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基因XI

LEWIN'S GENES XI

JOCELYN E. KREBS
ELLIOTT S. GOLDSTEIN
STEPHEN T. KILPATRICK

高等教育出版社

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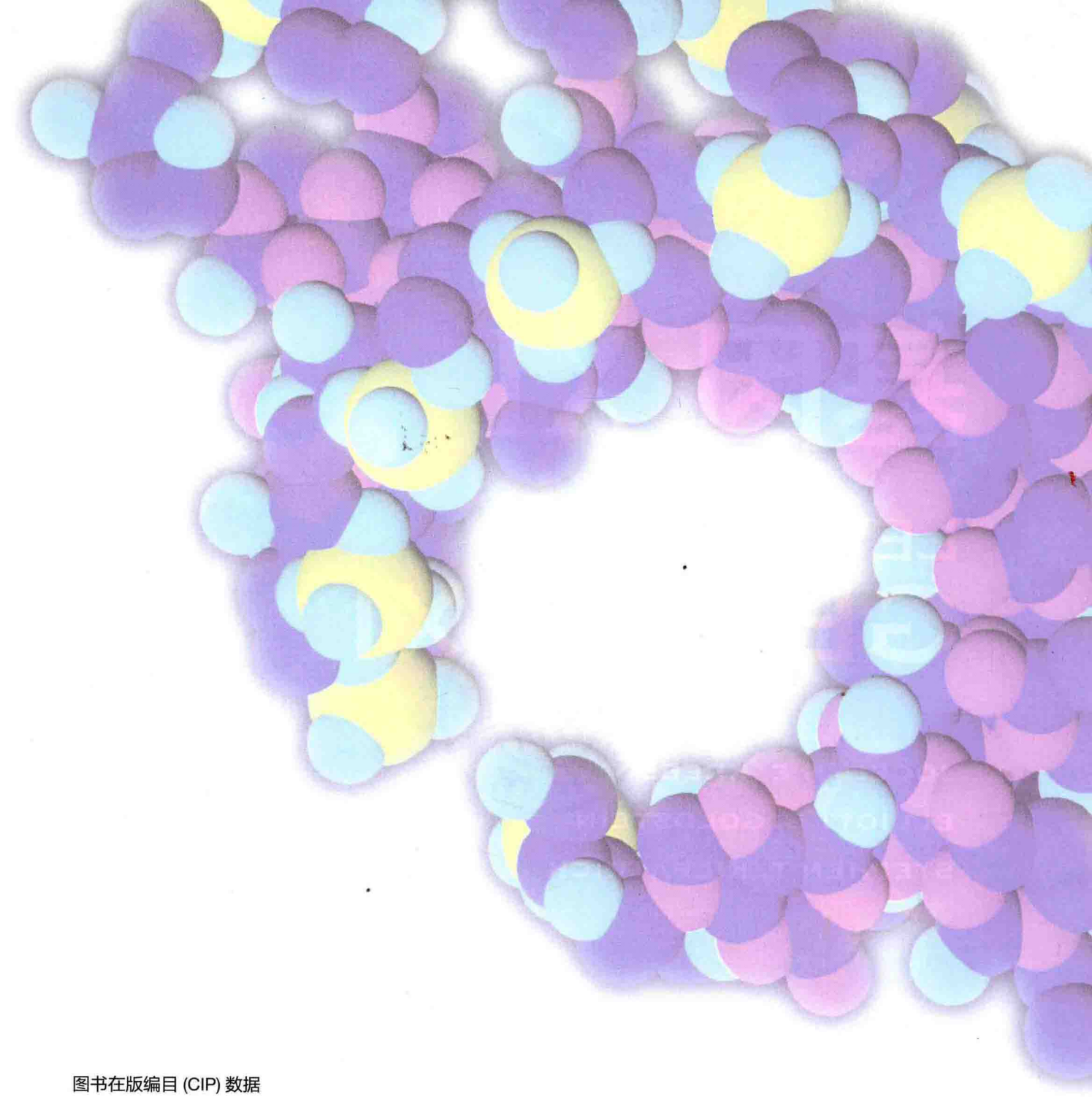

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LEWIN'S GENES XI

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Dedication

To Benjamin Lewin, for setting the bar high.

To my mother, Ellen Baker, for raising me with a love of science; to the memory of my stepfather, Barry Kiefer, for convincing me science would stay fun; to my partner, Susannah Morgan, for always pretending my biology jokes are funny; and to my sons, Rhys and Frey, who have each gestated during the writing of two editions of this book. Finally, I would like to dedicate this edition to the memory of my PhD mentor, Dr. Marietta Dunaway, a great inspiration who set my feet on the exciting path of chromatin biology.

Jocelyn Krebs

To my family: my wife, Suzanne, whose patience, understanding, and confidence in me are amazing; my children, Andy, Hyla, and Gary, who have taught me so much about using the computer; and my grandchildren, Seth and Elena, whose smiles and giggles inspire me. And to the memory of my mentor and dear friend, Lee A. Snyder, whose professionalism, guidance, and insight demonstrated the skills necessary to be a scientist and teacher. I have tried to live up to his expectations. This is for you, Doc.

Elliott Goldstein

To my wife, Lori, for our many years of love, support, and sometimes tolerance; to my daughter, Jennifer, who will actually read this book; to my son, Andrew, who continually renews my faith in humanity; and to my daughter, Sarah, who brings me joy daily.

Stephen Kilpatrick

Preface

Of the diverse ways to study the living world, molecular biology has been most remarkable in the speed and breadth of its expansion. New data are acquired daily, and new insights into well-studied processes come on a scale measured in weeks or months rather than years. It's difficult to believe that the first complete organismal genome sequence was obtained less than 20 years ago. The structure and function of genes and genomes and their associated cellular processes are sometimes elegantly and deceptively simple but frequently amazingly complex, and no single book can do justice to the realities and diversities of natural genetic systems.

This book is aimed at advanced students in molecular genetics and molecular biology. In order to provide the most current understanding of the rapidly changing subjects in molecular biology, we have enlisted 21 scientists to provide revisions and content updates in their individual fields of expertise. Their expert knowledge has been incorporated throughout the text. Much of the revision and reorganization of this edition follows that of the third edition of *Lewin's Essential GENES*, but there are many updates and features that are new to this book. This edition follows a logical flow of topics; in particular, discussion of chromatin organization and nucleosome structure precedes the discussion of eukaryotic transcription, because chromosome organization is critical to all DNA transactions in the cell, and current research in the field of transcriptional regulation is heavily biased toward the study of the role of chromatin in this process. Many new figures are included in this book, some reflecting new developments in the field, particularly in the topics of chromatin structure and function, epigenetics, and regulation by noncoding and microRNAs in eukaryotes.

This book is organized into four parts. **Part 1 (Genes and Chromosomes)** comprises Chapters 1 through 10. Chapters 1 and 2 serve as an introduction to the structure and function of DNA and contain basic coverage of DNA replication and gene expression. Chapter 3 provides information on molecular laboratory techniques. Chapter 4 introduces the interrupted structures of eukaryotic genes, and Chapters 5 through 8 discuss genome structure and evolution. Chapters 9 and 10 discuss the structure of eukaryotic chromosomes.

Part 2 (DNA Replication and Recombination) comprises Chapters 11 through 18. Chapters 11 to 14 provide detailed discussions of DNA replication in plasmids, viruses, and prokaryotic and eukaryotic cells. Chapters 15 through 18 cover recombination and its roles in DNA repair and the human immune system, with Chapter 16 discussing DNA repair pathways in detail and Chapter 17 focusing on different types of transposable elements.

Part 3 (Transcription and Posttranscriptional Mechanisms) includes Chapters 19 through 25. Chapters 19 and 20 provide more in-depth coverage of bacterial and eukaryotic transcription. Chapters 21 through 23 are concerned with RNA, discussing messenger RNA, RNA stability and localization, RNA processing, and the catalytic roles of RNA. Chapters 24 and 25 discuss translation and the genetic code.

Part 4 (Gene Regulation) comprises Chapters 26 through 30. In Chapter 26, the regulation of bacterial gene expression via operons is discussed. Chapter 27 covers the regulation of expression of genes during phage development as they infect bacterial cells. Chapters 28 and 29 cover eukaryotic gene regulation, including epigenetic modifications. Finally, Chapter 30 covers RNA-based control of gene expression in prokaryotes and eukaryotes.

For instructors who prefer to order topics with the essentials of DNA replication and gene expression followed by more advanced topics, the following chapter sequence is suggested:

Introduction: Chapters 1–2
Gene and Genome Structure: Chapters 5–7
DNA Replication: Chapters 11–14
Transcription: Chapters 19–22
Translation: Chapters 24–25
Regulation of Gene Expression: Chapters 9–10 and 26–30

Other chapters can be covered at the instructor's discretion.

Pedagogical Features

This edition contains several features to help students learn as they read. Each chapter begins with a *Chapter Outline*, and each section is summarized with a bulleted list of *Key Concepts*. *Key Terms* are highlighted in bold type in the text and compiled in the *Glossary* at the end of the book. Finally, each chapter concludes with an expanded and updated list of *References*, which provides both primary literature and current reviews to supplement and reinforce the chapter content. Additional instructional tools are available online and on the Instructor's Media CD.

Ancillaries

Jones & Bartlett Learning offers an impressive array of traditional and interactive multimedia supplements to assist instructors and aid students in mastering molecular biology. Additional information and review copies of any of the following items are available through your Jones & Bartlett sales representative or by visiting http://www.jblearning.com/science/molecular/.

For the Student

Interactive Student Study Guide

Jones & Bartlett Learning has developed an interactive, electronic study guide dedicated exclusively to this title. Students will find a variety of study aids and resources at http://biology.jbpub.com/lewin/genesxi/, all designed to explore the concepts of molecular biology in more depth and to help students master the material in the book. A variety of activities are available to help students review class material, such as chapter summaries, Web-based learning exercises, study quizzes, a searchable glossary, and links to animations, videos, and podcasts, all to help students master important terms and concepts.

For Instructors

Instructor's Media CD

The *Instructor's Media CD* provides the instructor with the following resources:

- The **PowerPoint® Image Bank** provides all of the illustrations, photographs, and tables (to which Jones & Bartlett Learning holds the copyright or has permission to reprint digitally) inserted into PowerPoint slides. With the Microsoft® PowerPoint program, you can quickly and easily copy individual image slides into your existing lecture slides.
- The **PowerPoint Lecture Outline** presentation package developed by author Stephen Kilpatrick, of the University of Pittsburgh at Johnstown, provides outline summaries and relevant images for each chapter of *Lewin's GENES XI*. A PowerPoint viewer is provided on the CD, and instructors with the Microsoft PowerPoint software can customize the outlines, figures, and order of presentation.

Online Instructor Resources

The **Test Bank**, updated and expanded by author Stephen Kilpatrick, is provided as a text file with 750 questions in a variety of formats. The Test Bank is easily compatible with most course management software.

Acknowledgments

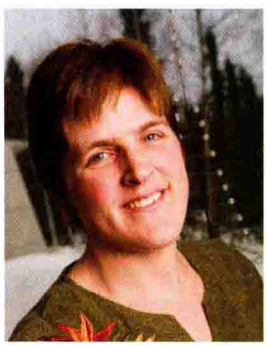
The authors would like to thank the following individuals for their assistance in the preparation of this book: The editorial, production, marketing, and sales teams at Jones & Bartlett have been exemplary in all aspects of this project. Cathy Sether, Erin O'Connor, Rachel Isaacs, Lauren Miller, Leah Corrigan, and Wendy Swanson deserve special mention. Cathy brought us together on this project and in doing so launched an efficient and amiable partnership. She has provided able leadership and has been an excellent resource as we ventured into new territories. Rachel, Wendy, and Leah have handled the daily responsibilities of the writing and production phases with friendly professionalism and helpful guidance. Lauren has made the process of choosing and revising figures very smooth.

We thank the editors of individual chapters, whose expertise, enthusiasm, and careful judgment brought the manuscript up to date in many critical areas.

Jocelyn E. Krebs
Elliott S. Goldstein
Stephen T. Kilpatrick

About the Authors

Benjamin Lewin founded the journal *Cell* in 1974 and was Editor until 1999. He founded the Cell Press journals *Neuron*, *Immunity*, and *Molecular Cell*. In 2000, he founded Virtual Text, which was acquired by Jones and Bartlett Publishers in 2005. He is also the author of *Essential GENES* and *CELLS*.



Jocelyn E. Krebs received a B.A. in Biology from Bard College, Annandale-on-Hudson, NY, and a Ph.D. in Molecular and Cell Biology from the University of California, Berkeley. For her Ph.D. thesis, she studied the roles of DNA topology and insulator elements in transcriptional regulation.

She performed her postdoctoral training as an American Cancer Society Fellow at the University of Massachusetts Medical School in the laboratory of Dr. Craig Peterson, where she focused on the roles of histone acetylation and chromatin remodeling in transcription. In 2000, Dr. Krebs joined the faculty in the Department of Biological Sciences at the University of Alaska, Anchorage, where she is now an Associate Professor. She directs a research group studying chromatin structure and function in transcription and DNA repair in the yeast *Saccharomyces cerevisiae* and the role of chromatin remodeling in embryonic development in the frog *Xenopus*. She teaches courses in molecular biology for undergraduates, graduate students, and first-year medical students. She also teaches a Molecular Biology of Cancer course and has taught Genetics and Introductory Biology. She lives in Eagle River, AK, with her partner and son, and a house full of dogs and cats. Her non-work passions include hiking, camping, and snowshoeing.

Elliott S. Goldstein earned his B.S. in Biology from the University of Hartford (Connecticut) and his Ph.D. in Genetics from the University of Minnesota, Department of Genetics and Cell Biology. Following this, he was awarded an N.I.H. Postdoctoral Fellowship to work with Dr. Sheldon Penman at the Massachusetts Institute of Technology. After leaving Boston, he joined the faculty at Arizona State University in Tempe, AZ, where he is an Associate Professor in the Cellular, Molecular, and Biosciences program in the School of Life Sciences and in the Honors Disciplinary Program. His research interests are in the area of molecular and developmental genetics of early embryogenesis in *Drosophila melanogaster*. In recent years, he has focused on the *Drosophila* counterparts of the human proto-oncogenes *jun* and *fos*. His primary teaching responsibilities are in the undergraduate General Genetics course as well as the graduate level Molecular Genetics course. Dr. Goldstein lives in Tempe with his wife, his high school sweetheart. They have three children and two grandchildren. He is a bookworm who loves reading as well as underwater photography. His pictures can be found at http://www.public.asu.edu/~elliotg/.

Stephen T. Kilpatrick received a B.S. in Biology from Eastern College (now Eastern University) in St. Davids, PA, and a Ph.D. from the Program in Ecology and Evolutionary Biology at Brown University. His thesis research was an investigation of the population genetics

of interactions between the mitochondrial and nuclear genomes of *Drosophila melanogaster*. Since 1995, Dr. Kilpatrick has taught at the University of Pittsburgh at Johnstown in Johnstown, PA. His regular teaching duties include undergraduate courses in nonmajors biology, introductory majors biology, and advanced undergraduate courses in genetics, evolution, molecular genetics, and biostatistics. He has also supervised a number of undergraduate research projects in evolutionary genetics. Dr. Kilpatrick's major professional focus has been in biology education. He has participated in the development and authoring of ancillary materials for several introductory biology, genetics, and molecular genetics texts as well as writing articles for educational reference publications. For his classes at Pitt-Johnstown, Dr. Kilpatrick has developed many active learning exercises in introductory biology, genetics, and evolution. Dr. Kilpatrick resides in Johnstown, PA, with his wife and three children. Outside of scientific interests, he enjoys music, literature, and theater and occasionally performs in local community theater groups.

Chapter Editors

Esther Siegfried completed her work on this book while teaching at the University of Pittsburgh at Johnstown. She is now an Assistant Professor of Biology at Pennsylvania State University, Altoona. Her research interests include signal transduction pathways in *Drosophila* development.

John Brunstein is a Clinical Assistant Professor with the Department of Pathology and Laboratory Medicine at the University of British Columbia. His research interests focus on the development of, validation strategies for, and implementation of novel molecular diagnostic technologies.

Donald Forsdyke, emeritus professor of biochemistry at Queen's University in Canada, studied lymphocyte activation/inactivation and the associated genes. In the 1990s he obtained evidence supporting his 1981 hypothesis on the origin of introns, and immunologists in Australia shared a Nobel Prize for work that supported his 1975 hypothesis on the positive selection of the lymphocyte repertoire. His books include *The Origin of Species, Revisited* (2001), *Evolutionary Bioinformatics* (2006), and *"Treasure Your Exceptions": The Science and Life of William Bateson* (2008).

Hank W. Bass is an Associate Professor of Biological Science at Florida State University. His laboratory works on the structure and function of meiotic chromosomes and telomeres in maize using molecular cytology and genetics.

Stephen D. Bell is the Professor of Microbiology in the Sir William Dunn School of Pathology, Oxford University. His research group is studying gene transcription, DNA replication, and cell division in the Archaeal domain of life.

Søren Johannes Sørensen is a Professor in the Department of Biology and Head of the Section of Microbiology at the University of Copenhagen. The main objective of his studies is to evaluate the extent of genetic flow within natural communities and the responses to environmental perturbations. Molecular techniques such as DGGE and high-throughput sequencing are used to investigate resilience and resistance of microbial community structure. Dr Sørensen has more than twenty years' experience in teaching molecular microbiology at both the bachelor and graduate levels.

Lars Hestbjerg Hansen is an Associate Professor in the Section of Microbiology, Department of Biology, at the University of Copenhagen. His research interests include the bacterial maintenance and interchange of plasmid DNA, especially focused on plasmidborne mechanisms of bacterial resistance to antibiotics. Dr. Hansen's laboratory has developed and is currently working with new flow-cytometric methods for estimating plasmid transfer and stability. Dr. Hansen is the Science Director of Prokaryotic Genomics at Copenhagen High-Throughput Sequencing Facility, focusing on using high-throughput sequencing to describe bacterial and plasmid diversity in natural environments.

Barbara Funnell is a Professor of Molecular Genetics at the University of Toronto. Her laboratory studies chromosome dynamics in bacterial cells and, in particular, the mechanisms of action of proteins involved in plasmid and chromosome segregation.

Peter Burgers is Professor of Biochemistry and Molecular Biophysics at Washington University School of Medicine. His laboratory has a long-standing interest in the biochemistry and genetics of DNA replication in eukaryotic cells, and in the study of responses to DNA damage and replication stress that result in mutagenesis and in cell cycle checkpoints.

Hannah L. Klein is a Professor of Biochemistry, Medicine, and Pathology at New York University Langone Medical Center. She studies pathways of DNA damage repair and recombination and genome stability.

Samantha Hoot is a postdoctoral researcher in the laboratory of Dr. Hannah Klein at New York University Langone Medical Center. She received her Ph.D. from the University of Washington. Her interests include the role of recombination in genome stability in yeast and the molecular mechanisms of drug resistance in pathogenic fungi.

Damon Lisch is an Associate Research Professional at the University of California at Berkeley. He is interested in the regulation of transposable elements in plants and the ways in which transposon activity has shaped plant genome evolution. His laboratory investigates the complex behavior and epigenetic regulation of the *Mutator* system of transposons in maize and related species.

Paolo Casali, M.D., is the Donald L. Bren Professor of Medicine, Molecular Biology & Biochemistry, and Director of the Institute for Immunology at the University of California, Irvine. He works on B lymphocyte differentiation and regulation of antibody gene expression as well as molecular mechanisms of generation of autoantibodies. He has been Editor-in-Chief of *Autoimmunity* since 2002. He is a member of the American Association of Immunologists, an elected "Young Turk" of the American Society for Clinical Investigation, and an elected Fellow of the American Association for Advancement of Science. He has served on several NIH immunology study sections and scientific panels.

Richard Gourse is a Professor in the Department of Bacteriology at the University of Wisconsin, Madison, and an Editor of the *Journal of Bacteriology*. His primary interests lie in transcription initiation and the regulation of gene expression in bacteria. His laboratory has long focused on rRNA promoters and the control of ribosome synthesis as a means of uncovering fundamental mechanisms responsible for regulation of transcription and translation.

Xiang-Dong Fu is a Professor of Cellular and Molecular Medicine at the University of California, San Diego. His laboratory studies mechanisms underlying constitutive and regulated pre-mRNA splicing in mammalian cells, coupling between transcription and RNA processing, RNA genomics, and roles of RNA processing in development and diseases.

Ellen Baker is an Associate Professor of Biology at the University of Nevada, Reno. Her research interests have focused on the role of polyadenylation in mRNA stability and translation.

Douglas J. Briant teaches at the University of Victoria in British Columbia. His research has investigated bacterial RNA processing and the role of ubiquitin in cell signalling pathways.

Cheryl Keller Capone is an Instructor in the Department of Biology at The Pennsylvania State University and teaches cell and molecular biology. Her research interests include embryonic muscle development in *Drosophila melanogaster* and the molecular mechanisms involved in the clustering and postsynaptic targeting of $GABA_A$ receptors.

John Perona is a Professor of Biochemistry in the Department of Chemistry and Biochemistry, and the Interdepartmental Program in Biomolecular Science and Engineering, at the University of California, Santa Barbara. His laboratory studies structuré-function relationships and catalytic mechanisms in aminoacyl-tRNA synthetases, tRNA-dependent amino acid modification enzymes, and tRNA-modifying enzymes.

Liskin Swint-Kruse is an Assistant Professor in Biochemistry and Molecular Biology at the University of Kansas School of Medicine. Her research utilizes bacterial transcription regulators in studies that bridge biophysics of DNA-binding and bioinformatics analyses of transcription repressor families to advance the principles of protein engineering.

Trygve Tollefsbol is a Professor of Biology at the University of Alabama at Birmingham and a Senior Scientist of the Center for Aging, Comprehensive Cancer Center, and Clinical Nutrition Research Center. He has long been involved with elucidating epigenetic mechanisms, especially as they pertain to cancer, aging, and differentiation. He has been the editor and primary contributor of numerous books including *Epigenetic Protocols*, *Cancer Epigenetics*, and *Epigenetics of Aging*.

Chapter Opener Credits and Captions

Part 1

Photo courtesy of S. V. Flores, A. Mena, and B. F. McAllister. Used with permission of Bryant McAllister, Department of Biology, University of Iowa.

Chapter 1

A strand of DNA in blue and red. DNA is the genetic material of eukaryotic cells, bacteria, and many viruses. © Artsilensecome/ShutterStock, Inc.

Chapter 2

A visual representation of gene expression analysis that allows researchers to see patterns in a network of expressed genes. Each dot represents a gene, and links between the dots occur where there are similar patterns of expression between the genes. © Anton Enright, The Sanger Institute/Wellcome Images.

Chapter 3

DNA fragments separated by gel electrophoresis. © Nicemonkey/Dreamstime.com.

Chapter 4

A self-splicing intron in an rRNA of the large ribosomal subunit. © Kenneth Eward/Photo Researchers, Inc.

Chapter 5

Scanning electron micrograph (SEM) of human X and Y chromosomes in metaphase (35,000×). Most of the content of the genome is found in chromosomal DNA, though some organelles contain their own genomes. © Biophoto Associates/Photo Researchers, Inc.

Chapter 6

Mouse and human chromosomes. Both species' genomes have undergone chromosomal rearrangements from the genome of their most recent common ancestor. The colors and corresponding numbers on the mouse chromosomes indicate the human chromosomes containing homologous segments. Photo courtesy of U.S. Department of Energy. Used with permission of Lisa J. Stubbs, University of Illinois at Urbana–Champaign.

Chapter 7

Scanning electron micrograph (SEM) of red blood cells. Genes that encode the protein subunits of hemoglobin, the oxygen-carrying complex found in red blood cells, are members of a large gene family that have evolved by duplication and divergence. © Sebastian Kaulitzki/ShutterStock. Inc.

Chapter 8

A circular genome map showing shared (syntenic) regions between humans (outer ring) and (from inner ring outward) chimpanzee, mouse, rat, dog, chicken, and zebrafish genomes. Similar colors among rings show synteny. © Martin Krzywinski/Photo Researchers, Inc.

Chapter 9

Microphotograph of living cells undergoing mitosis. Individual chromosomes lined up at the metaphase plate or separating are visible in several cells. © Dimarion/ShutterStock, Inc.

Chapter 10

A three-dimensional model of chromatin showing one possible arrangement for the nucleosomes in the 30-nm fiber. Photo courtesy of Thomas Bishop, Tulane University, using VDNA plug-in for VMD (http://www.ks.uiuc.edu/research/vmd/plugins/vdna/).

Part 2

Image courtesy of Teresa Larsen, The Foundation for Scientific Literacy.

Chapter 11

A transmission electron micrograph of an *E. coli* bacterium in the mid to late stages of binary fission, the process by which the bacterium divides. The hair-like appendages around the bacterium are pili, structures used for bacterial conjugation (magnification: 17,500×). © CNRI/Photo Researchers, Inc.

Chapter 12
Computer model of DNA polymerase replicating a strand of DNA (across center). The secondary structure of the DNA polymerase and the primary structure of the DNA molecule are shown. DNA polymerases are enzymes that synthesize strands of DNA from a complementary template strand during DNA replication. This molecule is in the Y family of DNA polymerases, which are translesion synthesis polymerases, that is, they are able to replicate damaged areas of DNA that stall other DNA polymerases. The replication is not always accurate and can lead to mutagenesis or cancer. © Laguna Design/Photo Researchers, Inc.

Chapter 13
A type II topoisomerase acting on a knotted or supercoiled DNA substrate. The cleaved DNA is shown in green. The DNA that is being passed through the break is viewed end-on. Photo courtesy of James Berger, University of California, Berkeley.

Chapter 14
Plasmids. © Deco Images II/Almay Images.

Chapter 15
A model demonstrating the interaction of a RuvA tetramer with a DNA Holliday junction, an intermediate of recombination. Reproduced with permission from J. B. Rafferty et al., *Science* 274 (1996): 415–421. © 1996 AAAS. Photo courtesy of David W. Rice and John B. Rafferty, University of Sheffield.

Chapter 16
The XPD helicase, involved in both transcription and nucleotide excision repair, is shown unwinding DNA. Colors indicate different domains of XPD; the helicase domain is green. Photo courtesy of M. Pique, Li Fan, Jill Fuss, and John Tainer, The Scripps Research Institute and Lawrence Berkeley National Laboratory. More information available at L. Fan et al., *Cell* 133 (2008): 789–800.

Chapter 17
Artist's rendering of an electron micrograph showing retroviruses. © MedicalRF/Photo Researchers, Inc.

Chapter 18
Human Ig autoantibody binding double-strand DNA. Rendered by UCSF Chimera, P. Casali & E.J. Pone, 2012.

Part 3
Photo courtesy of Jie Ren and Jun Ma, University of Cincinnati College of Medicine and Cincinnati Children's Hospital.

Chapter 19
Transcription factor and DNA molecules. Molecular model showing the secondary structure (helices) of the transcription factor Brachyury (purple) binding to a molecule of DNA (deoxyribonucleic acid, running horizontally from left to right). Brachyury, also known as T, is a protein that controls the transcription of DNA to RNA (ribonucleic acid) by the enzyme RNA polymerase. RNA is the intermediate product in the formation of a protein from its gene. Brachyury binds to a specific sequence of bases in the DNA called a T-box. Brachyury has been found to be crucial in embryonic development in animals. It is necessary to form the mesoderm, the precursor tissue that eventually develops into the internal organs and bones. © Phantatomix/Photo Researchers, Inc.

Chapter 20
Biomedical illustration of transcription showing RNA polymerase at work. A DNA sequence is copied by RNA polymerase to produce a complementary nucleotide RNA strand, called messenger RNA (mRNA). © Carol & Mike Werner/Visuals Unlimited.

Chapter 21
A three-dimensional structure of the mammalian spliceosomal C complex. Spliceosome structure courtesy of Nikolaus Grigorieff, Brandeis University. Background photo © Bella D/ShutterStock, Inc.

Chapter 22
Computer artwork of aconitase (blue), in complex with ferritin mRNA (red). Aconitase is involved in the citric acid cycle, but here it is performing a secondary function as an iron regulatory protein (IRP). It does this by binding to ferritin mRNA, which prevents translation into the protein product (ferritin). Ferritin acts like a sponge and helps to protect cells from the toxic effects of excess iron. © Equinox Graphics/Photo Researchers, Inc.

Chapter 23
The figure shows the RNA/protein architecture of the large ribosomal subunit with the active site highlighted. The background shows a schematic diagram of the peptidyl transferase active site of the ribosome. Photo courtesy of Nenad Ban, Institute for Molecular Biology & Biophysics, Zurich.

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An aminoacyl-tRNA synthetase is shown complexed to a tRNA. Reproduced from M. Blaise et al., Nucleic Acids Res. 32, (2004): 2768–2775. Used with permission of Oxford University Press. Photo courtesy of Pr. Daniel Kern, Université Louis Pasteur, Institut de Biologie Moléculaire et Cellulaire, UPR 9002 du SNRS, Strasbourg.

Part 4

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Chapter 26
A visualization showing the structure of the lac repressor protein as it binds with DNA. Figure created by Elizabeth Villa using VMD and under copyright of the Theoretical and Computational Biophysics Group, NIH Resource for Macromolecular Modeling and Bioinformatics, at the Beckman Institute, University of Illinois at Urbana–Champaign. The work was partially supported by the National Center for Supercomputing Applications under National Institutes of Health Grant PHS5P41RR05969-04 and National Science Foundation Grant MCB-9982629. Computer time was provided by National Resource Allocations Committee Grant MCA93S028.

Chapter 27
A transmission electron micrograph of a T4 phage (magnification: 450,000,000×). © Dr. Harold Fisher/Visuals Unlimited.

Chapter 28
A model of the ATP-dependent chromatin-remodeling complex RSC bound to a nucleosome. Photo courtesy of Andres Leschziner, Harvard University.

Chapter 29
Structural model for the cohesin complex consisting of Smc1 (red), Smc3 (blue), and Scc1 (green) proteins encircling two sister chromatids, and DNA (gold) wrapped around nucleosomes (gray). Photo courtesy of Christian Haering, European Molecular Biology Laboratory—Germany. Used with permission of Kim Nasmyth, University of Oxford—United Kingdom.

Chapter 30
A hammerhead ribozyme that catalyzes a self-cleaving reaction. Many plant viroids are hammerhead RNAs. Reproduced from M. Martick et al., Solvent Structure and Hammerhead Ribozyme Catalysis. Chem. Bio. 15, pp. 332-342. Copyright 2008, with permission from Elsevier (http://www.sciencedirect.com/science/journal/10745521). Photo courtesy of William Scott, University of California, Santa Cruz.

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