Zhengqing Ouyang

List of Publications by Year
in descending order

44 papers	3,772 citations	394421 19 h-index	345221 36 g-index
44 all docs	44 docs citations	44 times ranked	8046 citing authors

#	Article	IF	Citations
1	Architecture of the human regulatory network derived from ENCODE data. Nature, 2012, 489, 91-100.	27.8	1,384
2	Landscape and variation of RNA secondary structure across the human transcriptome. Nature, 2014, 505, 706-709.	27.8	519
3	Multiplexed detection of proteins, transcriptomes, clonotypes and CRISPR perturbations in single cells. Nature Methods, 2019, 16, 409-412.	19.0	364
4	ChIP-Seq of transcription factors predicts absolute and differential gene expression in embryonic stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 21521-21526.	7.1	312
5	Genome-wide Measurement of RNA Folding Energies. Molecular Cell, 2012, 48, 169-181.	9.7	192
6	Hedgehog pathway-regulated gene networks in cerebellum development and tumorigenesis. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9736-9741.	7.1	109
7	Exon arrays provide accurate assessments of gene expression. Genome Biology, 2007, 8, R82.	9.6	103
8	SeqFold: Genome-scale reconstruction of RNA secondary structure integrating high-throughput sequencing data. Genome Research, 2013, 23, 377-387.	5.5	102
9	Single-cell transcriptomics–based MacSpectrum reveals macrophage activation signatures in diseases. JCI Insight, 2019, 4, .	5.0	86
10	Genome-wide mapping of RNA structure using nuclease digestion and high-throughput sequencing. Nature Protocols, 2013, 8, 849-869.	12.0	85
11	HSA: integrating multi-track Hi-C data for genome-scale reconstruction of 3D chromatin structure. Genome Biology, 2016, 17, 40.	8.8	60
12	DNA methylomes of bovine gametes and in vivo produced preimplantation embryos. Biology of Reproduction, 2018, 99, 949-959.	2.7	59
13	Assessing the Conservation of Mammalian Gene Expression Using High-Density Exon Arrays. Molecular Biology and Evolution, 2007, 24, 1283-1285.	8.9	49
14	Multimodal single-cell analysis of cutaneous T-cell lymphoma reveals distinct subclonal tissue-dependent signatures. Blood, 2021, 138, 1456-1464.	1.4	39
15	Direct DNA crosslinking with CAP-C uncovers transcription-dependent chromatin organization at high resolution. Nature Biotechnology, 2021, 39, 225-235.	17.5	37
16	Correlation of Global MicroRNA Expression With Basal Cell Carcinoma Subtype. G3: Genes, Genomes, Genetics, 2012, 2, 279-286.	1.8	36
17	STAT3 Targets Suggest Mechanisms of Aggressive Tumorigenesis in Diffuse Large B-Cell Lymphoma. G3: Genes, Genomes, Genetics, 2013, 3, 2173-2185.	1.8	34
18	c-MYC regulates mRNA translation efficiency and start-site selection in lymphoma. Journal of Experimental Medicine, 2019, 216, 1509-1524.	8.5	32

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19	A New FACS Approach Isolates hESC Derived Endoderm Using Transcription Factors. PLoS ONE, 2011, 6, e17536.	2.5	23
20	Gene selection for optimal prediction of cell position in tissues from single-cell transcriptomics data. Life Science Alliance, 2020, 3, e202000867.	2.8	20
21	A statistical framework for data integration through graphical models with application to cancer genomics. Annals of Applied Statistics, 2017, 11, 161-184.	1.1	19
22	MULTIVARIATE ENTROPY DISTANCE METHOD FOR PROKARYOTIC GENE IDENTIFICATION. Journal of Bioinformatics and Computational Biology, 2004, 02, 353-373.	0.8	17
23	Targeting eIF4A-Dependent Translation of KRAS Signaling Molecules. Cancer Research, 2021, 81, 2002-2014.	0.9	17
24	Scaling and Hierarchical Structures in DNA Sequences. Physical Review Letters, 2004, 93, 078103.	7.8	15
25	Identification and analysis of RNA structural disruptions induced by single nucleotide variants using Riprap and RiboSNitchDB. NAR Genomics and Bioinformatics, 2020, 2, lqaa057.	3.2	10
26	Dissecting Pathway Disturbances Using Network Topology and Multi-platform Genomics Data. Statistics in Biosciences, 2018, 10, 86-106.	1.2	9
27	PRAS: Predicting functional targets of RNA binding proteins based on CLIP-seq peaks. PLoS Computational Biology, 2019, 15, e1007227.	3.2	8
28	Joint modeling of RNase footprint sequencing profiles for genome-wide inference of RNA structure. Nucleic Acids Research, 2015, 43, 9187-9197.	14.5	7
29	Low SATB1 Expression Promotes IL-5 and IL-9 Expression in Sézary Syndrome. Journal of Investigative Dermatology, 2020, 140, 713-716.	0.7	5
30	Genome-Wide Probing of RNA Structures In Vitro Using Nucleases and Deep Sequencing. Methods in Molecular Biology, 2016, 1361, 141-160.	0.9	4
31	Joint Principal Trend Analysis for Longitudinal High-dimensional Data. Biometrics, 2018, 74, 430-438.	1.4	4
32	Differential RNA methylation using multivariate statistical methods. Briefings in Bioinformatics, 2022, 23, .	6.5	3
33	Hierarchical structure analysis describing abnormal base composition of genomes. Physical Review E, 2005, 72, 041915.	2.1	2
34	Noncoding RNA Landmarks of Pluripotency and Reprogramming. Cell Stem Cell, 2010, 7, 649-650.	11.1	2
35	LISA: Accurate reconstruction of cell trajectory and pseudo-time for massive single cell RNA-seq data. , 2018, , .		2
36	A new graph-based clustering method with application to single-cell RNA-seq data from human pancreatic islets. NAR Genomics and Bioinformatics, 2021, 3, lqaa087.	3.2	2

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37	LISA2: Learning Complex Single-Cell Trajectory and Expression Trends. Frontiers in Genetics, 2021, 12, 681206.	2.3	1
38	Large‐scale analysis of the position‐dependent binding and regulation of human RNA binding proteins. Quantitative Biology, 2020, 8, 119-129.	0.5	0
39	Unsupervised gene selection for predicting cell spatial positions in the Drosophila embryo. F1000Research, 0, 9, 124.	1.6	0
40	Structural inference of time‐varying mixed graphical models. Stat, 0, , e414.	0.4	0
41	An unsupervised learning method for reconstructing cell spatial organization withÂapplication to the DREAM Single Cell Transcriptomics Challenge. F1000Research, 0, 9, 124.	1.6	0
42	Meta-analysis of peptides to detect protein significance. Statistics and Its Interface, 2020, 13, 465-474.	0.3	0
43	PATH: An interactive web platform for analysis of time-course high-dimensional genomic data. International Journal of Computational Biology and Drug Design, 2020, 13, 529.	0.3	0
44	PATH: An interactive web platform for analysis of time-course high-dimensional genomic data. International Journal of Computational Biology and Drug Design, 2020, 13, 529.	0.3	0