

Jeffrey Fillingham

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

1,907
citations

623734

14
h-index

642732

23
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24
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24
docs citations

24
times ranked

2797
citing authors

#	ARTICLE	IF	CITATIONS
1	Functional proteomics protocol for the identification of interaction partners in <i>Tetrahymena thermophila</i> . STAR Protocols, 2021, 2, 100362.	1.2	3
2	Functional characterization of RebL1 highlights the evolutionary conservation of oncogenic activities of the RBBP4/7 orthologue in <i>Tetrahymena thermophila</i> . Nucleic Acids Research, 2021, 49, 6196-6212.	14.5	14
3	Exploring the Histone Acetylation Cycle in the Protozoan Model <i>Tetrahymena thermophila</i> . Frontiers in Cell and Developmental Biology, 2020, 8, 509.	3.7	10
4	Nucleus-specific linker histones Hho1 and Mlh1 form distinct protein interactions during growth, starvation and development in <i>Tetrahymena thermophila</i> . Scientific Reports, 2020, 10, 168.	3.3	10
5	The Med31 Conserved Component of the Divergent Mediator Complex in <i>Tetrahymena thermophila</i> Participates in Developmental Regulation. Current Biology, 2019, 29, 2371-2379.e6.	3.9	13
6	RACS: rapid analysis of ChIP-Seq data for contig based genomes. BMC Bioinformatics, 2019, 20, 533.	2.6	4
7	Functional Proteomics of Nuclear Proteins in <i>Tetrahymena thermophila</i> : A Review. Genes, 2019, 10, 333.	2.4	11
8	Proteomic Analysis of Histones H2A/H2B and Variant Hv1 in <i>Tetrahymena thermophila</i> Reveals an Ancient Network of Chaperones. Molecular Biology and Evolution, 2019, 36, 1037-1055.	8.9	12
9	Functional Analysis of Hif1 Histone Chaperone in <i>Saccharomyces cerevisiae</i> . G3: Genes, Genomes, Genetics, 2018, 8, 1993-2006.	1.8	8
10	The bromodomain-containing protein Ibd1 links multiple chromatin-related protein complexes to highly expressed genes in <i>Tetrahymena thermophila</i> . Epigenetics and Chromatin, 2018, 11, 10.	3.9	16
11	Regulation of histone gene transcription in yeast. Cellular and Molecular Life Sciences, 2014, 71, 599-613.	5.4	58
12	Cell cycle-regulated oscillator coordinates core histone gene transcription through histone acetylation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 14124-14129.	7.1	32
13	Molecular evolution of NASP and conserved histone H3/H4 transport pathway. BMC Evolutionary Biology, 2014, 14, 139.	3.2	30
14	The Replication-independent Histone H3-H4 Chaperones HIR, ASF1, and RTT106 Co-operate to Maintain Promoter Fidelity. Journal of Biological Chemistry, 2012, 287, 1709-1718.	3.4	54
15	Restriction of histone gene transcription to S phase by phosphorylation of a chromatin boundary protein. Genes and Development, 2011, 25, 2489-2501.	5.9	40
16	The program for processing newly synthesized histones H3.1 and H4. Nature Structural and Molecular Biology, 2010, 17, 1343-1351.	8.2	214
17	Defining the budding yeast chromatin-associated interactome. Molecular Systems Biology, 2010, 6, 448.	7.2	58
18	An acetylated form of histone H2A.Z regulates chromosome architecture in <i>Schizosaccharomyces pombe</i> . Nature Structural and Molecular Biology, 2009, 16, 1286-1293.	8.2	77

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19	Two-Color Cell Array Screen Reveals Interdependent Roles for Histone Chaperones and a Chromatin Boundary Regulator in Histone Gene Repression. <i>Molecular Cell</i> , 2009, 35, 340-351.	9.7	88
20	A Histone Code for Chromatin Assembly. <i>Cell</i> , 2008, 134, 206-208.	28.9	21
21	Chaperone Control of the Activity and Specificity of the Histone H3 Acetyltransferase Rtt109. <i>Molecular and Cellular Biology</i> , 2008, 28, 4342-4353.	2.3	165
22	Functional dissection of protein complexes involved in yeast chromosome biology using a genetic interaction map. <i>Nature</i> , 2007, 446, 806-810.	27.8	806
23	γH2AX and its role in DNA double-strand break repair This paper is one of a selection of papers published in this Special Issue, entitled 27th International West Coast Chromatin and Chromosome Conference, and has undergone the Journal's usual peer review process.. <i>Biochemistry and Cell Biology</i> , 2006, 84, 568-577.	2.0	163