

Richard D Kolodner

List of Publications by Year in descending order

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134
papers

20,723
citations

15504

65
h-index

13771

129
g-index

138
all docs

138
docs citations

138
times ranked

13549
citing authors

#	ARTICLE	IF	CITATIONS
1	Ligation of newly replicated DNA controls the timing of DNA mismatch repair. <i>Current Biology</i> , 2021, 31, 1268-1276.e6.	3.9	19
2	Rad27 and Exo1 function in different excision pathways for mismatch repair in <i>Saccharomyces cerevisiae</i> . <i>Nature Communications</i> , 2021, 12, 5568.	12.8	9
3	FEN1 endonuclease as a therapeutic target for human cancers with defects in homologous recombination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 19415-19424.	7.1	53
4	Tumour predisposition and cancer syndromes as models to study gene-environment interactions. <i>Nature Reviews Cancer</i> , 2020, 20, 533-549.	28.4	93
5	Mechanisms underlying genome instability mediated by formation of foldback inversions in <i>Saccharomyces cerevisiae</i> . <i>ELife</i> , 2020, 9, .	6.0	10
6	Essential <i>Saccharomyces cerevisiae</i> genome instability suppressing genes identify potential human tumor suppressors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17377-17382.	7.1	8
7	Alternative splicing regulates stochastic NLRP3 activity. <i>Nature Communications</i> , 2019, 10, 3238.	12.8	44
8	Guidelines for DNA recombination and repair studies: Cellular assays of DNA repair pathways. <i>Microbial Cell</i> , 2019, 6, 1-64.	3.2	47
9	Inhibition of Nuclear PTEN Tyrosine Phosphorylation Enhances Glioma Radiation Sensitivity through Attenuated DNA Repair. <i>Cancer Cell</i> , 2019, 35, 504-518.e7.	16.8	102
10	Analyzing Genome Rearrangements in <i>Saccharomyces cerevisiae</i> . <i>Methods in Molecular Biology</i> , 2018, 1672, 43-61.	0.9	9
11	The properties of Msh2-Msh6 ATP binding mutants suggest a signal amplification mechanism in DNA mismatch repair. <i>Journal of Biological Chemistry</i> , 2018, 293, 18055-18070.	3.4	24
12	DNA Mismatch Repair: Mechanisms and Cancer Genetics. , 2018, , .		1
13	The Swr1 chromatin-remodeling complex prevents genome instability induced by replication fork progression defects. <i>Nature Communications</i> , 2018, 9, 3680.	12.8	17
14	Identification of Exo1-Msh2 interaction motifs in DNA mismatch repair and new Msh2-binding partners. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 650-659.	8.2	35
15	Cdc73 suppresses genome instability by mediating telomere homeostasis. <i>PLoS Genetics</i> , 2018, 14, e1007170.	3.5	15
16	SUMO E3 ligase Mms21 prevents spontaneous DNA damage induced genome rearrangements. <i>PLoS Genetics</i> , 2018, 14, e1007250.	3.5	16
17	Reconstitution of <i>Saccharomyces cerevisiae</i> DNA polymerase δ -dependent mismatch repair with purified proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 3607-3612.	7.1	24
18	Pathways and Mechanisms that Prevent Genome Instability in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2017, 206, 1187-1225.	2.9	49

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19	Uner Tan syndrome caused by a homozygous TUBB2B mutation affecting microtubule stability. <i>Human Molecular Genetics</i> , 2016, 26, ddw383.	2.9	11
20	A genetic network that suppresses genome rearrangements in <i>Saccharomyces cerevisiae</i> and contains defects in cancers. <i>Nature Communications</i> , 2016, 7, 11256.	12.8	36
21	A personal historical view of DNA mismatch repair with an emphasis on eukaryotic DNA mismatch repair. <i>DNA Repair</i> , 2016, 38, 3-13.	2.8	44
22	Activation of <i>Saccharomyces cerevisiae</i> Mlh1-Pms1 Endonuclease in a Reconstituted Mismatch Repair System. <i>Journal of Biological Chemistry</i> , 2015, 290, 21580-21590.	3.4	29
23	New insights into the mechanism of DNA mismatch repair. <i>Chromosoma</i> , 2015, 124, 443-462.	2.2	103
24	Exonuclease 1-dependent and independent mismatch repair. <i>DNA Repair</i> , 2015, 32, 24-32.	2.8	115
25	S-Score: A Scoring System for the Identification and Prioritization of Predicted Cancer Genes. <i>PLoS ONE</i> , 2014, 9, e94147.	2.5	8
26	Loss of the Thioredoxin Reductase Trr1 Suppresses the Genomic Instability of Peroxiredoxin tsa1 Mutants. <i>PLoS ONE</i> , 2014, 9, e108123.	2.5	14
27	Mismatch-specific Recruitment of the Mlh1-Pms1 Complex Identifies Repair Substrates of the <i>Saccharomyces cerevisiae</i> Msh2-Msh3 Complex. <i>Journal of Biological Chemistry</i> , 2014, 289, 9352-9364.	3.4	42
28	DNA Repair Pathway Selection Caused by Defects in TEL1, SAE2, and De Novo Telomere Addition Generates Specific Chromosomal Rearrangement Signatures. <i>PLoS Genetics</i> , 2014, 10, e1004277.	3.5	20
29	Mlh2 Is an Accessory Factor for DNA Mismatch Repair in <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2014, 10, e1004327.	3.5	36
30	A <i>Saccharomyces cerevisiae</i> RNase H2 Interaction Network Functions To Suppress Genome Instability. <i>Molecular and Cellular Biology</i> , 2014, 34, 1521-1534.	2.3	46
31	PCNA and Msh2-Msh6 Activate an Mlh1-Pms1 Endonuclease Pathway Required for Exo1-Independent Mismatch Repair. <i>Molecular Cell</i> , 2014, 55, 291-304.	9.7	89
32	Template homology determines the genetics and mechanisms of gross chromosomal rearrangements in <i>S. cerevisiae</i> (736.11). <i>FASEB Journal</i> , 2014, 28, 736.11.	0.5	0
33	Checkpoint Kinases Regulate a Global Network of Transcription Factors in Response to DNA Damage. <i>Cell Reports</i> , 2013, 4, 174-188.	6.4	61
34	Reconstitution of long and short patch mismatch repair reactions using <i>Saccharomyces cerevisiae</i> proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 18472-18477.	7.1	53
35	Distinct SUMO Ligases Cooperate with Esc2 and Slx5 to Suppress Duplication-Mediated Genome Rearrangements. <i>PLoS Genetics</i> , 2013, 9, e1003670.	3.5	68
36	Dominant Mutations in <i>S. cerevisiae</i> PMS1 Identify the Mlh1-Pms1 Endonuclease Active Site and an Exonuclease 1-Independent Mismatch Repair Pathway. <i>PLoS Genetics</i> , 2013, 9, e1003869.	3.5	52

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37	DNA conformations in mismatch repair probed in solution by X-ray scattering from gold nanocrystals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 17308-17313.	7.1	53
38	Rapid Analysis of <i>Saccharomyces cerevisiae</i> Genome Rearrangements by Multiplex Ligation-Dependent Probe Amplification. <i>PLoS Genetics</i> , 2012, 8, e1002539.	3.5	15
39	Bioinformatic identification of genes suppressing genome instability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E3251-9.	7.1	25
40	A chemical-genetic screen to unravel the genetic network of CDC28/CDK1 links ubiquitin and Rad6-Bre1 to cell cycle progression. <i>FASEB Journal</i> , 2012, 26, 590.1.	0.5	0
41	Aneuploidy Drives a Mutator Phenotype in Cancer. <i>Science</i> , 2011, 333, 942-943.	12.6	45
42	Visualization of Eukaryotic DNA Mismatch Repair Reveals Distinct Recognition and Repair Intermediates. <i>Cell</i> , 2011, 147, 1040-1053.	28.9	183
43	Mismatch Repair, But Not Heteroduplex Rejection, Is Temporally Coupled to DNA Replication. <i>Science</i> , 2011, 334, 1713-1716.	12.6	109
44	A Genetic and Structural Study of Genome Rearrangements Mediated by High Copy Repeat Ty1 Elements. <i>PLoS Genetics</i> , 2011, 7, e1002089.	3.5	65
45	An overview of Cdk1-controlled targets and processes. <i>Cell Division</i> , 2010, 5, 11.	2.4	338
46	Functional Studies and Homology Modeling of Msh2-Msh3 Predict that Mismatch Recognition Involves DNA Bending and Strand Separation. <i>Molecular and Cellular Biology</i> , 2010, 30, 3321-3328.	2.3	33
47	Determination of Cross Chromosomal Rearrangement Rates. <i>Cold Spring Harbor Protocols</i> , 2010, 2010, pdb.prot5492.	0.3	39
48	Interaction between the Msh2 and Msh6 Nucleotide-binding Sites in the <i>Saccharomyces cerevisiae</i> Msh2-Msh6 Complex. <i>Journal of Biological Chemistry</i> , 2010, 285, 9301-9310.	3.4	50
49	Post-Replication Repair Suppresses Duplication-Mediated Genome Instability. <i>PLoS Genetics</i> , 2010, 6, e1000933.	3.5	39
50	Rewiring of Genetic Networks in Response to DNA Damage. <i>Science</i> , 2010, 330, 1385-1389.	12.6	408
51	Stabilization of Dicentric Translocations through Secondary Rearrangements Mediated by Multiple Mechanisms in <i>S. cerevisiae</i> . <i>PLoS ONE</i> , 2009, 4, e6389.	2.5	34
52	Cdc28/Cdk1 positively and negatively affects genome stability in <i>S. cerevisiae</i> . <i>Journal of Cell Biology</i> , 2009, 185, 423-437.	5.2	37
53	A conserved MutS homolog connector domain interface interacts with MutL homologs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 22223-22228.	7.1	69
54	The <i>Saccharomyces cerevisiae</i> Rad6 Postreplication Repair and Siz1/Srs2 Homologous Recombination-Inhibiting Pathways Process DNA Damage That Arises in <i>asf1</i> Mutants. <i>Molecular and Cellular Biology</i> , 2009, 29, 5226-5237.	2.3	23

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55	Perspectives on the DNA damage and replication checkpoint responses in <i>Saccharomyces cerevisiae</i> . <i>DNA Repair</i> , 2009, 8, 974-982.	2.8	68
56	Specific pathways prevent duplication-mediated genome rearrangements. <i>Nature</i> , 2009, 460, 984-989.	27.8	122
57	<i>Escherichia coli</i> MutS Tetramerization Domain Structure Reveals That Stable Dimers but Not Tetramers Are Essential for DNA Mismatch Repair in Vivo. <i>Journal of Biological Chemistry</i> , 2007, 282, 16345-16354.	3.4	55
58	Chimeric <i>Saccharomyces cerevisiae</i> Msh6 protein with an Msh3 mispair-binding domain combines properties of both proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 10956-10961.	7.1	35
59	Coupling distant sites in DNA during DNA mismatch repair. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 12953-12954.	7.1	41
60	Lynch Syndrome (Hereditary Nonpolyposis Colorectal Cancer) Diagnostics. <i>Journal of the National Cancer Institute</i> , 2007, 99, 291-299.	6.3	201
61	<i>Saccharomyces cerevisiae</i> Msh2-Msh3 Acts in Repair of Base-Base Mismatches. <i>Molecular and Cellular Biology</i> , 2007, 27, 6546-6554.	2.3	89
62	Oxygen metabolism and reactive oxygen species cause chromosomal rearrangements and cell death. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 9747-9752.	7.1	84
63	The C-terminal domain of yeast PCNA is required for physical and functional interactions with Cdc9 DNA ligase. <i>Nucleic Acids Research</i> , 2007, 35, 1624-1637.	14.5	70
64	The N Terminus of <i>Saccharomyces cerevisiae</i> Msh6 Is an Unstructured Tether to PCNA. <i>Molecular Cell</i> , 2007, 26, 565-578.	9.7	110
65	The clinical continuum of cryopyrinopathies: Novel CIAS1 mutations in North American patients and a new cryopyrin model. <i>Arthritis and Rheumatism</i> , 2007, 56, 1273-1285.	6.7	362
66	Control of Translocations between Highly Diverged Genes by Sgs1, the <i>Saccharomyces cerevisiae</i> Homolog of the Bloom's Syndrome Protein. <i>Molecular and Cellular Biology</i> , 2006, 26, 5406-5420.	2.3	62
67	Analysis of Gross Chromosomal Rearrangements in <i>Saccharomyces cerevisiae</i> . <i>Methods in Enzymology</i> , 2006, 409, 462-476.	1.0	50
68	Genetic analysis of ionizing radiation-induced mutagenesis in <i>Saccharomyces cerevisiae</i> reveals TransLesion Synthesis (TLS) independent of PCNA K164 SUMOylation and ubiquitination. <i>DNA Repair</i> , 2006, 5, 1475-1488.	2.8	21
69	Inhibition of Msh6 ATPase Activity by Mismatched DNA Induces a Msh2(ATP)-Msh6(ATP) State Capable of Hydrolysis-Independent Movement along DNA. <i>Molecular Cell</i> , 2006, 22, 39-49.	9.7	87
70	Chromosome healing by de novo telomere addition in <i>Saccharomyces cerevisiae</i> . <i>Molecular Microbiology</i> , 2006, 59, 1357-1368.	2.5	85
71	Checkpoint functions are required for normal S-phase progression in <i>Saccharomyces cerevisiae</i> RCAF- and CAF-I-defective mutants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 3710-3715.	7.1	29
72	Biochemical basis for dominant mutations in the <i>Saccharomyces cerevisiae</i> MSH6 gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 558-563.	7.1	27

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73	An FHA domain-mediated protein interaction network of Rad53 reveals its role in polarized cell growth. <i>Journal of Cell Biology</i> , 2006, 175, 743-753.	5.2	85
74	Suppression of spontaneous genome rearrangements in yeast DNA helicase mutants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 18196-18201.	7.1	42
75	Checkpoint proteins control morphogenetic events during DNA replication stress in <i>Saccharomyces cerevisiae</i> . <i>Journal of Cell Biology</i> , 2006, 175, 729-741.	5.2	79
76	Mutation in Rpa1 results in defective DNA double-strand break repair, chromosomal instability and cancer in mice. <i>Nature Genetics</i> , 2005, 37, 750-755.	21.4	141
77	<i>Saccharomyces cerevisiae</i> as a Model System To Define the Chromosomal Instability Phenotype. <i>Molecular and Cellular Biology</i> , 2005, 25, 7226-7238.	2.3	51
78	Analysis of the Interaction between the <i>Saccharomyces cerevisiae</i> MSH2-MSH6 and MLH1-PMS1 Complexes with DNA Using a Reversible DNA End-blocking System. <i>Journal of Biological Chemistry</i> , 2005, 280, 22245-22257.	3.4	116
79	A Biological Network in <i>Saccharomyces cerevisiae</i> Prevents the Deleterious Effects of Endogenous Oxidative DNA Damage. <i>Molecular Cell</i> , 2005, 17, 709-720.	9.7	104
80	Suppression of gross chromosomal rearrangements by the multiple functions of the Mre11-Rad50-Xrs2 complex in <i>Saccharomyces cerevisiae</i> . <i>DNA Repair</i> , 2005, 4, 606-617.	2.8	34
81	Chromosome healing through terminal deletions generated by de novo telomere additions in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 13262-13267.	7.1	51
82	Mitotic checkpoint function in the formation of gross chromosomal rearrangements in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 15980-15985.	7.1	49
83	Recombination and the Tel1 and Mec1 checkpoints differentially effect genome rearrangements driven by telomere dysfunction in yeast. <i>Nature Genetics</i> , 2004, 36, 612-617.	21.4	61
84	Dominant effects of an Msh6 missense mutation on DNA repair and cancer susceptibility. <i>Cancer Cell</i> , 2004, 6, 139-150.	16.8	140
85	Induction of genome instability by DNA damage in <i>Saccharomyces cerevisiae</i> . <i>DNA Repair</i> , 2003, 2, 243-258.	2.8	74
86	Transfer of the MSH2-MSH6 Complex from Proliferating Cell Nuclear Antigen to Mismatched Bases in DNA. <i>Journal of Biological Chemistry</i> , 2003, 278, 14-17.	3.4	87
87	Inactivation of Exonuclease 1 in mice results in DNA mismatch repair defects, increased cancer susceptibility, and male and female sterility. <i>Genes and Development</i> , 2003, 17, 603-614.	5.9	282
88	A genomewide screen in <i>Saccharomyces cerevisiae</i> for genes that suppress the accumulation of mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 11529-11534.	7.1	248
89	The Recombination-deficient Mutant RPA (rfa1-t11) Is Displaced Slowly from Single-stranded DNA by Rad51 Protein. <i>Journal of Biological Chemistry</i> , 2003, 278, 23410-23417.	3.4	85
90	<i>Saccharomyces cerevisiae</i> chromatin-assembly factors that act during DNA replication function in the maintenance of genome stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 6640-6645.	7.1	136

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91	EXO1 variants occur commonly in normal population: evidence against a role in hereditary nonpolyposis colorectal cancer. <i>Cancer Research</i> , 2003, 63, 154-8.	0.9	46
92	Maintenance of Genome Stability in <i>Saccharomyces cerevisiae</i> . <i>Science</i> , 2002, 297, 552-557.	12.6	442
93	Haploinsufficiency of Flap endonuclease (Fen1) leads to rapid tumor progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9924-9929.	7.1	227
94	Isolation and Characterization of New Proliferating Cell Nuclear Antigen (POL30) Mutator Mutants That Are Defective in DNA Mismatch Repair. <i>Molecular and Cellular Biology</i> , 2002, 22, 6669-6680.	2.3	61
95	Dominant <i>Saccharomyces cerevisiae</i> msh6 Mutations Cause Increased Mismatch Binding and Decreased Dissociation from Mismatches by Msh2-Msh6 in the Presence of ATP. <i>Journal of Biological Chemistry</i> , 2002, 277, 25545-25553.	3.4	59
96	Suppression of genome instability by redundant S-phase checkpoint pathways in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 4500-4507.	7.1	135
97	Replication Protein A Is Required for Meiotic Recombination in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2002, 161, 535-547.	2.9	57
98	A hereditary nonpolyposis colorectal carcinoma case associated with hypermethylation of the MLH1 gene in normal tissue and loss of heterozygosity of the unmethylated allele in the resulting microsatellite instability-high tumor. <i>Cancer Research</i> , 2002, 62, 3925-8.	0.9	174
99	Suppression of Spontaneous Chromosomal Rearrangements by S Phase Checkpoint Functions in <i>Saccharomyces cerevisiae</i> . <i>Cell</i> , 2001, 104, 397-408.	28.9	301
100	SGS1, the <i>Saccharomyces cerevisiae</i> homologue of BLM and WRN, suppresses genome instability and homologous recombination. <i>Nature Genetics</i> , 2001, 27, 113-116.	21.4	309
101	Mutation of a new gene encoding a putative pyrin-like protein causes familial cold autoinflammatory syndrome and Muckle-Wells syndrome. <i>Nature Genetics</i> , 2001, 29, 301-305.	21.4	1,488
102	Multiple pathways cooperate in the suppression of genome instability in <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 2001, 411, 1073-1076.	27.8	336
103	The MER3 Helicase Involved in Meiotic Crossing Over Is Stimulated by Single-stranded DNA-binding Proteins and Unwinds DNA in the 3' to 5' Direction. <i>Journal of Biological Chemistry</i> , 2001, 276, 31487-31493.	3.4	54
104	exo1-Dependent Mutator Mutations: Model System for Studying Functional Interactions in Mismatch Repair. <i>Molecular and Cellular Biology</i> , 2001, 21, 5142-5155.	2.3	177
105	Novel dominant mutations in <i>Saccharomyces cerevisiae</i> MSH6. <i>Nature Genetics</i> , 2000, 24, 53-56.	21.4	58
106	Proliferating cell nuclear antigen and Msh2p-Msh6p interact to form an active mismatch recognition complex. <i>Nature Genetics</i> , 2000, 26, 375-378.	21.4	215
107	Guarding against mutation. <i>Nature</i> , 2000, 407, 687-689.	27.8	18
108	Links between replication, recombination and genome instability in eukaryotes. <i>Trends in Biochemical Sciences</i> , 2000, 25, 196-200.	7.5	111

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109	Characterization of Hereditary Nonpolyposis Colorectal Cancer Families From a Population-Based Series of Cases. <i>Journal of the National Cancer Institute</i> , 2000, 92, 1517-1522.	6.3	80
110	The Yeast HSM3 Gene Is Not Involved in DNA Mismatch Repair in Rapidly Dividing Cells. <i>Genetics</i> , 2000, 154, 491-493.	2.9	4
111	Biochemical Characterization of the Interaction between the <i>Saccharomyces cerevisiae</i> MSH2-MSH6 Complex and Mispaiored Bases in DNA. <i>Journal of Biological Chemistry</i> , 1999, 274, 26668-26682.	3.4	121
112	Gross chromosomal rearrangements in <i>Saccharomyces cerevisiae</i> replication and recombination defective mutants. <i>Nature Genetics</i> , 1999, 23, 81-85.	21.4	360
113	Eukaryotic DNA mismatch repair. <i>Current Opinion in Genetics and Development</i> , 1999, 9, 89-96.	3.3	781
114	<i>Saccharomyces cerevisiae</i> pol30 (Proliferating Cell Nuclear Antigen) Mutations Impair Replication Fidelity and Mismatch Repair. <i>Molecular and Cellular Biology</i> , 1999, 19, 7801-7815.	2.3	100
115	Interpretation of Genetic Test Results for Hereditary Nonpolyposis Colorectal Cancer. <i>JAMA - Journal of the American Medical Association</i> , 1999, 282, 247.	7.4	118
116	Germ-line msh6 mutations in colorectal cancer families. <i>Cancer Research</i> , 1999, 59, 5068-74.	0.9	241
117	Functional analysis of human MLH1 mutations in <i>Saccharomyces cerevisiae</i> . <i>Nature Genetics</i> , 1998, 19, 384-389.	21.4	136
118	Chromosomal Rearrangements Occur in <i>S. cerevisiae</i> rfa1 Mutator Mutants Due to Mutagenic Lesions Processed by Double-Strand-Break Repair. <i>Molecular Cell</i> , 1998, 2, 9-22.	9.7	153
119	<i>Saccharomyces</i> Ku70, Mre11/Rad50, and RPA Proteins Regulate Adaptation to G2/M Arrest after DNA Damage. <i>Cell</i> , 1998, 94, 399-409.	28.9	729
120	The Evolutionarily Conserved Zinc Finger Motif in the Largest Subunit of Human Replication Protein A Is Required for DNA Replication and Mismatch Repair but Not for Nucleotide Excision Repair. <i>Journal of Biological Chemistry</i> , 1998, 273, 1453-1461.	3.4	130
121	Genetic Analysis of Yeast RPA1 Reveals Its Multiple Functions in DNA Metabolism. <i>Genetics</i> , 1998, 148, 989-1005.	2.9	185
122	Mutation in the Mismatch Repair Gene Msh6 Causes Cancer Susceptibility. <i>Cell</i> , 1997, 91, 467-477.	28.9	326
123	A Novel Mutation Avoidance Mechanism Dependent on <i>S. cerevisiae</i> RAD27 Is Distinct from DNA Mismatch Repair. <i>Cell</i> , 1997, 88, 253-263.	28.9	452
124	Low frequency of hMSH2 mutations in Swedish HNPCC families. , 1997, 74, 134-137.		20
125	Meiotic Pachytene Arrest in MLH1-Deficient Mice. <i>Cell</i> , 1996, 85, 1125-1134.	28.9	528
126	Mutation in the DNA mismatch repair gene homologue hMLH 1 is associated with hereditary non-polyposis colon cancer. <i>Nature</i> , 1994, 368, 258-261.	27.8	2,001

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127	Homologous pairing proteins encoded by the Escherichia coli recE and recT genes. Molecular Microbiology, 1994, 11, 23-30.	2.5	92
128	Structure of the Human MSH2 Locus and Analysis of Two Muir-Torre Kindreds for msh2 Mutations. Genomics, 1994, 24, 516-526.	2.9	276
129	The human mutator gene homolog MSH2 and its association with hereditary nonpolyposis colon cancer. Cell, 1993, 75, 1027-1038.	28.9	2,706
130	Characterization of DNA-binding and strand-exchange stimulation properties of γ -RPA, a yeast single-strand-DNA-binding protein. Journal of Molecular Biology, 1992, 227, 54-71.	4.2	180
131	The role of heteroduplex correction in gene conversion in Saccharomyces cerevisiae. Nature, 1987, 328, 362-364.	27.8	108
132	Isolation of genetic elements that increase frequencies of plasmid recombinants. Nature, 1983, 303, 256-259.	27.8	29
133	recA-independent general genetic recombination of plasmids. Nature, 1981, 294, 184-186.	27.8	168
134	Rad5 and Its Human Homologs, HLTF and SHPRH, Are Novel Interactors of Mismatch Repair. Frontiers in Cell and Developmental Biology, 0, 10, .	3.7	1