

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	A new strategy for using historical imbalanced yield data to conduct genome-wide association studies and develop genomic prediction models for wheat breeding. <i>Molecular Breeding</i> , 2022, 42, 1.	2.1	0
2	<i>Brucella</i> activates the host RIDD pathway to subvert BLOS1-directed immune defense. <i>ELife</i> , 2022, 11, .	6.0	4
3	Genetic dissection of end-use quality traits in two widely adapted wheat cultivars "TAM 111" and "TAM 112". <i>Crop Science</i> , 2021, 61, 1944-1959.	1.8	9
4	RNA-seq analysis reveals different drought tolerance mechanisms in two broadly adapted wheat cultivars "TAM 111" and "TAM 112". <i>Scientific Reports</i> , 2021, 11, 4301.	3.3	19
5	Genome-wide QTL mapping of yield and agronomic traits in two widely adapted winter wheat cultivars from multiple mega-environments. <i>PeerJ</i> , 2021, 9, e12350.	2.0	6
6	Accurate Genomic Predictions for Chronic Wasting Disease in U.S. White-Tailed Deer. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1433-1441.	1.8	17
7	Genome wide identification of QTL associated with yield and yield components in two popular wheat cultivars TAM 111 and TAM 112. <i>PLoS ONE</i> , 2020, 15, e0237293.	2.5	17
8	Developing KASP Markers on a Major Stripe Rust Resistance QTL in a Popular Wheat TAM 111 Using 90K Array and Genotyping-by-Sequencing SNPs. <i>Crop Science</i> , 2019, 59, 165-175.	1.8	14
9	Examining De Novo Transcriptome Assemblies via a Quality Assessment Pipeline. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 494-505.	3.0	4
10	Functional RNAs in Stallion Sperm: Potential Indicators of Sperm Quality and Contributors to Fertility. <i>Journal of Equine Veterinary Science</i> , 2018, 66, 31.	0.9	0
11	Horse Y chromosome assembly displays unique evolutionary features and putative stallion fertility genes. <i>Nature Communications</i> , 2018, 9, 2945.	12.8	56
12	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
13	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. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3047-3058.	1.8	20
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	HiMMe: using genetic patterns as a proxy for genome assembly reliability assessment. <i>BMC Genomics</i> , 2017, 18, 694.	2.8	3
16	Computational Considerations in Transcriptome Assemblies and Their Evaluation, using High Quality Human RNA-Seq data. , 2016, , .		1
17	Northern Bobwhite (<i>Colinus virginianus</i>) Mitochondrial Population Genomics Reveals Structure, Divergence, and Evidence for Heteroplasmy. <i>PLoS ONE</i> , 2015, 10, e0144913.	2.5	5
18	De novo transcriptome assemblies and annotation for pacific whiteleg shrimp. , 2014, , .		0

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19	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
20	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
21	Novel transcriptome assembly and improved annotation of the whiteleg shrimp (<i>Litopenaeus</i>) Tj ETQq1 1 0.784314 rrgBT /Overlock 10	3.5	89
22	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. <i>PLoS ONE</i> , 2014, 9, e90240.	2.5	34
23	Modeling the next generation sequencing sample processing pipeline for the purposes of classification. <i>BMC Bioinformatics</i> , 2013, 14, 307.	2.6	27
24	OBGene: Optimal barcode generator for NGS experiments. , 2012, , .		0
25	Fast DNA barcode generating algorithm using Radix Coding method. , 2012, , .		0
26	Whole-Genome sequencing and genetic variant analysis of a quarter Horse mare. <i>BMC Genomics</i> , 2012, 13, 78.	2.8	60
27	Evaluation of the coverage and depth of transcriptome by RNA-Seq in chickens. <i>BMC Bioinformatics</i> , 2011, 12, S5.	2.6	86
28	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
29	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
30	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
31	Neural crest and mesoderm lineage-dependent gene expression in orofacial development. <i>Differentiation</i> , 2007, 75, 463-477.	1.9	48
32	Insight into redox-regulated gene networks in vascular cells. <i>Bioinformatics</i> , 2007, 1, 379-383.	0.5	7
33	[2] Analyzing MicroRNA Expression Using Microarrays. <i>Methods in Enzymology</i> , 2006, 411, 14-34.	1.0	80
34	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
35	Using RNA sample titrations to assess microarray platform performance and normalization techniques. <i>Nature Biotechnology</i> , 2006, 24, 1123-1131.	17.5	168
36	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

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37	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
38	Unraveling gene-gene interactions regulated by ligands of the aryl hydrocarbon receptor.. Environmental Health Perspectives, 2004, 112, 403-412.	6.0	54
39	Genomic profiles and predictive biological networks in oxidant-induced atherogenesis. Physiological Genomics, 2003, 13, 263-275.	2.3	34
40	Unraveling gene-gene interactions regulated by ligands of the aryl hydrocarbon receptor. Environmental Health Perspectives, 0, , .	6.0	0