

Bo Zhang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8599550/publications.pdf>

Version: 2024-02-01

28
papers

6,952
citations

430442

18
h-index

500791

28
g-index

31
all docs

31
docs citations

31
times ranked

18805
citing authors

#	ARTICLE	IF	CITATIONS
1	A genome-wide CRISPR-Cas9 knockout screen identifies essential and growth-restricting genes in human trophoblast stem cells. <i>Nature Communications</i> , 2022, 13, 2548.	5.8	25
2	Chronologically modified androgen receptor in recurrent castration-resistant prostate cancer and its therapeutic targeting. <i>Science Translational Medicine</i> , 2022, 14, .	5.8	12
3	A synthetic mechanogenetic gene circuit for autonomous drug delivery in engineered tissues. <i>Science Advances</i> , 2021, 7, .	4.7	40
4	Common DNA methylation dynamics in endometrioid adenocarcinoma and glioblastoma suggest universal epigenomic alterations in tumorigenesis. <i>Communications Biology</i> , 2021, 4, 607.	2.0	9
5	AIAP: A Quality Control and Integrative Analysis Package to Improve ATAC-seq Data Analysis. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 641-651.	3.0	19
6	OCT4 cooperates with distinct ATP-dependent chromatin remodelers in naïve and primed pluripotent states in human. <i>Nature Communications</i> , 2021, 12, 5123.	5.8	17
7	Identification of an FGF18-expressing alveolar myofibroblast that is developmentally cleared during alveologenesis. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	30
8	Tissue-specific usage of transposable element-derived promoters in mouse development. <i>Genome Biology</i> , 2020, 21, 255.	3.8	55
9	Comparison of differential accessibility analysis strategies for ATAC-seq data. <i>Scientific Reports</i> , 2020, 10, 10150.	1.6	32
10	Chamber-specific transcriptional responses in atrial fibrillation. <i>JCI Insight</i> , 2020, 5, .	2.3	10
11	Uncovering the transcriptomic and epigenomic landscape of nicotinic receptor genes in non-neuronal tissues. <i>BMC Genomics</i> , 2017, 18, 439.	1.2	15
12	Mapping of Variable DNA Methylation Across Multiple Cell Types Defines a Dynamic Regulatory Landscape of the Human Genome. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 973-986.	0.8	41
13	Transcriptome Analysis of Chemically-Induced Sensory Neuron Ablation in Zebrafish. <i>PLoS ONE</i> , 2016, 11, e0148726.	1.1	5
14	RNA Microarray Analysis of Macroscopically Normal Articular Cartilage from Knees Undergoing Partial Medial Meniscectomy: Potential Prediction of the Risk for Developing Osteoarthritis. <i>PLoS ONE</i> , 2016, 11, e0155373.	1.1	20
15	Epigenomic annotation of genetic variants using the Roadmap Epigenome Browser. <i>Nature Biotechnology</i> , 2015, 33, 345-346.	9.4	83
16	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	18.7	5,653
17	Developmental enhancers revealed by extensive DNA methylome maps of zebrafish early embryos. <i>Nature Communications</i> , 2015, 6, 6315.	5.8	73
18	Combining MeDIP-seq and MRE-seq to investigate genome-wide CpG methylation. <i>Methods</i> , 2015, 72, 29-40.	1.9	93

#	ARTICLE	IF	CITATIONS
19	Monoacylglycerol lipase (MGLL) polymorphism rs604300 interacts with childhood adversity to predict cannabis dependence symptoms and amygdala habituation: Evidence from an endocannabinoid system-level analysis.. <i>Journal of Abnormal Psychology</i> , 2015, 124, 860-877.	2.0	39
20	Comparative DNA methylome analysis of endometrial carcinoma reveals complex and distinct deregulation of cancer promoters and enhancers. <i>BMC Genomics</i> , 2014, 15, 868.	1.2	49
21	Regulatory network decoded from epigenomes of surface ectoderm-derived cell types. <i>Nature Communications</i> , 2014, 5, 5442.	5.8	25
22	Recurrent epimutations activate gene body promoters in primary glioblastoma. <i>Genome Research</i> , 2014, 24, 761-774.	2.4	39
23	DNA hypomethylation within specific transposable element families associates with tissue-specific enhancer landscape. <i>Nature Genetics</i> , 2013, 45, 836-841.	9.4	207
24	Functional DNA methylation differences between tissues, cell types, and across individuals discovered using the M&M algorithm. <i>Genome Research</i> , 2013, 23, 1522-1540.	2.4	162
25	Distinct MicroRNA Subcellular Size and Expression Patterns in Human Cancer Cells. <i>International Journal of Cell Biology</i> , 2012, 2012, 1-9.	1.0	22
26	Estimating the Quality of Reprogrammed Cells Using ES Cell Differentiation Expression Patterns. <i>PLoS ONE</i> , 2011, 6, e15336.	1.1	2
27	Estimating developmental states of tumors and normal tissues using a linear time-ordered model. <i>BMC Bioinformatics</i> , 2011, 12, 53.	1.2	4
28	Transcriptional inhibition of Hoxd4 expression by miRNA-10a in human breast cancer cells. <i>BMC Molecular Biology</i> , 2009, 10, 12.	3.0	167