

James J Cai

List of Publications by Citations

Source: <https://exaly.com/author-pdf/6262900/james-j-cai-publications-by-citations.pdf>

Version: 2024-04-26

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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 | 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 |
| 72 | 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 |
| 71 | Pervasive hitchhiking at coding and regulatory sites in humans. <i>PLoS Genetics</i> , 2009 , 5, e1000336 | 6 | 99 |
| 70 | 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 |
| 69 | Diverse splicing patterns of exonized Alu elements in human tissues. <i>PLoS Genetics</i> , 2008 , 4, e1000225 | 6 | 85 |
| 68 | 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 |
| 67 | Genetic variants contribute to gene expression variability in humans. <i>Genetics</i> , 2013 , 193, 95-108 | 4 | 77 |
| 66 | 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 |
| 65 | 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 |
| 64 | 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 |
| 63 | 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 |
| 62 | Broker genes in human disease. <i>Genome Biology and Evolution</i> , 2010 , 2, 815-25 | 3.9 | 52 |
| 61 | 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 |
| 60 | 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 |
| 59 | Aberrant gene expression in humans. <i>PLoS Genetics</i> , 2015 , 11, e1004942 | 6 | 43 |
| 58 | Exploring the <i>Penicillium marneffei</i> genome. <i>Archives of Microbiology</i> , 2003 , 179, 339-53 | 3 | 42 |
| 57 | The lncRNA RZE1 Controls Cryptococcal Morphological Transition. <i>PLoS Genetics</i> , 2015 , 11, e1005692 | 6 | 41 |

| | | | |
|----|--|-----|----|
| 56 | 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 |
| 55 | 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 |
| 54 | MBEToolbox: a MATLAB toolbox for sequence data analysis in molecular biology and evolution. <i>BMC Bioinformatics</i> , 2005 , 6, 64 | 3.6 | 34 |
| 53 | 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 |
| 52 | Natural selection retains overrepresented out-of-frame stop codons against frameshift peptides in prokaryotes. <i>BMC Genomics</i> , 2010 , 11, 491 | 4.5 | 33 |
| 51 | SBEToolbox: A Matlab Toolbox for Biological Network Analysis. <i>Evolutionary Bioinformatics</i> , 2013 , 9, 355-62 | 4.6 | 31 |
| 50 | Gene expression responses of threespine stickleback to salinity: implications for salt-sensitive hypertension. <i>Frontiers in Genetics</i> , 2014 , 5, 312 | 4.5 | 30 |
| 49 | Draft genome sequence of <i>Penicillium marneffei</i> strain PM1. <i>Eukaryotic Cell</i> , 2011 , 10, 1740-1 | | 30 |
| 48 | Morphotype transition and sexual reproduction are genetically associated in a ubiquitous environmental pathogen. <i>PLoS Pathogens</i> , 2014 , 10, e1004185 | 7.6 | 29 |
| 47 | Novel Partitivirus Enhances Virulence of and Causes Aberrant Gene Expression in <i>Talaromyces marneffei</i> . <i>MBio</i> , 2018 , 9, | 7.8 | 28 |
| 46 | 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 |
| 45 | 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 |
| 44 | 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 |
| 43 | 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 |
| 42 | PGEToolbox: A Matlab toolbox for population genetics and evolution. <i>Journal of Heredity</i> , 2008 , 99, 438-40 | 4.0 | 20 |
| 41 | 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 |
| 40 | Exploiting aberrant mRNA expression in autism for gene discovery and diagnosis. <i>Human Genetics</i> , 2016 , 135, 797-811 | 6.3 | 18 |
| 39 | Context-dependent robustness to 5' splice site polymorphisms in human populations. <i>Human Molecular Genetics</i> , 2011 , 20, 1084-96 | 5.6 | 18 |

| | | | |
|----|--|-----|----|
| 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 | Microsatellite variation in the equine MHC. <i>Animal Genetics</i> , 2013 , 44, 267-75 | 2.5 | 16 |
| 36 | Adaptive selection of an incretin gene in Eurasian populations. <i>Genome Research</i> , 2011 , 21, 21-32 | 9.7 | 14 |
| 35 | Single-cell RNA sequencing of a European and an African lymphoblastoid cell line. <i>Scientific Data</i> , 2019 , 6, 112 | 8.2 | 13 |
| 34 | Single-Cell Expression Variability Implies Cell Function. <i>Cells</i> , 2019 , 9, | 7.9 | 12 |
| 33 | Expression profiling of disease progression in canine model of Duchenne muscular dystrophy. <i>PLoS ONE</i> , 2018 , 13, e0194485 | 3.7 | 11 |
| 32 | Identification of metabolic modifiers that underlie phenotypic variations in energy-balance regulation. <i>Diabetes</i> , 2011 , 60, 726-34 | 0.9 | 9 |
| 31 | Overdispersed gene expression in schizophrenia. <i>NPJ Schizophrenia</i> , 2020 , 6, 9 | 5.5 | 8 |
| 30 | 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 |
| 29 | scGEAToolbox: a Matlab toolbox for single-cell RNA sequencing data analysis. <i>Bioinformatics</i> , 2019 , | 7.2 | 7 |
| 28 | 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 |
| 27 | 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 |
| 26 | 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 |
| 25 | 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 |
| 24 | Systematic determination of the mitochondrial proportion in human and mice tissues for single-cell RNA sequencing data quality control | | 6 |
| 23 | 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 |
| 22 | Adaptive human CDKAL1 variants underlie hormonal response variations at the enteroinsular axis. <i>PLoS ONE</i> , 2014 , 9, e105410 | 3.7 | 5 |
| 21 | 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 |

| | | | |
|----|---|-----|---|
| 20 | 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 |
| 19 | 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 |
| 18 | AECS: identifying aberrantly expressed gene sets for differential variability analysis. <i>Bioinformatics</i> , 2018 , 34, 881-883 | 7.2 | 3 |
| 17 | Simulating variance heterogeneity in quantitative genome wide association studies. <i>BMC Bioinformatics</i> , 2018 , 19, 72 | 3.6 | 3 |
| 16 | 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 |
| 15 | Overdispersed gene expression characterizes schizophrenic brains | | 2 |
| 14 | Osmoregulation in freshwaters: Gene expression in the gills of a Neotropical cichlid in contrasting pH and ionic environments | | 2 |
| 13 | scGEApp: a Matlab app for feature selection on single-cell RNA sequencing data | | 2 |
| 12 | 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 |
| 11 | Single-cell RNA sequencing of a European and an African lymphoblastoid cell line | | 1 |
| 10 | Epistasis and destabilizing mutations shape gene expression variability in humans via distinct modes of action | | 1 |
| 9 | scTenifoldNet: a machine learning workflow for constructing and comparing transcriptome-wide gene regulatory networks from single-cell data | | 1 |
| 8 | Extent, heritability, and functional relevance of single cell expression variability in highly homogeneous populations of human cells | | 1 |
| 7 | 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 |
| 6 | 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 |
| 5 | scTenifoldKnk: a machine learning workflow performing virtual knockout experiments on single-cell gene regulatory networks | | 1 |
| 4 | 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 |
| 3 | 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 |

- 2 Corrigendum to Genomic and experimental evidence for a potential sexual cycle in the pathogenic thermal dimorphic fungus *Penicillium marneffei* [FEBS Lett. 580 (2006) 3409-3416]. *FEBS Letters*, **2006**, 580, 4976-4977 3.8
- 1 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 0.9