

Hongkai Ji

List of Publications by Year in descending order

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Version: 2024-02-01

99
papers

7,950
citations

117625

34
h-index

56724

83
g-index

108
all docs

108
docs citations

108
times ranked

14764
citing authors

#	ARTICLE	IF	CITATIONS
1	Differential Cytokine Signatures of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) and Influenza Infection Highlight Key Differences in Pathobiology. <i>Clinical Infectious Diseases</i> , 2022, 74, 254-262.	5.8	28
2	Understanding Patients' Perceived Health After Critical Illness. <i>Chest</i> , 2022, 161, 407-417.	0.8	6
3	GLI transcriptional repression is inert prior to Hedgehog pathway activation. <i>Nature Communications</i> , 2022, 13, 808.	12.8	15
4	NTR 2.0: a rationally engineered prodrug-converting enzyme with substantially enhanced efficacy for targeted cell ablation. <i>Nature Methods</i> , 2022, 19, 205-215.	19.0	29
5	EDClust: an EM-MM hybrid method for cell clustering in multiple-subject single-cell RNA sequencing. <i>Bioinformatics</i> , 2022, 38, 2692-2699.	4.1	4
6	Epigenome-wide association analyses of active injection drug use. <i>Drug and Alcohol Dependence</i> , 2022, 235, 109431.	3.2	5
7	SARS-CoV-2 vaccination diversifies the CD4+ spike-reactive T cell repertoire in patients with prior SARS-CoV-2 infection. <i>EBioMedicine</i> , 2022, 80, 104048.	6.1	12
8	Repeated exposure to heterologous hepatitis C viruses associates with enhanced neutralizing antibody breadth and potency. <i>Journal of Clinical Investigation</i> , 2022, 132, .	8.2	5
9	Genome-wide prediction of chromatin accessibility based on gene expression. <i>Wiley Interdisciplinary Reviews: Computational Statistics</i> , 2021, 13, e1544.	3.9	5
10	Genome-wide association study identifies a novel maternal gene-stress interaction associated with spontaneous preterm birth. <i>Pediatric Research</i> , 2021, 89, 1549-1556.	2.3	11
11	Single-cell transcriptomic reveals molecular diversity and developmental heterogeneity of human stem cell-derived oligodendrocyte lineage cells. <i>Nature Communications</i> , 2021, 12, 652.	12.8	47
12	A Nonlinear Relation Between Maternal Red Blood Cell Manganese Concentrations and Child Blood Pressure at Age 6-12 y: A Prospective Birth Cohort Study. <i>Journal of Nutrition</i> , 2021, 151, 570-578.	2.9	3
13	Profiling Chromatin Accessibility at Single-cell Resolution. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 172-190.	6.9	18
14	63438 Differential chromatin accessibility at dorsal root ganglia enhancers is associated with nerve injury. <i>Journal of Clinical and Translational Science</i> , 2021, 5, 5-5.	0.6	0
15	Functional characterization of CD4+ T cell receptors crossreactive for SARS-CoV-2 and endemic coronaviruses. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	72
16	Converging genetic and epigenetic drivers of paediatric acute lymphoblastic leukaemia identified by an information-theoretic analysis. <i>Nature Biomedical Engineering</i> , 2021, 5, 360-376.	22.5	10
17	EGFR Activates a TAZ-Driven Oncogenic Program in Glioblastoma. <i>Cancer Research</i> , 2021, 81, 3580-3592.	0.9	12
18	Discussion of Exponential-Family Embedding With Application to Cell Developmental Trajectories for Single-Cell RNA-seq Data. <i>Journal of the American Statistical Association</i> , 2021, 116, 471-474.	3.1	0

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19	Distinct Cytokine and Chemokine Dysregulation in Hospitalized Children With Acute Coronavirus Disease 2019 and Multisystem Inflammatory Syndrome With Similar Levels of Nasopharyngeal Severe Acute Respiratory Syndrome Coronavirus 2 Shedding. <i>Journal of Infectious Diseases</i> , 2021, 224, 606-615.	4.0	30
20	Large-scale phenotypic drug screen identifies neuroprotectants in zebrafish and mouse models of retinitis pigmentosa. <i>ELife</i> , 2021, 10, .	6.0	15
21	Transcriptional programs of neoantigen-specific TIL in anti-PD-1-treated lung cancers. <i>Nature</i> , 2021, 596, 126-132.	27.8	234
22	A prospective cohort study on the intersectionality of obesity, chronic disease, social factors, and incident risk of COVID-19 in US low-income minority middle-age mothers. <i>International Journal of Obesity</i> , 2021, 45, 2577-2584.	3.4	7
23	Global gene expression and chromatin accessibility of the peripheral nervous system in animal models of persistent pain. <i>Journal of Neuroinflammation</i> , 2021, 18, 185.	7.2	6
24	Prenatal exposure to mercury and precocious puberty: a prospective birth cohort study. <i>Human Reproduction</i> , 2021, 36, 712-720.	0.9	14
25	286â€¦Sex differences in the transcriptional profiles of mucosal-associated invariant T cells in neoadjuvant anti-PD-1 treated non-small cell lung cancer (NSCLC). , 2021, 9, A310-A310.		0
26	Can social support during pregnancy affect maternal DNA methylation? Findings from a cohort of African-Americans. <i>Pediatric Research</i> , 2020, 88, 131-138.	2.3	8
27	Altered 3D chromatin structure permits inversional recombination at the <i>IgH</i> locus. <i>Science Advances</i> , 2020, 6, eaaz8850.	10.3	13
28	A systematic evaluation of single-cell RNA-sequencing imputation methods. <i>Genome Biology</i> , 2020, 21, 218.	8.8	188
29	Single-cell ATAC-seq signal extraction and enhancement with SCATE. <i>Genome Biology</i> , 2020, 21, 161.	8.8	34
30	Compartmental Analysis of T-cell Clonal Dynamics as a Function of Pathologic Response to Neoadjuvant PD-1 Blockade in Resectable Nonâ€“Small Cell Lung Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 1327-1337.	7.0	90
31	GLI transcriptional repression regulates tissue-specific enhancer activity in response to Hedgehog signaling. <i>ELife</i> , 2020, 9, .	6.0	29
32	Epigenome-wide association scan identifies methylation sites associated with HIV infection. <i>Epigenomics</i> , 2020, 12, 1917-1927.	2.1	7
33	Maternal postpartum plasma folate status and preterm birth in a high-risk US population. <i>Public Health Nutrition</i> , 2019, 22, 1-11.	2.2	10
34	Global prediction of chromatin accessibility using small-cell-number and single-cell RNA-seq. <i>Nucleic Acids Research</i> , 2019, 47, e121-e121.	14.5	24
35	Prenatal Risk Factors and Perinatal and Postnatal Outcomes Associated With Maternal Opioid Exposure in an Urban, Low-Income, Multiethnic US Population. <i>JAMA Network Open</i> , 2019, 2, e196405.	5.9	98
36	TCF-1-Centered Transcriptional Network Drives an Effector versus Exhausted CD8Â“T Cell-Fate Decision. <i>Immunity</i> , 2019, 51, 840-855.e5.	14.3	409

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37	Association Between Maternal Exposure to Lead, Maternal Folate Status, and Intergenerational Risk of Childhood Overweight and Obesity. <i>JAMA Network Open</i> , 2019, 2, e1912343.	5.9	35
38	Maternal triacylglycerol signature and risk of food allergy in offspring. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 144, 729-737.	2.9	12
39	Sex differences in gene regulation in the dorsal root ganglion after nerve injury. <i>BMC Genomics</i> , 2019, 20, 147.	2.8	53
40	Pseudotime Reconstruction Using TSCAN. <i>Methods in Molecular Biology</i> , 2019, 1935, 115-124.	0.9	6
41	Paternal involvement and support and risk of preterm birth: findings from the Boston birth cohort. <i>Journal of Psychosomatic Obstetrics and Gynaecology</i> , 2019, 40, 48-56.	2.1	24
42	Stress response factors drive regrowth of quiescent cells. <i>Current Genetics</i> , 2018, 64, 807-810.	1.7	8
43	ATAC-Seq analysis reveals a widespread decrease of chromatin accessibility in age-related macular degeneration. <i>Nature Communications</i> , 2018, 9, 1364.	12.8	124
44	Dynamic motif occupancy (DynaMO) analysis identifies transcription factors and their binding sites driving dynamic biological processes. <i>Nucleic Acids Research</i> , 2018, 46, e2-e2.	14.5	11
45	Sequential Enhancer Sequestration Dysregulates Recombination Center Formation at the IgH Locus. <i>Molecular Cell</i> , 2018, 70, 21-33.e6.	9.7	35
46	Genome-wide DNA methylation associations with spontaneous preterm birth in US blacks: findings in maternal and cord blood samples. <i>Epigenetics</i> , 2018, 13, 163-172.	2.7	38
47	Transcriptional outcomes and kinetic patterning of gene expression in response to NF- κ B activation. <i>PLoS Biology</i> , 2018, 16, e2006347.	5.6	37
48	Maternal smoking during pregnancy and cord blood DNA methylation: new insight on sex differences and effect modification by maternal folate levels. <i>Epigenetics</i> , 2018, 13, 505-518.	2.7	32
49	A Prospective Birth Cohort Study on Maternal Cholesterol Levels and Offspring Attention Deficit Hyperactivity Disorder: New Insight on Sex Differences. <i>Brain Sciences</i> , 2018, 8, 3.	2.3	14
50	Maternal Biomarkers of Acetaminophen Use and Offspring Attention Deficit Hyperactivity Disorder. <i>Brain Sciences</i> , 2018, 8, 127.	2.3	23
51	Immunomodulation-accelerated neuronal regeneration following selective rod photoreceptor cell ablation in the zebrafish retina. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3719-E3728.	7.1	155
52	Single-cell regulome data analysis by SCRAT. <i>Bioinformatics</i> , 2017, 33, 2930-2932.	4.1	47
53	Genome-wide approach identifies a novel gene-maternal pre-pregnancy BMI interaction on preterm birth. <i>Nature Communications</i> , 2017, 8, 15608.	12.8	31
54	Genome-wide prediction of DNase I hypersensitivity using gene expression. <i>Nature Communications</i> , 2017, 8, 1038.	12.8	34

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55	Two approaches reveal a new paradigm of "switchable or genetics-influenced allele-specific DNA methylation"™ with potential in human disease. <i>Cell Discovery</i> , 2017, 3, 17038.	6.7	25
56	Single-Cell Co-expression Analysis Reveals Distinct Functional Modules, Co-regulation Mechanisms and Clinical Outcomes. <i>PLoS Computational Biology</i> , 2016, 12, e1004892.	3.2	36
57	Computational Prediction of the Global Functional Genomic Landscape: Applications, Methods, and Challenges. <i>Human Heredity</i> , 2016, 81, 88-105.	0.8	3
58	PRMT5 is essential for the maintenance of chondrogenic progenitor cells in the limb bud. <i>Development (Cambridge)</i> , 2016, 143, 4608-4619.	2.5	19
59	ARQiv-HTS, a versatile whole-organism screening platform enabling in vivo drug discovery at high-throughput rates. <i>Nature Protocols</i> , 2016, 11, 2432-2453.	12.0	50
60	TSCAN: Pseudo-time reconstruction and evaluation in single-cell RNA-seq analysis. <i>Nucleic Acids Research</i> , 2016, 44, e117-e117.	14.5	491
61	Association Between Maternal Prepregnancy Body Mass Index and Plasma Folate Concentrations With Child Metabolic Health. <i>JAMA Pediatrics</i> , 2016, 170, e160845.	6.2	67
62	Turning publicly available gene expression data into discoveries using gene set context analysis. <i>Nucleic Acids Research</i> , 2016, 44, e8-e8.	14.5	11
63	The Pluripotency Factor NANOG Binds to GLI Proteins and Represses Hedgehog-mediated Transcription. <i>Journal of Biological Chemistry</i> , 2016, 291, 7171-7182.	3.4	22
64	Cormotif: An R Package for Jointly Detecting Differential Gene Expression in Multiple Studies. , 2016, , 28-47.		0
65	A novel DNA sequence motif in human and mouse genomes. <i>Scientific Reports</i> , 2015, 5, 10444.	3.3	0
66	Joint analysis of differential gene expression in multiple studies using correlation motifs. <i>Biostatistics</i> , 2015, 16, 31-46.	1.5	31
67	Gata6 potently initiates reprogramming of pluripotent and differentiated cells to extraembryonic endoderm stem cells. <i>Genes and Development</i> , 2015, 29, 1239-1255.	5.9	120
68	HOXB7 Is an ER α Cofactor in the Activation of HER2 and Multiple ER Target Genes Leading to Endocrine Resistance. <i>Cancer Discovery</i> , 2015, 5, 944-959.	9.4	72
69	Spatiotemporal regulation of GLI target genes in the mammalian limb bud. <i>Developmental Biology</i> , 2015, 406, 92-103.	2.0	55
70	PolyaPeak: Detecting Transcription Factor Binding Sites from ChIP-seq Using Peak Shape Information. <i>PLoS ONE</i> , 2014, 9, e89694.	2.5	13
71	Kruppel-like Factor-9 (KLF9) Inhibits Glioblastoma Stemness through Global Transcription Repression and Integrin $\beta 6$ Inhibition. <i>Journal of Biological Chemistry</i> , 2014, 289, 32742-32756.	3.4	67
72	High-temporal-resolution view of transcription and chromatin states across distinct metabolic states in budding yeast. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 854-863.	8.2	70

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73	Global Mapping of Transcription Factor Binding Sites by Sequencing Chromatin Surrogates: a Perspective on Experimental Design, Data Analysis, and Open Problems. <i>Statistics in Biosciences</i> , 2013, 5, 156-178.	1.2	4
74	ChIPXpress: using publicly available gene expression data to improve ChIP-seq and ChIP-chip target gene ranking. <i>BMC Bioinformatics</i> , 2013, 14, 188.	2.6	15
75	TRIB2 Acts Downstream of Wnt/TCF in Liver Cancer Cells to Regulate YAP and C/EBP β Function. <i>Molecular Cell</i> , 2013, 51, 211-225.	9.7	136
76	Construction of human activity-based phosphorylation networks. <i>Molecular Systems Biology</i> , 2013, 9, 655.	7.2	153
77	ChIP-PED enhances the analysis of ChIP-seq and ChIP-chip data. <i>Bioinformatics</i> , 2013, 29, 1182-1189.	4.1	12
78	Differential principal component analysis of ChIP-seq. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6789-6794.	7.1	48
79	Gene set bagging for estimating the probability a statistically significant result will replicate. <i>BMC Bioinformatics</i> , 2013, 14, 360.	2.6	7
80	iASeq: integrative analysis of allele-specificity of protein-DNA interactions in multiple ChIP-seq datasets. <i>BMC Genomics</i> , 2012, 13, 681.	2.8	22
81	Dynamics of Regulatory Networks in the Developing Mouse Retina. <i>PLoS ONE</i> , 2012, 7, e46521.	2.5	9
82	Cell-Type Independent MYC Target Genes Reveal a Primordial Signature Involved in Biomass Accumulation. <i>PLoS ONE</i> , 2011, 6, e26057.	2.5	147
83	MLL fusion proteins preferentially regulate a subset of wild-type MLL target genes in the leukemic genome. <i>Blood</i> , 2011, 117, 6895-6905.	1.4	103
84	Analyzing 'omics data using hierarchical models. <i>Nature Biotechnology</i> , 2010, 28, 337-340.	17.5	58
85	Sox17 promotes differentiation in mouse embryonic stem cells by directly regulating extraembryonic gene expression and indirectly antagonizing self-renewal. <i>Genes and Development</i> , 2010, 24, 312-326.	5.9	270
86	Hedgehog pathway-regulated gene networks in cerebellum development and tumorigenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 9736-9741.	7.1	109
87	Computational Analysis of ChIP-seq Data. <i>Methods in Molecular Biology</i> , 2010, 674, 143-159.	0.9	6
88	Integration of Brassinosteroid Signal Transduction with the Transcription Network for Plant Growth Regulation in Arabidopsis. <i>Developmental Cell</i> , 2010, 19, 765-777.	7.0	790
89	Mobile Interspersed Repeats Are Major Structural Variants in the Human Genome. <i>Cell</i> , 2010, 141, 1171-1182.	28.9	242
90	MLL Fusion Proteins Directly Regulate a Small Set of Wild Type MLL Target Genes.. <i>Blood</i> , 2009, 114, 1279-1279.	1.4	0

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91	An integrated software system for analyzing ChIP-chip and ChIP-seq data. Nature Biotechnology, 2008, 26, 1293-1300.	17.5	662
92	A genome-scale analysis of the cis-regulatory circuitry underlying sonic hedgehog-mediated patterning of the mammalian limb. Genes and Development, 2008, 22, 2651-2663.	5.9	269
93	Genomic characterization of Gli-activator targets in sonic hedgehog-mediated neural patterning. Development (Cambridge), 2007, 134, 1977-1989.	2.5	256
94	FoxOs Are Lineage-Restricted Redundant Tumor Suppressors and Regulate Endothelial Cell Homeostasis. Cell, 2007, 128, 309-323.	28.9	952
95	Computational Biology: Toward Deciphering Gene Regulatory Information in Mammalian Genomes. Biometrics, 2006, 62, 645-663.	1.4	31
96	An improved distance measure between the expression profiles linking co-expression and co-regulation in mouse. BMC Bioinformatics, 2006, 7, 44.	2.6	21
97	A comparative analysis of genome-wide chromatin immunoprecipitation data for mammalian transcription factors. Nucleic Acids Research, 2006, 34, e146-e146.	14.5	59
98	Why do human diversity levels vary at a megabase scale?. Genome Research, 2005, 15, 1222-1231.	5.5	156
99	Integrative Analysis of Multiple ChIP-X Data Sets Using Correlation Motifs. , 0, , 110-132.		0