

Hehuang Xie

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

46
papers

1,107
citations

18
h-index

32
g-index

52
ext. papers

1,342
ext. citations

7
avg, IF

3.82
L-index

#	Paper	IF	Citations
46	nMOWChIP-seq: low-input genome-wide mapping of non-histone targets.. <i>NAR Genomics and Bioinformatics</i> , 2022 , 4, lqac030	3.7	0
45	EGR2 is elevated and positively regulates inflammatory IFN γ production in lupus CD4 T cells. <i>BMC Immunology</i> , 2020 , 21, 41	3.7	0
44	Epigenetic regulation of neuronal cell specification inferred with single cell "Omics" data. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 942-952	6.8	3
43	Advances in methods and software for RNA cytosine methylation analysis. <i>Genomics</i> , 2020 , 112, 1840-1846	4.9	3
42	EGR1 recruits TET1 to shape the brain methylome during development and upon neuronal activity. <i>Nature Communications</i> , 2019 , 10, 3892	17.4	47
41	Divergent age-dependent peripheral immune transcriptomic profile following traumatic brain injury. <i>Scientific Reports</i> , 2019 , 9, 8564	4.9	10
40	Recursive Motif Analyses Identify Brain Epigenetic Transcription Regulatory Modules. <i>Computational and Structural Biotechnology Journal</i> , 2019 , 17, 507-515	6.8	7
39	Retinal-input-induced epigenetic dynamics in the developing mouse dorsal lateral geniculate nucleus. <i>Epigenetics and Chromatin</i> , 2019 , 12, 13	5.8	4
38	Virtual methylome dissection facilitated by single-cell analyses. <i>Epigenetics and Chromatin</i> , 2019 , 12, 66	5.8	1
37	Identifying Transcriptional Regulatory Modules Among Different Chromatin States in Mouse Neural Stem Cells. <i>Frontiers in Genetics</i> , 2018 , 9, 731	4.5	3
36	Cell-type-specific brain methylomes profiled via ultralow-input microfluidics. <i>Nature Biomedical Engineering</i> , 2018 , 2, 183-194	19	18
35	Integrative single-cell omics analyses reveal epigenetic heterogeneity in mouse embryonic stem cells. <i>PLoS Computational Biology</i> , 2018 , 14, e1006034	5	12
34	Mammalian Brain Development is Accompanied by a Dramatic Increase in Bipolar DNA Methylation. <i>Scientific Reports</i> , 2016 , 6, 32298	4.9	9
33	Impairment of DNA Methylation Maintenance Is the Main Cause of Global Demethylation in Naive Embryonic Stem Cells. <i>Molecular Cell</i> , 2016 , 62, 848-861	17.6	129
32	A Bayesian Assignment Method for Ambiguous Bisulfite Short Reads. <i>PLoS ONE</i> , 2016 , 11, e0151826	3.7	2
31	Endothelial-Specific EphA4 Negatively Regulates Native Pial Collateral Formation and Re-Perfusion following Hindlimb Ischemia. <i>PLoS ONE</i> , 2016 , 11, e0159930	3.7	12
30	Activation of Endogenous Retroviruses in Dnmt1(-/-) ESCs Involves Disruption of SETDB1-Mediated Repression by NP95 Binding to Hemimethylated DNA. <i>Cell Stem Cell</i> , 2016 , 19, 81-94	18	53

29	Nonparametric Bayesian clustering to detect bipolar methylated genomic loci. <i>BMC Bioinformatics</i> , 2015 , 16, 11	3.6	9
28	Characterization and machine learning prediction of allele-specific DNA methylation. <i>Genomics</i> , 2015 , 106, 331-9	4.3	9
27	Investigating bisulfite short-read mapping failure with hairpin bisulfite sequencing data. <i>BMC Genomics</i> , 2015 , 16 Suppl 11, S2	4.5	5
26	HBS-Tools for Hairpin Bisulfite Sequencing Data Processing and Analysis. <i>Advances in Bioinformatics</i> , 2015 , 2015, 760423	5.5	7
25	Improving bisulfite short-read mapping efficiency with hairpin-bisulfite data 2014 ,		1
24	Human rhinovirus infection causes different DNA methylation changes in nasal epithelial cells from healthy and asthmatic subjects. <i>BMC Medical Genomics</i> , 2014 , 7, 37	3.7	30
23	The dynamics of DNA methylation fidelity during mouse embryonic stem cell self-renewal and differentiation. <i>Genome Research</i> , 2014 , 24, 1296-307	9.7	54
22	Objective and comprehensive evaluation of bisulfite short read mapping tools. <i>Advances in Bioinformatics</i> , 2014 , 2014, 472045	5.5	31
21	Deciphering the heterogeneity in DNA methylation patterns during stem cell differentiation and reprogramming. <i>BMC Genomics</i> , 2014 , 15, 978	4.5	13
20	Dynamic Alu methylation during normal development, aging, and tumorigenesis. <i>BioMed Research International</i> , 2014 , 2014, 784706	3	48
19	DMEAS: DNA methylation entropy analysis software. <i>Bioinformatics</i> , 2013 , 29, 2044-5	7.2	16
18	Methylation alterations of WT1 and homeobox genes in inflamed muscle biopsy samples from patients with untreated juvenile dermatomyositis suggest self-renewal capacity. <i>Arthritis and Rheumatism</i> , 2012 , 64, 3478-85		22
17	DNA methylation alterations in response to pesticide exposure in vitro. <i>Environmental and Molecular Mutagenesis</i> , 2012 , 53, 542-9	3.2	60
16	Genome-wide study of DNA methylation alterations in response to diazinon exposure in vitro. <i>Environmental Toxicology and Pharmacology</i> , 2012 , 34, 959-68	5.8	44
15	Individual variation and longitudinal pattern of genome-wide DNA methylation from birth to the first two years of life. <i>Epigenetics</i> , 2012 , 7, 594-605	5.7	69
14	Histone deacetylase 1 deficiency impairs differentiation and electrophysiological properties of cardiomyocytes derived from induced pluripotent cells. <i>Stem Cells</i> , 2012 , 30, 2412-22	5.8	15
13	BTECH: a platform to integrate genomic, transcriptomic and epigenomic alterations in brain tumors. <i>Neuroinformatics</i> , 2011 , 9, 59-67	3.2	5
12	Genetic and epigenetic variations contributed by Alu retrotransposition. <i>BMC Genomics</i> , 2011 , 12, 617	4.5	14

11	Genome-wide quantitative assessment of variation in DNA methylation patterns. <i>Nucleic Acids Research</i> , 2011 , 39, 4099-108	20.1	64
10	Epigenomic analysis of Alu repeats in human ependymomas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 6952-7	11.5	51
9	Microenvironment alters epigenetic and gene expression profiles in Swarm rat chondrosarcoma tumors. <i>BMC Cancer</i> , 2010 , 10, 471	4.8	29
8	A Primer Design Algorithm for Global Analysis of CpG Methylation 2009 ,		1
7	SNP-based prediction of the human germ cell methylation landscape. <i>Genomics</i> , 2009 , 93, 434-40	4.3	14
6	High-throughput sequence-based epigenomic analysis of Alu repeats in human cerebellum. <i>Nucleic Acids Research</i> , 2009 , 37, 4331-40	20.1	75
5	Global demethylation of rat chondrosarcoma cells after treatment with 5-aza-2-deoxycytidine results in increased tumorigenicity. <i>PLoS ONE</i> , 2009 , 4, e8340	3.7	44
4	Monosomy of chromosome 10 associated with dysregulation of epidermal growth factor signaling in glioblastomas. <i>JAMA - Journal of the American Medical Association</i> , 2009 , 302, 276-89	27.4	45
3	Recent patents on the identification and clinical application of microRNAs and target genes. <i>Recent Patents on DNA & Gene Sequences</i> , 2007 , 1, 116-24		3
2	Robust semiparametric microarray normalization and significance analysis. <i>Biometrics</i> , 2006 , 62, 555-61	1.8	5
1	A robust two-way semi-linear model for normalization of cDNA microarray data. <i>BMC Bioinformatics</i> , 2005 , 6, 14	3.6	11