Wei Vivian Li

List of Publications by Year
in descending order

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	An accurate and robust imputation method scImpute for single-cell RNA-seq data. Nature Communications, 2018, 9, 997.	12.8	495
2	Immune suppressive landscape in the human esophageal squamous cell carcinoma microenvironment. Nature Communications, 2020, 11, 6268.	12.8	206
3	Modeling and analysis of RNA‑seq data: a review from a statistical perspective. Quantitative Biology, 2018, 6, 195-209.	0.5	49
4	A statistical simulator scDesign for rational scRNA-seq experimental design. Bioinformatics, 2019, 35, i41-i50.	4.1	48
5	scDesign2: a transparent simulator that generates high-fidelity single-cell gene expression count data with gene correlations captured. Genome Biology, 2021, 22, 163.	8.8	48
6	Maternal cecal microbiota transfer rescues early-life antibiotic-induced enhancement of type 1 diabetes in mice. Cell Host and Microbe, 2021, 29, 1249-1265.e9.	11.0	32
7	mbImpute: an accurate and robust imputation method for microbiome data. Genome Biology, 2021, 22, 192.	8.8	23
8	scLink: Inferring Sparse Gene Co-expression Networks from Single-cell Expression Data. Genomics, Proteomics and Bioinformatics, 2021, 19, 475-492.	6.9	23
9	Selecting gene features for unsupervised analysis of single-cell gene expression data. Briefings in Bioinformatics, 2021, 22, .	6.5	20
10	TROM: A Testing-Based Method for Finding Transcriptomic Similarity of Biological Samples. Statistics in Biosciences, 2017, 9, 105-136.	1.2	16
11	MAAPER: model-based analysis of alternative polyadenylation using 3′ end-linked reads. Genome Biology, 2021, 22, 222.	8.8	12
12	AIDE: annotation-assisted isoform discovery with high precision. Genome Research, 2019, 29, 2056-2072.	5.5	10
13	scINSIGHT for interpreting single-cell gene expression from biologically heterogeneous data. Genome Biology, 2022, 23, 82.	8.8	8
14	Epigenome overlap measure (EPOM) for comparing tissue/cell types based on chromatin states. BMC Genomics, 2016, 17, 10.	2.8	7
15	Trends and prediction in daily incidence of novel coronavirus infection in China, Hubei Province and Wuhan City: an application of Farr's law. American Journal of Translational Research (discontinued), 2020, 12, 1355-1361.	0.0	7
16	EpiAlign: an alignment-based bioinformatic tool for comparing chromatin state sequences. Nucleic Acids Research, 2019, 47, e77-e77.	14.5	6
17	MSIQ: Joint modeling of multiple RNA-seq samples for accurate isoform quantification. Annals of Applied Statistics, 2018, 12, 510-539.	1.1	5
18	Simulating Single-Cell Gene Expression Count Data with Preserved Gene Correlations by scDesign2. Journal of Computational Biology, 2022, 29, 23-26.	1.6	3

#	Article	IF	Citations
19	Phitest for analyzing the homogeneity of single-cell populations. Bioinformatics, 2022, 38, 2639-2641.	4.1	3
20	A computational pipeline for functional gene discovery. Scientific Reports, 2021, 11, 23522.	3.3	1
21	Cecal Microbiota Transfer Rescues Antibiotic-Induced Acceleration of Type 1 DiabetesÂ and Alteration of Intestinal Gene Expression. SSRN Electronic Journal, 0, , .	0.4	0