MOLECULAR BIOLOGY

PRINCIPLES AND PRACTICE

All March 200 SECOND EDITION

Michael M. Cox Jennifer A. Doudna **Michael O'Donnell**

Molecular Biology

This page intentionally left blank

Molecular Biology Principles and Practice Second Edition

Michael M. Cox *University of Wisconsin–Madison*

Jennifer A. Doudna *University of California, Berkeley*

Michael O'Donnell *The Rockefeller University*

A Macmillan Education Imprint New York

Publisher: Kate Ahr Parker Senior Acquisitions Editor: Lauren Schultz Developmental Editors: Anna Bristow, Erica Pantages Frost, Lisa Samols Media Editors: Anna Bristow, Erica Pantages Frost Assistant Editor: Tue Tran Art Director: Diana Blume Cover and text designer: Diana Andrews, DreamIt, Inc. Senior Project Editor: Elizabeth Geller Manuscript Editors: Linda Strange, Brook Soltvedt Illustrations: H. Adam Steinberg, Dragonfly Media Group Photo Editor: Jennifer Atkins Photo Researcher: Teri Stratford Illustration Coordinator: Janice Donnola Production Coordinator: Paul Rohloff Marketing Director: John Britch Marketing Assistant: Bailey James Composition: MPS Limited Printing and Binding: Quad Versailles

Front cover image: Courtesy Illumina, Inc.

Throughout the text, a number of illustrations have been adapted from *Lehninger Principles of Biochemistry*, Sixth Edition, by David L. Nelson and Michael M. Cox.

Library of Congress Control Number: 2015930844

ISBN-13: 978-1-4641-2614-7 ISBN-10: 1-4641-2614-3

© 2015, 2012 by W. H. Freeman and Company All rights reserved

Printed in the United States of America

First Printing

W. H. Freeman and Company 41 Madison Avenue New York, NY 10010 Houndmills, Basingstoke RG21 6XS, England

www.whfreeman.com

To our students, for the inspiration they provide every day, and to our mentors, in gratitude for their guidance:

> *Tom Cech Fred Grieman Bill Jencks Arthur Kornberg Bob Lehman Sharon Panasenko David Sheppard Jack Szostak Hal White Charles Williams*

About the Authors

Michael M. cox was born in Wilmington, Delaware. After graduating from the University of Delaware, he went to Brandeis University to do his doctoral work with William P. Jencks, and then to Stanford for postdoctoral study with I. Robert Lehman. He is currently Professor of Biochemistry at the University of Wisconsin–Madison. His research focuses on recombinational DNA repair processes. Cox has received awards for both teaching and research, including the 1989 Eli Lilly Award in Biological Chemistry from the American Chemical Society and two major teaching awards from the University of Wisconsin. He has coauthored five editions of *Lehninger Principles of Biochemistry.*

Sam Willard *Photo by Sam Willard*

JENNIFER A. DOUDNA grew up on the Big Island of Hawaii and became interested in chemistry and biochemistry in high school. She received her B.A. in biochemistry from Pomona College and her Ph.D. from Harvard University, working in the laboratory of Jack Szostak, with whom she also did postdoctoral research. She then went to the University of Colorado as a Lucille P. Markey scholar and postdoctoral fellow with Thomas Cech. Doudna is currently Professor of Molecular and Cell Biology and Professor of Chemistry at the University of California, Berkeley, and an Investigator of the Howard Hughes Medical Institute. She is a member of the National Academy of Sciences, the American Academy of Arts and Sciences, and the Institute of Medicine. She is also a Fellow of the American Association for the Advancement of Science.

MICHAEL O'DONNELL grew up in a neighborhood on the banks of the Columbia River outside Vancouver, Washington. He had several inspirational teachers at Hudson Bay High School who led him into science. He received his B.A. in biochemistry from the University of Portland and his Ph.D. from the University of Michigan, where he worked under Charles Williams, Jr., on electron transfer in the flavoprotein thioredoxin reductase. He performed postdoctoral work on *E. coli* replication with Arthur Kornberg and then on herpes simplex virus replication with I. Robert Lehman in the Biochemistry Department at Stanford University. O'Donnell is currently Professor of Biochemistry and Structural Biology at The Rockefeller University and an Investigator of the Howard Hughes Medical Institute. He is a member of the National Academy of Sciences.

Contents in Brief

I FOUNDATIONS

Glossary **G-1** Solutions to Problems **S-1** Index I-1

Contents

MOMENT OF DISCOVERY James Berger, on his discovery of the structure and mechanism of topoisomerase II 23

2.1 Mendelian Genetics 25

Mendel's First Law: Allele Pairs Segregate during Gamete Formation 26 Mendel's Second Law: Different Genes Assort Independently during Gamete Formation 28 There Are Exceptions to Mendel's Laws 28 2.2 Cytogenetics: Chromosome Movements during Mitosis and Meiosis 31 Cells Contain Chromosomes and Other Internal Structures 31 Mitosis: Cells Evenly Divide Chromosomes between New Cells 33 Meiosis: Chromosome Number Is Halved during Gamete Formation 35 2.3 The Chromosome Theory of Inheritance 37 Sex-Linked Genes in the Fruit Fly Reveal That Genes Are on Chromosomes 37 Linked Genes Do Not Segregate Independently 38 Recombination Unlinks Alleles 40 Recombination Frequency Can Be Used to Map Genes along Chromosomes 41 2.4 Foundations of Molecular Genetics 43 DNA Is the Chemical of Heredity 43 Genes Encode Polypeptides and Functional RNAs 45 The Central Dogma: Information Flows from DNA to RNA to Protein—Usually 46 Mutations in DNA Give Rise to Phenotypic Change 49 **HIGHLIGHT 2-1** MEDICINE The Molecular Biology of Sickle-Cell Anemia, a Recessive Genetic Disease of Hemoglobin 52 HOW WE KNOW 55 Chromosome Pairs Segregate during Gamete Formation in a Way That Mirrors the Mendelian Behavior of Genes 55 Corn Crosses Uncover the Molecular Mechanism of Crossing Over 56 Hershey and Chase Settle the Matter: DNA Is the Genetic Material 57 3 chemical Basis of Information Molecules 61

MOMENT OF DISCOVERY Roxana Georgescu, on her discovery of how beta processivity clamps bind DNA 61

CONTENTS **ix**

3.1 Chemical Building Blocks of Nucleic Acids and Proteins 62 Nucleic Acids Are Long Chains of Nucleotides 62 Proteins Are Long Polymers of Amino Acids 64 Chemical Composition Helps Determine Nucleic Acid and Protein Structure 65 Chemical Composition Can Be Altered by Postsynthetic Changes 65 3.2 Chemical Bonds 68 Electrons Are Shared in Covalent Bonds and Transferred in Ionic Bonds 68 Chemical Bonds Are Explainable in Quantum Mechanical Terms 70 Forming and Breaking of Chemical Bonds Involves Energy Transfer 72 Electron Distribution between Bonded Atoms Determines Molecular Behavior 72 **3.3** Weak Chemical Interactions 73 van der Waals Forces Are Nonspecific Contacts between Atoms 74 The Hydrophobic Effect Brings Together Nonpolar Molecules 74 Adjacent Bases in Nucleic Acids Participate in Noncovalent Interactions 75 Hydrogen Bonds Are a Special Kind of Noncovalent Bond 75 Combined Effects of Weak Chemical Interactions Stabilize Macromolecular Structures 76 Weak Chemical Bonds Also Facilitate Macromolecular Interactions 77 **3.4** Stereochemistry 78 Three-Dimensional Atomic Arrangements Define Molecules 78 Biological Molecules and Processes Selectively Use One Stereoisomer 79 Proteins and Nucleic Acids Are Chiral 79 HIGHLIGHT 3-1 MEDICINE The Behavior of a Peptide Made of D-Amino Acids 80 **3.5** The Role of pH and Ionization 81 The Hydrogen Ion Concentration of a Solution Is Measured by pH 81 Buffers Prevent Dramatic Changes in pH 81 The Henderson-Hasselbalch Equation Estimates the pH of a Buffered Solution 83 **3.6** Chemical Reactions in Biology 83

The Mechanism and Speed of Chemical Transformation Define Chemical Reactions 83 Biological Systems Follow the Laws of

- Thermodynamics 85
- Catalysts Increase the Rates of Biological Reactions 86
- Energy Is Stored and Released by Making and Breaking Phosphodiester Bonds 86

HIGHLIGHT 3-2 EVOLUTION ATP: The Critical Molecule of Energy Exchange in All Cells 87

HOW WE KNOW 89

Single Hydrogen Atoms Are Speed Bumps in Enzyme-Catalyzed Reactions 89 Peptide Bonds Are (Mostly) Flat 90

4 Protein Structure 23

MOMENT OF DISCOVERY Steve Mayo, on his discovery of the first successful method for computational protein design 93

4.1 Primary Structure 95 Amino Acids Are Categorized by Chemical Properties 95 Amino Acids Are Connected in a Polypeptide Chain 96 Evolutionary Relationships Can Be Determined from Primary Sequence Comparisons 98 HIGHLIGHT 4-1 A CLOSER LOOK Purification of Proteins by Column Chromatography and SDS-PAGE 100 4.2 Secondary Structure 102 The α Helix Is a Common Form of Secondary Protein Structure 102 The β Conformation Forms Sheetlike Structures 103 Reverse Turns Allow Secondary Structures to Fold 104 **4.3** Tertiary and Quaternary Structures 105 Tertiary and Quaternary Structures Can Be Represented in Different Ways 105 Domains Are Independent Folding Units within the Protein 105 Supersecondary Structural Elements Are Building Blocks of Domains 106 Quaternary Structures Range from Simple to Complex 110 Intrinsically Unstructured Proteins Have versatile Binding Properties 111 Protein Structures Help Explain Protein Evolution 112 HIGHLIGHT 4-2 | A CLOSER LOOK Protein Structure Databases 112 4.4 Protein Folding 113 Predicting Protein Folding Is a Goal of Computational

Biology 113 Polypeptides Fold through a Molten Globule Intermediate 115

HIGHLIGHT 4-3 MEDICINE Prion-Based Misfolding Diseases 116

Chaperones and Chaperonins Can Facilitate Protein Folding 118

x CONTENTS

Protein Isomerases Assist in the Folding of Some Proteins 118

4.5 Determining the Atomic Structure of Proteins 120 Most Protein Structures Are Solved by X-Ray Crystallography 120

Smaller Protein Structures Can Be Determined by NMR 122

HOW WE KNOW 126

Sequence Comparisons Yield an Evolutionary Roadmap from Bird Influenza to a Deadly Human Pandemic 126

We Can Tell That a Protein Binds ATP by Looking at Its Sequence 127

Disulfide Bonds Act as Molecular Cross-Braces to Stabilize a Protein 128

5 Protein Function 133

MOMENT OF DISCOVERY Smita Patel, on her early work with the T7 gene 4–encoded DNA helicase **133**

5.1 Protein-Ligand Interactions 134

Reversible Binding of Proteins to Other Molecules Follows Defined Principles 134

Protein-Ligand Interactions Can Be Quantified 135

DNA-Binding Proteins Guide Genome Structure and Function 136

5.2 Enzymes: The Reaction Catalysts of Biological Systems 142

Enzymes Catalyze Specific Biological Reactions 142 Enzymes Increase the Rate of a Reaction by Lowering the Activation Energy 145

The Rates of Enzyme-Catalyzed Reactions Can Be Quantified 146

HIGHLIGHT 5-1 A CLOSER LOOK Reversible and Irreversible Inhibition 148

DNA Ligase Activity Illustrates Some Principles of Catalysis 150

5.3 Motor Proteins 151

Helicases Abound in DNA and RNA Metabolism 151 Helicase Mechanisms Have Characteristic Molecular

Parameters 155

5.4 The Regulation of Protein Function 157

Modulator Binding Causes Conformational Changes in Allosteric Proteins 158

Allosteric Enzymes Have Distinctive Binding and/or Kinetic Properties 158

Autoinhibition Can Affect Enzyme Activity 159

Some Proteins Are Regulated by Reversible Covalent Modification 160

Phosphoryl Groups Affect the Structure and Catalytic Activity of Proteins 162

Some Proteins Are Regulated by Proteolytic Cleavage 162

HIGHLIGHT 5-2 MEDICINE HIv Protease: Rational Drug Design Using Protein Structure 164

HOW WE KNOW | 166

The Discovery of the Lactose Repressor: One of the Great Sagas of Molecular Biology 166 The *lacI* Gene Encodes a Repressor 167 Discovery of the Lactose Repressor Helped Give Rise to DNA Sequencing 168

II NUCLEIC ACID STRUCTURE AND **METHODS**

6 DNA and RNA Structure 173

MOMENT OF DISCOVERY Jamie Cate, on determining the molecular structure of the bacterial ribosome 173

6.1 The Structure and Properties of Nucleotides 174 Nucleotides Comprise Phosphates and Characteristic Bases and Sugars 175

Phosphodiester Bonds Link the Nucleotide Units in Nucleic Acids 177

The Properties of Nucleotide Bases Affect the Three-Dimensional Structure of Nucleic Acids 178

Nucleotides Play Additional Roles in Cells 179 6.2 DNA Structure 182

DNA Molecules Have Distinctive Base Compositions 182

DNA Is Usually a Right-Handed Double Helix 183

DNA Adopts Different Helical Forms 185

Certain DNA Sequences Adopt Unusual

Structures 187

HIGHLIGHT 6-1 TECHNOLOGY DNA Nanotechnology 190

6.3 RNA Structure 192

RNAs Have Helical Secondary Structures 192

RNAs Form various Stable Three-Dimensional Structures 193

6.4 Chemical and Thermodynamic Properties of Nucleic Acids 195

HIGHLIGHT 6-2 MEDICINE RNA Structure Governing HIV Gene Expression 196

Double-Helical DNA and RNA Can Be Denatured 196 Nucleic Acids from Different Species Can Form

Hybrids 198

Nucleotides and Nucleic Acids Undergo Uncatalyzed Chemical Transformations 199

Base Methylation in DNA Plays an Important Role in Regulating Gene Expression 200

- RNA Molecules Are Often Site-Specifically Modified In vivo 201
- The Chemical Synthesis of DNA and RNA Has Been Automated 201

HOW WE KNOW 204

DNA Is a Double Helix 204

- DNA Helices Have Unique Geometries That Depend on Their Sequence 205
- Ribosomal RNA Sequence Comparisons Provided the First Hints of the Structural Richness of RNA 206

7 studying Genes 211

MOMENT OF DISCOVERY Norman Arnheim, on the discovery of interspersed CA repeats in genomic DNA 211

- **7.1** Isolating Genes for Study (Cloning) 212
- Genes Are Cloned by Insertion into Cloning vectors 213
- Cloning vectors Allow Amplification of Inserted DNA Segments 215
- DNA Libraries Provide Specialized Catalogs of Genetic Information 220
- **7.2** Working with Genes and Their Products 221 Gene Sequences Can Be Amplified with the
- Polymerase Chain Reaction 221

HIGHLIGHT 7-1 TECHNOLOGY A Potent Weapon in Forensic Medicine 224

- The Sanger Method Identifies Nucleotide Sequences in Cloned Genes 226
- Genomic Sequencing Is Aided by New Generations of DNA Sequencing Methods 228
- Cloned Genes Can Be Expressed to Amplify Protein Production 232

Many Different Systems Are Used to Express Recombinant Proteins 232

Alteration of Cloned Genes Produces Altered Proteins 235

- Terminal Tags Provide Handles for Affinity Purification 237
- **7.3** Understanding the Functions of Genes and Their Products 239

Protein Fusions and Immunofluorescence Can Localize Proteins in Cells 239

- Proteins Can Be Detected in Cellular Extracts with the Aid of Western Blots 241
- Protein-Protein Interactions Can Help Elucidate Protein Function 241
- DNA Microarrays Reveal Cellular Protein Expression Patterns and Other Information 244
- A Gene's Function Can Be Elucidated by Examining the Effects of Its Absence 245

HOW WE KNOW 250

New Enzymes Take Molecular Biologists from Cloning to Genetically Modified Organisms 250 A Dreamy Night Ride on a California Byway Gives Rise

to the Polymerase Chain Reaction 251 Coelenterates Show Biologists the Light 252

8 Genomes, Transcriptomes, and Proteomes 259

MOMENT OF DISCOVERY Joe DeRisi, on his discovery of the SARS virus 259

8.1 Genomes and Genomics 260 Many Genomes Have Been Sequenced in Their Entirety 260 Annotation Provides a Description of the Genome 262 Genome Databases Provide Information about Every Type of Organism 264 **HIGHLIGHT 8-1** TECHNOLOGY Sampling Biodiversity with Metagenomics 266 The Human Genome Contains Many Types of Sequences 267 Genome Sequencing Informs Us about Our Humanity 269 Genome Comparisons Help Locate Genes Involved in Disease 272 8.2 Transcriptomes and Proteomes 275 Special Cellular Functions Are Revealed in a Cell's Transcriptome 275 High-Throughput DNA Sequencing Is Used in Transcriptome Analysis 276 The Proteins Generated by a Cell Constitute Its Proteome 276 Electrophoresis and Mass Spectrometry Support Proteomics Research 277 Computational Approaches Help Elucidate Protein Function 279 Experimental Approaches Reveal Protein Interaction Networks 280 8.3 Our Genetic History 280 All Living Things Have a Common Ancestor 281 Genome Comparisons Provide Clues to Our Evolutionary Past 281

HIGHLIGHT 8-2 EVOLUTION Phylogenetics Solves a Crime 282

The Human Journey Began in Africa 284 Human Migrations Are Recorded in Haplotypes 287

HIGHLIGHT 8-3 EVOLUTION Getting to Know the Neanderthals 288

xii CONTENTS

HOW WE KNOW 292

Haemophilus influenzae Ushers in the Era of Genome Sequences 292

9 Topology: Functional Deformations of DNA 297

MOMENT OF DISCOVERY Carlos Bustamante, on discovering the elasticity of DNA 297

9.1 Chromosomes: An Overview 298

Chromosome Function Relies on Specialized Genomic Sequences 298

Chromosomes Are Longer Than the Cellular or viral Packages Containing Them 300

HIGHLIGHT 9-1 MEDICINE The Dark Side of Antibiotics 303

9.2 DNA Supercoiling 304 Most Cellular DNA Is Underwound 305 DNA Underwinding Is Defined by the Topological

Linking Number 307

DNA Compaction Requires a Special Form of Supercoiling 309

9.3 The Enzymes That Promote DNA Compaction 311 Topoisomerases Catalyze Changes in the Linking Number of DNA 311

HIGHLIGHT 9-2 MEDICINE Curing Disease by Inhibiting Topoisomerases 312

The Two Bacterial Type II Topoisomerases Have Distinct Functions 313 Eukaryotic Topoisomerases Have Specialized Functions in DNA Metabolism 316 SMC Proteins Facilitate the Condensation of Chromatin 317

HOW WE KNOW 322

The Discovery of Supercoiled DNA Goes through Twists and Turns 322 The First DNA Topoisomerase Unravels Some Mysteries 323 DNA Gyrase Passes the Strand Test 324

10 Nucleosomes, Chromatin, and chromosome structure 331

MOMENT OF DISCOVERY C. David Allis, on establishing that p55 from *Tetrahymena* is a histone acetylase, as is transcription factor Gcn5 331

- 10.1 Nucleosomes: The Basic Units of DNA Condensation 332
- Histone Octamers Organize DNA into Repeating Units 332

DNA Wraps around a Single Histone Octamer 334 Histone Tails Mediate Internucleosome Connections That Regulate the Accessibility of DNA 336 10.2 Higher-Order Chromosome Structure 337 Histone H1 Binds the Nucleosome 338 Chromosomes Condense into a Compact Chromatin Filament 338 Higher-Order Chromosome Structure Involves Loops and Coils 341 Bacterial DNA, Like Eukaryotic DNA, Is Highly Organized 341 **10.3** Regulation of Chromosome Structure 343 Nucleosomes Are Intrinsically Dynamic 344 ATP-Driven Chromatin Remodeling Complexes Can Reposition Nucleosomes 344 variant Histone Subunits Alter DNA-Binding Affinity 346 Nucleosome Assembly Requires Chaperones 348 Modifications of Histone Tails Alter DNA

Accessibility 348

HIGHLIGHT 10-1 A CLOSER LOOK The Use of a Histone Variant in X Chromosome Inactivation 350

- Proteins with Bromodomains and Chromodomains Bind Modified Histones 353
- Histone Modifications and Remodeling Complexes May Read a Histone Code 354
- Histone Modifying Enzymes Maintain Epigenetic States through Cell Division 355

HIGHLIGHT 10-2 MEDICINE Defects in Epigenetic Maintenance Proteins Associated with Cancer 356

HOW WE KNOW 359

Kornberg Wrapped His Mind around the Histone Octamer 359

A Transcription Factor Can Acetylate Histones 360

III INFORMATION TRANSFER

11 DNA Replication 363

MOMENT OF DISCOVERY Robert Lehman, on discovering DNA ligase 363

11.1 DNA Transactions during Replication 364 DNA Replication Is Semiconservative 364 Replication Is Initiated at Origins and Proceeds Bidirectionally 366

Replication Is Semidiscontinuous 368

11.2 The Chemistry of DNA Polymerases 369

DNA Polymerases Elongate DNA in the 5'→3' Direction 369

Most DNA Polymerases Have DNA Exonuclease Activity 371

Five *E. coli* DNA Polymerases Function in DNA Replication and Repair 373 DNA Polymerase Structure Reveals the Basis for Its

Accuracy 373 Processivity Increases the Efficiency of DNA Polymerase Activity 376

11.3 Mechanics of the DNA Replication Fork 377

DNA Polymerase III Is the Replicative Polymerase in *E. coli* 377

A DNA Sliding Clamp Increases the Speed and Processivity of the Chromosomal Replicase 379

Many Different Proteins Advance a Replication Fork 381

Helicase Activity Is Stimulated by Its Connection to the DNA Polymerase 384

DNA Loops Repeatedly Grow and Collapse on the Lagging Strand 384

Okazaki Fragments Require Removal of RNA and Ligase-Mediated Joining of DNA 386

The Replication Fork Is More Complex in Eukaryotes Than in Bacteria 387

11.4 Initiation of DNA Replication 391

Assembly of the Replication Fork Follows an Ordered Sequence of Events 391

Replication Initiation in *E. coli* Is Controlled at Multiple Steps 393

Eukaryotic Origins "Fire" Only Once per Cell Cycle 394

HIGHLIGHT 11-1 TECHNOLOGY Two-Dimensional Gel Analysis of Replication Origins 396

11.5 Termination of DNA Replication 398

E. coli Chromosome Replication Terminates Opposite the Origin 398

Telomeres and Telomerase Solve the End Replication Problem in Eukaryotes 399

Telomere Length Is Associated with Immortality and Cancer 401

Telomeres are Protected and Regulated by Proteins 401

HIGHLIGHT 11-2 MEDICINE Short Telomeres Portend Aging Diseases 403

HOW WE KNOW 406

DNA Polymerase Reads the Sequence of the DNA Template to Copy the DNA 406 Polymerase Processivity Depends on a Circular Protein That Slides along DNA 407 Replication Requires an Origin 408

12 DNA Mutation and Repair 413

MOMENT OF DISCOVERY Rose Byrne, on her discovery that *E. coli* could become a radiation-resistant extremophile 413

12.1 Types of DNA Mutations 414 A Point Mutation Can Alter One Amino Acid 415 Small Insertion and Deletion Mutations Change Protein Length 416 Some Mutations Are very Large and Form Abnormal Chromosomes 418 12.2 DNA Alterations That Lead to Mutations 420 Spontaneous DNA Damage by Water Can Cause Point Mutations 421 Oxidative Damage and Alkylating Agents Can Create Point Mutations and Strand Breaks 422 The Ames Test Identifies DNA-Damaging Chemicals 423 DNA-Damaging Agents Are Used in Cancer Chemotherapy 425 Solar Radiation Causes Interbase Cross-Links and Strand Breaks 425 Errant Replication and Recombination Lead to DNA Damage 428 12.3 Mechanisms of DNA Repair 428 Mismatch Repair Fixes Misplaced-Nucleotide Replication Errors 428 Direct Repair Corrects a Damaged Nucleotide Base in One Step 430

HIGHLIGHT 12-1 MEDICINE Mismatch Repair and Colon Cancer 433

Base Excision Repairs Subtle Alterations in Nucleotide Bases 435

Nucleotide Excision Repair Removes Bulky Damaged Bases 437

HIGHLIGHT 12-2 MEDICINE Nucleotide Excision Repair and Xeroderma Pigmentosum 439

Recombination Repairs Lesions That Break DNA 440 Specialized Translesion DNA Polymerases Extend DNA Past a Lesion 440

HOW WE KNOW 443

Mismatch Repair in *E. coli* Requires DNA Methylation 443 Uv Lights Up the Pathway to DNA Damage Repair 444 Translesion DNA Polymerases Produce DNA Mutations 445

13 Recombinational DNA Repair and Homologous Recombination 449

MOMENT OF DISCOVERY Lorraine Symington, on discovering how DNA ends are processed to initiate DNA recombination 449

xiv CONTENTS

13.1 Recombination as a DNA Repair Process 451 Double-Strand Breaks Are Repaired by Recombination 452 Collapsed Replication Forks Are Reconstructed by Double-Strand Break Repair 453 A Stalled Replication Fork Requires Fork Regression 454 Single-Stranded DNA Regions Are Filled In by Gap Repair 456 13.2 Enzymatic Machines in Bacterial Recombinational DNA Repair 457 RecBCD and RecFOR Initiate Recombinational Repair 457 RecA Protein Is the Bacterial Recombinase 459 RecA Protein Is Subject to Regulation 461 Multiple Enzymes Process DNA Intermediates Created by RecA 463 **HIGHLIGHT 13-1** EVOLUTION A Tough Organism in a Tough Environment: *Deinococcus radiodurans* 464 Repair of the Replication Fork in Bacteria Can Lead to Dimeric Chromosomes 466 13.3 Homologous Recombination in Eukaryotes 467 HIGHLIGHT 13-2 MEDICINE Why Proper Chromosomal Segregation Matters 468 Meiotic Recombination Is Initiated at Double-Strand Breaks 469 Meiotic Recombination Is Completed by a Classic DSBR Pathway 471 Meiotic Recombination Contributes to Genetic Diversity 471 Recombination during Mitosis Is Also Initiated at Double-Strand Breaks 472 Programmed Gene Conversion Events Can Affect Gene Function and Regulation 473 Some Introns Move via Homologous Recombination 475 13.4 Nonhomologous End Joining 475 Nonhomologous End Joining Repairs Double-Strand Breaks 475 Nonhomologous End Joining Is Promoted by a Set of Conserved Enzymes 476 Recombination Systems Are Being Harnessed for Genome Editing 477 HOW WE KNOW 479 A Motivated Graduate Student Inspires the Discovery of Recombination Genes in Bacteria 479 A Biochemical Masterpiece Catches a Recombination Protein in the Act 480

14 Site-Specific Recombination and Transposition **485**

MOMENT OF DISCOVERY Wei Yang, on researching the structure and molecular mechanisms of $\gamma\delta$ resolvase 485

14.1 Mechanisms of Site-Specific Recombination 487 Precise DNA Rearrangements Are Promoted by Site-Specific Recombinases 487

Site-Specific Recombination Complements Replication 490

- Site-Specific Recombination Can Be a Stage in a Viral Infection Cycle 491
- Site-Specific Recombination Systems Are Used in Biotechnology 491

Gene Expression Can Be Regulated by Site-Specific Recombination 492

HIGHLIGHT 14-1 TECHNOLOGY Using Site-Specific Recombination to Trace Neurons 494

14.2 Mechanisms of Transposition 496 Transposition Takes Place by Three Major Pathways 496

Bacteria Have Three Common Classes of Transposons 500

Retrotransposons Are Especially Common in Eukaryotes 502

HIGHLIGHT 14-2 EVOLUTION Awakening Sleeping Beauty 503

Retrotransposons and Retroviruses Are Closely Related 504

A Retrovirus Causes AIDS 506

HIGHLIGHT 14-3 MEDICINE Fighting AIDS with HIv Reverse Transcriptase Inhibitors 507

- 14.3 The Evolutionary Interplay of Transposons and Their Hosts 508
- viruses, Transposons, and Introns Have an Interwoven Evolutionary History 508
- A Hybrid Recombination Process Assembles Immunoglobulin Genes 510

HOW WE KNOW 513

Bacteriophage λ Provided the First Example of Site-Specific Recombination 513

If You Leave Out the Polyvinyl Alcohol, Transposition Gets Stuck 514

15 Transcription: DNA-Dependent Synthesis of RNA 519

MOMENT OF DISCOVERY Robert Tjian, on discovering the first specific eukaryotic transcription factor 519

15.1 RNA Polymerases and Transcription Basics 520 RNA Polymerases Differ in Details but Share Many Features 520

HIGHLIGHT 15-1 A CLOSER LOOK The ABCs of RNA: Complexity of the Transcriptome 521

- Transcription Initiation, Elongation, and Termination Occur in Discrete Steps 524
- DNA-Dependent RNA Polymerases Can Be Specifically Inhibited 524

Transcriptional Regulation Is a Central Mechanism in the Control of Gene Expression 526

15.2 Transcription in Bacteria 527

Promoter Sequences Alter the Strength and Frequency of Transcription 527

- Sigma Factors Specify Polymerase Binding to Particular Promoters 529
- Structural Changes Lead to Formation of the Transcription-Competent Open Complex 531
- Initiation Is Primer-Independent and Produces Short, Abortive Transcripts 531
- Transcription Elongation Is Continuous until Termination 533

Specific Sequences in the Template Strand Stop Transcription 535

15.3 Transcription in Eukaryotes 537

Eukaryotic Polymerases Recognize Characteristic Promoters 537

HIGHLIGHT 15-2 MEDICINE Using Transcription Factors to Reprogram Cells 538

Pol II Transcription Parallels Bacterial RNA Transcription 540 Transcription Factors Play Specific Roles in the Transcription Process 540 Transcription Initiation In vivo Requires the Mediator Complex 543 Termination Mechanisms Vary among RNA Polymerases 544 Transcription Is Coupled to DNA Repair, RNA Processing, and mRNA Transport 545

HOW WE KNOW 547

RNA Polymerase Is Recruited to Promoter Sequences 547 RNA Polymerases Are Both Fast and Slow 548

16 RNA Processing 553

MOMENT OF DISCOVERY Melissa Jurica, on determining the first electron microscopic structures of spliceosomes 553

16.1 Messenger RNA Capping and Polyadenylation 555

Eukaryotic mRNAs Are Capped at the 5' End 555 Eukaryotic mRNAs Have a Distinctive 3'-End Structure 557

mRNA Capping, Polyadenylation, and Splicing Are Coordinately Regulated during Transcription 557

HIGHLIGHT 16-1 EvOLUTION Eukaryotic mRNAs with Unusual 3' Tails 558

16.2 Pre-mRNA Splicing and Editing 559 Eukaryotic mRNAs Are Synthesized as Precursors Containing Introns 560 Alternative RNA Splicing Can Generate Multiple

- Products from a Gene 561 The Spliceosome Catalyzes Most Pre-mRNA
- Splicing 562
- Some Introns Can Self-Splice without Protein or Spliceosome Assistance 564

Exons from Different RNA Molecules Can Be Fused by *Trans*-Splicing 568

RNA Editing Can Involve the Insertion or Deletion of Bases 569

HIGHLIGHT 16-2 EVOLUTION The Origin of Introns 570

RNA Editing by Substitution Involves Deamination of A or C Residues 571

16.3 RNA Transport and Degradation 573 Different Kinds of RNA Use Different Nuclear Export Pathways 573

mRNA Export from the Nucleus Is Coupled to Pre-mRNA Splicing 574

Some mRNAs Are Localized to Specific Regions of the Cytoplasm 575

Cellular mRNAs Are Degraded at Different Rates 575 Processing Bodies Are the Sites of mRNA Storage and Degradation in Eukaryotic Cells 576

16.4 Processing of Non-Protein-Coding RNAs 577 Maturation of tRNAs Involves Site-Specific Cleavage and Chemical Modification 577

- Maturation of rRNA Involves Site-Specific Cleavage and Chemical Modification 578
- Small Regulatory RNAs Are Derived from Larger Precursor Transcripts 579

16.5 RNA Catalysis and the RNA World Hypothesis 580 Ribozymes Catalyze Similar Kinds of Reactions But Have Diverse Functions 580

HIGHLIGHT 16-3 EvOLUTION A viral Ribozyme Derived from the Human Genome? 581

Could RNA Have Formed the Basis for Early Life on Earth? 581

HOW WE KNOW 583

Studying Autoimmunity Led to the Discovery of snRNPs 583

xvi CONTENTS

RNA Molecules Are Fine-Tuned for Stability or Function 584 Ribozyme Form Explains Function 585

17 The Genetic Code 589

MOMENT OF DISCOVERY Steve Benner, on discovering that borate minerals stabilize ribose 589

17.1 Deciphering the Genetic Code: tRNA as Adaptor 590 All tRNAs Have a Similar Structure 591 The Genetic Code Is Degenerate 592 Wobble Enables One tRNA to Recognize Two or More Codons 593 Specific Codons Start and Stop Translation 594 The Genetic Code Resists Single-Base Substitution Mutations 595 Some Mutations Are Suppressed by Special tRNAs 596 17.2 The Rules of the Code 597 The Genetic Code Is Nonoverlapping 597 There Are No Gaps in the Genetic Code 598 The Genetic Code Is Read in Triplets 599 Protein Synthesis Is Linear 599 17.3 Cracking the Code 600 Random Synthetic RNA Polymers Direct Protein Synthesis in Cell Extracts 600 RNA Polymers of Defined Sequence Complete the Code 602 The Genetic Code Is Validated in Living Cells 604 17.4 Exceptions Proving the Rules 604 Evolution of the Translation Machinery Is a Mystery 604 Mitochondrial tRNAs Deviate from the Universal Genetic Code 605 **HIGHLIGHT 17-1** EVOLUTION The Translation

Machinery 606

Initiation and Termination Rules Have Exceptions 608

HOW WE KNOW 610

Transfer RNA Connects mRNA and Protein 610 Proteins Are Synthesized from the N-Terminus to the C-Terminus 611

The Genetic Code In vivo Matches the Genetic Code In vitro 612

18 Protein Synthesis 617

MOMENT OF DISCOVERY Harry Noller, on discovering the functional importance of ribosomal RNA 617 18.1 The Ribosome 618

The Ribosome Is an RNA-Protein Complex Composed of Two Subunits 619 Ribosomal Subunits Associate and Dissociate in Each Cycle of Translation 621 The Ribosome Is a Ribozyme 622 The Ribosome Structure Facilitates Peptide Bond Formation 623 HIGHLIGHT 18-1 EvOLUTION Mitochondrial Ribosomes: A Window into Ribosome Evolution? 624 **18.2** Activation of Amino Acids for Protein Synthesis 626 Amino Acids Are Activated and Linked to Specific tRNAs 626 Aminoacyl-tRNA Synthetases Attach the Correct Amino Acids to Their tRNAs 626 The Structure of tRNA Allows Accurate Recognition by tRNA Synthetases 628 Proofreading Ensures the Fidelity of Aminoacyl-tRNA Synthetases 628 18.3 Initiation of Protein Synthesis 630 HIGHLIGHT 18-2 TECHNOLOGY Genetic Incorporation of Unnatural Amino Acids into Proteins 631 Base Pairing Recruits the Small Ribosomal Subunit to Bacterial mRNAs 631 Eukaryotic mRNAs Recruit the Small Ribosomal Subunit Indirectly 632 A Specific Amino Acid Initiates Protein Synthesis 632

Initiation in Bacterial Cells Requires Three Initiation Factors 635

Initiation in Eukaryotic Cells Requires Additional Initiation Factors 636

Some mRNAs Use 5' End–Independent Mechanisms of Initiation 637

18.4 Elongation and Termination of the Polypeptide Chain 639

Peptide Bonds Are Formed in the Translation Elongation Stage 639

Substrate Positioning and the Incoming tRNA Contribute to Peptide Bond Formation 640

EF-G Drives Translocation by Displacing the A-Site tRNA 641

GTP Binding and Hydrolysis Regulate Successive Elongation Cycles 642

An mRNA Stop Codon Signals Completion of a Polypeptide Chain 643

Ribosome Recycling Factor Prepares Ribosomes for New Rounds of Translation 644

Fast and Accurate Protein Synthesis Requires Energy 644

Antibiotics and Toxins Frequently Target Protein Synthesis 646

Cox_2e_FM.indd 16 05/02/15 12:34 PM

HIGHLIGHT 18-3 MEDICINE Toxins That Target the Ribosome 647

18.5 Translation-Coupled Removal of Defective mRNA 650 Ribosomes Stalled on Truncated mRNAs Are Rescued by tmRNA 650 Eukaryotes Have Other Mechanisms to Detect Defective mRNAs 651 18.6 Protein Folding, Covalent Modification, and Targeting 653 Protein Folding Sometimes Requires the Assistance of Chaperones 653 Covalent Modifications Are Common in Newly Synthesized Proteins 653 Proteins Are Targeted to Correct Locations during or after Synthesis 654 Some Chemical Modifications of Eukaryotic Proteins Take Place in the Endoplasmic Reticulum 654 Glycosylation Plays a Key Role in Eukaryotic Protein Targeting 655 Signal Sequences for Nuclear Transport Are Not Removed 656 Bacteria Also Use Signal Sequences for Protein Targeting 657

HOW WE KNOW 659

The Ribosome Is a Ribozyme 659 Ribosomes Check the Accuracy of Codon-Anticodon Pairing, but Not the Identity of the Amino Acid 660

IV REGULATION

19 Regulating the Flow of Information 665

MOMENT OF DISCOVERY Lin He, on discovering that microRNA overexpression accelerates tumor development 665

19.1 Regulation of Transcription Initiation 667 Activators and Repressors Control RNA Polymerase Function at a Promoter 667 Transcription Factors Can Function by DNA Looping 668 Regulators Often Work Together for Signal Integration 670 Gene Expression Is Regulated through Feedback Loops 671 Related Sets of Genes Are Often Regulated Together 672 Eukaryotic Promoters Use More Regulators Than Bacterial Promoters 672 Multiple Regulators Provide Combinatorial Control 673

Regulation by Nucleosomes Is Specific to Eukaryotes 674 19.2 The Structural Basis of Transcriptional Regulation 675 Transcription Factors Interact with DNA and Proteins through Structural Motifs 675 Transcription Activators Have Separate DNA-Binding and Regulatory Domains 679 **19.3 Posttranscriptional Regulation** of Gene Expression 680 Some Regulatory Mechanisms Act on the Nascent RNA Transcript 680 Small RNAs Can Affect mRNA Stability 681 Some Genes Are Regulated at the Level of Translation 681 Some Covalent Modifications Regulate Protein Function 682 Gene Expression Can Be Regulated by Intracellular Localization 682

HIGHLIGHT 19-1 MEDICINE Insulin Regulation: Control by Phosphorylation 684

Protein Degradation by Ubiquitination Modulates Gene Expression 686

HOW WE KNOW 689

Plasmids Have the Answer to Enhancer Action 689

20 The Regulation of Gene Expression in Bacteria 693

MOMENT OF DISCOVERY Bonnie Bassler, on her discovery of interspecies quorum sensing 693

20.1 Transcriptional Regulation 694 The *lac* Operon Is Subject to Negative Regulation 694 The *lac* Operon Also Undergoes Positive Regulation 699

HIGHLIGHT 20-1 TECHNOLOGY Classical Techniques in the Analysis of Gene Regulation 700

- CRP Functions with Activators or Repressors to Control Gene Transcription 702
- Transcription Attenuation Often Controls Amino Acid Biosynthesis 704
- The SOS Response Leads to Coordinated Transcription of Many Genes 705
- 20.2 Beyond Transcription: Control of Other Steps in the Gene Expression Pathway 707
- RNA Sequences or Structures Can Control Gene Expression Levels 707
- Translation of Ribosomal Proteins Is Coordinated with rRNA Synthesis 711

xviii CONTENTS

HIGHLIGHT 20-2 A CLOSER LOOK T-Box Riboswitches 713

20.3 Control of Gene Expression in

Bacteriophages 715

Phage Propagation Can Take One of Two Forms 716 Differential Activation of Promoters Regulates λ Phage Infection 717

The λ Repressor Functions as Both an Activator and a Repressor 718

More Regulation Levels Are Invoked during the λ Phage Life Cycle 719

HOW WE KNOW 722

TRAPped RNA Inhibits Expression of Tryptophan Biosynthetic Genes in *Bacillus subtilis* 722 Autoinducer Analysis Reveals Possibilities for Treating Cholera 723

21 The Transcriptional Regulation of Gene Expression in Eukaryotes 727

MOMENT OF DISCOVERY Tracy Johnson, on discovering that pre-mRNA splicing requires specific histone acetylation 727

21.1 Basic Mechanisms of Eukaryotic Transcriptional Activation 728

Eukaryotic Transcription Is Regulated by Chromatin Structure 728

Positive Regulation of Eukaryotic Promoters Involves Multiple Protein Activators 730

HIGHLIGHT 21-1 A CLOSER LOOK The Intertwining of Transcription and mRNA Splicing 732

- Transcription Activators and Coactivators Help Assemble General Transcription Factors 733
- 21.2 Combinatorial Control of Gene Expression 736
- Combinatorial Control of the Yeast *GAL* Genes Involves Positive and Negative Regulation 736

HIGHLIGHT 21-2 TECHNOLOGY Discovering and Analyzing DNA-Binding Proteins 738

Combinatorial Control of Transcription Causes Mating-Type Switches in Yeast 738

Combinatorial Mixtures of Heterodimers Regulate Transcription 740

Differentiation Requires Extensive Use of Combinatorial Control 741

21.3 Transcriptional Regulation Mechanisms Unique to Eukaryotes 743

Insulators Separate Adjacent Genes in a Chromosome 743

Some Activators Assemble into Enhanceosomes 744

Gene Silencing Can Inactivate Large Regions of Chromosomes 745

Imprinting Allows Selective Gene Expression from One Allele Only 745

HIGHLIGHT 21-3 A CLOSER LOOK Gene Silencing by Small RNAs 746

Dosage Compensation Balances Gene Expression from Sex Chromosomes 747

Steroid Hormones Bind Nuclear Receptors That Regulate Gene Expression 749

Nonsteroid Hormones Control Gene Expression by Triggering Protein Phosphorylation 750

HOW WE KNOW 753

Transcription Factors Bind Thousands of Sites in the Fruit Fly Genome 753

Muscle Tissue Differentiation Reveals Surprising Plasticity in the Basal Transcription Machinery 754

22 The Posttranscriptional Regulation of Gene Expression in Eukaryotes 759

MOMENT OF DISCOVERY Judith Kimble, on the discovery that noncoding regions of mRNA regulate cell fate 759

22.1 Posttranscriptional Control inside the Nucleus 760

Alternative Splicing Controls Sex Determination in Fruit Flies 761

Multiple mRNA Cleavage Sites Allow the Production of Multiple Proteins 762

Nuclear Transport Regulates Which mRNAs Are Selected for Translation 764

22.2 Translational Control in the Cytoplasm 765

Initiation Can Be Suppressed by Phosphorylation of eIF2 766

The 3'UTR of Some mRNAs Controls Translational Efficiency 766

Upstream Open Reading Frames Control the Translation of *GCN4* mRNA 768

mRNA Degradation Rates Can Control Translational Efficiency 769

22.3 The Large-Scale Regulation of Groups of Genes 770

Some Sets of Genes Are Regulated by Pre-mRNA Splicing in the Nucleus 770

5'UTRs and 3'UTRs Coordinate the Translation of Multiple mRNAs 771

HIGHLIGHT 22-1 EVOLUTION Regulation of Splicing in Response to Stress 771

Conserved AU-Rich Elements in 3'UTRs Control Global mRNA Stability for Some Genes 772

22.4 RNA Interference 774 Eukaryotic MicroRNAs Target mRNAs for Gene Silencing 774 Short Interfering RNAs Target mRNAs for Degradation 776 RNAi Pathways Regulate viral Gene Expression 777 RNAi Provides a Useful Tool for Molecular Biologists 778

HIGHLIGHT 22-2 MEDICINE Viral Takeover Using a Cell Type-Specific miRNA 779

RNAs Regulate a Wide Range of Cellular Processes 780 22.5 Putting It All Together: Gene Regulation in Development 781 Development Depends on Asymmetric Cell Divisions and Cell-Cell Signaling 781 Early Development Is Mediated by Maternal Genes 784 Segmentation Genes Specify the Development of Body Segments and Tissues 785 Homeotic Genes Control the Development of Organs and Appendages 787 Stem Cells Have Developmental Potential That Can Be Controlled 788 22.6 Finale: Molecular Biology, Developmental Biology, and Evolution 791 The Interface of Evolutionary and Developmental Biology Defines a New Field 791 Small Genetic Differences Can Produce Dramatic Phenotypic Changes 792

HOW WE KNOW 794

A Natural Collaboration Reveals a Binding Protein for a 3'UTR 794 Little RNAs Play a Big Role in Controlling Gene Expression 795 Everything Old Is New Again: Beauty at the Turn of a Developmental Switch 796

Model Organisms Appendix **A-1**

A Few Organisms Are Models for Understanding Common Life Processes A-1 Three Approaches Are Used to Study Human Disease A-2

Bacterium, *Escherichia coli* A-6 Early Studies of *E. coli* as a Model Organism A-6 Life Cycle A-6 Genetic Techniques A-7 *E. coli* as a Model Organism Today A-7 **Budding Yeast, Saccharomyces cerevisiae A-8** Early Studies of Yeast as a Model Organism A-8 Life Cycle A-8 Genetic Techniques A-8 Yeast as a Model Organism Today A-9 **Bread Mold, Neurospora crassa A-10** Early Studies of *Neurospora* as a Model Organism A-10 Life Cycle A-10 Genetic Techniques A-11 *Neurospora* as a Model Organism Today A-11 **Nematode, Caenorhabditis elegans** A-12 Early Studies of *C. elegans* as a Model Organism A-12 Life Cycle A-12 Genetic Techniques A-13 *C. elegans* as a Model Organism Today A-13 **Mustard Weed, Arabidopsis thaliana A-14** Early Studies of *Arabidopsis* as a Model Organism A-14 Life Cycle A-14 Genetic Techniques A-15 *Arabidopsis* as a Model Organism Today A-15 Fruit Fly, *Drosophila melanogaster* A-16 Early Studies of *Drosophila* as a Model Organism A-16 Life Cycle A-16 Genetic Techniques A-17 *Drosophila* as a Model Organism Today A-17 **House Mouse, Mus musculus A-18** Early Studies of the Mouse as a Model Organism A-18 Life Cycle A-18 Genetic Techniques A-18 The Mouse as a Model Organism Today A-19 Glossary **G-1** Solutions to Problems states of the Second Seco

Index **I-1**

[Preface](#page-8-0)

As teachers, we know that undergraduate science education is evolving. Simply conveying facts does not produce a scientifically literate student, a long-held perception now reinforced by numerous studies. Students of science need more: a better window on what science is and how it is done, a clear presentation of key concepts that rises above the recitation of details, an articulation of the philosophical underpinnings of the scientific discipline at hand, exercises that demand analysis of real data, and an appreciation for the contributions of science to the well-being of humans throughout the world. As undergraduate science educators rise to these challenges, we are faced with both higher numbers of students and declining resources. How can we all do more with less?

Textbooks are an important part of the equation. A good textbook must now be more than a guide to the information that defines a discipline. For instructors, a textbook must organize information, incorporate assessment tools, and provide resources to help bring a discipline to life. For students, a textbook must relate science to everyday experience, highlight the key concepts, and show each student the process that generated those key concepts.

This book had its genesis at a meeting of the authors in Napa Valley in January 2006. From the outset, we set ambitious goals designed to address the key challenges we face as teachers.

students see science as a set of facts rather than an active human **endeavor.** Molecular biology has a wealth of important stories to tell. We wanted to convey the excitement that drives modern molecular biology, the creativity at the bench, and the genuine wonder that takes hold as the workings of a new biological process are revealed. This theme is set in the first chapter, dedicated in large measure

to an introduction to the scientific process. Every chapter then begins with a *Moment of Discovery,* highlighting a researcher's own description of a memorable moment in his or her career. After Chapter 1, every chapter ends with a *How We Know* section, with stories relating the often circuitous path to a new insight. Additional anecdotes— scientists in action—are woven into the text and the accompanying *Highlights.* As students read the text, the laboratories and the people behind the discoveries will never be far away.

This second edition is an update, and much more. It has allowed us to refine the initial vision we had when we started this project and to augment that vision with unparalleled resources that will bring the subject to life for students and educators alike.

4 MOMENT OF DISCOVERY

Scientific breakthroughs represent the exhilarating culmination of a lot of hard work. Each chapter opens with a description of a significant breakthrough in molecular biology, told by the scientist who made the discovery. The scientists featured in the Moments of Discovery are David Allis, Norm Arnheim, Bonnie Bassler, Steve Benner, James Berger, Carlos Bustamante,

Rose Byrne, Jamie Cate, Joe DeRisi, Roxana Georgescu, Lin He, Tracy Johnson, Melissa Jurica, Judith Kimble, Robert Lehman, Steve Mayo, Harry Noller, Smita Patel, Lorraine Symington, Jack Szostak, Robert Tjian, and Wei Yang.

A HOW WE KNOW

Each chapter ends with a How We Know section that combines fascinating stories of research and researchers with experimental data for students to analyze.

Students often view science as a completed story. The reality is far different. Data can take a researcher in unexpected directions. An experiment designed to test one hypothesis can end up revealing something quite different. The analysis of real data is a fundamental skill to be honed by every student of science. We have tried to address this need aggressively. Each chapter in this text features a challenging set of problems, including at least one requiring the analysis of data from the scientific literature. Many of these are linked to the discoveries described in the How We Know sections. Each chapter also ends with some *Unanswered Questions,* providing just a sampling of the endless challenges that remain for those with the motivation to tackle them.

UNANSWERED QUESTIONS

A short section at the end of each chapter describes important areas still open to discovery, showing students that even wellcovered subjects, such as nucleic acid structure and DNA replication, are far from fully explored.

R.A. Lowe, R. Hitteglia, N. Ro. $-$ that is **BOOK Millery** VII. The is also credy the of front a for a showing choose as a state of and registers (I Just Jinel 13:283-708 duce had developed a first lary α is the positive of the step of a first large system of the procedure of the procedure of the state is a system of the state o contributes and the contribution of the state of the state of the property of the state of is requires to the slip markets in All of the All-Acts
that and only the bur density Panty I give a post exact the labels of personal of \$4.40 .
Marie More in 1945, et l'Alt auto-Marie restorant la coult la f Callenge, and a IFC Mixed **TTE** ITT.641w46/ ٠ and serve **FOUND 1 Structure & Hutchison and Linux Box 12000 ATL 79-11**

TUNANSWERED QUESTIONS

The study of protein function is, arguably, the oldest subdiscipline in biochemistry and molecular biology. But there is still much to learn. The relatively young science of genomics keeps pointing to genes that encode proteins about which we know little or nothing at all. Some shortcuts to functional discovery are discussed in later chapters.

L. How does protein structure relate to function? This is an old but still very relevant question for every scientist who studies proteins. Advanced methods of structural analysis are providing more information than ever before, but many of these structural pictures are static. A clear picture of a complete binding or catalytic cycle can require a detailed knowledge of the structure of multiple protein conformations. Certain structural motifs and domains (e.g., the OB fold of single-stranded DNAbinding proteins and other proteins, the AAA' ATPase domain, and simple B-barrel structures) appear in proteins that often have seemingly unrelated functions. The manner in which particulan structures are adapted to different functions is an ongoing area of investigation.

End-oF-chaPtEr ProBlEMs

Extensive problem sets at the end of each chapter give students the opportunity to think about and work with the chapter's key ideas. New problems have been added in each chapter for this second edition. Each problem set concludes with a Data Analysis Problem, giving students the critical experience of interpreting real research data. Solutions to all problems can be found at the back of the book.

Students get lost in the details. Presenting the major concepts clearly, in the text as well as in the illustrations, is crucial to teaching students how science is done. We have worked to use straightforward language and a conversational writing style to draw students in to the material. We have collaborated closely with our illustrator, Adam Steinberg, to create clean, focused figures. Featured *Key Conventions* highlight the implicit but often unstated conventions used when sequences and structures are displayed and in naming biological molecules.

DNA and RNA are defined by the type of sugar in the polynucleotide backbone (deoxyribose or ribose), not by the presence of thymine or uracil.

KEY CONVENTIONS

In brief paragraphs, the Key Conventions clearly lay out for students some fundamental principles often glossed over.

to refluorable) from the spee or 2002 as. The starte-maritantsings has a
red child allows some

IllustratIons

Good figures should speak for themselves. We have worked to keep our figures simple and the figure legends as brief as possible. The illustrations in the text are the product of close collaboration with our colleague Adam Steinberg. Together with the talented artists at Dragonfly Media Group, Adam has helped to hone and implement our vision.

students see evolution as an abstract theory.

Every time a molecular biologist studies a developmental pathway in nematodes, identifies key parts of an enzyme active site by determining what parts are conserved among species, or searches for the gene underlying a human genetic disease, he or she is relying on evolutionary theory. *Evolution is a foundational concept, upon which every discipline in the biological sciences is built*. In this text, evolution is a theme that pervades every chapter, beginning with a major section in Chapter 1 and continuing as the topic of many Highlights and chapter segments.

4 HIGHLIGHTS

These discussions are designed to enhance students' understanding and appreciation of the relevance of each chapter's material. There are four categories of Highlights:

• Medicine explores diseases that arise from defects in biochemical pathways, and how concepts uncovered in molecular biology have contributed to drug therapies and other treatments.

• Technology focuses on cutting-edge molecular biology methods.

• Evolution reveals the role of molecular biology research in understanding key biological processes and the connections among organisms.

• A Closer Look examines a wide variety of additional, intriguing topics.

ExPErIMEntal tEchnIQuEs

As researchers, we know that it is critical to understand the benefits and limitations of experimental techniques. We strive to give students a sense of how an experiment is designed and what makes the use of a particular technique or model organism appropriate. The techniques covered in this book are:

Ames test 424 Chemical modification interference 700 Chemical protection footprinting 700 Chemical synthesis of nucleic acids 201 ChIP-Chip 345 ChIP-Seq 345 Chromatography Affinity chromatography 100 Using terminal tags 237 Using tandem affinity purification (TAP) tags 242 Column chromatography 100 Gel-exclusion chromatography 100 Ion-exchange chromatography 100 Thin-layer chromatography 584 CRISPR/Cas 246 Detecting A=T-rich segments of DNA by denaturation analysis 197 DNA cloning 212 DNA cloning with artificial chromosomes (BACs, YACs) 218 DNA footprinting 700 DNA genotyping (DNA fingerprinting, DNA profiling, STR analysis) 224 DNA library creation (cDNA, genomic) 220 DNA microarrays 244 DNA sequencing Automated Sanger sequencing 226 Deep sequencing 232 Genome sequencing techniques 260 Ion torrent 232 Next generation sequencing 229 Pyrosequencing 229 Reversible terminator sequencing 230 Sanger sequencing 226 Single molecule real time (SMRT) sequencing 230 Electrophoresis Agarose gel electrophoresis 199 Isoelectric focusing 277

Pulsed field gel electrophoresis (PFGE) 220 Sodium dodecyl sulfate–polyacrylamide gel electrophoresis (SDS-PAGE) 100 Two-dimensional gel electrophoresis 277 Electrophoretic mobility shift assay (EMSA) 700 Electroporation 217 Epitope tagging 240 Haplotype analysis 269 Immunoprecipitation 242 Linkage analysis 272 Localization of GFP fusion proteins 239 Mass spectrometry 278 Northern blotting 199 Nuclear magnetic resonance (NMR) 115 Optical trapping 344 Photolithography 244 Phylogenetic analysis 270 Phylogenetic profiling 279 Polymerase chain reaction (PCR) 222 Quantitative PCR (qPCR) 222 Reverse transcriptase PCR (RT-PCR) 222 Protein chips 280 Protein localization via indirect immunofluorescence 240 Recombinant protein expression 232 RNA interference (RNAi) 774 RNA-Seq 276 Selection and screening 217 Site-directed mutagenesis 235 Somatic cell nuclear transfer (SCNT) 538 Southern blotting 199 Transformation 217 Western blotting 241 X-ray crystallography 120 Yeast three-hybrid analysis 243 Yeast two-hybrid analysis 243

nEW and uPdatEd contEnt

The second edition addresses recent discoveries and advances, corresponding to our ever-changing understanding of molecular biology. In addition to the text updates listed here, there are numerous new figures and photos, along with significantly updated figures in every chapter. There are also new end-of-chapter problems for every chapter and many new Unanswered Questions.

chapter 1

• Updated discussions of evolution and the scientific method

chapter 2

- Updated discussion of the central dogma
- Updated and expanded discussion of the types of RNA

chapter 3

- New Moment of Discovery
- Expanded discussion of nucleosides
- Revised and expanded section: The Hydrophobic Effect Brings Together Nonpolar Molecules
- New section: Electronic Interactions between Bases in Nucleic Acids

chapter 4

- Expanded section: Amino Acids Are Categorized by Chemical Properties
- Significantly expanded discussion of protein purification, including Highlight 4-1
- New section: Intrinsically Unstructured Proteins Have Versatile Binding Properties
- Expanded section on protein families
- Significantly expanded section on protein folding and computational biology

chapter 5

• New Moment of Discovery

chapter 6

- Expanded discussion of the instability of RNA
- New Highlight 6-1: DNA Nanotechnology
- New discussion of riboswitches

chapter 7

- Expanded discussion on obtaining DNA fragments to clone
- Thoroughly updated section on next-gen and other modern DNA sequencing technologies.
- New section: Genomic Sequencing Is Aided by New Generations of DNA Sequencing Methods, incorporating the exciting new advances with programmable nucleases

chapter 8

- Expanded Highlight 8-1, now including discussion of the microbiome
- Updated section on noncoding DNA
- Expanded section on mass spectrometry

chapter 10

- New Moment of Discovery
- Significantly expanded discussion of histone modifications, including a new table

chapter 11

- Expanded discussion of the β sliding clamp
- Expanded discussion of the Pol III holoenzyme
- Updated and expanded discussion of eukaryotic replication forks
- Updated and expanded section: Eukaryotic Origins "Fire" Only Once per Cell Cycle
- New section: Telomeres and Telomerase Solve the End Replication Problem in Eukaryotes
- New Highlight 11-2: Short Telomeres Portend Aging Diseases

chapter 12

- New Moment of Discovery
- New table presenting overview of DNA repair processes

chapter 13

- Updated and expanded sections on double-strand break repair and reconstruction of replication forks
- Updated section on meiotic recombination

chapter 14

- Updated and expanded introductory section on transposable elements and sitespecific recombination
- Updated and expanded section: Precise DNA Rearrangements Are Promoted by Site-Specific Recombinases
- Reorganized section on the use of site-specific recombination systems in biotechnology
- Updated and expanded sections on transposition

chapter 15

- Updated section on transcription elongation
- Updated and expanded discussion of the role of transcription factors
- Updated and expanded discussion of termination mechanisms among RNA polymerases

chapter 16

- Streamlined chapter organization
- Expanded discussion of P bodies

chapter 18

- Streamlined chapter organization
- Updated discussion of protein release factors
- Updated discussion of nuclear export signals

chapter 19

• Updated section: Gene Expression Is Regulated through Feedback Loops, now including inducer exclusion

chapter 22

- Expanded section on alternative splicing, including ESEs and ESSs
- Updated section on RNA interference
- New section: RNAs Regulate a Wide Range of Cellular Processes
- Updated section on the developmental potential of stem cells

MEDIA

Simulations

One of our central goals in tackling the revision of this textbook was to provide special resources to engage students (and educators) in molecular biology. New to the second edition are simulations that cover core molecular biology concepts and techniques. Created using the art from the text, the simulations reinforce students' understanding by allowing them to interact with the structures and processes they have encountered. A gamelike format guides students through the simulations, unlocking them in order, and multiple-choice questions after each simulation ensure that instructors can assess whether students have thoroughly understood each topic. These simulations are the product of many days of meetings among the authors, editors, and media developers. From storyboarding to the finished product, these simulations were one of the most challenging as well as stimulating efforts associated with preparing the second edition. We are excited to present this new approach to learning key concepts.

Nucleotide Structure (Chapter 3) DNA/RNA Structure (Chapter 6) PCR (Chapter 7) Sanger Sequencing (Chapter 7) CRISPR (Chapters 7 and 19) DNA Replication (Chapter 11) DNA Polymerase (Chapter 11) Mutation and Repair (Chapter 12) Transcription (Chapter 15) mRNA Processing (Chapter 16) Translation (Chapter 18)

Nature Articles with Assessment

These articles engage students in reading about primary research and encourage critical thinking. Specifically selected for both alignment with the text coverage and exploration of identi-

fied difficult topics, the *Nature* articles include assessment questions that can be automatically graded. Also included are open-ended questions that are suitable for use in flipped classrooms and active learning discussions either in class or online.

The simulations and *Nature* articles for *Molecular Biology: Principles and Practice* are available in our LaunchPad system, along with many additional resources.

This dynamic, fully integrated learning environment brings together all of our teaching and learning resources in one place. It also contains the fully interactive **e-Book** and other newly updated resources for students and instructors, including the following:

new clicker Questions allow instructors to integrate active learning in the classroom and to assess students' understanding of key concepts during lectures.

updated Test Bank contains at least 40 multiple-choice and short-answer questions for each chapter.

allows students to test their comprehension of the chapter concepts. The system adapts to students' individual level of preparedness by giving them questions at varying levels of difficulty, depending on whether they answer a question without help, or they need help but eventually get the question right, or they are unable to answer the question. Links to the appropriate e-Book section, hints, and feedback help students realize where they need more practice on a topic.

Key Term flashcards allow students to review the definitions of all the glossary terms and quiz themselves.

Textbook images and Tables are offered as high-resolution JPEG files. Each image has been fully optimized to increase type size and adjust color saturation. These images have been tested in a large lecture hall to ensure maximum clarity and visibility.

[Acknowledgment](#page-8-0)s

This text represents our best effort to synthesize a complex and ever-shifting field and to contribute to the broadening requirements of twenty-first-century education in molecular biology. We welcome your comments and suggestions. We thank our many colleagues whose input has helped shape this book:

Steven Ackerman, *University of Massachusetts* Ravi Allada, *Northwestern University* Rick Amasino, *University of Wisconsin–Madison* Andrew Andres, *University of Nevada, Las Vegas* Brian Ashburner, *University of Toledo* Matthew Bahamonde, *Farmingdale State College* Kenneth Belanger, *Colgate University* Joel Belasco, *NYU School of Medicine* Morgan Benowitz-Fredericks, *Bucknell University* Bradford Berges, *Brigham Young University* Xin Bi, *University of Rochester* Robert Borgon, *University of Central Florida* David Bourgaize, *Whittier College* Nicole Bournias-Vardiabasis, *California State University, San Bernardino* John Boyle, *Mississippi State University* Jeremy Bruenn, *University at Buffalo* Douglas Burks, *Wilmington College* Aaron Cassill, *University of Texas, San Antonio* Karl Chai, *University of Central Florida* Davis Cheng, *California State University, Fresno* William Cody, *University of Dallas* Mary Connell, *Appalachian State University* Scott Covey, *University of British Columbia* Fred Cross, *Rockefeller University* Cristina Cummings, *Providence College* Rodney Dale, *Loyola University Chicago* Susan DiBartolomeis, *Millersville University* Dessislava Dimova, *Rutgers University, New Brunswick* David Donze, *Louisiana State University, Baton Rouge* Arri Eisen, *Emory University* Danielle Ellis, *California State University, Pomona* R. Paul Evans, *Brigham Young University* Nicholas Ewing, *California State University, Sacramento* Jason Fitzgerald, *Southeastern Illinois College* Gerald Frenkel, *Rutgers University, Newark* Louise Glass, *University of California, Berkeley*

Ann Grens, *Indiana University South Bend* Theresa Grove, *Valdosta State University* Nancy Guild, *University of Colorado Boulder* Immo Hansen, *New Mexico State University* Daniel Herman, *University of Wisconsin–Eau Claire* Margaret Hollingsworth, *University at Buffalo* Stan Ivey, *Delaware State University* Russell Johnson, *Colby College* Jason Kahn, *University of Maryland* Mijung Kim, *Chicago State University* Timothy Lane, *University of California, Los Angeles* Curtis Loer, *University of San Diego* Charles Mallery, *University of Miami, College of Arts and Sciences* Kathryn McMenimen, *Mount Holyoke College* Mitch McVey, *Tufts University* Thomas Mennella, *Bay Path College* Karl Miletti, *Delaware State University* Yuko Miyamoto, *Elon University* Evangelos Moudrianakis, *Johns Hopkins University* Arunachalam Muthaiyan, *Chicago State University* Hao Nguyen, *California State University, Sacramento* Brent Nielsen, *Brigham Young University* James Ntambi, *University of Wisconsin–Madison* Greg Odorizzi, *University of Colorado* James Olesen, *Ball State University* Harold Olivey, *Indiana University Northwest* Anthony Otsuka, *Illinois State University* Rekha Patel, *University of South Carolina* Bruce Patterson, *University of Arizona, Tucson* Brian Poole, *Brigham Young University* Megan Porter, *University of South Dakota* Ted Powers, *University of California, Davis* April Pyle, *University of California, Los Angeles* Brian Ring, *Valdosta State University* Herve Roy, *University of Central Florida* Edmund Rucker, *University of Kentucky* Ivan Sadowski, *University of British Columbia* Steven Sandler, *University of Massachusetts Amherst* Brian Sato, *University of California, Irvine* Mary Schuler, *University of Illinois Urbana-Champaign* William Scovell, *Bowling Green State University* Andrei Seluanov, *University of Rochester* Konstantin Severinov, *Rutgers University, New Brunswick*

xxvii

xxviii ACKNOWLEDGMENTS

Xueyan Shan, *Mississippi State University* Elaine Sia, *University of Rochester* Ron Siu, *University of California, Los Angeles, Extension* Agnes Southgate, *College of Charleston* Daniel Stoebel, *Harvey Mudd College* Derek Tan, *Sloan-Kettering Institute for Cancer Research* Ignatius Tan, *New York University* Lloyd Turniten, *University of Wisconsin–Eau Claire* Jill Wildonger, *University of Wisconsin–Madison* Bruce Wolff, *University of Waterloo* Michael Yu, *University at Buffalo*

This book would not have been possible without the support of our publishers at W. H. Freeman. A book of this sort is an undertaking measured not just in hours but in sleepless nights, almost-met deadlines, conference calls, and occasional levity. It is an enterprise in which teachers sometimes become students. The needed guidance has been provided by an exceptionally talented team of editors and copy editors. Kate Ahr Parker has overseen the effort from the beginning. Few human beings are as gifted in the art of articulating urgency with grace.

Mike Cox, Jennifer Doudna, and Mike O'Donnell *December 2014*

Anna Bristow, Erica Frost, and Lisa Samols have been our development editors. Guided by their capable hands, first-draft chapters have been created, reworked, broken up, and sometimes merged. They provided encouragement and pointed out deficiencies. They have been our partners throughout, scrutinizing every word we produced. As the project progressed, the work was honed and the chapters integrated with the help of Brook Soltvedt and Linda Strange. Both Brook and Linda are longtime veterans of the *Lehninger Biochemistry* series, and their expertise added immeasurably to the final product in your hands. In the end, they have managed the impressive feat of merging three voices into one. We are extraordinarily grateful to all of the editors for their dedication to this project. We are fortunate to have had the benefit of their insights and expertise.

The artwork for this book was a labor of love handled by Adam Steinberg and the artists at Dragonfly Media. Adam is also a *Lehninger Principles of Biochemistry* veteran, and his experience and skill are evident on almost every page of this book. He worked hand in hand with the authors to create illustrations that convey concepts concisely and in a unified style.

Our thanks also go to the consummate professionals who ensured the high quality in the production of the book: art director Diana Blume, project editor Elizabeth Geller, production coordinator Paul Rohloff, illustration coordinator Janice Donnola, photo editor Jennifer Atkins, and photo researcher Teri Stratford. We greatly appreciated their flexibility and creativity in working with complex material and ever-shifting schedules.

We express our appreciation to our colleagues, friends, and families for their patience and support.

Last, but certainly not least, we are grateful to the Moment of Discovery authors, who shared some of their favorite scientific career moments with us. Each of them provided valuable time and effort for this project and helped us add a personal touch to every chapter.

Michael M. Cox Jennifer A. Doudna Michael O'Donnell

Evolution, Science,
and Molecular Biology

Jack Szostak *[Source: © Jim Sugar/Corbis.]*

MoMent of Discovery

A big question in the origin of life concerns how primitive cells might have evolved. My own approach to this question involved lots of discussions with Irene Chen and others in my lab about how lipid vesicles containing RNA, which might mimic a simple self-replicating life form, could be capable of dividing. In other words, as the amount of genetic material (here, RNA) increased by making more copies of itself, *how*

would the increased RNA content affect the physical properties of the vesicle? We envisioned that osmotic pressure might make vesicles grow by extracting lipids from neighboring vesicles, ultimately leading to division by rupture and resealing. This idea seemed pretty far out, though, until Irene began doing experiments with vesicles containing lipids bearing fluorescent dyes. We could encapsulate RNA inside the vesicles and watch the vesicles change in size (or not) under different conditions by following the level of fluorescence as a function of vesicle surface area. Irene found that empty vesicles or vesicles "swollen" with RNA were stable over time, but when she mixed them together, the swollen vesicles started to grow by stealing lipid molecules from neighboring empty vesicles! So the system worked exactly as we had imagined, demonstrating that vesicle growth and division is a process that can occur spontaneously.

More recently, we found that vesicles loaded with RNA can also take up nucleotides (the building blocks of RNA and DNA) from the environment, disproving an old idea that it would be hard for primitive cells to survive by taking up small molecules, including negatively charged nucleotides, from their surroundings. It has been very exciting to find that each potential roadblock to primitive cellular replication that we have explored so far can be overcome, often without requiring specialized catalysts or input energy.

—Jack Szostak, on his discovery of self-dividing vesicles that mimic growing cells

1.1 The Evolution of Life on Earth: 2

1.2 How Scientists Do Science: 12

Online resources related to this chapter:

Nature exercise Genome dynamics

1

Form in the second half of the twentieth century,

Broadly speaking, **molecular biology** is the study

of essential cellular macromolecules, including DNA molecular biology has only recently come of age. of essential cellular macromolecules, including DNA, RNA, and proteins, and the biological pathways between them. Over the decades, molecular biology has become firmly associated with the structure, function, and regulation of information pathways at the molecular level. All of the processes required to reliably pass genetic information from one generation to another and from DNA to RNA to protein are included in this area of study. Of the requirements for life, it is the information in our genetic material that links all organisms to each other and documents their intertwined history. The biological information pathways that maintain, use, and transmit that information are the focus of this book.

Molecular biology may have a relatively short history, but its impact on the human experience is already considerable. Medicine, modern agriculture, forensic science, and many other endeavors rely on technologies developed by molecular biologists. Our current understanding of information pathways has given rise to diagnostic tests for genetic diseases, forensic DNA analysis, crops with improved yields and resistance to disease, new cancer therapies, an unprecedented ability to track pandemics, new wastewater treatment methods, new approaches to the generation of energy, and much more. Many of these advances are chronicled throughout this textbook.

This first chapter introduces three of the most important themes that link the book's topics. The first theme concerns the two key requirements for life: **biological information**, the genetic instructions that shape every living cell and virus, and **catalysis**, a capacity to accelerate critical molecular processes. Molecular biology deals with both, and much of the discipline focuses on the interplay between information-containing polymers (nucleic acids and proteins) and the enzymes that catalyze and regulate their synthesis, modification, function, and degradation.

The second theme is **evolution**. Many of the processes we will consider can be traced back billions of years, and a few can be traced to the last universal common ancestor. Genetic information is a kind of molecular clock that can help define ancestral relationships among species. Shared information pathways connect humans to every other living organism on Earth and to all the organisms that came before.

The third theme in this book is how we look at molecular biology as a scientific endeavor. Any scientific discipline is a construct not only of the knowledge it has generated but also of the human processes behind that knowledge. Molecular biology has both an inspirational history and a promising future, to be forged by contributors as yet unnamed. Breakthroughs rely on more than technology and ideas: they require an understanding of the scientific process and are informed by [the struggles of the past.](#page-8-0)

1.1 THE EVOLUTION OF LIFE ON EARTH

All organisms on Earth are connected by an evolutionary journey spanning more than 3 billion years. The diversity of life we see around us is the sum of a limitless number of **mutations**, changes in genetic information that are usually subtle but sometimes dramatic. When Charles Darwin proposed that natural selection acts on variation in populations, he had no knowledge of the mechanisms [that give r](#page-8-0)ise to that variation. Such mechanisms lie at the heart of modern molecular biology.

What is life?

Almost anyone can distinguish a living organism from an inanimate object. However, a rigorous scientific description of life is harder to achieve. Life differs from nonlife in identifiable ways, as summarized in **Figure 1-1**. Organisms move, reproduce, grow, and alter their environment in ways that inanimate objects cannot. But such characteristics alone provide an unsatisfying definition of life, particularly when a few of them may be shared by inanimate substances. In 1994, the United States National Aeronautics and Space Administration (NASA) convened a panel to consider the question, "What is life?" A simple definition resulted: *Life is a chemical system capable of Darwinian evolution*. The importance of evolutionary theory to all biological sciences gains full expression in this concise statement.

Every living system we know about has several requirements for its existence. Two of these—raw materials and energy—are supplied by a home planet endowed with an abundance of both. Molecules in Earth's life forms are made up largely of the elements hydrogen, oxygen, nitrogen, and carbon. These are the smallest and most abundant atoms that can make, respectively, one, two, three, and four covalent bonds with other atoms. The molecules formed by these elements tend to be quite stable and can be very complex. The energy required for life is derived from the sun. Plants and photosynthetic microorganisms collect and store the energy derived from sunlight in the chemical bonds of complex biomolecules.

A third requirement for a living system is an envelope, creating a barrier between the living and inanimate worlds and establishing a means of selective interaction between a cell and its environment. The work of Jack Szostak, chronicled in this chapter's Moment of Discovery, may be replicating some key evolutionary moments that led to enveloped living systems (**Figure 1-2** on p. 4).

FIGURE 1-1 Characteristics of living systems. Each characteristic distinguishes living organisms from inanimate matter.

The final two requirements—catalysis and biological information—are particularly important, truly distinguishing a living organism from an inanimate object. These requirements are the domain of molecular biology. The energy transactions that support homeostasis (the maintenance of parameters such as pH and biomolecule concentrations within the narrow range needed to support life) and enable the transmission of genetic information from one generation to the next are initiated by powerful catalysts called **enzymes**. Enzymes are highly specific, and each enzyme accelerates only one or a small number of chemical reactions. Most enzymes are proteins, although a few catalytic RNA molecules play important roles in cells. The catalysts that a particular organism possesses define which reactions can occur in that organism. Enzymes determine what a cell takes in for nourishment, how fast the cell grows, how it discards wastes, how it constructs its cellular membranes, how it responds to other cells, and how it reproduces.

The presence of enzymes in a cell depends on the faithful transmission of the genetic information that encodes them from one generation to the next. Enzymes, as well as the myriad other proteins and RNA molecules that regulate their synthesis and function, are the actual molecular targets of evolution. When a cell acquires a new function, it generally reflects the presence of a new enzyme or set of enzymes, or an alteration in the regulation or function of an existing enzyme or process. The new functions arise through changes in genes—changes that are shaped by evolutionary processes. In the biosphere of today, DNA is the standard macromolecule for the long-term storage and transmission of biological information. It is exquisitely adapted to that function (**Figure 1-3** on p. 5). However, as we shall see, there were probably stages in the evolution of life when DNA did not serve as the primary genetic library in living systems.

Evolution Underpins Molecular Biology

In 1973, the geneticist Theodosius Dobzhansky published an article in the professional journal *The American Biology Teacher* entitled "Nothing in Biology Makes Sense Except in the Light of Evolution." This sentiment has special meaning in molecular biology, because the pathways and processes in living systems give rise to the genetic variation on which natural selection acts (**Figure 1-4**). They also inform the ongoing investigations into how life arose on Earth.

Evolution relies on spontaneous and generally random changes in an organism's genomic material, called mutations. In spite of the elaborate cellular mechanisms we consider in this book, all of which help ensure accurate transmission of genetic information from one generation to the next, mutations regularly occur. Mutations can be as simple as a change in a single base pair of DNA or base of RNA or as substantial as the inversion, deletion,

by lipid molecules (green circle in the first panel), can be made from fatty acids. Fatty acids in aqueous solution are external concentration of fatty acids increases (more local micelles), the mostly spherical vesicles (top) grow slowly into a filamentous form (bottom) by incorporation of the added fatty acids. The micelle concentration declines as the micelles are incorporated into the larger vesicles. Gentle agitation produces a solution that again consists of mainly spherical vesicles, as shown in the schematic. *[Source: J. Am. Chem. Soc.* 30 mm *134(51):20812–20819, 2012, Fig. 7.]*

> or insertion of large segments of genetic material. As we will be discussing in detail, errors can arise during replication (Chapter 11), and DNA damage can lead to permanent mutation when repair systems (Chapter 12) go awry. Larger chromosomal changes can arise from recombination (Chapter 13) or transposition (Chapter 14). Some mutations affect genes directly; others affect the ways in which DNA is transcribed into RNA or RNA is processed or translated (Chapters 15–18). Relatively minor changes in genes involved in regulatory processes (Chapters 19– 22) can give rise to dramatic changes in the organism; this realization has created a new field, essentially a modern merger of the fields of evolutionary and developmental biology, dubbed "evo-devo" (described in Chapter 22). All the processes that contribute to information transfer are highly, but not perfectly, accurate, and the slow accumulation of alterations is inevitable. Many organisms even have mechanisms to speed up the pace of mutational change, which they draw upon in times of stress.

FIGURE 1-3 DNA structure. Because of its structural properties, DNA is well suited for longterm information storage. Genomic DNA almost always consists of two complementary strands of deoxyribonucleic acid. Each strand has a backbone consisting of deoxyribose residues connected by phosphate groups, and a base is attached to each ribose. Strand complementarity is enforced by specific interactions between the bases in each strand. The interactions create base pairs. (a) The $G\!\equiv\!\mathsf{C}$ and A $=$ T base pairs are similarly sized, giving the DNA double helix a uniform width and allowing base pairs, in any sequence, to stack. Complementary base pairing facilitates replication and transmission from one generation to the next. (b) The double-helical structure and base stacking confer stability. Major and minor helical grooves in the structure provide access to genetic information for a wide range of DNAbinding proteins. The uniform structure of the DNA backbone allows the synthesis of very long polymers.

FIGURE 1-4 Pathways of biological information flow. In almost all living systems, information is stored in DNA, then transcribed into RNA, which is processed and translated into protein. DNA is replicated to prepare for cell division. The transfer and maintenance of genetic information are regulated at each of these stages. Exceptions to this general pattern are found in certain viruses (RNA viruses and retroviruses) that store their genetic information in RNA. Viruses with RNA genomes make use of additional pathways (denoted by the red arrows)—RNA replication and reverse transcription (creation of DNA from RNA, instead of the other way around)—to maintain their genomes. The yellow highlighting represents points of regulation. Processes in the gray shaded box, along with occasional errors in replication, reverse transcription, and RNA replication, give rise to genomic alterations (mutations) that fuel evolution.

An understanding of these processes has also given us insights into the origins of life and the process of evolution. Continuing explorations of RNA structure (Chapter 6) and metabolism (Chapters 15 and 16) have informed new theories of prebiotic evolution. The genetic code (Chapter 17) provides a particularly vivid look at the shared history of every organism on Earth.

Molecular biology has provided the enzymes that make most of the methods of biotechnology possible (Chapter 7). These increasingly powerful methods for studying the genes of many different organisms allow us to trace their evolution. Through modern genomics (Chapter 8), molecular biology is opening a window onto evolution that Charles Darwin would marvel at.

The interrelationship of molecular biology and evolution is of more than academic interest. Human beings exist in a world where every organism continues to evolve. Microorganisms, with their short life cycles, evolve most rapidly (**Highlight 1-1**). Of special concern are human pathogens, as well as the microorganisms, fungi, insects, and other organisms that affect our food crops, livestock, and water supply. Molecular biology

HIGHLIGHT 1-1 **EVOLUTION**

Observing Evolution in the Laboratory

The bacterium *Deinococcus radiodurans* has a remarkable capacity to survive the effects of ionizing radiation (IR, or gamma rays). A human being would be killed by exposure to 2 Gy (1 Gy (gray) = 100 rads) of IR, but cultures of *Deinococcus* routinely survive 5,000 Gy with no lethality. *Deinococcus* is a desert dweller, and this characteristic reflects its adaptation to the effects of desiccation. In dry conditions, the bacterium cannot grow and its cellular metabolism shuts down. Spontaneous damage to the cellular DNA accumulates, including strand breaks. DNA repair processes, which require ATP generated by cellular metabolism, do not take place. However, the bacterium can repair its genome quickly when conditions favorable for growth return. Like desiccation, IR also generates numerous DNA strand breaks, and that same extraordinary capacity for DNA repair is put to use after exposure to IR.

How long does it take for a bacterium to evolve extreme resistance to IR? A recent study demonstrated that *Escherichia coli*, the common laboratory bacterium, can acquire this resistance by directed evolution. Twenty cycles of exposure to enough IR to kill more than 99% of the cells, with each cycle followed by the outgrowth of survivors, produced an *E. coli* population with a radiation resistance approaching that of *Deinococcus*. The entire selection process can be achieved in less than a month. Complete genomic sequencing of cells isolated from the evolved populations typically reveals 40 to 80 mutations. The answer to survival varies from cell to cell, with different cells displaying different arrays of mutations, even when they come from the same evolved population. In just a single, small bacterial culture, evolution can take many paths, and a variety of solutions are found that lead to acquisition of a new trait.

This is just one of many experiments demonstrating that dramatic changes in microorganisms can be readily generated and observed in the laboratory within short periods of time. The same kind of evolutionary processes are occurring constantly in microorganisms in our environment, including human pathogens. When AIDS appeared as a new threat to human health in the early 1980s, the power of evolutionary theory was quickly on display. The causative agent, HIV, was soon isolated and its genomic sequence determined.

provides essential tools for use in tracking pandemics, investigating new microbial pathogens, identifying the genes underlying human genetic diseases, solving crimes, tracing the origin of diseases, treating cancer, and engineering microorganisms for new purposes in bioremediation and bioenergy. All of these efforts rely heavily on the concepts of evolutionary biology. Indeed, modern society relies on countless innovations in medicine and agriculture that would not exist but for Darwin's great insight.

Characterizing this novel and very dangerous virus from scratch would have delayed treatments for years. But scientists had a shortcut at hand. A deep reservoir of information about viruses and their evolutionary relationships had already been built up over decades of research. The small HIV genome thus held all the clues that science needed for a rapid understanding of its infection cycle and the development of a medical response. Its genome revealed that HIV is a type of RNA virus called a retrovirus, with clear evolutionary relationships to other viruses that were already known and understood (Figure 1). It was immediately evident which HIV genes encode the enzymes essential to the virus life cycle, and these enzymes rapidly became drug targets. One result was the development of highly effective treatments at an unprecedented rate, ranging from AZT to protease inhibitors (see Highlights 5-2 and 14-3 for more detailed descriptions of the retrovirus life cycle). Millions of lives have been saved, in large measure because all biological and medical research is carried out in the context of evolutionary theory.

FIGURE 1 HIV is a retrovirus. Like other retroviruses, it has an RNA genome condensed within a proteinaceous capsid. The capsid is surrounded by a spherical lipid envelope derived from its host cell's cytoplasmic (plasma) membrane. Its relationship to other retroviruses is not just structural but embedded in definable ways in its chromosome. *[Source: Hans [Gelderblom / Getty Images.\]](#page-8-0)*

Life on Earth Probably Began with RNA

About 4.6 billion years ago, the sun and Earth and the other planets and asteroids of our solar system were formed. Within the first billion years of our planet's existence, life appeared on its surface. How did this happen, and how likely is it that this has happened on other, similar worlds? Modern geologists, paleontologists, and molecular biologists are slowly piecing together the history of life on Earth from the rich trove of clues in the

>3.5 billion years ago

FIGURE 1-5 Prebiotic chemistry. Over hundreds of millions of years, and with constant energy input from solar radiation, volcanism, and other sources, the molecular constituents of Earth's early atmosphere were converted from simple molecules such as water, methane, ammonia, hydrogen, nitrogen, and carbon dioxide into a range of more complex organic molecules and polymers. The resulting tarry substance may have coated the planet's surface and turned bodies of water into concentrated and complex solutions.

geologic, fossil, and genomic records. A plausible sequence emerges, providing a wide range of hypotheses that can be tested using modern chemical and physical methods.

The first few hundred million years were a time of prebiotic chemistry (**Figure 1-5**). No life was present, but chemical reactions were happening everywhere. The atmosphere contained primarily water, methane, ammonia, hydrogen, nitrogen, and carbon dioxide. Reactions driven by the constant stream of energy coming from the sun were slowly yielding more complex molecules such as simple sugars, amino acids, and nucleotide bases. And the accumulation of organic material was supplemented by materials from a multitude of collisions between early Earth and meteors laden with organic matter. Prebiotic chemistry is being studied by a large community of researchers. A small sampling of their work is presented in the How We Know section at the end of this chapter.

Over a period of millions of years, the accumulation of reaction products yielded a soup containing molecules and polymers. As they grew increasingly complex, particular polymers acquired the capacity to duplicate themselves. The first self-replicating polymer, possessing two of the key requirements for life—catalysis and biological information—might be considered the first life form.

We do not know what this first "living" polymer was. However, modern molecular biology has given us many reasons to think that RNA either was the first self-replicator or arose as a much-improved descendant of that first self-replicator. RNA differs from DNA only in that it uses ribose instead of deoxyribose in its backbone. That single additional hydroxyl group in each monomeric unit of the polymer allows RNA to take up a plethora of complex structures that are inaccessible to DNA. The structural malleability of RNA gives it a capacity for both catalysis and information storage that has made it indispensable for life, from its beginnings to the present time.

The **RNA world hypothesis** was first proposed as a stage in evolution by molecular biologists Carl Woese, Francis Crick, and Leslie Orgel, in separate papers published in the late 1960s. The hypothesis describes a living system (or set of living systems) based on RNA. In this system, a variety of RNA enzymes could catalyze all of the reactions needed to synthesize the molecules required for life from simpler molecules available in the environment. The RNA enzymes would include replicators to duplicate all of the RNA catalysts. The "RNA organism," out of equilibrium with its surroundings, would have to be defined by a boundary. The experiments of Szostak and colleagues show one way in which lipid-enclosed RNA systems can arise (see the How We Know section at the end of this chapter).

Four more-recent lines of evidence have added much breadth and depth to the RNA world proposal. The first was the discovery by Thomas Cech and Sidney Altman, in the early 1980s, of **catalytic RNAs**, or **ribozymes** enzymes that are made of RNA instead of protein. Thus we learned that some extant RNA molecules catalyze reactions and so possess both of the key conditions for life—biological information and catalysis. In modern organisms, ribozymes catalyze a relatively narrow range of reactions, such as the cleavage and ligation of other RNA molecules—a range insufficient to support an RNA world.

What is the real catalytic potential of RNA? The second line of supportive research demonstrated that RNA molecules generated in the laboratory can catalyze almost any imaginable reaction needed in a living system certainly a range of reactions much broader than those attributable to ribozymes existing today. Early RNA molecules could clearly have catalyzed all of the reactions required to set up a primordial cellular metabolism.

The third and fourth discoveries have further broadened our perspectives on RNA function. We now know that in ribosomes, the large ribonucleoprotein complexes that translate RNA into protein, the RNA is the active component with the capacity to catalyze protein synthesis (**Figure 1-6**; see also the Moment of Discovery for Chapter 18). Finally, and most recently, RNA sequences capable of simple forms of self -replication have been discovered (discussed in Chapter 16).

Ongoing research thus makes it possible to visualize a highly plausible sequence of events unfolding on the pathway from prebiotic soup to living systems. Arising from a myriad random primordial polymers, an RNA world came into being and gradually became more complex. An RNA capable of reliable self-replication may have been the first living entity. Self-replicators would have diversified to synthesize other ribozymes, leading to an RNA-based metabolism capable of providing a greater supply of needed RNA

FIGURE 1-6 The 50S subunit of a bacterial ribosome. The gray parts of the subunit are RNA and the blue parts are protein. The structure is a huge ribozyme that evolved for the synthesis of protein. *[Source: PDB ID 1VSA.]*

precursors. Ribozyme groupings became enclosed within lipid membranes. Particular groupings were successful, resulting in the first cells and a capacity to maintain a metabolic state out of equilibrium with the surroundings. As the RNA molecules in those cells increased in size and structural complexity, a need for stabilization and auxiliary functions arose. Peptides (proteins) were synthesized to neutralize the negative charges of the phosphates in the RNA backbone, to stabilize RNA structure in other ways, and to augment early metabolism. As more peptides were synthesized, some with catalytic activities arose. Proteins gradually supplanted RNA as catalysts, because the greater catalytic potential of proteins yielded an advantage. The protein world emerged, but not without retaining [important vestiges of the RNA world \(ribosom](#page-8-0)es and some other RNA catalysts), as we find them today.

The Last Universal Common Ancestor Is the Root of the Tree of Life

Countless nascent life forms probably arose from the primordial soup, along with many biological advances that improved their fitness. Successful combinations of RNA catalysts gave way to systems based on protein catalysts. Improvements in catalytic efficiency appeared, along with systematized genetic codes to link genetic information in RNA and DNA to protein sequences. Additional changes facilitated cellular metabolism and reproduction. Protein synthesis was systematized through the evolution of an efficient ribosome machine. RNA became more specialized for information storage and transmission. Cell membranes became more structured and specialized, eventually including mechanisms to selectively transport materials into and out of the cell as needed. And some processes became regulated. In this way, a variety of primitive cells may have evolved—each of them a viable living system. Organisms living today exhibit shared properties, telling us that one of these early experimental cells won out over the others. This cell, sometimes called **LUCA (last universal common ancestor)** (**Figure 1-7**), ultimately gave rise to all life now present on Earth.

LUCA is a special source of fascination for molecular biologists. Although LUCA probably lived more than 3 billion years ago, our speculation about what this cell was like is informed by experiment. One approach is to determine the minimum protein and genetic requirements for life. Attempts to create a minimal life form, either by reconstituting basic components or by taking bacteria and stripping them of all unnecessary parts, are underway in laboratories around the world. These experiments are not only defining properties that must have been present in LUCA; they are also setting the stage for the laboratory generation of engineered bacterial cells that can be used to manufacture chemicals for bioenergy, agriculture, and medicine.

Simple metabolism RNA genetic material Primitive ribosome and protein biosynthetic apparatus Transcriptional machinery Genetic code

FIGURE 1-7 The last universal common ancestor. LUCA and its immediate descendants probably had a simple metabolism and a form of transcriptional machinery to replicate their RNA genome. A primitive ribosome and protein-biosynthetic apparatus would have used the same universal genetic code found in all modern organisms.

Another approach to understanding LUCA is to survey all types of living systems on Earth to determine which genes or characteristics are universal. The only genes that are truly universal in living systems are those encoding the cellular machinery for protein synthesis and some components of RNA transcription. All organisms also share (with very minor modifications discussed in Chapter 17) the same genetic code. That same code must have been present in LUCA. To support protein synthesis and RNA synthesis, a simple metabolism must have been present that allowed the uptake of chemical energy and its use to synthesize amino acids, nucleotides, and whatever lipids existed in the cell membrane

from precursors available in the environment. The study of LUCA is described in more detail in Chapter 8.

The appearance of LUCA signaled the beginning of biological evolution on Earth. New types of cells gradually appeared, and new environments were exploited. The first cells were capable of taking up organic molecules from their surroundings and converting them to the molecules needed to support protein and RNA synthesis. Cellular complexity resulted in ever-increasing requirements for cellular genomic information. DNA, with a more uniform structure and some stability advantages relative to RNA, may first have appeared in viruses. It then gradually supplanted RNA as the most stable platform for the longterm storage and transmission of genetic information, and DNA replication and systems for the segregation of replicated DNA chromosomes into daughter cells evolved.

The early single-celled organisms derived from LUCA diversified to inhabit all niches in the ecosystem of this early Earth. The diversification eventually generated the three major groups of organisms that we recognize today: **bacteria**, **archaea**, and **eukaryotes** (**Figure 1-8**).

Many additional events helped shape the life we see around us. Notably, photosynthesis appeared about 2.5 billion years ago, as evidenced by the sudden rise in the concentration of atmospheric oxygen documented in the geologic record. As cells engulfed other cells, some endosymbiotic relationships developed and became permanent. The engulfed cells became organelles within their hosts more than 1 billion years ago, and we see these organelles today as chloroplasts and mitochondria. Loose

FIGURE 1-8 The universal tree of life. A current version of the tree is shown here, with branches for the three main groups of known organisms: bacteria, archaea, and eukaryotes. Particular types of bacteria, engulfed by other cells, gave rise to mitochondria and chloroplasts. *[Source: Data from J. R. Brown, "Universal tree of life," in* Encyclopedia of Life Sciences*, Wiley InterScience (online), 2005.]*