SECOND EDITION

# DNA Repair and Mutagenesis

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*Cover and interior design:* Susan Brown Schmidler
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*Cover illustration:* The MutS protein (red and white ribbon) is a sensor of mismatched base pairs in DNA (gold), coupling ATP turnover with mismatch recognition (1, 2). The disk-shaped MutS dimer encircles the bound DNA and stabilizes a sharp kink in the double helix. ATP binds to the dimer interface (bottom of figure) opposite the DNA and allosterically regulates DNA-binding affinity.

**1. Lammers, M. H., A. Perrakis, J. Enzlin, H. H. K. Winterwerp, N. de Wind, and T. K. Sixma.** 2000. The crystal structure of DNA mismatch repair protein MutS binding to a GT mismatch. *Nature* **407:**711–717.

**2. Obmolova, G., C. Ban, P. Hsieh, and W. Yang.** 2000. Crystal structures of mismatch repair protein MutS and its complex with a substrate DNA. *Nature* **407:**703–710.

*For Rhonda, Jan, Jenny, Enid, Lisa, and Mary*

# *About the Authors*

(*Left to right*) Tom Ellenberger, Rick Wood, Roger Schultz, Errol Friedberg, Wolfram Siede, Graham Walker

**Errol C. Friedberg, MD,** received his training as a medical student at the University of the Witwatersrand, Johannesburg, South Africa, and did postdoctoral training in pathology and in biochemistry at Case Western Reserve University, Cleveland, Ohio. Following 19 years on the faculty at Stanford University, he assumed his present position as the Senator Betty and Dr. Andy Andujar Distinguished Chair in Pathology at the University of Texas Southwestern Medical Center at Dallas in 1990. He is the author of *DNA Repair* and is the senior author of the first edition of *DNA Repair and Mutagenesis*. He also authored *Cancer Answers—Encouraging Answers to 21 Questions You Were Always Afraid To Ask*, *Correcting the Blueprint of Life—an Historical Account of the Discovery of DNA Repair Mechanisms*, and *The Writing Life of James D. Watson*, and he edited and annotated the work *Sydney Brenner—My Life in Science*. He is the recipient of the Rous-Whipple Award from the American Society of Investigative Pathology and is a Fellow of the American Academy of Microbiology. He has contributed over 300 papers to the scientific literature, mainly on biological responses to DNA damage.

**Graham C. Walker, PhD,** is a Professor in the Department of Biology at the Massachusetts Institute of Technology. He has worked in the area of DNA repair and mutagenesis for 30 years and also carries out research on the *Rhizobium*-legume symbiosis and its relationship to chronic *Brucella* pathogenesis. He has been named an American Cancer Society Research Professor for his contributions to basic research and an HHMI Professor for his contributions to undergraduate education. He has been elected to the American Academy of Arts and Sciences and to the American Academy of Microbiology. He served as the Editor in Chief of *Journal of Bacteriology* for 10 years and is a member of various editorial boards. Long active in undergraduate education, he was in charge of the undergraduate program in biology at MIT for 15 years, served as Housemaster of an MIT dormitory, was named a Margaret MacVicar Faculty Fellow for his undergraduate teaching, and has founded an HHMI Education Group. He has contributed over 250 papers to the scientific literature and is a coauthor of the first edition of *DNA Repair and Mutagenesis*.

**Wolfram Siede, PhD,** received his doctorate in microbiology from the University of Frankfurt, Frankfurt, Germany. He did his postdoctoral training in the Departments of Pathology at Stanford University and the University of Texas Southwestern Medical Center. In 1996, he became Assistant Professor in a joint appointment by the Department of Radiation Oncology and the Winship Cancer Institute at Emory University, Atlanta, Ga. He is currently Associate Professor and Graduate Advisor in the Department of Cell Biology and Genetics at the University of North Texas Health Science Center in Fort Worth. His research focus is on DNA repair, mutagenesis, and cell cycle regulation in yeast. He has published extensively on many aspects of eukaryotic DNA damage responses and is a coauthor of the first edition of *DNA Repair and Mutagenesis*.

**Richard D. Wood, PhD,** performed his graduate study in biophysics at the University of California, Berkeley, and obtained his PhD in 1981. This was followed by postdoctoral work at Yale University and at the Imperial Cancer Research Fund (ICRF) in the United Kingdom. After leading a research group at the Clare Hall Laboratories of the ICRF until 2001, he was appointed the Richard Cyert Professor of Molecular Oncology at the University of Pittsburgh. His research has focused on the molecular biology and biochemistry of DNA repair and mutagenesis. He is a recipient of the Meyenburg Prize for Cancer Research, an elected member of the European Molecular Biology Organization (EMBO), and a Fellow of the Royal Society.

**Roger A. Schultz, PhD,** performed his graduate training in an interdepartmental program in genetics at Michigan State University in East Lansing in 1980. Following postdoctoral work in the Department of Pathology at Stanford University, he assumed a faculty position at the University of Maryland at Baltimore in the Division of Human Genetics in the School of Medicine. He moved to the McDermott Center for Human Growth and Development and the Department of Pathology at the University of Texas Southwestern Medical Center at Dallas in 1993. He has focused his research interests on human diseases with relevance to genomic instability. He served as Director of the Chromosome 15 DNA Sequencing Project within the Genome Sciences and Technology Center at UT Southwestern, again with a focus on human genomic integrity. More recently, he has added a more clinical focus to his activities as Associate Director of the Veripath Clinical Cytogenetic Laboratory at UT Southwestern.

**Tom Ellenberger, DVM PhD,** was trained as a veterinarian at Iowa State University before pursuing graduate studies in molecular biology and pharmacology at Harvard Medical School. Following postdoctoral studies in structural biology at Harvard College, he joined the faculty of Harvard Medical School in 1993, where he is the Hsien Wu and Daisy Yen Wu Professor of Biological Chemistry and Molecular Pharmacology. His research interests are focused on the structural enzymology of DNA repair, replication, and recombination processes.

# Contents

# Preface

It has been a decade since the publication of the first edition of *DNA Repair and Mutagenesis*. It was noted in the preface then that "[I]n very recent times, progress in the DNA repair and mutagenesis fields has been particularly rapid. . . ." In fact, in recognition of the importance of mutagenesis as a fundamental aspect of DNA metabolism and the impressive gains made in our understanding of the intricate relationships between DNA repair and mutagenesis, the authors of the first edition elaborated the title *DNA Repair* used for the book published by W. H. Freeman in 1984.

The unabated progress of the DNA damage response field is reflected in further major changes in the present edition. The field has progressed to the point that a comprehensive treatment of the manifold responses to DNA damage (including sensing and signaling the presence of damage and other perturbations of DNA metabolism) now requires the efforts of an author group with expertise in multiple and diverse areas. Richard D. (Rick) Wood and Roger A. Schultz were invited to provide such expertise to bolster the team that wrote the first edition. Additionally, the inclusion of structural biologist Tom Ellenberger reflects our desire to incorporate the considerable recent contributions of protein structure to biology in general and the DNA repair field in particular. The six authors have labored to achieve a text that is seamlessly integrated.

The second edition of *DNA Repair and Mutagenesis* was initiated in late 1999. Our efforts to keep the final product manageable for the average reader notwithstanding, the size of the present work appropriately reflects the substantial growth of the field in the past decade. This edition is more a rewriting than a revision, and little of the text from the first edition remains. The first edition of *DNA Repair and Mutagenesis* comprised 14 chapters and contained about 400 illustrations. The present edition consists of 30 chapters divided into five major sections, and the text is adorned with more than 700 illustrations, including more than 80 structural representations. Additionally, more than ten thousand primary literature references are provided in full, reflecting the massive increase in the scientific literature through 2004.

We have strived to present readers with a comprehensive survey of the field, stressing basic principles wherever feasible but mainly describing the extensive progress achieved to date and highlighting the many problems remaining to be solved. We trust that our desire to represent the dynamic state of this active field of research will not hinder the primary educational purpose of this book, a basic text for advanced undergraduate and graduate students and a reference source for all students of DNA metabolism.

As was the case in the first edition, we have continued to present the field in a historical context, with the intent of sensitizing and inspiring students (and others) to the realities of how research progress unfolds and how ideas develop and attain maturity—or not. We have refrained

wherever possible from unadulterated dogma and from presenting the field of biological responses to DNA damage as anywhere near total clarification. While we are aware of presenting viewpoints that are sometimes controversial and even conflicting, we trust that readers, especially students, are not unduly confused or frustrated by our reluctance to always provide the final word, as it were. Rather, it is our hope that such controversies and complexities will inspire further studies.

The names of genes and their polypeptide products sometimes change with good reason as more is known about them and the families they belong to. Additionally, the value and utility of long-standing terminology are often challenged by new information. A textbook provides a valuable opportunity to address such revisions, and we have done so in some areas. However, we have consciously retained much original nomenclature in deference to historic recognition and popular usage.

No work of this sort can come to fruition without special assistance at every level. We owe an enormous debt of gratitude to many individuals for the help they have provided at every level of this labor. We have enjoyed scientific dialogues with an outstanding cadre of professional colleagues who have given unstintingly of their time, energy, and knowledge to review and discuss every chapter with us. In this respect, we owe particular thanks to Rafael Alvarez-Gonzalez, Carl Anderson, Daniel Bogenhagen, Rhona Borts, Vilhelm Bohr, Anne Casper, Stuart Clarkson, James Cleaver, Nils Confer, Richard Cunningham, Bruce Demple, Friederike Eckardt-Schupp, Andre Eker, Paula Fischhaber, Ann Ganesan, Myron Goodman, Thomas Glover, Philip Hanawalt, Ian Hickson, Peggy Hsieh, Sue Jinks-Robertson, Caroline Kisker, Beate Köberle, Nicole Kosarek, Y. W. Kow, Kenneth Kraemer, Susan LeDoux, Alan Lehmann, Michael Lieber, Tomas Lindahl, Sue Lovett, Carolina Marchetto, Lisa McDaniel, M. Stephen Meyn, Paul Modrich, Harvey Mohrenweiser, Robb Moses, Laura Niedernhofer, Shwetal Patel, Tony Pegg, Dean Rupp, Aziz Sancar, Gwen Sancar, Barbara Sedgwick, the late Erling Seeberg, Mutsuo Sekiguchi, Michael Smerdon, Kendric Smith, Robert Sobol, David Stern, James Stivers, John Tainer, Gail Thomlinson, Takeshi Todo, Bennett van Houten, Harry van Steeg, Greg Verdine, Zhigang Wang, Bernard Weiss, Dale Wigley, Sam Wilson, Birgitte Wittschieben, John Wittschieben, Roger Woodgate, and Akira Yasui. Final responsibility naturally rests with us, and we apologize for any inaccuracies and omissions that remain in this publication. Readers are encouraged to inform us of these if and when they are discovered.

We particularly wish to acknowledge the outstanding artistic talent and the dedication and commitment of Marty Burgin, who also worked as illustrator for the first edition. This book is as much hers as ours. We are also extremely grateful to Patrick Lane, whose technological wizardry solved tricky problems in the rendering of crystal structures in shades of just two colors. We thank Jeff Holtmeier of ASM Press for providing his strong personal commitment and that of his staff throughout the production of this work. The magnificent job of editing of the manuscript by Yvonne Strong merits special mention. Thanks are also due to Susan Birch, Production Manager at ASM Press, and to Cathy Balogh and Susan Schmidler.

Each of us owes special thanks to particular individuals who provided indispensable logistical and spiritual support. E.C.F. thanks Angela Ceplis and Meredith Thomas for extraordinary secretarial and editorial assistance and Angela for her invaluable help in coordinating author meetings held in various parts of the country. He also thanks Rhonda Friedberg for editorial assistance and for unstinting moral support. For belief in the importance of the project and for help in bringing it to fruition, R.D.W. thanks his research group, as well as Enid Wood, Patrick Moore, Yuan Chang, Vesna Rapic-Otrin, Ron Herberman, and Arthur Levine. R.S. thanks Lisa McDaniel for extensive editorial assistance and expert help in coordinating and citing the literature and Carmencita Ordu for her invaluable secretarial support. G.W. thanks Jan and Gordon Walker for their cheerleading and understanding, Marianne White for her always cheerful help, Evelyn Witkin for her inspiration, and Priscilla Cooper, Judi Neal, Bill Broughton, and Anne Hills for their constant support. W.S. offers special thanks to Nina Patel and Gulnaz Bachlani.

Over the course of many meetings, most of which took place over weekends, as well as innumerable phone calls and e-mails, each of us came to know and respect our fellow authors from unique perspectives. We are unanimous in our view that the camaraderie and friendships forged through these meetings have enormously enriched our lives, not to mention our taste in fine beverages and the musical pursuits of some of us—such as they are!

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*December 2004*

# Abbreviations

This text employs many standard (and some not so standard) abbreviations. In an effort to reduce confusion for the reader, abbreviations are spelled out in full when first employed in each chapter. Additionally, the following list includes the abbreviations most frequently used.

| | |
|---|---|
| AAF | Acetylaminofluorine |
| ALL | Acute lymphoblastic leukemia |
| AML | Acute myeloid leukemia |
| AT | Ataxia telangiectasia |
| BER | Base excision repair |
| BIR | Break-induced replication |
| BPDE | Benzo[*a*]pyrene-diol-epoxide |
| BrdU | 5-Bromodeoxyuridine |
| BrU | 5-Bromouracil |
| BS | Bloom syndrome |
| CHO | Chinese hamster ovary |
| CPD | Cyclobutane pyrimidine dimer(s) |
| CS | Cockayne syndrome |
| dNTP | Deoxyribonucleoside triphosphate(s) |
| DSB | Double-strand break(s) |
| dsDNA | Double-stranded DNA |
| EMS | Ethyl methanesulfonate |
| ESS | Enzyme-sensitive site(s) |
| FA | Fanconi anemia |
| FdU | 5-Fluorodeoxyuridine |
| GFP | Green fluorescent protein |
| Gy | Gray |
| HNPCC | Hereditary nonpolyposis colon cancer |
| HR | Homologous recombination |
| HU | Hydroxyurea |
| ICL | Interstrand cross-link(s) |
| IR | Ionizing radiation |
| MEF | Mouse embryonic fibroblast(s) |
| MMC | Mitomycin C |
| MMR | Mismatch repair |
| MMS | Methyl methanesulfonate |
| MNase | Micrococcal nuclease |
| MSI | Microsatellite instability |
| NER | Nucleotide excision repair |
| NHEJ | Nonhomologous end joining |
| 4-NQO | 4-Nitroquinoline 1-oxide |
| NTP | Nucleoside triphosphate(s) |
| OR | Odds ratio |
| ORF | Open reading frame(s) |
| Pol | Polymerase |
| (6-4)PP | (6-4) photoproduct(s) |
| RNAPII | RNA polymerase II |
| ROS | Reactive oxygen species |
| RR | Risk ratio |
| RS | Roberts syndrome |
| RT-PCR | Reverse transcription-polymerase chain reaction |
| SCE | Sister chromatid exchange(s) |
| SNP | Single-nucleotide polymorphism(s) |
| SSA | Single-strand annealing |
| SSB | Single-strand break(s) |
| ssDNA | Single-stranded DNA |
| TC-NER | Transcription-coupled nucleotide excision repair |
| TLS | Translesion DNA synthesis |
| TTD | Trichothiodystrophy |
| UAS | Upstream activating sequence(s) |
| WS | Werner syndrome |
| XP | Xeroderma pigmentosum |

# Appendix

**Table 1** Nomenclature of DNA repair genes[a]

| Pathway | Gene(s) in[b]: *E. coli* | *S. cerevisiae* | *S. pombe* | *Drosophila* | Human | Activity |
|---|---|---|---|---|---|---|
| **Base excision repair (BER)** DNA glycosylases | | | | | | Major altered base released: |
| | *ung*$^+$ | *UNG1* | *ung1*$^+$ | — | *UNG* | U |
| | — | — | — | *CG5285* | *SMUG1* | U, hydroxymethyl U |
| | — | — | — | — | *MBD4* (*MED1*) | U or T opposite G at CpG sequences |
| | *mug*$^+$ | — | *thp1*$^+$ | *Thd1* | *TDG* | U, T, or ethenoC opposite G |
| | *fpg*$^+$ (*mutM*$^+$) | *OGG1* | | *Ogg1* | *OGG1* | 8-oxoG opposite C |
| | *mutY*$^+$ | | *myh1*$^+$ | | *MYH* | A opposite 8-oxoG |
| | *nth*$^+$ | *NTG1, NTG2* | *nth1*$^+$ | *CG9272* | *NTHL1* (*NTH1*) | Ring-saturated or fragmented pyrimidines |
| | *alkA*$^+$, *tagA*$^+$ | *MAG1* | *mag1*$^+$, *SPBC23G7.11* | | *MPG* (*MAG, AAG*) | 3-meA, ethenoA, hypoxanthine |
| | *nei*$^+$ | — | — | — | *NEIL1* | Thymine glycol |
| | | — | — | — | *NEIL2* | Oxidative products of C, U |
| | | — | — | — | *NEIL3* | Not known |
| Other BER factors | *xthA*$^+$ | *APN2* (*ETH1*) | *apn2*$^+$ | *Rrp1* | *APEX1* (*HAP1, APE1, REF1*) | AP endonuclease |
| | — | — | — | *ApII* | *APEX2* (*APE2*) | AP endonuclease |
| | *nfo*$^+$ | *APN1* | *apn1*$^+$ | | | AP endonuclease |
| | — | — | — | *CG17227* | *LIG3* | DNA ligase |
| | | — | — | *XRCC1* | *XRCC1* | Accessory factor for LIG3 and BER |
| | — | — | — | *Parp* | *PARP1* (*ADPRT*) | Poly(ADP-ribose) polymerase |
| | — | — | — | | *PARP2* (*ADPRTL2*) | ADPRT-like enzyme |
| **Direct reversal of damage** | *phrA*$^+$ | *PHR1* | — | *phr* | — | CPD photolyase |
| | — | — | — | *phr6-4* | — | (6-4) photolyase |
| | — | — | *uve1*$^+$ (*uvde*$^+$) | — | — | UV damage endonuclease |
| | *ada*$^+$, *ogt*$^+$ | *MGT1* | *SPAC1250.04c* | *agt* | *MGMT* (*AGT*) | $O^6$-meG alkyltransferase |
| | *alkB*$^+$ | | | | *ABH2* | Reversal of alkylation damage (1-meA and 3-meC) |

*(continued)*

**Table 1** Nomenclature of DNA repair genes[a] (*continued*)

| | Gene(s) in[b]: | | | | | |
|---|---|---|---|---|---|---|
| Pathway | *E. coli* | *S. cerevisiae* | *S. pombe* | *Drosophila* | Human | Activity |
| | | | | | *ABH3* (*DEPC-1*) | Reversal of alkylation damage (1-meA and 3-meC) |
| Repair of DNA-protein cross-links | | *TDP1* | *SPCP31B10.05* | *Tdp1* | *TDP1* | Removes covalently bound Topo I-DNA complexes |
| Mismatch repair (MMR) | *mutS*$^+$ | *MSH2* | *swi8*$^+$ | *spel1* (*spellchecker1*) | *MSH2* | Mismatch and loop recognition |
| | | *MSH3* | *swi4* | — | *MSH3* | |
| | | *MSH6* | — | *CG7003* | *MSH6* | |
| | | | | | *MSH4* | MutS homologs specialized for meiosis |
| | | | | | *MSH5* | |
| | *mutL*$^+$ | | | *mlh1* | *MLH1* | MutL homologs, forming dimer |
| | | *PMS1* | *mlh1*$^+$ | *pms2* | *PMS2* | |
| | | | | | *PMS1* | MutL homolog |
| | | | | | *MLH3* | MutL homologs of unknown function |
| | | | | | *PMS2L3* | |
| | | | | | *PMS2L4* (*PMS6*) | |
| | *mutH*$^+$ | | | | | GATC recognition |
| | *uvrD*$^+$ (*mutU*$^+$) | | | | | Helicase aiding excision in MMR and NER |
| Nucleotide excision repair (NER) | | | | | | |
| DNA binding | | *RAD4* | *rhp41*$^+$, *rhp42*$^+$ | *mus210* | *XPC* | Binds distorted DNA as complex |
| | | *RAD23* | *rhp23*$^+$ | *Rad23* | *RAD23B* (*HR23B*) | |
| | | | | | *RAD23A* (*HR23A*) | RAD23B paralog |
| | | *RAD14* | *rhp14*$^+$ | *Xpac* | *XPA* | Binds DNA and proteins in preincision complex |
| | *uvrA*$^+$ | — | — | — | — | Binds damaged DNA in complex with UvrB |
| | *uvrB*$^+$ | — | — | — | — | Catalyzes unwinding in preincision complex |
| TFIIH subunits | | *SSL2* (*RAD25*) | *ercc3sp*$^+$ | *hay* (*haywire*) | *XPB* (*ERCC3*) | 3′–to–5′ DNA helicase TFIIH subunit |
| | | *RAD3* | *rad15*$^+$ (*rad5*$^+$) | *Xpd* | *XPD* (*ERCC2*) | 5′–to–3′ DNA helicase TFIIH subunit |
| | | *TFB1* | *tfb1*$^+$ | *Tfb1* | *GTF2H1* | TFIIH subunit p62 |
| | | *SSL1* | *ssl1*$^+$ | *Ssl1* | *GTF2H2* | TFIIH subunit p44 |
| | | *TFB4* | *tfb4*$^+$ | *Tfb4* | *GTF2H3* | TFIIH subunit p34 |
| | | *TFB2* | *tfb2*$^+$ | *Tfb2* | *GTF2H4* | TFIIH subunit p52 |
| | | *TFB5* | | *CG31917* | *GTF2H5* (*TTDA*) | TFIIH subunit p8 |
| | | *KIN28* | — | *Cdk7* | *CDK7* | Kinase subunits of TFIIH |
| | | *CCL1* | — | *CycH* | *CCNH* | |
| | | *TFB3* | — | *Mat1* | *MNAT1* (*MAT1*) | TFIIH subunit |
| NER nucleases | *uvrC*$^+$, *cho*$^+$ | | | | | 3′ and 5′ incision nuclease |
| | | *RAD2* | *rad13*$^+$ | *mus201* | *XPG* (*ERCC5*) | 3′ incision nuclease |
| | | *RAD10* | *swi10*$^+$ | *Ercc1* | *ERCC1* | 5′ incision nuclease subunits |
| | | *RAD1* | *rad16*$^+$ | *mei9* | *XPF* (*ERCC4*) | |

**Table 1** (*continued*)

| Pathway | Gene(s) in[b]: *E. coli* | *S. cerevisiae* | *S. pombe* | *Drosophila* | Human | Activity |
|---|---|---|---|---|---|---|
| Other factors | | *RAD28* | — | — | *CSA* (*CKN1*, *ERCC8*) | Cockayne syndrome; needed for TC-NER |
| | *mfd*$^+$ | *RAD26* | *rhp26*$^+$ | — | *CSB* (*ERCC6*) | Cockayne syndrome; needed for TC-NER |
| | — | — | *ddb1*$^+$ | *Ddb1* | *DDB1* | p127 subunit of DDB |
| | — | — | — | — | *DDB2* (*XPE*) | p48 subunit of DDB, defective in XP-E |
| | | *RAD7* | *rhp7*$^+$ | | — | E3 ubiquitin ligase and damage binding |
| | | *RAD16* | *rhp16*$^+$ | | — | |
| | | *MMS19* | | *Mms19* | *MMS19L* (*MMS19*) | Transcription and NER |
| DNA ligase I | *ligA*$^+$ | *CDC9* | *cdc17*$^+$ | *DNA-ligI* | *LIG1* | DNA joining |
| **Single-stranded-DNA-binding protein** | *ssb*$^+$ | *RFA1* | *ssb1*$^+$ | *RpA-70* | *RPA1* | Binds ssDNA intermediates in recombination, NER, and gap-filling pathways |
| | | *RFA2* | *ssb2*$^+$ | *RpA-30* | *RPA2* | |
| | | *RFA3* | *ssb3*$^+$ | *RpA-8* | *RPA3* | |
| **Homologous recombination (HR)** | *recA*$^+$ | *RAD51* | *rhp51*$^+$ | *Rad51* (*spn-A*) | *RAD51* | Formation of protein filament to mediate homologous pairing |
| | | | | | *RAD51L1* (*RAD51B*) | Rad51 paralog |
| | | | | *spn-D* | *RAD51C* (*RAD51L2*) | Rad51 paralog |
| | | | | | *RAD51L3* (*RAD51D*) | Rad51 paralog |
| | | *DMC1* | *dmc1*$^+$ | — | *DMC1* | Rad51 paralog for meiosis |
| | | | | *Rad51D* | *XRCC2* | DNA break and cross-link repair |
| | *recB*$^+$, *recC*$^+$, *recD*$^+$ | | | | | Generation of ssDNA to allow formation of RecA filament |
| | | | | *spn-B* | *XRCC3* | DNA break and cross-link repair |
| | *recF*$^+$, *recO*$^+$, *recR*$^+$ | *RAD52* | *rad22*$^+$ (*rad22a*$^+$), *rti1*$^+$ (*rad22b*$^+$) | — | *RAD52* | Accessory factor for recombination |
| | | *RAD54* | *rhp54*$^+$ | *okra* | *RAD54L* | Accessory factor for recombination |
| | | *RDH54 (TID1)* | *rdh54*$^+$ | — | *RAD54B* | |
| | | *RAD55* | *rhp55*$^+$ | — | — | Recombination mediator function |
| | | *RAD57* | *rhp57*$^+$ | — | — | |
| | | *RAD59* | — | — | — | |
| | | *RHC18* | *rad18*$^+$ | | | |
| | | | | | *BRCA1* | Recombination; E3 ubiquitin ligase |
| | | | | | *BRCA2* (*FANCD1*) | Cooperation with RAD51, essential function |
| | *sbcC*$^+$ | *RAD50* | *rad50*$^+$ | *rad50* | *RAD50* | ATPase in complex with MRE11A, NBS1 |
| | *sbcD*$^+$ | *MRE11* | | *mre11* | *MRE11A* | 3′ exonuclease |
| | | *XRS2* | *nbs1*$^+$ | *nbs* | *NBS1* | Mutated in Nijmegen breakage syndrome |
| | *ruvA*, *ruvB* | | | | | Branch migration of Holliday junctions |
| | *ruvC* | | (*mus81-eme1*)$^+$? | | | Nuclease to cleave Holliday junctions |

*(continued)*

**Table 1** Nomenclature of DNA repair genes[a] (*continued*)

| Pathway | Gene(s) in[b]: *E. coli* | *S. cerevisiae* | *S. pombe* | *Drosophila* | Human | Activity |
|---|---|---|---|---|---|---|
| Nonhomologous end joining (NHEJ) | | *YKU70* (*HDF1*) | *pku70*$^+$ | *Irbp* | *Ku70* (*G22P1*) | DNA end binding |
| | | *YKU80* (*HDF2*) | *pku80*$^+$ | *Ku80* | *Ku80* (*XRCC5*) | DNA end binding |
| | | | | | *PRKDC* (*DNA-PKcs*, *XRCC7*) | DNA-dependent protein kinase catalytic subunit |
| | | *LIG4* | | *ligase4* | *LIG4* | Ligase |
| | | *LIF4* | | | *XRCC4* | Ligase accessory factor |
| | | | | | *Artemis* (*SNM1C*) | Nuclease |
| Modulation of nucleotide pools | *MutT*$^+$ | — | — | *CG10898* | *MTH1* (*NUDT1*) | 8-oxoGTPase |
| | *Dut*$^+$ | | | *dUTPase* | *DUT* | dUTPase |
| | | | | | *p53R2* | p53-inducible ribonucleotide reductase small subunit 2 |
| DNA polymerases (catalytic subunits) | *polB*$^+$ (*dinA*, *pol II*) | | | | | Damage responses |
| | | | | — | *POLB* | Pol β; BER in nuclear DNA |
| | | *MIP1* | *SPCC24B10.22*$^+$ | *tam* (*tamas*) | *POLG* | Pol γ; replication and BER in mitochondrial DNA |
| | | *CDC2* (*POL3*) | *cdc6*$^+$ | *DNA-pold* | *POLD1* | Pol δ; NER and MMR |
| | | *POL2* | *cdc20*$^+$ | *DNA-pole* | *POLE1* | Pol ε; NER and MMR |
| | | *REV3* | *rev3*$^+$ | *mus205* | *REV3L* (*PSO1*) | DNA Pol ζ catalytic subunit |
| | | *REV7* | *SPAC12D12.09* | *rev7* | *REV7* (*MAD2L2*) | *DNA* Pol β subunit |
| | | *REV1* | *SPBC1347.01c* | *Rev1* | *REV1L* (*REV1*) | dCMP transferase and other roles in TLS |
| | *umuC*$^+$ | | | | | Catalytic subunit of Pol V for lesion bypass |
| | | *RAD30* | *eso1*$^+$ | *DNA-polh* | *POLH* | Pol η; bypass of CPD, defective in XP-V |
| | | | | | *POLI* (*RAD30B*) | Pol ι; lesion bypass |
| | — | — | — | *mus308* | *POLQ* | Pol θ Lesion bypass; DNA crosslink repair? |
| | *dinB*$^+$ (*Pol IV*) | — | — | | *POLK* (*DINB1*) | Pol κ Lesion bypass |
| | | *POL4* | *SPAC2F7.06c* | — | *POLL* | Pol λ Gap filling during nonhomologous end joining |
| | | | | — | *POLM* | |
| | — | — | — | — | *POLN* (*POL4P*) | Pol μ DNA cross-link repair? |
| | | *POL5* | *pol5*$^+$ | | | |
| DNA polymerase accessory factors | *dnaN*$^+$ | *POL30* | *pcn1*$^+$ | *mus209* | *PCNA* | Sliding clamp |
| | *dnaX*$^+$ (γ-δ) complex | *CDC44* | *rfc1*$^+$ | *Gnf1* | *RFC1* | Clamp loader, large subunit |
| Processing nucleases | | *MUS81* | *mus81*$^+$ | *mus81* | *MUS81* | Structure-specific nuclease subunits |
| | | *MMS4* | *eme1*$^+$ | *MMS4* (*CG12936*) | *EME1* (*MMS4L*) | |
| | *polA*$^+$ (5′ to 3′ exo) | *RAD27* (*RTH1*) | *rad2*$^+$ | *I(3)04108* | *FEN1* (*DNase IV*) | 5′ nuclease |
| | | | | | *TREX1* (*DNase III*) | 3′ exonuclease |
| | | | | | *TREX2* | 3′ exonuclease |
| | *recJ*$^+$, *Exo1*$^+$ | *EXO1* | *exo1*$^+$ | *tos* (*tosca*) | *EXO1* (*HEX1*) | Exonuclease for MMR and other pathways |

**Table 1** (*continued*)

| Pathway | Gene(s) in[b]: *E. coli* | *S. cerevisiae* | *S. pombe* | *Drosophila* | Human | Activity |
|---|---|---|---|---|---|---|
| | | *SPO11* | | *meiW-68* | *SPO11* | Recombination endonuclease |
| | *nfi*$^+$ (*EndoV*$^+$) | — | *SPAC1F12.06c* | — | *ENDOV* (*FLJ35220*) | Incision 3′ of hypoxanthine and uracil |
| Rad6 pathway | | *RAD6* | | *UbcD6* | *UBE2A* (*RAD6A*) | E2 ubiquitin-conjugating enzyme |
| | | | | | *UBE2B* (*RAD6B*) | E2 ubiquitin-conjugating enzyme |
| | | *RAD18* | *rhp18*$^+$ | | *RAD18* | RING domain E3 ubiquitin ligase |
| | | *HPR5* (*SRS2*, *RADH*) | *srs2*$^+$ | | | |
| | | *RAD5* (*SNM2*, *REV2*) | | | | RING domain E3 ubiquitin ligase |
| | | *MMS2* | | | *UBE2V2* (*MMS2*) | DNA helicase |
| | | *UBC13* | | | *UBE2N* (*UBC13*, *BTG1*) | E2 ubiquitin-conjugating complex |
| Genes defective in diseases associated with sensitivity to DNA damaging agent | *recQ*$^+$ | *SGS1* | *rqh1*$^+$ (*hus1*$^+$, *rad12*$^+$) | *mus309* | *BLM* | Bloom syndrome helicase |
| | | | | *CG7670* (exo only) | *WRN* | Werner syndrome helicase / 3′-exonuclease |
| | | | | *RecQ4* | *RECQL4* | Rothmund-Thomson syndrome |
| | | *TEL1* | *tefu tel1*$^+$ | *CG6535* | *ATM* | Ataxia telangiectasia |
| | | *HNT3* | *SPCC18.09c* | *CG5316* | *APTX* | Ataxia-oculomotor apraxia syndrome (aprataxin; interaction with XRCC1, XRCC4) |
| | — | — | — | — | *FANCA* | Fanconi anemia gene |
| | — | — | — | — | *FANCB* | Fanconi anemia gene |
| | — | — | — | — | *FANCC* | Fanconi anemia gene |
| | — | — | — | *fancd2* | *FANCD2* | Fanconi anemia gene |
| | — | — | — | — | *FANCE* | Fanconi anemia gene |
| | — | — | — | — | *FANCF* | |
| | — | — | — | — | *FANCG* (*XRCC9*) | Fanconi anemia gene |
| | — | — | — | *CG12812* | *FANCL* | Ubiquitin ligase for monoubiquitination of FANCD2 |
| Other genes related to DNA repair | | *PSO2* (*SNM1*) | | *mus322* | *DCLRE1A* (*PSO2*, *SNM1*) | DNA cross-link repair nuclease |
| | | | | | *SNM1B* (*DCLRE1B*) | Related to SNM1 |
| | | | | | *PNKP* (*PNK*) | Converts some DNA breaks to ligatable ends |
| | | | | *mus301* (*spn-C*) | *HEL308* | Similar to helicase domain of Mus308 |
| Other conserved DNA damage response genes | — | *H2A* | *hta1*$^+$, *hta2*$^+$ | *His2av* | *H2AFX* (*H2AX*) | Histone, phosphorylated after DNA damage |
| | — | — | — | *p53* | *p53* (*TP53*) | Transcription factor and DNA binding |
| | | *MEC1* | *rad3*$^+$ | *mei-41* | *ATR* | ATM- and PI3K-like essential kinase |

*(continued)*

**Table 1** Nomenclature of DNA repair genes[a] (*continued*)

| Pathway | Gene(s) in[b]: *E. coli* | *S. cerevisiae* | *S. pombe* | *Drosophila* | Human | Activity |
|---|---|---|---|---|---|---|
| | | *LCD1* (*DDC2*) | *rad26*$^+$ | *mus304* | *ATRIP* | ATR interacting |
| | | *RAD17* | *rad1*$^+$ | *rad1* | *RAD1* | PCNA-like DNA damage sensor (9-1-1 complex) |
| | | *DDC1* | *rad9*$^+$ | *rad9* | *RAD9* | |
| | | *MEC3* | *hus1*$^+$ | *Hus1*-like | *HUS1* | |
| | | *RAD24* | *rad17*$^+$ | *Rad17* | *RAD17* | RFC1-like DNA damage sensor |
| | | *RAD9* | *crb2*$^+$ (*rhp9*$^+$) | | | Checkpoint function |
| | | *CHK1* | *chk1*$^+$ (*rad27*$^+$) | *grp* (*grapes*) | *CHEK1* (*CHK1*) | Effector kinase |
| | | *RAD53* | *cds1*$^+$ | *lok* (*loki*) | *CHK2* (*CHEK2*) | Effector kinase |

[a]Entries in Table 1 are organized according to DNA repair pathway, emphasizing functional orthologs. In many cases, but not all, these are also sequence or structural homologs. Caution is recommended in this respect, and the text should be consulted for details, together with public DNA sequence databases. For example, the major DNA glycosylase for removal of 7,8-dihydro-8-oxoguanine (8-oxoG) from DNA is encoded by *fpg*$^+$ in *Escherichia coli* and *OGG1* in human cells, but the two gene products are not related by amino acid sequence and do not fall into the same structural family. The symbol "−" indicates that no ortholog is detected. Some DNA repair genes play roles in more than one pathway but are listed here only once for simplicity. HUGO-approved gene names (http://www.gene.ucl.ac.uk/nomenclature) are presented in nearly all cases, with a few of the commonly used synonyms provided in parentheses. The name used most commonly in this book is usually presented first here. See also the table "Human DNA Repair Genes" (http://www.cgal.icnet.uk/DNA_Repair_Genes.html). For *Drosophila*, official gene names from http://flybase.bio.indiana.edu are used. For *Schizosaccharomyces pombe*, official gene names from http://www.genedb.org/genedb/pombe/index.jsp are used. For *Saccharomyces cerevisiae*, official gene names from http://www.yeastgenome.org/ are used. For *E. coli*, official gene names from http://www.ncbi.nlm.nih.gov/ are used.

[b]Dashes indicate that no gene exists. Blank spaces indicate that the status is unknown.

**Table 2** Human hereditary diseases and defective cellular responses to DNA damage

**A.** Human hereditary diseases with defective cellular responses to DNA damage

| Human disease | Gene(s) | Principal defective response | Principal clinical features |
|---|---|---|---|
| Xeroderma pigmentosum (XP) | *XPA–XPG; XPV* | Nucleotide excision repair (NER); translesion DNA synthesis | Dermatitis, freckling, skin cancer, sometimes neurological defects |
| Cockayne syndrome (CS) | *CSA, CSB* | Transcription-coupled NER | Post-natal developmental defects, neurological defects |
| Combined XP/CS complex (XP/CS) | *XPB, XPD, XPG* | NER and basal transcription by RNA polymerase II | Features of both XP and CS |
| Trichothiodystrophy (TTD) | *XPB, XPD, TTDA* | NER and basal transcription by RNA polymerase II | Photosensitivity, brittle hair, post-natal developmental defects, neurological defects |
| Cerebro-oculo-facio-skeletal (COFS) syndrome | *CSB* | Transcription-coupled NER | Post-natal developmental defects, neurological defects |
| UV-sensitive ($UV^s$) syndrome | *CSB* | Transcription-coupled NER | Photosensitivity |
| Ataxia telangiectasia (AT) | *ATM* | Repair of DNA strand breaks | Cerebellar ataxia, defective immune function, neurological problems, predisposition to hematolymphoid cancer |
| Nijmegen breakage syndrome (NBS) | *NBS1* | Repair of DNA strand breaks | Developmental abnormalities, growth retardation, cancer predisposition |
| AT-like disorder (ATLD) | *MRE11A* | Repair of DNA strand breaks | Defective immune function, neurological problems, predisposition to hematolymphoid cancer |
| LIG4 syndrome | *LIG4* | Repair of DNA strand breaks | Defective immune function, neurological problems, predisposition to hematolymphoid cancer |
| Seckel syndrome | *ATR* | Chromosome stability in response to specific treatments | Developmental, immunological, and hematolymphoid abnormalities |
| Severe combined immunodeficiency (SCID) | *RAG1, RAG2,* SNM1C (*Artemis*) | V(D)J recombination | Severe immunodeficiency |
| Spinocerebellar ataxia with axonal neuropathy (SCAN1) | *TDP1* | Processing of topoisomerase-DNA intermediates | Neurodegeneration |
| Ataxia-ocular apraxia 1 (AOA1) | APTX (*Aprataxin*) | None known; possibly double-strand break repair | Neurodegeneration |
| Bloom syndrome (BS) | *BLM* | Resolution of stalled replication/ transcription intermediates | Dwarfism, immunodeficiency, cancer predisposition |
| Werner syndrome (WS) | *WRN* | Resolution of stalled replication/ transcription intermediates | Premature aging, cancer predisposition |
| Rothmund-Thomson syndrome (RTS) | *RECQL4* | Resolution of stalled replication/ transcription intermediates | Skin, hair, and skeletal abnormalities, cancer |

*(continued)*

**Table 2** Human hereditrary diseases with defective cellular responses to DNA damage (*continued*)

**A.** Human hereditary diseases and defective cellular responses to DNA damage *(continued)*

| Human disease | Gene(s) | Principal defective response | Principal clinical features |
|---|---|---|---|
| RAPADILINO syndrome (RS) | *RECQL4* | Resolution of stalled replication/ transcription intermediates | Skeletal abnormalities |
| 46BR syndrome | *LIG1* | Modest chromosome instability | Immunodeficiency, cancer |
| Hereditary nonpolyposis colon cancer (HNPCC) | *MLH1, MSH2, MSH6, PMS1, PMS2, MLH3, EXO1* | Mismatch repair | Colon and other cancers |
| Fanconi anemia (FA) | *FANCA, FANCB, FANCC, FANCD1 BRCA2, FANCD2, FANCE, FANCF, FANCG, FANCI, FANCJ, FANCL* | Chromosomal stability, spontaneous and in response to cross-linking agents | Limb defects, anemia, cancer disposition |
| Hyper-IgM syndrome | *UNG* | Removal of uracil during class switch recombination | Immune deficiency |

**B.** Human hereditary diseases implicated in defective cellular responses to DNA damage

| Human disease | Gene(s) | Principal defective response | Principal clinical features |
|---|---|---|---|
| Retinoblastoma (RB) | *RB1* | Cell cycle response to DNA damage | Retinoblastoma and other cancers |
| Li-Fraumeni syndrome (LFS) | *p53, CHEK2* | Cell cycle response to DNA damage | Broad spectrum of cancer |
| Hereditary breast cancer | *BRCA1, BRCA2* | Cell cycle response to DNA damage | Breast and ovarian cancer |
| Familial adenomatous polyposis (FAP) | *APC* | Cell proliferation and chromosomal stability | Gastrointestinal cancer and thyroid cancer |
| MYH-associated polyposis (MAP) | *MYH* | None noted, despite mutations in a base excision repair gene | Gastrointestinal cancer |
| Juvenile polyposis syndrome (JPS) | *SMAD4, BMPR1A* | Cell-signaling and "landscaper" functions | Juvenile polyps and gastrointestinal malignancy |
| Cowden syndrome and Bannayan-Riley-Ruvalcaba syndrome | *PTEN* | Cell cycle responses and apoptosis (but not in response to DNA damage) | Breast, thyroid, and endometrial cancer |
| Peutz-Jeghers syndrome (PJS) | *STK11* | Cell cycle responses and apoptosis | Hamartomas, gastrointestinal and non-gastrointestinal tumors |
| Basal cell nevus syndrome (BCNS) | *PTCH2* | Cell-signaling pathways | Malignant melanoma |
| Cutaneous malignant melanoma | *CDKN2A, CDK4* | Cell cycle responses and apoptosis | Malignant melanoma |

**Table 2** (*continued*)

**B. Human hereditary diseases implicated in defective cellular responses to DNA damage**

| Human disease | Gene(s) | Principal defective response | Principal clinical features |
|---|---|---|---|
| Wilm's tumor (WT) | *WT1* | Transcriptional regulation | Pediatric kidney tumors |
| Hereditary papillary renal cell carcinoma (HPRCC) | *MET* | Cell signaling | Papillary renal cell carcinoma |
| von Hippel-Lindau (VHL) | *VHL* | Multiple associated functions, possibly defective in cell cycle regulation | Renal cell and other cancers |
| TSC Tuberous sclerosis complex | *TSC1, TSC2* | Cytoskeleton maintenance | Multiple hamartomas, renal cell cancer |
| Neurofibromatoses type 1 and type 2 (NF1, NF2) | *NF1, NF2* | RAS protein regulation or cytoskeleton maintenance | Neurofibrosarcoma and other tumors |

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