

Dustin E Schones

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

16,107
citations

147566
31
h-index

214527
47
g-index

56
all docs

56
docs citations

56
times ranked

21819
citing authors

#	ARTICLE	IF	CITATIONS
1	Sequence features of retrotransposons allow for epigenetic variability. <i>ELife</i> , 2021, 10, .	2.8	9
2	Hyperinsulinemia promotes aberrant histone acetylation in triple-negative breast cancer. <i>Epigenetics and Chromatin</i> , 2019, 12, 44.	1.8	23
3	Chromatin modifications in metabolic disease: Potential mediators of long-term disease risk. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2018, 10, e1416.	6.6	19
4	LTRs activated by Epstein-Barr virus-induced transformation of B cells alter the transcriptome. <i>Genome Research</i> , 2018, 28, 1791-1798.	2.4	25
5	Diabetes Mellitus-induced Long Noncoding RNA <i>Dnm3os</i> Regulates Macrophage Functions and Inflammation via Nuclear Mechanisms. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2018, 38, 1806-1820.	1.1	93
6	Estrogens and selective estrogen receptor modulators differentially antagonize Runx2 in ST2 mesenchymal progenitor cells. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2018, 183, 10-17.	1.2	6
7	Hyperinsulinemia-induced Changes In Chromatin Acetylation In Triple Negative Breast Cancer. <i>FASEB Journal</i> , 2018, 32, 1b12.	0.2	0
8	Vertical sleeve gastrectomy reverses diet-induced gene-regulatory changes impacting lipid metabolism. <i>Scientific Reports</i> , 2017, 7, 5274.	1.6	14
9	Vertical sleeve gastrectomy activates GPCR1/TGR5 to sustain weight loss, improve fatty liver, and remit insulin resistance in mice. <i>Hepatology</i> , 2016, 64, 760-773.	3.6	143
10	Epigenomic profiling reveals an association between persistence of DNA methylation and metabolic memory in the DCCT/EDIC type 1 diabetes cohort. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3002-11.	3.3	179
11	Regional glutamine deficiency in tumours promotes dedifferentiation through inhibition of histone demethylation. <i>Nature Cell Biology</i> , 2016, 18, 1090-1101.	4.6	291
12	Chromatin variation associated with liver metabolism is mediated by transposable elements. <i>Epigenetics and Chromatin</i> , 2016, 9, 28.	1.8	37
13	Persistent Chromatin Modifications Induced by High Fat Diet*. <i>Journal of Biological Chemistry</i> , 2016, 291, 10446-10455.	1.6	71
14	Transgenerational programming of longevity through E(z)-mediated histone H3K27 trimethylation in <i>Drosophila</i> . <i>Aging</i> , 2016, 8, 2988-3008.	1.4	38
15	Distinct roles of DNMT1-dependent and DNMT1-independent methylation patterns in the genome of mouse embryonic stem cells. <i>Genome Biology</i> , 2015, 16, 115.	3.8	70
16	Chromatin Modifications Associated With Diabetes and Obesity. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015, 35, 1557-1561.	1.1	24
17	C9a/GLP-dependent H3K9me2 patterning alters chromatin structure at CpG islands in hematopoietic progenitors. <i>Epigenetics and Chromatin</i> , 2014, 7, 23.	1.8	18
18	Epigenetic dysregulation by nickel through repressive chromatin domain disruption. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 14631-14636.	3.3	39

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19	Differential Effects of RUNX2 on the Androgen Receptor in Prostate Cancer: Synergistic Stimulation of a Gene Set Exemplified by SNAI2 and Subsequent Invasiveness. <i>Cancer Research</i> , 2014, 74, 2857-2868.	0.4	30
20	Open Chromatin Profiling in Mice Livers Reveals Unique Chromatin Variations Induced by High Fat Diet. <i>Journal of Biological Chemistry</i> , 2014, 289, 23557-23567.	1.6	67
21	The ATP-dependent Chromatin Remodeling Enzyme Fun30 Represses Transcription by Sliding Promoter-proximal Nucleosomes. <i>Journal of Biological Chemistry</i> , 2013, 288, 23182-23193.	1.6	31
22	High Mobility Group Protein N5 (HMGN5) and Lamina-associated Polypeptide 2 \pm (LAP2 \pm) Interact and Reciprocally Affect Their Genome-wide Chromatin Organization. <i>Journal of Biological Chemistry</i> , 2013, 288, 18104-18109.	1.6	21
23	Novel Long Noncoding RNAs Are Regulated by Angiotensin II in Vascular Smooth Muscle Cells. <i>Circulation Research</i> , 2013, 113, 266-278.	2.0	258
24	A Structural-Based Strategy for Recognition of Transcription Factor Binding Sites. <i>PLoS ONE</i> , 2013, 8, e52460.	1.1	13
25	Using epigenetic mechanisms to understand the impact of common disease causing alleles. <i>Current Opinion in Immunology</i> , 2012, 24, 558-563.	2.4	20
26	Regulation of nucleosome landscape and transcription factor targeting at tissue-specific enhancers by BRG1. <i>Genome Research</i> , 2011, 21, 1650-1658.	2.4	160
27	The Chromatin-binding Protein HMGN1 Regulates the Expression of Methyl CpG-binding Protein 2 (MECP2) and Affects the Behavior of Mice. <i>Journal of Biological Chemistry</i> , 2011, 286, 42051-42062.	1.6	42
28	Genomic Profiling of HMGN1 Reveals an Association with Chromatin at Regulatory Regions. <i>Molecular and Cellular Biology</i> , 2011, 31, 700-709.	1.1	44
29	Genome-Wide Approaches to Studying Yeast Chromatin Modifications. <i>Methods in Molecular Biology</i> , 2011, 759, 61-71.	0.4	4
30	Global analysis of the insulator binding protein CTCF in chromatin barrier regions reveals demarcation of active and repressive domains. <i>Genome Research</i> , 2009, 19, 24-32.	2.4	587
31	Down-regulation of Gfi-1 expression by TGF- β 2 is important for differentiation of Th17 and CD103+ inducible regulatory T cells. <i>Journal of Experimental Medicine</i> , 2009, 206, 329-341.	4.2	124
32	Chromatin poises miRNA- and protein-coding genes for expression. <i>Genome Research</i> , 2009, 19, 1742-1751.	2.4	135
33	Global Mapping of H3K4me3 and H3K27me3 Reveals Specificity and Plasticity in Lineage Fate Determination of Differentiating CD4+ T Cells. <i>Immunity</i> , 2009, 30, 155-167.	6.6	1,005
34	Genome-wide Analysis of Histone Methylation Reveals Chromatin State-Based Regulation of Gene Transcription and Function of Memory CD8+ T Cells. <i>Immunity</i> , 2009, 30, 912-925.	6.6	256
35	Genome-wide Mapping of HATs and HDACs Reveals Distinct Functions in Active and Inactive Genes. <i>Cell</i> , 2009, 138, 1019-1031.	13.5	1,174
36	Characterization of human epigenomes. <i>Current Opinion in Genetics and Development</i> , 2009, 19, 127-134.	1.5	144

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37	Chromatin Signatures in Multipotent Human Hematopoietic Stem Cells Indicate the Fate of Bivalent Genes during Differentiation. <i>Cell Stem Cell</i> , 2009, 4, 80-93.	5.2	548
38	Integrated Expression Profiling and CHIP-seq Analyses of the Growth Inhibition Response Program of the Androgen Receptor. <i>PLoS ONE</i> , 2009, 4, e6589.	1.1	77
39	Combinatorial patterns of histone acetylations and methylations in the human genome. <i>Nature Genetics</i> , 2008, 40, 897-903.	9.4	2,034
40	Priming for T helper type 2 differentiation by interleukin 2-mediated induction of interleukin 4 receptor α -chain expression. <i>Nature Immunology</i> , 2008, 9, 1288-1296.	7.0	234
41	Genome-wide approaches to studying chromatin modifications. <i>Nature Reviews Genetics</i> , 2008, 9, 179-191.	7.7	343
42	Dynamic Regulation of Nucleosome Positioning in the Human Genome. <i>Cell</i> , 2008, 132, 887-898.	13.5	1,211
43	Interferon Regulatory Factors Are Transcriptional Regulators of Adipogenesis. <i>Cell Metabolism</i> , 2008, 7, 86-94.	7.2	122
44	Neural Potential of a Stem Cell Population in the Hair Follicle. <i>Cell Cycle</i> , 2007, 6, 2161-2170.	1.3	79
45	High-Resolution Profiling of Histone Methylations in the Human Genome. <i>Cell</i> , 2007, 129, 823-837.	13.5	6,036
46	Response: Mapping Nucleosome Positions Using ChIP-Seq Data. <i>Cell</i> , 2007, 131, 832-833.	13.5	32
47	Statistical significance of cis-regulatory modules. <i>BMC Bioinformatics</i> , 2007, 8, 19.	1.2	68
48	Similarity of position frequency matrices for transcription factor binding sites. <i>Bioinformatics</i> , 2005, 21, 307-313.	1.8	97