

Weisheng Wu

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

4,399
citations

394421

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580821

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docs citations

26
times ranked

9223
citing authors

#	ARTICLE	IF	CITATIONS
1	Spatial and Transcriptomic Analysis of Perineural Invasion in Oral Cancer. <i>Clinical Cancer Research</i> , 2022, 28, 3557-3572.	7.0	15
2	Targeted RNA-seq improves efficiency, resolution, and accuracy of allele specific expression for human term placentas. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	4
3	APOBEC3A drives deaminase domain-independent chromosomal instability to promote pancreatic cancer metastasis. <i>Nature Cancer</i> , 2021, 2, 1338-1356.	13.2	35
4	Loss of Imprinting in Human Placentas Is Widespread, Coordinated, and Predicts Birth Phenotypes. <i>Molecular Biology and Evolution</i> , 2020, 37, 429-441.	8.9	15
5	Transposon Insertion Site Sequencing of <i>Providencia stuartii</i> : Essential Genes, Fitness Factors for Catheter-Associated Urinary Tract Infection, and the Impact of Polymicrobial Infection on Fitness Requirements. <i>MSphere</i> , 2020, 5, .	2.9	14
6	Twin arginine translocation, ammonia incorporation, and polyamine biosynthesis are crucial for <i>Proteus mirabilis</i> fitness during bloodstream infection. <i>PLoS Pathogens</i> , 2019, 15, e1007653.	4.7	29
7	Identification of Pathogenicity-Associated Loci in <i>Klebsiella pneumoniae</i> from Hospitalized Patients. <i>MSystems</i> , 2018, 3, .	3.8	38
8	Bayesian Analysis of RNA-Seq Data Using a Family of Negative Binomial Models. <i>Bayesian Analysis</i> , 2018, 13, 411-436.	3.0	5
9	The Pathogenic Potential of <i>Proteus mirabilis</i> Is Enhanced by Other Uropathogens during Polymicrobial Urinary Tract Infection. <i>Infection and Immunity</i> , 2017, 85, .	2.2	81
10	Genome-wide transposon mutagenesis of <i>Proteus mirabilis</i> : Essential genes, fitness factors for catheter-associated urinary tract infection, and the impact of polymicrobial infection on fitness requirements. <i>PLoS Pathogens</i> , 2017, 13, e1006434.	4.7	97
11	TnseqDiff: identification of conditionally essential genes in transposon sequencing studies. <i>BMC Bioinformatics</i> , 2017, 18, 326.	2.6	42
12	Occupancy by key transcription factors is a more accurate predictor of enhancer activity than histone modifications or chromatin accessibility. <i>Epigenetics and Chromatin</i> , 2015, 8, 16.	3.9	100
13	Genome-Wide Identification of <i>Klebsiella pneumoniae</i> Fitness Genes during Lung Infection. <i>MBio</i> , 2015, 6, e00775.	4.1	168
14	Complete Genome Sequence of <i>Klebsiella pneumoniae</i> Strain ATCC 43816 KPPR1, a Rifampin-Resistant Mutant Commonly Used in Animal, Genetic, and Molecular Biology Studies. <i>Genome Announcements</i> , 2014, 2, .	0.8	52
15	CD1d-unrestricted NKT cells are endowed with a hybrid function far superior than that of iNKT cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 12841-12846.	7.1	19
16	Divergent functions of hematopoietic transcription factors in lineage priming and differentiation during erythro-megakaryopoiesis. <i>Genome Research</i> , 2014, 24, 1932-1944.	5.5	88
17	Dynamic shifts in occupancy by TAL1 are guided by GATA factors and drive large-scale reprogramming of gene expression during hematopoiesis. <i>Genome Research</i> , 2014, 24, 1945-1962.	5.5	71
18	Principles of regulatory information conservation between mouse and human. <i>Nature</i> , 2014, 515, 371-375.	27.8	259

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19	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	27.8	1,444
20	Topologically associating domains are stable units of replication-timing regulation. <i>Nature</i> , 2014, 515, 402-405.	27.8	779
21	An encyclopedia of mouse DNA elements (Mouse ENCODE). <i>Genome Biology</i> , 2012, 13, 418.	9.6	410
22	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. <i>Genome Research</i> , 2011, 21, 1659-1671.	5.5	110
23	Erythroid GATA1 function revealed by genome-wide analysis of transcription factor occupancy, histone modifications, and mRNA expression. <i>Genome Research</i> , 2009, 19, 2172-2184.	5.5	184
24	Primary sequence and epigenetic determinants of in vivo occupancy of genomic DNA by GATA1. <i>Nucleic Acids Research</i> , 2009, 37, 7024-7038.	14.5	29
25	A GATA-1-regulated microRNA locus essential for erythropoiesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3333-3338.	7.1	309