

Aaron E Darling

List of Publications by Year in descending order

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Version: 2024-02-01

90
papers

36,015
citations

66234

42
h-index

46693

89
g-index

107
all docs

107
docs citations

107
times ranked

42827
citing authors

#	ARTICLE	IF	CITATIONS
1	MrBayes 3.2: Efficient Bayesian Phylogenetic Inference and Model Choice Across a Large Model Space. <i>Systematic Biology</i> , 2012, 61, 539-542.	2.7	20,458
2	progressiveMauve: Multiple Genome Alignment with Gene Gain, Loss and Rearrangement. <i>PLoS ONE</i> , 2010, 5, e11147.	1.1	3,652
3	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013, 499, 431-437.	13.7	2,239
4	A5-miseq: an updated pipeline to assemble microbial genomes from Illumina MiSeq data. <i>Bioinformatics</i> , 2015, 31, 587-589.	1.8	973
5	The <i>Amphimedon queenslandica</i> genome and the evolution of animal complexity. <i>Nature</i> , 2010, 466, 720-726.	13.7	917
6	Critical Assessment of Metagenome Interpretation—a benchmark of metagenomics software. <i>Nature Methods</i> , 2017, 14, 1063-1071.	9.0	635
7	PhyloSift: phylogenetic analysis of genomes and metagenomes. <i>PeerJ</i> , 2014, 2, e243.	0.9	633
8	BEAGLE: An Application Programming Interface and High-Performance Computing Library for Statistical Phylogenetics. <i>Systematic Biology</i> , 2012, 61, 170-173.	2.7	555
9	Reordering contigs of draft genomes using the Mauve Aligner. <i>Bioinformatics</i> , 2009, 25, 2071-2073.	1.8	532
10	Assemblathon 1: A competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011, 21, 2224-2241.	2.4	443
11	An Integrated Pipeline for de Novo Assembly of Microbial Genomes. <i>PLoS ONE</i> , 2012, 7, e42304.	1.1	436
12	Nitrogen fixation in a landrace of maize is supported by a mucilage-associated diazotrophic microbiota. <i>PLoS Biology</i> , 2018, 16, e2006352.	2.6	236
13	Dynamics of Genome Rearrangement in Bacterial Populations. <i>PLoS Genetics</i> , 2008, 4, e1000128.	1.5	216
14	Patterns of Gene Flow Define Species of Thermophilic Archaea. <i>PLoS Biology</i> , 2012, 10, e1001265.	2.6	214
15	Metagenomic Sequencing of an In Vitro-Simulated Microbial Community. <i>PLoS ONE</i> , 2010, 5, e10209.	1.1	200
16	MetAMOS: a modular and open source metagenomic assembly and analysis pipeline. <i>Genome Biology</i> , 2013, 14, R2.	13.9	174
17	Inference of Homologous Recombination in Bacteria Using Whole-Genome Sequences. <i>Genetics</i> , 2010, 186, 1435-1449.	1.2	155
18	ASAP, a systematic annotation package for community analysis of genomes. <i>Nucleic Acids Research</i> , 2003, 31, 147-151.	6.5	152

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19	DESMAN: a new tool for de novo extraction of strains from metagenomes. <i>Genome Biology</i> , 2017, 18, 181.	3.8	152
20	Impact of homologous and non-homologous recombination in the genomic evolution of <i>Escherichia coli</i> . <i>BMC Genomics</i> , 2012, 13, 256.	1.2	141
21	BEAGLE 3: Improved Performance, Scaling, and Usability for a High-Performance Computing Library for Statistical Phylogenetics. <i>Systematic Biology</i> , 2019, 68, 1052-1061.	2.7	139
22	Phylogeny of Bacterial and Archaeal Genomes Using Conserved Genes: Supertrees and Supermatrices. <i>PLoS ONE</i> , 2013, 8, e62510.	1.1	138
23	Phylogenetically Driven Sequencing of Extremely Halophilic Archaea Reveals Strategies for Static and Dynamic Osmo-response. <i>PLoS Genetics</i> , 2014, 10, e1004784.	1.5	136
24	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	9.0	133
25	Progressive genome-wide introgression in agricultural <i>Campylobacter coli</i> . <i>Molecular Ecology</i> , 2013, 22, 1051-1064.	2.0	128
26	CAMISIM: simulating metagenomes and microbial communities. <i>Microbiome</i> , 2019, 7, 17.	4.9	117
27	Strain- and plasmid-level deconvolution of a synthetic metagenome by sequencing proximity ligation products. <i>PeerJ</i> , 2014, 2, e415.	0.9	111
28	Mauve Assembly Metrics. <i>Bioinformatics</i> , 2011, 27, 2756-2757.	1.8	108
29	Alignathon: a competitive assessment of whole-genome alignment methods. <i>Genome Research</i> , 2014, 24, 2077-2089.	2.4	102
30	A longitudinal study of the diabetic skin and wound microbiome. <i>PeerJ</i> , 2017, 5, e3543.	0.9	93
31	Porcine commensal <i>Escherichia coli</i> : a reservoir for class 1 integrons associated with IS26. <i>Microbial Genomics</i> , 2017, 3, .	1.0	89
32	Near full-length 16S rRNA gene next-generation sequencing revealed <i>Asaia</i> as a common midgut bacterium of wild and domesticated Queensland fruit fly larvae. <i>Microbiome</i> , 2018, 6, 85.	4.9	82
33	bin3C: exploiting Hi-C sequencing data to accurately resolve metagenome-assembled genomes. <i>Genome Biology</i> , 2019, 20, 46.	3.8	66
34	Genome-wide detection and analysis of homologous recombination among sequenced strains of <i>Escherichia coli</i> . <i>Genome Biology</i> , 2006, 7, R44.	13.9	63
35	Visualization of Biomedical Data. <i>Annual Review of Biomedical Data Science</i> , 2018, 1, 275-304.	2.8	63
36	Phylogenetic and molecular analysis of hydrogen-producing green algae. <i>Journal of Experimental Botany</i> , 2009, 60, 1691-1702.	2.4	62

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37	Are Protein Domains Modules of Lateral Genetic Transfer?. <i>PLoS ONE</i> , 2009, 4, e4524.	1.1	60
38	Lateral Transfer of Genes and Gene Fragments in Prokaryotes. <i>Genome Biology and Evolution</i> , 2009, 1, 429-438.	1.1	59
39	A method for high precision sequencing of near full-length 16S rRNA genes on an Illumina MiSeq. <i>PeerJ</i> , 2016, 4, e2492.	0.9	59
40	ASAP: a resource for annotating, curating, comparing, and disseminating genomic data. <i>Nucleic Acids Research</i> , 2006, 34, D41-D45.	6.5	56
41	The rapid <i>in vivo</i> evolution of <i>Pseudomonas aeruginosa</i> in ventilator-associated pneumonia patients leads to attenuated virulence. <i>Open Biology</i> , 2017, 7, 170029.	1.5	50
42	Diversification of a single ancestral gene into a successful toxin superfamily in highly venomous Australian funnel-web spiders. <i>BMC Genomics</i> , 2014, 15, 177.	1.2	49
43	Sequencing of Seven Haloarchaeal Genomes Reveals Patterns of Genomic Flux. <i>PLoS ONE</i> , 2012, 7, e41389.	1.1	42
44	GRIL: genome rearrangement and inversion locator. <i>Bioinformatics</i> , 2004, 20, 122-124.	1.8	41
45	The Common Oceanographer: Crowdsourcing the Collection of Oceanographic Data. <i>PLoS Biology</i> , 2014, 12, e1001947.	2.6	41
46	Swabs to genomes: a comprehensive workflow. <i>PeerJ</i> , 2015, 3, e960.	0.9	37
47	Tutorial: assessing metagenomics software with the CAMI benchmarking toolkit. <i>Nature Protocols</i> , 2021, 16, 1785-1801.	5.5	36
48	Inferring genomic flux in bacteria. <i>Genome Research</i> , 2009, 19, 306-317.	2.4	35
49	Indigenous <i>Vibrio cholerae</i> strains from a non-endemic region are pathogenic. <i>Open Biology</i> , 2013, 3, 120181.	1.5	35
50	Comparative genomic analysis of a multiple antimicrobial resistant enterotoxigenic <i>E. coli</i> O157 lineage from Australian pigs. <i>BMC Genomics</i> , 2015, 16, 165.	1.2	34
51	TraDIS-Xpress: a high-resolution whole-genome assay identifies novel mechanisms of triclosan action and resistance. <i>Genome Research</i> , 2020, 30, 239-249.	2.4	32
52	Bacterial Communities Vary between Sinuses in Chronic Rhinosinusitis Patients. <i>Frontiers in Microbiology</i> , 2015, 6, 1532.	1.5	30
53	Effective Online Bayesian Phylogenetics via Sequential Monte Carlo with Guided Proposals. <i>Systematic Biology</i> , 2018, 67, 490-502.	2.7	29
54	Human milk oligosaccharide profiles and allergic disease up to 18 years. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 1041-1048.	1.5	29

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55	The genome of <i>Clostridium difficile</i> 5.3. <i>Gut Pathogens</i> , 2014, 6, 4.	1.6	27
56	Sim3C: simulation of Hi-C and Meta3C proximity ligation sequencing technologies. <i>GigaScience</i> , 2018, 7, .	3.3	27
57	High contiguity genome sequence of a multidrug-resistant hospital isolate of <i>Enterobacter hormaechei</i> . <i>Gut Pathogens</i> , 2019, 11, 3.	1.6	26
58	Strainberry: automated strain separation in low-complexity metagenomes using long reads. <i>Nature Communications</i> , 2021, 12, 4485.	5.8	25
59	Analysis of <i>Theileria orientalis</i> draft genome sequences reveals potential species-level divergence of the Ikeda, Chitose and Buffeli genotypes. <i>BMC Genomics</i> , 2018, 19, 298.	1.2	24
60	Comparative Genomics of the Genus <i>Porphyromonas</i> Identifies Adaptations for Heme Synthesis within the Prevalent Canine Oral Species <i>Porphyromonas cangingivalis</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 3397-3413.	1.1	23
61	Whole Genome Sequencing Analysis of Porcine Faecal Commensal <i>Escherichia coli</i> Carrying Class 1 Integrons from Sows and Their Offspring. <i>Microorganisms</i> , 2020, 8, 843.	1.6	22
62	Online Bayesian Phylogenetic Inference: Theoretical Foundations via Sequential Monte Carlo. <i>Systematic Biology</i> , 2018, 67, 503-517.	2.7	21
63	Hackflex: low-cost, high-throughput, Illumina Nextera Flex library construction. <i>Microbial Genomics</i> , 2022, 8, .	1.0	20
64	Evaluating probabilistic programming and fast variational Bayesian inference in phylogenetics. <i>PeerJ</i> , 2019, 7, e8272.	0.9	18
65	Local and relaxed clocks: the best of both worlds. <i>PeerJ</i> , 2018, 6, e5140.	0.9	17
66	Efficient Sampling of Parsimonious Inversion Histories with Application to Genome Rearrangement in <i>Yersinia</i> . <i>Genome Biology and Evolution</i> , 2009, 1, 153-164.	1.1	14
67	A Novel Heuristic for Local Multiple Alignment of Interspersed DNA Repeats. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 180-189.	1.9	14
68	Metagenomic Chromosome Conformation Capture (3C): techniques, applications, and challenges. <i>F1000Research</i> , 2015, 4, 1377.	0.8	13
69	Comparative genomic analysis of toxin-negative strains of <i>Clostridium difficile</i> from humans and animals with symptoms of gastrointestinal disease. <i>BMC Microbiology</i> , 2016, 16, 41.	1.3	13
70	Deconvoluting simulated metagenomes: the performance of hard- and soft- clustering algorithms applied to metagenomic chromosome conformation capture (3C). <i>PeerJ</i> , 2016, 4, e2676.	0.9	11
71	Evaluation of ddRADseq for reduced representation metagenome sequencing. <i>PeerJ</i> , 2017, 5, e3837.	0.9	11
72	Draft Genome Sequence of an Actinobacterium, <i>Brachybacterium muris</i> Strain UCD-AY4. <i>Genome Announcements</i> , 2013, 1, e0008613.	0.8	9

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73	Draft Genome Sequences of 26 <i>Porphyromonas</i> Strains Isolated from the Canine Oral Microbiome. <i>Genome Announcements</i> , 2015, 3, .	0.8	9
74	Metagenomic Hi-C of a Healthy Human Fecal Microbiome Transplant Donor. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	9
75	A large-scale metagenomic survey dataset of the post-weaning piglet gut lumen. <i>GigaScience</i> , 2021, 10, .	3.3	9
76	Post-weaning shifts in microbiome composition and metabolism revealed by over 25,000 pig gut metagenome-assembled genomes. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
77	A draft genome of <i>Escherichia coli</i> sequence type 127 strain 2009-46. <i>Gut Pathogens</i> , 2014, 6, 32.	1.6	8
78	Draft Genome Sequence of <i>Curtobacterium flaccumfaciens</i> Strain UCD-AKU (Phylum Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 542 Td (<i>A	0.8	7
79	Genomes from bacteria associated with the canine oral cavity: A test case for automated genome-based taxonomic assignment. <i>PLoS ONE</i> , 2019, 14, e0214354.	1.1	7
80	Identification of a novel lineage of plasmids within phylogenetically diverse subclades of IncHI2-ST1 plasmids. <i>Plasmid</i> , 2019, 102, 56-61.	0.4	6
81	Seevolution: visualizing chromosome evolution. <i>Bioinformatics</i> , 2009, 25, 960-961.	1.8	5
82	Draft Genome Sequence of <i>Microbacterium</i> sp. Strain UCD-TDU (Phylum <i>Actinobacteria</i>). <i>Genome Announcements</i> , 2013, 1, e0012013.	0.8	5
83	Draft Genome Sequence of <i>Kocuria</i> sp. Strain UCD-OTCP (Phylum <i>Actinobacteria</i>). <i>Genome Announcements</i> , 2013, 1, .	0.8	5
84	Draft Genome Sequence of <i>Leucobacter</i> sp. Strain UCD-THU (Phylum <i>Actinobacteria</i>). <i>Genome Announcements</i> , 2013, 1, .	0.8	5
85	Draft Genome Sequence of <i>Dietzia</i> sp. Strain UCD-THP (Phylum <i>Actinobacteria</i>). <i>Genome Announcements</i> , 2013, 1, .	0.8	5
86	Molecular techniques and their limitations shape our view of the holobiont. <i>Zoology</i> , 2019, 137, 125695.	0.6	5
87	qc3C: Reference-free quality control for Hi-C sequencing data. <i>PLoS Computational Biology</i> , 2021, 17, e1008839.	1.5	5
88	Phylogenetic diversity analysis of shotgun metagenomic reads describes gut microbiome development and treatment effects in the post-weaned pig. <i>PLoS ONE</i> , 2022, 17, e0270372.	1.1	5
89	<i>Escherichia coli</i> ST8196 is a novel, locally evolved, and extensively drug resistant pathogenic lineage within the ST131 clonal complex. <i>Emerging Microbes and Infections</i> , 2020, 9, 1780-1792.	3.0	3
90	Hidden Breakpoints in Genome Alignments. <i>Lecture Notes in Computer Science</i> , 2012, , 391-403.	1.0	0