

Rodney Rothstein

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

130
papers

20,571
citations

57
h-index

138
g-index

138
ext. papers

22,070
ext. citations

12.2
avg, IF

6.91
L-index

#	Paper	IF	Citations
130	Measuring Chromosome Pairing During Homologous Recombination in Yeast. <i>Methods in Molecular Biology</i> , 2021 , 2153, 253-265	1.4	0
129	The Ultimate (Mis)match: When DNA Meets RNA. <i>Cells</i> , 2021 , 10,	7.9	4
128	DNA damage triggers increased mobility of chromosomes in G1-phase cells. <i>Molecular Biology of the Cell</i> , 2019 , 30, 2620-2625	3.5	9
127	Rad5 dysregulation drives hyperactive recombination at replication forks resulting in cisplatin sensitivity and genome instability. <i>Nucleic Acids Research</i> , 2019 , 47, 9144-9159	20.1	9
126	Guidelines for DNA recombination and repair studies: Cellular assays of DNA repair pathways. <i>Microbial Cell</i> , 2019 , 6, 1-64	3.9	27
125	Defining the influence of Rad51 and Dmc1 lineage-specific amino acids on genetic recombination. <i>Genes and Development</i> , 2019 , 33, 1191-1207	12.6	21
124	Xrs2 and Tel1 Independently Contribute to MR-Mediated DNA Tethering and Replisome Stability. <i>Cell Reports</i> , 2018 , 25, 1681-1692.e4	10.6	13
123	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	14.4	15
122	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	12.6	14
121	Poetry in motion: Increased chromosomal mobility after DNA damage. <i>DNA Repair</i> , 2017 , 56, 102-108	4.3	17
120	CRISPR-Mediated Base Editing Enables Efficient Disruption of Eukaryotic Genes through Induction of STOP Codons. <i>Molecular Cell</i> , 2017 , 67, 1068-1079.e4	17.6	191
119	Multi-scale tracking reveals scale-dependent chromatin dynamics after DNA damage. <i>Molecular Biology of the Cell</i> , 2017 ,	3.5	44
118	Recombination-Mediated Telomere Maintenance in <i>Saccharomyces cerevisiae</i> Is Not Dependent on the Shu Complex. <i>PLoS ONE</i> , 2016 , 11, e0151314	3.7	6
117	A Synthetic Dosage Lethal Genetic Interaction Between CKS1B and PLK1 Is Conserved in Yeast and Human Cancer Cells. <i>Genetics</i> , 2016 , 204, 807-819	4	19
116	Cell biology of mitotic recombination. <i>Cold Spring Harbor Perspectives in Biology</i> , 2015 , 7, a016535	10.2	34
115	Mechanisms and regulation of mitotic recombination in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2014 , 198, 795-835	4	217
114	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	4.8	78

113	Phosphorylation-regulated transitions in an oligomeric state control the activity of the Sae2 DNA repair enzyme. <i>Molecular and Cellular Biology</i> , 2014 , 34, 778-93	4.8	36
112	DNA in motion during double-strand break repair. <i>Trends in Cell Biology</i> , 2013 , 23, 529-36	18.3	48
111	Repair of strand breaks by homologous recombination. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013 , 5, a012740	10.2	543
110	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, 1241-51	4	12
109	The Shu complex regulates Rad52 localization during rDNA repair. <i>DNA Repair</i> , 2013 , 12, 786-90	4.3	5
108	Gene Targeting and Homologous Recombination in <i>Saccharomyces cerevisiae</i> . <i>Topics in Current Genetics</i> , 2013 , 71-89		1
107	Telomere length homeostasis responds to changes in intracellular dNTP pools. <i>Genetics</i> , 2013 , 193, 1095-1105	4.105	32
106	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	6	63
105	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, 7389-94	11.5	12
104	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	3.7	8
103	Visualizing global effects of the DNA damage response. <i>Nature Cell Biology</i> , 2012 , 14, 900-1	23.4	1
102	Increased chromosome mobility facilitates homology search during recombination. <i>Nature Cell Biology</i> , 2012 , 14, 510-7	23.4	250
101	Sec24p and Sec16p cooperate to regulate the GTP cycle of the COPII coat. <i>EMBO Journal</i> , 2012 , 31, 1014-17	4.37	76
100	Rif2 promotes a telomere fold-back structure through Rpd3L recruitment in budding yeast. <i>PLoS Genetics</i> , 2012 , 8, e1002960	6	24
99	ScreenTroll: a searchable database to compare genome-wide yeast screens. <i>Database: the Journal of Biological Databases and Curation</i> , 2012 , 2012, bas022	5	3
98	Impaired manganese metabolism causes mitotic misregulation. <i>Journal of Biological Chemistry</i> , 2012 , 287, 18717-29	5.4	9
97	Cell biology of homologous recombination in yeast. <i>Methods in Molecular Biology</i> , 2011 , 745, 523-36	1.4	23
96	Long telomeres are preferentially extended during recombination-mediated telomere maintenance. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 451-6	17.6	33

95	HDACs link the DNA damage response, processing of double-strand breaks and autophagy. <i>Nature</i> , 2011 , 471, 74-79	50.4	305
94	Srs2 overexpression reveals a helicase-independent role at replication forks that requires diverse cell functions. <i>DNA Repair</i> , 2011 , 10, 506-17	4.3	15
93	Rif1/2 and Tel1 function in separate pathways during replicative senescence. <i>Cell Cycle</i> , 2011 , 10, 3798-94.7		6
92	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, 1599-607	3.5	65
91	Selective ploidy ablation, a high-throughput plasmid transfer protocol, identifies new genes affecting topoisomerase I-induced DNA damage. <i>Genome Research</i> , 2011 , 21, 477-86	9.7	65
90	Bringing Rad52 foci into focus. <i>Journal of Cell Biology</i> , 2011 , 194, 665-7	7.3	11
89	The ribonucleotide reductase inhibitor, Sml1, is sequentially phosphorylated, ubiquitylated and degraded in response to DNA damage. <i>Nucleic Acids Research</i> , 2010 , 38, 6490-501	20.1	55
88	The RecQ DNA helicases in DNA repair. <i>Annual Review of Genetics</i> , 2010 , 44, 393-417	14.5	215
87	Most, but not all, yeast strains in the deletion library contain the [PIN(+)] prion. <i>Yeast</i> , 2010 , 27, 159-66	3.4	15
86	ScreenMill: a freely available software suite for growth measurement, analysis and visualization of high-throughput screen data. <i>BMC Bioinformatics</i> , 2010 , 11, 353	3.6	64
85	The rad52-Y66A allele alters the choice of donor template during spontaneous chromosomal recombination. <i>DNA Repair</i> , 2010 , 9, 23-32	4.3	7
84	Cooperativity of Mus81.Mms4 with Rad54 in the resolution of recombination and replication intermediates. <i>Journal of Biological Chemistry</i> , 2009 , 284, 7733-45	5.4	47
83	Kinetochore asymmetry defines a single yeast lineage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 6673-8	11.5	27
82	Localization of recombination proteins and Srs2 reveals anti-recombinase function in vivo. <i>Journal of Cell Biology</i> , 2009 , 185, 969-81	7.3	61
81	Role of the Rad52 amino-terminal DNA binding activity in DNA strand capture in homologous recombination. <i>Journal of Biological Chemistry</i> , 2009 , 284, 33275-84	5.4	38
80	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, 6429-38	20.1	9
79	Telomerase is essential to alleviate pif1-induced replication stress at telomeres. <i>Genetics</i> , 2009 , 183, 779-91	4	22
78	Rad52. <i>Current Biology</i> , 2009 , 19, R676-7	6.3	64

77	Choreography of recombination proteins during the DNA damage response. <i>DNA Repair</i> , 2009 , 8, 1068-74	6.3	88
76	Sgs1 function in the repair of DNA replication intermediates is separable from its role in homologous recombinational repair. <i>EMBO Journal</i> , 2009 , 28, 915-25	13	55
75	Rad52 recruitment is DNA replication independent and regulated by Cdc28 and the Mec1 kinase. <i>EMBO Journal</i> , 2009 , 28, 1121-30	13	54
74	At loose ends: resecting a double-strand break. <i>Cell</i> , 2009 , 137, 807-10	56.2	80
73	Quality control of DNA break metabolism: in the 'end', it's a good thing. <i>EMBO Journal</i> , 2008 , 27, 581-8	13	53
72	Rad52 multimerization is important for its nuclear localization in <i>Saccharomyces cerevisiae</i> . <i>DNA Repair</i> , 2008 , 7, 57-66	4.3	13
71	The genetic consequences of ablating helicase activity and the Top3 interaction domain of Sgs1. <i>DNA Repair</i> , 2008 , 7, 558-71	4.3	19
70	Differential regulation of the cellular response to DNA double-strand breaks in G1. <i>Molecular Cell</i> , 2008 , 30, 73-85	17.6	132
69	Chromosome-scale genetic mapping using a set of 16 conditionally stable <i>Saccharomyces cerevisiae</i> chromosomes. <i>Genetics</i> , 2008 , 180, 1799-808	4	35
68	Alu elements mediate MYB gene tandem duplication in human T-ALL. <i>Journal of Experimental Medicine</i> , 2007 , 204, 3059-66	16.6	71
67	The Smc5-Smc6 complex and SUMO modification of Rad52 regulates recombinational repair at the ribosomal gene locus. <i>Nature Cell Biology</i> , 2007 , 9, 923-31	23.4	292
66	Rad52 and Rad59 exhibit both overlapping and distinct functions. <i>DNA Repair</i> , 2007 , 6, 27-37	4.3	30
65	Genome-wide analysis of Rad52 foci reveals diverse mechanisms impacting recombination. <i>PLoS Genetics</i> , 2007 , 3, e228	6	141
64	The Slx5-Slx8 complex affects sumoylation of DNA repair proteins and negatively regulates recombination. <i>Molecular and Cellular Biology</i> , 2007 , 27, 6153-62	4.8	119
63	More is not always better: the genetic constraints of polyploidy. <i>Trends in Genetics</i> , 2007 , 23, 263-6	8.5	24
62	The cell biology of mitotic recombination in <i>Saccharomyces cerevisiae</i> . <i>Topics in Current Genetics</i> , 2007 , 317-333		
61	The Cell Biology of Mitotic Recombination in <i>Saccharomyces Cerevisiae</i> 2006 , 317-333		
60	Multiple start codons and phosphorylation result in discrete Rad52 protein species. <i>Nucleic Acids Research</i> , 2006 , 34, 2587-97	20.1	28

59	The role of DNA double-strand breaks in spontaneous homologous recombination in <i>S. cerevisiae</i> . <i>PLoS Genetics</i> , 2006 , 2, e194	6	77
58	The absence of Top3 reveals an interaction between the Sgs1 and Pif1 DNA helicases in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2006 , 174, 555-73	4	38
57	Cells expressing murine RAD52 splice variants favor sister chromatid repair. <i>Molecular and Cellular Biology</i> , 2006 , 26, 3752-63	4.8	9
56	Functional genomics of the yeast DNA-damage response. <i>Genome Biology</i> , 2006 , 7, 233	18.3	7
55	Systematic hybrid LOH: a new method to reduce false positives and negatives during screening of yeast gene deletion libraries. <i>Yeast</i> , 2006 , 23, 1097-106	3.4	23
54	Localization of checkpoint and repair proteins in eukaryotes. <i>Biochimie</i> , 2005 , 87, 579-89	4.6	51
53	RMI1/NCE4, a suppressor of genome instability, encodes a member of the RecQ helicase/Topo III complex. <i>EMBO Journal</i> , 2005 , 24, 2024-33	13	139
52	A genetic screen for top3 suppressors in <i>Saccharomyces cerevisiae</i> identifies SHU1, SHU2, PSY3 and CSM2: four genes involved in error-free DNA repair. <i>Genetics</i> , 2005 , 169, 1275-89	4	82
51	DNA repair: keeping it together. <i>Current Biology</i> , 2004 , 14, R994-6	6.3	34
50	DNA damage checkpoint and repair centers. <i>Current Opinion in Cell Biology</i> , 2004 , 16, 328-34	9	126
49	Choreography of the DNA damage response: spatiotemporal relationships among checkpoint and repair proteins. <i>Cell</i> , 2004 , 118, 699-713	56.2	735
48	Sml1p is a dimer in solution: characterization of denaturation and renaturation of recombinant Sml1p. <i>Biochemistry</i> , 2004 , 43, 8568-78	3.2	13
47	Stay close to your sister. <i>Molecular Cell</i> , 2004 , 14, 418-20	17.6	5
46	Cell Cycle-Regulated Centers of DNA Double-Strand Break Repair. <i>Cell Cycle</i> , 2003 , 2, 477-481	4.7	44
45	Colocalization of multiple DNA double-strand breaks at a single Rad52 repair centre. <i>Nature Cell Biology</i> , 2003 , 5, 572-7	23.4	346
44	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	56.2	343
43	Cell cycle-regulated centers of DNA double-strand break repair. <i>Cell Cycle</i> , 2003 , 2, 479-83	4.7	32
42	Efficient PCR-based gene disruption in <i>Saccharomyces</i> strains using intergenic primers. <i>Yeast</i> , 2002 , 19, 319-28	3.4	57

41	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, 3746-51	11.5	213
40	Kar-mediated plasmid transfer between yeast strains: alternative to traditional transformation methods. <i>Methods in Enzymology</i> , 2002 , 350, 278-89	1.7	11
39	Cloning-free genome alterations in <i>Saccharomyces cerevisiae</i> using adaptamer-mediated PCR. <i>Methods in Enzymology</i> , 2002 , 350, 258-77	1.7	83
38	Interaction with Rad51 is indispensable for recombination mediator function of Rad52. <i>Journal of Biological Chemistry</i> , 2002 , 277, 40132-41	5.4	92
37	A molecular genetic dissection of the evolutionarily conserved N terminus of yeast Rad52. <i>Genetics</i> , 2002 , 161, 549-62	4	65
36	Mutations in homologous recombination genes rescue top3 slow growth in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2002 , 162, 647-62	4	76
35	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, 3544-53	13	214
34	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, 8276-82	11.5	345
33	YAC transgene-mediated olfactory receptor gene choice. <i>Developmental Dynamics</i> , 2000 , 217, 225-31	2.9	21
32	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, 224-32	4.8	14
31	Mutational and structural analyses of the ribonucleotide reductase inhibitor Sml1 define its Rnr1 interaction domain whose inactivation allows suppression of mec1 and rad53 lethality. <i>Molecular and Cellular Biology</i> , 2000 , 20, 9076-83	4.8	75
30	Characterization of genetic interactions with RFA1: the role of RPA in DNA replication and telomere maintenance. <i>Biochimie</i> , 2000 , 82, 71-8	4.6	60
29	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, 1900-4	11	42
28	Evolutionary implications of the frequent horizontal transfer of mismatch repair genes. <i>Cell</i> , 2000 , 103, 711-21	56.2	198
27	Replication fork pausing and recombination or "give me a break" <i>Genes and Development</i> , 2000 , 14, 1-10	12.6	155
26	Three-dimensional microscopy of the Rad51 recombination protein during meiotic prophase. <i>Plant Cell</i> , 1999 , 11, 809-24	11.6	150
25	An allele of RFA1 suppresses RAD52-dependent double-strand break repair in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 1999 , 151, 447-58	4	55
24	A suppressor of two essential checkpoint genes identifies a novel protein that negatively affects dNTP pools. <i>Molecular Cell</i> , 1998 , 2, 329-40	17.6	605

23	High-resolution YAC-cosmid-STS map of human chromosome 13. <i>Genomics</i> , 1998 , 47, 26-43	4.3	21
22	Cloning-free PCR-based allele replacement methods. <i>Genome Research</i> , 1997 , 7, 1174-83	9.7	146
21	The complete set of predicted genes from <i>Saccharomyces cerevisiae</i> in a readily usable form. <i>Genome Research</i> , 1997 , 7, 1169-73	9.7	115
20	Holliday junctions accumulate in replication mutants via a RecA homolog-independent mechanism. <i>Cell</i> , 1997 , 90, 87-96	56.2	243
19	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, 10729-34	11.5	385
18	Direct association between the yeast Rad51 and Rad54 recombination proteins. <i>Journal of Biological Chemistry</i> , 1996 , 271, 33181-6	5.4	129
17	New vectors for manipulation and selection of functional yeast artificial chromosomes (YACs) containing human DNA inserts. <i>Gene</i> , 1995 , 155, 167-74	3.8	14
16	Transfer of yeast artificial chromosomes into mammalian cells and comparative study of their integrity. <i>Gene</i> , 1995 , 163, 27-33	3.8	7
15	Creation of a deletion series of mouse YACs covering a 500 kb region around Xist. <i>Nucleic Acids Research</i> , 1994 , 22, 1830-7	20.1	20
14	A yeast mating-selection scheme for detection of protein-protein interactions. <i>Nucleic Acids Research</i> , 1994 , 22, 1778-9	20.1	117
13	Assembly of ordered contigs of cosmids selected with YACs of human chromosome 13. <i>Genomics</i> , 1994 , 21, 525-37	4.3	15
12	Identification of a mouse homologue of the <i>Saccharomyces cerevisiae</i> recombination and repair gene, RAD52. <i>Genomics</i> , 1994 , 23, 300-3	4.3	41
11	DNA-damaging agents stimulate the formation of directed reciprocal translocations in <i>Saccharomyces cerevisiae</i> . <i>Mutation Research DNA Repair</i> , 1994 , 314, 121-33		24
10	Sex, maps, and imprinting. <i>Cell</i> , 1991 , 64, 1-3	56.2	102
9	Targeting, disruption, replacement, and allele rescue: integrative DNA transformation in yeast. <i>Methods in Enzymology</i> , 1991 , 194, 281-301	1.7	1115
8	A hyper-recombination mutation in <i>S. cerevisiae</i> identifies a novel eukaryotic topoisomerase. <i>Cell</i> , 1989 , 58, 409-19	56.2	507
7	Elevated recombination rates in transcriptionally active DNA. <i>Cell</i> , 1989 , 56, 619-30	56.2	1496
6	Genetic applications of yeast transformation with linear and gapped plasmids. <i>Methods in Enzymology</i> , 1983 , 101, 228-45	1.7	449

5	One-step gene disruption in yeast. <i>Methods in Enzymology</i> , 1983 , 101, 202-11	1.7	2980
4	The double-strand-break repair model for recombination. <i>Cell</i> , 1983 , 33, 25-35	56.2	2305
3	Modification of the bacteriophage vector M13mp2: introduction of new restriction sites for cloning. <i>Gene</i> , 1981 , 15, 167-76	3.8	11
2	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, 6354-8	11.5	1379
1	Deletions of a tyrosine tRNA gene in <i>S. cerevisiae</i> . <i>Cell</i> , 1979 , 17, 185-90	56.2	60