

# Rodney Rothstein

## List of Publications by Citations

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130  
papers

20,571  
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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	One-step gene disruption in yeast. <i>Methods in Enzymology</i> , <b>1983</b> , 101, 202-11	1.7	2980
129	The double-strand-break repair model for recombination. <i>Cell</i> , <b>1983</b> , 33, 25-35	56.2	2305
128	Elevated recombination rates in transcriptionally active DNA. <i>Cell</i> , <b>1989</b> , 56, 619-30	56.2	1496
127	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> , <b>1981</b> , 78, 6354-8	11.5	1379
126	Targeting, disruption, replacement, and allele rescue: integrative DNA transformation in yeast. <i>Methods in Enzymology</i> , <b>1991</b> , 194, 281-301	1.7	1115
125	Choreography of the DNA damage response: spatiotemporal relationships among checkpoint and repair proteins. <i>Cell</i> , <b>2004</b> , 118, 699-713	56.2	735
124	A suppressor of two essential checkpoint genes identifies a novel protein that negatively affects dNTP pools. <i>Molecular Cell</i> , <b>1998</b> , 2, 329-40	17.6	605
123	Repair of strand breaks by homologous recombination. <i>Cold Spring Harbor Perspectives in Biology</i> , <b>2013</b> , 5, a012740	10.2	543
122	A hyper-recombination mutation in <i>S. cerevisiae</i> identifies a novel eukaryotic topoisomerase. <i>Cell</i> , <b>1989</b> , 58, 409-19	56.2	507
121	Genetic applications of yeast transformation with linear and gapped plasmids. <i>Methods in Enzymology</i> , <b>1983</b> , 101, 228-45	1.7	449
120	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> , <b>1996</b> , 93, 10729-34	11.5	385
119	Colocalization of multiple DNA double-strand breaks at a single Rad52 repair centre. <i>Nature Cell Biology</i> , <b>2003</b> , 5, 572-7	23.4	346
118	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> , <b>2001</b> , 98, 8276-82	11.5	345
117	Survival of DNA damage in yeast directly depends on increased dNTP levels allowed by relaxed feedback inhibition of ribonucleotide reductase. <i>Cell</i> , <b>2003</b> , 112, 391-401	56.2	343
116	HDACs link the DNA damage response, processing of double-strand breaks and autophagy. <i>Nature</i> , <b>2011</b> , 471, 74-79	50.4	305
115	The Smc5-Smc6 complex and SUMO modification of Rad52 regulates recombinational repair at the ribosomal gene locus. <i>Nature Cell Biology</i> , <b>2007</b> , 9, 923-31	23.4	292
114	Increased chromosome mobility facilitates homology search during recombination. <i>Nature Cell Biology</i> , <b>2012</b> , 14, 510-7	23.4	250

113	Holliday junctions accumulate in replication mutants via a RecA homolog-independent mechanism. <i>Cell</i> , <b>1997</b> , 90, 87-96	56.2	243
112	Mechanisms and regulation of mitotic recombination in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , <b>2014</b> , 198, 795-835	4	217
111	The RecQ DNA helicases in DNA repair. <i>Annual Review of Genetics</i> , <b>2010</b> , 44, 393-417	14.5	215
110	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> , <b>2001</b> , 20, 3544-53	13	214
109	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> , <b>2002</b> , 99, 3746-51	11.5	213
108	Evolutionary implications of the frequent horizontal transfer of mismatch repair genes. <i>Cell</i> , <b>2000</b> , 103, 711-21	56.2	198
107	CRISPR-Mediated Base Editing Enables Efficient Disruption of Eukaryotic Genes through Induction of STOP Codons. <i>Molecular Cell</i> , <b>2017</b> , 67, 1068-1079.e4	17.6	191
106	Replication fork pausing and recombination or "gimme a break" <i>Genes and Development</i> , <b>2000</b> , 14, 1-10	12.6	155
105	Three-dimensional microscopy of the Rad51 recombination protein during meiotic prophase. <i>Plant Cell</i> , <b>1999</b> , 11, 809-24	11.6	150
104	Cloning-free PCR-based allele replacement methods. <i>Genome Research</i> , <b>1997</b> , 7, 1174-83	9.7	146
103	Genome-wide analysis of Rad52 foci reveals diverse mechanisms impacting recombination. <i>PLoS Genetics</i> , <b>2007</b> , 3, e228	6	141
102	RMI1/NCE4, a suppressor of genome instability, encodes a member of the RecQ helicase/Topo III complex. <i>EMBO Journal</i> , <b>2005</b> , 24, 2024-33	13	139
101	Differential regulation of the cellular response to DNA double-strand breaks in G1. <i>Molecular Cell</i> , <b>2008</b> , 30, 73-85	17.6	132
100	Direct association between the yeast Rad51 and Rad54 recombination proteins. <i>Journal of Biological Chemistry</i> , <b>1996</b> , 271, 33181-6	5.4	129
99	DNA damage checkpoint and repair centers. <i>Current Opinion in Cell Biology</i> , <b>2004</b> , 16, 328-34	9	126
98	The Slx5-Slx8 complex affects sumoylation of DNA repair proteins and negatively regulates recombination. <i>Molecular and Cellular Biology</i> , <b>2007</b> , 27, 6153-62	4.8	119
97	A yeast mating-selection scheme for detection of protein-protein interactions. <i>Nucleic Acids Research</i> , <b>1994</b> , 22, 1778-9	20.1	117
96	The complete set of predicted genes from <i>Saccharomyces cerevisiae</i> in a readily usable form. <i>Genome Research</i> , <b>1997</b> , 7, 1169-73	9.7	115

95	Sex, maps, and imprinting. <i>Cell</i> , <b>1991</b> , 64, 1-3	56.2	102
94	Interaction with Rad51 is indispensable for recombination mediator function of Rad52. <i>Journal of Biological Chemistry</i> , <b>2002</b> , 277, 40132-41	5.4	92
93	Choreography of recombination proteins during the DNA damage response. <i>DNA Repair</i> , <b>2009</b> , 8, 1068-76	4.3	88
92	Cloning-free genome alterations in <i>Saccharomyces cerevisiae</i> using adaptamer-mediated PCR. <i>Methods in Enzymology</i> , <b>2002</b> , 350, 258-77	1.7	83
91	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> , <b>2005</b> , 169, 1275-89	4	82
90	At loose ends: resecting a double-strand break. <i>Cell</i> , <b>2009</b> , 137, 807-10	56.2	80
89	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> , <b>2014</b> , 34, 4213-4213	4.8	78
88	The role of DNA double-strand breaks in spontaneous homologous recombination in <i>S. cerevisiae</i> . <i>PLoS Genetics</i> , <b>2006</b> , 2, e194	6	77
87	Sec24p and Sec16p cooperate to regulate the GTP cycle of the COPII coat. <i>EMBO Journal</i> , <b>2012</b> , 31, 1014-27	4.7	76
86	Mutations in homologous recombination genes rescue top3 slow growth in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , <b>2002</b> , 162, 647-62	4	76
85	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> , <b>2000</b> , 20, 9076-83	4.8	75
84	Alu elements mediate MYB gene tandem duplication in human T-ALL. <i>Journal of Experimental Medicine</i> , <b>2007</b> , 204, 3059-66	16.6	71
83	The Shu complex, which contains Rad51 paralogues, promotes DNA repair through inhibition of the Srs2 anti-recombinase. <i>Molecular Biology of the Cell</i> , <b>2011</b> , 22, 1599-607	3.5	65
82	Selective ploidy ablation, a high-throughput plasmid transfer protocol, identifies new genes affecting topoisomerase I-induced DNA damage. <i>Genome Research</i> , <b>2011</b> , 21, 477-86	9.7	65
81	A molecular genetic dissection of the evolutionarily conserved N terminus of yeast Rad52. <i>Genetics</i> , <b>2002</b> , 161, 549-62	4	65
80	Rad52. <i>Current Biology</i> , <b>2009</b> , 19, R676-7	6.3	64
79	ScreenMill: a freely available software suite for growth measurement, analysis and visualization of high-throughput screen data. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 353	3.6	64
78	Histone H3K56 acetylation, Rad52, and non-DNA repair factors control double-strand break repair choice with the sister chromatid. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003237	6	63

77	Localization of recombination proteins and Srs2 reveals anti-recombinase function in vivo. <i>Journal of Cell Biology</i> , <b>2009</b> , 185, 969-81	7.3	61
76	Characterization of genetic interactions with RFA1: the role of RPA in DNA replication and telomere maintenance. <i>Biochimie</i> , <b>2000</b> , 82, 71-8	4.6	60
75	Deletions of a tyrosine tRNA gene in <i>S. cerevisiae</i> . <i>Cell</i> , <b>1979</b> , 17, 185-90	56.2	60
74	Efficient PCR-based gene disruption in <i>Saccharomyces</i> strains using intergenic primers. <i>Yeast</i> , <b>2002</b> , 19, 319-28	3.4	57
73	The ribonucleotide reductase inhibitor, Sml1, is sequentially phosphorylated, ubiquitylated and degraded in response to DNA damage. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, 6490-501	20.1	55
72	Sgs1 function in the repair of DNA replication intermediates is separable from its role in homologous recombinational repair. <i>EMBO Journal</i> , <b>2009</b> , 28, 915-25	13	55
71	An allele of RFA1 suppresses RAD52-dependent double-strand break repair in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , <b>1999</b> , 151, 447-58	4	55
70	Rad52 recruitment is DNA replication independent and regulated by Cdc28 and the Mec1 kinase. <i>EMBO Journal</i> , <b>2009</b> , 28, 1121-30	13	54
69	Quality control of DNA break metabolism: in the 'end', it's a good thing. <i>EMBO Journal</i> , <b>2008</b> , 27, 581-8	13	53
68	Localization of checkpoint and repair proteins in eukaryotes. <i>Biochimie</i> , <b>2005</b> , 87, 579-89	4.6	51
67	DNA in motion during double-strand break repair. <i>Trends in Cell Biology</i> , <b>2013</b> , 23, 529-36	18.3	48
66	Cooperativity of Mus81.Mms4 with Rad54 in the resolution of recombination and replication intermediates. <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 7733-45	5.4	47
65	Multi-scale tracking reveals scale-dependent chromatin dynamics after DNA damage. <i>Molecular Biology of the Cell</i> , <b>2017</b> ,	3.5	44
64	Cell Cycle-Regulated Centers of DNA Double-Strand Break Repair. <i>Cell Cycle</i> , <b>2003</b> , 2, 477-481	4.7	44
63	Intragenic inversion of mtDNA: a new type of pathogenic mutation in a patient with mitochondrial myopathy. <i>American Journal of Human Genetics</i> , <b>2000</b> , 66, 1900-4	11	42
62	Identification of a mouse homologue of the <i>Saccharomyces cerevisiae</i> recombination and repair gene, RAD52. <i>Genomics</i> , <b>1994</b> , 23, 300-3	4.3	41
61	Role of the Rad52 amino-terminal DNA binding activity in DNA strand capture in homologous recombination. <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 33275-84	5.4	38
60	The absence of Top3 reveals an interaction between the Sgs1 and Pif1 DNA helicases in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , <b>2006</b> , 174, 555-73	4	38

59	Phosphorylation-regulated transitions in an oligomeric state control the activity of the Sae2 DNA repair enzyme. <i>Molecular and Cellular Biology</i> , <b>2014</b> , 34, 778-93	4.8	36
58	Chromosome-scale genetic mapping using a set of 16 conditionally stable <i>Saccharomyces cerevisiae</i> chromosomes. <i>Genetics</i> , <b>2008</b> , 180, 1799-808	4	35
57	Cell biology of mitotic recombination. <i>Cold Spring Harbor Perspectives in Biology</i> , <b>2015</b> , 7, a016535	10.2	34
56	DNA repair: keeping it together. <i>Current Biology</i> , <b>2004</b> , 14, R994-6	6.3	34
55	Long telomeres are preferentially extended during recombination-mediated telomere maintenance. <i>Nature Structural and Molecular Biology</i> , <b>2011</b> , 18, 451-6	17.6	33
54	Telomere length homeostasis responds to changes in intracellular dNTP pools. <i>Genetics</i> , <b>2013</b> , 193, 1095-1105	4.1	32
53	Cell cycle-regulated centers of DNA double-strand break repair. <i>Cell Cycle</i> , <b>2003</b> , 2, 479-83	4.7	32
52	Rad52 and Rad59 exhibit both overlapping and distinct functions. <i>DNA Repair</i> , <b>2007</b> , 6, 27-37	4.3	30
51	Multiple start codons and phosphorylation result in discrete Rad52 protein species. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, 2587-97	20.1	28
50	Guidelines for DNA recombination and repair studies: Cellular assays of DNA repair pathways. <i>Microbial Cell</i> , <b>2019</b> , 6, 1-64	3.9	27
49	Kinetochores asymmetry defines a single yeast lineage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 6673-8	11.5	27
48	Rif2 promotes a telomere fold-back structure through Rpd3L recruitment in budding yeast. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002960	6	24
47	More is not always better: the genetic constraints of polyploidy. <i>Trends in Genetics</i> , <b>2007</b> , 23, 263-6	8.5	24
46	DNA-damaging agents stimulate the formation of directed reciprocal translocations in <i>Saccharomyces cerevisiae</i> . <i>Mutation Research DNA Repair</i> , <b>1994</b> , 314, 121-33		24
45	Cell biology of homologous recombination in yeast. <i>Methods in Molecular Biology</i> , <b>2011</b> , 745, 523-36	1.4	23
44	Systematic hybrid LOH: a new method to reduce false positives and negatives during screening of yeast gene deletion libraries. <i>Yeast</i> , <b>2006</b> , 23, 1097-106	3.4	23
43	Telomerase is essential to alleviate pif1-induced replication stress at telomeres. <i>Genetics</i> , <b>2009</b> , 183, 779-91	4	22
42	Defining the influence of Rad51 and Dmc1 lineage-specific amino acids on genetic recombination. <i>Genes and Development</i> , <b>2019</b> , 33, 1191-1207	12.6	21

41	YAC transgene-mediated olfactory receptor gene choice. <i>Developmental Dynamics</i> , <b>2000</b> , 217, 225-31	2.9	21
40	High-resolution YAC-cosmid-STS map of human chromosome 13. <i>Genomics</i> , <b>1998</b> , 47, 26-43	4.3	21
39	Creation of a deletion series of mouse YACs covering a 500 kb region around Xist. <i>Nucleic Acids Research</i> , <b>1994</b> , 22, 1830-7	20.1	20
38	The genetic consequences of ablating helicase activity and the Top3 interaction domain of Sgs1. <i>DNA Repair</i> , <b>2008</b> , 7, 558-71	4.3	19
37	A Synthetic Dosage Lethal Genetic Interaction Between CKS1B and PLK1 Is Conserved in Yeast and Human Cancer Cells. <i>Genetics</i> , <b>2016</b> , 204, 807-819	4	19
36	Poetry in motion: Increased chromosomal mobility after DNA damage. <i>DNA Repair</i> , <b>2017</b> , 56, 102-108	4.3	17
35	Srs2 overexpression reveals a helicase-independent role at replication forks that requires diverse cell functions. <i>DNA Repair</i> , <b>2011</b> , 10, 506-17	4.3	15
34	Most, but not all, yeast strains in the deletion library contain the [PIN(+)] prion. <i>Yeast</i> , <b>2010</b> , 27, 159-66	3.4	15
33	Assembly of ordered contigs of cosmids selected with YACs of human chromosome 13. <i>Genomics</i> , <b>1994</b> , 21, 525-37	4.3	15
32	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> , <b>2018</b> , 10, 90	14.4	15
31	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> , <b>2000</b> , 20, 224-32	4.8	14
30	New vectors for manipulation and selection of functional yeast artificial chromosomes (YACs) containing human DNA inserts. <i>Gene</i> , <b>1995</b> , 155, 167-74	3.8	14
29	Increased chromosomal mobility after DNA damage is controlled by interactions between the recombination machinery and the checkpoint. <i>Genes and Development</i> , <b>2018</b> , 32, 1242-1251	12.6	14
28	Rad52 multimerization is important for its nuclear localization in <i>Saccharomyces cerevisiae</i> . <i>DNA Repair</i> , <b>2008</b> , 7, 57-66	4.3	13
27	Sml1p is a dimer in solution: characterization of denaturation and renaturation of recombinant Sml1p. <i>Biochemistry</i> , <b>2004</b> , 43, 8568-78	3.2	13
26	Xrs2 and Tel1 Independently Contribute to MR-Mediated DNA Tethering and Replisome Stability. <i>Cell Reports</i> , <b>2018</b> , 25, 1681-1692.e4	10.6	13
25	Resection activity of the Sgs1 helicase alters the affinity of DNA ends for homologous recombination proteins in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , <b>2013</b> , 195, 1241-51	4	12
24	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> , <b>2013</b> , 110, 7389-94	11.5	12

23	Bringing Rad52 foci into focus. <i>Journal of Cell Biology</i> , <b>2011</b> , 194, 665-7	7.3	11
22	Kar-mediated plasmid transfer between yeast strains: alternative to traditional transformation methods. <i>Methods in Enzymology</i> , <b>2002</b> , 350, 278-89	1.7	11
21	Modification of the bacteriophage vector M13mp2: introduction of new restriction sites for cloning. <i>Gene</i> , <b>1981</b> , 15, 167-76	3.8	11
20	DNA damage triggers increased mobility of chromosomes in G1-phase cells. <i>Molecular Biology of the Cell</i> , <b>2019</b> , 30, 2620-2625	3.5	9
19	Rad5 dysregulation drives hyperactive recombination at replication forks resulting in cisplatin sensitivity and genome instability. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 9144-9159	20.1	9
18	Rad10 exhibits lesion-dependent genetic requirements for recruitment to DNA double-strand breaks in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , <b>2009</b> , 37, 6429-38	20.1	9
17	Impaired manganese metabolism causes mitotic misregulation. <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 18717-29	5.4	9
16	Cells expressing murine RAD52 splice variants favor sister chromatid repair. <i>Molecular and Cellular Biology</i> , <b>2006</b> , 26, 3752-63	4.8	9
15	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> , <b>2013</b> , 8, e82630	3.7	8
14	The rad52-Y66A allele alters the choice of donor template during spontaneous chromosomal recombination. <i>DNA Repair</i> , <b>2010</b> , 9, 23-32	4.3	7
13	Functional genomics of the yeast DNA-damage response. <i>Genome Biology</i> , <b>2006</b> , 7, 233	18.3	7
12	Transfer of yeast artificial chromosomes into mammalian cells and comparative study of their integrity. <i>Gene</i> , <b>1995</b> , 163, 27-33	3.8	7
11	Rif1/2 and Tel1 function in separate pathways during replicative senescence. <i>Cell Cycle</i> , <b>2011</b> , 10, 3798-94.7		6
10	Recombination-Mediated Telomere Maintenance in <i>Saccharomyces cerevisiae</i> Is Not Dependent on the Shu Complex. <i>PLoS ONE</i> , <b>2016</b> , 11, e0151314	3.7	6
9	The Shu complex regulates Rad52 localization during rDNA repair. <i>DNA Repair</i> , <b>2013</b> , 12, 786-90	4.3	5
8	Stay close to your sister. <i>Molecular Cell</i> , <b>2004</b> , 14, 418-20	17.6	5
7	The Ultimate (Mis)match: When DNA Meets RNA. <i>Cells</i> , <b>2021</b> , 10,	7.9	4
6	ScreenTroll: a searchable database to compare genome-wide yeast screens. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2012</b> , 2012, bas022	5	3



- 5 Visualizing global effects of the DNA damage response. *Nature Cell Biology*, **2012**, 14, 900-1 23.4 1
- 4 Gene Targeting and Homologous Recombination in *Saccharomyces cerevisiae*. *Topics in Current Genetics*, **2013**, 71-89 1
- 3 Measuring Chromosome Pairing During Homologous Recombination in Yeast. *Methods in Molecular Biology*, **2021**, 2153, 253-265 1.4 0
- 2 The Cell Biology of Mitotic Recombination in *Saccharomyces Cerevisiae* **2006**, 317-333
- 1 The cell biology of mitotic recombination in *Saccharomyces cerevisiae*. *Topics in Current Genetics*, **2007**, 317-333