

Jennifer A Cobb

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

778
citations

840776

11
h-index

677142

22
g-index

34
all docs

34
docs citations

34
times ranked

1018
citing authors

#	ARTICLE	IF	CITATIONS
1	Mechanistically distinct roles for Sgs1p in checkpoint activation and replication fork maintenance. <i>EMBO Journal</i> , 2005, 24, 405-417.	7.8	132
2	Cohesin Association to Replication Sites Depends on Rad50 and Promotes Fork Restart. <i>Molecular Cell</i> , 2012, 48, 98-108.	9.7	108
3	PolySUMOylation by Siz2 and Mms21 triggers relocation of DNA breaks to nuclear pores through the Slx5/Slx8 STUbL. <i>Genes and Development</i> , 2016, 30, 931-945.	5.9	107
4	The yeast Shu complex couples error-free post-replication repair to homologous recombination. <i>Molecular Microbiology</i> , 2009, 73, 89-102.	2.5	88
5	The MRX complex stabilizes the replisome independently of the S phase checkpoint during replication stress. <i>EMBO Journal</i> , 2009, 28, 1142-1156.	7.8	79
6	During Replication Stress, Non-Smc Element 5 (Nse5) Is Required for Smc5/6 Protein Complex Functionality at Stalled Forks. <i>Journal of Biological Chemistry</i> , 2012, 287, 11374-11383.	3.4	46
7	Nej1 Interacts with Mre11 to Regulate Tethering and Dna2 Binding at DNA Double-Strand Breaks. <i>Cell Reports</i> , 2019, 28, 1564-1573.e3.	6.4	27
8	Smc5/6 Is a Telomere-Associated Complex that Regulates Sir4 Binding and TPE. <i>PLoS Genetics</i> , 2016, 12, e1006268.	3.5	26
9	The C-terminus of Nej1 is critical for nuclear localization and non-homologous end-joining. <i>DNA Repair</i> , 2014, 14, 9-16.	2.8	21
10	The non-homologous end-joining factor Nej1 inhibits resection mediated by Dna2-Sgs1 nuclease-helicase at DNA double strand breaks. <i>Journal of Biological Chemistry</i> , 2017, 292, 14576-14586.	3.4	19
11	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. <i>PLoS Genetics</i> , 2020, 16, e1008422.	3.5	17
12	A Role for the Mre11-Rad50-Xrs2 Complex in Gene Expression and Chromosome Organization. <i>Molecular Cell</i> , 2021, 81, 183-197.e6.	9.7	15
13	The NuA4 Complex Promotes Translesion Synthesis (TLS)-Mediated DNA Damage Tolerance. <i>Genetics</i> , 2015, 199, 1065-1076.	2.9	14
14	Non-Smc element 5 (Nse5) of the Smc5/6 complex interacts with SUMO pathway components. <i>Biology Open</i> , 2016, 5, 777-785.	1.2	14
15	A high-throughput alpha particle irradiation system for monitoring DNA damage repair, genome instability and screening in human cell and yeast model systems. <i>Nucleic Acids Research</i> , 2020, 48, e111-e111.	14.5	13
16	Mapping Genomic Targets of DNA Helicases by Chromatin Immunoprecipitation in <i>Saccharomyces cerevisiae</i> . <i>Methods in Molecular Biology</i> , 2009, 587, 113-126.	0.9	11
17	The Mre11-Rad50-Xrs2 Complex Is Required for Yeast DNA Postreplication Repair. <i>PLoS ONE</i> , 2014, 9, e109292.	2.5	9
18	SUNny Ways: The Role of the SUN-Domain Protein Mps3 Bridging Yeast Nuclear Organization and Lipid Homeostasis. <i>Frontiers in Genetics</i> , 2020, 11, 136.	2.3	7

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19	Smc5/6 in the rDNA modulates lifespan independently of Fob1. Aging Cell, 2021, 20, e13373.	6.7	7
20	Nej1 interacts with Sae2 at DNA double-stranded breaks to inhibit DNA resection. Journal of Biological Chemistry, 2022, 298, 101937.	3.4	7
21	Multifunctional properties of Nej1XLF C-terminus promote end-joining and impact DNA double-strand break repair pathway choice. DNA Repair, 2022, 115, 103332.	2.8	4
22	A decade of understanding spatio-temporal regulation of DNA repair by the nuclear architecture. Biochemistry and Cell Biology, 2016, 94, 433-440.	2.0	2
23	Nej1 Interacts with Mre11 to Regulate-Tethering and Dna2 Binding at DNA Double-Strand Breaks. SSRN Electronic Journal, 0, , .	0.4	0
24	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
25	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
26	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
27	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
28	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
29	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0