

James J Cai

List of Publications by Year in Descending Order

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Version: 2024-04-26

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

73
papers

2,785
citations

28
h-index

52
g-index

84
ext. papers

3,375
ext. citations

4.7
avg, IF

4.99
L-index

#	Paper	IF	Citations
73	scTenifoldKnk: An efficient virtual knockout tool for gene function predictions via single-cell gene regulatory network perturbation.. <i>Patterns</i> , 2022 , 3, 100434	5.1	0
72	rPanglaoDB: an R package to download and merge labeled single-cell RNA-seq data from the PanglaoDB database. <i>Bioinformatics</i> , 2021 ,	7.2	1
71	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	7.2	19
70	Single-Cell Gene Regulatory Network Analysis Reveals Potential Mechanisms of Action of Antimalarials Against SARS-CoV-2. <i>Lecture Notes in Computer Science</i> , 2021 , 88-94	0.9	
69	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	5.9	4
68	Adipocyte inducible 6-phosphofructo-2-kinase suppresses adipose tissue inflammation and promotes macrophage anti-inflammatory activation. <i>Journal of Nutritional Biochemistry</i> , 2021 , 95, 108764	6.3	1
67	Antecedent presentation of neurological phenotypes in the Collaborative Cross reveals four classes with complex sex-dependencies. <i>Scientific Reports</i> , 2020 , 10, 7918	4.9	6
66	Overdispersed gene expression in schizophrenia. <i>NPJ Schizophrenia</i> , 2020 , 6, 9	5.5	8
65	scTenifoldNet: A Machine Learning Workflow for Constructing and Comparing Transcriptome-wide Gene Regulatory Networks from Single-Cell Data. <i>Patterns</i> , 2020 , 1, 100139	5.1	6
64	Site-specific and substrate-specific control of accurate mRNA editing by a helicase complex in trypanosomes. <i>Rna</i> , 2020 , 26, 1862-1881	5.8	1
63	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	8.6	33
62	Single-cell RNA sequencing of a European and an African lymphoblastoid cell line. <i>Scientific Data</i> , 2019 , 6, 112	8.2	13
61	scGEAToolbox: a Matlab toolbox for single-cell RNA sequencing data analysis. <i>Bioinformatics</i> , 2019 ,	7.2	7
60	Single-Cell Expression Variability Implies Cell Function. <i>Cells</i> , 2019 , 9,	7.9	12
59	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	6	38
58	AECS: identifying aberrantly expressed gene sets for differential variability analysis. <i>Bioinformatics</i> , 2018 , 34, 881-883	7.2	3
57	Simulating variance heterogeneity in quantitative genome wide association studies. <i>BMC Bioinformatics</i> , 2018 , 19, 72	3.6	3

56	Novel Partitivirus Enhances Virulence of and Causes Aberrant Gene Expression in <i>Talaromyces marneffei</i> . <i>MBio</i> , 2018 , 9,	7.8	28
55	Expression profiling of disease progression in canine model of Duchenne muscular dystrophy. <i>PLoS ONE</i> , 2018 , 13, e0194485	3.7	11
54	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	5	7
53	Genome-wide association study to identify potential genetic modifiers in a canine model for Duchenne muscular dystrophy. <i>BMC Genomics</i> , 2016 , 17, 665	4.5	7
52	Epistasis and destabilizing mutations shape gene expression variability in humans via distinct modes of action. <i>Human Molecular Genetics</i> , 2016 , 25, 4911-4919	5.6	4
51	Exploiting aberrant mRNA expression in autism for gene discovery and diagnosis. <i>Human Genetics</i> , 2016 , 135, 797-811	6.3	18
50	Aging Shapes the Population-Mean and -Dispersion of Gene Expression in Human Brains. <i>Frontiers in Aging Neuroscience</i> , 2016 , 8, 183	5.3	22
49	Aberrant gene expression in humans. <i>PLoS Genetics</i> , 2015 , 11, e1004942	6	43
48	A framework radiation hybrid map of buffalo chromosome 1 ordering scaffolds from buffalo genome sequence assembly. <i>Genetics and Molecular Research</i> , 2015 , 14, 13096-104	1.2	1
47	The lncRNA RZE1 Controls Cryptococcal Morphological Transition. <i>PLoS Genetics</i> , 2015 , 11, e1005692	6	41
46	Population-level expression variability of mitochondrial DNA-encoded genes in humans. <i>European Journal of Human Genetics</i> , 2014 , 22, 1093-9	5.3	7
45	Adaptive human CDKAL1 variants underlie hormonal response variations at the enteroinsular axis. <i>PLoS ONE</i> , 2014 , 9, e105410	3.7	5
44	Gene expression responses of threespine stickleback to salinity: implications for salt-sensitive hypertension. <i>Frontiers in Genetics</i> , 2014 , 5, 312	4.5	30
43	Morphotype transition and sexual reproduction are genetically associated in a ubiquitous environmental pathogen. <i>PLoS Pathogens</i> , 2014 , 10, e1004185	7.6	29
42	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	6	22
41	Additive, epistatic, and environmental effects through the lens of expression variability QTL in a twin cohort. <i>Genetics</i> , 2014 , 196, 413-25	4	28
40	Microsatellite variation in the equine MHC. <i>Animal Genetics</i> , 2013 , 44, 267-75	2.5	16
39	Genetic variants contribute to gene expression variability in humans. <i>Genetics</i> , 2013 , 193, 95-108	4	77

38	Unraveling the molecular basis of temperature-dependent genetic regulation in <i>Penicillium marneffei</i> . <i>Eukaryotic Cell</i> , 2013 , 12, 1214-24		17
37	SBEToolbox: A Matlab Toolbox for Biological Network Analysis. <i>Evolutionary Bioinformatics</i> , 2013 , 9, 355-62		31
36	Identification of metabolic modifiers that underlie phenotypic variations in energy-balance regulation. <i>Diabetes</i> 2011;60:726-734. <i>Diabetes</i> , 2013 , 62, 4284-4284	0.9	78
35	Widespread divergence of the CEACAM/PSG genes in vertebrates and humans suggests sensitivity to selection. <i>PLoS ONE</i> , 2013 , 8, e61701	3.7	21
34	Evolutionary Analysis of Sequence Divergence and Diversity of Duplicate Genes in <i>Aspergillus fumigatus</i> . <i>Evolutionary Bioinformatics</i> , 2012 , 8, 623-44	1.9	6
33	Context-dependent robustness to 5' splice site polymorphisms in human populations. <i>Human Molecular Genetics</i> , 2011 , 20, 1084-96	5.6	18
32	Draft genome sequence of <i>Penicillium marneffei</i> strain PM1. <i>Eukaryotic Cell</i> , 2011 , 10, 1740-1		30
31	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, 1032-8	3.3	104
30	Identification of metabolic modifiers that underlie phenotypic variations in energy-balance regulation. <i>Diabetes</i> , 2011 , 60, 726-34	0.9	9
29	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, 2837-42	11.5	98
28	Adaptive selection of an incretin gene in Eurasian populations. <i>Genome Research</i> , 2011 , 21, 21-32	9.7	14
27	High diversity of polyketide synthase genes and the melanin biosynthesis gene cluster in <i>Penicillium marneffei</i> . <i>FEBS Journal</i> , 2010 , 277, 3750-8	5.7	76
26	Relaxed purifying selection and possibly high rate of adaptation in primate lineage-specific genes. <i>Genome Biology and Evolution</i> , 2010 , 2, 393-409	3.9	70
25	Broker genes in human disease. <i>Genome Biology and Evolution</i> , 2010 , 2, 815-25	3.9	52
24	Natural selection retains overrepresented out-of-frame stop codons against frameshift peptides in prokaryotes. <i>BMC Genomics</i> , 2010 , 11, 491	4.5	33
23	Similarly strong purifying selection acts on human disease genes of all evolutionary ages. <i>Genome Biology and Evolution</i> , 2009 , 1, 131-44	3.9	41
22	Pervasive hitchhiking at coding and regulatory sites in humans. <i>PLoS Genetics</i> , 2009 , 5, e1000336	6	99
21	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	6	45

20	Diverse splicing patterns of exonized Alu elements in human tissues. <i>PLoS Genetics</i> , 2008 , 4, e1000225	6	85
19	PGEToolbox: A Matlab toolbox for population genetics and evolution. <i>Journal of Heredity</i> , 2008 , 99, 438-40	4	20
18	MBEToolbox 2.0: an enhanced version of a MATLAB toolbox for molecular biology and evolution. <i>Evolutionary Bioinformatics</i> , 2007 , 2, 179-82	1.9	4
17	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	3.1	48
16	Genomic and experimental evidence for a potential sexual cycle in the pathogenic thermal dimorphic fungus <i>Penicillium marneffei</i> . <i>FEBS Letters</i> , 2006 , 580, 3409-16	3.8	53
15	Corrigendum to "Genomic and experimental evidence for a potential sexual cycle in the pathogenic thermal dimorphic fungus <i>Penicillium marneffei</i> " [FEBS Lett. 580 (2006) 3409-16]. <i>FEBS Letters</i> , 2006 , 580, 4976-4977	3.8	
14	MBEToolbox 2.0: An enhanced version of a MATLAB toolbox for Molecular Biology and Evolution. <i>Evolutionary Bioinformatics</i> , 2006 , 2, 117693430600200	1.9	2
13	Characterization and complete genome sequence of a novel coronavirus, coronavirus HKU1, from patients with pneumonia. <i>Journal of Virology</i> , 2005 , 79, 884-95	6.6	1028
12	MBEToolbox: a MATLAB toolbox for sequence data analysis in molecular biology and evolution. <i>BMC Bioinformatics</i> , 2005 , 6, 64	3.6	34
11	Exploring the <i>Penicillium marneffei</i> genome. <i>Archives of Microbiology</i> , 2003 , 179, 339-53	3	42
10	The mitochondrial genome of the thermal dimorphic fungus <i>Penicillium marneffei</i> is more closely related to those of molds than yeasts. <i>FEBS Letters</i> , 2003 , 555, 469-77	3.8	54
9	Single-cell RNA sequencing of a European and an African lymphoblastoid cell line		1
8	Epistasis and destabilizing mutations shape gene expression variability in humans via distinct modes of action		1
7	scTenifoldNet: a machine learning workflow for constructing and comparing transcriptome-wide gene regulatory networks from single-cell data		1
6	Systematic determination of the mitochondrial proportion in human and mice tissues for single-cell RNA sequencing data quality control		6
5	Overdispersed gene expression characterizes schizophrenic brains		2
4	Osmoregulation in freshwaters: Gene expression in the gills of a Neotropical cichlid in contrasting pH and ionic environments		2
3	scGEApp: a Matlab app for feature selection on single-cell RNA sequencing data		2

2	Extent, heritability, and functional relevance of single cell expression variability in highly homogeneous populations of human cells	1
1	scTenifoldKnk: a machine learning workflow performing virtual knockout experiments on single-cell gene regulatory networks	1