

# James J Cai

## List of Publications by Year in descending order

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Version: 2024-02-01

69  
papers

3,640  
citations

172207

29  
h-index

143772

57  
g-index

84  
all docs

84  
docs citations

84  
times ranked

5795  
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization and Complete Genome Sequence of a Novel Coronavirus, Coronavirus HKU1, from Patients with Pneumonia. <i>Journal of Virology</i> , 2005, 79, 884-895.	1.5	1,269
2	Pervasive Hitchhiking at Coding and Regulatory Sites in Humans. <i>PLoS Genetics</i> , 2009, 5, e1000336.	1.5	134
3	Widespread establishment and regulatory impact of Alu exons in human genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 2837-2842.	3.3	119
4	Perceived and objective measures of the food store environment and the association with weight and diet among low-income women in North Carolina. <i>Public Health Nutrition</i> , 2011, 14, 1032-1038.	1.1	118
5	Diverse Splicing Patterns of Exonized Alu Elements in Human Tissues. <i>PLoS Genetics</i> , 2008, 4, e1000225.	1.5	105
6	High diversity of polyketide synthase genes and the melanin biosynthesis gene cluster in <i>Penicillium marneffeii</i> . <i>FEBS Journal</i> , 2010, 277, 3750-3758.	2.2	105
7	Relaxed Purifying Selection and Possibly High Rate of Adaptation in Primate Lineage-Specific Genes. <i>Genome Biology and Evolution</i> , 2010, 2, 393-409.	1.1	100
8	Genetic Variants Contribute to Gene Expression Variability in Humans. <i>Genetics</i> , 2013, 193, 95-108.	1.2	98
9	Systematic determination of the mitochondrial proportion in human and mice tissues for single-cell RNA-sequencing data quality control. <i>Bioinformatics</i> , 2021, 37, 963-967.	1.8	80
10	Broker Genes in Human Disease. <i>Genome Biology and Evolution</i> , 2010, 2, 815-825.	1.1	68
11	Accelerated Evolutionary Rate May Be Responsible for the Emergence of Lineage-Specific Genes in Ascomycota. <i>Journal of Molecular Evolution</i> , 2006, 63, 1-11.	0.8	64
12	Commonality in dysregulated expression of gene sets in cortical brains of individuals with autism, schizophrenia, and bipolar disorder. <i>Translational Psychiatry</i> , 2019, 9, 152.	2.4	61
13	Genomic and experimental evidence for a potential sexual cycle in the pathogenic thermal dimorphic fungus <i>Penicillium marneffeii</i> . <i>FEBS Letters</i> , 2006, 580, 3409-3416.	1.3	60
14	Aberrant Gene Expression in Humans. <i>PLoS Genetics</i> , 2015, 11, e1004942.	1.5	60
15	Long noncoding RNA MALAT1 regulates generation of reactive oxygen species and the insulin responses in male mice. <i>Biochemical Pharmacology</i> , 2018, 152, 94-103.	2.0	60
16	The mitochondrial genome of the thermal dimorphic fungus <i>Penicillium marneffeii</i> is more closely related to those of molds than yeasts. <i>FEBS Letters</i> , 2003, 555, 469-477.	1.3	56
17	Novel Partitivirus Enhances Virulence of and Causes Aberrant Gene Expression in <i>Talaromyces marneffeii</i> . <i>MBio</i> , 2018, 9, .	1.8	54
18	The Complete Genome and Proteome of <i>Laribacter hongkongensis</i> Reveal Potential Mechanisms for Adaptations to Different Temperatures and Habitats. <i>PLoS Genetics</i> , 2009, 5, e1000416.	1.5	52

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19	The lncRNA RZE1 Controls Cryptococcal Morphological Transition. <i>PLoS Genetics</i> , 2015, 11, e1005692.	1.5	49
20	Exploring the <i>Penicillium marneffei</i> genome. <i>Archives of Microbiology</i> , 2003, 179, 339-353.	1.0	45
21	Similarly Strong Purifying Selection Acts on Human Disease Genes of All Evolutionary Ages. <i>Genome Biology and Evolution</i> , 2009, 1, 131-144.	1.1	45
22	Draft Genome Sequence of <i>Penicillium marneffei</i> Strain PM1. <i>Eukaryotic Cell</i> , 2011, 10, 1740-1741.	3.4	42
23	MBEToolbox: a MATLAB toolbox for sequence data analysis in molecular biology and evolution. <i>BMC Bioinformatics</i> , 2005, 6, 64.	1.2	41
24	Morphotype Transition and Sexual Reproduction Are Genetically Associated in a Ubiquitous Environmental Pathogen. <i>PLoS Pathogens</i> , 2014, 10, e1004185.	2.1	41
25	Additive, Epistatic, and Environmental Effects Through the Lens of Expression Variability QTL in a Twin Cohort. <i>Genetics</i> , 2014, 196, 413-425.	1.2	41
26	SBEToolbox: A Matlab Toolbox for Biological Network Analysis. <i>Evolutionary Bioinformatics</i> , 2013, 9, EBO.S12012.	0.6	40
27	Gene expression responses of threespine stickleback to salinity: implications for salt-sensitive hypertension. <i>Frontiers in Genetics</i> , 2014, 5, 312.	1.1	39
28	Natural selection retains overrepresented out-of-frame stop codons against frameshift peptides in prokaryotes. <i>BMC Genomics</i> , 2010, 11, 491.	1.2	38
29	Signature Gene Expression Reveals Novel Clues to the Molecular Mechanisms of Dimorphic Transition in <i>Penicillium marneffei</i> . <i>PLoS Genetics</i> , 2014, 10, e1004662.	1.5	38
30	Unraveling the Molecular Basis of Temperature-Dependent Genetic Regulation in <i>Penicillium marneffei</i> . <i>Eukaryotic Cell</i> , 2013, 12, 1214-1224.	3.4	32
31	Aging Shapes the Population-Mean and -Dispersion of Gene Expression in Human Brains. <i>Frontiers in Aging Neuroscience</i> , 2016, 8, 183.	1.7	31
32	Exploiting aberrant mRNA expression in autism for gene discovery and diagnosis. <i>Human Genetics</i> , 2016, 135, 797-811.	1.8	30
33	Single-Cell Expression Variability Implies Cell Function. <i>Cells</i> , 2020, 9, 14.	1.8	27
34	scTenifoldNet: A Machine Learning Workflow for Constructing and Comparing Transcriptome-wide Gene Regulatory Networks from Single-Cell Data. <i>Patterns</i> , 2020, 1, 100139.	3.1	25
35	Widespread Divergence of the CEACAM/PSG Genes in Vertebrates and Humans Suggests Sensitivity to Selection. <i>PLoS ONE</i> , 2013, 8, e61701.	1.1	25
36	Single-cell RNA sequencing of a European and an African lymphoblastoid cell line. <i>Scientific Data</i> , 2019, 6, 112.	2.4	23

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37	PGEToolbox: A Matlab Toolbox for Population Genetics and Evolution. <i>Journal of Heredity</i> , 2008, 99, 438-440.	1.0	22
38	Overdispersed gene expression in schizophrenia. <i>NPJ Schizophrenia</i> , 2020, 6, 9.	2.0	20
39	Adaptive selection of an incretin gene in Eurasian populations. <i>Genome Research</i> , 2011, 21, 21-32.	2.4	19
40	Context-dependent robustness to 5â€² splice site polymorphisms in human populations. <i>Human Molecular Genetics</i> , 2011, 20, 1084-1096.	1.4	18
41	scTenifoldKnk: An efficient virtual knockout tool for gene function predictions via single-cell gene regulatory network perturbation. <i>Patterns</i> , 2022, 3, 100434.	3.1	17
42	Microsatellite variation in the equine <scp>MHC</scp>. <i>Animal Genetics</i> , 2013, 44, 267-275.	0.6	16
43	Expression profiling of disease progression in canine model of Duchenne muscular dystrophy. <i>PLoS ONE</i> , 2018, 13, e0194485.	1.1	16
44	scGEAToolbox: a Matlab toolbox for single-cell RNA sequencing data analysis. <i>Bioinformatics</i> , 2020, 36, 1948-1949.	1.8	14
45	Adipose tissue inflammation and systemic insulin resistance in mice with diet-induced obesity is possibly associated with disruption of PFKFB3 in hematopoietic cells. <i>Laboratory Investigation</i> , 2021, 101, 328-340.	1.7	14
46	Identification of Metabolic Modifiers That Underlie Phenotypic Variations in Energy-Balance Regulation. <i>Diabetes</i> , 2011, 60, 726-734.	0.3	13
47	Antecedent presentation of neurological phenotypes in the Collaborative Cross reveals four classes with complex sex-dependencies. <i>Scientific Reports</i> , 2020, 10, 7918.	1.6	12
48	Ablation of long noncoding RNA MALAT1 activates antioxidant pathway and alleviates sepsis in mice. <i>Redox Biology</i> , 2022, 54, 102377.	3.9	12
49	Evolutionary Analysis of Sequence Divergence and Diversity of Duplicate Genes in <i>Aspergillus fumigatus</i>. <i>Evolutionary Bioinformatics</i> , 2012, 8, EBO.S10372.	0.6	10
50	Population-level expression variability of mitochondrial DNA-encoded genes in humans. <i>European Journal of Human Genetics</i> , 2014, 22, 1093-1099.	1.4	10
51	Site-specific and substrate-specific control of accurate mRNA editing by a helicase complex in trypanosomes. <i>Rna</i> , 2020, 26, 1862-1881.	1.6	9
52	Genome-wide association study to identify potential genetic modifiers in a canine model for Duchenne muscular dystrophy. <i>BMC Genomics</i> , 2016, 17, 665.	1.2	8
53	Integrating multiple fitting regression and Bayes decision for cancer diagnosis with transcriptomic data from tumor-educated blood platelets. <i>Analyst, The</i> , 2017, 142, 3588-3597.	1.7	8
54	rPanglaoDB: an R package to download and merge labeled single-cell RNA-seq data from the PanglaoDB database. <i>Bioinformatics</i> , 2022, 38, 580-582.	1.8	7

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55	Adaptive Human CDKAL1 Variants Underlie Hormonal Response Variations at the Enteroinsular Axis. PLoS ONE, 2014, 9, e105410.	1.1	6
56	Simulating variance heterogeneity in quantitative genome wide association studies. BMC Bioinformatics, 2018, 19, 72.	1.2	6
57	Single-cell RNA Sequencing Reveals How the Aryl Hydrocarbon Receptor Shapes Cellular Differentiation Potency in the Mouse Colon. Cancer Prevention Research, 2022, 15, 17-28.	0.7	6
58	Epistasis and destabilizing mutations shape gene expression variability in humans via distinct modes of action. Human Molecular Genetics, 2016, 25, ddw314.	1.4	5
59	AECS: identifying aberrantly expressed gene sets for differential variability analysis. Bioinformatics, 2018, 34, 881-883.	1.8	4
60	MBEToolbox 2.0: an enhanced version of a MATLAB toolbox for molecular biology and evolution. Evolutionary Bioinformatics, 2007, 2, 179-82.	0.6	4
61	scInTime: A Computational Method Leveraging Single-Cell Trajectory and Gene Regulatory Networks to Identify Master Regulators of Cellular Differentiation. Genes, 2022, 13, 371.	1.0	4
62	MBEToolbox 2.0: An enhanced version of a MATLAB toolbox for Molecular Biology and Evolution. Evolutionary Bioinformatics, 2006, 2, 117693430600200.	0.6	3
63	Adipocyte inducible 6-phosphofructo-2-kinase suppresses adipose tissue inflammation and promotes macrophage anti-inflammatory activation. Journal of Nutritional Biochemistry, 2021, 95, 108764.	1.9	3
64	Corrigendum to "Genomic and experimental evidence for a potential sexual cycle in the pathogenic thermal dimorphic fungus <i>Penicillium marneffeii</i> " [FEBS Lett. 580 (2006) 3409-3416]. FEBS Letters, 2006, 580, 4976-4977.	1.3	1
65	A framework radiation hybrid map of buffalo chromosome 1 ordering scaffolds from buffalo genome sequence assembly. Genetics and Molecular Research, 2015, 14, 13096-13104.	0.3	1
66	Identification of metabolic modifiers that underlie phenotypic variations in energy-balance regulation. Diabetes 2011;60:726-734. Diabetes, 2013, 62, 4284-4284.	0.3	0
67	Simulating Variance Heterogeneity in Quantitative Genome Wide Association Studies. , 2017, , .		0
68	Single-Cell Gene Regulatory Network Analysis Reveals Potential Mechanisms of Action of Antimalarials Against SARS-CoV-2. Lecture Notes in Computer Science, 2021, , 88-94.	1.0	0
69	Extent, Heritability, and Functional Relevance of Single Cell Expression Variability in Highly Homogeneous Populations of Human Cells. SSRN Electronic Journal, 0, , .	0.4	0