

# Wei Vivian Li

## List of Publications by Year in descending order

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Version: 2024-02-01

21  
papers

1,057  
citations

933447

10  
h-index

752698

20  
g-index

34  
all docs

34  
docs citations

34  
times ranked

1458  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	scINSIGHT for interpreting single-cell gene expression from biologically heterogeneous data. <i>Genome Biology</i> , 2022, 23, 82.	8.8	8
3	Phitest for analyzing the homogeneity of single-cell populations. <i>Bioinformatics</i> , 2022, 38, 2639-2641.	4.1	3
4	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
5	mblmpute: an accurate and robust imputation method for microbiome data. <i>Genome Biology</i> , 2021, 22, 192.	8.8	23
6	scLink: Inferring Sparse Gene Co-expression Networks from Single-cell Expression Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 475-492.	6.9	23
7	Selecting gene features for unsupervised analysis of single-cell gene expression data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	20
8	MAAPER: model-based analysis of alternative polyadenylation using 3' end-linked reads. <i>Genome Biology</i> , 2021, 22, 222.	8.8	12
9	Maternal cecal microbiota transfer rescues early-life antibiotic-induced enhancement of type 1 diabetes in mice. <i>Cell Host and Microbe</i> , 2021, 29, 1249-1265.e9.	11.0	32
10	A computational pipeline for functional gene discovery. <i>Scientific Reports</i> , 2021, 11, 23522.	3.3	1
11	Immune suppressive landscape in the human esophageal squamous cell carcinoma microenvironment. <i>Nature Communications</i> , 2020, 11, 6268.	12.8	206
12	Trends and prediction in daily incidence of novel coronavirus infection in China, Hubei Province and Wuhan City: an application of Farr's law. <i>American Journal of Translational Research (discontinued)</i> , 2020, 12, 1355-1361.	0.0	7
13	A statistical simulator scDesign for rational scRNA-seq experimental design. <i>Bioinformatics</i> , 2019, 35, i41-i50.	4.1	48
14	AIDE: annotation-assisted isoform discovery with high precision. <i>Genome Research</i> , 2019, 29, 2056-2072.	5.5	10
15	EpiAlign: an alignment-based bioinformatic tool for comparing chromatin state sequences. <i>Nucleic Acids Research</i> , 2019, 47, e77-e77.	14.5	6
16	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
17	An accurate and robust imputation method scImpute for single-cell RNA-seq data. <i>Nature Communications</i> , 2018, 9, 997.	12.8	495
18	Modeling and analysis of RNA-seq data: a review from a statistical perspective. <i>Quantitative Biology</i> , 2018, 6, 195-209.	0.5	49

#	ARTICLE	IF	CITATIONS
19	TROM: A Testing-Based Method for Finding Transcriptomic Similarity of Biological Samples. <i>Statistics in Biosciences</i> , 2017, 9, 105-136.	1.2	16
20	Epigenome overlap measure (EPOM) for comparing tissue/cell types based on chromatin states. <i>BMC Genomics</i> , 2016, 17, 10.	2.8	7
21	Cecal Microbiota Transfer Rescues Antibiotic-Induced Acceleration of Type 1 Diabetes and Alteration of Intestinal Gene Expression. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0