

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	Hackflex: low-cost, high-throughput, Illumina Nextera Flex library construction. <i>Microbial Genomics</i> , 2022, 8, .	1.0	20
2	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	9.0	133
3	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
4	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
5	Tutorial: assessing metagenomics software with the CAMI benchmarking toolkit. <i>Nature Protocols</i> , 2021, 16, 1785-1801.	5.5	36
6	A large-scale metagenomic survey dataset of the post-weaning piglet gut lumen. <i>GigaScience</i> , 2021, 10, .	3.3	9
7	Strainberry: automated strain separation in low-complexity metagenomes using long reads. <i>Nature Communications</i> , 2021, 12, 4485.	5.8	25
8	Post-weaning shifts in microbiome composition and metabolism revealed by over 25â€š000 pig gut metagenome-assembled genomes. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
9	qc3C: Reference-free quality control for Hi-C sequencing data. <i>PLoS Computational Biology</i> , 2021, 17, e1008839.	1.5	5
10	<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
11	Metagenomic Hi-C of a Healthy Human Fecal Microbiome Transplant Donor. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	9
12	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
13	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
14	Molecular techniques and their limitations shape our view of the holobiont. <i>Zoology</i> , 2019, 137, 125695.	0.6	5
15	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
16	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
17	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
18	bin3C: exploiting Hi-C sequencing data to accurately resolve metagenome-assembled genomes. <i>Genome Biology</i> , 2019, 20, 46.	3.8	66

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19	CAMISIM: simulating metagenomes and microbial communities. <i>Microbiome</i> , 2019, 7, 17.	4.9	117
20	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
21	Evaluating probabilistic programming and fast variational Bayesian inference in phylogenetics. <i>PeerJ</i> , 2019, 7, e8272.	0.9	18
22	Effective Online Bayesian Phylogenetics via Sequential Monte Carlo with Guided Proposals. <i>Systematic Biology</i> , 2018, 67, 490-502.	2.7	29
23	Sim3C: simulation of Hi-C and Meta3C proximity ligation sequencing technologies. <i>GigaScience</i> , 2018, 7, .	3.3	27
24	Online Bayesian Phylogenetic Inference: Theoretical Foundations via Sequential Monte Carlo. <i>Systematic Biology</i> , 2018, 67, 503-517.	2.7	21
25	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
26	Visualization of Biomedical Data. <i>Annual Review of Biomedical Data Science</i> , 2018, 1, 275-304.	2.8	63
27	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
28	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
29	Local and relaxed clocks: the best of both worlds. <i>PeerJ</i> , 2018, 6, e5140.	0.9	17
30	Critical Assessment of Metagenome Interpretationâ€”a benchmark of metagenomics software. <i>Nature Methods</i> , 2017, 14, 1063-1071.	9.0	635
31	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
32	DESMAN: a new tool for de novo extraction of strains from metagenomes. <i>Genome Biology</i> , 2017, 18, 181.	3.8	152
33	Porcine commensal <i>Escherichia coli</i> : a reservoir for class 1 integrons associated with IS26. <i>Microbial Genomics</i> , 2017, 3, .	1.0	89
34	A longitudinal study of the diabetic skin and wound microbiome. <i>PeerJ</i> , 2017, 5, e3543.	0.9	93
35	Evaluation of ddRADseq for reduced representation metagenome sequencing. <i>PeerJ</i> , 2017, 5, e3837.	0.9	11
36	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

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37	A method for high precision sequencing of near full-length 16S rRNA genes on an Illumina MiSeq. PeerJ, 2016, 4, e2492.	0.9	59
38	Deconvoluting simulated metagenomes: the performance of hard- and soft- clustering algorithms applied to metagenomic chromosome conformation capture (3C). PeerJ, 2016, 4, e2676.	0.9	11
39	Metagenomic Chromosome Conformation Capture (3C): techniques, applications, and challenges. F1000Research, 2015, 4, 1377.	0.8	13
40	Comparative Genomics of the Genus <i>Porphyromonas</i> Identifies Adaptations for Heme Synthesis within the Prevalent Canine Oral Species <i>Porphyromonas cangingivalis</i> . Genome Biology and Evolution, 2015, 7, 3397-3413.	1.1	23
41	Draft Genome Sequences of 26 <i>Porphyromonas</i> Strains Isolated from the Canine Oral Microbiome. Genome Announcements, 2015, 3, .	0.8	9
42	A5-miseq: an updated pipeline to assemble microbial genomes from Illumina MiSeq data. Bioinformatics, 2015, 31, 587-589.	1.8	973
43	Comparative genomic analysis of a multiple antimicrobial resistant enterotoxigenic <i>E. coli</i> O157 lineage from Australian pigs. BMC Genomics, 2015, 16, 165.	1.2	34
44	Bacterial Communities Vary between Sinuses in Chronic Rhinosinusitis Patients. Frontiers in Microbiology, 2015, 6, 1532.	1.5	30
45	Swabs to genomes: a comprehensive workflow. PeerJ, 2015, 3, e960.	0.9	37
46	Phylogenetically Driven Sequencing of Extremely Halophilic Archaea Reveals Strategies for Static and Dynamic Osmo-response. PLoS Genetics, 2014, 10, e1004784.	1.5	136
47	The Common Oceanographer: Crowdsourcing the Collection of Oceanographic Data. PLoS Biology, 2014, 12, e1001947.	2.6	41
48	Alignathon: a competitive assessment of whole-genome alignment methods. Genome Research, 2014, 24, 2077-2089.	2.4	102
49	A draft genome of <i>Escherichia coli</i> sequence type 127 strain 2009-46. Gut Pathogens, 2014, 6, 32.	1.6	8
50	The genome of <i>Clostridium difficile</i> 5.3. Gut Pathogens, 2014, 6, 4.	1.6	27
51	Diversification of a single ancestral gene into a successful toxin superfamily in highly venomous Australian funnel-web spiders. BMC Genomics, 2014, 15, 177.	1.2	49
52	PhyloSift: phylogenetic analysis of genomes and metagenomes. PeerJ, 2014, 2, e243.	0.9	633
53	Strain- and plasmid-level deconvolution of a synthetic metagenome by sequencing proximity ligation products. PeerJ, 2014, 2, e415.	0.9	111
54	MetAMOS: a modular and open source metagenomic assembly and analysis pipeline. Genome Biology, 2013, 14, R2.	13.9	174

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55	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013, 499, 431-437.	13.7	2,239
56	Indigenous <i>Vibrio cholerae</i> strains from a non-endemic region are pathogenic. <i>Open Biology</i> , 2013, 3, 120181.	1.5	35
57	Draft Genome Sequence of an Actinobacterium, <i>Brachybacterium muris</i> Strain UCD-AY4. <i>Genome Announcements</i> , 2013, 1, e0008613.	0.8	9
58	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
59	Draft Genome Sequence of <i>Kocuria</i> sp. Strain UCD-OTCP (Phylum <i>Actinobacteria</i>). <i>Genome Announcements</i> , 2013, 1, .	0.8	5
60	Draft Genome Sequence of <i>Curtobacterium flaccumfaciens</i> Strain UCD-AKU (Phylum <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 542 Td (<i></i>	0.8	7
61	Progressive genome-wide introgression in agricultural <i>Campylobacter coli</i> . <i>Molecular Ecology</i> , 2013, 22, 1051-1064.	2.0	128
62	Draft Genome Sequence of <i>Leucobacter</i> sp. Strain UCD-THU (Phylum <i>Actinobacteria</i>). <i>Genome Announcements</i> , 2013, 1, .	0.8	5
63	Draft Genome Sequence of <i>Dietzia</i> sp. Strain UCD-THP (Phylum <i>Actinobacteria</i>). <i>Genome Announcements</i> , 2013, 1, .	0.8	5
64	Phylogeny of Bacterial and Archaeal Genomes Using Conserved Genes: Supertrees and Supermatrices. <i>PLoS ONE</i> , 2013, 8, e62510.	1.1	138
65	Patterns of Gene Flow Define Species of Thermophilic Archaea. <i>PLoS Biology</i> , 2012, 10, e1001265.	2.6	214
66	BEAGLE: An Application Programming Interface and High-Performance Computing Library for Statistical Phylogenetics. <i>Systematic Biology</i> , 2012, 61, 170-173.	2.7	555
67	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
68	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
69	An Integrated Pipeline for de Novo Assembly of Microbial Genomes. <i>PLoS ONE</i> , 2012, 7, e42304.	1.1	436
70	Sequencing of Seven Haloarchaeal Genomes Reveals Patterns of Genomic Flux. <i>PLoS ONE</i> , 2012, 7, e41389.	1.1	42
71	Hidden Breakpoints in Genome Alignments. <i>Lecture Notes in Computer Science</i> , 2012, , 391-403.	1.0	0
72	Mauve Assembly Metrics. <i>Bioinformatics</i> , 2011, 27, 2756-2757.	1.8	108

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73	Assemblathon 1: A competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011, 21, 2224-2241.	2.4	443
74	The <i>Amphimedon queenslandica</i> genome and the evolution of animal complexity. <i>Nature</i> , 2010, 466, 720-726.	13.7	917
75	Inference of Homologous Recombination in Bacteria Using Whole-Genome Sequences. <i>Genetics</i> , 2010, 186, 1435-1449.	1.2	155
76	Metagenomic Sequencing of an In Vitro-Simulated Microbial Community. <i>PLoS ONE</i> , 2010, 5, e10209.	1.1	200
77	progressiveMauve: Multiple Genome Alignment with Gene Gain, Loss and Rearrangement. <i>PLoS ONE</i> , 2010, 5, e11147.	1.1	3,652
78	Inferring genomic flux in bacteria. <i>Genome Research</i> , 2009, 19, 306-317.	2.4	35
79	Are Protein Domains Modules of Lateral Genetic Transfer?. <i>PLoS ONE</i> , 2009, 4, e4524.	1.1	60
80	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
81	Reordering contigs of draft genomes using the Mauve Aligner. <i>Bioinformatics</i> , 2009, 25, 2071-2073.	1.8	532
82	Lateral Transfer of Genes and Gene Fragments in Prokaryotes. <i>Genome Biology and Evolution</i> , 2009, 1, 429-438.	1.1	59
83	Seevolution: visualizing chromosome evolution. <i>Bioinformatics</i> , 2009, 25, 960-961.	1.8	5
84	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
85	Phylogenetic and molecular analysis of hydrogen-producing green algae. <i>Journal of Experimental Botany</i> , 2009, 60, 1691-1702.	2.4	62
86	Dynamics of Genome Rearrangement in Bacterial Populations. <i>PLoS Genetics</i> , 2008, 4, e1000128.	1.5	216
87	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
88	ASAP: a resource for annotating, curating, comparing, and disseminating genomic data. <i>Nucleic Acids Research</i> , 2006, 34, D41-D45.	6.5	56
89	GRIL: genome rearrangement and inversion locator. <i>Bioinformatics</i> , 2004, 20, 122-124.	1.8	41
90	ASAP, a systematic annotation package for community analysis of genomes. <i>Nucleic Acids Research</i> , 2003, 31, 147-151.	6.5	152