Bo Zhang

List of Publications by Year
in descending order

		430442	500791
28	6,952	18	28
papers	citations	h-index	g-index

31	31	31	18805
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	13.7	5,653
2	DNA hypomethylation within specific transposable element families associates with tissue-specific enhancer landscape. Nature Genetics, 2013, 45, 836-841.	9.4	207
3	Transcriptional inhibiton of Hoxd4 expression by miRNA-10a in human breast cancer cells. BMC Molecular Biology, 2009, 10, 12.	3.0	167
4	Functional DNA methylation differences between tissues, cell types, and across individuals discovered using the M&M algorithm. Genome Research, 2013, 23, 1522-1540.	2.4	162
5	Combining MeDIP-seq and MRE-seq to investigate genome-wide CpG methylation. Methods, 2015, 72, 29-40.	1.9	93
6	Epigenomic annotation of genetic variants using the Roadmap Epigenome Browser. Nature Biotechnology, 2015, 33, 345-346.	9.4	83
7	Developmental enhancers revealed by extensive DNA methylome maps of zebrafish early embryos. Nature Communications, 2015, 6, 6315.	5.8	73
8	Tissue-specific usage of transposable element-derived promoters in mouse development. Genome Biology, 2020, 21, 255.	3.8	55
9	Comparative DNA methylome analysis of endometrial carcinoma reveals complex and distinct deregulation of cancer promoters and enhancers. BMC Genomics, 2014, 15, 868.	1.2	49
10	Mapping of Variable DNA Methylation Across Multiple Cell Types Defines a Dynamic Regulatory Landscape of the Human Genome. G3: Genes, Genomes, Genetics, 2016, 6, 973-986.	0.8	41
11	A synthetic mechanogenetic gene circuit for autonomous drug delivery in engineered tissues. Science Advances, 2021, 7, .	4.7	40
12	Recurrent epimutations activate gene body promoters in primary glioblastoma. Genome Research, 2014, 24, 761-774.	2.4	39
13	Monoacylglycerol lipase (MGLL) polymorphism rs604300 interacts with childhood adversity to predict cannabis dependence symptoms and amygdala habituation: Evidence from an endocannabinoid system-level analysis.. Journal of Abnormal Psychology, 2015, 124, 860-877.	2.0	39
14	Comparison of differential accessibility analysis strategies for ATAC-seq data. Scientific Reports, 2020, 10, 10150.	1.6	32
15	Identification of an FGF18-expressing alveolar myofibroblast that is developmentally cleared during alveologenesis. Development (Cambridge), 2020, 147, .	1.2	30
16	Regulatory network decoded from epigenomes of surface ectoderm-derived cell types. Nature Communications, 2014, 5, 5442.	5.8	25
17	A genome-wide CRISPR-Cas9 knockout screen identifies essential and growth-restricting genes in human trophoblast stem cells. Nature Communications, 2022, 13, 2548.	5.8	25
18	Distinct MicroRNA Subcellular Size and Expression Patterns in Human Cancer Cells. International Journal of Cell Biology, 2012, 2012, 1-9.	1.0	22

#	ARTICLE	IF	CITATIONS
19	RNA Microarray Analysis of Macroscopically Normal Articular Cartilage from Knees Undergoing Partial Medial Meniscectomy: Potential Prediction of the Risk for Developing Osteoarthritis. PLoS ONE, 2016, 11, e0155373.	1.1	20
20	AIAP: A Quality Control and Integrative Analysis Package to Improve ATAC-seq Data Analysis. Genomics, Proteomics and Bioinformatics, 2021, 19, 641-651.	3.0	19
21	OCT4 cooperates with distinct ATP-dependent chromatin remodelers in naÃ¯ve and primed pluripotent states in human. Nature Communications, 2021, 12, 5123.	5.8	17
22	Uncovering the transcriptomic and epigenomic landscape of nicotinic receptor genes in non-neuronal tissues. BMC Genomics, 2017, 18, 439.	1.2	15
23	Chronologically modified androgen receptor in recurrent castration-resistant prostate cancer and its therapeutic targeting. Science Translational Medicine, 2022, 14, .	5.8	12
24	Chamber-specific transcriptional responses in atrial fibrillation. JCI Insight, 2020, 5, .	2.3	10
25	Common DNA methylation dynamics in endometriod adenocarcinoma and glioblastoma suggest universal epigenomic alterations in tumorigenesis. Communications Biology, 2021, 4, 607.	2.0	9
26	Transcriptome Analysis of Chemically-Induced Sensory Neuron Ablation in Zebrafish. PLoS ONE, 2016, 11, e0148726.	1.1	5
27	Estimating developmental states of tumors and normal tissues using a linear time-ordered model. BMC Bioinformatics, 2011, 12, 53.	1.2	4
28	Estimating the Quality of Reprogrammed Cells Using ES Cell Differentiation Expression Patterns. PLoS ONE, 2011, 6, e15336.	1.1	2