

Charles D Johnson

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

6,115
citations

361413

20
h-index

395702

33
g-index

45
all docs

45
docs citations

45
times ranked

10032
citing authors

#	ARTICLE	IF	CITATIONS
1	The MicroArray Quality Control (MAQC) project shows inter- and intraplatform reproducibility of gene expression measurements. <i>Nature Biotechnology</i> , 2006, 24, 1151-1161.	17.5	1,927
2	The <i>let-7</i> MicroRNA Represses Cell Proliferation Pathways in Human Cells. <i>Cancer Research</i> , 2007, 67, 7713-7722.	0.9	1,177
3	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. <i>Nature Biotechnology</i> , 2014, 32, 903-914.	17.5	883
4	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. <i>Nature Biotechnology</i> , 2010, 28, 827-838.	17.5	795
5	Genome-Scale MicroRNA and Small Interfering RNA Screens Identify Small RNA Modulators of TRAIL-Induced Apoptosis Pathway. <i>Cancer Research</i> , 2007, 67, 10782-10788.	0.9	204
6	Using RNA sample titrations to assess microarray platform performance and normalization techniques. <i>Nature Biotechnology</i> , 2006, 24, 1123-1131.	17.5	168
7	Novel transcriptome assembly and improved annotation of the whiteleg shrimp (<i>Litopenaeus</i>) Tj ETQq1 1 0.784314 rsgBT /Overlock 10 T	3.3	89
8	Evaluation of the coverage and depth of transcriptome by RNA-Seq in chickens. <i>BMC Bioinformatics</i> , 2011, 12, S5.	2.6	86
9	[2] Analyzing MicroRNA Expression Using Microarrays. <i>Methods in Enzymology</i> , 2006, 411, 14-34.	1.0	80
10	Toxicogenomic Profile of 2,3,7,8-Tetrachlorodibenzo-p-Dioxin in the Murine Fetal Heart: Modulation of Cell Cycle and Extracellular Matrix Genes. <i>Toxicological Sciences</i> , 2005, 88, 231-241.	3.1	71
11	Modulation of RNA Polymerase II Phosphorylation Downstream of Pathogen Perception Orchestrates Plant Immunity. <i>Cell Host and Microbe</i> , 2014, 16, 748-758.	11.0	70
12	Whole-Genome sequencing and genetic variant analysis of a quarter Horse mare. <i>BMC Genomics</i> , 2012, 13, 78.	2.8	60
13	Translational control of lipogenic enzymes in the cell cycle of synchronous, growing yeast cells. <i>EMBO Journal</i> , 2017, 36, 487-502.	7.8	59
14	Genome-wide identification of soybean microRNA responsive to soybean cyst nematodes infection by deep sequencing. <i>BMC Genomics</i> , 2017, 18, 572.	2.8	56
15	Horse Y chromosome assembly displays unique evolutionary features and putative stallion fertility genes. <i>Nature Communications</i> , 2018, 9, 2945.	12.8	56
16	Unraveling gene-gene interactions regulated by ligands of the aryl hydrocarbon receptor.. <i>Environmental Health Perspectives</i> , 2004, 112, 403-412.	6.0	54
17	Neural crest and mesoderm lineage-dependent gene expression in orofacial development. <i>Differentiation</i> , 2007, 75, 463-477.	1.9	48
18	Genomic profiles and predictive biological networks in oxidant-induced atherogenesis. <i>Physiological Genomics</i> , 2003, 13, 263-275.	2.3	34

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19	A Draft De Novo Genome Assembly for the Northern Bobwhite (<i>Colinus virginianus</i>) Reveals Evidence for a Rapid Decline in Effective Population Size Beginning in the Late Pleistocene. PLoS ONE, 2014, 9, e90240.	2.5	34
20	Modeling the next generation sequencing sample processing pipeline for the purposes of classification. BMC Bioinformatics, 2013, 14, 307.	2.6	27
21	Annotated Draft Genome Assemblies for the Northern Bobwhite (<i>Colinus virginianus</i>) and the Scaled Quail (<i>Callipepla squamata</i>) Reveal Disparate Estimates of Modern Genome Diversity and Historic Effective Population Size. G3: Genes, Genomes, Genetics, 2017, 7, 3047-3058.	1.8	20
22	RNA-seq analysis reveals different drought tolerance mechanisms in two broadly adapted wheat cultivars "TAM 111" and "TAM 112". Scientific Reports, 2021, 11, 4301.	3.3	19
23	Accurate Genomic Predictions for Chronic Wasting Disease in U.S. White-Tailed Deer. G3: Genes, Genomes, Genetics, 2020, 10, 1433-1441.	1.8	17
24	Genome wide identification of QTL associated with yield and yield components in two popular wheat cultivars TAM 111 and TAM 112. PLoS ONE, 2020, 15, e0237293.	2.5	17
25	Developing KASP Markers on a Major Stripe Rust Resistance QTL in a Popular Wheat TAM 111 Using 90K Array and Genotyping-by-sequencing SNPs. Crop Science, 2019, 59, 165-175.	1.8	14
26	Genetic dissection of end-use quality traits in two widely adapted wheat cultivars "TAM 111" and "TAM 112". Crop Science, 2021, 61, 1944-1959.	1.8	9
27	Insight into redox-regulated gene networks in vascular cells. Bioinformation, 2007, 1, 379-383.	0.5	7
28	In vitro models to evaluate acute and chronic injury to the heart and vascular systems. Toxicology in Vitro, 2005, 19, 631-644.	2.4	6
29	Genome-wide QTL mapping of yield and agronomic traits in two widely adapted winter wheat cultivars from multiple mega-environments. PeerJ, 2021, 9, e12350.	2.0	6
30	Northern Bobwhite (<i>Colinus virginianus</i>) Mitochondrial Population Genomics Reveals Structure, Divergence, and Evidence for Heteroplasmy. PLoS ONE, 2015, 10, e0144913.	2.5	5
31	Examining De Novo Transcriptome Assemblies via a Quality Assessment Pipeline. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 494-505.	3.0	4
32	Brucella activates the host RIDD pathway to subvert BLOS1-directed immune defense. ELife, 2022, 11, .	6.0	4
33	HiMMe: using genetic patterns as a proxy for genome assembly reliability assessment. BMC Genomics, 2017, 18, 694.	2.8	3
34	Computational Considerations in Transcriptome Assemblies and Their Evaluation, using High Quality Human RNA-Seq data. , 2016, , .		1
35	OBGene: Optimal barcode generator for NGS experiments. , 2012, , .		0
36	Fast DNA barcode generating algorithm using Radix Coding method. , 2012, , .		0

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37	De novo transcriptome assemblies and annotation for pacific whiteleg shrimp. , 2014, , .		0
38	Functional RNAs in Stallion Sperm: Potential Indicators of Sperm Quality and Contributors to Fertility. Journal of Equine Veterinary Science, 2018, 66, 31.	0.9	0
39	Unraveling gene-gene interactions regulated by ligands of the aryl hydrocarbon receptor. Environmental Health Perspectives, 0, , .	6.0	0
40	A new strategy for using historical imbalanced yield data to conduct genome-wide association studies and develop genomic prediction models for wheat breeding. Molecular Breeding, 2022, 42, 1.	2.1	0