

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
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103
all docs

103
docs citations

103
times ranked

4245
citing authors

#	ARTICLE	IF	CITATIONS
1	Recurrent mutations in topoisomerase II \pm 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
2	Mitotic recombination in yeast: what we know and what we don't know. Current Opinion in Genetics and Development, 2021, 71, 78-85.	3.3	18
3	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
4	High-Throughput Analysis of Heteroduplex DNA in Mitotic Recombination Products. Methods in Molecular Biology, 2021, 2153, 503-519.	0.9	1
5	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
6	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
7	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
8	Characterization of long G4-rich enhancer-associated genomic regions engaging in a novel loop:loop α -G4 Kissing interaction. Nucleic Acids Research, 2020, 48, 5907-5925.	14.5	17
9	Role of the Srs2-Rad51 Interaction Domain in Crossover Control in <i>Saccharomyces cerevisiae</i> . Genetics, 2019, 212, 1133-1145.	2.9	4
10	Guidelines for DNA recombination and repair studies: Cellular assays of DNA repair pathways. Microbial Cell, 2019, 6, 1-64.	3.2	47
11	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
12	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
13	Mitotic Recombination and Adaptive Genomic Changes in Human Pathogenic Fungi. Genes, 2019, 10, 901.	2.4	30
14	Topoisomerase I and Genome Stability: The Good and the Bad. Methods in Molecular Biology, 2018, 1703, 21-45.	0.9	17
15	DNA strand-exchange patterns associated with double-strand break-induced and spontaneous mitotic crossovers in <i>Saccharomyces cerevisiae</i> . PLoS Genetics, 2018, 14, e1007302.	3.5	14
16	The Top1 paradox: Friend and foe of the eukaryotic genome. DNA Repair, 2017, 56, 33-41.	2.8	35
17	Effects of camptothecin or TOP1 overexpression on genetic stability in <i>Saccharomyces cerevisiae</i> . DNA Repair, 2017, 59, 69-75.	2.8	9
18	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

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19	Regulation of hetDNA Length during Mitotic Double-Strand Break Repair in Yeast. <i>Molecular Cell</i> , 2017, 67, 539-549.e4.	9.7	36
20	Ribonucleotides and Transcription-Associated Mutagenesis in Yeast. <i>Journal of Molecular Biology</i> , 2017, 429, 3156-3167.	4.2	11
21	Parallel analysis of ribonucleotide-dependent deletions produced by yeast Top1 <i>in vitro</i> and <i>in vivo</i> . <i>Nucleic Acids Research</i> , 2016, 44, 7714-7721.	14.5	15
22	SMRT Sequencing for Parallel Analysis of Multiple Targets and Accurate SNP Phasing. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2801-2808.	1.8	25
23	Topoisomerase 1-dependent deletions initiated by incision at ribonucleotides are biased to the non-transcribed strand of a highly activated reporter. <i>Nucleic Acids Research</i> , 2015, 43, 9306-9313.	14.5	17
24	Ribonucleotides in DNA: hidden in plain sight. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 176-178.	8.2	29
25	Genome-Destabilizing Effects Associated with Top1 Loss or Accumulation of Top1 Cleavage Complexes in Yeast. <i>PLoS Genetics</i> , 2015, 11, e1005098.	3.5	24
26	Elevated Genome-Wide Instability in Yeast Mutants Lacking RNase H Activity. <i>Genetics</i> , 2015, 201, 963-975.	2.9	60
27	Topoisomerase I Plays a Critical Role in Suppressing Genome Instability at a Highly Transcribed G-Quadruplex-Forming Sequence. <i>PLoS Genetics</i> , 2014, 10, e1004839.	3.5	43
28	Shared Genetic Pathways Contribute to the Tolerance of Endogenous and Low-Dose Exogenous DNA Damage in Yeast. <i>Genetics</i> , 2014, 198, 519-530.	2.9	6
29	The Role of Dbf4-Dependent Protein Kinase in DNA Polymerase η -Dependent Mutagenesis in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2014, 197, 1111-1122.	2.9	20
30	Transcription-Associated Mutagenesis. <i>Annual Review of Genetics</i> , 2014, 48, 341-359.	7.6	104
31	Roles of exonucleases and translesion synthesis DNA polymerases during mitotic gap repair in yeast. <i>DNA Repair</i> , 2013, 12, 1024-1030.	2.8	8
32	Removal of N-6-methyladenine by the nucleotide excision repair pathway triggers the repair of mismatches in yeast gap-repair intermediates. <i>DNA Repair</i> , 2013, 12, 1053-1061.	2.8	4
33	Two distinct mechanisms of Topoisomerase 1-dependent mutagenesis in yeast. <i>DNA Repair</i> , 2013, 12, 205-211.	2.8	45
34	The Mechanism of Nucleotide Excision Repair-Mediated UV-Induced Mutagenesis in Nonproliferating Cells. <i>Genetics</i> , 2013, 193, 803-817.	2.9	23
35	DNA Repair Mechanisms and the Bypass of DNA Damage in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2013, 193, 1025-1064.	2.9	191
36	Heteroduplex DNA Position Defines the Roles of the Sgs1, Srs2, and Mph1 Helicases in Promoting Distinct Recombination Outcomes. <i>PLoS Genetics</i> , 2013, 9, e1003340.	3.5	79

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37	The 2013 Thomas Hunt Morgan Medal. <i>Genetics</i> , 2013, 194, 1-4.	2.9	0
38	RNA-DNA Hybrids Initiate Quasi-Palindrome-Associated Mutations in Highly Transcribed Yeast DNA. <i>PLoS Genetics</i> , 2013, 9, e1003924.	3.5	18
39	The 2012 Novitski Prize. <i>Genetics</i> , 2012, 191, 305-306.	2.9	0
40	Frameshift Mutagenesis: The Roles of Primer-Template Misalignment and the Nonhomologous End-Joining Pathway in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2012, 190, 501-510.	2.9	18
41	Transcription as a source of genome instability. <i>Nature Reviews Genetics</i> , 2012, 13, 204-214.	16.3	253
42	Formaldehyde-induced mutagenesis in <i>Saccharomyces cerevisiae</i> : Molecular properties and the roles of repair and bypass systems. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2012, 731, 92-98.	1.0	11
43	Mutagenic Processing of Ribonucleotides in DNA by Yeast Topoisomerase I. <i>Science</i> , 2011, 332, 1561-1564.	12.6	251
44	Guanine repeat-containing sequences confer transcription-dependent instability in an orientation-specific manner in yeast. <i>DNA Repair</i> , 2011, 10, 953-960.	2.8	46
45	The dCMP transferase activity of yeast Rev1 is biologically relevant during the bypass of endogenously generated AP sites. <i>DNA Repair</i> , 2011, 10, 1262-1271.	2.8	36
46	Role for topoisomerase 1 in transcription-associated mutagenesis in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 698-703.	7.1	80
47	Abasic Sites in the Transcribed Strand of Yeast DNA Are Removed by Transcription-Coupled Nucleotide Excision Repair. <i>Molecular and Cellular Biology</i> , 2010, 30, 3206-3215.	2.3	58
48	Molecular Structures of Crossover and Noncrossover Intermediates during Gap Repair in Yeast: Implications for Recombination. <i>Molecular Cell</i> , 2010, 38, 211-222.	9.7	61
49	Seeking Resolution: Budding Yeast Enzymes Finally Make the Cut. <i>Molecular Cell</i> , 2010, 40, 858-859.	9.7	1
50	The Polymerase δ -Translesion Synthesis DNA Polymerase Acts Independently of the Mismatch Repair System To Limit Mutagenesis Caused by 7,8-Dihydro-8-Oxoguanine in Yeast. <i>Molecular and Cellular Biology</i> , 2009, 29, 5316-5326.	2.3	25
51	The mismatch repair system promotes DNA polymerase δ -dependent translesion synthesis in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5749-5754.	7.1	27
52	dUTP incorporation into genomic DNA is linked to transcription in yeast. <i>Nature</i> , 2009, 459, 1150-1153.	27.8	59
53	Role of Proliferating Cell Nuclear Antigen Interactions in the Mismatch Repair-Dependent Processing of Mitotic and Meiotic Recombination Intermediates in Yeast. <i>Genetics</i> , 2008, 178, 1221-1236.	2.9	26
54	Sequence Divergence Impedes Crossover More Than Noncrossover Events During Mitotic Gap Repair in Yeast. <i>Genetics</i> , 2008, 179, 1251-1262.	2.9	36

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55	The effect of sequence context on spontaneous Pol η -dependent mutagenesis in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2008, 36, 2082-2093.	14.5	19
56	Oligonucleotide transformation of yeast reveals mismatch repair complexes to be differentially active on DNA replication strands. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 11352-11357.	7.1	40
57	Transcription-associated mutagenesis in yeast is directly proportional to the level of gene expression and influenced by the direction of DNA replication. <i>DNA Repair</i> , 2007, 6, 1285-1296.	2.8	100
58	Identification of a strand-related bias in the PCNA-mediated bypass of spontaneous lesions by yeast Pol δ . <i>DNA Repair</i> , 2007, 6, 1307-1318.	2.8	10
59	The in Vivo Characterization of Translesion Synthesis Across UV-Induced Lesions in <i>Saccharomyces cerevisiae</i> : Insights Into Pol η - and Pol δ -Dependent Frameshift Mutagenesis. <i>Genetics</i> , 2006, 172, 1487-1498.	2.9	35
60	The effect of oxidative metabolism on spontaneous Pol η -dependent translesion synthesis in <i>Saccharomyces cerevisiae</i> . <i>DNA Repair</i> , 2006, 5, 226-234.	2.8	18
61	Mutagenesis and the three R's in yeast. <i>DNA Repair</i> , 2006, 5, 409-421.	2.8	13
62	Novel PMS1 Alleles Preferentially Affect the Repair of Primer Strand Loops during DNA Replication. <i>Molecular and Cellular Biology</i> , 2005, 25, 9221-9231.	2.3	17
63	The 9-1-1 Checkpoint Clamp Physically Interacts with Pol η and Is Partially Required for Spontaneous Pol η -dependent Mutagenesis in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 38657-38665.	3.4	104
64	Roles of RAD6 Epistasis Group Members in Spontaneous Pol η -Dependent Translesion Synthesis in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2005, 169, 1939-1955.	2.9	54
65	Mutagenic effects of abasic and oxidized abasic lesions in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2005, 33, 6196-6202.	14.5	41
66	Identification of a Distinctive Mutation Spectrum Associated with High Levels of Transcription in Yeast. <i>Molecular and Cellular Biology</i> , 2004, 24, 4801-4809.	2.3	21
67	Examination of the Roles of Sgs1 and Srs2 Helicases in the Enforcement of Recombination Fidelity in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2004, 168, 1855-1865.	2.9	79
68	Involvement of two endonuclease III homologs in the base excision repair pathway for the processing of DNA alkylation damage in <i>Saccharomyces cerevisiae</i> . <i>DNA Repair</i> , 2004, 3, 51-59.	2.8	39
69	Effects of mismatch repair and Hpr1 on transcription-stimulated mitotic recombination in the yeast <i>Saccharomyces cerevisiae</i> . <i>DNA Repair</i> , 2004, 3, 1437-1446.	2.8	5
70	Determination of Mitotic Recombination Rates by Fluctuation Analysis in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2004, 262, 003-012.		83
71	Delineating the Requirements for Spontaneous DNA Damage Resistance Pathways in Genome Maintenance and Viability in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2003, 164, 443-455.	2.9	8
72	Role of Mismatch Repair in the Fidelity of RAD51- and RAD59-Dependent Recombination in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2003, 165, 1733-1744.	2.9	35

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73	Base Composition of Mononucleotide Runs Affects DNA Polymerase Slippage and Removal of Frameshift Intermediates by Mismatch Repair in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2002, 22, 8756-8762.	2.3	82
74	The genome's best friend. <i>Nature Genetics</i> , 2002, 31, 331-332.	21.4	4
75	Genetic Requirements for Spontaneous and Transcription-Stimulated Mitotic Recombination in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2002, 162, 15-27.	2.9	24
76	Alleles of the Yeast PMS1 Mismatch-Repair Gene That Differentially Affect Recombination- and Replication-Related Processes. <i>Genetics</i> , 2002, 162, 1131-1145.	2.9	28
77	Yeast base excision repair: Interconnections and networks. <i>Progress in Molecular Biology and Translational Science</i> , 2001, 68, 29-39.	1.9	37
78	Spontaneous Frameshift Mutations in <i>Saccharomyces cerevisiae</i> : Accumulation During DNA Replication and Removal by Proofreading and Mismatch Repair Activities. <i>Genetics</i> , 2001, 159, 65-75.	2.9	42
79	Discrete in vivo roles for the MutL homologs Mlh2p and Mlh3p in the removal of frameshift intermediates in budding yeast. <i>Current Biology</i> , 2000, 10, 145-148.	3.9	118
80	Stimulation of Mitotic Recombination Events by High Levels of RNA Polymerase II Transcription in Yeast. <i>Molecular and Cellular Biology</i> , 2000, 20, 5404-5414.	2.3	45
81	DNA Polymerase η Introduces Multiple Mutations when Bypassing Spontaneous DNA Damage in <i>Saccharomyces cerevisiae</i> . <i>Molecular Cell</i> , 2000, 6, 1491-1499.	9.7	114
82	DNA MISMATCH REPAIR AND GENETIC INSTABILITY. <i>Annual Review of Genetics</i> , 2000, 34, 359-399.	7.6	561
83	Genetic Analysis of Transcription-Associated Mutation in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2000, 154, 109-120.	2.9	52
84	Regulation of Mitotic Homeologous Recombination in Yeast: Functions of Mismatch Repair and Nucleotide Excision Repair Genes. <i>Genetics</i> , 2000, 154, 133-146.	2.9	107
85	Sequence Composition and Context Effects on the Generation and Repair of Frameshift Intermediates in Mononucleotide Runs in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2000, 156, 571-578.	2.9	53
86	Comparison of spontaneous and adaptive mutation spectra in yeast. <i>Journal of Genetics</i> , 1999, 78, 51-55.	0.7	9
87	<i>Saccharomyces cerevisiae</i> Ntg1p and Ntg2p: Broad Specificity N-Glycosylases for the Repair of Oxidative DNA Damage in the Nucleus and Mitochondria. <i>Biochemistry</i> , 1999, 38, 11298-11306.	2.5	110
88	Overlapping Specificities of Base Excision Repair, Nucleotide Excision Repair, Recombination, and Translesion Synthesis Pathways for DNA Base Damage in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 1999, 19, 2929-2935.	2.3	205
89	Removal of Frameshift Intermediates by Mismatch Repair Proteins in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 1999, 19, 4766-4773.	2.3	56
90	The Role of the Mismatch Repair Machinery in Regulating Mitotic and Meiotic Recombination Between Diverged Sequences in Yeast. <i>Genetics</i> , 1999, 151, 1299-1313.	2.9	162

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91	Mismatch Repair Proteins Regulate Heteroduplex Formation during Mitotic Recombination in Yeast. <i>Molecular and Cellular Biology</i> , 1998, 18, 6525-6537.	2.3	111
92	Genetic control of microsatellite stability. <i>Mutation Research DNA Repair</i> , 1997, 383, 61-70.	3.7	127
93	Meiotic Crossing Over Between Nonhomologous Chromosomes Affects Chromosome Segregation in Yeast. <i>Genetics</i> , 1997, 146, 69-78.	2.9	21
94	Destabilization of Simple Repetitive DNA Sequences by Transcription in Yeast. <i>Genetics</i> , 1996, 143, 713-721.	2.9	99
95	Time-dependent mitotic recombination in <i>Saccharomyces cerevisiae</i> . <i>Current Genetics</i> , 1993, 23, 423-429.	1.7	6
96	[46] Experimental determination of rates of concerted evolution. <i>Methods in Enzymology</i> , 1993, 224, 631-646.	1.0	19
97	Nucleotide sequence of the <i>LYS2</i> gene of <i>Saccharomyces cerevisiae</i> : homology to <i>Bacillus brevis</i> tyrocidine synthetase 1. <i>Gene</i> , 1991, 98, 141-145.	2.2	63
98	CHROMOSOMAL TRANSLOCATIONS GENERATED BY HIGH-FREQUENCY MEIOTIC RECOMBINATION BETWEEN REPEATED YEAST GENES. <i>Genetics</i> , 1986, 114, 731-752.	2.9	178
99	Expression of rRNA and tRNA genes in <i>Escherichia coli</i> : Evidence for feedback regulation by products of rRNA operons. <i>Cell</i> , 1983, 33, 865-876.	28.9	239