

Hongkai Ji

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5496900/publications.pdf>

Version: 2024-02-01

99
papers

7,950
citations

117571

34
h-index

56687

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.	2.9	28
2	Understanding Patients'™ Perceived Health After Critical Illness. <i>Chest</i> , 2022, 161, 407-417.	0.4	6
3	GLI transcriptional repression is inert prior to Hedgehog pathway activation. <i>Nature Communications</i> , 2022, 13, 808.	5.8	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.	9.0	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.	1.8	4
6	Epigenome-wide association analyses of active injection drug use. <i>Drug and Alcohol Dependence</i> , 2022, 235, 109431.	1.6	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.	2.7	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, .	3.9	5
9	Genome-wide prediction of chromatin accessibility based on gene expression. <i>Wiley Interdisciplinary Reviews: Computational Statistics</i> , 2021, 13, e1544.	2.1	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.	1.1	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.	5.8	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.	1.3	3
13	Profiling Chromatin Accessibility at Single-cell Resolution. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 172-190.	3.0	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.	0.3	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, .	3.9	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.	11.6	10
17	EGFR Activates a TAZ-Driven Oncogenic Program in Glioblastoma. <i>Cancer Research</i> , 2021, 81, 3580-3592.	0.4	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.	1.8	0

#	ARTICLE	IF	CITATIONS
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.	1.9	30
20	Large-scale phenotypic drug screen identifies neuroprotectants in zebrafish and mouse models of retinitis pigmentosa. <i>ELife</i> , 2021, 10, .	2.8	15
21	Transcriptional programs of neoantigen-specific TIL in anti-PD-1-treated lung cancers. <i>Nature</i> , 2021, 596, 126-132.	13.7	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.	1.6	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.	3.1	6
24	Prenatal exposure to mercury and precocious puberty: a prospective birth cohort study. <i>Human Reproduction</i> , 2021, 36, 712-720.	0.4	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.	1.1	8
27	Altered 3D chromatin structure permits inversional recombination at the <i>IgH</i> locus. <i>Science Advances</i> , 2020, 6, eaaz8850.	4.7	13
28	A systematic evaluation of single-cell RNA-sequencing imputation methods. <i>Genome Biology</i> , 2020, 21, 218.	3.8	188
29	Single-cell ATAC-seq signal extraction and enhancement with SCATE. <i>Genome Biology</i> , 2020, 21, 161.	3.8	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.	3.2	90
31	GLI transcriptional repression regulates tissue-specific enhancer activity in response to Hedgehog signaling. <i>ELife</i> , 2020, 9, .	2.8	29
32	Epigenome-wide association scan identifies methylation sites associated with HIV infection. <i>Epigenomics</i> , 2020, 12, 1917-1927.	1.0	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.	1.1	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.	6.5	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.	2.8	98
36	TCF-1-Centered Transcriptional Network Drives an Effector versus Exhausted CD8âˆ† Cell-Fate Decision. <i>Immunity</i> , 2019, 51, 840-855.e5.	6.6	409

#	ARTICLE	IF	CITATIONS
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.	2.8	35
38	Maternal triacylglycerol signature and risk of food allergy in offspring. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 144, 729-737.	1.5	12
39	Sex differences in gene regulation in the dorsal root ganglion after nerve injury. <i>BMC Genomics</i> , 2019, 20, 147.	1.2	53
40	Pseudotime Reconstruction Using TSCAN. <i>Methods in Molecular Biology</i> , 2019, 1935, 115-124.	0.4	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.	1.1	24
42	Stress response factors drive regrowth of quiescent cells. <i>Current Genetics</i> , 2018, 64, 807-810.	0.8	8
43	ATAC-Seq analysis reveals a widespread decrease of chromatin accessibility in age-related macular degeneration. <i>Nature Communications</i> , 2018, 9, 1364.	5.8	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.	6.5	11
45	Sequential Enhancer Sequestration Dysregulates Recombination Center Formation at the IgH Locus. <i>Molecular Cell</i> , 2018, 70, 21-33.e6.	4.5	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.	1.3	38
47	Transcriptional outcomes and kinetic patterning of gene expression in response to NF- κ B activation. <i>PLoS Biology</i> , 2018, 16, e2006347.	2.6	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.	1.3	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.	1.1	14
50	Maternal Biomarkers of Acetaminophen Use and Offspring Attention Deficit Hyperactivity Disorder. <i>Brain Sciences</i> , 2018, 8, 127.	1.1	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.	3.3	155
52	Single-cell regulome data analysis by SCRAT. <i>Bioinformatics</i> , 2017, 33, 2930-2932.	1.8	47
53	Genome-wide approach identifies a novel gene-maternal pre-pregnancy BMI interaction on preterm birth. <i>Nature Communications</i> , 2017, 8, 15608.	5.8	31
54	Genome-wide prediction of DNase I hypersensitivity using gene expression. <i>Nature Communications</i> , 2017, 8, 1038.	5.8	34

#	ARTICLE	IF	CITATIONS
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.	3.1	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.	1.5	36
57	Computational Prediction of the Global Functional Genomic Landscape: Applications, Methods, and Challenges. <i>Human Heredity</i> , 2016, 81, 88-105.	0.4	3
58	PRMT5 is essential for the maintenance of chondrogenic progenitor cells in the limb bud. <i>Development (Cambridge)</i> , 2016, 143, 4608-4619.	1.2	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.	5.5	50
60	TSCAN: Pseudo-time reconstruction and evaluation in single-cell RNA-seq analysis. <i>Nucleic Acids Research</i> , 2016, 44, e117-e117.	6.5	491
61	Association Between Maternal Prepregnancy Body Mass Index and Plasma Folate Concentrations With Child Metabolic Health. <i>JAMA Pediatrics</i> , 2016, 170, e160845.	3.3	67
62	Turning publicly available gene expression data into discoveries using gene set context analysis. <i>Nucleic Acids Research</i> , 2016, 44, e8-e8.	6.5	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.	1.6	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.	1.6	0
66	Joint analysis of differential gene expression in multiple studies using correlation motifs. <i>Biostatistics</i> , 2015, 16, 31-46.	0.9	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.	2.7	120
68	HOXB7 Is an ER \pm Cofactor in the Activation of HER2 and Multiple ER Target Genes Leading to Endocrine Resistance. <i>Cancer Discovery</i> , 2015, 5, 944-959.	7.7	72
69	Spatiotemporal regulation of GLI target genes in the mammalian limb bud. <i>Developmental Biology</i> , 2015, 406, 92-103.	0.9	55
70	PolyaPeak: Detecting Transcription Factor Binding Sites from ChIP-seq Using Peak Shape Information. <i>PLoS ONE</i> , 2014, 9, e89694.	1.1	13
71	Kruppel-like Factor-9 (KLF9) Inhibits Glioblastoma Stemness through Global Transcription Repression and Integrin β 6 Inhibition. <i>Journal of Biological Chemistry</i> , 2014, 289, 32742-32756.	1.6	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.	3.6	70

#	ARTICLE	IF	CITATIONS
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.	0.6	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.	1.2	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.	4.5	136
76	Construction of human activity-based phosphorylation networks. <i>Molecular Systems Biology</i> , 2013, 9, 655.	3.2	153
77	ChIP-PED enhances the analysis of ChIP-seq and ChIP-chip data. <i>Bioinformatics</i> , 2013, 29, 1182-1189.	1.8	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.	3.3	48
79	Gene set bagging for estimating the probability a statistically significant result will replicate. <i>BMC Bioinformatics</i> , 2013, 14, 360.	1.2	7
80	iASeq: integrative analysis of allele-specificity of protein-DNA interactions in multiple ChIP-seq datasets. <i>BMC Genomics</i> , 2012, 13, 681.	1.2	22
81	Dynamics of Regulatory Networks in the Developing Mouse Retina. <i>PLoS ONE</i> , 2012, 7, e46521.	1.1	9
82	Cell-Type Independent MYC Target Genes Reveal a Primordial Signature Involved in Biomass Accumulation. <i>PLoS ONE</i> , 2011, 6, e26057.	1.1	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.	0.6	103
84	Analyzing 'omics data using hierarchical models. <i>Nature Biotechnology</i> , 2010, 28, 337-340.	9.4	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.	2.7	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.	3.3	109
87	Computational Analysis of ChIP-seq Data. <i>Methods in Molecular Biology</i> , 2010, 674, 143-159.	0.4	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.	3.1	790
89	Mobile Interspersed Repeats Are Major Structural Variants in the Human Genome. <i>Cell</i> , 2010, 141, 1171-1182.	13.5	242
90	MLL Fusion Proteins Directly Regulate a Small Set of Wild Type MLL Target Genes.. <i>Blood</i> , 2009, 114, 1279-1279.	0.6	0

#	ARTICLE	IF	CITATIONS
91	An integrated software system for analyzing ChIP-chip and ChIP-seq data. Nature Biotechnology, 2008, 26, 1293-1300.	9.4	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.	2.7	269
93	Genomic characterization of Gli-activator targets in sonic hedgehog-mediated neural patterning. Development (Cambridge), 2007, 134, 1977-1989.	1.2	256
94	FoxOs Are Lineage-Restricted Redundant Tumor Suppressors and Regulate Endothelial Cell Homeostasis. Cell, 2007, 128, 309-323.	13.5	952
95	Computational Biology: Toward Deciphering Gene Regulatory Information in Mammalian Genomes. Biometrics, 2006, 62, 645-663.	0.8	31
96	An improved distance measure between the expression profiles linking co-expression and co-regulation in mouse. BMC Bioinformatics, 2006, 7, 44.	1.2	21
97	A comparative analysis of genome-wide chromatin immunoprecipitation data for mammalian transcription factors. Nucleic Acids Research, 2006, 34, e146-e146.	6.5	59
98	Why do human diversity levels vary at a megabase scale?. Genome Research, 2005, 15, 1222-1231.	2.4	156
99	Integrative Analysis of Multiple ChIP-X Data Sets Using Correlation Motifs. , 0, , 110-132.		0