Jonathan H Dennis

List of Publications by Year
in descending order

27 papers	1,634 citations	567281 15 h-index	526287 27 g-index
28 all docs	28 docs citations	28 times ranked	2758 citing authors

#	Article	IF	Citations
1	Topologically associating domains are stable units of replication-timing regulation. Nature, 2014, 515, 402-405.	27.8	779
2	Expression of the Brn-3b Transcription Factor Correlates with Expression of HSP-27 in Breast Cancer Biopsies and Is Required for Maximal Activation of the HSP-27 Promoter. Cancer Research, 2005, 65, 3072-3080.	0.9	203
3	Predicting Human Nucleosome Occupancy from Primary Sequence. PLoS Computational Biology, 2008, 4, e1000134.	3.2	111
4	Differential Nuclease Sensitivity Profiling of Chromatin Reveals Biochemical Footprints Coupled to Gene Expression and Functional DNA Elements in Maize. Plant Cell, 2014, 26, 3883-3893.	6.6	72
5	Pre-replication complex proteins assemble at regions of low nucleosome occupancy within the Chinese hamster dihydrofolate reductase initiation zone. Nucleic Acids Research, 2011, 39, 3141-3155.	14.5	61
6	Chromatin-interaction compartment switch at developmentally regulated chromosomal domains reveals an unusual principle of chromatin folding. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 12574-12579.	7.1	59
7	BAF250a Protein Regulates Nucleosome Occupancy and Histone Modifications in Priming Embryonic Stem Cell Differentiation. Journal of Biological Chemistry, 2015, 290, 19343-19352.	3.4	55
8	Independent and complementary methods for large-scale structural analysis of mammalian chromatin. Genome Research, 2007, 17, 928-939.	5.5	38
9	Regulated large-scale nucleosome density patterns and precise nucleosome positioning correlate with V(D)J recombination. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E6427-E6436.	7.1	31
10	The spring-loaded genome: Nucleosome redistributions are widespread, transient, and DNA-directed. Genome Research, 2014, 24, 251-259.	5.5	28
11	Label-Free Relative Quantitation of Isobaric and Isomeric Human Histone H2A and H2B Variants by Fourier Transform Ion Cyclotron Resonance Top-Down MS/MS. Journal of Proteome Research, 2016, 15, 3196-3203.	3.7	27
12	Genome-Wide Prediction of Nucleosome Occupancy in Maize Reveals Plant Chromatin Structural Features at Genes and Other Elements at Multiple Scales Â Â. Plant Physiology, 2013, 162, 1127-1141.	4.8	24
13	Multiple roles of H2A.Z in regulating promoter chromatin architecture in human cells. Nature Communications, 2021, 12, 2524.	12.8	22
14	The native cistrome and sequence motif families of the maize ear. PLoS Genetics, 2021, 17, e1009689.	3.5	19
15	Chromatin patterns associated with lung adenocarcinoma progression. Cell Cycle, 2013, 12, 1536-1543.	2.6	18
16	Evaluation of procalcitonin-guided antimicrobial stewardship in patients admitted to hospital with COVID-19 pneumonia. JAC-Antimicrobial Resistance, 2021, 3, dlab133.	2.1	18
17	Comprehensive nucleosome mapping of the human genome in cancer progression. Oncotarget, 2016, 7, 13429-13445.	1.8	17
18	Hierarchical regulation of the genome: global changes in nucleosome organization potentiate genome response. Oncotarget, 2016, 7, 6460-6475.	1.8	12

#	Article	IF	Citations
19	Nucleosome Repositioning: A Novel Mechanism for Nicotine- and Cocaine-Induced Epigenetic Changes. PLoS ONE, 2015, 10, e0139103.	2.5	11
20	iSeg: an efficient algorithm for segmentation of genomic and epigenomic data. BMC Bioinformatics, 2018, 19, 131.	2.6	9
21	Commentary: Epigenetic Regulation of Phosphodiesterases 2A and 3A Underlies Compromised Î²-Adrenergic Signaling in an iPSC Model of Dilated Cardiomyopathy. Frontiers in Physiology, 2016, 7, 418.	2.8	5
22	Chromatin structure profile data from DNS-seq: Differential nuclease sensitivity mapping of four reference tissues of B73 maize (Zea mays L). Data in Brief, 2018, 20, 358-363.	1.0	5
23	Changes in nucleosome occupancy occur in a chromosome specific manner. Genomics Data, 2014, 2, 114-116.	1.3	3
24	DNA-Encoded Chromatin Structural Intron Boundary Signals Identify Conserved Genes with Common Function. International Journal of Genomics, 2015, 2015, 1-10.	1.6	3
25	Functional interaction between Brn-3a and Src-1 co-activates Brn-3a-mediated transactivation. Biochemical and Biophysical Research Communications, 2002, 294, 487-495.	2.1	2
26	Stimulation of the Drosophila immune system alters genome-wide nucleosome occupancy. Genomics Data, 2015, 3, 146-147.	1.3	1
27	MNase Profiling of Promoter Chromatin in Salmonella typhimurium-Stimulated GM12878 Cells Reveals Dynamic and Response-Specific Nucleosome Architecture. G3: Genes, Genomes, Genetics, 2020, 10, 2171-2178.	1.8	1