

Index

A

Abf1, 458
Aging. *See* Oogenesis
Aneuploidy. *See* Oogenesis
Angelman syndrome, 381
APC/C, 527
Apj1, 229
Apollo, 293–294
Archaea
 double-strand break end resection mechanism and regulation, 58
 end resection in homologous recombination, 183–185
 Holliday junction resolvases, 149–150
Arp5, 459
Asc1, 229
ASF, 242–243
Ataxia-telangiectasia-like disease (ATLD), 176
ATLD. *See* Ataxia-telangiectasia-like disease
ATM, 65, 174–176, 222, 292, 295–296, 301, 438, 451, 497, 499, 502–505, 508–509
ATR, 65, 223, 292, 294, 430, 451, 477, 497, 499, 502–505, 508–509
ATRIP, 223, 505
ATRX, 300
Aurora B, 527

B

Bacteria
 double-strand break end resection mechanism and regulation, 57
 DNA motor proteins in DNA pairing, 19–20
 DNA pairing and annealing, 11–13
 Holliday junction dissolution and resolution, 22
 homologous recombination suppression, 274
 RecA/RAD51 filament formation regulation, 15–16
 recombination
 initiation and DNA break processing, 6–8
 DNA repair overview, 3–5
BARD1, 337–338
BCDX2, 82
BIR. *See* Break-induced replication
BLM, 9–10, 18, 20–23, 44, 58, 61–62, 65, 110–111, 113–114, 116, 128–132, 134, 155–156, 177, 181–183, 201, 205, 227, 281, 296, 373, 375

Bloom syndrome, 111

BRCA1, 2, 6, 175, 177, 206, 208, 223, 497, 505
 cancer mutations, 336
 domains, 336–337
 homologous recombination function
 defects, 339
 end resection, 339–341
 RAD51 loading, 351
 interactions
 BARD1, 337–338
 overview, 336–339
 PALB2, 338
BRCA2, 2, 17, 42, 82, 98–100, 110, 204, 206, 208, 217, 223, 259, 298, 300
 cancer mutations, 341–342
 domains, 342
 homologous recombination function, 344–345
 interactions
 DNA binding, 343–344
 DSS1, 343–344
 overview, 342
 RAD51, 342–343
Break-induced replication (BIR), double-strand break repair, 47–48, 76–77
Breakage–fusion–bridge cycle. *See* Gene duplication
BRIP1, 338–339
BTBD12, 376
BTR complex, 114, 375–376, 378

C

Cce1, 152–153
Cdc13, 294
Cdc28, 64, 222
Cdc45, 45
Cdc5, 375
CDK-S, 437
Cdk1, 44
CDK2, 60, 372
Cds1, 22, 155
Centromere
 double-strand break-independent homolog pairing, 406
 function and recombination in heterochromatin, 201
 homologous recombination function, 200
Charcot–Marie–Tooth disease, 381
CHK2, 222, 497–499, 502–510

Index

- CHK-2, 432, 506
Class-switch recombination (CSR), 241–242
Cmr1, 229
CNTD1, 371
COMPASS, 457
COSA-1, 371
Crossover interference. *See* Meiotic recombination
Csm2, 16, 102–103, 217
CSR. *See* Class-switch recombination
Ctc1, 295
CTCF, 453
CTCF, 453
CtIP, 9–10, 44, 58, 60–65, 175, 177–178, 185, 208, 222, 295–296, 178, 180, 185, 339–340, 502
Cytidine deaminase, 244
- D**
- DNA ends, 483
Ddc1, 223, 477
Ddc2, 223
DDK, 437
DFO, 431
DinG, 245
D-loop
 causes, 2–3
 homologous recombination, 110–111
 independent formation at DNA breaks. *See also* Double-strand breaks
 recombination initiation and processing
 bacteria, 6–8
 humans, 9–10
 yeast, 8–9
 reversibility
 extended D-loops, 205–206
 nascent D-loops, 204–205
 RTEL disruption, 117
 synthesis-dependent strand annealing, 84
DMC1, 343, 430, 431, 472, 494, 503
Dmc1, 62, 206, 404, 450, 464, 466–477, 479–480, 483
DNA2, 9–10, 43–44, 177, 181–183
Dna2, 8–9, 58, 61–63, 183, 185, 207, 223
DNA replication. *See also* Break-induced replication
 double-strand break formation control, 497–499
 initiation by recombination, 255–256
 recombination and genomic maintenance, 200
 replication forks
 blocked forks
 processing with fork regression, 261–263
 processing without fork regression, 260–261
 structure, 257–258
 collisions, 263–264
 recombination enzymes and fork movement, 258–259
 stability, 259–260
 transcription conflicts. *See* Transcription-associated recombination
Double Holliday junction. *See* Holliday junction
Double-strand breaks (DSBs). *See also* Homologous recombination
 end recognition
 Mre11, 172–174
 Mre11-Rad50 mechanism, 174–175
 MRN complex, 170–172, 176
 Nbs1, 175–176
 Rad50, 174
 end resection mechanism and regulation
 Archaea, 58
 bacteria, 57
 cell cycle and DNA damage checkpoint regulation, 64–65
 chromatin protein regulation
 chromatin-remodeling complexes, 65–66
 53BP1, 65
 Rad9, 65
 RIF1, 65
 endonuclease-generated double-strand breaks, 62–64
 meiotic double-strand breaks, 62
 overview, 56
 prospects for study, 66
 structure and characterization
 Exo1, 61
 MRX/N complex, 58–60
 Sae2/Ctp1/CtIP, 60–61
 Sgs1/BLM-Dna2-RPA, 61–62
 yeast, 58
 end resection
 Archaea, 183–185
 Exo1 resection pathway, 180–181
 initiation in eukaryotes, 177–180
 overview, 176–177
 Sgs1/BLM-DNA2 resection pathway, 181–183
 meiosis. *See* Meiotic recombination
 mitotic homologous recombination dynamics, 227–228
 programmed breaks, 40–41, 366, 398–399
 programmed double-strand break formation in meiosis, 366
 repair control in meiotic prophase
 crossover formation and interference, 503–504
 ectopic recombination suppression, 503
 end processing activation, 502
 intersister recombination suppression, 502–503
 repair
 break-induced replication, 47–48
 double Holliday junction mechanism, 45–46
 gene conversion, 45
 homologous recombination, 41–44
 overview, 41–42, 109–110

- prospects for study, 48
 - single-strand annealing, 44–45
 - synthesis-dependent strand-annealing, 46–47
 - sources, 37–40
 - telomere. *See* Telomere
 - Dpb11, 223
 - DSB-1, 432, 438, 502
 - DSB-2, 432, 438, 502
 - DSBs. *See* Double-strand breaks
 - DSS1, 343–344
 - Dun1, 198
 - DYAD, 431
- E**
- Ecm11, 409–410
 - EME1, 23, 152, 155–159, 219, 224, 248, 298, 374–375, 377
 - Eme1, 156
 - EME2, 23
 - ERCC1, 45, 155, 157, 281, 155, 370, 373, 377
 - EXO1, 9–10, 44, 227, 294–296, 301, 375, 502
 - Exo1, 9, 43, 56, 58, 61–62, 65, 113, 177, 180–181, 207, 281, 375
 - Exo2, 9
 - ExoI, 271
 - ExoVII, 271
 - ExoX, 271
- F**
- FANCA, 300
 - FANCD1, 6
 - FANCD2, 198, 300
 - FANCI, 6, 119
 - FANCM, 6, 116–117, 134, 205, 217, 378
 - FANCN, 6
 - Fanconi anemia, 342
 - FBH1, 18, 204, 217, 224
 - Fbh1, 119
 - FEN1, 154, 180–181, 300
 - 53BP1, 65, 196, 223, 227, 295–296, 301, 339–341
 - Fml1, 116–117, 205
 - FTSK, 184
 - FtsK, 58
 - Fun30, 9, 65, 207, 458
- G**
- GC. *See* Gene conversion
 - GEN1, 22–23, 152, 154–155, 219, 248, 298, 377
 - Gene conversion (GC), double-strand break repair, 45, 75
 - Gene duplication
 - amplifications in cancer and microbes, 324–328
 - growth under selection studies, 323–324
 - measurement
 - duplication detection
 - cell selection with increased copy number, 309
 - hybrid junction sequence detection, 310
 - trapping, 309–310
 - between long repeats
 - duplication between tandem copies of rDNA genes, 313–314
 - reciprocal recombination in duplication/deletion system, 312–313
 - small plasmid reciprocal duplication/deletion, 314–315
 - transposable elements and duplications, 315–316
 - rates, 310–312
 - tandem duplications between short repeats
 - amplifications during long-term bacterial growth on lactose, 317–318
 - duplication using short recombining sequences, 318
 - selected amplifications with very short junction sequences, 317
 - overview, 307–308
 - short-junction duplication formation
 - breakage–fusion–bridge cycles, 321–323
 - illegitimate recombination, 319
 - tandem inversion duplication formation and processing, 319–321
 - template switching, 321
- GINS, 45
- Gmc2, 409
- Gp32, 80, 82–83, 95–96
- Gp41, 245
- H**
- Hed1, 466, 480, 482
 - HEI10, 370–372, 454
 - HER2, 336
 - HerA, 58, 177, 184
 - Hereditary nonpolyposis colorectal cancer (HNPCC), 270
 - Heteroduplex rejection. *See* Mismatch repair
 - HEX1, 9
 - HIM-5, 432–433
 - HIM-6, 156
 - HIM-17, 432–433
 - HJ. *See* Holliday junction
 - HNPCC. *See* Hereditary nonpolyposis colorectal cancer
 - HO endonuclease, 41–42, 44, 63, 65, 241, 450
 - Holliday junction (HJ)
 - dissolution and resolution
 - bacteria, 22
 - humans, 23–24
 - overview, 21–22

Index

- Holliday junction (HJ) (*Continued*)
 yeast, 22–23
 double Holliday junction
 break-induced replication, 76–77
 dissolution
 convergent branch migration, 131–132
 decatenation, 130–131
 history of study, 126–129
 overview, 125–126
 protein complex formation, 130
 Rmi1 role, 132–134
 mechanism of double-strand break repair,
 45–46, 75
 overview, 139–141
 resolvases
 Archaea, 149–150
 bacteria, 143
 bacteriophage, 150–152
 humans, 158–160
 mechanism of resolution, 132
 overview, 142–144–149
 yeast, 152–158
 single versus double, 3
 structure
 antiparallel geometry, 141–142
 conformation, 141
 crossover isomers, 141
- Homologous recombination (HR). *See also* Double-strand breaks; Mitotic homologous recombination; Meiotic recombination; Transcription-associated recombination
- DNA pairing and annealing reactions
 annealing proteins, 82–83
 double Holliday junction, 75
 endonuclease and annealing protein-mediated recombination, 86–87
 overview, 73–75
 pairing mediation
 BRCA2, 98–99
 helicases, 111–114
 MPH1, 116–117
 overview, 93–95
 PCSS complex, 102–103
 prospects for study, 103–104
 RAD51, 99–101
 RAD52, 97–98
 RAD54, 117–118
 RDH54, 117–118
 RecBCD, 96
 RecFOR, 96
 RECQ5, 116
 RTEL, 117
 single-stranded DNA packaging in eukaryotes, 96–97
 Sir1, 101–102
 Srs2, 114–115
 Swi5, 101–102
 UvsY, 95–96
 pairing proteins
 overview, 77–78
 RecA, 77–80
 single-stranded DNA-binding proteins, 80
 RecA-promoted homologous pairing
 homology detection and strand exchange, 85–86
 target location, 84–85
 recombination mediator proteins
 annealing protein activity, 80–82
 BRCA2, 82
 Rad51, 82
 Rad54, 82
 single-strand annealing, 77
 synthesis-dependent strand-annealing, 75–76, 83–84
 double-strand break repair, 41–44
 overview, 110–111, 334–336
 regulation and genomic maintenance
 centromere function, 201
 coordination and nuclear structure and function, 201–202
 diseases, 208–209
 DNA replication, 200
 genetic implications of reversible pathways, 206
 homologous recombination pathway control
 D-loop reversibility, 204–205
 quality control by reversibility, 202, 206
 Rad51 filament stage reversibility, 202–204
 subpathway control, 202
 protein posttranslational modifications in pathway regulation, 207–208
 repair pathway choice, 196–199
 substrate modification, 206–207
 telomere function, 200
 template choice, 196
 transcription and connections to RNA processing and nuclear export, 199–200
- Hop1, 404, 424, 426, 437, 477, 479
Hop2, 474–476, 483, 485
HORMAD1, 433, 437, 503, 505, 509
HORMAD2, 503, 505, 509
Hos2, 229
HOT1, 240
HR. *See* Homologous recombination
Hrp3, 458
HTP-3, 432–433
Humans
 DNA motor proteins in DNA pairing, 20–21
 DNA pairing and annealing, 15
 Holliday junction dissolution and resolution, 23–24, 158–160
 RecA/RAD51 filament formation regulation, 17–18

- recombination
 - DNA repair overview, 4–6
 - initiation and DNA break processing, 9–10
- HUS1, 497, 503, 507
- I**
- ICP8, 86
- IH recombination. *See* Interhomolog recombination
- INO80, 65, 458–459
- Interhomolog (IH) recombination
 - bias
 - models
 - anchor pad model, 484
 - homology-independent steric hindrance, 484–485
 - strand exchange activation in distal regions, 485
 - overview, 477, 480–481
 - positive regulation, 482–483
- K**
- KaiC, 101
- Kms1, 226
- Ku, 64–65
- KU70, 298–299, 301
- Ku70, 41, 196
- KU80, 298–299, 300–301
- Ku80, 41, 196
- L**
- Lim15, 464
- M**
- MCM, 299, 373
- MDC1, 175, 222–223, 505
- Mde2, 429–430, 498
- Mec1, 65, 222–223, 227, 430, 451, 477
- Mec3, 223
- MEI1, 430–431
- MEI4, 430–431, 437
- Mei4, 426–427
- Mei5, 472–474
- MEI9, 373, 377
- MEI217, 373
- MEI218, 373
- MEIOB, 373, 477
- Meiotic recombination. *See also* Oogenesis
 - alternative programs, 399
 - canonical features, 398–399
 - checkpoint network. *See* Prophase, meiosis
 - clinical significance
 - aneuploidy, 379–380
 - genomic syndromes, 381
 - infertility, 381
 - crossover control
 - assurance and interference, 367–369
 - crossover/noncrossover differentiation, 369–372
 - recombination-associated DNA synthesis, 372–374
 - synaptonemal complex pro-crossover role, 372
 - crossover/noncrossover formation differential timing, 374
 - crossover resolution, 374–378
 - DNA strand exchange
 - Dmc1
 - cytological localization, 470–472
 - Hop2 function, 474–476
 - Mei5 function, 472–474
 - MEIOB function, 477
 - Mnd1 function, 474–476
 - Rad51 activity comparison, 466–470
 - Rad54 function, 476–477
 - Sae3 function, 472–474
 - SPATA22 function, 477
 - Tid1/Rdh54 function, 476–477
 - overview, 463–466
 - Rad51
 - cytological localization, 470–472
 - Dmc1 activity comparison, 466–470
 - template choice regulation
 - Dmc1, 479–480, 483
 - double-strand break–independent synapsis, 483–484
 - independent D-loops, 483
 - interhomolog bias models, 484–485
 - negative regulation of IS recombination, 480–482
 - overview, 477–479
 - positive regulation of interhomolog recombination, 482–483
 - prospects for study, 485
 - Rad51, 479–480
 - history of study, 361–362
 - initiation
 - double-strand break formation
 - Arabidopsis*, 431
 - Caenorhabditis elegans*, 432–433
 - chromatin remodeling role, 457–459
 - Drosophila*, 431–432
 - histone modifications in regulation, 454–457
 - miscellaneous proteins, 426–427
 - mouse, 430–431
 - Spo11, 425
 - yeast, 427–430
 - double-strand break formation integration with chromosome loop-axis structure
 - mouse, 436–437
 - yeast, 435–436
 - double-strand break spatial distribution

Index

- Meiotic recombination (*Continued*)
 mouse, 434–435
 overview, 449–451
 regulation, 451–454
 yeast, 433–434
 double-strand break timing, 437–438
 feedback control of double-strand break
 numbers, 438
 overview, 423–425, 447–449
 prospects for study, 438, 459
interhomolog interactions, 365–366
molecular models, 362–365
MUS81 in joint molecule processing, 375
noncrossover formation, 478
pairing
 double-strand break-mediated pairing
 bouquet configuration and entanglement
 resolution, 407–409
 entanglement prevention, 407
 partner identification, 406–407
 recombination-dependent pairing of homologs
 chromosome structural axes and
 synaptonemal complex recombination,
 400–402
 coalignment via interaxis bridges, 402–404
 homolog bias, 404
 Spo11-mediated double-strand breaks,
 399–400
 recombination-independent pairing of
 homologs
 Caenorhabditis elegans, 405
 centromeres and telomeres, 406
 Drosophila meiosis, 405
 fungus, 406
 mechanisms, 406
 mouse, 405
 RIP/MIP, 404–405
 roles, 406
 yeast, 405–406
 programmed double-strand break formation, 366,
 398–399
 prospects for study, 381
 spatial patterning of double-strand breaks and
 crossovers
 crossover homeostasis, 413
 crossover interference, 414–416
 double-strand break patterning, 416
 obligatory crossover and precursor distribution,
 415
STR/BTR in joint molecule metabolism, 375–376
synaptonemal complex
 functional overview, 411–413
 length correlation with crossover frequency, 411
 nucleation and limited extension followed by
 nonhomologous synapsis, 410–411
 structure, 409–410
Meiotic silencing of unsynapsed chromatin (MSUC),
 505, 509
Mei-P22, 431–432
Mek1, 404, 479–480, 482–485
MER2, 437, 498
Mer2, 426–427, 429, 435, 456–457
Mer3, 370
Mfd, 245
Mhf1, 378
Mhf2, 378
Microtubule organizing center (MTOC), 407–408
MIP, 404–406
Mismatch repair (MMR)
 heteroduplex rejection during single-strand
 annealing, 279–283
 heterologous flap processing, 280–281
 machinery in recombination
 homeologous recombination
 overview, 274
 suppression in *Escherichia coli*, 274
 suppression in yeast, 278–279
 homologous recombination, 270–274
 overview, 269–270
 proteins and biochemical activity, 275–278
Mitotic homologous recombination
 BLM role, 111, 113–114
 double-stranded break dynamics, 227–228
 focus formation, 220–226
 genome-wide cell biology screens, 228–229
 nuclear compartments, 226–227
 overview, 217–220
 prospects for study, 229
 recombination centers, 224–225
 Sgs1 role, 111, 113–114
MLH1, 281, 374
Mlh1, 279–280, 525
MLH3, 374
Mlh3, 280, 525
MMR. *See* Mismatch repair
Mms4, 23, 155–156, 219, 224, 248, 374, 376–378
Mms21, 378
Mnd1, 474–476, 483, 485
Mph1, 20, 46, 116–117, 205, 217, 273, 378
MRB complex, 196
MRE11, 9, 176, 196, 222, 298, 339, 430, 497, 502
MRE-11, 432–433
Mre11, 8, 43, 58–60, 62–63, 170–176, 178, 184, 196,
 204, 207, 221–222, 426–427, 429
MRN complex, 9–10, 58–60, 170–172, 174, 176–178,
 185, 222, 225, 298, 339, 497, 502, 508
MRX complex, 8, 58–62, 64, 83, 170, 178, 221–222,
 225–226, 427, 429
MSH2, 281–282
Msh2, 275, 279–280
MSH3, 281, 279–280
MSH4, 454

Msh4, 369–370
Msh5, 369–370
MSH6, 282–283
Msh6, 275, 279
MSUC. *See* Meiotic silencing of unsynapsed chromatin
Mto1, 226
MTOC. *See* Microtubule organizing center
Mug20, 429, 436, 438
Mup84, 226
MUS309, 373
MUS-309, 156
MUS312, 373
MUS81, 23, 152, 155–159, 219, 224, 248, 260, 298,
374–375, 378, 503
Mus81, 23, 117, 155–156, 219, 224, 248, 374,
376–378
MutH, 270, 274–275, 278
MutL, 270–271, 274–275, 277–278, 282, 372, 374–376,
378
MutS, 270–271, 274–275, 277–278, 282–283, 371, 373,
376, 454
MutU, 270

N

Nab2, 242
NBS. *See* Nijmegen breakage syndrome
NBS1, 9, 196, 222, 298, 339, 430, 497
Nbs1, 60, 170–172, 175–176, 198
NBSLD. *See* Nijmegen breakage syndrome–like disorder
NHEJ. *See* Nonhomologous end-joining
NHK-1, 504
Nijmegen breakage syndrome (NBS), 176
Nijmegen breakage syndrome–like disorder (NBSLD),
176
9-1-1 complex, 497
Nns1, 429
Nonhomologous end-joining (NHEJ)
double-strand break repair, 41–42, 109–110
error potential, 2
mammalian cells, 314–316
repression at telomeres
alternative end-joining, 301
classical end-joining, 300–301
Nse2, 378
NurA, 58, 184

O

Oogenesis
aging and aneuploidy
clinical overview, 379–380, 519–520
mechanisms, 528–533
prospects for study, 533–534
chromosome segregation in meiosis and aneuploidy,
527–528

chromosome structure in meiosis and aneuploidy,
523–527
meiosis overview, 520–523
Orc1, 456

P

PALB2, 18–19, 98, 208, 223, 338–339, 341, 345
PAR1, 19, 204, 217, 224
PARP, 24, 206, 339
Pch2, 456
PCNA, 47–48, 115, 198–199, 204–205, 208, 224,
372–373, 497
PCSS complex, 102–103
Pds5, 525
Pif1, 48, 200, 224
PLK2, 505
Pms1, 279–281
PMS2, 281
POH1, 223, 340
Pol32, 47–48
Pol η , 374
Pol ζ , 374
POT1, 292–294, 299, 301
POT1a, 292–293, 295
POT1b, 292–293, 295
PP2A, 526
Pph21, 229
Prader–Willi syndrome, 381
PRD1, 430–431
PRD2, 431
PRD3, 431
PRDM9, 206, 434, 436–437, 453, 459, 523, 525
PriC, 258
Prophase, meiosis
asynapsis and transcriptional silencing, 505
cell death from persistent defects, 506–507
chromosome pairing and bouquet formation, 508
double-strand break formation control
DNA replication, 497–499
levels, 499, 502
double-strand break repair control
crossover formation and interference, 503–504
ectopic recombination suppression, 503
end processing activation, 502
intersister recombination suppression, 502–503
exit control, 506
meiotic checkpoint network
architecture, 507–508
developmental function, 507
overview, 496–497, 501
phosphorylation events, 50
prospects for study, 510
response modulation, 509
signal generation, 508–509
signal integration and separation, 509–510

Index

- Prophase, meiosis (*Continued*)
 nuclear organization checkpoint control, 504
 overview, 493–496
 synapsis initiation control, 508–509
- Psf1, 45
Psf2, 45
Psf3, 45
PSO2, 293
Psy3, 16, 102–103, 217
PTEN, 208
- R**
- RAD1, 497
Rad1, 224
Rad2, 22, 154, 248, 375
RAD3, 477
Rad6, 114, 198
RAD9, 497
Rad9, 65, 196, 222, 224, 227
Rad10, 224
RAD17, 223
Rad17, 223
Rad18, 114, 198
Rad24, 223
Rad32, 429
RAD50, 9, 196, 298, 300, 339, 430, 497
RAD-50, 432–433
Rad50, 8, 43, 58–60, 170–175, 178, 184, 196, 207, 221, 426–427, 429
RAD51, 6, 10–11, 14–21, 94, 97–101, 104, 116, 119, 139, 201, 203–204, 208, 223, 273, 282, 298, 335, 431, 472, 477, 494, 502–503
 BRCA1 in loading, 341
 BRCA2 binding, 342–343
 cancer mutations, 346
 filament formation regulation
 bacteria, 15–16
 humans, 17–18
 overview, 14
 yeast, 16–17
 knockout mice, 347–349
 mutant cellular phenotypes, 347
 protein–protein interactions, 346–347
 reversibility, 202–204
RAD-51, 438
Rad51, 13–14, 16, 20, 38, 41, 43–44, 63, 77, 79, 82–84, 97, 103, 110, 114–115, 118, 204–206, 217, 220, 224, 226–227, 240, 243, 259, 262, 273, 404, 450, 464, 466–473, 475–477, 479–480, 482, 484
RAD51B, 17–18, 44, 82, 99–100, 208, 217, 224, 346–347
Rad51b, 347–348
RAD51C, 17–18, 44, 82, 99–100, 208, 217, 224, 346–347
Rad51c, 347–349
RAD51D, 17–18, 44, 82, 99, 102–103, 208, 217, 346–347
Rad51d, 347–349
RAD52, 13–14, 17–18, 38, 83, 97–98, 223–224, 281
Rad52, 3, 6, 13–14, 16, 41, 44–45, 77, 81–84, 97, 102, 217, 220, 223–224, 226–228, 240, 280
Rad53, 16, 222
RAD54, 17, 19–20, 23, 155, 503
Rad54, 16–17, 20, 44, 82, 84, 117–118, 206, 218, 220, 458, 470, 480, 482, 485, 476–477
RAD54A, 224
RAD54B, 17, 224
Rad55, 16, 82, 84, 99, 100, 217, 224, 226
Rad57, 16, 18, 82, 84, 99, 100, 217, 224
Rad59, 45, 83, 226
RAD211, 453
RadA, 101
RadB, 101
RAG, 336
RAG complex, 40
Rap1, 292, 299, 458
RAP80, 223, 340
Ras, 510
Rdh54, 17, 117–118, 204, 470, 476–477, 503
Reb1, 458
Rec6, 429–430
Rec7, 429–430
Rec8, 429, 436, 456, 483, 525–526
Rec10, 429–430
Rec11, 429
Rec12, 429–430, 436, 454, 456
Rec14, 429–430
Rec15, 429–430
Rec24, 429–430
Rec25, 429–430, 436, 438
Rec27, 429–430, 436, 438
REC102, 437
Rec102, 426–427
REC104, 437
Rec104, 426–427
REC114, 430–431, 437, 426–427, 429, 498, 502
RecA, 10–17, 19–20, 44, 85–86, 94, 96, 101, 139, 240, 259, 273, 282, 309, 312–315, 318, 464, 466–467, 477, 480, 483
 family of proteins, 77–80
 homologous pairing promotion
 homology detection and strand exchange, 85–86
 target location, 84–85
 RAD51 filament formation regulation
 bacteria, 15–16
 humans, 17–18
 overview, 14
 yeast, 16–17
RecB, 56
RecBC, 245
RecBCD complex, 56, 86, 96

- RecBCD pathway, 3, 6–7, 15
RecD, 9, 56–57
RecE, 86
RecF pathway, 3, 15, 57
RecFOR complex, 96
RecG, 21
RecJ, 15, 57, 271
RecO, 13, 81–83
RecOR complex, 15, 96
RECQ, 296
RecQ, 8–9, 15, 19, 22, 57, 102, 111, 113, 126–128,
130–131, 134, 181–183, 375
RECQ1, 20–21, 113, 116, 205, 281
RECQ4, 113, 116, 127
RECQ5, 18, 113, 116, 127, 204–205
RECQL5, 245, 247
RecR, 15
RecT, 86–87
RecX, 16, 19
Red1, 404, 424–426, 477, 479–480
Red β , 86
Rep, 245
Repetitive extragenetic palindromic elements, 318–319
Replication fork. *See* DNA replication
Rev1, 374
RFC, 223, 373, 477
RIF1, 65, 196, 223, 296, 340
RIP, 404–406
R-loop. *See* Transcription-associated recombination
RMI1, 24, 113, 133–134, 181, 375–376
Rmi1, 8, 43, 45, 58, 61, 84, 113, 132–133, 218, 375–376
RMI2, 24, 134, 375–376
RNA polymerase, 240–241, 243–245, 247
RNASE H, 184
RNase U, 39
RNF168, 222
RNF212, 370–372, 453, 505
RNF8, 222
RPA, 8–11, 14, 16–18, 23, 38, 44, 61–63, 82–83,
96–101, 110, 115–116, 181, 196, 217,
223, 282, 294, 373, 431, 472–473, 497, 503
Rqh1, 156
RSC, 65
Rsc3, 458
RTEL, 117–118, 378
RTEL1, 205, 299
RuvA, 143, 145
RuvABC, 143, 149
RuvB, 143, 145
RuvC, 143, 145–149, 152–153
- S**
Sad1, 226
Sae2, 8, 43–44, 58, 60–61, 63–64, 178, 185, 208, 103,
222, 225
Sae3, 472–474
SbcCD, 3, 7, 56–57
Scc1, 526
Scc3, 525
SCP1, 409, 504
SDSA. *See* Synthesis-dependent strand-annealing
Sen1, 243
SETX, 243
SF2, 242–243
SFR1, 17, 19
Sfr1, 103, 472–474
Sgol2, 527
Sgs1, 8–9, 20–21, 43–45, 58, 61–62, 102, 117, 127–131,
134, 155–156, 177, 181–183, 185, 207,
218, 273, 279, 375
meiotic homologous recombination role, 114
mitotic homologous recombination role, 111,
113–114
Sgs2, 44
Shelterin, 291–293
SHOC1, 370
Shu1, 16, 102–103, 217
Shu2, 16, 102–103, 217
Single-strand annealing (SSA), double-strand break
repair, 44–45, 77
Sir1, 101–102
Sir2, 456, 508
Ski8, 426–427, 430–431
Sld5, 45
SLX1, 23, 152, 155, 157–159, 248, 298, 376–377
Slx1, 22–23, 45, 155, 157–158, 219, 248, 377–378
SLX4, 23, 152, 157–159, 248, 298, 376–377
Slx4, 22–23, 45, 155, 157–158, 219, 248, 377–378
Slx5, 224
Slx8, 224, 226
SMAR, 21
SMARCAD1, 65
SMARCAL1, 118
Smc1, 526–527
SMC5, 300, 377–378
Smc5, 226, 377–378
SMC6, 377–378
Smc6, 226, 377–378
SMN1B, 293
SNF, 65, 458, 503
Snf2, 17, 118
SNF22, 458
SPATA, 477
SPATA22, 373, 477
SPO11, 366, 430–433, 437–438, 494, 498–499, 505,
509–510
Spo11, 40, 62, 114, 272, 399–400, 405, 423,
425–427, 449–450, 453–454, 456–457,
463
Spo16, 370
Spp1, 435, 456

Index

- Srs2, 16, 18, 20, 84, 100–101, 114–115, 117, 204, 206, 217, 224, 273, 279
- SSA. *See* Single-strand annealing
- SSB, 83
- STAG3, 525
- Stn1, 294–295
- STR complex, 8, 45, 62, 64–65, 114, 218, 375–378
- Sub2, 242
- SUMO-1, 410
- SUN-1, 504–505
- SWI, 65, 458, 503
- SWI1, 431
- Swi2, 17, 118
- SWI5, 17, 19
- Swi5, 101–102, 472–474
- SWR1, 458
- SWS1, 18, 103, 217
- Sws1, 102–103
- SWSAP1, 18, 103
- SYCE1, 409
- SYCE2, 409
- SYCE3, 409
- SYCP1, 409
- Synaptonemal complex. *See* Meiotic recombination
- Synthesis-dependent strand-annealing (SDSA)
 double-strand break repair, 46–47, 75–76, 110
 entry control, 202
 Srs2 role, 114–115
- SYP-1, 409
- SYP-2, 409
- SYP-4, 409
- T**
- T4 endonuclease VII, 150–151
- T7 endonuclease I, 151–152, 157
- Tandem inversion duplication. *See* Gene duplication
- TAR. *See* Transcription-associated recombination
- Tcn1, 294
- Tel1, 65, 222, 438, 451
- Telomere
 double-strand break–independent homolog pairing, 406
 function and homologous recombination, 200
 homology-directed repair
 alternative lengthening, 299–300
 homologous recombination repression between sister telomeres, 299
 T-loop formation and function, 296–298
 T-loop protection from homologous recombination, 298–299
 nonhomologous end-joining repression
 alternative end-joining, 301
 classical end-joining, 300–301
 resection
 hyperresection at dysfunctional telomeres, 295–296
 overhang generation, 293–295
 shelterin and end-protection problem, 291–293
 transcription-associated recombination, 246–247
 Telomeric repeat-containing RNA (TERRA), 246
 Ten1, 295
 TERRA. *See* Telomeric repeat-containing RNA
 Tex12, 409
 TFIIH, 240
 THO, 242, 244–246, 249
 Tho1, 242
 THSC, 242
 Tid1, 204, 470, 476–477
 TIN2, 292
 T-loop. *See* Telomere
 Top1, 241–242
 Top2, 247
 Top3, 8, 20, 23, 43, 45, 58, 61, 113, 129, 131, 133, 218, 273, 375–376
 TOPBP1, 223, 497, 505
 TOPO III, 2, 113–114, 128, 131, 133, 205, 375–376
 TopoIII, 281
 TPP1, 292, 294–295
 Transcription-associated recombination (TAR)
 class-switch recombination comparison, 241–242
 genomic maintenance connections to RNA processing and nuclear export, 199–200
 overview, 239–242
 prospects for study, 249
 R-loop mediation, 242–243
 rDNA region, 245–246
 replication–transcription conflicts, 244–245, 247–247
 telomeres, 246–247
 Trem, 431–432
 TREX-2, 242
 TRF1, 292, 295
 TRF2, 292–293, 295, 298, 300–301
 TRIP13, 508
 Trisomies. *See* Oogenesis
- U**
- UAP56, 242
- UBC13, 338
- Ubc9, 410
- Ulp1, 226
- UvrC, 376
- UvrD, 18, 20, 115–116, 204, 245, 270–271, 274–275, 277–278, 282
- UvsX, 79, 81–82, 94–95
- UvsY, 81–83, 95–96
- V**
- V(D)J recombination, 227

W

WDR61, 430
WEE1, 506
WRN, 9–10, 20–21, 61, 113, 116, 116, 281

X

XLF1, 198
XPD, 240
XPE, 45, 155, 157, 281, 377
XPG, 181, 248, 375
XRCC2, 17–19, 44, 82, 99, 102, 208, 217, 346–347
Xrcc2, 347–349
XRCC3, 17, 44, 82, 99, 208, 217, 346–347
Xrs2, 8, 43, 58–60, 196, 207, 221–222, 426–427

Y

Ydc2, 152–154
Yeast
 DNA motor proteins in DNA pairing, 20
 DNA pairing and annealing, 13–14
 double-strand break end resection mechanism and regulation, 58
 Holliday junction dissolution and resolution, 22–23, 152–158
 homeologous recombination suppression, 278–279

meiotic recombination

 double-strand break
 formation, 427–430
 formation integration with chromosome
 loop-axis structure, 435–436
 spatial distribution, 433–434
 recombination-independent pairing of
 homologs, 405–406
 RecA/RAD51 filament formation regulation, 16–17
 recombination
 DNA repair overview, 3–6
 initiation and DNA break processing, 8–9
 Yen1, 23, 154–155, 219, 248, 377–378
 Yku70, 221
 Yku80, 221

Z

ZEP1, 409
ZHP-3, 370–371
ZIP1, 409
Zip1, 369–370, 409, 412, 504
Zip2, 369–370
Zip3, 369–373
Zip4, 369–370, 381
ZRANB, 21
ZRANB3, 118