Scott A Lujan

List of Publications by Year
in descending order

34 papers	1,928 citations	304743 22 h-index	377865 34 g-index
35 all docs	35 docs citations	35 times ranked	2083 citing authors

#	Article	IF	Citations
1	Tracking replication enzymology in vivo by genome-wide mapping of ribonucleotide incorporation. Nature Structural and Molecular Biology, 2015, 22, 185-191.	8.2	167
2	Ribonucleotides Are Signals for Mismatch Repair of Leading-Strand Replication Errors. Molecular Cell, 2013, 50, 437-443.	9.7	166
3	Processing ribonucleotides incorporated during eukaryotic DNA replication. Nature Reviews Molecular Cell Biology, 2016, 17, 350-363.	37.0	152
4	Heterogeneous polymerase fidelity and mismatch repair bias genome variation and composition. Genome Research, 2014, 24, 1751-1764.	5.5	141
5	Topoisomerase 1-Mediated Removal of Ribonucleotides from Nascent Leading-Strand DNA. Molecular Cell, 2013, 49, 1010-1015.	9.7	130
6	DNA Polymerases Divide the Labor of Genome Replication. Trends in Cell Biology, 2016, 26, 640-654.	7.9	123
7	Mismatch Repair Balances Leading and Lagging Strand DNA Replication Fidelity. PLoS Genetics, 2012, 8, e1003016.	3.5	107
8	Genome-wide model for the normal eukaryotic DNA replication fork. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 17674-17679.	7.1	88
9	Disrupting antibiotic resistance propagation by inhibiting the conjugative DNA relaxase. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 12282-12287.	7.1	78
10	Evidence that DNA polymerase Î´ contributes to initiating leading strand DNA replication in Saccharomyces cerevisiae. Nature Communications, 2018, 9, 858.	12.8	77
11	Roles for DNA polymerase Î´ in initiating and terminating leading strand DNA replication. Nature Communications, 2019, 10, 3992.	12.8	68
12	DNA Polymerase Delta Synthesizes Both Strands during Break-Induced Replication. Molecular Cell, 2019, 76, 371-381.e4.	9.7	65
13	Genome-wide analysis of the specificity and mechanisms of replication infidelity driven by imbalanced dNTP pools. Nucleic Acids Research, 2016, 44, 1669-1680.	14.5	62
14	Mismatch repair-independent tandem repeat sequence instability resulting from ribonucleotide incorporation by DNA polymerase É›. DNA Repair, 2011, 10, 476-482.	2.8	56
15	DNA polymerase zeta generates clustered mutations during bypass of endogenous DNA lesions in <i>Saccharomyces cerevisiae</i>. Environmental and Molecular Mutagenesis, 2012, 53, 777-786.	2.2	54
16	Quantifying the contributions of base selectivity, proofreading and mismatch repair to nuclear DNA replication in Saccharomyces cerevisiae. DNA Repair, 2015, 31, 41-51.	2.8	51
17	Ultrasensitive deletion detection links mitochondrial DNA replication, disease, and aging. Genome Biology, 2020, 21, 248.	8.8	48
18	Evidence that processing of ribonucleotides in DNA by topoisomerase 1 is leading-strand specific. Nature Structural and Molecular Biology, 2015, 22, 291-297.	8.2	45

#	Article	IF	Citations
19	Stimulation of Chromosomal Rearrangements by Ribonucleotides. Genetics, 2015, 201, 951-961.	2.9	43
20	Differences in genome-wide repeat sequence instability conferred by proofreading and mismatch repair defects. Nucleic Acids Research, 2015, 43, 4067-4074.	14.5	28
21	Low-fidelity DNA synthesis by the L979F mutator derivative of Saccharomyces cerevisiae DNA polymerase Î¶. Nucleic Acids Research, 2009, 37, 3774-3787.	14.5	26
22	The mechanism and control of DNA transfer by the conjugative relaxase of resistance plasmid pCU1. Nucleic Acids Research, 2010, 38, 5929-5943.	14.5	25
23	The absence of the catalytic domains of Saccharomyces cerevisiae DNA polymerase Ïµ strongly reduces DNA replication fidelity. Nucleic Acids Research, 2019, 47, 3986-3995.	14.5	19
24	Hypermutation signature reveals a slippage and realignment model of translesion synthesis by Rev3 polymerase in cisplatin-treated yeast. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2663-2668.	7.1	18
25	Ribonucleotide incorporation into DNA during DNA replication and its consequences. Critical Reviews in Biochemistry and Molecular Biology, 2021, 56, 109-124.	5.2	15
26	Eukaryotic genome instability in light of asymmetric DNA replication. Critical Reviews in Biochemistry and Molecular Biology, 2016, 51, 43-52.	5.2	12
27	Muver, a computational framework for accurately calling accumulated mutations. BMC Genomics, 2018, 19, 345.	2.8	12
28	How asymmetric DNA replication achieves symmetrical fidelity. Nature Structural and Molecular Biology, 2021, 28, 1020-1028.	8.2	12
29	Energy-minimized structures and MO levels of catalysts related to [RuO(hpsd)(bpy)]+ that competently hydroxylate benzene (hpsd(2-)=(2-hydroxyphenyl)salicyldiminato). Inorganica Chimica Acta, 2004, 357, 785-796.	2.4	10
30	Genome-wide mutagenesis resulting from topoisomerase 1-processing of unrepaired ribonucleotides in DNA. DNA Repair, 2019, 84, 102641.	2.8	10
31	Stability across the Whole Nuclear Genome in the Presence and Absence of DNA Mismatch Repair. Cells, 2021, 10, 1224.	4.1	8
32	Mapping Ribonucleotides Incorporated into DNA by Hydrolytic End-Sequencing. Methods in Molecular Biology, 2018, 1672, 329-345.	0.9	5
33	Opportunities for new studies of nuclear DNA replication enzymology in budding yeast. Current Genetics, 2020, 66, 299-302.	1.7	4
34	The fidelity of DNA replication, particularly on GC-rich templates, is reduced by defects of the Feâ€"S cluster in DNA polymerase Î´. Nucleic Acids Research, 2021, 49, 5623-5636.	14.5	3