

# 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	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
2	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
3	Development and validation of a parsimonious TB gene signature using the digital NanoString nCounter platform. <i>Clinical Infectious Diseases</i> , 2022, , .	5.8	2
4	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
5	Robustifying genomic classifiers to batch effects via ensemble learning. <i>Bioinformatics</i> , 2021, 37, 1521-1527.	4.1	13
6	Inhibition of colony stimulating factor 1 receptor corrects maternal inflammation-induced microglial and synaptic dysfunction and behavioral abnormalities. <i>Molecular Psychiatry</i> , 2021, 26, 1808-1831.	7.9	44
7	Comparing tuberculosis gene signatures in malnourished individuals using the TBSignatureProfiler. <i>BMC Infectious Diseases</i> , 2021, 21, 106.	2.9	10
8	animalcules: interactive microbiome analytics and visualization in R. <i>Microbiome</i> , 2021, 9, 76.	11.1	18
9	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
10	Wolframín-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
11	High-resolution within-sewer SARS-CoV-2 surveillance facilitates informed intervention. <i>Water Research</i> , 2021, 204, 117613.	11.3	38
12	Tuberculosis 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
13	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
14	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
15	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
16	ComBat-seq: batch effect adjustment for RNA-seq count data. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa078.	3.2	591
17	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
18	Decontamination of ambient RNA in single-cell RNA-seq with DecontX. <i>Genome Biology</i> , 2020, 21, 57.	8.8	209

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19	The Cancer Microbiome: Distinguishing Direct and Indirect Effects Requires a Systemic View. <i>Trends in Cancer</i> , 2020, 6, 192-204.	7.4	162
20	Evaluation of computational methods for human microbiome analysis using simulated data. <i>PeerJ</i> , 2020, 8, e9688.	2.0	14
21	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
22	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
23	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
24	Existing blood transcriptional classifiers accurately discriminate active tuberculosis from latent infection in individuals from south India. <i>Tuberculosis</i> , 2018, 109, 41-51.	1.9	51
25	Exploring Host-Microbe Interactions in Lung Cancer. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 198, 1116-1118.	5.6	1
26	Alternative empirical Bayes models for adjusting for batch effects in genomic studies. <i>BMC Bioinformatics</i> , 2018, 19, 262.	2.6	47
27	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
28	Casein kinase 1ε deletion increases mu opioid receptor-dependent behaviors and binge eating <sup>1</sup> . <i>Genes, Brain and Behavior</i> , 2017, 16, 725-738.	2.2	21
29	Combating subclonal evolution of resistant cancer phenotypes. <i>Nature Communications</i> , 2017, 8, 1231.	12.8	124
30	Cytoplasmic FMR1-Interacting Protein 2 Is a Major Genetic Factor Underlying Binge Eating. <i>Biological Psychiatry</i> , 2017, 81, 757-769.	1.3	78
31	Shared Gene Expression Alterations in Nasal and Bronchial Epithelium for Lung Cancer Detection. <i>Journal of the National Cancer Institute</i> , 2017, 109, .	6.3	44
32	Metataxonomic and Metagenomic Approaches vs. Culture-Based Techniques for Clinical Pathology. <i>Frontiers in Microbiology</i> , 2016, 7, 484.	3.5	78
33	Striatal transcriptome analysis of a congenic mouse line (chromosome 11: 50-60Mb) exhibiting reduced methamphetamine sensitivity. <i>Genomics Data</i> , 2016, 8, 77-80.	1.3	3
34	BatchQC: interactive software for evaluating sample and batch effects in genomic data. <i>Bioinformatics</i> , 2016, 32, 3836-3838.	4.1	50
35	Discovery and Subsequent Confirmation of Novel Serum Biomarkers Diagnosing Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2015, 49, 317-327.	2.6	10
36	Gene-expression patterns in peripheral blood classify familial breast cancer susceptibility. <i>BMC Medical Genomics</i> , 2015, 8, 72.	1.5	13

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37	ASSIGN: context-specific genomic profiling of multiple heterogeneous biological pathways. <i>Bioinformatics</i> , 2015, 31, 1745-1753.	4.1	28
38	Serum biomarkers predictive of pre-eclampsia. <i>Biomarkers in Medicine</i> , 2015, 9, 563-575.	1.4	8
39	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
40	Xenosurveillance: A Novel Mosquito-Based Approach for Examining the Human-Pathogen Landscape. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003628.	3.0	67
41	Genome-wide profiling of the <i>C. elegans</i> dsRNAome. <i>Rna</i> , 2015, 21, 786-800.	3.5	41
42	Integrating microbial and host transcriptomics to characterize asthma-associated microbial communities. <i>BMC Medical Genomics</i> , 2015, 8, 50.	1.5	63
43	Assessment of microRNA differential expression and detection in multiplexed small RNA sequencing data. <i>Rna</i> , 2015, 21, 164-171.	3.5	31
44	Hnrnp1 Is A Quantitative Trait Gene for Methamphetamine Sensitivity. <i>PLoS Genetics</i> , 2015, 11, e1005713.	3.5	57
45	Concordance and discordance of sequence survey methods for molecular epidemiology. <i>PeerJ</i> , 2015, 3, e761.	2.0	5
46	A Field Guide to Genomics Research. <i>PLoS Biology</i> , 2014, 12, e1001744.	5.6	13
47	Low concordance of multiple variant-calling pipelines: practical implications for exome and genome sequencing. <i>Genome Medicine</i> , 2013, 5, 28.	8.2	381
48	Probabilistic alignment leads to improved accuracy and read coverage for bisulfite sequencing data. <i>BMC Bioinformatics</i> , 2013, 14, 337.	2.6	7
49	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
50	Multiplatform single-sample estimates of transcriptional activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 17778-17783.	7.1	86
51	<i>Pathoscope</i> : Species identification and strain attribution with unassembled sequencing data. <i>Genome Research</i> , 2013, 23, 1721-1729.	5.5	132
52	The <i>sva</i> package for removing batch effects and other unwanted variation in high-throughput experiments. <i>Bioinformatics</i> , 2012, 28, 882-883.	4.1	3,912
53	Effects of ADARs on small RNA processing pathways in <i>C. elegans</i> . <i>Genome Research</i> , 2012, 22, 1488-1498.	5.5	52
54	Parallel Pair-HMM SNP Detection. , 2012, , .		0

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55	A single-sample microarray normalization method to facilitate personalized-medicine workflows. <i>Genomics</i> , 2012, 100, 337-344.	2.9	212
56	Parallel Mapping Approaches for GNUMAP. , 2011, 2011, 435-443.		8
57	A pharmacogenomic method for individualized prediction of drug sensitivity. <i>Molecular Systems Biology</i> , 2011, 7, 513.	7.2	43
58	Dynamic Linear Model for the Identification of miRNAs in Next-Generation Sequencing Data. <i>Biometrics</i> , 2011, 67, 1206-1214.	1.4	2
59	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
60	Improved annotation of <i>C. elegans</i> microRNAs by deep sequencing reveals structures associated with processing by Drosha and Dicer. <i>Rna</i> , 2011, 17, 563-577.	3.5	47
61	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
62	The GNUMAP algorithm: unbiased probabilistic mapping of oligonucleotides from next-generation sequencing. <i>Bioinformatics</i> , 2010, 26, 38-45.	4.1	122
63	DNA Demethylase Activity Maintains Intestinal Cells in an Undifferentiated State Following Loss of APC. <i>Cell</i> , 2010, 142, 930-942.	28.9	96
64	ETS-4 Is a Transcriptional Regulator of Life Span in <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , 2010, 6, e1001125.	3.5	44
65	Doubly stochastic continuous-time hidden Markov approach for analyzing genome tiling arrays. <i>Annals of Applied Statistics</i> , 2009, 3, .	1.1	5
66	DNA Specificity Determinants Associate with Distinct Transcription Factor Functions. <i>PLoS Genetics</i> , 2009, 5, e1000778.	3.5	161
67	Analysis of ChIP-chip Data on Genome Tiling Microarrays. <i>Frontiers of Statistics</i> , 2009, , 239-257.	0.2	0
68	A Flexible and Powerful Bayesian Hierarchical Model for ChIP-Chip Experiments. <i>Biometrics</i> , 2008, 64, 468-478.	1.4	31
69	Adjusting batch effects in microarray expression data using empirical Bayes methods. <i>Biostatistics</i> , 2007, 8, 118-127.	1.5	6,399
70	Model-based analysis of two-color arrays (MA2C). <i>Genome Biology</i> , 2007, 8, R178.	9.6	95
71	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
72	Adjusting Batch Effects in Microarray Experiments with Small Sample Size Using Empirical Bayes Methods. , 0, , 113-129.		6