Sue Jinks-Robertson

List of Publications by Year
in descending order

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99 papers	5,464 citations	87888 38 h-index	91884 69 g-index
103 all docs	103 docs citations	103 times ranked	4245 citing authors

#	Article	IF	Citations
1	DNA MISMATCH REPAIR AND GENETIC INSTABILITY. Annual Review of Genetics, 2000, 34, 359-399.	7.6	561
2	Transcription as a source of genome instability. Nature Reviews Genetics, 2012, 13, 204-214.	16.3	253
3	Mutagenic Processing of Ribonucleotides in DNA by Yeast Topoisomerase I. Science, 2011, 332, 1561-1564.	12.6	251
4	Expression of rRNA and tRNA genes in Escherichia coli: Evidence for feedback regulation by products of rRNA operons. Cell, 1983, 33, 865-876.	28.9	239
5	Overlapping Specificities of Base Excision Repair, Nucleotide Excision Repair, Recombination, and Translesion Synthesis Pathways for DNA Base Damage in <i>Saccharomyces cerevisiae</i>. Molecular and Cellular Biology, 1999, 19, 2929-2935.	2.3	205
6	DNA Repair Mechanisms and the Bypass of DNA Damage in <i>Saccharomyces cerevisiae</i>. Genetics, 2013, 193, 1025-1064.	2.9	191
7	CHROMOSOMAL TRANSLOCATIONS GENERATED BY HIGH-FREQUENCY MEIOTIC RECOMBINATION BETWEEN REPEATED YEAST GENES. Genetics, 1986, 114, 731-752.	2.9	178
8	The Role of the Mismatch Repair Machinery in Regulating Mitotic and Meiotic Recombination Between Diverged Sequences in Yeast. Genetics, 1999, 151, 1299-1313.	2.9	162
9	Genetic control of microsatellite stability. Mutation Research DNA Repair, 1997, 383, 61-70.	3.7	127
10	Discrete in vivo roles for the MutL homologs Mlh2p and Mlh3p in the removal of frameshift intermediates in budding yeast. Current Biology, 2000, 10, 145-148.	3.9	118
11	DNA Polymerase Î¶ Introduces Multiple Mutations when Bypassing Spontaneous DNA Damage in Saccharomyces cerevisiae. Molecular Cell, 2000, 6, 1491-1499.	9.7	114
12	Mismatch Repair Proteins Regulate Heteroduplex Formation during Mitotic Recombination in Yeast. Molecular and Cellular Biology, 1998, 18, 6525-6537.	2.3	111
13	Saccharomyces cerevisiaeNtg1p and Ntg2p:Â Broad SpecificityN-Glycosylases for the Repair of Oxidative DNA Damage in the Nucleus and Mitochondriaâ€. Biochemistry, 1999, 38, 11298-11306.	2.5	110
14	Regulation of Mitotic Homeologous Recombination in Yeast: Functions of Mismatch Repair and Nucleotide Excision Repair Genes. Genetics, 2000, 154, 133-146.	2.9	107
15	The 9-1-1 Checkpoint Clamp Physically Interacts with PolÎ¶ and Is Partially Required for Spontaneous PolÎ¶-dependent Mutagenesis in Saccharomyces cerevisiae. Journal of Biological Chemistry, 2005, 280, 38657-38665.	3.4	104
16	Transcription-Associated Mutagenesis. Annual Review of Genetics, 2014, 48, 341-359.	7.6	104
17	Transcription-associated mutagenesis in yeast is directly proportional to the level of gene expression and influenced by the direction of DNA replication. DNA Repair, 2007, 6, 1285-1296.	2.8	100
18	Destabilization of Simple Repetitive DNA Sequences by Transcription in Yeast. Genetics, 1996, 143, 713-721.	2.9	99

#	ARTICLE	IF	CITATIONS
19	Determination of Mitotic Recombination Rates by Fluctuation Analysis in <I>Saccharomyces cerevisiae</I>. , 2004, 262, 003-012.		83
20	Base Composition of Mononucleotide Runs Affects DNA Polymerase Slippage and Removal of Frameshift Intermediates by Mismatch Repair in Saccharomyces cerevisiae. Molecular and Cellular Biology, 2002, 22, 8756-8762.	2.3	82
21	Role for topoisomerase 1 in transcription-associated mutagenesis in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 698-703.	7.1	80
22	Examination of the Roles of Sgs1 and Srs2 Helicases in the Enforcement of Recombination Fidelity in Saccharomyces cerevisiae. Genetics, 2004, 168, 1855-1865.	2.9	79
23	Heteroduplex DNA Position Defines the Roles of the Sgs1, Srs2, and Mph1 Helicases in Promoting Distinct Recombination Outcomes. PLoS Genetics, 2013, 9, e1003340.	3.5	79
24	Nucleotide sequence of the LYS2 gene of Saccharomyces cerevisiae: homology to Bacillus brevis tyrocidine synthetase 1. Gene, 1991, 98, 141-145.	2.2	63
25	Molecular Structures of Crossover and Noncrossover Intermediates during Gap Repair in Yeast: Implications for Recombination. Molecular Cell, 2010, 38, 211-222.	9.7	61
26	Elevated Genome-Wide Instability in Yeast Mutants Lacking RNase H Activity. Genetics, 2015, 201, 963-975.	2.9	60
27	dUTP incorporation into genomic DNA is linked to transcription in yeast. Nature, 2009, 459, 1150-1153.	27.8	59
28	Abasic Sites in the Transcribed Strand of Yeast DNA Are Removed by Transcription-Coupled Nucleotide Excision Repair. Molecular and Cellular Biology, 2010, 30, 3206-3215.	2.3	58
29	Removal of Frameshift Intermediates by Mismatch Repair Proteins in <i>Saccharomyces cerevisiae</i>. Molecular and Cellular Biology, 1999, 19, 4766-4773.	2.3	56
30	Roles of RAD6 Epistasis Group Members in Spontaneous PolÎ¶-Dependent Translesion Synthesis in Saccharomyces cerevisiae. Genetics, 2005, 169, 1939-1955.	2.9	54
31	Sequence Composition and Context Effects on the Generation and Repair of Frameshift Intermediates in Mononucleotide Runs in Saccharomyces cerevisiae. Genetics, 2000, 156, 571-578.	2.9	53
32	Genetic Analysis of Transcription-Associated Mutation in Saccharomyces cerevisiae. Genetics, 2000, 154, 109-120.	2.9	52
33	Guidelines for DNA recombination and repair studies: Cellular assays of DNA repair pathways. Microbial Cell, 2019, 6, 1-64.	3.2	47
34	Guanine repeat-containing sequences confer transcription-dependent instability in an orientation-specific manner in yeast. DNA Repair, 2011, 10, 953-960.	2.8	46
35	Stimulation of Mitotic Recombination Events by High Levels of RNA Polymerase II Transcription in Yeast. Molecular and Cellular Biology, 2000, 20, 5404-5414.	2.3	45
36	Two distinct mechanisms of Topoisomerase 1-dependent mutagenesis in yeast. DNA Repair, 2013, 12, 205-211.	2.8	45

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37	Topoisomerase I Plays a Critical Role in Suppressing Genome Instability at a Highly Transcribed G-Quadruplex-Forming Sequence. PLoS Genetics, 2014, 10, e1004839.	3.5	43
38	Spontaneous Frameshift Mutations in <i>Saccharomyces cerevisiae</i>: Accumulation During DNA Replication and Removal by Proofreading and Mismatch Repair Activities. Genetics, 2001, 159, 65-75.	2.9	42
39	Mutagenic effects of abasic and oxidized abasic lesions in Saccharomyces cerevisiae. Nucleic Acids Research, 2005, 33, 6196-6202.	14.5	41
40	Oligonucleotide transformation of yeast reveals mismatch repair complexes to be differentially active on DNA replication strands. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11352-11357.	7.1	40
41	Involvement of two endonuclease III homologs in the base excision repair pathway for the processing of DNA alkylation damage in Saccharomyces cerevisiae. DNA Repair, 2004, 3, 51-59.	2.8	39
42	Yeast base excision repair: Interconnections and networks. Progress in Molecular Biology and Translational Science, 2001, 68, 29-39.	1.9	37
43	Sequence Divergence Impedes Crossover More Than Noncrossover Events During Mitotic Gap Repair in Yeast. Genetics, 2008, 179, 1251-1262.	2.9	36
44	The dCMP transferase activity of yeast Rev1 is biologically relevant during the bypass of endogenously generated AP sites. DNA Repair, 2011, 10, 1262-1271.	2.8	36
45	Regulation of hetDNA Length during Mitotic Double-Strand Break Repair in Yeast. Molecular Cell, 2017, 67, 539-549.e4.	9.7	36
46	The in Vivo Characterization of Translesion Synthesis Across UV-Induced Lesions in Saccharomyces cerevisiae: Insights Into PolÎ¶- and PolÎ·-Dependent Frameshift Mutagenesis. Genetics, 2006, 172, 1487-1498.	2.9	35
47	The Top1 paradox: Friend and foe of the eukaryotic genome. DNA Repair, 2017, 56, 33-41.	2.8	35
48	Role of Mismatch Repair in the Fidelity ofRAD51- andRAD59-Dependent Recombination inSaccharomyces cerevisiae. Genetics, 2003, 165, 1733-1744.	2.9	35
49	Transposon mobilization in the human fungal pathogen <i>Cryptococcus</i> is mutagenic during infection and promotes drug resistance in vitro. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 9973-9980.	7.1	32
50	Mitotic Recombination and Adaptive Genomic Changes in Human Pathogenic Fungi. Genes, 2019, 10, 901.	2.4	30
51	Ribonucleotides in DNA: hidden in plain sight. Nature Structural and Molecular Biology, 2015, 22, 176-178.	8.2	29
52	Alleles of the Yeast PMS1 Mismatch-Repair Gene That Differentially Affect Recombination- and Replication-Related Processes. Genetics, 2002, 162, 1131-1145.	2.9	28
53	The mismatch repair system promotes DNA polymerase Î¶-dependent translesion synthesis in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5749-5754.	7.1	27
54	Role of Proliferating Cell Nuclear Antigen Interactions in the Mismatch Repair-Dependent Processing of Mitotic and Meiotic Recombination Intermediates in Yeast. Genetics, 2008, 178, 1221-1236.	2.9	26

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55	The Polymerase Î· Translesion Synthesis DNA Polymerase Acts Independently of the Mismatch Repair System To Limit Mutagenesis Caused by 7,8-Dihydro-8-Oxoguanine in Yeast. Molecular and Cellular Biology, 2009, 29, 5316-5326.	2.3	25
56	SMRT Sequencing for Parallel Analysis of Multiple Targets and Accurate SNP Phasing. G3: Genes, Genomes, Genetics, 2015, 5, 2801-2808.	1.8	25
57	Genome-Destabilizing Effects Associated with Top1 Loss or Accumulation of Top1 Cleavage Complexes in Yeast. PLoS Genetics, 2015, 11, e1005098.	3.5	24
58	Genetic Requirements for Spontaneous and Transcription-Stimulated Mitotic Recombination in <i>Saccharomyces cerevisiae</i>. Genetics, 2002, 162, 15-27.	2.9	24
59	The Mechanism of Nucleotide Excision Repair-Mediated UV-Induced Mutagenesis in Nonproliferating Cells. Genetics, 2013, 193, 803-817.	2.9	23
60	Mismatch recognition and subsequent processing have distinct effects on mitotic recombination intermediates and outcomes in yeast. Nucleic Acids Research, 2019, 47, 4554-4568.	14.5	23
61	Recurrent mutations in topoisomerase IIÎ± cause a previously undescribed mutator phenotype in human cancers. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	22
62	Identification of a Distinctive Mutation Spectrum Associated with High Levels of Transcription in Yeast. Molecular and Cellular Biology, 2004, 24, 4801-4809.	2.3	21
63	Meiotic Crossing Over Between Nonhomologous Chromosomes Affects Chromosome Segregation in Yeast. Genetics, 1997, 146, 69-78.	2.9	21
64	The Role of Dbf4-Dependent Protein Kinase in DNA Polymerase Î¶-Dependent Mutagenesis in <i>Saccharomyces cerevisiae</i>. Genetics, 2014, 197, 1111-1122.	2.9	20
65	[46] Experimental determination of rates of concerted evolution. Methods in Enzymology, 1993, 224, 631-646.	1.0	19
66	The effect of sequence context on spontaneous PolÎ¶-dependent mutagenesis in Saccharomyces cerevisiae. Nucleic Acids Research, 2008, 36, 2082-2093.	14.5	19
67	Mitotic Gene Conversion Tracts Associated with Repair of a Defined Double-Strand Break in <i>Saccharomyces cerevisiae</i>. Genetics, 2017, 207, 115-128.	2.9	19
68	The effect of oxidative metabolism on spontaneous PolÎ¶-dependent translesion synthesis in Saccharomyces cerevisiae. DNA Repair, 2006, 5, 226-234.	2.8	18
69	Frameshift Mutagenesis: The Roles of Primerâ€“Template Misalignment and the Nonhomologous End-Joining Pathway in <i>Saccharomyces cerevisiae</i>. Genetics, 2012, 190, 501-510.	2.9	18
70	RNAâˆ¶DNA Hybrids Initiate Quasi-Palindrome-Associated Mutations in Highly Transcribed Yeast DNA. PLoS Genetics, 2013, 9, e1003924.	3.5	18
71	Mitotic recombination in yeast: what we know and what we donâ€™t know. Current Opinion in Genetics and Development, 2021, 71, 78-85.	3.3	18
72	Novel PMS1 Alleles Preferentially Affect the Repair of Primer Strand Loops during DNA Replication. Molecular and Cellular Biology, 2005, 25, 9221-9231.	2.3	17

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73	Topoisomerase 1-dependent deletions initiated by incision at ribonucleotides are biased to the non-transcribed strand of a highly activated reporter. Nucleic Acids Research, 2015, 43, 9306-9313.	14.5	17
74	Topoisomerase I and Genome Stability: The Good and the Bad. Methods in Molecular Biology, 2018, 1703, 21-45.	0.9	17
75	Trapped topoisomerase II initiates formation of de novo duplications via the nonhomologous end-joining pathway in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 26876-26884.	7.1	17
76	Characterization of long G4-rich enhancer-associated genomic regions engaging in a novel loop:loop â€˜G4 Kissingâ€™ interaction. Nucleic Acids Research, 2020, 48, 5907-5925.	14.5	17
77	Parallel analysis of ribonucleotide-dependent deletions produced by yeast Top1<i>in vitro</i>and<i>in vivo</i>. Nucleic Acids Research, 2016, 44, 7714-7721.	14.5	15
78	Deletions associated with stabilization of the Top1 cleavage complex in yeast are products of the nonhomologous end-joining pathway. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 22683-22691.	7.1	15
79	DNA strand-exchange patterns associated with double-strand break-induced and spontaneous mitotic crossovers in Saccharomyces cerevisiae. PLoS Genetics, 2018, 14, e1007302.	3.5	14
80	Mutagenesis and the three R's in yeast. DNA Repair, 2006, 5, 409-421.	2.8	13
81	Formaldehyde-induced mutagenesis in Saccharomyces cerevisiae: Molecular properties and the roles of repair and bypass systems. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2012, 731, 92-98.	1.0	11
82	Ribonucleotides and Transcription-Associated Mutagenesis in Yeast. Journal of Molecular Biology, 2017, 429, 3156-3167.	4.2	11
83	Identification of a strand-related bias in the PCNA-mediated bypass of spontaneous lesions by yeast PolÎ·. DNA Repair, 2007, 6, 1307-1318.	2.8	10
84	Comparison of spontaneous and adaptive mutation spectra in yeast. Journal of Genetics, 1999, 78, 51-55.	0.7	9
85	Effects of camptothecin or TOP1 overexpression on genetic stability in Saccharomyces cerevisiae. DNA Repair, 2017, 59, 69-75.	2.8	9
86	Roles of exonucleases and translesion synthesis DNA polymerases during mitotic gap repair in yeast. DNA Repair, 2013, 12, 1024-1030.	2.8	8
87	Delineating the Requirements for Spontaneous DNA Damage Resistance Pathways in Genome Maintenance and Viability in Saccharomyces cerevisiae. Genetics, 2003, 164, 443-455.	2.9	8
88	Time-dependent mitotic recombination in Saccharomyces cerevisiae. Current Genetics, 1993, 23, 423-429.	1.7	6
89	Shared Genetic Pathways Contribute to the Tolerance of Endogenous and Low-Dose Exogenous DNA Damage in Yeast. Genetics, 2014, 198, 519-530.	2.9	6
90	Effects of mismatch repair and Hpr1 on transcription-stimulated mitotic recombination in the yeast Saccharomyces cerevisiae. DNA Repair, 2004, 3, 1437-1446.	2.8	5

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91	The genome's best friend. Nature Genetics, 2002, 31, 331-332.	21.4	4
92	Removal of N-6-methyladenine by the nucleotide excision repair pathway triggers the repair of mismatches in yeast gap-repair intermediates. DNA Repair, 2013, 12, 1053-1061.	2.8	4
93	Role of the Srs2â€"Rad51 Interaction Domain in Crossover Control in Saccharomyces cerevisiae. Genetics, 2019, 212, 1133-1145.	2.9	4
94	Mutagenic repair of a ZFN-induced double-strand break in yeast: Effects of cleavage site sequence and spacer size. DNA Repair, 2021, 108, 103228.	2.8	3
95	Seeking Resolution: Budding Yeast Enzymes Finally Make the Cut. Molecular Cell, 2010, 40, 858-859.	9.7	1
96	High-Throughput Analysis of Heteroduplex DNA in Mitotic Recombination Products. Methods in Molecular Biology, 2021, 2153, 503-519.	0.9	1
97	The 2012 Novitski Prize. Genetics, 2012, 191, 305-306.	2.9	0
98	The 2013 Thomas Hunt Morgan Medal. Genetics, 2013, 194, 1-4.	2.9	0
99	Recombinational Repair of Nuclease-Generated Mitotic Double-Strand Breaks with Different End Structures in Yeast. G3: Genes, Genomes, Genetics, 2020, 10, 3821-3829.	1.8	0