

Corbin D Jones

List of Publications by Year in descending order

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92
papers

15,406
citations

61984

43
h-index

43889

91
g-index

98
all docs

98
docs citations

98
times ranked

23142
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498.	27.0	2,582
2	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	27.8	1,886
3	Salicylic acid modulates colonization of the root microbiome by specific bacterial taxa. <i>Science</i> , 2015, 349, 860-864.	12.6	957
4	Practical innovations for high-throughput amplicon sequencing. <i>Nature Methods</i> , 2013, 10, 999-1002.	19.0	787
5	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	28.9	738
6	Root microbiota drive direct integration of phosphate stress and immunity. <i>Nature</i> , 2017, 543, 513-518.	27.8	669
7	Population Genomics: Whole-Genome Analysis of Polymorphism and Divergence in <i>Drosophila simulans</i> . <i>PLoS Biology</i> , 2007, 5, e310.	5.6	583
8	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017, 31, 181-193.	16.8	532
9	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016, 29, 723-736.	16.8	482
10	Dynamic Evolution of Pathogenicity Revealed by Sequencing and Comparative Genomics of 19 <i>Pseudomonas syringae</i> Isolates. <i>PLoS Pathogens</i> , 2011, 7, e1002132.	4.7	413
11	Accurate sampling and deep sequencing of the HIV-1 protease gene using a Primer ID. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20166-20171.	7.1	358
12	SARS-CoV-2 infection is effectively treated and prevented by EIDD-2801. <i>Nature</i> , 2021, 591, 451-457.	27.8	320
13	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017, 31, 411-423.	16.8	309
14	Novel genes derived from noncoding DNA in <i>Drosophila melanogaster</i> are frequently X-linked and exhibit testis-biased expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 9935-9939.	7.1	288
15	A single bacterial genus maintains root growth in a complex microbiome. <i>Nature</i> , 2020, 587, 103-108.	27.8	245
16	Origin and Spread of de Novo Genes in <i>Drosophila melanogaster</i> Populations. <i>Science</i> , 2014, 343, 769-772.	12.6	220
17	Systemic HIV and SIV latency reversal via non-canonical NF- κ B signalling in vivo. <i>Nature</i> , 2020, 578, 160-165.	27.8	210
18	Gene Transposition as a Cause of Hybrid Sterility in <i>Drosophila</i> . <i>Science</i> , 2006, 313, 1448-1450.	12.6	195

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19	Evidence for de Novo Evolution of Testis-Expressed Genes in the <i>Drosophila yakuba</i> / <i>Drosophila erecta</i> Clade. <i>Genetics</i> , 2007, 176, 1131-1137.	2.9	182
20	Design of synthetic bacterial communities for predictable plant phenotypes. <i>PLoS Biology</i> , 2018, 16, e2003962.	5.6	182
21	Evidence for extensive horizontal gene transfer from the draft genome of a tardigrade. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15976-15981.	7.1	145
22	Detecting the Undetected: Estimating the Total Number of Loci Underlying a Quantitative Trait. <i>Genetics</i> , 2000, 156, 2093-2107.	2.9	144
23	DiffSplice: the genome-wide detection of differential splicing events with RNA-seq. <i>Nucleic Acids Research</i> , 2013, 41, e39-e39.	14.5	138
24	De novo assembly using low-coverage short read sequence data from the rice pathogen <i>Pseudomonas syringae</i> pv. <i>oryzae</i> . <i>Genome Research</i> , 2009, 19, 294-305.	5.5	129
25	The effects of soil phosphorus content on plant microbiota are driven by the plant phosphate starvation response. <i>PLoS Biology</i> , 2019, 17, e3000534.	5.6	126
26	De Novo ORFs in <i>Drosophila</i> Are Important to Organismal Fitness and Evolved Rapidly from Previously Non-coding Sequences. <i>PLoS Genetics</i> , 2013, 9, e1003860.	3.5	124
27	The tardigrade <i>Hypsibius dujardini</i> , a new model for studying the evolution of development. <i>Developmental Biology</i> , 2007, 312, 545-559.	2.0	119
28	HIV-1 Populations in Semen Arise through Multiple Mechanisms. <i>PLoS Pathogens</i> , 2010, 6, e1001053.	4.7	119
29	The Genetic Basis of <i>Drosophila sechellia</i> 's Resistance to a Host Plant Toxin. <i>Genetics</i> , 1998, 149, 1899-1908.	2.9	118
30	Parallel Geographic Variation in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2014, 197, 361-373.	2.9	113
31	Primer ID Validates Template Sampling Depth and Greatly Reduces the Error Rate of Next-Generation Sequencing of HIV-1 Genomic RNA Populations. <i>Journal of Virology</i> , 2015, 89, 8540-8555.	3.4	111
32	Highly contiguous assemblies of 101 drosophilid genomes. <i>ELife</i> , 2021, 10, .	6.0	108
33	FMLRC: Hybrid long read error correction using an FM-index. <i>BMC Bioinformatics</i> , 2018, 19, 50.	2.6	94
34	Genetic Changes Accompanying the Evolution of Host Specialization in <i>Drosophila sechellia</i> . <i>Genetics</i> , 2009, 181, 721-736.	2.9	91
35	The genetics of adaptation in <i>Drosophila sechellia</i> . <i>Genetica</i> , 2005, 123, 137-145.	1.1	82
36	Specific modulation of the root immune system by a community of commensal bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	81

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37	A complex immune response to flagellin epitope variation in commensal communities. <i>Cell Host and Microbe</i> , 2021, 29, 635-649.e9.	11.0	73
38	Evolution of Gene Expression in the <i>Drosophila</i> Olfactory System. <i>Molecular Biology and Evolution</i> , 2008, 25, 1081-1092.	8.9	67
39	Parallel evolution of chimeric fusion genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 11373-11378.	7.1	62
40	Evolution of an MCM Complex in Flies That Promotes Meiotic Crossovers by Blocking BLM Helicase. <i>Science</i> , 2012, 338, 1363-1365.	12.6	61
41	Molecular Population Genetics of Male Accessory Gland Proteins in the <i>Drosophila simulans</i> Complex. <i>Genetics</i> , 2004, 167, 725-735.	2.9	56
42	The <i>Pseudomonas viridiflava</i> phylogroups in the <i>Pseudomonas syringae</i> species complex are characterized by genetic variability and phenotypic plasticity of pathogenicity-related traits. <i>Environmental Microbiology</i> , 2014, 16, 2301-2315.	3.8	51
43	Combinations of DIPs and Dprs control organization of olfactory receptor neuron terminals in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2018, 14, e1007560.	3.5	48
44	Relaxed Genetic Constraint is Ancestral to the Evolution of Phenotypic Plasticity. <i>Integrative and Comparative Biology</i> , 2012, 52, 16-30.	2.0	46
45	Signatures of antagonistic pleiotropy in a bacterial flagellin epitope. <i>Cell Host and Microbe</i> , 2021, 29, 620-634.e9.	11.0	44
46	The genetic basis of larval resistance to a host plant toxin in <i>Drosophila sechellia</i> . <i>Genetical Research</i> , 2001, 78, 225-233.	0.9	43
47	Origin and Evolution of a Chimeric Fusion Gene in <i>Drosophila subobscura</i> , <i>D. madeirensis</i> and <i>D. guanche</i> . Sequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY874360, AY874361, AY874362, AY874363, AY874364, AY874365, AY874366, AY874367, AY874368, AY874369, AY874370, AY874371, AY874372, AY874373, AY874374, AY874375, AY874376, AY874377, AY874378. <i>Genetics</i> , 2005, 170, 207-219.	2.9	43
48	Rapid and Predictable Evolution of Admixed Populations Between Two <i>Drosophila</i> Species Pairs. <i>Genetics</i> , 2020, 214, 211-230.	2.9	42
49	Variable Suites of Non-effector Genes Are Co-regulated in the Type III Secretion Virulence Regulon across the <i>Pseudomonas syringae</i> Phylogeny. <i>PLoS Pathogens</i> , 2014, 10, e1003807.	4.7	39
50	Bigger is not always better: Transmission and fitness burden of a 11MB <i>Pseudomonas syringae</i> megaplasmid pMPPla107. <i>Plasmid</i> , 2014, 73, 16-25.	1.4	37
51	An aberrant NOTCH2-BCR signaling axis in B cells from patients with chronic GVHD. <i>Blood</i> , 2017, 130, 2131-2145.	1.4	37
52	A Functionally Conserved Gene Regulatory Network Module Governing Olfactory Neuron Diversity. <i>PLoS Genetics</i> , 2016, 12, e1005780.	3.5	36
53	Genetic testing reveals some mislabeling but general compliance with a ban on herbivorous fish harvesting in Belize. <i>Conservation Letters</i> , 2013, 6, 132-140.	5.7	35
54	Comparative Genomics of Multiple Strains of <i>Pseudomonas cannabina</i> pv. <i>alisalensis</i> , a Potential Model Pathogen of Both Monocots and Dicots. <i>PLoS ONE</i> , 2013, 8, e59366.	2.5	34

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55	A Locus in <i>Drosophila sechellia</i> Affecting Tolerance of a Host Plant Toxin. <i>Genetics</i> , 2013, 195, 1063-1075.	2.9	32
56	Genome Reference and Sequence Variation in the Large Repetitive Central Exon of Human <i>MUC5AC</i> . <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2014, 50, 223-232.	2.9	32
57	Overcoming Redundancy: An RNAi Enhancer Screen for Morphogenesis Genes in <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2011, 188, 549-564.	2.9	30
58	Hepatitis C Virus (HCV) NS3 Sequence Diversity and Antiviral Resistance-Associated Variant Frequency in HCV/HIV Coinfection. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 6079-6092.	3.2	29
59	Phylogeny of Toll-Like Receptor Signaling: Adapting the Innate Response. <i>PLoS ONE</i> , 2013, 8, e54156.	2.5	27
60	Selective single cell isolation for genomics using microarray arrays. <i>Nucleic Acids Research</i> , 2016, 44, 8292-8301.	14.5	24
61	Next-Generation Mapping of Complex Traits with Phenotype-Based Selection and Introgression. <i>Genetics</i> , 2011, 189, 1203-1209.	2.9	23
62	Evolution of a Signaling Nexus Constrained by Protein Interfaces and Conformational States. <i>PLoS Computational Biology</i> , 2010, 6, e1000962.	3.2	22
63	MT-Toolbox: improved amplicon sequencing using molecule tags. <i>BMC Bioinformatics</i> , 2014, 15, 284.	2.6	22
64	CIB1 depletion impairs cell survival and tumor growth in triple-negative breast cancer. <i>Breast Cancer Research and Treatment</i> , 2015, 152, 337-346.	2.5	22
65	Virus expression detection reveals RNA-sequencing contamination in TCGA. <i>BMC Genomics</i> , 2020, 21, 79.	2.8	21
66	Suppressor Analysis Reveals a Role for SecY in the SecA2-Dependent Protein Export Pathway of Mycobacteria. <i>Journal of Bacteriology</i> , 2013, 195, 4456-4465.	2.2	20
67	Prediction of Protein-Protein Interfaces on G-Protein β Subunits Reveals a Novel Phospholipase C β 2 Binding Domain. <i>Journal of Molecular Biology</i> , 2009, 392, 1044-1054.	4.2	19
68	Root Microbiome Modulates Plant Growth Promotion Induced by Low Doses of Glyphosate. <i>MSphere</i> , 2020, 5, .	2.9	19
69	Genomic Effects of Nucleotide Substitutions in <i>Drosophila simulans</i> . <i>Genetics</i> , 2002, 162, 1753-1761.	2.9	19
70	Natural variation in sugar tolerance associates with changes in signaling and mitochondrial ribosome biogenesis. <i>eLife</i> , 2018, 7, .	6.0	12
71	Patterns of Amino Acid Evolution in the <i>Drosophila ananassae</i> Chimeric Gene, <i>siren</i> , Parallel Those of Other <i>Adh</i> -Derived Chimeras. <i>Genetics</i> , 2008, 180, 1261-1263.	2.9	11
72	A suite of molecular markers for identifying species, detecting introgression and describing population structure in spadefoot toads (<i>Spea</i> spp.). <i>Molecular Ecology Resources</i> , 2012, 12, 909-917.	4.8	11

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73	Cognitive Phenotype and Differential Gene Expression in a Hippocampal Homologue in Two Species of Frog. <i>Integrative and Comparative Biology</i> , 2020, 60, 1007-1023.	2.0	11
74	Alterations in airway microbiota in patients with PaO ₂ /FiO ₂ ratio \hat{a}% 300 after burn and inhalation injury. <i>PLoS ONE</i> , 2017, 12, e0173848.	2.5	11
75	Transcriptional profiling of olfactory system development identifies distal antenna as a regulator of subset of neuronal fates. <i>Scientific Reports</i> , 2017, 7, 40873.	3.3	10
76	Plastic potential: how the phenotypes and adaptations of pathogens are influenced by microbial interactions within plants. <i>Current Opinion in Plant Biology</i> , 2017, 38, 78-83.	7.1	9
77	Patterns of transcriptional parallelism and variation in the developing olfactory system of <i>Drosophila</i> species. <i>Scientific Reports</i> , 2017, 7, 8804.	3.3	8
78	Parasites, niche modification and the host microbiome: A field survey of multiple parasites. <i>Molecular Ecology</i> , 2021, 30, 2404-2416.	3.9	8
79	A scalable and memory-efficient algorithm for de novo transcriptome assembly of non-model organisms. <i>BMC Genomics</i> , 2017, 18, 387.	2.8	7
80	Variation in hybrid gene expression: Implications for the evolution of genetic incompatibilities in interbreeding species. <i>Molecular Ecology</i> , 2019, 28, 4667-4679.	3.9	7
81	Systematic Identification of Balanced Transposition Polymorphisms in <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2009, 5, e1000502.	3.5	6
82	Two Rapidly Evolving Genes Contribute to Male Fitness in <i>Drosophila</i> . <i>Journal of Molecular Evolution</i> , 2013, 77, 246-259.	1.8	6
83	Comparative analysis of behavioral and transcriptional variation underlying CO ₂ sensory neuron function and development in <i>Drosophila</i> . <i>Fly</i> , 2017, 11, 239-252.	1.7	5
84	Challenges and solutions for analysing dual $\langle scp \rangle$RNA$\langle /scp \rangle$seq data for non-model host-pathogen systems. <i>Methods in Ecology and Evolution</i> , 2019, 10, 401-414.	5.2	5
85	A prospective study of asymptomatic SARS-CoV-2 infection among individuals involved in academic research under limited operations during the COVID-19 pandemic. <i>PLoS ONE</i> , 2022, 17, e0267353.	2.5	5
86	Collaboration between Clinical and Academic Laboratories for Sequencing SARS-CoV-2 Genomes. <i>Journal of Clinical Microbiology</i> , 2022, 60, JCM0128821.	3.9	4
87	Fast alignment filtering of nanopore sequencing reads using locality-sensitive hashing. , 2015, , .		3
88	Evolutionary Genetics: You Are What You Evolve to Eat. <i>Current Biology</i> , 2015, 25, R341-R344.	3.9	2
89	Acute Leukemia Classification Using Transcriptional Profiles From Low-Cost Nanopore mRNA Sequencing. <i>JCO Precision Oncology</i> , 2022, 6, e2100326.	3.0	2
90	A note on optimal sampling strategy for structural variant detection using optical mapping. <i>Communications in Statistics - Theory and Methods</i> , 2020, , 1-15.	1.0	1

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91	REC: fast sparse regression-based multicategory classification. <i>Statistics and Its Interface</i> , 2017, 10, 175-185.	0.3	1
92	The Use of the Dahl Rat to Understand the Genetics of Human Hypertension: 35 Years of Data. <i>Current Hypertension Reviews</i> , 2005, 1, 97-99.	0.9	0