

# Detailed Contents

<b>Chapter 1: To the Cell and Beyond: The Realm of Molecular Biology</b>	<b>000</b>		
<b>1.1 INTRODUCTION</b>	<b>000</b>		
<b>1.2 THE VITAL ROLE OF MICROSCOPY IN BIOLOGY</b>	<b>000</b>		
The light microscope led to the first revolution in biology	000		
Biochemistry led to the discovery of the importance of macromolecules in life's structure and processes	000		
The electron microscope provided another order of resolution	000		
<b>1.3 FINE STRUCTURE OF CELLS AND VIRUSES AS REVEALED BY MICROSCOPY</b>	<b>000</b>		
<b>1.4 ULTRAHIGH RESOLUTION: BIOLOGY AT THE MOLECULAR LEVEL</b>	<b>000</b>		
Fluorescence techniques allow for one approach to ultrasresolution	000		
Confocal fluorescence microscopy allows observation of the fluorescence emitted by a particular substance in a cell	000		
FIONA provides ultimate optical resolution by use of fluorescence	000		
FRET allows distance measurements at the molecular level	000		
Single-molecule cryo-electron microscopy is a powerful new technique	000		
The atomic force microscope feels molecular structure	000		
X-ray diffraction and NMR provide resolution to the atomic level	000		
<b>1.5 MOLECULAR GENETICS: ANOTHER FACE OF MOLECULAR BIOLOGY</b>	<b>000</b>		
Key concepts	000		
Further reading	000		
<b>Chapter 2: From Classical Genetics to Molecular Genetics</b>	<b>000</b>		
<b>2.1 INTRODUCTION</b>	<b>000</b>		
<b>2.2 CLASSICAL GENETICS AND THE RULES OF TRAIT INHERITANCE</b>	<b>000</b>		
Gregor Mendel developed the formal rules of genetics	000		
Mendel's laws have extensions and exceptions	000		
Genes are arranged linearly on chromosomes and can be mapped	000		
The nature of genes and how they determine phenotypes was long a mystery	000		
<b>2.3 THE GREAT BREAKTHROUGH TO MOLECULAR GENETICS</b>	<b>000</b>		
Bacteria and bacteriophage exhibit genetic behavior and serve as model systems	000		
		Transformation and transduction allow transfer of genetic information	000
		The Watson-Crick model of DNA structure provided the final key to molecular genetics	000
		<b>2.4 MODEL ORGANISMS</b>	<b>000</b>
		Key concepts	000
		Further reading	000
		<b>Chapter 3: Proteins</b>	<b>000</b>
		<b>3.1 INTRODUCTION</b>	<b>000</b>
		Proteins are macromolecules with enormous variety in size, structure, and function	000
		Proteins are essential for the structure and functioning of all organisms	000
		<b>3.2 PROTEIN STRUCTURE</b>	<b>000</b>
		Amino acids are the building blocks of proteins	000
		In proteins, amino acids are covalently connected to form polypeptides	000
		<b>3.3 LEVELS OF STRUCTURE IN THE POLYPEPTIDE CHAIN</b>	<b>000</b>
		The primary structure of a protein is a unique sequence of amino acids	000
		A protein's secondary structure involves regions of regular folding stabilized by hydrogen bonds	000
		Each protein has a unique three-dimensional tertiary structure	000
		The tertiary structure of most proteins is divided into distinguishable folded domains	000
		Algorithms are now used to identify and classify domains in proteins of known sequence	000
		Some domains or proteins are intrinsically disordered	000
		Quaternary structure involves associations between protein molecules to form aggregated structures	000
		<b>3.4 HOW DO PROTEINS FOLD?</b>	<b>000</b>
		Folding can be a problem	000
		Chaperones help or allow proteins to fold	000
		<b>3.5 HOW ARE PROTEINS DESTROYED?</b>	<b>000</b>
		The proteasome is the general protein destruction system	000
		<b>3.6 THE PROTEOME AND PROTEIN INTERACTION NETWORKS</b>	<b>000</b>
		New technologies allow a census of an organism's proteins and their interactions	000
		Key concepts	000
		Further reading	000

<b>Chapter 4: Nucleic Acids</b>	<b>000</b>	<b>5.7 POLYMERASE CHAIN REACTION AND SITE-DIRECTED MUTAGENESIS</b>	<b>000</b>
<b>4.1 INTRODUCTION</b>	<b>000</b>	<b>5.8 SEQUENCING OF ENTIRE GENOMES</b>	<b>000</b>
Protein sequences are dictated by nucleic acids	000	Genomic libraries contain the entire genome of an organism as a collection of recombinant DNA molecules	000
<b>4.2 CHEMICAL STRUCTURE OF NUCLEIC ACIDS</b>	<b>000</b>	There are two approaches for sequencing large genomes	000
DNA and RNA have similar but different chemical structures	000	<b>5.9 MANIPULATING THE GENETIC CONTENT OF EUKARYOTIC ORGANISMS</b>	<b>000</b>
Nucleic acids (polynucleotides) are polymers of nucleotides	000	Making a transgenic mouse involves numerous steps	000
<b>4.3 PHYSICAL STRUCTURES OF DNA</b>	<b>000</b>	To inactivate, replace, or otherwise modify a particular gene, the vector must be targeted for homologous recombination at that particular site	000
Discovery of the B-DNA structure was a breakthrough in molecular biology	000	<b>5.10 PRACTICAL APPLICATIONS OF RECOMBINANT DNA TECHNOLOGIES</b>	<b>000</b>
A number of alternative DNA structures exist	000	Hundreds of pharmaceutical compounds are produced in recombinant bacteria	000
Although the double helix is quite rigid, it can be bent by bound proteins	000	Plant genetic engineering is a huge but controversial industry	000
DNA can also form folded tertiary structures	000	Gene therapy is a complex multistep process aiming to correct defective genes or gene functions that are responsible for disease	000
Closed DNA circles can be twisted into supercoils	000	Delivering a gene into sufficient cells within a specific tissue and ensuring its subsequent long-term expression is a challenge	000
<b>4.4 PHYSICAL STRUCTURES OF RNA</b>	<b>000</b>	Whole animals can be cloned by nuclear transfer	000
RNA can adopt a variety of complex structures but not the B-form helix	000	Key concepts	000
<b>4.5 THE CENTRAL DOGMA OF MOLECULAR BIOLOGY: ONE-WAY FLOW OF GENETIC INFORMATION</b>	<b>000</b>	Further reading	000
<b>4.6 METHODS USED TO STUDY NUCLEIC ACIDS</b>	<b>000</b>	<b>Chapter 6: Protein–Nucleic Acid Interactions</b>	<b>000</b>
Key concepts	000	<b>6.1 INTRODUCTION</b>	<b>000</b>
Further reading	000	<b>6.2 DNA–PROTEIN INTERACTIONS</b>	<b>000</b>
<b>Chapter 5: Recombinant DNA: Principles and Applications</b>	<b>000</b>	DNA–protein binding occurs by many modes and mechanisms	000
<b>5.1 INTRODUCTION</b>	<b>000</b>	Site-specific binding is the most widely used mode	000
Cloning of DNA involves several fundamental steps	000	Most recognition sites fall into a limited number of classes	000
<b>5.2 CONSTRUCTION OF RECOMBINANT DNA MOLECULES</b>	<b>000</b>	Most specific binding requires the insertion of protein into a DNA groove	000
Restriction endonucleases and ligases are essential tools in cloning	000	Some proteins cause DNA looping	000
<b>5.3 VECTORS FOR CLONING</b>	<b>000</b>	There are a few major protein motifs of DNA-binding domains	000
Genes coding for selectable markers are inserted into vectors during their construction	000	Helix–turn–helix motif interacts with the major groove	000
Bacterial plasmids were the first cloning vectors	000	Zinc fingers also probe the major groove	000
Recombinant bacteriophages can serve as bacterial vectors	000	Leucine zippers are especially suited for dimeric sites	000
Cosmids and phagemids expand the repertoire of cloning vectors	000	<b>6.3 RNA–PROTEIN INTERACTIONS</b>	<b>000</b>
<b>5.4 ARTIFICIAL CHROMOSOMES AS VECTORS</b>	<b>000</b>	<b>6.4 STUDYING PROTEIN–NUCLEIC ACID INTERACTIONS</b>	<b>000</b>
Bacterial artificial chromosomes meet the need for cloning very large DNA fragments in bacteria	000	Key concepts	000
Eukaryotic artificial chromosomes provide proper maintenance and expression of very large DNA fragments in eukaryotic cells	000	Further reading	000
<b>5.5 EXPRESSION OF RECOMBINANT GENES</b>	<b>000</b>	<b>Chapter 7: The Genetic Code, Genes, and Genomes</b>	<b>000</b>
Expression vectors allow regulated and efficient expression of cloned genes	000	<b>7.1 INTRODUCTION</b>	<b>000</b>
Shuttle vectors can replicate in more than one organism	000	<b>7.2 GENES AS NUCLEIC ACID REPOSITORIES OF GENETIC INFORMATION</b>	<b>000</b>
<b>5.6 INTRODUCING RECOMBINANT DNA INTO HOST CELLS</b>	<b>000</b>	Our understanding of the nature of genes is constantly evolving	000
Numerous host-specific techniques are used to introduce recombinant DNA molecules into living cells	000	The central dogma states that information flows from DNA to protein	000

It was necessary to separate cellular RNAs to seek the adaptors	000	Centromeres and telomeres are chromosome regions with special functions	000
Messenger RNA, tRNA, and ribosomes constitute the protein factories of the cell	000	There are a number of models of mitotic chromosome structure	000
<b>7.3 RELATING PROTEIN SEQUENCE TO DNA SEQUENCE IN THE GENETIC CODE</b>	<b>000</b>	Key concepts	000
The first task was to define the nature of the code	000	Further reading	000
<b>7.4 SURPRISES FROM THE EUKARYOTIC CELL: INTRONS AND SPLICING</b>	<b>000</b>	<b>Chapter 9: Transcription in Bacteria</b>	<b>000</b>
Eukaryotic genes usually contain interspersed noncoding sequences	000	<b>9.1 INTRODUCTION</b>	<b>000</b>
<b>7.5 GENES FROM A NEW AND BROADER PERSPECTIVE</b>	<b>000</b>	<b>9.2 OVERVIEW OF TRANSCRIPTION</b>	<b>000</b>
Protein-coding genes are complex	000	There are aspects of transcription common to all organisms	000
Genome sequencing has revolutionized the gene concept	000	Transcription requires the participation of many proteins	000
Mutations, pseudogenes, and alternative splicing all contribute to gene diversity	000	Transcription is rapid but is often interrupted by pauses	000
<b>7.6 COMPARING WHOLE GENOMES AND NEW PERSPECTIVES ON EVOLUTION</b>	<b>000</b>	Transcription can be visualized by electron microscopy	000
Genome sequencing reveals puzzling features of genomes	000	<b>9.3 RNA POLYMERASES TRANSCRIPTION CATALYSIS</b>	<b>000</b>
How are DNA sequence types and functions distributed in eukaryotes?	000	RNA polymerases are a large family of enzymes that produce RNA transcripts of polynucleotide templates	000
Key concepts	000	<b>9.4 MECHANICS OF TRANSCRIPTION IN BACTERIA</b>	<b>000</b>
Further reading	000	Initiation requires a multisubunit polymerase complex, termed the holoenzyme	000
<b>Chapter 8: Physical Structure of the Genomic Material</b>	<b>000</b>	The initiation phase of bacterial transcription is frequently aborted	000
<b>8.1 INTRODUCTION</b>	<b>000</b>	Elongation in bacteria must overcome topological problems	000
<b>8.2 CHROMOSOMES OF VIRUSES AND BACTERIA</b>	<b>000</b>	There are two mechanisms for transcription termination in bacteria	000
Viruses are packages for minimal genomes	000	Understanding transcription in bacteria is useful in clinical practice	000
Bacterial chromosomes are organized structures in the cytoplasm	000	Key concepts	000
DNA-bending proteins and DNA-bridging proteins help to pack bacterial DNA	000	Further reading	000
<b>8.3 EUKARYOTIC CHROMATIN</b>	<b>000</b>	<b>Chapter 10: Transcription in Eukaryotes</b>	<b>000</b>
Eukaryotic chromosomes are highly condensed DNA-protein complexes segregated into a nucleus	000	<b>10.1 INTRODUCTION</b>	<b>000</b>
The nucleosome is the basic repeating unit of eukaryotic chromatin	000	Transcription in eukaryotes is a complex, highly regulated process	000
Histone nonallelic variants and postsynthetic modifications create a heterogeneous population of nucleosomes	000	Eukaryotic cells contain multiple RNA polymerases, each specific for distinct functional subsets of genes	000
The nucleosome family is dynamic	000	<b>10.2 TRANSCRIPTION BY RNA POLYMERASE II</b>	<b>000</b>
Nucleosome assembly <i>in vivo</i> uses histone chaperones	000	The yeast Pol II structure provides insights into transcriptional mechanisms	000
<b>8.4 HIGHER-ORDER CHROMATIN STRUCTURE</b>	<b>000</b>	The structure of Pol II is more evolutionarily conserved than its sequence	000
Nucleosomes along the DNA form a chromatin fiber	000	Nucleotide addition during transcription elongation is cyclic	000
The chromatin fiber is folded, but its structure remains controversial	000	Transcription initiation depends on multisubunit protein complexes that assemble at core promoters	000
The organization of chromosomes in the interphase nucleus is still obscure	000	An additional protein complex is needed to connect Pol II to regulatory proteins	000
<b>8.5 MITOTIC CHROMOSOMES</b>	<b>000</b>	Termination of eukaryotic transcription is coupled to polyadenylation of the RNA transcript	000
Chromosomes condense and separate in mitosis	000	<b>10.3 TRANSCRIPTION BY RNA POLYMERASE I</b>	<b>000</b>
A number of proteins are needed to form and maintain mitotic chromosomes	000	<b>10.4 TRANSCRIPTION BY RNA POLYMERASE III</b>	<b>000</b>
		RNA polymerase III specializes in transcription of small genes	000

<b>10.5 TRANSCRIPTION IN EUKARYOTES: PERVASIVE AND SPATIALLY ORGANIZED</b>	<b>000</b>	Some eukaryotic transcription factors are activators, others are repressors, and still others can be either, depending on context	000
Most of the eukaryotic genome is transcribed	000	Regulation can use alternative components of the basal transcriptional machinery	000
Transcription in eukaryotes is not uniform within the nucleus	000	Mutations in gene regulatory regions and in transcriptional machinery components lead to human diseases	000
Active and inactive genes are spatially separated in the nucleus	000	<b>12.3 REGULATION OF TRANSCRIPTIONAL ELONGATION</b>	<b>000</b>
<b>10.6 METHODS FOR STUDYING EUKARYOTIC TRANSCRIPTION</b>	<b>000</b>	The polymerase may stall close to the promoter	000
A battery of methods is available for the study of transcription	000	Transcription elongation rate can be regulated by elongation factors	000
Key concepts	000	<b>12.4 TRANSCRIPTION REGULATION AND CHROMATIN STRUCTURE</b>	<b>000</b>
Further reading	000	What happens to nucleosomes during transcription?	000
<b>Chapter 11: Regulation of Transcription in Bacteria</b>	<b>000</b>	<b>12.5 REGULATION OF TRANSCRIPTION BY HISTONE MODIFICATIONS AND VARIANTS</b>	<b>000</b>
<b>11.1 INTRODUCTION</b>	<b>000</b>	Modification of histones provides epigenetic control of transcription	000
<b>11.2 GENERAL MODELS FOR REGULATION OF TRANSCRIPTION</b>	<b>000</b>	Gene expression is often regulated by histone post-translational modifications	000
Regulation can occur via differences in promoter strength or use of alternative $\sigma$ factors	000	Readout of histone post-translational modification marks involves specialized protein molecules	000
Regulation through ligand binding to RNA polymerase is called stringent control	000	Post-translational histone marks distinguish transcriptionally active and inactive chromatin regions	000
<b>11.3 SPECIFIC REGULATION OF TRANSCRIPTION</b>	<b>000</b>	Some genes are specifically silenced by post-translational modification in some cell lines	000
Regulation of specific genes occurs through <i>cis-trans</i> interactions with transcription factors	000	Polycomb protein complexes silence genes through H3K27 trimethylation and H2AK119 ubiquitylation	000
Transcription factors are activators and repressors whose own activity is regulated in a number of ways	000	Heterochromatin formation at telomeres in yeast silences genes through H4K16 deacetylation	000
Several transcription factors can act synergistically or in opposition to activate or repress transcription	000	HP1-mediated gene repression in the majority of eukaryotic organisms involves H3K9 methylation	000
<b>11.4 TRANSCRIPTIONAL REGULATION OF OPERONS IMPORTANT TO BACTERIAL PHYSIOLOGY</b>	<b>000</b>	Poly(ADP)ribosylation of proteins is involved in transcriptional regulation	000
The <i>lac</i> operon is controlled by a dissociable repressor and an activator	000	Histone variants H2A.Z, H3.3, and H2A.Bbd are present in active chromatin	000
Control of the <i>trp</i> operon involves both repression and attenuation	000	MacroH2A is a histone variant prevalent in inactive chromatin	000
The same protein can serve as an activator or a repressor: the <i>ara</i> operon	000	Problems caused by chromatin structure can be fixed by remodeling	000
<b>11.5 OTHER MODES OF GENE REGULATION IN BACTERIA</b>	<b>000</b>	Endogenous metabolites can exert rheostat control of transcription	000
DNA supercoiling is involved in both global and local regulation of transcription	000	<b>12.6 DNA METHYLATION</b>	<b>000</b>
DNA methylation can provide specific regulation	000	DNA methylation patterns in genomic DNA may participate in regulation of transcription	000
<b>11.6 COORDINATION OF GENE EXPRESSION IN BACTERIA</b>	<b>000</b>	Carcinogenesis alters the pattern of CpG methylation	000
Networks of transcription factors form the basis of coordinated gene expression	000	DNA methylation changes during embryonic development	000
Key concepts	000	DNA methylation is governed by complex enzymatic machinery	000
Further reading	000	There are proteins that read the DNA methylation mark	000
<b>Chapter 12: Regulation of Transcription in Eukaryotes</b>	<b>000</b>	<b>12.7 LONG NONCODING RNAs IN TRANSCRIPTIONAL REGULATION</b>	<b>000</b>
<b>12.1 INTRODUCTION</b>	<b>000</b>	Noncoding RNAs play surprising roles in regulating transcription	000
<b>12.2 REGULATION OF TRANSCRIPTION INITIATION: REGULATORY REGIONS AND TRANSCRIPTION FACTORS</b>	<b>000</b>	The sizes and genomic locations of noncoding transcripts are remarkably diverse	000
Core and proximal promoters are needed for basal and regulated transcription	000		
Enhancers, silencers, insulators, and locus control regions are all distal regulatory elements	000		



<b>12.8 METHODS FOR MEASURING THE ACTIVITY OF TRANSCRIPTIONAL REGULATORY ELEMENTS</b>	<b>000</b>	<b>14.3 PROCESSING OF EUKARYOTIC mRNA: END MODIFICATIONS</b>	<b>000</b>
Key concepts	000	Eukaryotic mRNA capping is co-transcriptional	000
Further reading	000	Polyadenylation at the 3'-end serves a number of functions	000
<b>Chapter 13: Transcription Regulation in the Human Genome</b>	<b>000</b>	<b>14.4 PROCESSING OF EUKARYOTIC mRNA: SPLICING</b>	<b>000</b>
<b>13.1 INTRODUCTION</b>	<b>000</b>	The splicing process is complex and requires great precision	000
Rapid full-genome sequencing allows deep analysis	000	Splicing is carried out by spliceosomes	000
<b>13.2 BASIC CONCEPTS OF ENCODE</b>	<b>000</b>	Splicing can produce alternative mRNAs	000
ENCODE depends on high-throughput, massively processive sequencing and sophisticated computer algorithms for analysis	000	Tandem chimerism links exons from separate genes	000
The ENCODE project integrates diverse data relevant to transcription in the human genome	000	<i>Trans</i> -splicing combines exons residing in the two complementary DNA strands	000
<b>13.3 REGULATORY DNA SEQUENCE ELEMENTS</b>	<b>000</b>	<b>14.5 REGULATION OF SPLICING AND ALTERNATIVE SPLICING</b>	<b>000</b>
Seven classes of regulatory DNA sequence elements make up the transcriptional landscape	000	Splice sites differ in strength	000
<b>13.4 SPECIFIC FINDINGS CONCERNING CHROMATIN STRUCTURE FROM ENCODE</b>	<b>000</b>	Exon-intron architecture affects splice-site usage	000
Millions of DNase I hypersensitive sites mark regions of accessible chromatin	000	<i>Cis-trans</i> interactions may stimulate or inhibit splicing	000
DNase I signatures at promoters are asymmetric and stereotypic	000	RNA secondary structure can regulate alternative splicing	000
Nucleosome positioning at promoters and around TF-binding sites is highly heterogeneous	000	Sometimes alternative splicing regulation needs no auxiliary regulators	000
The chromatin environment at regulatory elements and in gene bodies is also heterogeneous and asymmetric	000	The rate of transcription and chromatin structure may help regulate splicing	000
<b>13.5 ENCODE INSIGHTS INTO GENE REGULATION</b>	<b>000</b>	<b>14.6 SELF-SPLICING: INTRONS AND RIBOZYMES</b>	<b>000</b>
Distal control elements are connected to promoters in a complex network	000	A fraction of introns is excised by self-splicing RNA	000
Transcription factor binding defines the structure and function of regulatory regions	000	There are two classes of self-splicing introns	000
Transcription factors interact in a huge network	000	<b>14.7 OVERVIEW: THE HISTORY OF AN mRNA MOLECULE</b>	<b>000</b>
TF-binding sites and TF structure co-evolve	000	Proceeding from the primary transcript to a functioning mRNA requires a number of steps	000
DNA methylation patterns show a complex relationship with transcription	000	mRNA is exported from the nucleus to the cytoplasm through nuclear pore complexes	000
<b>13.6 ENCODE OVERVIEW</b>	<b>000</b>	RNA sequence can be edited by enzymatic modification even after transcription	000
What have we learned from ENCODE, and where is it leading?	000	<b>14.8 RNA QUALITY CONTROL AND DEGRADATION</b>	<b>000</b>
Certain methods are essential to ENCODE project studies	000	Bacteria, archaea, and eukaryotes all have mechanisms for RNA quality control	000
Key concepts	000	Archaea and eukaryotes utilize specific pathways to deal with different RNA defects	000
Further reading	000	<b>14.9 BIOGENESIS AND FUNCTIONS OF SMALL SILENCING RNAS</b>	<b>000</b>
<b>Chapter 14: RNA Processing</b>	<b>000</b>	All ssRNAs are produced by processing from larger precursors	000
<b>14.1 INTRODUCTION</b>	<b>000</b>	Key concepts	000
Most RNA molecules undergo post-transcriptional processing	000	Further reading	000
There are four general categories of processing	000	<b>Chapter 15: Translation: The Players</b>	<b>000</b>
Eukaryotic RNAs exhibit much more processing than bacterial RNAs	000	<b>15.1 INTRODUCTION</b>	<b>000</b>
<b>14.2 PROCESSING OF tRNAs AND rRNAs</b>	<b>000</b>	<b>15.2 A BRIEF OVERVIEW OF TRANSLATION</b>	<b>000</b>
tRNA processing is similar in all organisms	000	Three participants are needed for translation to occur	000
All three mature ribosomal RNA molecules are cleaved from a single long precursor RNA	000	<b>15.3 TRANSFER RNA</b>	<b>000</b>
		tRNA molecules fold into four-arm cloverleaf structures	000
		tRNAs are aminoacylated by a set of specific enzymes, aminoacyl-tRNA synthetases	000
		Aminoacylation of tRNA is a two-step process	000
		Quality control or proofreading occurs during the aminoacylation reaction	000

Insertion of noncanonical amino acids into polypeptide chains is guided by stop codons	000		
<b>15.4 MESSENGER RNA</b>	<b>000</b>		
The Shine–Dalgarno sequence in bacterial mRNAs aligns the message on the ribosome	000		
Eukaryotic mRNAs do not have Shine–Dalgarno sequences but more complex 5'- and 3'-untranslated regions	000		
Overall translation efficiency depends on a number of factors	000		
<b>15.5 RIBOSOMES</b>	<b>000</b>		
The ribosome is a two-subunit structure comprising rRNAs and numerous ribosomal proteins	000		
Functional ribosomes require both subunits, with specific complements of RNA and protein molecules	000		
The small subunit can accept mRNA but must join with the large subunit for peptide synthesis to occur	000		
Ribosome assembly has been studied both <i>in vivo</i> and <i>in vitro</i>	000		
Key concepts	000		
Further reading	000		
<b>Chapter 16: Translation: The Process</b>	<b>000</b>		
<b>16.1 INTRODUCTION</b>	<b>000</b>		
<b>16.2 AN OVERVIEW OF TRANSLATION: HOW FAST AND HOW ACCURATE?</b>	<b>000</b>		
<b>16.3 ADVANCED METHODOLOGY FOR THE ANALYSIS OF TRANSLATION</b>	<b>000</b>		
Cryo-EM allows visualization of discrete kinetic states of ribosomes	000		
X-ray crystallography provides the highest resolution	000		
Single-pair fluorescence resonance energy transfer allows dynamic studies at the single-particle level	000		
<b>16.4 INITIATION OF TRANSLATION</b>	<b>000</b>		
Initiation of translation begins on a free small ribosomal subunit	000		
Cryo-EM provides details of initiation complexes	000		
Start site selection in eukaryotes is complex	000		
<b>16.5 TRANSLATIONAL ELONGATION</b>	<b>000</b>		
Decoding means matching the codon to the anticodon-carrying aminoacyl-tRNA	000		
Accommodation denotes a relaxation of distorted tRNA to allow peptide bond formation	000		
Peptide bond formation is accelerated by the ribosome	000		
The formation of hybrid states is an essential part of translocation	000		
Structural information on bacterial elongation factors provides insights into mechanisms	000		
There is an exit tunnel for the peptide chain in the ribosome	000		
Translation elongation in eukaryotes involves even more factors	000		
<b>16.6 TERMINATION OF TRANSLATION</b>	<b>000</b>		
RF3 aids in removing RF1 and RF2	000		
Ribosomes are recycled after termination	000		
Our views of translation continue to evolve	000		
Key concepts	000		
Further reading	000		
<b>Chapter 17: Regulation of Translation</b>	<b>000</b>		
<b>17.1 INTRODUCTION</b>	<b>000</b>		
<b>17.2 REGULATION OF TRANSLATION BY CONTROLLING RIBOSOME NUMBER</b>	<b>000</b>		
Ribosome numbers in bacteria are responsive to the environment	000		
Synthesis of ribosomal components in bacteria is coordinated	000		
Regulation of the synthesis of ribosomal components in eukaryotes involves chromatin structure	000		
<b>17.3 REGULATION OF TRANSLATION INITIATION</b>	<b>000</b>		
Regulation of translation initiation is ubiquitous and remarkably varied	000		
Regulation may depend on protein factors binding to the 5'- or 3'-ends of mRNA	000		
Cap-dependent regulation is the major pathway for controlling initiation	000		
Initiation may utilize internal ribosome entry sites	000		
5'-3'-UTR interactions provide a novel mechanism that regulates initiation in eukaryotes	000		
Riboswitches are RNA sequence elements that regulate initiation in response to stimuli	000		
MicroRNAs can bind to mRNA, thereby regulating translation	000		
<b>17.4 mRNA STABILITY AND DECAY IN EUKARYOTES</b>	<b>000</b>		
The two major pathways of decay for nonfaulty mRNA molecules start with mRNA deadenylation	000		
The 5' → 3' pathway is initiated by the activities of the decapping enzyme Dcp2	000		
The 3' → 5' pathway uses the exosome, followed by a different decapping enzyme, DcpS	000		
There are additional pathways for mRNA degradation	000		
Unused mRNA is sequestered in P bodies and stress granules	000		
Cells have several mechanisms that destroy faulty mRNA molecules	000		
mRNA molecules that contain premature stop codons are degraded through nonsense-mediated decay or NMD	000		
No-go decay or NGD functions when the ribosome stalls during elongation	000		
Non-stop decay or NSD functions when mRNA does not contain a stop codon	000		
<b>17.5 MECHANISMS OF TRANSLATION</b>	<b>000</b>		
Key concepts	000		
Further reading	000		
<b>Chapter 18: Protein Processing and Modification</b>	<b>000</b>		
<b>18.1 INTRODUCTION</b>	<b>000</b>		
<b>18.2 STRUCTURE OF BIOLOGICAL MEMBRANES</b>	<b>000</b>		
Biological membranes are protein-rich lipid bilayers	000		
Numerous proteins are associated with biomembranes	000		
<b>18.3 PROTEIN TRANSLOCATION THROUGH BIOLOGICAL MEMBRANES</b>	<b>000</b>		
Protein translocation can occur during or after translation	000		
Membrane translocation in bacteria and archaea primarily functions for secretion	000		

Membrane translocation in eukaryotes serves a multitude of functions	000	The full complement of proteins in the replisome is organized in a complex and dynamic way	000
Integral membrane proteins have special mechanisms for membrane insertion	000	DNA polymerase I is necessary for maturation of Okazaki fragments	000
Vesicles transport proteins between compartments in eukaryotic cells	000	<b>19.4 THE PROCESS OF BACTERIAL REPLICATION</b>	<b>000</b>
<b>18.4 PROTEOLYTIC PROTEIN PROCESSING: CUTTING, SPLICING, AND DEGRADATION</b>	<b>000</b>	The replisome is a dynamic structure during elongation	000
Proteolytic cleavage is sometimes used to produce mature proteins from precursors	000	<b>19.5 INITIATION AND TERMINATION OF BACTERIAL REPLICATION</b>	<b>000</b>
Some proteases can catalyze protein splicing	000	Initiation involves both specific DNA sequence elements and numerous proteins	000
Controlled proteolysis is also used to destroy proteins no longer needed	000	Termination of replication also employs specific DNA sequences and protein factors that bind to them	000
<b>18.5 POST-TRANSLATIONAL CHEMICAL MODIFICATIONS OF SIDE CHAINS</b>	<b>000</b>	<b>19.6 BACTERIOPHAGE AND PLASMID REPLICATION</b>	<b>000</b>
Modification of side chains can affect protein structure and function	000	Rolling-circle replication is an alternative mechanism	000
Phosphorylation plays a major role in signaling	000	Phage replication can involve both bidirectional and rolling-circle mechanisms	000
Acetylation mainly modifies interactions	000	Key concepts	000
Several classes of glycosylated proteins contain added sugar moieties	000	Further reading	000
Mechanisms of glycosylation depend on the type of modification	000	<b>Chapter 20: DNA Replication in Eukaryotes</b>	<b>000</b>
Ubiquitylation adds single or multiple ubiquitin molecules to proteins through an enzymatic cascade	000	<b>20.1 INTRODUCTION</b>	<b>000</b>
Specificity of ubiquitin targeting is determined by a special class of enzymes	000	<b>20.2 REPLICATION INITIATION IN EUKARYOTES</b>	<b>000</b>
The structure of protein-ubiquitin conjugates determines the biological role of the modification	000	Replication initiation in eukaryotes proceeds from multiple origins	000
Polyubiquitin marks proteins for degradation by the proteasome	000	Eukaryotic origins of replication have diverse DNA and chromatin structure depending on the biological species	000
Sumoylation adds single or multiple SUMO molecules to proteins	000	There is a defined scenario for formation of initiation complexes	000
<b>18.6 THE GENOMIC ORIGIN OF PROTEINS</b>	<b>000</b>	Re-replication must be prevented	000
Key concepts	000	Histone methylation regulates onset of licensing	000
Further reading	000	<b>20.3 REPLICATION ELONGATION IN EUKARYOTES</b>	<b>000</b>
<b>Chapter 19: DNA Replication in Bacteria</b>	<b>000</b>	Eukaryotic replisomes both resemble and significantly differ from those of bacteria	000
<b>19.1 INTRODUCTION</b>	<b>000</b>	Other components of the bacterial replisome have functional counterparts in eukaryotes	000
<b>19.2 FEATURES OF DNA REPLICATION SHARED BY ALL ORGANISMS</b>	<b>000</b>	Eukaryotic elongation has some special dynamic features	000
Replication on both strands creates a replication fork	000	<b>20.4 REPLICATION OF CHROMATIN</b>	<b>000</b>
Mechanistically, synthesis of new DNA chains requires a template, a polymerase, and a primer	000	Dynamics of chromatin structure during replication	000
DNA replication requires the simultaneous action of two DNA polymerases	000	Histone chaperones may play multiple roles in replication	000
Other protein factors are obligatory at the replication fork	000	Both old and newly synthesized histones are required in replication	000
<b>19.3 DNA REPLICATION IN BACTERIA</b>	<b>000</b>	Epigenetic information in chromatin must also be replicated	000
Bacterial chromosome replication is bidirectional, from a single origin of replication	000	<b>20.5 THE DNA END-REPLICATION PROBLEM AND ITS RESOLUTION</b>	<b>000</b>
DNA polymerase III catalyzes replication in bacteria	000	Telomerase solves the end-replication problem	000
Sliding clamp $\beta$ , or processivity factor, is essential for processivity	000	Alternative lengthening of telomeres pathway is active in telomerase-deficient cells	000
The clamp loader organizes the replisome	000	<b>20.6 MITOCHONDRIAL DNA REPLICATION</b>	<b>000</b>
		Are circular mitochondrial genomes myth or reality?	000
		Models of mitochondrial genome replication are contentious	000

<b>20.7 REPLICATION IN VIRUSES THAT INFECT EUKARYOTES</b>	<b>000</b>	Immunoglobulin gene rearrangements also occur through site-specific recombination	000
Retroviruses use reverse transcriptase to copy RNA into DNA	000	Key concepts	000
Key concepts	000	Further reading	000
Further reading	000		
<b>Chapter 21: DNA Recombination</b>	<b>000</b>	<b>Chapter 22: DNA Repair</b>	<b>000</b>
<b>21.1 INTRODUCTION</b>	<b>000</b>	<b>22.1 INTRODUCTION</b>	<b>000</b>
<b>21.2 HOMOLOGOUS RECOMBINATION</b>	<b>000</b>	<b>22.2 TYPES OF LESIONS IN DNA</b>	<b>000</b>
Homologous recombination plays a number of roles in bacteria	000	Natural agents, from both within and outside a cell, can change the information content of DNA	000
Homologous recombination has multiple roles in mitotic cells	000	<b>22.3 PATHWAYS AND MECHANISMS OF DNA REPAIR</b>	<b>000</b>
Meiotic exchange is essential to eukaryotic evolution	000	DNA lesions are countered by a number of mechanisms of repair	000
<b>21.3 HOMOLOGOUS RECOMBINATION IN BACTERIA</b>	<b>000</b>	Thymine dimers are directly repaired by DNA photolyase	000
End resection requires the RecBCD complex	000	The enzyme <i>O</i> <sup>6</sup> -alkylguanine alkyltransferase is involved in the repair of alkylated bases	000
Strand invasion and strand exchange both depend on RecA	000	Nucleotide excision repair is active on helix-distorting lesions	000
Much concerning homologous recombination is still not understood	000	Base excision repair corrects damaged bases	000
Holliday junctions are the essential intermediary structures in HR	000	Mismatch repair corrects errors in base pairing	000
<b>21.4 HOMOLOGOUS RECOMBINATION IN EUKARYOTES</b>	<b>000</b>	Methyl-directed mismatch repair in bacteria uses methylation on adenines as a guide	000
Proteins involved in eukaryotic recombination resemble their bacterial counterparts	000	Mismatch repair pathways in eukaryotes may be directed by strand breaks during DNA replication	000
HR malfunction is connected with many human diseases	000	Repair of double-strand breaks can be error-free or error-prone	000
Meiotic recombination allows exchange of genetic information between homologous chromosomes in meiosis	000	Homologous recombination repairs double-strand breaks faithfully	000
<b>21.5 NONHOMOLOGOUS RECOMBINATION</b>	<b>000</b>	Nonhomologous end-joining restores the continuity of the DNA double helix in an error-prone process	000
Transposable elements or transposons are mobile DNA sequences that change positions in the genome	000	<b>22.4 TRANSLESION SYNTHESIS</b>	<b>000</b>
Many transposons are transcribed but only a few have known functions	000	Many repair pathways utilize RecQ helicases	000
There are several types of transposons	000	<b>22.5 CHROMATIN AS AN ACTIVE PLAYER IN DNA REPAIR</b>	<b>000</b>
DNA class II transposons can use either of two mechanisms to transpose themselves	000	Histone variants and their post-translational modifications are specifically involved in DNA repair	000
Retrotransposons, or class I transposons, require an RNA intermediate	000	<b>22.6 OVERVIEW: THE ROLE OF DNA REPAIR IN LIFE</b>	<b>000</b>
<b>21.6 SITE-SPECIFIC RECOMBINATION</b>	<b>000</b>	Key concepts	000
Bacteriophage $\lambda$ integrates into the bacterial genome by site-specific recombination	000	Further reading	000