Hehuang Xie

List of Publications by Year
in descending order

50 papers	**1,506** citations	393982 **19** h-index	329751 **37** g-index
52 all docs	**52** docs citations	**52** times ranked	**3346** citing authors

#	Article	IF	Citations
1	Impairment of DNA Methylation Maintenance Is the Main Cause of Global Demethylation in Naive Embryonic Stem Cells. Molecular Cell, 2016, 62, 848-861.	4.5	189
2	Genome-wide quantitative assessment of variation in DNA methylation patterns. Nucleic Acids Research, 2011, 39, 4099-4108.	6.5	96
3	EGR1 recruits TET1 to shape the brain methylome during development and upon neuronal activity. Nature Communications, 2019, 10, 3892.	5.8	95
4	High-throughput sequence-based epigenomic analysis of Alu repeats in human cerebellum. Nucleic Acids Research, 2009, 37, 4331-4340.	6.5	87
5	Activation of Endogenous Retroviruses in Dnmt1 â˜'/â˜' ESCs Involves Disruption of SETDB1-Mediated Repression by NP95 Binding to Hemimethylated DNA. Cell Stem Cell, 2016, 19, 81-94.	5.2	77
6	Individual variation and longitudinal pattern of genome-wide DNA methylation from birth to the first two years of life. Epigenetics, 2012, 7, 594-605.	1.3	76
7	The dynamics of DNA methylation fidelity during mouse embryonic stem cell self-renewal and differentiation. Genome Research, 2014, 24, 1296-1307.	2.4	72
8	Dynamic *Alu* Methylation during Normal Development, Aging, and Tumorigenesis. BioMed Research International, 2014, 2014, 1-12.	0.9	70
9	DNA methylation alterations in response to pesticide exposure *in vitro*. Environmental and Molecular Mutagenesis, 2012, 53, 542-549.	0.9	68
10	Monosomy of Chromosome 10 Associated With Dysregulation of Epidermal Growth Factor Signaling in Glioblastomas. JAMA - Journal of the American Medical Association, 2009, 302, 276.	3.8	60
11	Epigenomic analysis of Alu repeats in human ependymomas. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6952-6957.	3.3	57
12	Objective and Comprehensive Evaluation of Bisulfite Short Read Mapping Tools. Advances in Bioinformatics, 2014, 2014, 1-11.	5.7	52
13	Global Demethylation of Rat Chondrosarcoma Cells after Treatment with 5-Aza-2â€²-Deoxycytidine Results in Increased Tumorigenicity. PLoS ONE, 2009, 4, e8340.	1.1	51
14	Genome-wide study of DNA methylation alterations in response to diazinon exposure in vitro. Environmental Toxicology and Pharmacology, 2012, 34, 959-968.	2.0	47
15	Microenvironment alters epigenetic and gene expression profiles in Swarm rat chondrosarcoma tumors. BMC Cancer, 2010, 10, 471.	1.1	35
16	Human rhinovirus infection causes different DNA methylation changes in nasal epithelial cells from healthy and asthmatic subjects. BMC Medical Genomics, 2014, 7, 37.	0.7	35
17	Cell-type-specific brain methylomes profiled via ultralow-input microfluidics. Nature Biomedical Engineering, 2018, 2, 183-194.	11.6	29
18	Methylation alterations of WT1 and homeobox genes in inflamed muscle biopsy samples from patients with untreated juvenile dermatomyositis suggest selfâ€renewal capacity. Arthritis and Rheumatism, 2012, 64, 3478-3485.	6.7	27

#	Article	IF	Citations
19	DMEAS: DNA methylation entropy analysis software. Bioinformatics, 2013, 29, 2044-2045.	1.8	19
20	A robust two-way semi-linear model for normalization of cDNA microarray data. BMC Bioinformatics, 2005, 6, 14.	1.2	18
21	SNP-based prediction of the human germ cell methylation landscape. Genomics, 2009, 93, 434-440.	1.3	17
22	Genetic and epigenetic variations contributed by Alu retrotransposition. BMC Genomics, 2011, 12, 617.	1.2	17
23	Deciphering the heterogeneity in DNA methylation patterns during stem cell differentiation and reprogramming. BMC Genomics, 2014, 15, 978.	1.2	17
24	Endothelial-Specific EphA4 Negatively Regulates Native Pial Collateral Formation and Re-Perfusion following Hindlimb Ischemia. PLoS ONE, 2016, 11, e0159930.	1.1	17
25	Integrative single-cell omics analyses reveal epigenetic heterogeneity in mouse embryonic stem cells. PLoS Computational Biology, 2018, 14, e1006034.	1.5	17
26	Histone Deacetylase 1 Deficiency Impairs Differentiation and Electrophysiological Properties of Cardiomyocytes Derived from Induced Pluripotent Cells. Stem Cells, 2012, 30, 2412-2422.	1.4	15
27	Divergent age-dependent peripheral immune transcriptomic profile following traumatic brain injury. Scientific Reports, 2019, 9, 8564.	1.6	15
28	Mammalian Brain Development is Accompanied by a Dramatic Increase in Bipolar DNA Methylation. Scientific Reports, 2016, 6, 32298.	1.6	13
29	Nonparametric Bayesian clustering to detect bipolar methylated genomic loci. BMC Bioinformatics, 2015, 16, 11.	1.2	12
30	Characterization and machine learning prediction of allele-specific DNA methylation. Genomics, 2015, 106, 331-339.	1.3	12
31	Identifying Transcriptional Regulatory Modules Among Different Chromatin States in Mouse Neural Stem Cells. Frontiers in Genetics, 2018, 9, 731.	1.1	8
32	Recursive Motif Analyses Identify Brain Epigenetic Transcription Regulatory Modules. Computational and Structural Biotechnology Journal, 2019, 17, 507-515.	1.9	8
33	HBS-Tools for Hairpin Bisulfite Sequencing Data Processing and Analysis. Advances in Bioinformatics, 2015, 2015, 1-4.	5.7	7
34	Investigating bisulfite short-read mapping failure with hairpin bisulfite sequencing data. BMC Genomics, 2015, 16, S2.	1.2	6
35	Retinal-input-induced epigenetic dynamics in the developing mouse dorsal lateral geniculate nucleus. Epigenetics and Chromatin, 2019, 12, 13.	1.8	6
36	Epigenetic regulation of neuronal cell specification inferred with single cell â€œOmicsâ€•data. Computational and Structural Biotechnology Journal, 2020, 18, 942-952.	1.9	6

#	Article	IF	Citations
37	Systematic evaluation of parameters in RNA bisulfite sequencing data generation and analysis. NAR Genomics and Bioinformatics, 2022, 4, .	1.5	6
38	Association between cord blood metabolites in tryptophan pathway and childhood risk of autism spectrum disorder and attention-deficit hyperactivity disorder. Translational Psychiatry, 2022, 12, .	2.4	6
39	Robust Semiparametric Microarray Normalization and Significance Analysis. Biometrics, 2006, 62, 555-561.	0.8	5
40	BTECH: A Platform to Integrate Genomic, Transcriptomic and Epigenomic Alterations in Brain Tumors. Neuroinformatics, 2011, 9, 59-67.	1.5	5
41	Advances in methods and software for RNA cytosine methylation analysis. Genomics, 2020, 112, 1840-1846.	1.3	5
42	EGR2 is elevated and positively regulates inflammatory IFNÎ³ production in lupus CD4+ T cells. BMC Immunology, 2020, 21, 41.	0.9	5
43	Perinatal Acetaminophen Exposure and Childhood Attention-Deficit/Hyperactivity Disorder (ADHD): Exploring the Role of Umbilical Cord Plasma Metabolites in Oxidative Stress Pathways. Brain Sciences, 2021, 11, 1302.	1.1	5
44	Recent Patents on the Identification and Clinical Application of microRNAs and Target Genes. Recent Patents on DNA & Gene Sequences, 2007, 1, 116-24.	0.7	4
45	Virtual methylome dissection facilitated by single-cell analyses. Epigenetics and Chromatin, 2019, 12, 66.	1.8	4
46	A Bayesian Assignment Method for Ambiguous Bisulfite Short Reads. PLoS ONE, 2016, 11, e0151826.	1.1	2
47	A Primer Design Algorithm for Global Analysis of CpG Methylation. , 2009, , .		1
48	Improving bisulfite short-read mapping efficiency with hairpin-bisulfite data. , 2014, , .		1
49	nMOWChIP-seq: low-input genome-wide mapping of non-histone targets. NAR Genomics and Bioinformatics, 2022, 4, lqac030.	1.5	1
50	Neuronal Depolarization Induced RNA m5C Methylation Changes in Mouse Cortical Neurons. Biology, 2022, 11, 988.	1.3	1