

Jingyi Jessica Li

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6839936/publications.pdf>

Version: 2024-02-01

59
papers

18,930
citations

279798

23
h-index

149698

56
g-index

91
all docs

91
docs citations

91
times ranked

38027
citing authors

#	ARTICLE	IF	CITATIONS
1	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	27.8	15,516
2	An accurate and robust imputation method scImpute for single-cell RNA-seq data. <i>Nature Communications</i> , 2018, 9, 997.	12.8	495
3	Developmental roles of 21 <i>Drosophila</i> transcription factors are determined by quantitative differences in binding to an overlapping set of thousands of genomic regions. <i>Genome Biology</i> , 2009, 10, R80.	9.6	313
4	Statistics or biology: the zero-inflation controversy about scRNA-seq data. <i>Genome Biology</i> , 2022, 23, 31.	8.8	302
5	Comparative analysis of the transcriptome across distant species. <i>Nature</i> , 2014, 512, 445-448.	27.8	289
6	System wide analyses have underestimated protein abundances and the importance of transcription in mammals. <i>PeerJ</i> , 2014, 2, e270.	2.0	255
7	Comparative analysis of regulatory information and circuits across distant species. <i>Nature</i> , 2014, 512, 453-456.	27.8	184
8	Statistics requantitates the central dogma. <i>Science</i> , 2015, 347, 1066-1067.	12.6	155
9	DNA regions bound at low occupancy by transcription factors do not drive patterned reporter gene expression in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 21330-21335.	7.1	141
10	Sparse linear modeling of next-generation mRNA sequencing (RNA-Seq) data for isoform discovery and abundance estimation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 19867-19872.	7.1	135
11	Benchmarking Computational Doublet-Detection Methods for Single-Cell RNA Sequencing Data. <i>Cell Systems</i> , 2021, 12, 176-194.e6.	6.2	99
12	Comparison of <i>D. melanogaster</i> and <i>C. elegans</i> developmental stages, tissues, and cells by modENCODE RNA-seq data. <i>Genome Research</i> , 2014, 24, 1086-1101.	5.5	88
13	Exaggerated false positives by popular differential expression methods when analyzing human population samples. <i>Genome Biology</i> , 2022, 23, 79.	8.8	88
14	Large-scale comparative epigenomics reveals hierarchical regulation of non-CG methylation in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1069-E1074.	7.1	51
15	Oct4 was a novel target of Wnt signaling pathway. <i>Molecular and Cellular Biochemistry</i> , 2012, 362, 233-240.	3.1	49
16	Modeling and analysis of RNA-seq data: a review from a statistical perspective. <i>Quantitative Biology</i> , 2018, 6, 195-209.	0.5	49
17	A statistical simulator scDesign for rational scRNA-seq experimental design. <i>Bioinformatics</i> , 2019, 35, i41-i50.	4.1	48
18	scDesign2: a transparent simulator that generates high-fidelity single-cell gene expression count data with gene correlations captured. <i>Genome Biology</i> , 2021, 22, 163.	8.8	48

#	ARTICLE	IF	CITATIONS
19	Neyman-Pearson classification algorithms and NP receiver operating characteristics. <i>Science Advances</i> , 2018, 4, eaao1659.	10.3	46
20	Spliceosome Profiling Visualizes Operations of a Dynamic RNP at Nucleotide Resolution. <i>Cell</i> , 2018, 173, 1014-1030.e17.	28.9	39
21	DORGE: Discovery of Oncogenes and tumor suppressor genes using Genetic and Epigenetic features. <i>Science Advances</i> , 2020, 6, .	10.3	34
22	A quantitative proteomic analysis of cellular responses to high glucose media in Chinese hamster ovary cells. <i>Biotechnology Progress</i> , 2015, 31, 1026-1038.	2.6	30
23	Quantitative principles of cis-translational control by general mRNA sequence features in eukaryotes. <i>Genome Biology</i> , 2019, 20, 162.	8.8	29
24	The concurrence of DNA methylation and demethylation is associated with transcription regulation. <i>Nature Communications</i> , 2021, 12, 5285.	12.8	29
25	Quantitating translational control: mRNA abundance-dependent and independent contributions and the mRNA sequences that specify them. <i>Nucleic Acids Research</i> , 2017, 45, 11821-11836.	14.5	28
26	PseudotimeDE: inference of differential gene expression along cell pseudotime with well-calibrated p-values from single-cell RNA sequencing data. <i>Genome Biology</i> , 2021, 22, 124.	8.8	26
27	Statistical Hypothesis Testing versus Machine Learning Binary Classification: Distinctions and Guidelines. <i>Patterns</i> , 2020, 1, 100115.	5.9	24
28	mblImpute: an accurate and robust imputation method for microbiome data. <i>Genome Biology</i> , 2021, 22, 192.	8.8	23
29	Clipper: p-value-free FDR control on high-throughput data from two conditions. <i>Genome Biology</i> , 2021, 22, 288.	8.8	20
30	TROM: A Testing-Based Method for Finding Transcriptomic Similarity of Biological Samples. <i>Statistics in Biosciences</i> , 2017, 9, 105-136.	1.2	16
31	Word and Sentence Embedding Tools to Measure Semantic Similarity of Gene Ontology Terms by Their Definitions. <i>Journal of Computational Biology</i> , 2019, 26, 38-52.	1.6	16
32	Integrin-Src-YAP1 signaling mediates the melanoma acquired resistance to MAPK and PI3K/mTOR dual targeted therapy. <i>Molecular Biomedicine</i> , 2020, 1, 12.	4.4	16
33	Identifying the combinatorial control of signal-dependent transcription factors. <i>PLoS Computational Biology</i> , 2021, 17, e1009095.	3.2	15
34	Cellular Heterogeneityâ€Adjusted clonal Methylation (CHALM) improves prediction of gene expression. <i>Nature Communications</i> , 2021, 12, 400.	12.8	13
35	Protocol for executing and benchmarking eight computational doublet-detection methods in single-cell RNA sequencing data analysis. <i>STAR Protocols</i> , 2021, 2, 100699.	1.2	12
36	RAD: a web application to identify region associated differentially expressed genes. <i>Bioinformatics</i> , 2021, 37, 2741-2743.	4.1	11

#	ARTICLE	IF	CITATIONS
37	Large-scale mapping of mammalian transcriptomes identifies conserved genes associated with different cell states. <i>Nucleic Acids Research</i> , 2017, 45, gkw1256.	14.5	10
38	NMFP: a non-negative matrix factorization based preselection method to increase accuracy of identifying mRNA isoforms from RNA-seq data. <i>BMC Genomics</i> , 2016, 17, 11.	2.8	10
39	AIDE: annotation-assisted isoform discovery with high precision. <i>Genome Research</i> , 2019, 29, 2056-2072.	5.5	10
40	Bi-clustering of Li near P patterns In Gene Expression Data. <i>Journal of Computational Biology</i> , 2012, 19, 619-631.	1.6	9
41	scPNMF: sparse gene encoding of single cells to facilitate gene selection for targeted gene profiling. <i>Bioinformatics</i> , 2021, 37, i358-i366.	4.1	9
42	Epigenome overlap measure (EPOM) for comparing tissue/cell types based on chromatin states. <i>BMC Genomics</i> , 2016, 17, 10.	2.8	7
43	EpiAlign: an alignment-based bioinformatic tool for comparing chromatin state sequences. <i>Nucleic Acids Research</i> , 2019, 47, e77-e77.	14.5	6
44	Network Modeling in Biology: Statistical Methods for Gene and Brain Networks. <i>Statistical Science</i> , 2021, 36, 89-108.	2.8	6
45	MSIQ: Joint modeling of multiple RNA-seq samples for accurate isoform quantification. <i>Annals of Applied Statistics</i> , 2018, 12, 510-539.	1.1	5
46	A Bootstrap Lasso + Partial Ridge Method to Construct Confidence Intervals for Parameters in High-dimensional Sparse Linear Models. <i>Statistica Sinica</i> , 2020, , .	0.3	5
47	Hybrid Statistical and Mechanistic Mathematical Model Guides Mobile Health Intervention for Chronic Pain. <i>Journal of Computational Biology</i> , 2017, 24, 675-688.	1.6	3
48	Correspondence of <i>D. melanogaster</i> and <i>C. elegans</i> developmental stages revealed by alternative splicing characteristics of conserved exons. <i>BMC Genomics</i> , 2017, 18, 234.	2.8	3
49	Understanding patterns and correlates of daily pain using the Sickle cell disease Mobile Application to Record Symptoms via Technology (<sc>SMART</sc>). <i>British Journal of Haematology</i> , 2018, 183, 306-308.	2.5	3
50	Bipartite tight spectral clustering (BiTSC) algorithm for identifying conserved gene co-clusters in two species. <i>Bioinformatics</i> , 2021, 37, 1225-1233.	4.1	3
51	Postoperative Admission of Adult Craniotomy Patients to the Neuroscience Ward Reduces Length of Stay and Cost. <i>Neurosurgery</i> , 2021, 89, 85-93.	1.1	3
52	Simulating Single-Cell Gene Expression Count Data with Preserved Gene Correlations by scDesign2. <i>Journal of Computational Biology</i> , 2022, 29, 23-26.	1.6	3
53	Genomic Applications of the Neyman-Pearson Classification Paradigm. , 2016, , 145-167.		2
54	The interplay between translational efficiency, poly(A) tails, microRNAs, and neuronal activation. <i>Rna</i> , 2022, 28, 808-831.	3.5	2

#	ARTICLE	IF	CITATIONS
55	Single-cell generalized trend model (scGTM): a flexible and interpretable model of gene expression trend along cell pseudotime. <i>Bioinformatics</i> , 2022, 38, 3927-3934.	4.1	2
56	TRANSCRIPTOME ANALYSIS USING NEXT-GENERATION SEQUENCING. , 2015, , 915-936.		1
57	A new bioinformatics tool to recover missing gene expression in single-cell RNA sequencing data. <i>Journal of Molecular Cell Biology</i> , 2021, 13, 1-2.	3.3	1
58	scSampler: fast diversity-preserving subsampling of large-scale single-cell transcriptomic data. <i>Bioinformatics</i> , 2022, 38, 3126-3127.	4.1	1
59	A flexible model-free prediction-based framework for feature ranking.. <i>Journal of Machine Learning Research</i> , 2021, 22, .	62.4	0