

Hengyao Niu

List of Publications by Year in descending order

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45
papers

3,247
citations

172457

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254184

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all docs

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docs citations

45
times ranked

3611
citing authors

#	ARTICLE	IF	CITATIONS
1	Deciphering the mechanism of processive ssDNA digestion by the Dna2-RPA ensemble. <i>Nature Communications</i> , 2022, 13, 359.	12.8	12
2	Mechanistic insights into the multiple activities of the Rad5 family of enzymes. <i>Journal of Molecular Biology</i> , 2022, , 167581.	4.2	1
3	Structure of Rad5 provides insights into its role in tolerance to replication stress. <i>Molecular and Cellular Oncology</i> , 2021, 8, 1889348.	0.7	0
4	A PRC2-independent function for EZH2 in regulating rRNA 2â€²-O methylation and IRES-dependent translation. <i>Nature Cell Biology</i> , 2021, 23, 341-354.	10.3	54
5	Thermal Analysis of a Mixture of Ribosomal Proteins by vT-ESI-MS: Toward a Parallel Approach for Characterizing the Stabilitome. <i>Analytical Chemistry</i> , 2021, 93, 8484-8492.	6.5	8
6	Structural basis for the multi-activity factor Rad5 in replication stress tolerance. <i>Nature Communications</i> , 2021, 12, 321.	12.8	10
7	Rad52 Restrains Resection at DNA Double-Strand Break Ends in Yeast. <i>Molecular Cell</i> , 2019, 76, 699-711.e6.	9.7	37
8	Guidelines for DNA recombination and repair studies: Mechanistic assays of DNA repair processes. <i>Microbial Cell</i> , 2019, 6, 65-101.	3.2	10
9	DNA duplex recognition activates Exo1 nuclease activity. <i>Journal of Biological Chemistry</i> , 2019, 294, 11559-11567.	3.4	5
10	Apn2 resolves blocked 3â€² ends and suppresses Top1-induced mutagenesis at genomic rNMP sites. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 155-163.	8.2	28
11	Phospho-dependent recruitment of the yeast NuA4 acetyltransferase complex by MRX at DNA breaks regulates RPA dynamics during resection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10028-10033.	7.1	25
12	Multifunctional Roles of <i>Saccharomyces cerevisiae</i> Srs2 protein in Replication, Recombination and Repair. <i>FEMS Yeast Research</i> , 2017, 17, fow111.	2.3	38
13	Nucleosome-like, Single-stranded DNA (ssDNA)-Histone Octamer Complexes and the Implication for DNA Double Strand Break Repair. <i>Journal of Biological Chemistry</i> , 2017, 292, 5271-5281.	3.4	33
14	A novel role of the Dna2 translocase function in DNA break resection. <i>Genes and Development</i> , 2017, 31, 503-510.	5.9	33
15	Metal-mediated diradical tuning for DNA replication arrest via template strand scission. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7405-E7414.	7.1	11
16	RNA topoisomerase is prevalent in all domains of life and associates with polyribosomes in animals. <i>Nucleic Acids Research</i> , 2016, 44, 6335-6349.	14.5	63
17	Enrichment of Cdk1-cyclins at DNA double-strand breaks stimulates Fun30 phosphorylation and DNA end resection. <i>Nucleic Acids Research</i> , 2016, 44, 2742-2753.	14.5	39
18	Differential regulation of the anti-crossover and replication fork regression activities of Mph1 by Mte1. <i>Genes and Development</i> , 2016, 30, 687-699.	5.9	17

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19	Roles of DNA helicases and Exo1 in the avoidance of mutations induced by Top1-mediated cleavage at ribonucleotides in DNA. <i>Cell Cycle</i> , 2016, 15, 331-336.	2.6	9
20	Tel1 and Rif2 Regulate MRX Functions in End-Tethering and Repair of DNA Double-Strand Breaks. <i>PLoS Biology</i> , 2016, 14, e1002387.	5.6	44
21	Synthetic viability genomic screening defines Sae2 function in DNA repair. <i>EMBO Journal</i> , 2015, 34, 1509-1522.	7.8	37
22	Molecular Mechanism of Resolving Trinucleotide Repeat Hairpin by Helicases. <i>Structure</i> , 2015, 23, 1018-1027.	3.3	6
23	DNA Sequence Alignment by Microhomology Sampling during Homologous Recombination. <i>Cell</i> , 2015, 160, 856-869.	28.9	182
24	Biochemical mechanism of DSB end resection and its regulation. <i>DNA Repair</i> , 2015, 32, 66-74.	2.8	107
25	Selective modulation of the functions of a conserved DNA motor by a histone fold complex. <i>Genes and Development</i> , 2015, 29, 1000-1005.	5.9	17
26	Interplay between Ku and Replication Protein A in the Restriction of Exo1-mediated DNA Break End Resection. <i>Journal of Biological Chemistry</i> , 2015, 290, 18806-18816.	3.4	38
27	Phosphorylation of the Synaptonemal Complex Protein Zip1 Regulates the Crossover/Noncrossover Decision during Yeast Meiosis. <i>PLoS Biology</i> , 2015, 13, e1002329.	5.6	43
28	Multifaceted role of the Topo III±RMI1-RMI2 complex and DNA2 in the BLM-dependent pathway of DNA break end resection. <i>Nucleic Acids Research</i> , 2014, 42, 11083-11091.	14.5	60
29	Restriction of Replication Fork Regression Activities by a Conserved SMC Complex. <i>Molecular Cell</i> , 2014, 56, 436-445.	9.7	60
30	Protein dynamics during presynaptic-complex assembly on individual single-stranded DNA molecules. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 893-900.	8.2	81
31	Avoidance of ribonucleotide-induced mutations by RNase H2 and Srs2-Exo1 mechanisms. <i>Nature</i> , 2014, 511, 251-254.	27.8	75
32	Concentration-Dependent Exchange of Replication Protein A on Single-Stranded DNA Revealed by Single-Molecule Imaging. <i>PLoS ONE</i> , 2014, 9, e87922.	2.5	176
33	Pif1 helicase and PolÎ± promote recombination-coupled DNA synthesis via bubble migration. <i>Nature</i> , 2013, 502, 393-396.	27.8	265
34	Nucleosome dynamics regulates DNA processing. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 836-842.	8.2	130
35	Investigations of homologous recombination pathways and their regulation. <i>Yale Journal of Biology and Medicine</i> , 2013, 86, 453-61.	0.2	40
36	Overcoming natural replication barriers: differential helicase requirements. <i>Nucleic Acids Research</i> , 2012, 40, 1091-1105.	14.5	76

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37	Processing of DNA structures via DNA unwinding and branch migration by the <i>S. cerevisiae</i> Mph1 protein. <i>DNA Repair</i> , 2011, 10, 1034-1043.	2.8	54
38	Cell cycle regulation of DNA double-strand break end resection by Cdk1-dependent Dna2 phosphorylation. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1015-1019.	8.2	165
39	Deciphering Protein Kinase Specificity Through Large-Scale Analysis of Yeast Phosphorylation Site Motifs. <i>Science Signaling</i> , 2010, 3, ra12.	3.6	341
40	Mechanism of the ATP-dependent DNA end-resection machinery from <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 2010, 467, 108-111.	27.8	349
41	Multiplicity of DNA end resection machineries in chromosome break repair. <i>Genes and Development</i> , 2009, 23, 1481-1486.	5.9	32
42	Regulation of Meiotic Recombination via Mek1-Mediated Rad54 Phosphorylation. <i>Molecular Cell</i> , 2009, 36, 393-404.	9.7	158
43	DNA double-strand break processing: the beginning of the end. <i>Genes and Development</i> , 2008, 22, 2903-2907.	5.9	33
44	Cdc28â€œClb5 (CDK-S) and Cdc7â€œDbf4 (DDK) collaborate to initiate meiotic recombination in yeast. <i>Genes and Development</i> , 2008, 22, 386-397.	5.9	124
45	Mek1 Kinase Is Regulated To Suppress Double-Strand Break Repair between Sister Chromatids during Budding Yeast Meiosis. <i>Molecular and Cellular Biology</i> , 2007, 27, 5456-5467.	2.3	121