

Rodney Rothstein

List of Publications by Year in descending order

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133
papers

24,080
citations

25014

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h-index

13758

129
g-index

138
all docs

138
docs citations

138
times ranked

14775
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | [12] One-step gene disruption in yeast. <i>Methods in Enzymology</i> , 1983, 101, 202-211. | 0.4 | 3,452 |
| 2 | The double-strand-break repair model for recombination. <i>Cell</i> , 1983, 33, 25-35. | 13.5 | 2,687 |
| 3 | Elevated recombination rates in transcriptionally active DNA. <i>Cell</i> , 1989, 56, 619-630. | 13.5 | 1,692 |
| 4 | Yeast transformation: a model system for the study of recombination.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1981, 78, 6354-6358. | 3.3 | 1,559 |
| 5 | [19] Targeting, disruption, replacement, and allele rescue: Integrative DNA transformation in yeast. <i>Methods in Enzymology</i> , 1991, 194, 281-301. | 0.4 | 1,319 |
| 6 | Choreography of the DNA Damage Response. <i>Cell</i> , 2004, 118, 699-713. | 13.5 | 829 |
| 7 | Repair of Strand Breaks by Homologous Recombination. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013, 5, a012740-a012740. | 2.3 | 706 |
| 8 | A Suppressor of Two Essential Checkpoint Genes Identifies a Novel Protein that Negatively Affects dNTP Pools. <i>Molecular Cell</i> , 1998, 2, 329-340. | 4.5 | 681 |
| 9 | A hyper-recombination mutation in <i>S. cerevisiae</i> identifies a novel eukaryotic topoisomerase. <i>Cell</i> , 1989, 58, 409-419. | 13.5 | 542 |
| 10 | [14] Genetic applications of yeast transformation with linear and gapped plasmids. <i>Methods in Enzymology</i> , 1983, 101, 228-245. | 0.4 | 515 |
| 11 | DNA strand annealing is promoted by the yeast Rad52 protein.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 10729-10734. | 3.3 | 453 |
| 12 | Rad52 forms DNA repair and recombination centers during S phase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 8276-8282. | 3.3 | 409 |
| 13 | Colocalization of multiple DNA double-strand breaks at a single Rad52 repair centre. <i>Nature Cell Biology</i> , 2003, 5, 572-577. | 4.6 | 388 |
| 14 | Survival of DNA Damage in Yeast Directly Depends on Increased dNTP Levels Allowed by Relaxed Feedback Inhibition of Ribonucleotide Reductase. <i>Cell</i> , 2003, 112, 391-401. | 13.5 | 382 |
| 15 | HDACs link the DNA damage response, processing of double-strand breaks and autophagy. <i>Nature</i> , 2011, 471, 74-79. | 13.7 | 368 |
| 16 | The Smc5-Smc6 complex and SUMO modification of Rad52 regulates recombinational repair at the ribosomal gene locus. <i>Nature Cell Biology</i> , 2007, 9, 923-931. | 4.6 | 345 |
| 17 | Increased chromosome mobility facilitates homology search during recombination. <i>Nature Cell Biology</i> , 2012, 14, 510-517. | 4.6 | 325 |
| 18 | Mechanisms and Regulation of Mitotic Recombination in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2014, 198, 795-835. | 1.2 | 313 |

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|----|--|------|-----------|
| 19 | CRISPR-Mediated Base Editing Enables Efficient Disruption of Eukaryotic Genes through Induction of STOP Codons. <i>Molecular Cell</i> , 2017, 67, 1068-1079.e4. | 4.5 | 283 |
| 20 | Replication fork pausing and recombination or "œgimme a break": <i>Genes and Development</i> , 2000, 14, 1-10. | 2.7 | 279 |
| 21 | The RecQ DNA Helicases in DNA Repair. <i>Annual Review of Genetics</i> , 2010, 44, 393-417. | 3.2 | 265 |
| 22 | Holliday Junctions Accumulate in Replication Mutants via a RecA Homolog-Independent Mechanism. <i>Cell</i> , 1997, 90, 87-96. | 13.5 | 261 |
| 23 | The ribonucleotide reductase inhibitor Sml1 is a new target of the Mec1/Rad53 kinase cascade during growth and in response to DNA damage. <i>EMBO Journal</i> , 2001, 20, 3544-3553. | 3.5 | 248 |
| 24 | Evolutionary Implications of the Frequent Horizontal Transfer of Mismatch Repair Genes. <i>Cell</i> , 2000, 103, 711-721. | 13.5 | 246 |
| 25 | The Dun1 checkpoint kinase phosphorylates and regulates the ribonucleotide reductase inhibitor Sml1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 3746-3751. | 3.3 | 236 |
| 26 | Genome-Wide Analysis of Rad52 Foci Reveals Diverse Mechanisms Impacting Recombination. <i>PLoS Genetics</i> , 2007, 3, e228. | 1.5 | 176 |
| 27 | Three-Dimensional Microscopy of the Rad51 Recombination Protein during Meiotic Prophase. <i>Plant Cell</i> , 1999, 11, 809-824. | 3.1 | 167 |
| 28 | Cloning-Free PCR-Based Allele Replacement "Methods. <i>Genome Research</i> , 1997, 7, 1174-1183. | 2.4 | 162 |
| 29 | Direct Association between the Yeast Rad51 and Rad54 Recombination Proteins. <i>Journal of Biological Chemistry</i> , 1996, 271, 33181-33186. | 1.6 | 153 |
| 30 | RM11/NCE4, a suppressor of genome instability, encodes a member of the RecQ helicase/Topo III complex. <i>EMBO Journal</i> , 2005, 24, 2024-2033. | 3.5 | 150 |
| 31 | Differential Regulation of the Cellular Response to DNA Double-Strand Breaks in G1. <i>Molecular Cell</i> , 2008, 30, 73-85. | 4.5 | 149 |
| 32 | DNA damage checkpoint and repair centers. <i>Current Opinion in Cell Biology</i> , 2004, 16, 328-334. | 2.6 | 138 |
| 33 | A yeast mating-selection scheme for detection of protein " protein interactions. <i>Nucleic Acids Research</i> , 1994, 22, 1778-1779. | 6.5 | 125 |
| 34 | The Complete Set of Predicted Genes from <i>Saccharomyces cerevisiae</i> in a Readily Usable "Form. <i>Genome Research</i> , 1997, 7, 1169-1173. | 2.4 | 124 |
| 35 | The Slx5-Slx8 Complex Affects Sumoylation of DNA Repair Proteins and Negatively Regulates Recombination. <i>Molecular and Cellular Biology</i> , 2007, 27, 6153-6162. | 1.1 | 124 |
| 36 | Sex, maps, and imprinting. <i>Cell</i> , 1991, 64, 1-3. | 13.5 | 115 |

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|----|--|------|-----------|
| 37 | Choreography of recombination proteins during the DNA damage response. <i>DNA Repair</i> , 2009, 8, 1068-1076. | 1.3 | 103 |
| 38 | Interaction with Rad51 Is Indispensable for Recombination Mediator Function of Rad52. <i>Journal of Biological Chemistry</i> , 2002, 277, 40132-40141. | 1.6 | 102 |
| 39 | A Genetic Screen for top3 Suppressors in <i>Saccharomyces cerevisiae</i> Identifies SHU1, SHU2, PSY3 and CSM2. <i>Genetics</i> , 2005, 169, 1275-1289. | 1.2 | 92 |
| 40 | Cloning-free genome alterations in <i>saccharomyces cereuisiae</i> using adaptamer-mediated PCR. <i>Methods in Enzymology</i> , 2002, 350, 258-277. | 0.4 | 91 |
| 41 | At Loose Ends: Resecting a Double-Strand Break. <i>Cell</i> , 2009, 137, 807-810. | 13.5 | 89 |
| 42 | Sec24p and Sec16p cooperate to regulate the GTP cycle of the COPII coat. <i>EMBO Journal</i> , 2012, 31, 1014-1027. | 3.5 | 88 |
| 43 | Mutations in Homologous Recombination Genes Rescue <i>top3</i> Slow Growth in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2002, 162, 647-662. | 1.2 | 86 |
| 44 | Mutational and Structural Analyses of the Ribonucleotide Reductase Inhibitor Sml1 Define Its Rnr1 Interaction Domain Whose Inactivation Allows Suppression of <i>mec1</i> and <i>rad53</i> Lethality. <i>Molecular and Cellular Biology</i> , 2000, 20, 9076-9083. | 1.1 | 85 |
| 45 | Alu elements mediate <i>MYB</i> gene tandem duplication in human T-ALL. <i>Journal of Experimental Medicine</i> , 2007, 204, 3059-3066. | 4.2 | 85 |
| 46 | Histone H3K56 Acetylation, Rad52, and Non-DNA Repair Factors Control Double-Strand Break Repair Choice with the Sister Chromatid. <i>PLoS Genetics</i> , 2013, 9, e1003237. | 1.5 | 84 |
| 47 | The Role of DNA Double-Strand Breaks in Spontaneous Homologous Recombination in <i>S. cerevisiae</i> . <i>PLoS Genetics</i> , 2006, 2, e194. | 1.5 | 82 |
| 48 | ScreenMill: A freely available software suite for growth measurement, analysis and visualization of high-throughput screen data. <i>BMC Bioinformatics</i> , 2010, 11, 353. | 1.2 | 82 |
| 49 | The Shu complex, which contains Rad51 paralogues, promotes DNA repair through inhibition of the Srs2 anti-recombinase. <i>Molecular Biology of the Cell</i> , 2011, 22, 1599-1607. | 0.9 | 82 |
| 50 | Selective ploidy ablation, a high-throughput plasmid transfer protocol, identifies new genes affecting topoisomerase-induced DNA damage. <i>Genome Research</i> , 2011, 21, 477-486. | 2.4 | 81 |
| 51 | Rad52. <i>Current Biology</i> , 2009, 19, R676-R677. | 1.8 | 80 |
| 52 | The ribonucleotide reductase inhibitor, Sml1, is sequentially phosphorylated, ubiquitylated and degraded in response to DNA damage. <i>Nucleic Acids Research</i> , 2010, 38, 6490-6501. | 6.5 | 73 |
| 53 | A Molecular Genetic Dissection of the Evolutionarily Conserved N Terminus of Yeast Rad52. <i>Genetics</i> , 2002, 161, 549-562. | 1.2 | 73 |
| 54 | Localization of recombination proteins and Srs2 reveals anti-recombinase function in vivo. <i>Journal of Cell Biology</i> , 2009, 185, 969-981. | 2.3 | 72 |

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|----|---|------|-----------|
| 55 | Multi-scale tracking reveals scale-dependent chromatin dynamics after DNA damage. <i>Molecular Biology of the Cell</i> , 2017, 28, 3323-3332. | 0.9 | 71 |
| 56 | Deletions of a tyrosine tRNA gene in <i>S. cerevisiae</i> . <i>Cell</i> , 1979, 17, 185-190. | 13.5 | 69 |
| 57 | An Allele of RFA1 Suppresses RAD52-Dependent Double-Strand Break Repair in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 1999, 151, 447-458. | 1.2 | 68 |
| 58 | Characterization of genetic interactions with RFA1: the role of RPA in DNA replication and telomere maintenance. <i>Biochimie</i> , 2000, 82, 71-78. | 1.3 | 67 |
| 59 | DNA in motion during double-strand break repair. <i>Trends in Cell Biology</i> , 2013, 23, 529-536. | 3.6 | 64 |
| 60 | Sgs1 function in the repair of DNA replication intermediates is separable from its role in homologous recombinational repair. <i>EMBO Journal</i> , 2009, 28, 915-925. | 3.5 | 60 |
| 61 | Localization of checkpoint and repair proteins in eukaryotes. <i>Biochimie</i> , 2005, 87, 579-589. | 1.3 | 59 |
| 62 | Rad52 recruitment is DNA replication independent and regulated by Cdc28 and the Mec1 kinase. <i>EMBO Journal</i> , 2009, 28, 1121-1130. | 3.5 | 59 |
| 63 | Efficient PCR-based gene disruption in <i>Saccharomyces</i> strains using intergenic primers. <i>Yeast</i> , 2002, 19, 319-328. | 0.8 | 58 |
| 64 | Cooperativity of Mus81-Mms4 with Rad54 in the Resolution of Recombination and Replication Intermediates. <i>Journal of Biological Chemistry</i> , 2009, 284, 7733-7745. | 1.6 | 57 |
| 65 | Quality control of DNA break metabolism: in the $\hat{\epsilon}$ ™, it's a good thing. <i>EMBO Journal</i> , 2008, 27, 581-588. | 3.5 | 56 |
| 66 | Cell Biology of Mitotic Recombination. <i>Cold Spring Harbor Perspectives in Biology</i> , 2015, 7, a016535. | 2.3 | 54 |
| 67 | Cell Cycle-Regulated Centers of DNA Double-Strand Break Repair. <i>Cell Cycle</i> , 2003, 2, 477-481. | 1.3 | 53 |
| 68 | Chromosome-Scale Genetic Mapping Using a Set of 16 Conditionally Stable <i>Saccharomyces cerevisiae</i> Chromosomes. <i>Genetics</i> , 2008, 180, 1799-1808. | 1.2 | 53 |
| 69 | Identification of a Mouse Homologue of the <i>Saccharomyces cerevisiae</i> Recombination and Repair Gene, RAD52. <i>Genomics</i> , 1994, 23, 300-303. | 1.3 | 51 |
| 70 | Role of the Rad52 Amino-terminal DNA Binding Activity in DNA Strand Capture in Homologous Recombination. <i>Journal of Biological Chemistry</i> , 2009, 284, 33275-33284. | 1.6 | 50 |
| 71 | Intragenic Inversion of mtDNA: A New Type of Pathogenic Mutation in a Patient with Mitochondrial Myopathy. <i>American Journal of Human Genetics</i> , 2000, 66, 1900-1904. | 2.6 | 48 |
| 72 | Guidelines for DNA recombination and repair studies: Cellular assays of DNA repair pathways. <i>Microbial Cell</i> , 2019, 6, 1-64. | 1.4 | 47 |

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|----|---|-----|-----------|
| 73 | The Absence of Top3 Reveals an Interaction Between the Sgs1 and Pif1 DNA Helicases in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2006, 174, 555-573. | 1.2 | 45 |
| 74 | Telomere Length Homeostasis Responds to Changes in Intracellular dNTP Pools. <i>Genetics</i> , 2013, 193, 1095-1105. | 1.2 | 44 |
| 75 | Phosphorylation-Regulated Transitions in an Oligomeric State Control the Activity of the Sae2 DNA Repair Enzyme. <i>Molecular and Cellular Biology</i> , 2014, 34, 778-793. | 1.1 | 41 |
| 76 | DNA Repair: Keeping It Together. <i>Current Biology</i> , 2004, 14, R994-R996. | 1.8 | 40 |
| 77 | Multiple start codons and phosphorylation result in discrete Rad52 protein species. <i>Nucleic Acids Research</i> , 2006, 34, 2587-2597. | 6.5 | 38 |
| 78 | Defining the influence of Rad51 and Dmc1 lineage-specific amino acids on genetic recombination. <i>Genes and Development</i> , 2019, 33, 1191-1207. | 2.7 | 38 |
| 79 | Cell cycle-regulated centers of DNA double-strand break repair. <i>Cell Cycle</i> , 2003, 2, 479-83. | 1.3 | 36 |
| 80 | Rad52 and Rad59 exhibit both overlapping and distinct functions. <i>DNA Repair</i> , 2007, 6, 27-37. | 1.3 | 34 |
| 81 | Long telomeres are preferentially extended during recombination-mediated telomere maintenance. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 451-456. | 3.6 | 34 |
| 82 | DNA-damaging agents stimulate the formation of directed reciprocal translocations in <i>Saccharomyces cerevisiae</i> . <i>Mutation Research DNA Repair</i> , 1994, 314, 121-133. | 3.8 | 32 |
| 83 | Kinetochores asymmetry defines a single yeast lineage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6673-6678. | 3.3 | 30 |
| 84 | Cell Biology of Homologous Recombination in Yeast. <i>Methods in Molecular Biology</i> , 2011, 745, 523-536. | 0.4 | 30 |
| 85 | Rif2 Promotes a Telomere Fold-Back Structure through Rpd3L Recruitment in Budding Yeast. <i>PLoS Genetics</i> , 2012, 8, e1002960. | 1.5 | 30 |
| 86 | Increased chromosomal mobility after DNA damage is controlled by interactions between the recombination machinery and the checkpoint. <i>Genes and Development</i> , 2018, 32, 1242-1251. | 2.7 | 29 |
| 87 | Telomerase Is Essential to Alleviate Pif1-Induced Replication Stress at Telomeres. <i>Genetics</i> , 2009, 183, 779-791. | 1.2 | 28 |
| 88 | A role for the unfolded protein response stress sensor ERN1 in regulating the response to MEK inhibitors in KRAS mutant colon cancers. <i>Genome Medicine</i> , 2018, 10, 90. | 3.6 | 28 |
| 89 | Systematic hybrid LOH: a new method to reduce false positives and negatives during screening of yeast gene deletion libraries. <i>Yeast</i> , 2006, 23, 1097-1106. | 0.8 | 27 |
| 90 | A Synthetic Dosage Lethal Genetic Interaction Between <i>CKS1B</i> and <i>PLK1</i> Is Conserved in Yeast and Human Cancer Cells. <i>Genetics</i> , 2016, 204, 807-819. | 1.2 | 27 |

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|-----|--|-----|-----------|
| 91 | More is not always better: the genetic constraints of polyploidy. <i>Trends in Genetics</i> , 2007, 23, 263-266. | 2.9 | 25 |
| 92 | Poetry in motion: Increased chromosomal mobility after DNA damage. <i>DNA Repair</i> , 2017, 56, 102-108. | 1.3 | 24 |
| 93 | Creation of a deletion series of mouse YACs covering a 500 kb region around Xist. <i>Nucleic Acids Research</i> , 1994, 22, 1830-1837. | 6.5 | 23 |
| 94 | High-Resolution YAC-Cosmid-STS Map of Human Chromosome 13. <i>Genomics</i> , 1998, 47, 26-43. | 1.3 | 22 |
| 95 | YAC transgene-mediated olfactory receptor gene choice. , 2000, 217, 225-231. | | 22 |
| 96 | Timing is everything: cell cycle control of Rad52. <i>Cell Division</i> , 2010, 5, 7. | 1.1 | 21 |
| 97 | The genetic consequences of ablating helicase activity and the Top3 interaction domain of Sgs1. <i>DNA Repair</i> , 2008, 7, 558-571. | 1.3 | 20 |
| 98 | Most, but not all, yeast strains in the deletion library contain the [PIN ⁺] prion. <i>Yeast</i> , 2010, 27, 159-166. | 0.8 | 20 |
| 99 | Srs2 overexpression reveals a helicase-independent role at replication forks that requires diverse cell functions. <i>DNA Repair</i> , 2011, 10, 506-517. | 1.3 | 19 |
| 100 | Xrs2 and Tel1 Independently Contribute to MR-Mediated DNA Tethering and Replisome Stability. <i>Cell Reports</i> , 2018, 25, 1681-1692.e4. | 2.9 | 19 |
| 101 | Rad52 multimerization is important for its nuclear localization in <i>Saccharomyces cerevisiae</i> . <i>DNA Repair</i> , 2008, 7, 57-66. | 1.3 | 18 |
| 102 | DNA damage triggers increased mobility of chromosomes in G1-phase cells. <i>Molecular Biology of the Cell</i> , 2019, 30, 2620-2625. | 0.9 | 18 |
| 103 | Rad5 dysregulation drives hyperactive recombination at replication forks resulting in cisplatin sensitivity and genome instability. <i>Nucleic Acids Research</i> , 2019, 47, 9144-9159. | 6.5 | 17 |
| 104 | Modification of the bacteriophage vector M13mp2: introduction of new restriction sites for cloning. <i>Gene</i> , 1981, 15, 167-176. | 1.0 | 16 |
| 105 | Assembly of Ordered Contigs of Cosmids Selected with YACs of Human Chromosome 13. <i>Genomics</i> , 1994, 21, 525-537. | 1.3 | 16 |
| 106 | New vectors for manipulation and selection of functional yeast artificial chromosomes (YACs) containing human DNA inserts. <i>Gene</i> , 1995, 155, 167-174. | 1.0 | 16 |
| 107 | Rsp5, a Ubiquitin-Protein Ligase, Is Involved in Degradation of the Single-Stranded-DNA Binding Protein Rfa1 in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2000, 20, 224-232. | 1.1 | 16 |
| 108 | Physical and genetic-interaction density reveals functional organization and informs significance cutoffs in genome-wide screens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7389-7394. | 3.3 | 16 |

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|-----|--|------|-----------|
| 109 | Sml1p Is a Dimer in Solution: Characterization of Denaturation and Renaturation of Recombinant Sml1p. <i>Biochemistry</i> , 2004, 43, 8568-8578. | 1.2 | 14 |
| 110 | Impaired Manganese Metabolism Causes Mitotic Misregulation. <i>Journal of Biological Chemistry</i> , 2012, 287, 18717-18729. | 1.6 | 14 |
| 111 | The shuffling of a mortal coil. <i>Nature Genetics</i> , 1999, 22, 4-6. | 9.4 | 13 |
| 112 | Bringing Rad52 foci into focus. <i>Journal of Cell Biology</i> , 2011, 194, 665-667. | 2.3 | 13 |
| 113 | Resection Activity of the Sgs1 Helicase Alters the Affinity of DNA Ends for Homologous Recombination Proteins in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2013, 195, 1241-1251. | 1.2 | 13 |
| 114 | kar-mediated plasmid transfer between yeast strains: Alternative to traditional transformation methods. <i>Methods in Enzymology</i> , 2002, 350, 278-289. | 0.4 | 12 |
| 115 | Cells Expressing Murine RAD52 Splice Variants Favor Sister Chromatid Repair. <i>Molecular and Cellular Biology</i> , 2006, 26, 3752-3763. | 1.1 | 11 |
| 116 | Recombination-Mediated Telomere Maintenance in <i>Saccharomyces cerevisiae</i> Is Not Dependent on the Shu Complex. <i>PLoS ONE</i> , 2016, 11, e0151314. | 1.1 | 11 |
| 117 | Rad10 exhibits lesion-dependent genetic requirements for recruitment to DNA double-strand breaks in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2009, 37, 6429-6438. | 6.5 | 10 |
| 118 | The PCNA Interaction Protein Box Sequence in Rad54 Is an Integral Part of Its ATPase Domain and Is Required for Efficient DNA Repair and Recombination. <i>PLoS ONE</i> , 2013, 8, e82630. | 1.1 | 9 |
| 119 | Functional genomics of the yeast DNA-damage response. <i>Genome Biology</i> , 2006, 7, 233. | 13.9 | 8 |
| 120 | Transfer of yeast artificial chromosomes into mammalian cells and comparative study of their integrity. <i>Gene</i> , 1995, 163, 27-33. | 1.0 | 7 |
| 121 | The rad52-Y66A allele alters the choice of donor template during spontaneous chromosomal recombination. <i>DNA Repair</i> , 2010, 9, 23-32. | 1.3 | 7 |
| 122 | Rif1/2 and Tel1 function in separate pathways during replicative senescence. <i>Cell Cycle</i> , 2011, 10, 3798-3799. | 1.3 | 7 |
| 123 | Stay Close to Your Sister. <i>Molecular Cell</i> , 2004, 14, 418-420. | 4.5 | 6 |
| 124 | ScreenTroll: a searchable database to compare genome-wide yeast screens. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas022. | 1.4 | 6 |
| 125 | The Shu complex regulates Rad52 localization during rDNA repair. <i>DNA Repair</i> , 2013, 12, 786-790. | 1.3 | 6 |
| 126 | The Ultimate (Mis)match: When DNA Meets RNA. <i>Cells</i> , 2021, 10, 1433. | 1.8 | 5 |

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|-----|---|-----|-----------|
| 127 | Visualizing global effects of the DNA damage response. <i>Nature Cell Biology</i> , 2012, 14, 900-901. | 4.6 | 1 |
| 128 | Gene Targeting and Homologous Recombination in <i>Saccharomyces cerevisiae</i> . <i>Topics in Current Genetics</i> , 2013, , 71-89. | 0.7 | 1 |
| 129 | The cell biology of mitotic recombination in <i>Saccharomyces cerevisiae</i> . <i>Topics in Current Genetics</i> , 2007, , 317-333. | 0.7 | 1 |
| 130 | Measuring Chromosome Pairing During Homologous Recombination in Yeast. <i>Methods in Molecular Biology</i> , 2021, 2153, 253-265. | 0.4 | 1 |
| 131 | The Cell Biology of Mitotic Recombination in <i>Saccharomyces Cerevisiae</i> . , 2006, , 317-333. | | 0 |
| 132 | Correction for Fu et al., Phosphorylation-Regulated Transitions in an Oligomeric State Control the Activity of the Sae2 DNA Repair Enzyme. <i>Molecular and Cellular Biology</i> , 2014, 34, 4213-4213. | 1.1 | 0 |
| 133 | Editorial overview: Recombination “the ends justify the means. <i>Current Opinion in Genetics and Development</i> , 2021, 71, iii-vii. | 1.5 | 0 |