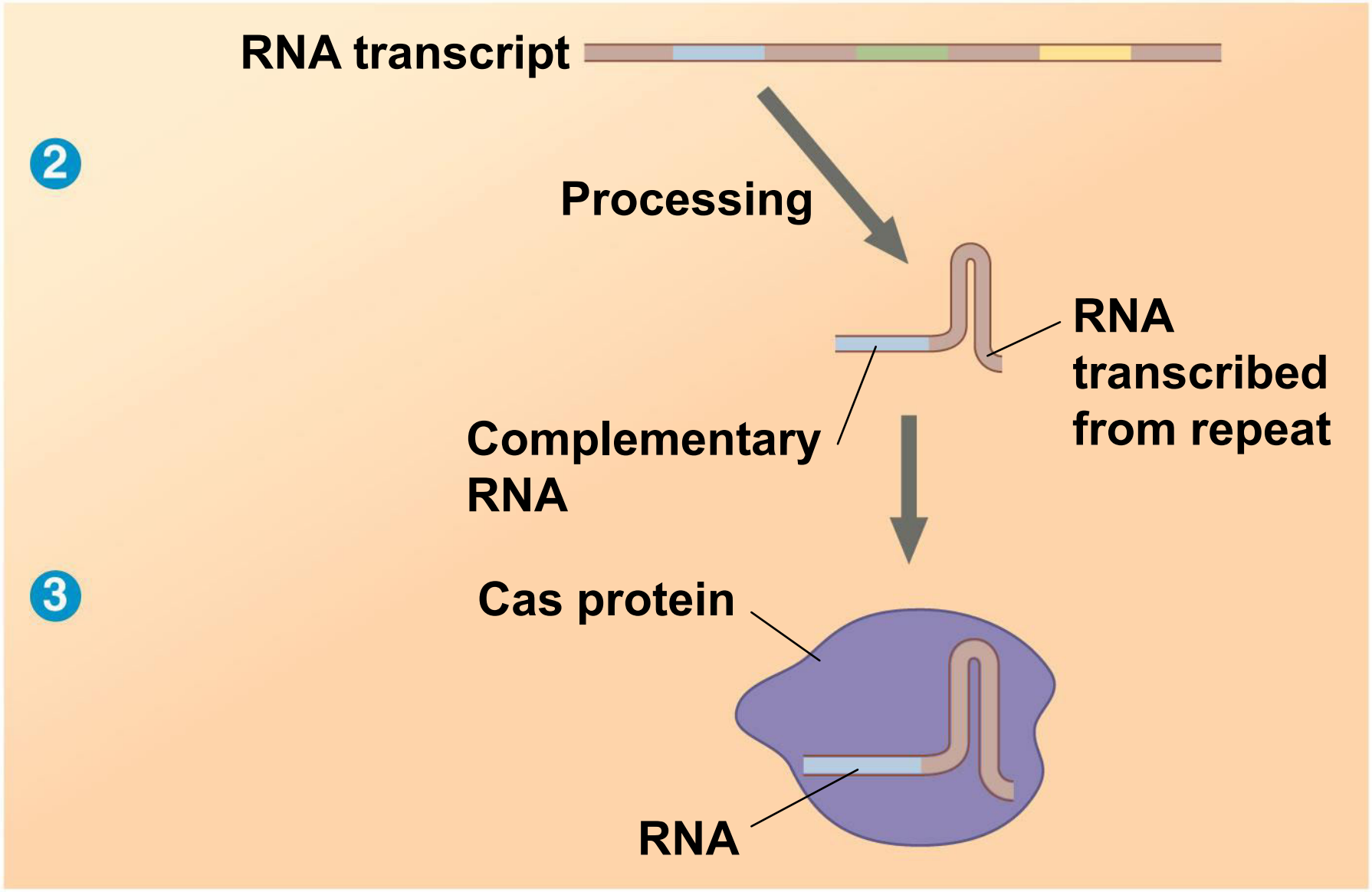
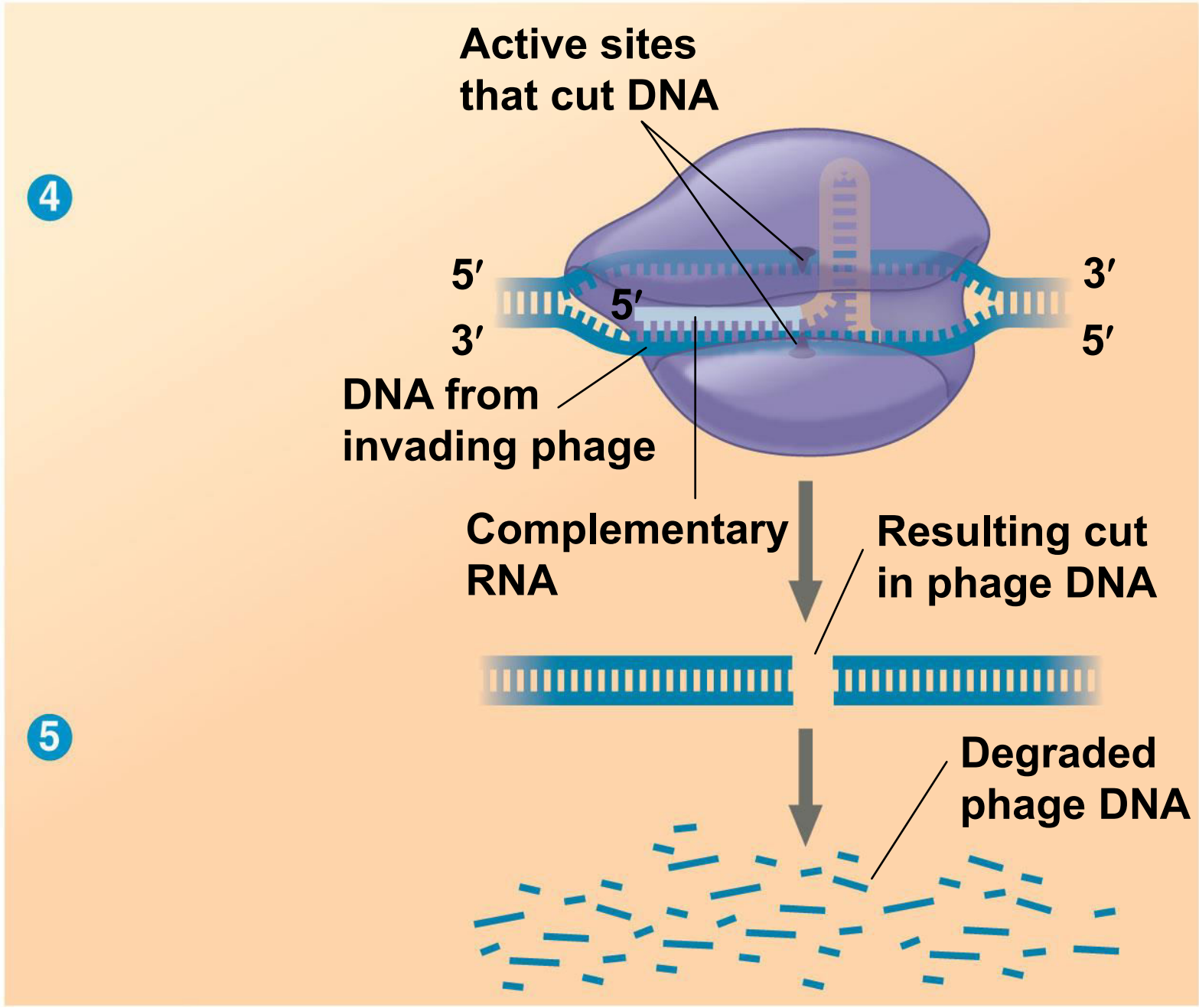


Figure 17.6-3



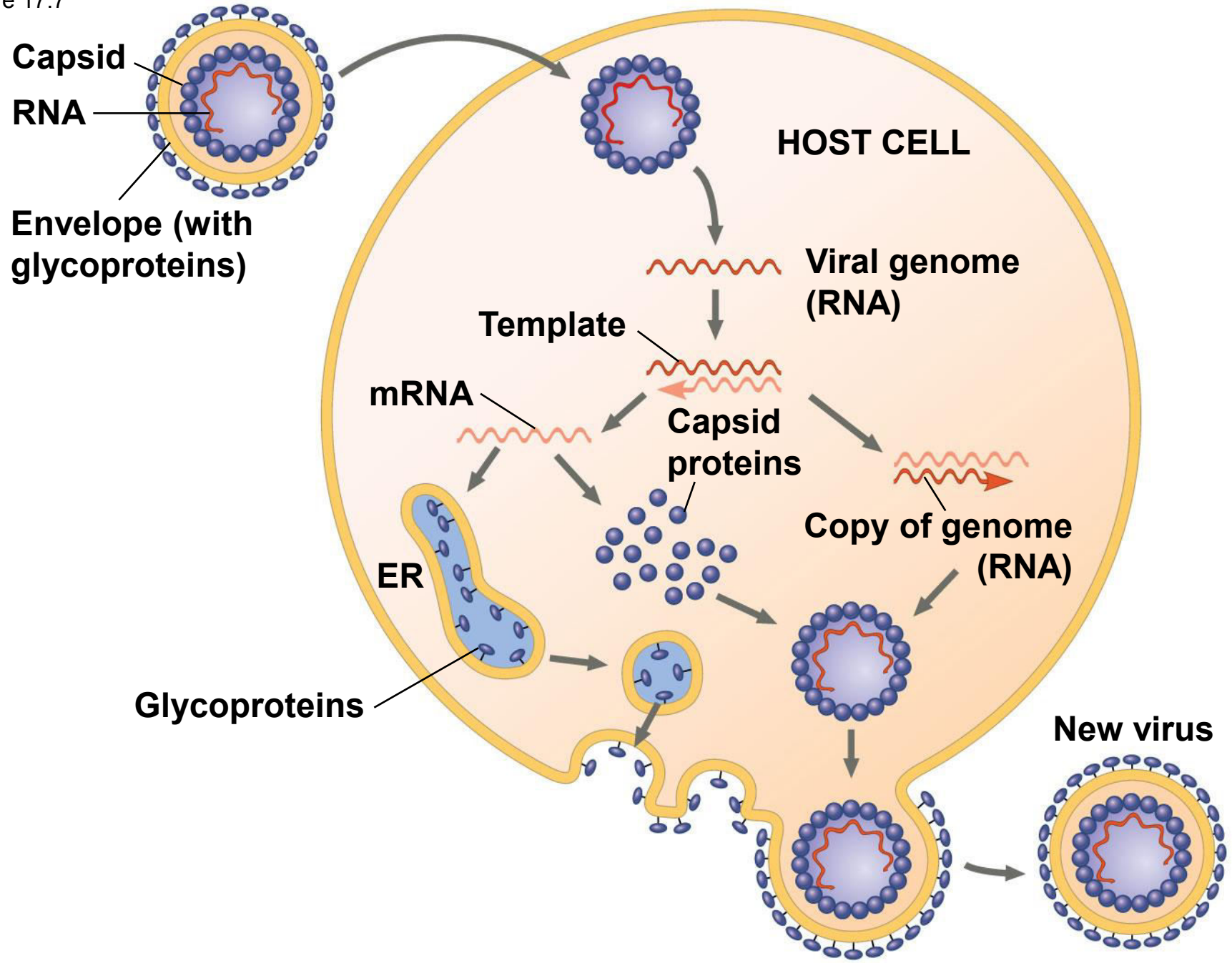
Replicative Cycles of Animal Viruses

- There are two key variables used to classify viruses that infect animals
  - The nature of the viral genome (single- or double-stranded DNA or RNA)
  - The presence or absence of an envelope

Viral Envelopes

- An animal virus with an envelope uses it to enter the host cell
- The envelope is derived from the plasma membrane of a host cell, although some of the molecules on the envelope are specified by the genome of the virus

Figure 17.7

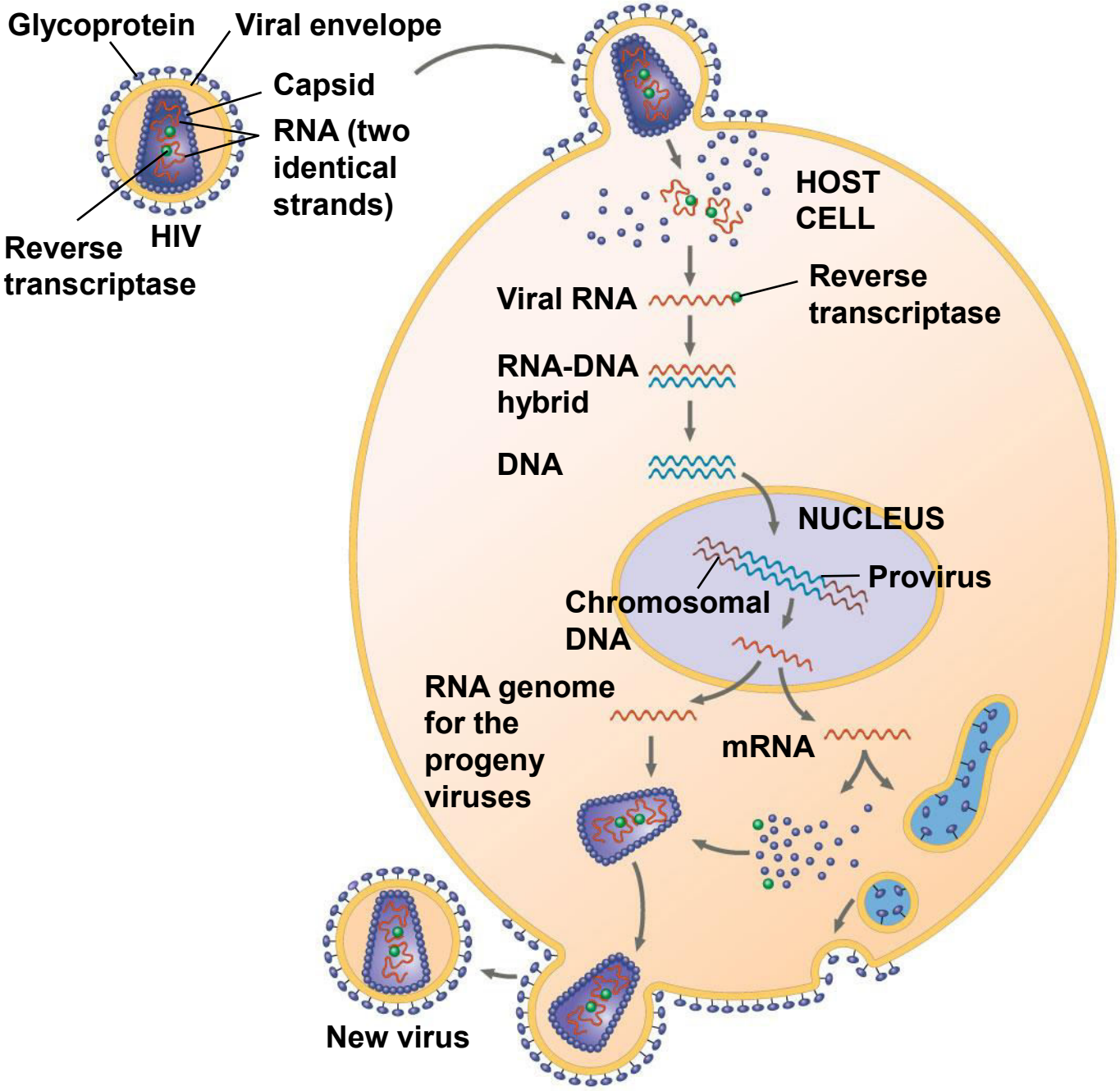


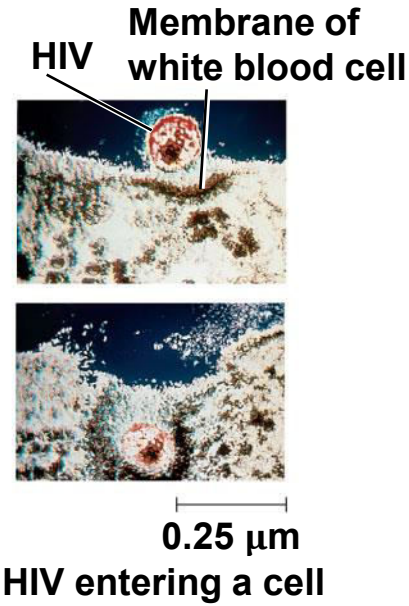
RNA as Viral Genetic Material

- The broadest variety of RNA genomes is found in viruses that infect animals
- **Retroviruses** use **reverse transcriptase** to copy their RNA genome into DNA
- **HIV** (**human immunodeficiency virus**) is the retrovirus that causes **AIDS** (**acquired immunodeficiency syndrome**)

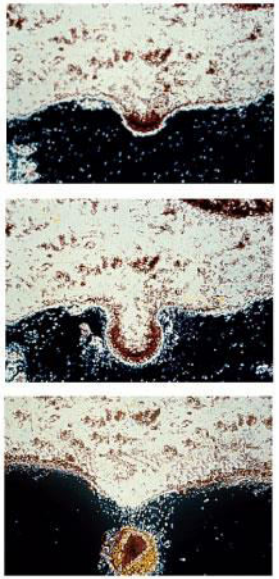
- Viral DNA that is integrated into the host genome is called a **provirus**
- A provirus is a permanent resident of the host cell
- The host's RNA polymerase transcribes the proviral DNA into RNA molecules
- The RNA molecules function both as mRNA for synthesis of viral proteins and as genomes for new viruses released from the cell

Figure 17.8





HIV entering a cell



New HIV leaving a cell

Figure 17.8-1

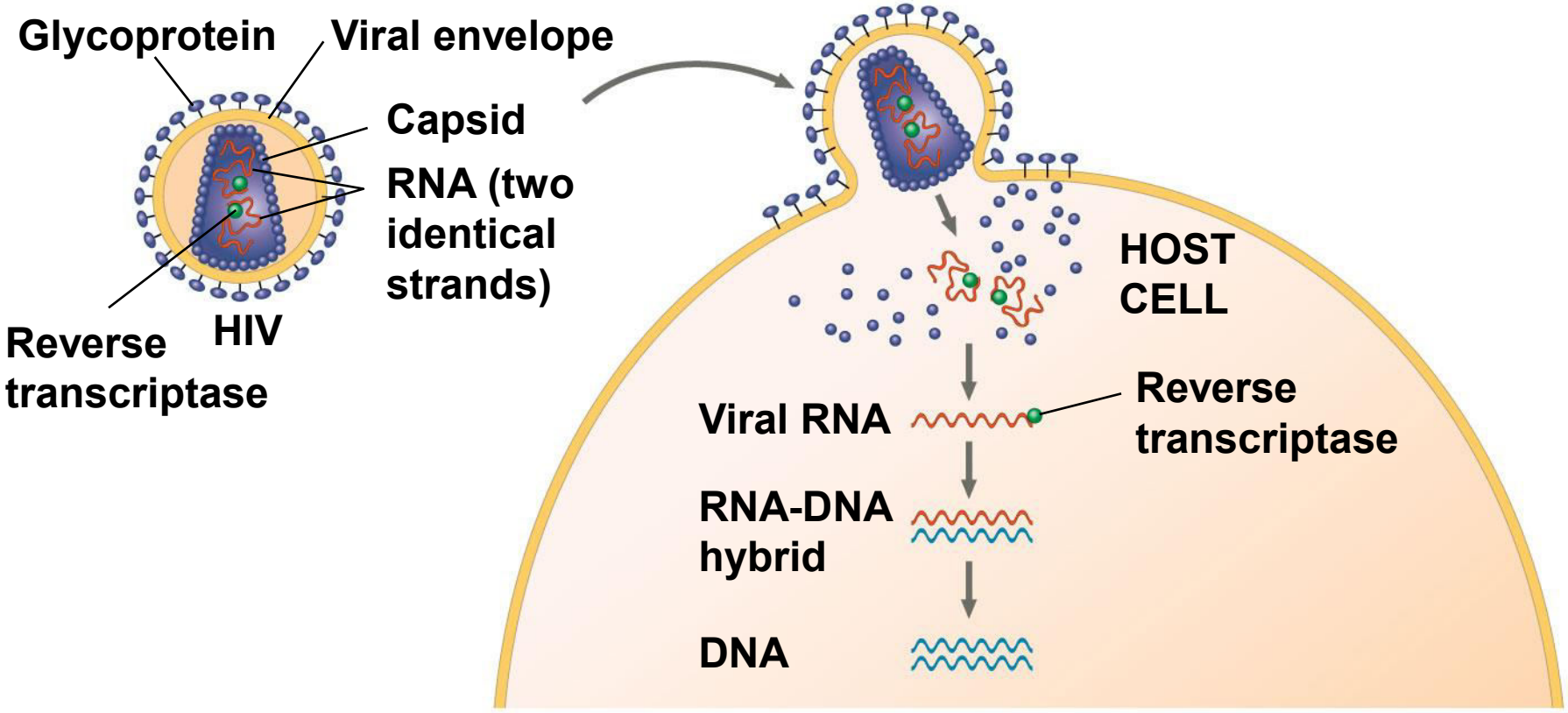


Figure 17.8-2

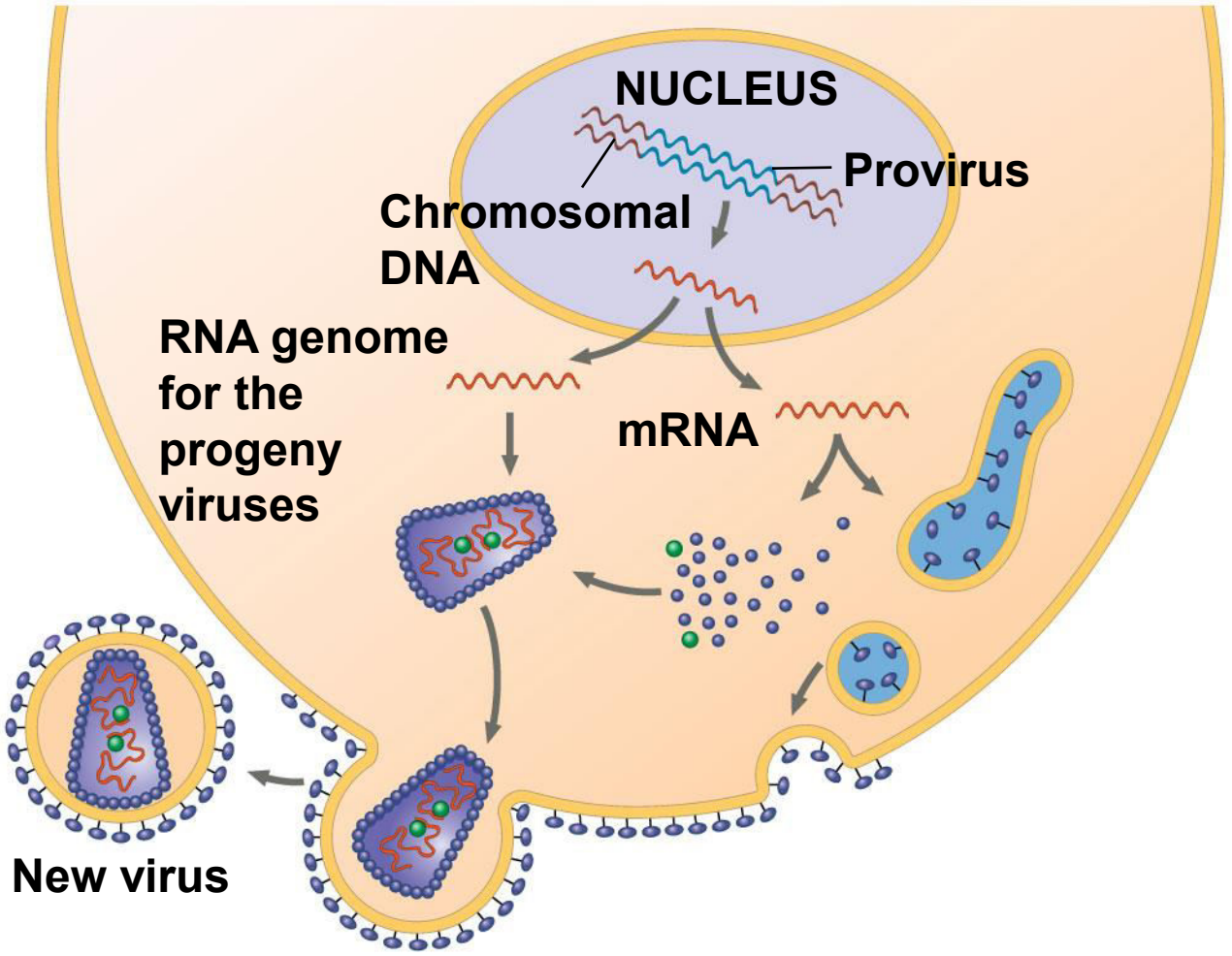


Figure 17.8-3

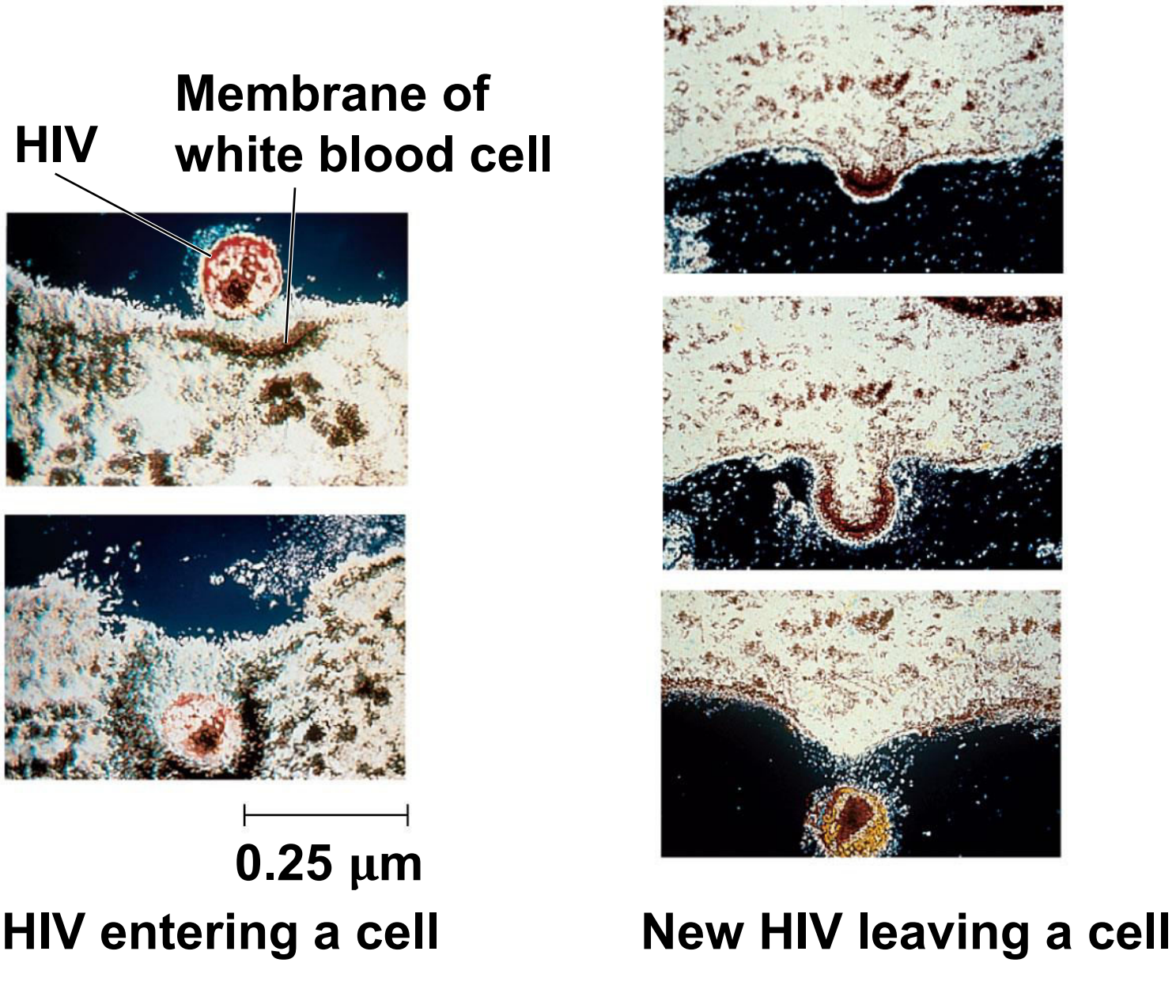
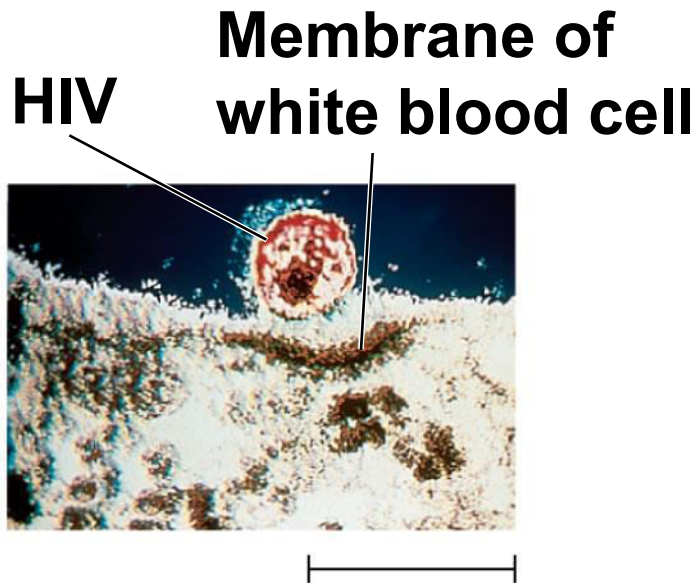
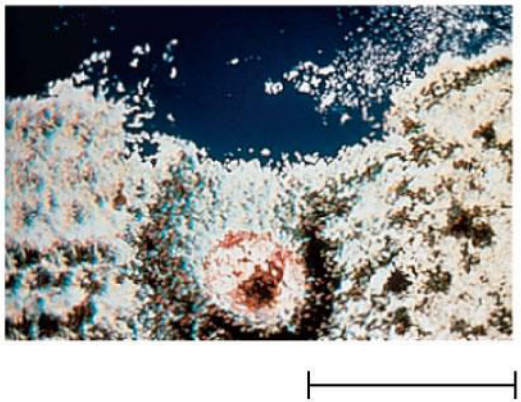


Figure 17.8-3a



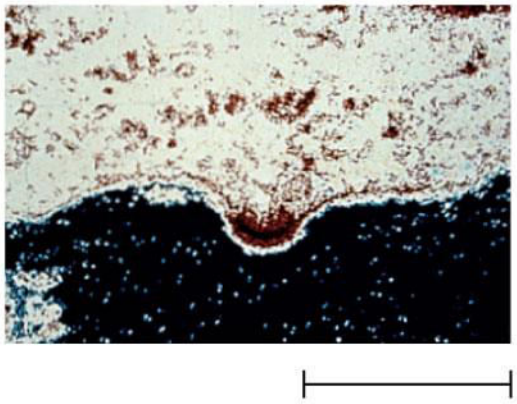
HIV entering a cell

Figure 17.8-3b



HIV entering a cell

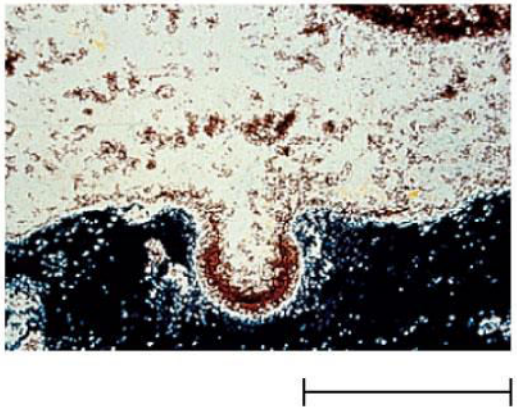
Figure 17.8-3c



0.25 μm

New HIV leaving a cell

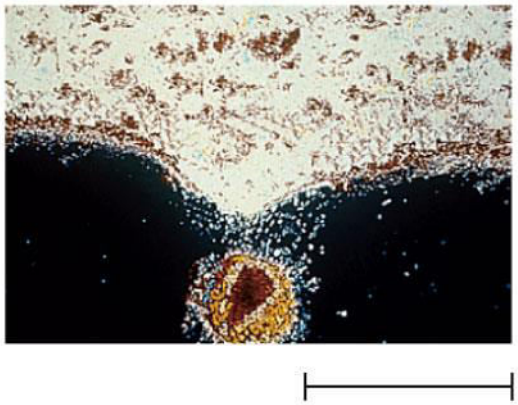
Figure 17.8-3d



0.25 μm

New HIV leaving a cell

Figure 17.8-3e



0.25 μm

New HIV leaving a cell

Evolution of Viruses

- Viruses do not fit our definition of living organisms
- Since viruses can replicate only within cells, they probably evolved after the first cells appeared
- Candidates for the source of viral genomes are plasmids (circular DNA in bacteria and yeasts) and transposons (small mobile DNA segments)
- Plasmids, transposons, and viruses are all mobile genetic elements

Concept 17.3: Viruses and prions are formidable pathogens in animals and plants

- Diseases caused by viral infections afflict humans, agricultural crops, and livestock worldwide
- Smaller, less complex entities known as prions also cause disease in animals

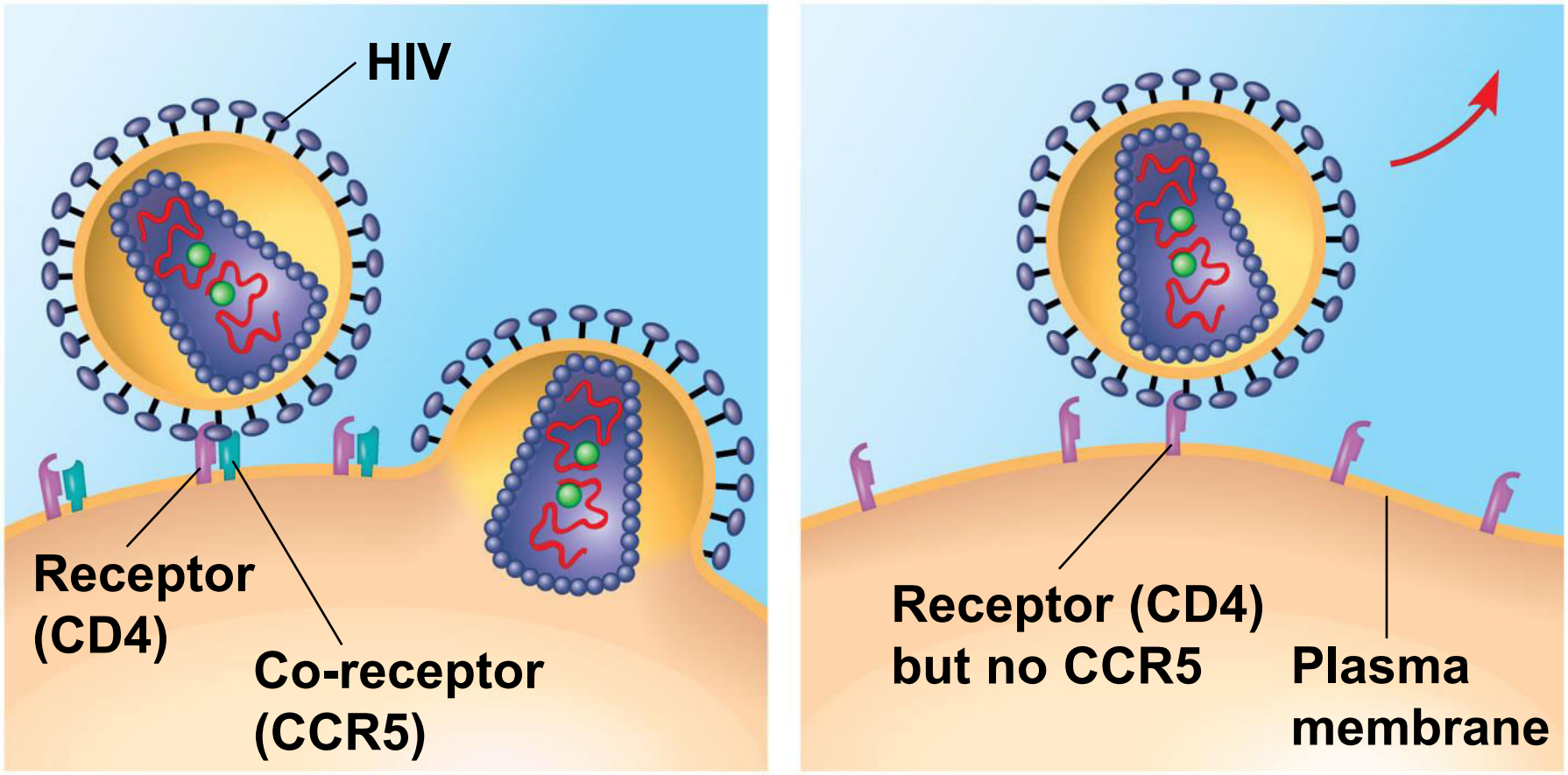
Viral Diseases in Animals

- Viruses may damage or kill cells by causing the release of hydrolytic enzymes from lysosomes
- Some viruses cause infected cells to produce toxins that lead to disease symptoms
- Others have molecular components such as envelope proteins that are toxic

- Vaccines are the major medical tool for preventing viral infections
- A **vaccine** is a harmless derivative of a pathogen that stimulates the immune system to mount defenses against the harmful pathogen
- Antibiotics are powerless against viruses
- Antiviral drugs can help to treat, though not cure, viral infections

- Receptor proteins on the surfaces of cells are important in treatment or prevention of viral infection
- Some people have been found to be resistant to HIV infection
- These people have an unusual form of the CCR5 protein, one of the proteins to which HIV must bind in order to infect most cells
- A drug that masks the CCR5 protein is being tested currently

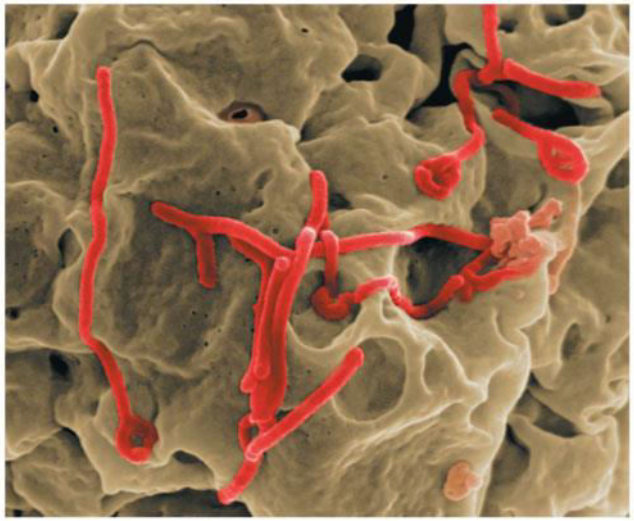
Figure 17.9



Emerging Viruses

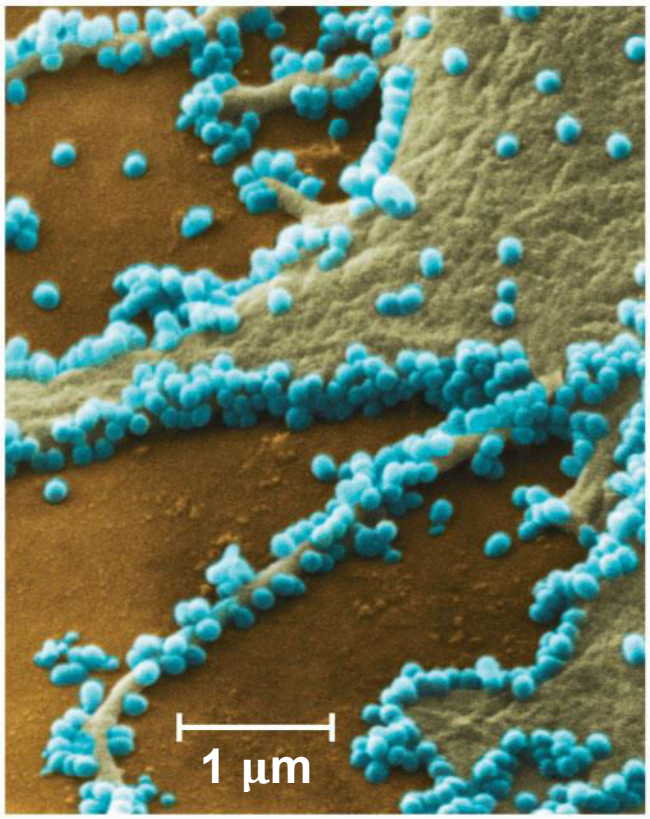
- Viruses that suddenly become apparent are called emerging viruses
- HIV is a classic example
- The Ebola virus, recognized initially in 1976 in central Africa, causes hemorrhagic fever, an often fatal syndrome

Figure 17.10



- In 2009 a general outbreak, or **epidemic**, of a flu-like illness occurred in Mexico and the United States; the virus responsible was named H1N1
- H1N1 spread rapidly, causing a **pandemic**, or global epidemic

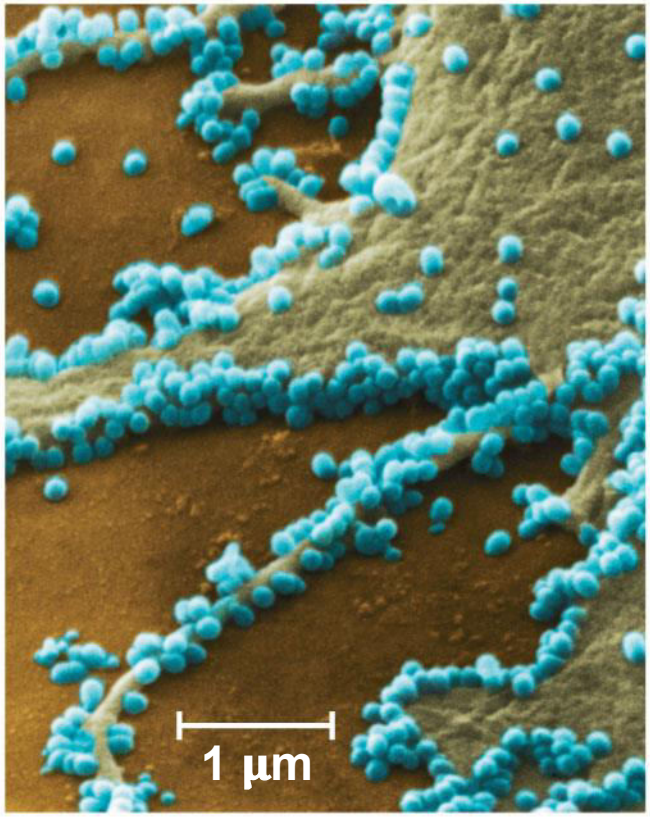
Figure 17.11



(a) 2009 pandemic H1N1 influenza A virus

(b) 2009 pandemic screening

Figure 17.11-1



(a) 2009 pandemic H1N1 influenza A virus

Figure 17.11-2

(b) 2009 pandemic screening

- Three processes contribute to the emergence of viral diseases
  - The mutation of existing viruses, which is especially high in RNA viruses
  - Dissemination of a viral disease from a small, isolated human population, allowing the disease to go unnoticed before it begins to spread
  - Spread of existing viruses from animal populations; about three-quarters of new human diseases originate this way

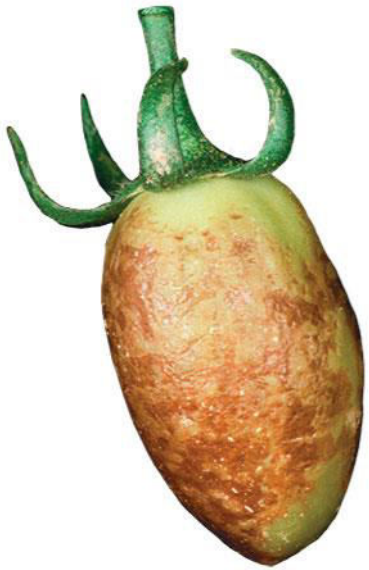
- Strains of influenza A are given standardized names
- The name H1N1 identifies forms of two viral surface proteins, hemagglutinin (H) and neuraminidase (N)
- There are numerous types of hemagglutinin and neuraminidase, identified by numbers

Viral Diseases in Plants

- More than 2,000 types of viral diseases of plants are known; these have enormous impacts on the agricultural and horticultural industries
- Plant viruses have the same basic structure and mode of replication as animal viruses
- Most plant viruses known thus far have an RNA genome and many have a helical capsid

- Plant viral diseases spread by two major routes
  - Infection from an external source of virus is called horizontal transmission
  - Herbivores, especially insects, pose a double threat because they can both carry a virus and help it get past the plant's outer layer of cells
  - Inheritance of the virus from a parent is called vertical transmission

Figure 17.12



Prions: Proteins as Infectious Agents

- There are proteins, called **prions**, that are known to be infectious
- These appear to cause a number of degenerative brain diseases in various animal species
- Prions can be transmitted in food
- Prions act very slowly, with an incubation period of at least 10 years
- Prions are also virtually indestructable

- To date, there is no known cure for prion diseases
- Prions, according to the leading model, are misfolded forms of proteins normally found in the brain
- The prion somehow converts the normal proteins to the incorrectly folded form
- The incorrectly folded form of the proteins forms aggregates that interfere with normal cell functions

Figure 17.13

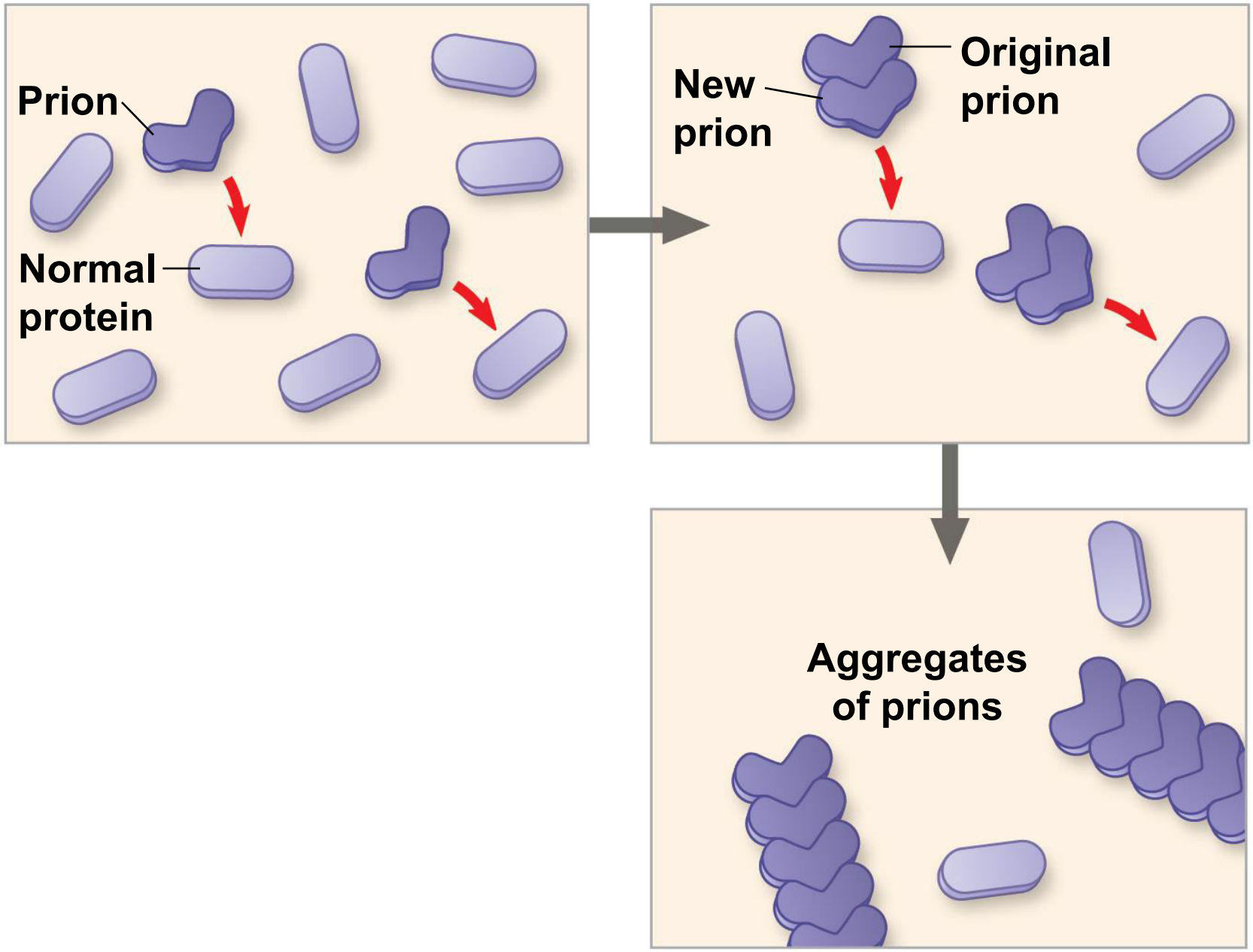


Figure 17.UN01-1

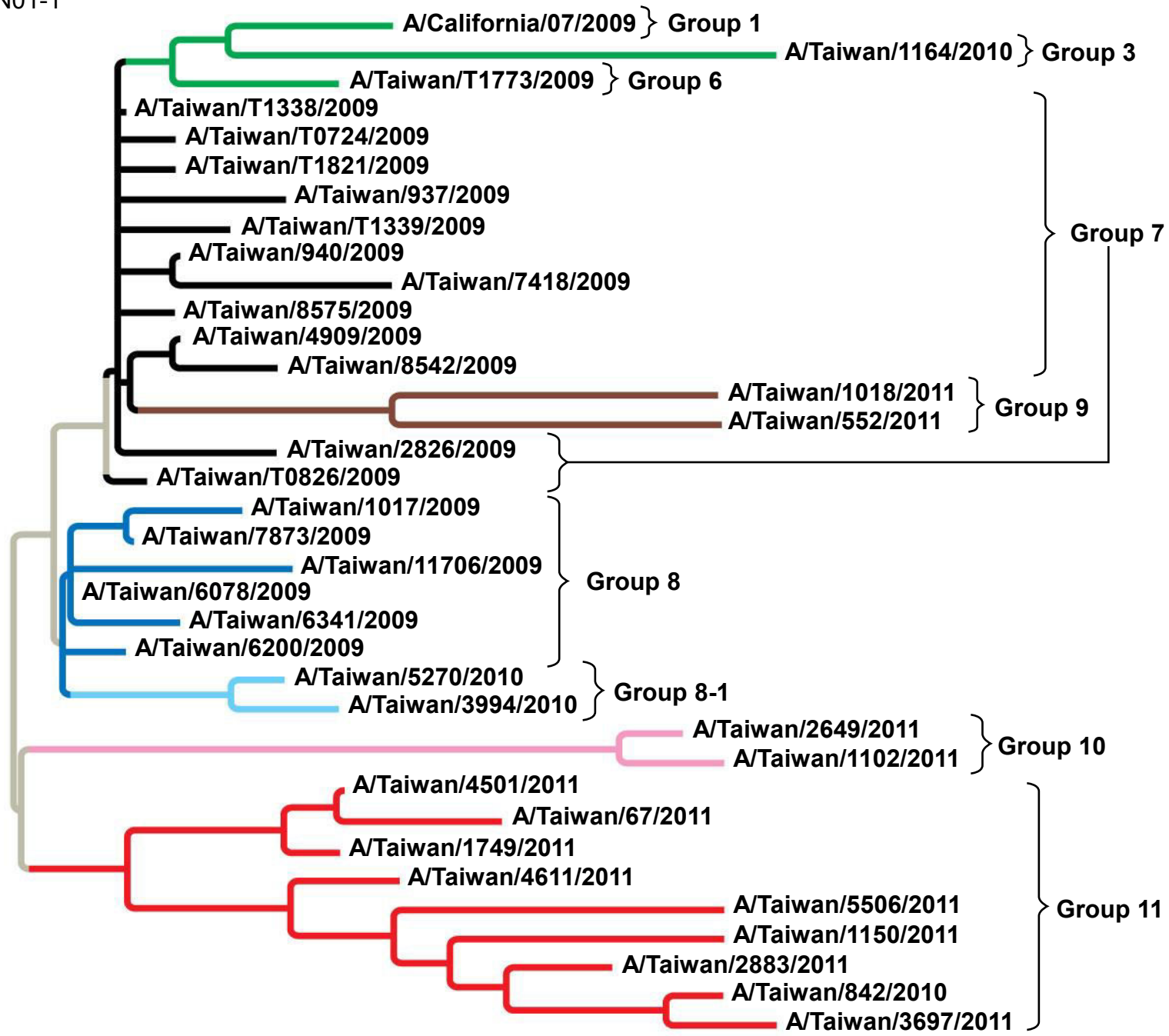


Figure 17.UN01-1a

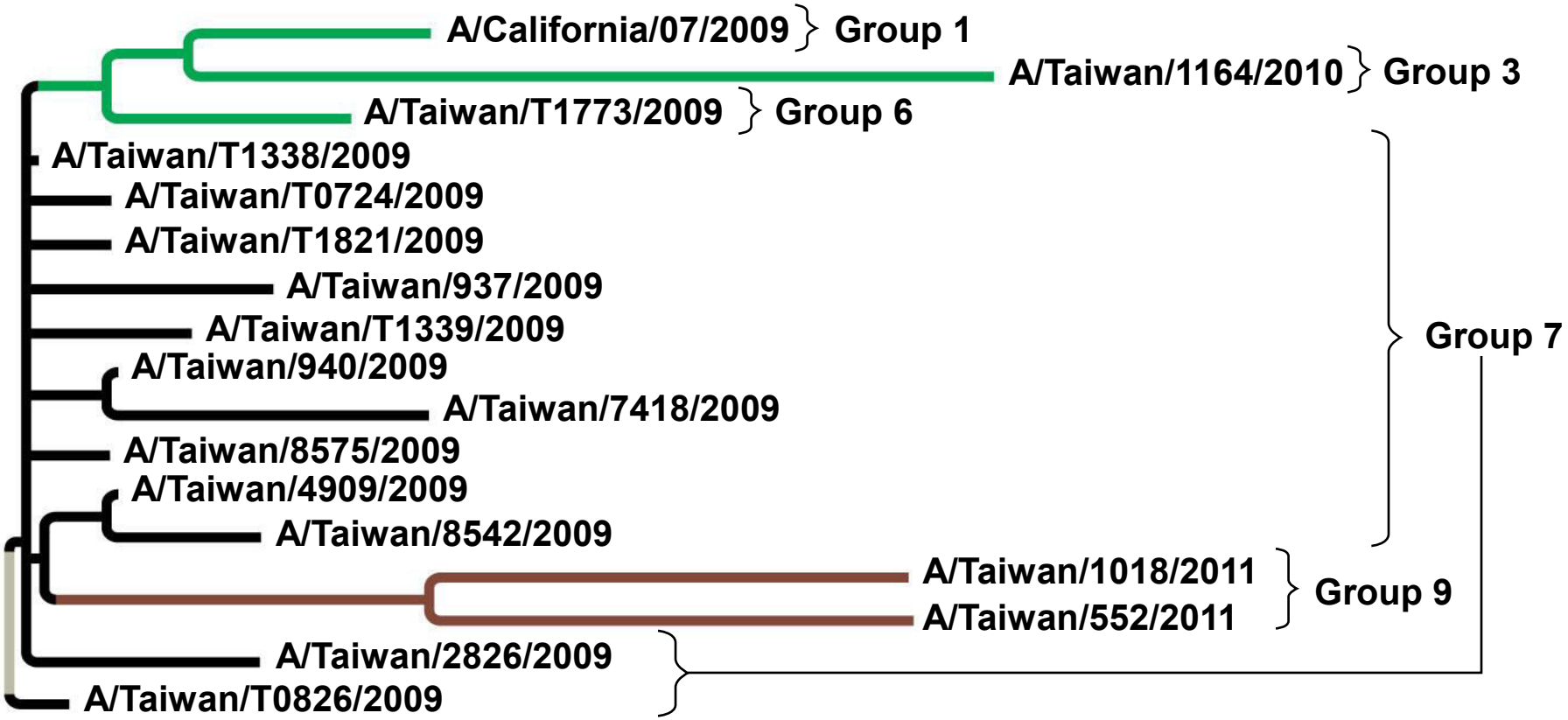


Figure 17.UN01-1b

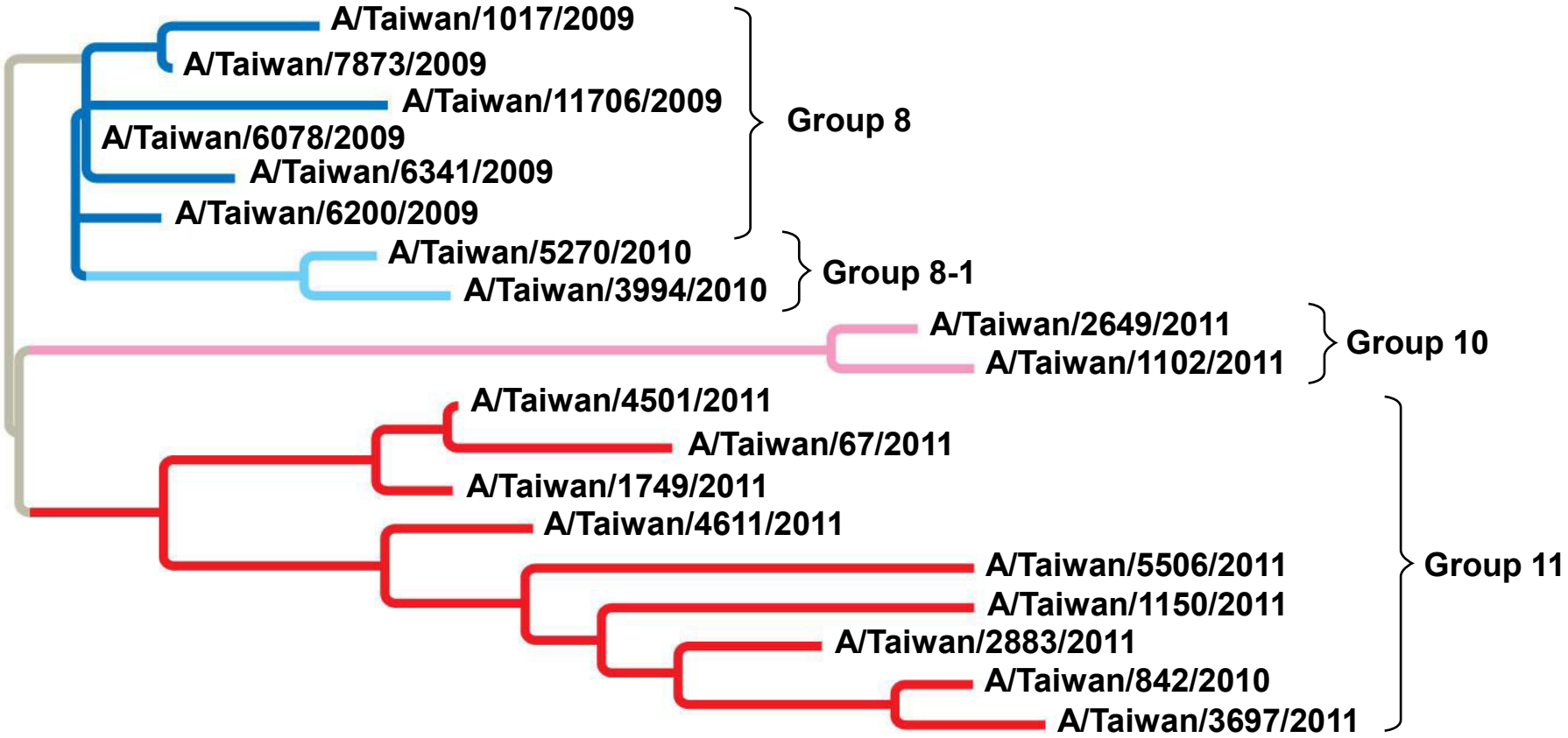


Figure 17.UN01-2

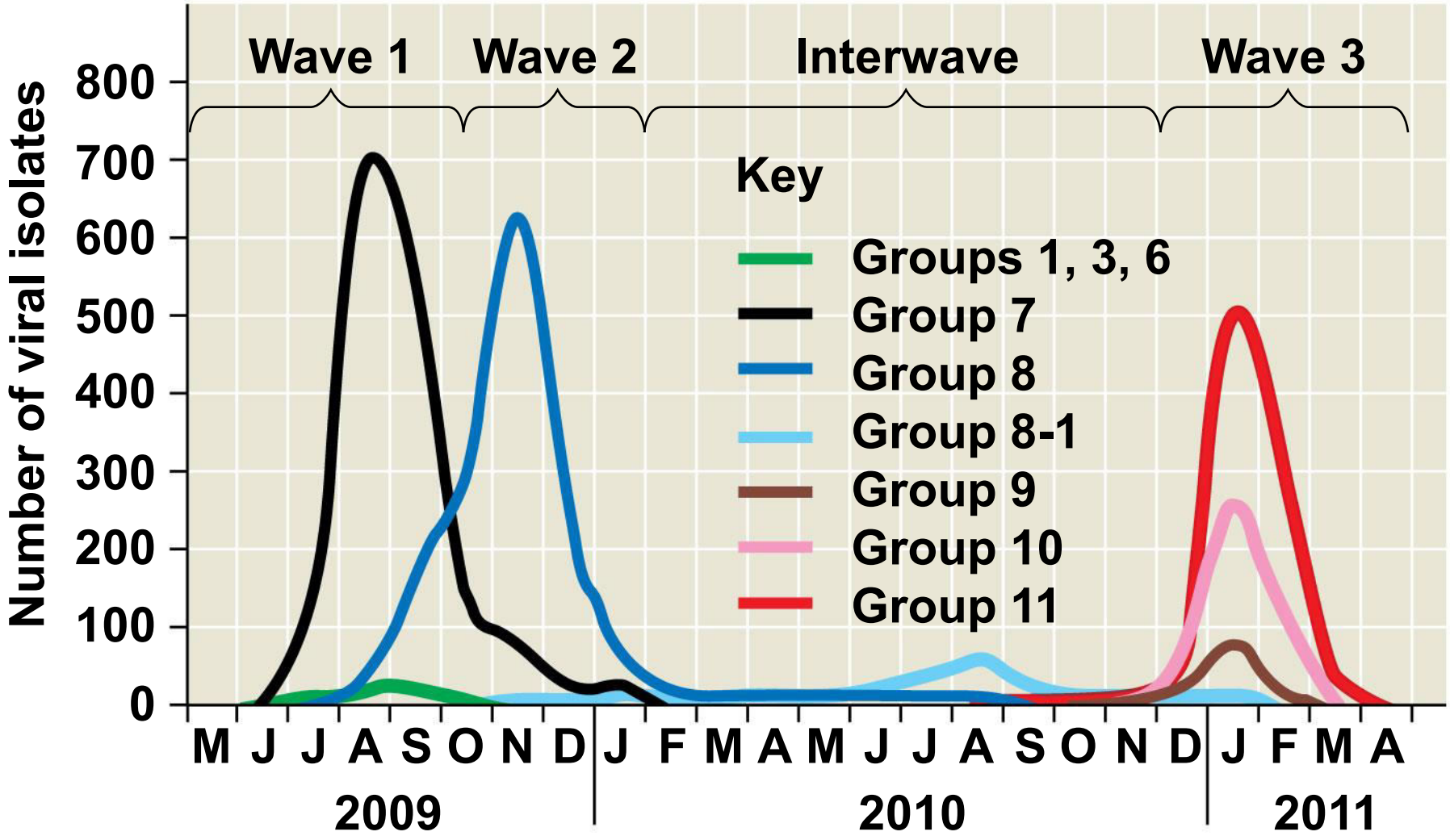
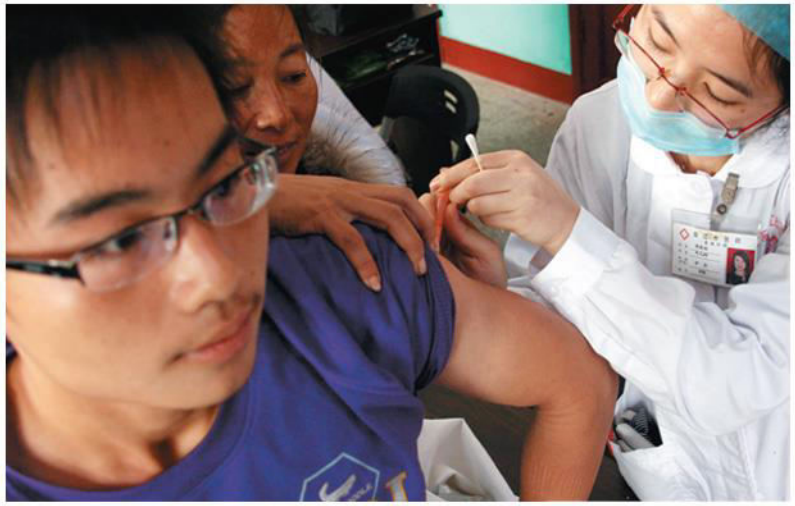
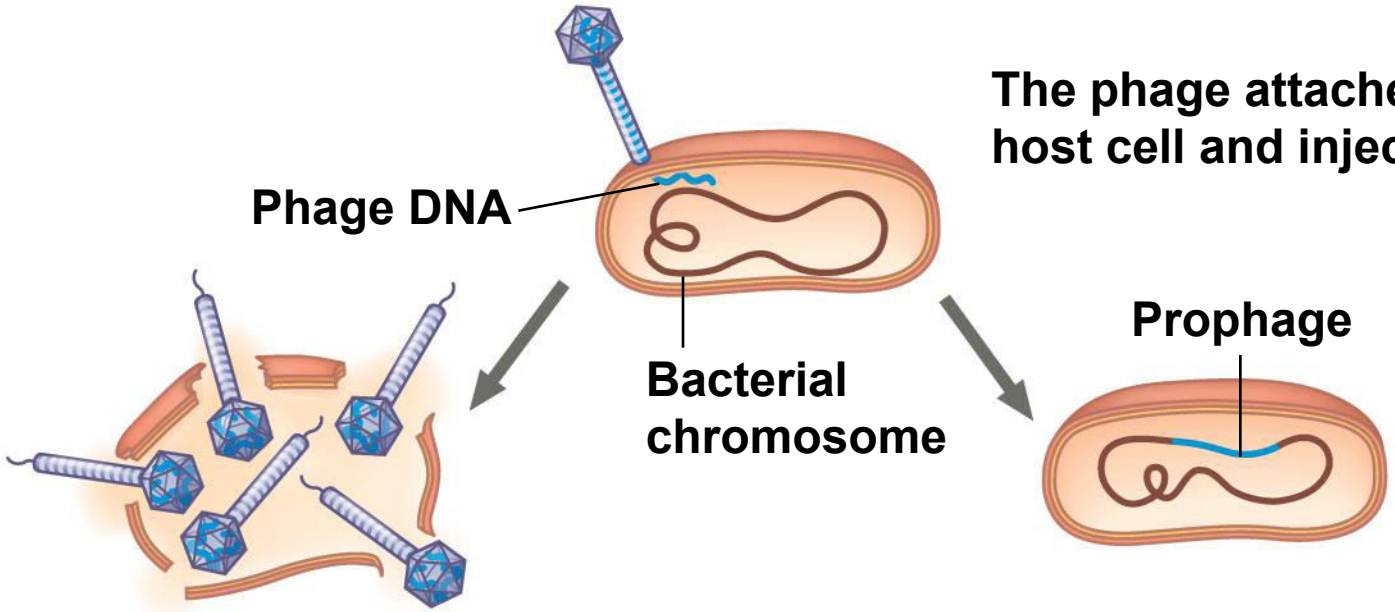


Figure 17.UN01-3



H1N1 flu vaccination

Figure 17.UN02



Lytic cycle

- Virulent or temperate phage
- Destruction of host DNA
- Production of new phages
- Lysis of host cell causes release of progeny phages

Lysogenic cycle

- Temperate phage only
- Genome integrates into bacterial chromosome as prophage, which (1) is replicated and passed on to daughter cells and (2) can be induced to leave the chromosome and initiate a lytic cycle

Figure 17.UN03