Michael I Love

List of Publications by Year
in descending order

72 papers	80,029 citations	172457 29 h-index	106344 65 g-index
110 all docs	110 docs citations	110 times ranked	118111 citing authors

#	Article	IF	Citations
1	Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. Genome Biology, 2014, 15, 550.	8.8	58,325
2	Salmon provides fast and bias-aware quantification of transcript expression. Nature Methods, 2017, 14, 417-419.	19.0	7,460
3	Orchestrating high-throughput genomic analysis with Bioconductor. Nature Methods, 2015, 12, 115-121.	19.0	3,070
4	Differential analyses for RNA-seq: transcript-level estimates improve gene-level inferences. F1000Research, 2015, 4, 1521.	1.6	2,612
5	Differential analyses for RNA-seq: transcript-level estimates improve gene-level inferences. F1000Research, 2015, 4, 1521.	1.6	1,848
6	MAGeCK enables robust identification of essential genes from genome-scale CRISPR/Cas9 knockout screens. Genome Biology, 2014, 15, 554.	8.8	1,614
7	Heavy-tailed prior distributions for sequence count data: removing the noise and preserving large differences. Bioinformatics, 2019, 35, 2084-2092.	4.1	1,085
8	RNA-Seq workflow: gene-level exploratory analysis and differential expression. F1000Research, 2015, 4, 1070.	1.6	304
9	X-exome sequencing of 405 unresolved families identifies seven novel intellectual disability genes. Molecular Psychiatry, 2016, 21, 133-148.	7.9	243
10	Static and Dynamic DNA Loops form AP-1-Bound Activation Hubs during Macrophage Development. Molecular Cell, 2017, 67, 1037-1048.e6.	9.7	242
11	Airway Epithelial miRNA Expression Is Altered in Asthma. American Journal of Respiratory and Critical Care Medicine, 2012, 186, 965-974.	5.6	222
12	Observation weights unlock bulk RNA-seq tools for zero inflation and single-cell applications. Genome Biology, 2018, 19, 24.	8.8	180
13	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. PLoS Computational Biology, 2020, 16, e1007664.	3.2	165
14	A benchmark for RNA-seq quantification pipelines. Genome Biology, 2016, 17, 74.	8.8	160
15	Modeling of RNA-seq fragment sequence bias reduces systematic errors in transcript abundance estimation. Nature Biotechnology, 2016, 34, 1287-1291.	17.5	159
16	Deletions of chromosomal regulatory boundaries are associated with congenital disease. Genome Biology, 2014, 15, 423.	8.8	144
17	ChIP-exo signal associated with DNA-binding motifs provides insight into the genomic binding of the glucocorticoid receptor and cooperating transcription factors. Genome Research, 2015, 25, 825-835.	5.5	113
18	SAFE-clustering: Single-cell Aggregated (from Ensemble) clustering for single-cell RNA-seq data. Bioinformatics, 2019, 35, 1269-1277.	4.1	104

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19	RNA Sequencing Data: Hitchhiker's Guide to Expression Analysis. Annual Review of Biomedical Data Science, 2019, 2, 139-173.	6.5	101
20	Alignment and mapping methodology influence transcript abundance estimation. Genome Biology, 2020, 21, 239.	8.8	96
21	Swimming downstream: statistical analysis of differential transcript usage following Salmon quantification. F1000Research, 2018, 7, 952.	1.6	87
22	Multisensory Logic of Infant-Directed Aggression by Males. Cell, 2018, 175, 1827-1841.e17.	28.9	73
23	An approach for normalization and quality control for NanoString RNA expression data. Briefings in Bioinformatics, 2021, 22, .	6.5	67
24	Swimming downstream: statistical analysis of differential transcript usage following Salmon quantification. F1000Research, 2018, 7, 952.	1.6	63
25	A framework for transcriptome-wide association studies in breast cancer in diverse study populations. Genome Biology, 2020, 21, 42.	8.8	60
26	Role of the chromatin landscape and sequence in determining cell type-specific genomic glucocorticoid receptor binding and gene regulation. Nucleic Acids Research, 2017, 45, 1805-1819.	14.5	56
27	RNA-Seq workflow: gene-level exploratory analysis and differential expression. F1000Research, 0, 4, 1070.	1.6	55
28	Flexible expressed region analysis for RNA-seq with<tt>derfinder</tt>. Nucleic Acids Research, 2017, 45, e9-e9.	14.5	54
29	Nonparametric expression analysis using inferential replicate counts. Nucleic Acids Research, 2019, 47, e105-e105.	14.5	54
30	Modeling Read Counts for CNV Detection in Exome Sequencing Data. Statistical Applications in Genetics and Molecular Biology, 2011, 10, .	0.6	52
31	Cell-type-specific effects of genetic variation on chromatin accessibility during human neuronal differentiation. Nature Neuroscience, 2021, 24, 941-953.	14.8	47
32	MOSTWAS: Multi-Omic Strategies for Transcriptome-Wide Association Studies. PLoS Genetics, 2021, 17, e1009398.	3.5	46
33	Adipose Tissue Gene Expression Associations Reveal Hundreds of Candidate Genes for Cardiometabolic Traits. American Journal of Human Genetics, 2019, 105, 773-787.	6.2	45
34	Brain-trait-associated variants impact cell-type-specific gene regulation during neurogenesis. American Journal of Human Genetics, 2021, 108, 1647-1668.	6.2	36
35	Generation of a Transcriptional Radiation Exposure Signature in Human Blood Using Long-Read Nanopore Sequencing. Radiation Research, 2019, 193, 143.	1.5	29
36	IncreasedSTAG2dosage defines a novel cohesinopathy with intellectual disability and behavioral problems. Human Molecular Genetics, 2015, 24, 7171-7181.	2.9	28

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37	Breakpointer: using local mapping artifacts to support sequence breakpoint discovery from single-end reads. Bioinformatics, 2012, 28, 1024-1025.	4.1	26
38	Consistency and overfitting of multi-omics methods on experimental data. Briefings in Bioinformatics, 2020, 21, 1277-1284.	6.5	24
39	MRLocus: Identifying causal genes mediating a trait through Bayesian estimation of allelic heterogeneity. PLoS Genetics, 2021, 17, e1009455.	3.5	24
40	Improving the completeness of public metadata accompanying omics studies. Genome Biology, 2021, 22, 106.	8.8	22
41	Evaluating brain structure traits as endophenotypes using polygenicity and discoverability. Human Brain Mapping, 2022, 43, 329-340.	3.6	19
42	A junction coverage compatibility score to quantify the reliability of transcript abundance estimates and annotation catalogs. Life Science Alliance, 2019, 2, e201800175.	2.8	19
43	Differences in race, molecular and tumor characteristics among women diagnosed with invasive ductal and lobular breast carcinomas. Cancer Causes and Control, 2019, 30, 31-39.	1.8	14
44	Outcomes of Hormone-Receptor Positive, HER2-Negative Breast Cancers by Race and Tumor Biological Features. JNCI Cancer Spectrum, 2021, 5, pkaa072.	2.9	14
45	Fast effect size shrinkage software for beta-binomialÂmodels of allelic imbalance. F1000Research, 2019, 8, 2024.	1.6	12
46	Terminus enables the discovery of data-driven, robust transcript groups from RNA-seq data. Bioinformatics, 2020, 36, i102-i110.	4.1	11
47	SCISSOR: a framework for identifying structural changes in RNA transcripts. Nature Communications, 2021, 12, 286.	12.8	10
48	Gene-Level Germline Contributions to Clinical Risk of Recurrence Scores in Black and White Patients with Breast Cancer. Cancer Research, 2022, 82, 25-35.	0.9	10
49	Intergenerational response to the endocrine disruptor vinclozolin is influenced by maternal genotype and crossing scheme. Reproductive Toxicology, 2018, 78, 9-19.	2.9	9
50	Reproductive risk factor associations with lobular and ductal carcinoma in the Carolina Breast Cancer Study. Cancer Causes and Control, 2018, 29, 25-32.	1.8	9
51	Chromatin accessibility and gene expression during adipocyte differentiation identify context-dependent effects at cardiometabolic GWAS loci. PLoS Genetics, 2021, 17, e1009865.	3.5	9
52	coTRaCTE predicts co-occurring transcription factors within cell-type specific enhancers. PLoS Computational Biology, 2018, 14, e1006372.	3.2	8
53	Fast effect size shrinkage software for beta-binomialÂmodels of allelic imbalance. F1000Research, 2019, 8, 2024.	1.6	8
54	A Genome-Wide Gene-Based Geneâ€“Environment Interaction Study of Breast Cancer in More than 90,000 Women. Cancer Research Communications, 2022, 2, 211-219.	1.7	6

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55	Assessing exposure effects on gene expression. Genetic Epidemiology, 2020, 44, 601-610.	1.3	4
56	DeCompress: tissue compartment deconvolution of targeted mRNA expression panels using compressed sensing. Nucleic Acids Research, 2021, 49, e48-e48.	14.5	4
57	Compression of quantification uncertainty for scRNA-seq counts. Bioinformatics, 2021, 37, 1699-1707.	4.1	4
58	ExploreModelMatrix: Interactive exploration for improved understanding of design matrices and linear models in R. F1000Research, 2020, 9, 512.	1.6	3
59	Molecular and Clinical Characterization of Postpartum-Associated Breast Cancer in the Carolina Breast Cancer Study Phase Iâ€“III, 1993â€“2013. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 561-568.	2.5	3
60	Hepatocyte growth factor pathway expression in breast cancer by race and subtype. Breast Cancer Research, 2021, 23, 80.	5.0	2
61	Fluent genomics withÂplyrangesÂandÂtximeta. F1000Research, 2020, 9, 109.	1.6	2
62	TP53 Pathway Function, Estrogen Receptor Status, and Breast Cancer Risk Factors in the Carolina Breast Cancer Study. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 124-131.	2.5	2
63	Statistical Modeling of High Dimensional Counts. Methods in Molecular Biology, 2021, 2284, 97-134.	0.9	1
64	Racial differences in breast cancer outcomes by hepatocyte growth factor pathway expression. Breast Cancer Research and Treatment, 2022, 192, 447-455.	2.5	1
65	Prognostic significance of RNA-based TP53 pathway function among estrogen receptor positive and negative breast cancer cases. Npj Breast Cancer, 2022, 8, .	5.2	1
66	ACTOR: a latent Dirichlet model to compare expressed isoform proportions to a reference panel. Biostatistics, 2023, 24, 388-405.	1.5	0
67	ExploreModelMatrix: Interactive exploration for improved understanding of design matrices and linear models in R. F1000Research, 0, 9, 512.	1.6	0
68	Breast cancer treatment patterns by age and time since last pregnancy in the Carolina Breast Cancer Study Phase III. Breast Cancer Research and Treatment, 2022, 192, 435-445.	2.5	0
69	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0
70	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0
71	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0
72	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0