Jeffrey Fillingham

List of Publications by Year
in descending order

23 papers	1,907 citations	623734 14 h-index	642732 23 g-index
24 all docs	24 docs citations	24 times ranked	2797 citing authors

#	Article	IF	Citations
1	Functional dissection of protein complexes involved in yeast chromosome biology using a genetic interaction map. Nature, 2007, 446, 806-810.	27.8	806
2	The program for processing newly synthesized histones H3.1 and H4. Nature Structural and Molecular Biology, 2010, 17, 1343-1351.	8.2	214
3	Chaperone Control of the Activity and Specificity of the Histone H3 Acetyltransferase Rtt109. Molecular and Cellular Biology, 2008, 28, 4342-4353.	2.3	165
4	Î³H2AX and its role in DNA double-strand break repairThis 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.. Biochemistry and Cell Biology, 2006, 84, 568-577.	2.0	163
5	Two-Color Cell Array Screen Reveals Interdependent Roles for Histone Chaperones and a Chromatin Boundary Regulator in Histone Gene Repression. Molecular Cell, 2009, 35, 340-351.	9.7	88
6	An acetylated form of histone H2A.Z regulates chromosome architecture in Schizosaccharomyces pombe. Nature Structural and Molecular Biology, 2009, 16, 1286-1293.	8.2	77
7	Defining the budding yeast chromatinâ€associated interactome. Molecular Systems Biology, 2010, 6, 448.	7.2	58
8	Regulation of histone gene transcription in yeast. Cellular and Molecular Life Sciences, 2014, 71, 599-613.	5.4	58
9	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
10	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
11	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
12	Molecular evolution of NASP and conserved histone H3/H4 transport pathway. BMC Evolutionary Biology, 2014, 14, 139.	3.2	30
13	A Histone Code for Chromatin Assembly. Cell, 2008, 134, 206-208.	28.9	21
14	The bromodomain-containing protein Ibd1 links multiple chromatin-related protein complexes to highly expressed genes in Tetrahymena thermophila. Epigenetics and Chromatin, 2018, 11, 10.	3.9	16
15	Functional characterization of RebL1 highlights the evolutionary conservation of oncogenic activities of the RBBP4/7 orthologue in Tetrahymena thermophila. Nucleic Acids Research, 2021, 49, 6196-6212.	14.5	14
16	The Med31 Conserved Component of the Divergent Mediator Complex in Tetrahymena thermophila Participates in Developmental Regulation. Current Biology, 2019, 29, 2371-2379.e6.	3.9	13
17	Proteomic Analysis of Histones H2A/H2B and Variant Hv1 in Tetrahymena thermophila Reveals an Ancient Network of Chaperones. Molecular Biology and Evolution, 2019, 36, 1037-1055.	8.9	12
18	Functional Proteomics of Nuclear Proteins in Tetrahymena thermophila: A Review. Genes, 2019, 10, 333.	2.4	11

#	Article	IF	Citations
19	Exploring the Histone Acetylation Cycle in the Protozoan Model Tetrahymena thermophila. Frontiers in Cell and Developmental Biology, 2020, 8, 509.	3.7	10
20	Nucleus-specific linker histones Hho1 and Mlh1 form distinct protein interactions during growth, starvation and development in Tetrahymena thermophila. Scientific Reports, 2020, 10, 168.	3.3	10
21	Functional Analysis of Hif1 Histone Chaperone in Saccharomyces cerevisiae. G3: Genes, Genomes, Genetics, 2018, 8, 1993-2006.	1.8	8
22	RACS: rapid analysis of ChIP-Seq data for contig based genomes. BMC Bioinformatics, 2019, 20, 533.	2.6	4
23	Functional proteomics protocol for the identification of interaction partners in Tetrahymena thermophila. STAR Protocols, 2021, 2, 100362.	1.2	3