Michael I Love

List of Publications by Year
in descending order

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Version: 2024-02-01

72 papers	80,029 citations	196777 29 h-index	120465 65 g-index
110 all docs	110 docs citations	110 times ranked	128514 citing authors

#	Article	IF	Citations
1	ACTOR: a latent Dirichlet model to compare expressed isoform proportions to a reference panel. Biostatistics, 2023, 24, 388-405.	0.9	0
2	Evaluating brain structure traits as endophenotypes using polygenicity and discoverability. Human Brain Mapping, 2022, 43, 329-340.	1.9	19
3	Gene-Level Germline Contributions to Clinical Risk of Recurrence Scores in Black and White Patients with Breast Cancer. Cancer Research, 2022, 82, 25-35.	0.4	10
4	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.	1.1	2
5	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.	1.1	3
6	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.	1.1	0
7	Racial differences in breast cancer outcomes by hepatocyte growth factor pathway expression. Breast Cancer Research and Treatment, 2022, 192, 447-455.	1.1	1
8	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.	0.7	6
9	Prognostic significance of RNA-based TP53 pathway function among estrogen receptor positive and negative breast cancer cases. Npj Breast Cancer, 2022, 8, .	2.3	1
10	Outcomes of Hormone-Receptor Positive, HER2-Negative Breast Cancers by Race and Tumor Biological Features. JNCI Cancer Spectrum, 2021, 5, pkaa072.	1.4	14
11	An approach for normalization and quality control for NanoString RNA expression data. Briefings in Bioinformatics, 2021, 22, .	3.2	67
12	Statistical Modeling of High Dimensional Counts. Methods in Molecular Biology, 2021, 2284, 97-134.	0.4	1
13	SCISSOR: a framework for identifying structural changes in RNA transcripts. Nature Communications, 2021, 12, 286.	5.8	10
14	DeCompress: tissue compartment deconvolution of targeted mRNA expression panels using compressed sensing. Nucleic Acids Research, 2021, 49, e48-e48.	6.5	4
15	MOSTWAS: Multi-Omic Strategies for Transcriptome-Wide Association Studies. PLoS Genetics, 2021, 17, e1009398.	1.5	46
16	MRLocus: Identifying causal genes mediating a trait through Bayesian estimation of allelic heterogeneity. PLoS Genetics, 2021, 17, e1009455.	1.5	24
17	Improving the completeness of public metadata accompanying omics studies. Genome Biology, 2021, 22, 106.	3.8	22
18	Cell-type-specific effects of genetic variation on chromatin accessibility during human neuronal differentiation. Nature Neuroscience, 2021, 24, 941-953.	7.1	47

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19	Hepatocyte growth factor pathway expression in breast cancer by race and subtype. Breast Cancer Research, 2021, 23, 80.	2.2	2
20	Brain-trait-associated variants impact cell-type-specific gene regulation during neurogenesis. American Journal of Human Genetics, 2021, 108, 1647-1668.	2.6	36
21	Compression of quantification uncertainty for scRNA-seq counts. Bioinformatics, 2021, 37, 1699-1707.	1.8	4
22	Chromatin accessibility and gene expression during adipocyte differentiation identify context-dependent effects at cardiometabolic GWAS loci. PLoS Genetics, 2021, 17, e1009865.	1.5	9
23	Consistency and overfitting of multi-omics methods on experimental data. Briefings in Bioinformatics, 2020, 21, 1277-1284.	3.2	24
24	Terminus enables the discovery of data-driven, robust transcript groups from RNA-seq data. Bioinformatics, 2020, 36, i102-i110.	1.8	11
25	Alignment and mapping methodology influence transcript abundance estimation. Genome Biology, 2020, 21, 239.	3.8	96
26	Assessing exposure effects on gene expression. Genetic Epidemiology, 2020, 44, 601-610.	0.6	4
27	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. PLoS Computational Biology, 2020, 16, e1007664.	1.5	165
28	A framework for transcriptome-wide association studies in breast cancer in diverse study populations. Genome Biology, 2020, 21, 42.	3.8	60
29	Fluent genomics withÂplyrangesÂandÂtximeta. F1000Research, 2020, 9, 109.	0.8	2
30	ExploreModelMatrix: Interactive exploration for improved understanding of design matrices and linear models in R. F1000Research, 2020, 9, 512.	0.8	3
31	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0
32	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0
33	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0
34	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0
35	Nonparametric expression analysis using inferential replicate counts. Nucleic Acids Research, 2019, 47, e105-e105.	6.5	54
36	Adipose Tissue Gene Expression Associations Reveal Hundreds of Candidate Genes for Cardiometabolic Traits. American Journal of Human Genetics, 2019, 105, 773-787.	2.6	45

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37	RNA Sequencing Data: Hitchhiker's Guide to Expression Analysis. Annual Review of Biomedical Data Science, 2019, 2, 139-173.	2.8	101
38	SAFE-clustering: Single-cell Aggregated (from Ensemble) clustering for single-cell RNA-seq data. Bioinformatics, 2019, 35, 1269-1277.	1.8	104
39	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.	0.8	14
40	Heavy-tailed prior distributions for sequence count data: removing the noise and preserving large differences. Bioinformatics, 2019, 35, 2084-2092.	1.8	1,085
41	Fast effect size shrinkage software for beta-binomialÂmodels of allelic imbalance. F1000Research, 2019, 8, 2024.	0.8	12
42	Generation of a Transcriptional Radiation Exposure Signature in Human Blood Using Long-Read Nanopore Sequencing. Radiation Research, 2019, 193, 143.	0.7	29
43	A junction coverage compatibility score to quantify the reliability of transcript abundance estimates and annotation catalogs. Life Science Alliance, 2019, 2, e201800175.	1.3	19
44	Fast effect size shrinkage software for beta-binomialÂmodels of allelic imbalance. F1000Research, 2019, 8, 2024.	0.8	8
45	Observation weights unlock bulk RNA-seq tools for zero inflation and single-cell applications. Genome Biology, 2018, 19, 24.	3.8	180
46	Intergenerational response to the endocrine disruptor vinclozolin is influenced by maternal genotype and crossing scheme. Reproductive Toxicology, 2018, 78, 9-19.	1.3	9
47	Reproductive risk factor associations with lobular and ductal carcinoma in the Carolina Breast Cancer Study. Cancer Causes and Control, 2018, 29, 25-32.	0.8	9
48	Swimming downstream: statistical analysis of differential transcript usage following Salmon quantification. F1000Research, 2018, 7, 952.	0.8	87
49	Multisensory Logic of Infant-Directed Aggression by Males. Cell, 2018, 175, 1827-1841.e17.	13.5	73
50	coTRaCTE predicts co-occurring transcription factors within cell-type specific enhancers. PLoS Computational Biology, 2018, 14, e1006372.	1.5	8
51	Swimming downstream: statistical analysis of differential transcript usage following Salmon quantification. F1000Research, 2018, 7, 952.	0.8	63
52	Salmon provides fast and bias-aware quantification of transcript expression. Nature Methods, 2017, 14, 417-419.	9.0	7,460
53	Static and Dynamic DNA Loops form AP-1-Bound Activation Hubs during Macrophage Development. Molecular Cell, 2017, 67, 1037-1048.e6.	4.5	242
54	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.	6.5	56

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55	Flexible expressed region analysis for RNA-seq with<tt>derfinder</tt>. Nucleic Acids Research, 2017, 45, e9-e9.	6.5	54
56	A benchmark for RNA-seq quantification pipelines. Genome Biology, 2016, 17, 74.	3.8	160
57	Modeling of RNA-seq fragment sequence bias reduces systematic errors in transcript abundance estimation. Nature Biotechnology, 2016, 34, 1287-1291.	9.4	159
58	X-exome sequencing of 405 unresolved families identifies seven novel intellectual disability genes. Molecular Psychiatry, 2016, 21, 133-148.	4.1	243
59	RNA-Seq workflow: gene-level exploratory analysis and differential expression. F1000Research, 2015, 4, 1070.	0.8	304
60	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.	2.4	113
61	IncreasedSTAG2dosage defines a novel cohesinopathy with intellectual disability and behavioral problems. Human Molecular Genetics, 2015, 24, 7171-7181.	1.4	28
62	Orchestrating high-throughput genomic analysis with Bioconductor. Nature Methods, 2015, 12, 115-121.	9.0	3,070
63	Differential analyses for RNA-seq: transcript-level estimates improve gene-level inferences. F1000Research, 2015, 4, 1521.	0.8	1,848
64	Differential analyses for RNA-seq: transcript-level estimates improve gene-level inferences. F1000Research, 2015, 4, 1521.	0.8	2,612
65	MAGeCK enables robust identification of essential genes from genome-scale CRISPR/Cas9 knockout screens. Genome Biology, 2014, 15, 554.	3.8	1,614
66	Deletions of chromosomal regulatory boundaries are associated with congenital disease. Genome Biology, 2014, 15, 423.	3.8	144
67	Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. Genome Biology, 2014, 15, 550.	3.8	58,325
68	Breakpointer: using local mapping artifacts to support sequence breakpoint discovery from single-end reads. Bioinformatics, 2012, 28, 1024-1025.	1.8	26
69	Airway Epithelial miRNA Expression Is Altered in Asthma. American Journal of Respiratory and Critical Care Medicine, 2012, 186, 965-974.	2.5	222
70	Modeling Read Counts for CNV Detection in Exome Sequencing Data. Statistical Applications in Genetics and Molecular Biology, 2011, 10, .	0.2	52
71	RNA-Seq workflow: gene-level exploratory analysis and differential expression. F1000Research, 0, 4, 1070.	0.8	55
72	ExploreModelMatrix: Interactive exploration for improved understanding of design matrices and linear models in R. F1000Research, 0, 9, 512.	0.8	0