James E Haber

List of Publications by Year
in descending order

234 papers	32,554 citations	4960 84 h-index	4548 171 g-index
263 all docs	263 docs citations	263 times ranked	29887 citing authors

#	Article	IF	Citations
1	DNA replication: the recombination connection. Trends in Cell Biology, 2022, 32, 45-57.	7.9	37
2	Loop extrusion as a mechanism for formation of DNA damage repair foci. Nature, 2021, 590, 660-665.	27.8	175
3	Modified chromosome structure caused by phosphomimetic H2A modulates the DNA damage response by increasing chromatin mobility in yeast. Journal of Cell Science, 2021, 134, .	2.0	8
4	Single-strand template repair: key insights to increase the efficiency of gene editing. Current Genetics, 2021, 67, 747-753.	1.7	14
5	Mechanisms restraining breakâ€induced replication at twoâ€ended DNA doubleâ€strand breaks. EMBO Journal, 2021, 40, e104847.	7.8	45
6	Learning Yeast Genetics from Miro Radman. Cells, 2021, 10, 945.	4.1	1
7	Local nucleosome dynamics and eviction following a double-strand break are reversible by NHEJ-mediated repair in the absence of DNA replication. Genome Research, 2021, 31, 775-788.	5.5	10
8	Monitoring Gene Conversion in Budding Yeast by Southern Blot Analysis. Methods in Molecular Biology, 2021, 2153, 221-238.	0.9	1
9	Determining the kinetics of break-induced replication (BIR) by the assay for monitoring BIR elongation rate (AMBER). Methods in Enzymology, 2021, 661, 139-154.	1.0	4
10	A Rad51-independent pathway promotes single-strand template repair in gene editing. PLoS Genetics, 2020, 16, e1008689.	3.5	33
11	Yeast ATM and ATR kinases use different mechanisms to spread histone H2A phosphorylation around a DNA double-strand break. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 21354-21363.	7.1	35
12	Genetic interaction mapping informs integrative structure determination of protein complexes. Science, 2020, 370, .	12.6	24
13	Checkpoint Responses to DNA Double-Strand Breaks. Annual Review of Biochemistry, 2020, 89, 103-133.	11.1	99
14	Patterns of somatic structural variation in human cancer genomes. Nature, 2020, 578, 112-121.	27.8	560
15	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	27.8	424
16	A Rad51-independent pathway promotes single-strand template repair in gene editing. , 2020, 16, e1008689.		0
17	A Rad51-independent pathway promotes single-strand template repair in gene editing. , 2020, 16, e1008689.		0
18	A Rad51-independent pathway promotes single-strand template repair in gene editing. , 2020, 16, e1008689.		0

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19	A Rad51-independent pathway promotes single-strand template repair in gene editing. , 2020, 16, e1008689.		0
20	Dephosphorylation of the Atg1 kinase complex by type 2C protein phosphatases. Molecular and Cellular Oncology, 2019, 6, 1588658.	0.7	2
21	Mec1ATR Autophosphorylation and Ddc2ATRIP Phosphorylation Regulates DNA Damage Checkpoint Signaling. Cell Reports, 2019, 28, 1090-1102.e3.	6.4	19
22	Network Rewiring of Homologous Recombination Enzymes during Mitotic Proliferation and Meiosis. Molecular Cell, 2019, 75, 859-874.e4.	9.7	38
23	PP2C phosphatases promote autophagy by dephosphorylation of the Atg1 complex. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 1613-1620.	7.1	48
24	Guidelines for DNA recombination and repair studies: Cellular assays of DNA repair pathways. Microbial Cell, 2019, 6, 1-64.	3.2	47
25	Live cell monitoring of double strand breaks in S. cerevisiae. PLoS Genetics, 2019, 15, e1008001.	3.5	28
26	Mating-type switching by homology-directed recombinational repair: a matter of choice. Current Genetics, 2019, 65, 351-362.	1.7	24
27	Evidence that DNA polymerase Î´ contributes to initiating leading strand DNA replication in Saccharomyces cerevisiae. Nature Communications, 2018, 9, 858.	12.8	77
28	DNA Repair: The Search for Homology. BioEssays, 2018, 40, e1700229.	2.5	106
29	CRISPR/Cas9 cleavages in budding yeast reveal templated insertions and strand-specific insertion/deletion profiles. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E2040-E2047.	7.1	152
30	Repair of a Site-Specific DNA Cleavage: Old-School Lessons for Cas9-Mediated Gene Editing. ACS Chemical Biology, 2018, 13, 397-405.	3.4	67
31	Functions and regulation of the Polo-like kinase Cdc5 in the absence and presence of DNA damage. Current Genetics, 2018, 64, 87-96.	1.7	30
32	New insights into donor directionality of mating-type switching in Schizosaccharomyces pombe. PLoS Genetics, 2018, 14, e1007424.	3.5	14
33	Assaying Mutations Associated With Gene Conversion Repair of a Double-Strand Break. Methods in Enzymology, 2018, 601, 145-160.	1.0	1
34	Multiplexed precision genome editing with trackable genomic barcodes in yeast. Nature Biotechnology, 2018, 36, 512-520.	17.5	138
35	A pathway of targeted autophagy is induced by DNA damage in budding yeast. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1158-E1167.	7.1	52
36	The budding yeast Polo-like kinase localizes to distinct populations at centrosomes during mitosis. Molecular Biology of the Cell, 2017, 28, 1011-1020.	2.1	15

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37	Rad51-mediated double-strand break repair and mismatch correction of divergent substrates. Nature, 2017, 544, 377-380.	27.8	120
38	Homology Requirements and Competition between Gene Conversion and Break-Induced Replication during Double-Strand Break Repair. Molecular Cell, 2017, 65, 515-526.e3.	9.7	77
39	Regulation of the DNA Damage Response by Autophagy. , 2017, , 213-236.		0
40	Position effects influencing intrachromosomal repair of a double-strand break in budding yeast. PLoS ONE, 2017, 12, e0180994.	2.5	16
41	Asf1 facilitates dephosphorylation of Rad53 after DNA double-strand break repair. Genes and Development, 2016, 30, 1211-1224.	5.9	23
42	The democratization of gene editing: Insights from site-specific cleavage and double-strand break repair. DNA Repair, 2016, 44, 6-16.	2.8	181
43	<i>MTE1</i> Functions with <i>MPH1</i> in Double-Strand Break Repair. Genetics, 2016, 203, 147-157.	2.9	13
44	The rule of three. Nature Reviews Molecular Cell Biology, 2016, 17, 333-333.	37.0	1
45	Re-establishment of nucleosome occupancy during double-strand break repair in budding yeast. DNA Repair, 2016, 47, 21-29.	2.8	9
46	A Life Investigating Pathways That Repair Broken Chromosomes. Annual Review of Genetics, 2016, 50, 1-28.	7.6	83
47	Chromosome-refolding model of mating-type switching in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E6929-E6938.	7.1	13
48	Sgs1 and Mph1 Helicases Enforce the Recombination Execution Checkpoint During DNA Double-Strand Break Repair in <i>Saccharomyces cerevisiae</i>. Genetics, 2016, 203, 667-675.	2.9	33
49	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). Autophagy, 2016, 12, 1-222.	9.1	4,701
50	Chromosomes at loose ends. Nature Cell Biology, 2016, 18, 257-259.	10.3	1
51	Chromosome position determines the success of double-strand break repair. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E146-54.	7.1	78
52	Role of Double-Strand Break End-Tethering during Gene Conversion in Saccharomyces cerevisiae. PLoS Genetics, 2016, 12, e1005976.	3.5	22
53	A Cohesin-Based Partitioning Mechanism Revealed upon Transcriptional Inactivation of Centromere. PLoS Genetics, 2016, 12, e1006021.	3.5	7
54	Mating-type Gene Switching in <i>Saccharomyces cerevisiae</i>. Microbiology Spectrum, 2015, 3, MDNA3-0013-2014.	3.0	56

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55	Caffeine impairs resection during DNA break repair by reducing the levels of nucleases Sae2 and Dna2. Nucleic Acids Research, 2015, 43, 6889-6901.	14.5	43
56	TOPping Off Meiosis. Molecular Cell, 2015, 57, 577-581.	9.7	14
57	Functional Interplay between the 53BP1-Ortholog Rad9 and the Mre11 Complex Regulates Resection, End-Tethering and Repair of a Double-Strand Break. PLoS Genetics, 2015, 11, e1004928.	3.5	103
58	Caffeine inhibits gene conversion by displacing Rad51 from ssDNA. Nucleic Acids Research, 2015, 43, 6902-6918.	14.5	17
59	Deciphering the DNA Damage Response. Cell, 2015, 162, 1183-1185.	28.9	18
60	The DNA Damage Response Induces Autophagy via Mec1(ATR) and Tel1(ATM) to Regulate the Initiation of Anaphase. FASEB Journal, 2015, 29, 879.16.	0.5	1
61	Nucleosome Dynamics Around a DNA Double Stranded Break During Repair by Gene Conversion.. FASEB Journal, 2015, 29, 709.8.	0.5	1
62	Break-Induced Replication Repair of Damaged Forks Induces Genomic Duplications in Human Cells. Science, 2014, 343, 88-91.	12.6	387
63	Dynamics of yeast histone H2A and H2B phosphorylation in response to a double-strand break. Nature Structural and Molecular Biology, 2014, 21, 103-109.	8.2	85
64	Chromosome rearrangements via template switching between diverged repeated sequences. Genes and Development, 2014, 28, 2394-2406.	5.9	114
65	Quantitative analysis of triple-mutant genetic interactions. Nature Protocols, 2014, 9, 1867-1881.	12.0	15
66	Sources of DNA Double-Strand Breaks and Models of Recombinational DNA Repair. Cold Spring Harbor Perspectives in Biology, 2014, 6, a016428-a016428.	5.5	561
67	Frequent Interchromosomal Template Switches during Gene Conversion in S. cerevisiae. Molecular Cell, 2014, 55, 615-625.	9.7	52
68	Effect of Chromosome Tethering on Nuclear Organization in Yeast. PLoS ONE, 2014, 9, e102474.	2.5	27
69	Chromatin modifications and chromatin remodeling during DNA repair in budding yeast. Current Opinion in Genetics and Development, 2013, 23, 166-173.	3.3	28
70	Systematic Triple-Mutant Analysis Uncovers Functional Connectivity between Pathways Involved in Chromosome Regulation. Cell Reports, 2013, 3, 2168-2178.	6.4	36
71	Migrating bubble during break-induced replication drives conservative DNA synthesis. Nature, 2013, 502, 389-392.	27.8	277
72	Break-Induced DNA Replication. Cold Spring Harbor Perspectives in Biology, 2013, 5, a010397-a010397.	5.5	191

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73	DNA damage checkpoint triggers autophagy to regulate the initiation of anaphase. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E41-9.	7.1	59
74	DNA damage signaling triggers the cytoplasm-to-vacuole pathway of autophagy to regulate cell cycle progression. Autophagy, 2013, 9, 440-441.	9.1	23
75	The DNA damage checkpoint triggers autophagy to regulate the initiation of anaphase. FASEB Journal, 2013, 27, 545.2.	0.5	0
76	Investigating the properties of a repair replicationâ€fork in the budding yeast Saccharomyces cerevisiae. FASEB Journal, 2013, 27, 542.5.	0.5	0
77	Role of the Recombination Enhancer in matingâ€type switching in budding yeast. FASEB Journal, 2013, 27, 542.7.	0.5	0
78	Regulation of Budding Yeast Mating-Type Switching Donor Preference by the FHA Domain of Fkh1. PLoS Genetics, 2012, 8, e1002630.	3.5	49
79	The <i>Saccharomyces cerevisiae</i> Chromatin Remodeler Fun30 Regulates DNA End Resection and Checkpoint Deactivation. Molecular and Cellular Biology, 2012, 32, 4727-4740.	2.3	143
80	Mutations Arising During Repair of Chromosome Breaks. Annual Review of Genetics, 2012, 46, 455-473.	7.6	117
81	Monitoring DNA Recombination Initiated by HO Endonuclease. Methods in Molecular Biology, 2012, 920, 349-370.	0.9	21
82	Mating-Type Genes and <i>MAT</i> Switching in <i>Saccharomyces cerevisiae</i>. Genetics, 2012, 191, 33-64.	2.9	359
83	Real-time analysis of double-strand DNA break repair by homologous recombination. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3108-3115.	7.1	87
84	Dynamics of Homology Searching During Gene Conversion in<i>Saccharomyces cerevisiae</i>Revealed by Donor Competition. Genetics, 2011, 189, 1225-1233.	2.9	28
85	Protein Phosphatases Pph3, Ptc2, and Ptc3 Play Redundant Roles in DNA Double-Strand Break Repair by Homologous Recombination. Molecular and Cellular Biology, 2011, 31, 507-516.	2.3	43
86	QnAs with James E. Haber. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5479-5479.	7.1	1
87	Mad2 Prolongs DNA Damage Checkpoint Arrest Caused by a Double-Strand Break via a Centromere-Dependent Mechanism. Current Biology, 2010, 20, 328-332.	3.9	147
88	Mec1/Tel1-dependent phosphorylation of Slx4 stimulates Rad1â€“Rad10-dependent cleavage of non-homologous DNA tails. DNA Repair, 2010, 9, 718-726.	2.8	54
89	Fast live simultaneous multiwavelength four-dimensional optical microscopy. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 16016-16022.	7.1	176
90	Increased Mutagenesis and Unique Mutation Signature Associated with Mitotic Gene Conversion. Science, 2010, 329, 82-85.	12.6	218

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91	Sgs1 and Exo1 Redundantly Inhibit Break-Induced Replication and De Novo Telomere Addition at Broken Chromosome Ends. PLoS Genetics, 2010, 6, e1000973.	3.5	78
92	Cdk1 Targets Srs2 to Complete Synthesis-Dependent Strand Annealing and to Promote Recombinational Repair. PLoS Genetics, 2010, 6, e1000858.	3.5	70
93	Break-induced replication requires all essential DNA replication factors except those specific for pre-RC assembly. Genes and Development, 2010, 24, 1133-1144.	5.9	146
94	Chromatin assembly factors Asf1 and CAF-1 have overlapping roles in deactivating the DNA damage checkpoint when DNA repair is complete. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1151-1156.	7.1	92
95	A recombination execution checkpoint regulates the choice of homologous recombination pathway during DNA double-strand break repair. Genes and Development, 2009, 23, 291-303.	5.9	121
96	Yeast Mph1 helicase dissociates Rad51-made D-loops: implications for crossover control in mitotic recombination. Genes and Development, 2009, 23, 67-79.	5.9	226
97	Replicon Dynamics, Dormant Origin Firing, and Terminal Fork Integrity after Double-Strand Break Formation. Cell, 2009, 137, 247-258.	28.9	110
98	Mre11â€"Rad50â€"Nbs1-dependent processing of DNA breaks generates oligonucleotides that stimulate ATM activity. EMBO Journal, 2008, 27, 1953-1962.	7.8	110
99	Histone methyltransferase Dot1 and Rad9 inhibit single-stranded DNA accumulation at DSBs and uncapped telomeres. EMBO Journal, 2008, 27, 1502-12.	7.8	159
100	Functional Interactions Between Sae2 and the Mre11 Complex. Genetics, 2008, 178, 711-723.	2.9	51
101	Alternative endings. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 405-406.	7.1	54
102	Mechanisms of Rad52-Independent Spontaneous and UV-Induced Mitotic Recombination in<i>Saccharomyces cerevisiae</i>. Genetics, 2008, 179, 199-211.	2.9	41
103	The yeast DNA damage checkpoint proteins control a cytoplasmic response to DNA damage. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11358-11363.	7.1	38
104	SMC Proteins, New Players in the Maintenance of Genomic Stability. Cell Cycle, 2007, 6, 914-918.	2.6	16
105	Anaphase Onset Before Complete DNA Replication with Intact Checkpoint Responses. Science, 2007, 315, 1411-1415.	12.6	121
106	Phosphorylation of Slx4 by Mec1 and Tel1 Regulates the Single-Strand Annealing Mode of DNA Repair in Budding Yeast. Molecular and Cellular Biology, 2007, 27, 6433-6445.	2.3	89
107	Mec1/Tel1 Phosphorylation of the INO80 Chromatin Remodeling Complex Influences DNA Damage Checkpoint Responses. Cell, 2007, 130, 499-511.	28.9	116
108	Heterochromatin is refractory to Î³-H2AX modification in yeast and mammals. Journal of Cell Biology, 2007, 178, 209-218.	5.2	234

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109	Histone chaperones: an escort network regulating histone traffic. Nature Structural and Molecular Biology, 2007, 14, 997-1007.	8.2	303
110	Break-induced replication and telomerase-independent telomere maintenance require Pol32. Nature, 2007, 448, 820-823.	27.8	425
111	Evolution of Models of Homologous Recombination. Genome Dynamics and Stability, 2007, , 1-64.	1.1	10
112	Multiple mechanisms of repairing meganuclease-induced double-strand DNA breaks in budding yeast. Topics in Current Genetics, 2007, , 285-316.	0.7	1
113	Surviving the Breakup: The DNA Damage Checkpoint. Annual Review of Genetics, 2006, 40, 209-235.	7.6	493
114	Break-Induced Replication and Recombinational Telomere Elongation in Yeast. Annual Review of Biochemistry, 2006, 75, 111-135.	11.1	294
115	Gene Amplification: Yeast Takes a Turn. Cell, 2006, 125, 1237-1240.	28.9	34
116	Transpositions and translocations induced by site-specific double-strand breaks in budding yeast. DNA Repair, 2006, 5, 998-1009.	2.8	60
117	Smc5â€“Smc6 mediate DNA double-strand-break repair by promoting sister-chromatid recombination. Nature Cell Biology, 2006, 8, 1032-1034.	10.3	170
118	A phosphatase complex that dephosphorylates Î³H2AX regulates DNA damage checkpoint recovery. Nature, 2006, 439, 497-501.	27.8	439
119	Corrections and Clarifications. Science, 2006, 313, 1045a-1045a.	12.6	4
120	Repair of DNA Double Strand Breaks: In Vivo Biochemistry. Methods in Enzymology, 2006, 408, 416-429.	1.0	52
121	Different Mating-Type-Regulated Genes Affect the DNA Repair Defects of Saccharomyces RAD51, RAD52 and RAD55 Mutants. Genetics, 2006, 174, 41-55.	2.9	37
122	Cell Cycle-Dependent Regulation of Saccharomyces cerevisiae Donor Preference during Mating-Type Switching by SBF (Swi4/Swi6) and Fkh1. Molecular and Cellular Biology, 2006, 26, 5470-5480.	2.3	21
123	Saccharomyces cerevisiae Donor Preference During Mating-Type Switching Is Dependent on Chromosome Architecture and Organization. Genetics, 2006, 173, 1197-1206.	2.9	24
124	Conservative Inheritance of Newly Synthesized DNA in Double-Strand Break-Induced Gene Conversion. Molecular and Cellular Biology, 2006, 26, 9424-9429.	2.3	56
125	Multiple Mechanisms of Repairing Meganuclease-Induced Double-Strand DNA Breaks in Budding Yeast. , 2006, , 285-316.		0
126	Chromosome Breakage and Repair. Genetics, 2006, 173, 1181-1185.	2.9	9

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127	RAD51 -Dependent Break-Induced Replication Differs in Kinetics and Checkpoint Responses from RAD51 -Mediated Gene Conversion. Molecular and Cellular Biology, 2005, 25, 933-944.	2.3	157
128	The MRE11-RAD50-XRS2 Complex, in Addition to Other Non-homologous End-joining Factors, Is Required for V(D)J Joining in Yeast*. Journal of Biological Chemistry, 2005, 280, 20247-20252.	3.4	17
129	Rad51-dependent DNA structures accumulate at damaged replication forks in sgs1 mutants defective in the yeast ortholog of BLM RecQ helicase. Genes and Development, 2005, 19, 339-350.	5.9	287
130	Inactivation of Ku-Mediated End Joining Suppresses mec1Î" Lethality by Depleting the Ribonucleotide Reductase Inhibitor Sml1 through a Pathway Controlled by Tel1 Kinase and the Mre11 Complex. Molecular and Cellular Biology, 2005, 25, 10652-10664.	2.3	13
131	Function and Evolution of HO and VDE Endonucleases in Fungi. , 2005, , 161-175.		12
132	Repairing a doubleâ€"strand chromosome break by homologous recombination: revisiting Robin Holliday's model. Philosophical Transactions of the Royal Society B: Biological Sciences, 2004, 359, 79-86.	4.0	67
133	Heteroduplex rejection during single-strand annealing requires Sgs1 helicase and mismatch repair proteins Msh2 and Msh6 but not Pms1. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 9315-9320.	7.1	187
134	Mating typeâ€"dependent constraints on the mobility of the left arm of yeast chromosome III. Journal of Cell Biology, 2004, 164, 361-371.	5.2	62
135	Gene Conversion and Crossing Over Along the 405-kb Left Arm of Saccharomyces cerevisiae Chromosome VII. Genetics, 2004, 168, 49-63.	2.9	90
136	Microhomology-Dependent End Joining and Repair of Transposon-Induced DNA Hairpins by Host Factors in Saccharomyces cerevisiae. Molecular and Cellular Biology, 2004, 24, 1351-1364.	2.3	61
137	Role of DNA Replication Proteins in Double-Strand Break-Induced Recombination in Saccharomyces cerevisiae. Molecular and Cellular Biology, 2004, 24, 6891-6899.	2.3	118
138	Role of Saccharomyces Single-Stranded DNA-Binding Protein RPA in the Strand Invasion Step of Double-Strand Break Repair. PLoS Biology, 2004, 2, e21.	5.6	127
139	In vivo assembly and disassembly of Rad51 and Rad52 complexes during double-strand break repair. EMBO Journal, 2004, 23, 939-949.	7.8	110
140	Checkpoint-mediated control of replisomeâ€"fork association and signalling in response to replication pausing. Oncogene, 2004, 23, 1206-1213.	5.9	147
141	DNA end resection, homologous recombination and DNA damage checkpoint activation require CDK1. Nature, 2004, 431, 1011-1017.	27.8	641
142	Distribution and Dynamics of Chromatin Modification Induced by a Defined DNA Double-Strand Break. Current Biology, 2004, 14, 1703-1711.	3.9	458
143	DNA Breaks Promote Genomic Instability by Impeding Proper Chromosome Segregation. Current Biology, 2004, 14, 2096-2106.	3.9	148
144	INO80 and Î³-H2AX Interaction Links ATP-Dependent Chromatin Remodeling to DNA Damage Repair. Cell, 2004, 119, 767-775.	28.9	512

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145	Telomeres Thrown for a Loop. Molecular Cell, 2004, 16, 502-503.	9.7	4
146	DNA Damage Response Pathway Uses Histone Modification to Assemble a Double-Strand Break-Specific Cohesin Domain. Molecular Cell, 2004, 16, 991-1002.	9.7	524
147	Aging: The Sins of the Parents. Current Biology, 2003, 13, R843-R845.	3.9	3
148	Srs2 and Sgs1â€"Top3 Suppress Crossovers during Double-Strand Break Repair in Yeast. Cell, 2003, 115, 401-411.	28.9	539
149	PP2C Phosphatases Ptc2 and Ptc3 Are Required for DNA Checkpoint Inactivation after a Double-Strand Break. Molecular Cell, 2003, 11, 827-835.	9.7	184
150	PP2C Phosphatases Ptc2 and Ptc3 Are Required for DNA Checkpoint Inactivation after a Double-Strand Break. Molecular Cell, 2003, 11, 1119.	9.7	2
151	In Vivo Roles of Rad52, Rad54, and Rad55 Proteins in Rad51-Mediated Recombination. Molecular Cell, 2003, 12, 209-219.	9.7	334
152	V(D)J Recombination and RAG-Mediated Transposition in Yeast. Molecular Cell, 2003, 12, 489-499.	9.7	46
153	Yeast Mre11 and Rad1 Proteins Define a Ku-Independent Mechanism To Repair Double-Strand Breaks Lacking Overlapping End Sequences. Molecular and Cellular Biology, 2003, 23, 8820-8828.	2.3	327
154	Yeast Rad52 and Rad51 Recombination Proteins Define a Second Pathway of DNA Damage Assessment in Response to a Single Double-Strand Break. Molecular and Cellular Biology, 2003, 23, 8913-8923.	2.3	50
155	Characterization of RAD51 -Independent Break-Induced Replication That Acts Preferentially with Short Homologous Sequences. Molecular and Cellular Biology, 2002, 22, 6384-6392.	2.3	172
156	Uses and abuses of HO endonuclease. Methods in Enzymology, 2002, 350, 141-164.	1.0	42
157	Saccharomyces forkhead protein Fkh1 regulates donor preference during mating-type switching through the recombination enhancer. Genes and Development, 2002, 16, 2085-2096.	5.9	44
158	Recovery from Checkpoint-Mediated Arrest after Repair of a Double-Strand Break Requires Srs2 Helicase. Molecular Cell, 2002, 10, 373-385.	9.7	310
159	Complementation between N-terminal Saccharomyces cerevisiae mre11 alleles in DNA repair and telomere length maintenance. DNA Repair, 2002, 1, 27-40.	2.8	67
160	Regulation of Saccharomyces Rad53 Checkpoint Kinase during Adaptation from DNA Damageâ€"Induced G2/M Arrest. Molecular Cell, 2001, 7, 293-300.	9.7	276
161	The Fuss about Mus81. Cell, 2001, 107, 551-554.	28.9	89
162	ASaccharomyces servazzii clone homologous toSaccharomyces cerevisiae chromosome III spanningKAR4,ARS 304 andSPB1 lacks the recombination enhancer but contains an unknown ORF. Yeast, 2001, 18, 789-795.	1.7	5

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163	NEJ1 controls non-homologous end joining in Saccharomyces cerevisiae. Nature, 2001, 414, 666-669.	27.8	213
164	Hypermutation: give us a break. Nature Immunology, 2001, 2, 902-903.	14.5	7
165	The Saccharomyces recombination protein Tid1p is required for adaptation from G2/M arrest induced by a double-strand break. Current Biology, 2001, 11, 1053-1057.	3.9	73
166	Genetic Requirements for RAD51 - and RAD54 -Independent Break-Induced Replication Repair of a Chromosomal Double-Strand Break. Molecular and Cellular Biology, 2001, 21, 2048-2056.	2.3	179
167	RAD51-independent break-induced replication to repair a broken chromosome depends on a distant enhancer site. Genes and Development, 2001, 15, 1055-1060.	5.9	68
168	Expansions and Contractions in 36-bp Minisatellites by Gene Conversion in Yeast. Genetics, 2001, 158, 155-166.	2.9	30
169	Recombination: a frank view of exchanges and vice versa. Current Opinion in Cell Biology, 2000, 12, 286-292.	5.4	76
170	Partners and pathways. Trends in Genetics, 2000, 16, 259-264.	6.7	519
171	Lucky breaks: analysis of recombination in Saccharomyces. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2000, 451, 53-69.	1.0	71
172	Recombination-induced CAG trinucleotide repeat expansions in yeast involve the MRE11â€“RAD50â€“XRS2 complex. EMBO Journal, 2000, 19, 2381-2390.	7.8	128
173	DNA Length Dependence of the Single-Strand Annealing Pathway and the Role of Saccharomyces cerevisiae RAD59 in Double-Strand Break Repair. Molecular and Cellular Biology, 2000, 20, 5300-5309.	2.3	264
174	The DNA Damage Checkpoint Signal in Budding Yeast Is Nuclear Limited. Molecular Cell, 2000, 6, 487-492.	9.7	44
175	The Saccharomyces cerevisiae Msh2 Mismatch Repair Protein Localizes to Recombination Intermediates In Vivo. Molecular Cell, 2000, 5, 789-799.	9.7	97
176	Multiple Pathways of Recombination Induced by Double-Strand Breaks in <i>Saccharomyces cerevisiae</i>. Microbiology and Molecular Biology Reviews, 1999, 63, 349-404.	6.6	1,989
177	Physical Monitoring of HO-Induced Homologous Recombination. , 1999, 113, 403-415.		18
178	Gatekeepers of recombination. Nature, 1999, 398, 665-667.	27.8	86
179	Role of yeast SIR genes and mating type in directing DNA double-strand breaks to homologous and non-homologous repair paths. Current Biology, 1999, 9, 767-770.	3.9	202
180	DNA recombination: the replication connection. Trends in Biochemical Sciences, 1999, 24, 271-275.	7.5	383

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