

R David Hawkins

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

22,893
citations

147801

31
h-index

189892

50
g-index

57
all docs

57
docs citations

57
times ranked

36417
citing authors

#	ARTICLE	IF	CITATIONS
1	dCas9 fusion to computer-designed PRC2 inhibitor reveals functional TATA box in distal promoter region. <i>Cell Reports</i> , 2022, 38, 110457.	6.4	12
2	Lysine-Specific Demethylase 1 (LSD1) epigenetically controls osteoblast differentiation. <i>PLoS ONE</i> , 2022, 17, e0265027.	2.5	10
3	In vivo HSPC gene therapy with base editors allows for efficient reactivation of fetal $\hat{1}^3$ -globin in $\hat{1}^2$ -YAC mice. <i>Blood Advances</i> , 2021, 5, 1122-1135.	5.2	50
4	Transcriptomes of an Array of Chicken Ovary, Intestinal, and Immune Cells and Tissues. <i>Frontiers in Genetics</i> , 2021, 12, 664424.	2.3	7
5	Sumoylation of the human histone H4 tail inhibits p300-mediated transcription by RNA polymerase II in cellular extracts. <i>ELife</i> , 2021, 10, .	6.0	12
6	The epigenetics of pluripotent stem cells. , 2020, , 25-74.		0
7	Candidate silencer elements for the human and mouse genomes. <i>Nature Communications</i> , 2020, 11, 1061.	12.8	107
8	Single-cell analysis of transcriptome and DNA methylome in human oocyte maturation. <i>PLoS ONE</i> , 2020, 15, e0241698.	2.5	27
9	CRISPR/Cas9 guided genome and epigenome engineering and its therapeutic applications in immune mediated diseases. <i>Seminars in Cell and Developmental Biology</i> , 2019, 96, 32-43.	5.0	9
10	Superovulation alters global DNA methylation in early mouse embryo development. <i>Epigenetics</i> , 2019, 14, 780-790.	2.7	23
11	Enhancer Chromatin and 3D Genome Architecture Changes from Naive to Primed Human Embryonic Stem Cell States. <i>Stem Cell Reports</i> , 2019, 12, 1129-1144.	4.8	33
12	Targeted Integration and High-Level Transgene Expression in AAVS1 Transgenic Mice after In Vivo HSC Transduction with HDAd5/35++ Vectors. <i>Molecular Therapy</i> , 2019, 27, 2195-2212.	8.2	28
13	DNA methylation dynamics during embryonic development and postnatal maturation of the mouse auditory sensory epithelium. <i>Scientific Reports</i> , 2018, 8, 17348.	3.3	27
14	Reactivation of $\hat{1}^3$ -globin in adult $\hat{1}^2$ -YAC mice after ex vivo and in vivo hematopoietic stem cell genome editing. <i>Blood</i> , 2018, 131, 2915-2928.	1.4	58
15	Muscle-specific CRISPR/Cas9 dystrophin gene editing ameliorates pathophysiology in a mouse model for Duchenne muscular dystrophy. <i>Nature Communications</i> , 2017, 8, 14454.	12.8	298
16	An Activating STAT3 Mutation Causes Neonatal Diabetes through Premature Induction of Pancreatic Differentiation. <i>Cell Reports</i> , 2017, 19, 281-294.	6.4	94
17	Methylome Analysis of Human Bone Marrow MSCs Reveals Extensive Age- and Culture-Induced Changes at Distal Regulatory Elements. <i>Stem Cell Reports</i> , 2017, 9, 999-1015.	4.8	32
18	First critical repressive H3K27me3 marks in embryonic stem cells identified using designed protein inhibitor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10125-10130.	7.1	39

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19	Epigenomic Landscapes of hESC-Derived Neural Rosettes: Modeling Neural Tube Formation and Diseases. <i>Cell Reports</i> , 2017, 20, 1448-1462.	6.4	28
20	Genome-wide, Single-Cell DNA Methylomics Reveals Increased Non-CpG Methylation during Human Oocyte Maturation. <i>Stem Cell Reports</i> , 2017, 9, 397-407.	4.8	77
21	Three-dimensional genome architecture and emerging technologies: looping in disease. <i>Genome Medicine</i> , 2017, 9, 87.	8.2	65
22	Epigenetic Silencing of the Key Antioxidant Enzyme Catalase in Karyotypically Abnormal Human Pluripotent Stem Cells. <i>Scientific Reports</i> , 2016, 6, 22190.	3.3	17
23	Genetic Variability Overrides the Impact of Parental Cell Type and Determines iPSC Differentiation Potential. <i>Stem Cell Reports</i> , 2016, 6, 200-212.	4.8	211
24	cChIP-seq: a robust small-scale method for investigation of histone modifications. <i>BMC Genomics</i> , 2015, 16, 1083.	2.8	14
25	Epigenomics of autoimmune diseases. <i>Immunology and Cell Biology</i> , 2015, 93, 271-276.	2.3	38
26	The metabolome regulates the epigenetic landscape during naive-to-primed human embryonic stem cell transition. <i>Nature Cell Biology</i> , 2015, 17, 1523-1535.	10.3	360
27	Identification of global regulators of T-helper cell lineage specification. <i>Genome Medicine</i> , 2015, 7, 122.	8.2	38
28	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	27.8	5,653
29	Comprehensive identification and analysis of human accelerated regulatory DNA. <i>Genome Research</i> , 2015, 25, 1245-1255.	5.5	105
30	Functional analysis of a chromosomal deletion associated with myelodysplastic syndromes using isogenic human induced pluripotent stem cells. <i>Nature Biotechnology</i> , 2015, 33, 646-655.	17.5	130
31	Derivation of naïve human embryonic stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4484-4489.	7.1	415
32	Global Chromatin State Analysis Reveals Lineage-Specific Enhancers during the Initiation of Human T helper 1 and T helper 2 Cell Polarization. <i>Immunity</i> , 2013, 38, 1271-1284.	14.3	83
33	Epigenomic Analysis of Multilineage Differentiation of Human Embryonic Stem Cells. <i>Cell</i> , 2013, 153, 1134-1148.	28.9	689
34	Optimized detection of transcription factor-binding sites in ChIP-seq experiments. <i>Nucleic Acids Research</i> , 2012, 40, e1-e1.	14.5	6
35	Methods for Identifying Higher-Order Chromatin Structure. <i>Annual Review of Genomics and Human Genetics</i> , 2012, 13, 59-82.	6.2	67
36	Global DNA hypomethylation coupled to repressive chromatin domain formation and gene silencing in breast cancer. <i>Genome Research</i> , 2012, 22, 246-258.	5.5	476

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37	Dynamic chromatin states in human ES cells reveal potential regulatory sequences and genes involved in pluripotency. <i>Cell Research</i> , 2011, 21, 1393-1409.	12.0	91
38	An assessment of histone-modification antibody quality. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 91-93.	8.2	369
39	Hotspots of aberrant epigenomic reprogramming in human induced pluripotent stem cells. <i>Nature</i> , 2011, 471, 68-73.	27.8	1,442
40	An RNA Interference-Based Screen of Transcription Factor Genes Identifies Pathways Necessary for Sensory Regeneration in the Avian Inner Ear. <i>Journal of Neuroscience</i> , 2011, 31, 4535-4543.	3.6	31
41	Genome-wide Profiling of Interleukin-4 and STAT6 Transcription Factor Regulation of Human Th2 Cell Programming. <i>Immunity</i> , 2010, 32, 852-862.	14.3	139
42	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. <i>Nature Biotechnology</i> , 2010, 28, 1097-1105.	17.5	647
43	Next-generation genomics: an integrative approach. <i>Nature Reviews Genetics</i> , 2010, 11, 476-486.	16.3	554
44	Distinct Epigenomic Landscapes of Pluripotent and Lineage-Committed Human Cells. <i>Cell Stem Cell</i> , 2010, 6, 479-491.	11.1	747
45	Predictive chromatin signatures in the mammalian genome. <i>Human Molecular Genetics</i> , 2009, 18, R195-R201.	2.9	196
46	Histone modifications at human enhancers reflect global cell-type-specific gene expression. <i>Nature</i> , 2009, 459, 108-112.	27.8	2,225
47	Human DNA methylomes at base resolution show widespread epigenomic differences. <i>Nature</i> , 2009, 462, 315-322.	27.8	4,063
48	Large Scale Gene Expression Profiles of Regenerating Inner Ear Sensory Epithelia. <i>PLoS ONE</i> , 2007, 2, e525.	2.5	71
49	Distinct and predictive chromatin signatures of transcriptional promoters and enhancers in the human genome. <i>Nature Genetics</i> , 2007, 39, 311-318.	21.4	2,898
50	Applying genomics to the avian inner ear: Development of subtractive cDNA resources for exploring sensory function and hair cell regeneration. <i>Genomics</i> , 2006, 87, 801-808.	2.9	19
51	Gene expression differences in quiescent versus regenerating hair cells of avian sensory epithelia: implications for human hearing and balance disorders. <i>Human Molecular Genetics</i> , 2003, 12, 1261-1272.	2.9	59
52	Computer Designed PRC2 Inhibitor, EBdCas9, Reveals Functional TATA Boxes in Distal Promoter Regions. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0