

William Johnson

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

16,559
citations

126907

33
h-index

95266

68
g-index

81
all docs

81
docs citations

81
times ranked

33893
citing authors

#	ARTICLE	IF	CITATIONS
1	Adjusting batch effects in microarray expression data using empirical Bayes methods. <i>Biostatistics</i> , 2007, 8, 118-127.	1.5	6,399
2	The <code>sva</code> package for removing batch effects and other unwanted variation in high-throughput experiments. <i>Bioinformatics</i> , 2012, 28, 882-883.	4.1	3,912
3	Tackling the widespread and critical impact of batch effects in high-throughput data. <i>Nature Reviews Genetics</i> , 2010, 11, 733-739.	16.3	1,641
4	ComBat-seq: batch effect adjustment for RNA-seq count data. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa078.	3.2	591
5	Model-based analysis of tiling-arrays for ChIP-chip. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 12457-12462.	7.1	390
6	Low concordance of multiple variant-calling pipelines: practical implications for exome and genome sequencing. <i>Genome Medicine</i> , 2013, 5, 28.	8.2	381
7	Using VAAST to Identify an X-Linked Disorder Resulting in Lethality in Male Infants Due to N-Terminal Acetyltransferase Deficiency. <i>American Journal of Human Genetics</i> , 2011, 89, 28-43.	6.2	222
8	A single-sample microarray normalization method to facilitate personalized-medicine workflows. <i>Genomics</i> , 2012, 100, 337-344.	2.9	212
9	Decontamination of ambient RNA in single-cell RNA-seq with DecontX. <i>Genome Biology</i> , 2020, 21, 57.	8.8	209
10	Alternative preprocessing of RNA-Sequencing data in The Cancer Genome Atlas leads to improved analysis results. <i>Bioinformatics</i> , 2015, 31, 3666-3672.	4.1	196
11	The Cancer Microbiome: Distinguishing Direct and Indirect Effects Requires a Systemic View. <i>Trends in Cancer</i> , 2020, 6, 192-204.	7.4	162
12	DNA Specificity Determinants Associate with Distinct Transcription Factor Functions. <i>PLoS Genetics</i> , 2009, 5, e1000778.	3.5	161
13	Nascent peptides that block protein synthesis in bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E878-87.	7.1	137
14	<i>Pathoscope</i> : Species identification and strain attribution with unassembled sequencing data. <i>Genome Research</i> , 2013, 23, 1721-1729.	5.5	132
15	Combating subclonal evolution of resistant cancer phenotypes. <i>Nature Communications</i> , 2017, 8, 1231.	12.8	124
16	The GNUMAP algorithm: unbiased probabilistic mapping of oligonucleotides from next-generation sequencing. <i>Bioinformatics</i> , 2010, 26, 38-45.	4.1	122
17	DNA Demethylase Activity Maintains Intestinal Cells in an Undifferentiated State Following Loss of APC. <i>Cell</i> , 2010, 142, 930-942.	28.9	96
18	Model-based analysis of two-color arrays (MA2C). <i>Genome Biology</i> , 2007, 8, R178.	9.6	95

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19	Multiplatform single-sample estimates of transcriptional activation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 17778-17783.	7.1	86
20	Metataxonomic and Metagenomic Approaches vs. Culture-Based Techniques for Clinical Pathology. Frontiers in Microbiology, 2016, 7, 484.	3.5	78
21	Cytoplasmic FMR1-Interacting Protein 2 Is a Major Genetic Factor Underlying Binge Eating. Biological Psychiatry, 2017, 81, 757-769.	1.3	78
22	Xenosurveillance: A Novel Mosquito-Based Approach for Examining the Human-Pathogen Landscape. PLoS Neglected Tropical Diseases, 2015, 9, e0003628.	3.0	67
23	Integrating microbial and host transcriptomics to characterize asthma-associated microbial communities. BMC Medical Genomics, 2015, 8, 50.	1.5	63
24	Hnrnp1 Is A Quantitative Trait Gene for Methamphetamine Sensitivity. PLoS Genetics, 2015, 11, e1005713.	3.5	57
25	Effects of ADARs on small RNA processing pathways in <i>C. elegans</i> . Genome Research, 2012, 22, 1488-1498.	5.5	52
26	Existing blood transcriptional classifiers accurately discriminate active tuberculosis from latent infection in individuals from south India. Tuberculosis, 2018, 109, 41-51.	1.9	51
27	BatchQC: interactive software for evaluating sample and batch effects in genomic data. Bioinformatics, 2016, 32, 3836-3838.	4.1	50
28	Improved annotation of <i>C. elegans</i> microRNAs by deep sequencing reveals structures associated with processing by Drosha and Dicer. Rna, 2011, 17, 563-577.	3.5	47
29	Alternative empirical Bayes models for adjusting for batch effects in genomic studies. BMC Bioinformatics, 2018, 19, 262.	2.6	47
30	Shared Gene Expression Alterations in Nasal and Bronchial Epithelium for Lung Cancer Detection. Journal of the National Cancer Institute, 2017, 109, .	6.3	44
31	Inhibition of colony stimulating factor 1 receptor corrects maternal inflammation-induced microglial and synaptic dysfunction and behavioral abnormalities. Molecular Psychiatry, 2021, 26, 1808-1831.	7.9	44
32	ETS-4 Is a Transcriptional Regulator of Life Span in <i>Caenorhabditis elegans</i> . PLoS Genetics, 2010, 6, e1001125.	3.5	44
33	A pharmacogenomic method for individualized prediction of drug sensitivity. Molecular Systems Biology, 2011, 7, 513.	7.2	43
34	Genome-wide profiling of the <i>C. elegans</i> dsRNAome. Rna, 2015, 21, 786-800.	3.5	41
35	High-resolution within-sewer SARS-CoV-2 surveillance facilitates informed intervention. Water Research, 2021, 204, 117613.	11.3	38
36	A Flexible and Powerful Bayesian Hierarchical Model for ChIP-Chip Experiments. Biometrics, 2008, 64, 468-478.	1.4	31

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37	Assessment of microRNA differential expression and detection in multiplexed small RNA sequencing data. <i>Rna</i> , 2015, 21, 164-171.	3.5	31
38	ASSIGN: context-specific genomic profiling of multiple heterogeneous biological pathways. <i>Bioinformatics</i> , 2015, 31, 1745-1753.	4.1	28
39	Comprehensive generation, visualization, and reporting of quality control metrics for single-cell RNA sequencing data. <i>Nature Communications</i> , 2022, 13, 1688.	12.8	23
40	Casein kinase 1 ϵ deletion increases mu opioid receptor ϵ -dependent behaviors and binge eating ¹ . <i>Genes, Brain and Behavior</i> , 2017, 16, 725-738.	2.2	21
41	Cross-validation of existing signatures and derivation of a novel 29-gene transcriptomic signature predictive of progression to TB in a Brazilian cohort of household contacts of pulmonary TB. <i>Tuberculosis</i> , 2020, 120, 101898.	1.9	20
42	Pathway activity profiling of growth factor receptor network and stemness pathways differentiates metaplastic breast cancer histological subtypes. <i>BMC Cancer</i> , 2019, 19, 881.	2.6	19
43	animalcules: interactive microbiome analytics and visualization in R. <i>Microbiome</i> , 2021, 9, 76.	11.1	18
44	Wolframin-1 ϵ -expressing neurons in the entorhinal cortex propagate tau to CA1 neurons and impair hippocampal memory in mice. <i>Science Translational Medicine</i> , 2021, 13, eabe8455.	12.4	17
45	Activity of distinct growth factor receptor network components in breast tumors uncovers two biologically relevant subtypes. <i>Genome Medicine</i> , 2017, 9, 40.	8.2	16
46	Evaluation of computational methods for human microbiome analysis using simulated data. <i>PeerJ</i> , 2020, 8, e9688.	2.0	14
47	A Field Guide to Genomics Research. <i>PLoS Biology</i> , 2014, 12, e1001744.	5.6	13
48	Gene-expression patterns in peripheral blood classify familial breast cancer susceptibility. <i>BMC Medical Genomics</i> , 2015, 8, 72.	1.5	13
49	Robustifying genomic classifiers to batch effects via ensemble learning. <i>Bioinformatics</i> , 2021, 37, 1521-1527.	4.1	13
50	A Parsimonious Host Inflammatory Biomarker Signature Predicts Incident Tuberculosis and Mortality in Advanced Human Immunodeficiency Virus. <i>Clinical Infectious Diseases</i> , 2020, 71, 2645-2654.	5.8	11
51	Exploring changes in the human gut microbiota and microbial-derived metabolites in response to diets enriched in simple, refined, or unrefined carbohydrate-containing foods: a post hoc analysis of a randomized clinical trial. <i>American Journal of Clinical Nutrition</i> , 2020, 112, 1631-1641.	4.7	11
52	Overcoming the impacts of two-step batch effect correction on gene expression estimation and inference. <i>Biostatistics</i> , 2023, 24, 635-652.	1.5	11
53	Discovery and Subsequent Confirmation of Novel Serum Biomarkers Diagnosing Alzheimer ϵ 's Disease. <i>Journal of Alzheimer's Disease</i> , 2015, 49, 317-327.	2.6	10
54	Comparing tuberculosis gene signatures in malnourished individuals using the TBSignatureProfiler. <i>BMC Infectious Diseases</i> , 2021, 21, 106.	2.9	10

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55	The oral microbiome in relation to pancreatic cancer risk in African Americans. <i>British Journal of Cancer</i> , 2022, 126, 287-296.	6.4	9
56	Parallel Mapping Approaches for GNUMAP. , 2011, 2011, 435-443.		8
57	Serum biomarkers predictive of pre-eclampsia. <i>Biomarkers in Medicine</i> , 2015, 9, 563-575.	1.4	8
58	Probabilistic alignment leads to improved accuracy and read coverage for bisulfite sequencing data. <i>BMC Bioinformatics</i> , 2013, 14, 337.	2.6	7
59	Adjusting Batch Effects in Microarray Experiments with Small Sample Size Using Empirical Bayes Methods. , 0, , 113-129.		6
60	A Western-type dietary pattern and atorvastatin induce epicardial adipose tissue interferon signaling in the Ossabaw pig. <i>Journal of Nutritional Biochemistry</i> , 2019, 67, 212-218.	4.2	6
61	Respiratory syncytial virus M2-1 protein associates non-specifically with viral messenger RNA and with specific cellular messenger RNA transcripts. <i>PLoS Pathogens</i> , 2021, 17, e1009589.	4.7	6
62	Doubly stochastic continuous-time hidden Markov approach for analyzing genome tiling arrays. <i>Annals of Applied Statistics</i> , 2009, 3, .	1.1	5
63	Concordance and discordance of sequence survey methods for molecular epidemiology. <i>PeerJ</i> , 2015, 3, e761.	2.0	5
64	Tuberculosisâ€”Learning the Impact of Nutrition (TB LION): protocol for an interventional study to decrease TB risk in household contacts. <i>BMC Infectious Diseases</i> , 2021, 21, 1058.	2.9	5
65	Novel temporal and spatial patterns of metastatic colonization from breast cancer rapid-autopsy tumor biopsies. <i>Genome Medicine</i> , 2021, 13, 170.	8.2	5
66	Striatal transcriptome analysis of a congenic mouse line (chromosome 11: 50â€”60Mb) exhibiting reduced methamphetamine sensitivity. <i>Genomics Data</i> , 2016, 8, 77-80.	1.3	3
67	Dynamic Linear Model for the Identification of miRNAs in Next-Generation Sequencing Data. <i>Biometrics</i> , 2011, 67, 1206-1214.	1.4	2
68	Development and validation of a parsimonious TB gene signature using the digital NanoString nCounter platform. <i>Clinical Infectious Diseases</i> , 2022, , .	5.8	2
69	Exploring Hostâ€”Microbe Interactions in Lung Cancer. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 198, 1116-1118.	5.6	1
70	A Western-Type Dietary Pattern Induces an Atherogenic Gene Expression Profile in the Coronary Arteries of the Ossabaw Pig. <i>Current Developments in Nutrition</i> , 2019, 3, nzz023.	0.3	1
71	Parallel Pair-HMM SNP Detection. , 2012, , .		0
72	Analysis of CHIP-chip Data on Genome Tiling Microarrays. <i>Frontiers of Statistics</i> , 2009, , 239-257.	0.2	0