Aaron E Darling

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/8328940/aaron-e-darling-publications-by-year.pdf
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97 papers	25,117 citations	38 h-index	107 g-index
107 ext. papers	32,148 ext. citations	8.2 avg, IF	6.85 L-index

#	Paper	IF	Citations
97	Critical Assessment of Metagenome Interpretation: the second round of challenges.. *Nature Methods*, **2022**,	21.6	14
96	qc3C: Reference-free quality control for Hi-C sequencing data. *PLoS Computational Biology*, **2021**, 17, e1008839	5	1
95	Tutorial: assessing metagenomics software with the CAMI benchmarking toolkit. *Nature Protocols*, **2021**, 16, 1785-1801	18.8	11
94	A large-scale metagenomic survey dataset of the post-weaning piglet gut lumen. *GigaScience*, **2021**, 10,	7.6	2
93	Strainberry: automated strain separation in low-complexity metagenomes using long reads. *Nature Communications*, **2021**, 12, 4485	17.4	9
92	Human milk oligosaccharide profiles and allergic disease up to 18 years. *Journal of Allergy and Clinical Immunology*, **2021**, 147, 1041-1048	11.5	14
91	Post-weaning shifts in microbiome composition and metabolism revealed by over 25 000 pig gut metagenome-assembled genomes. *Microbial Genomics*, **2021**, 7,	4.4	1
90	Metagenomic Hi-C of a Healthy Human Fecal Microbiome Transplant Donor. *Microbiology Resource Announcements*, **2020**, 9,	1.3	4
89	Whole Genome Sequencing Analysis of Porcine Faecal Commensal Carrying Class 1 Integrons from Sows and Their Offspring. *Microorganisms*, **2020**, 8,	4.9	11
88	TraDIS-Xpress: a high-resolution whole-genome assay identifies novel mechanisms of triclosan action and resistance. *Genome Research*, **2020**, 30, 239-249	9.7	15
87	ST8196 is a novel, locally evolved, and extensively drug resistant pathogenic lineage within the ST131 clonal complex. *Emerging Microbes and Infections*, **2020**, 9, 1780-1792	18.9	2
86	Genomes from bacteria associated with the canine oral cavity: A test case for automated genome-based taxonomic assignment. *PLoS ONE*, **2019**, 14, e0214354	3.7	4
85	BEAGLE 3: Improved Performance, Scaling, and Usability for a High-Performance Computing Library for Statistical Phylogenetics. *Systematic Biology*, **2019**, 68, 1052-1061	8.4	71
84	Identification of a novel lineage of plasmids within phylogenetically diverse subclades of IncHI2-ST1 plasmids. *Plasmid*, **2019**, 102, 56-61	3.3	4
83	bin3C: exploiting Hi-C sequencing data to accurately resolve metagenome-assembled genomes. *Genome Biology*, **2019**, 20, 46	18.3	33
82	CAMISIM: simulating metagenomes and microbial communities. *Microbiome*, **2019**, 7, 17	16.6	57
81	High contiguity genome sequence of a multidrug-resistant hospital isolate of. *Gut Pathogens*, **2019**, 11, 3	5.4	16

80	Molecular techniques and their limitations shape our view of the holobiont. *Zoology*, **2019**, 137, 125695	1.7	4
79	Evaluating probabilistic programming and fast variational Bayesian inference in phylogenetics. *PeerJ*, **2019**, 7, e8272	3.1	7
78	Effective Online Bayesian Phylogenetics via Sequential Monte Carlo with Guided Proposals. *Systematic Biology*, **2018**, 67, 490-502	8.4	14
77	Sim3C: simulation of Hi-C and Meta3C proximity ligation sequencing technologies. *GigaScience*, **2018**, 7,	7.6	14
76	Online Bayesian Phylogenetic Inference: Theoretical Foundations via Sequential Monte Carlo. *Systematic Biology*, **2018**, 67, 503-517	8.4	11
75	Analysis of Theileria orientalis draft genome sequences reveals potential species-level divergence of the Ikeda, Chitose and Buffeli genotypes. *BMC Genomics*, **2018**, 19, 298	4.5	14
74	Nitrogen fixation in a landrace of maize is supported by a mucilage-associated diazotrophic microbiota. *PLoS Biology*, **2018**, 16, e2006352	9.7	130
73	Near full-length 16S rRNA gene next-generation sequencing revealed Asaia as a common midgut bacterium of wild and domesticated Queensland fruit fly larvae. *Microbiome*, **2018**, 6, 85	16.6	39
72	Local and relaxed clocks: the best of both worlds. *PeerJ*, **2018**, 6, e5140	3.1	8
71	Visualization of Biomedical Data. *Annual Review of Biomedical Data Science*, **2018**, 1, 275-304	5.6	34
70	Critical Assessment of Metagenome Interpretation-a benchmark of metagenomics software. *Nature Methods*, **2017**, 14, 1063-1071	21.6	412
69	DESMAN: a new tool for de novo extraction of strains from metagenomes. *Genome Biology*, **2017**, 18, 181	18.3	103
68	The rapid evolution of in ventilator-associated pneumonia patients leads to attenuated virulence. *Open Biology*, **2017**, 7,	7	28
67	A longitudinal study of the diabetic skin and wound microbiome. *PeerJ*, **2017**, 5, e3543	3.1	58
66	Evaluation of ddRADseq for reduced representation metagenome sequencing. *PeerJ*, **2017**, 5, e3837	3.1	8
65	Porcine commensal Escherichia coli: a reservoir for class 1 integrons associated with IS26. *Microbial Genomics*, **2017**, 3,	4.4	43
64	Comparative genomic analysis of toxin-negative strains of Clostridium difficile from humans and animals with symptoms of gastrointestinal disease. *BMC Microbiology*, **2016**, 16, 41	4.5	9
63	A method for high precision sequencing of near full-length 16S rRNA genes on an Illumina MiSeq. *PeerJ*, **2016**, 4, e2492	3.1	39

62	Deconvoluting simulated metagenomes: the performance of hard- and soft- clustering algorithms applied to metagenomic chromosome conformation capture (3C). *PeerJ*, **2016**, 4, e2676	3.1	10
61	Comparative genomic analysis of a multiple antimicrobial resistant enterotoxigenic E. coli O157 lineage from Australian pigs. *BMC Genomics*, **2015**, 16, 165	4.5	21
60	Metagenomic Chromosome Conformation Capture (3C): techniques, applications, and challenges. *F1000Research*, **2015**, 4, 1377	3.6	11
59	Comparative Genomics of the Genus Porphyromonas Identifies Adaptations for Heme Synthesis within the Prevalent Canine Oral Species Porphyromonas cangingivalis. *Genome Biology and Evolution*, **2015**, 7, 3397-413	3.9	15
58	Draft genome sequences of 26 porphyromonas strains isolated from the canine oral microbiome. *Genome Announcements*, **2015**, 3,		8
57	A5-miseq: an updated pipeline to assemble microbial genomes from Illumina MiSeq data. *Bioinformatics*, **2015**, 31, 587-9	7.2	640
56	Swabs to genomes: a comprehensive workflow. *PeerJ*, **2015**, 3, e960	3.1	25
55	Bacterial Communities Vary between Sinuses in Chronic Rhinosinusitis Patients. *Frontiers in Microbiology*, **2015**, 6, 1532	5.7	16
54	Diversification of a single ancestral gene into a successful toxin superfamily in highly venomous Australian funnel-web spiders. *BMC Genomics*, **2014**, 15, 177	4.5	39
53	Phylogenetically driven sequencing of extremely halophilic archaea reveals strategies for static and dynamic osmo-response. *PLoS Genetics*, **2014**, 10, e1004784	6	95
52	The common oceanographer: crowdsourcing the collection of oceanographic data. *PLoS Biology*, **2014**, 12, e1001947	9.7	27
51	Alignathon: a competitive assessment of whole-genome alignment methods. *Genome Research*, **2014**, 24, 2077-89	9.7	74
50	A draft genome of Escherichia coli sequence type 127 strain 2009-46. *Gut Pathogens*, **2014**, 6, 32	5.4	7
49	The genome of Clostridium difficile 5.3. *Gut Pathogens*, **2014**, 6, 4	5.4	13
48	PhyloSift: phylogenetic analysis of genomes and metagenomes. *PeerJ*, **2014**, 2, e243	3.1	431
47	Strain- and plasmid-level deconvolution of a synthetic metagenome by sequencing proximity ligation products. *PeerJ*, **2014**, 2, e415	3.1	79
46	MetAMOS: a modular and open source metagenomic assembly and analysis pipeline. *Genome Biology*, **2013**, 14, R2	18.3	150
45	Insights into the phylogeny and coding potential of microbial dark matter. *Nature*, **2013**, 499, 431-7	50.4	1484

44	Indigenous Vibrio cholerae strains from a non-endemic region are pathogenic. *Open Biology*, **2013**, 3, 120181	7	23
43	Draft genome sequence of an Actinobacterium, Brachybacterium muris strain UCD-AY4. *Genome Announcements*, **2013**, 1, e0008613		9
42	Draft Genome Sequence of Microbacterium sp. Strain UCD-TDU (Phylum Actinobacteria). *Genome Announcements*, **2013**, 1, e0012013		5
41	Draft Genome Sequence of Kocuria sp. Strain UCD-OTCP (Phylum Actinobacteria). *Genome Announcements*, **2013**, 1,		5
40	Draft Genome Sequence of Curtobacterium flaccumfaciens Strain UCD-AKU (Phylum Actinobacteria). *Genome Announcements*, **2013**, 1,		6
39	Progressive genome-wide introgression in agricultural Campylobacter coli. *Molecular Ecology*, **2013**, 22, 1051-64	5.7	98
38	Draft Genome Sequence of Leucobacter sp. Strain UCD-THU (Phylum Actinobacteria). *Genome Announcements*, **2013**, 1,		5
37	Draft Genome Sequence of Dietzia sp. Strain UCD-THP (Phylum Actinobacteria). *Genome Announcements*, **2013**, 1,		5
36	Phylogeny of bacterial and archaeal genomes using conserved genes: supertrees and supermatrices. *PLoS ONE*, **2013**, 8, e62510	3.7	102
35	BEAGLE: an application programming interface and high-performance computing library for statistical phylogenetics. *Systematic Biology*, **2012**, 61, 170-3	8.4	374
34	MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic Biology*, **2012**, 61, 539-42	8.4	14368
33	Impact of homologous and non-homologous recombination in the genomic evolution of Escherichia coli. *BMC Genomics*, **2012**, 13, 256	4.5	95
32	An integrated pipeline for de novo assembly of microbial genomes. *PLoS ONE*, **2012**, 7, e42304	3.7	330
31	Patterns of gene flow define species of thermophilic Archaea. *PLoS Biology*, **2012**, 10, e1001265	9.7	152
30	Sequencing of seven haloarchaeal genomes reveals patterns of genomic flux. *PLoS ONE*, **2012**, 7, e41389	3.7	37
29	Hidden Breakpoints in Genome Alignments. *Lecture Notes in Computer Science*, **2012**, 391-403	0.9	
28	Mauve assembly metrics. *Bioinformatics*, **2011**, 27, 2756-7	7.2	71
27	Assemblathon 1: a competitive assessment of de novo short read assembly methods. *Genome Research*, **2011**, 21, 2224-41	9.7	364

26	The Amphimedon queenslandica genome and the evolution of animal complexity. *Nature*, **2010**, 466, 720-6	50.4	782
25	Inference of homologous recombination in bacteria using whole-genome sequences. *Genetics*, **2010** , 186, 1435-49	4	118
24	Metagenomic sequencing of an in vitro-simulated microbial community. *PLoS ONE*, **2010**, 5, e10209	3.7	163
23	progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. *PLoS ONE*, **2010**, 5, e11147	3.7	2526
22	Are protein domains modules of lateral genetic transfer?. *PLoS ONE*, **2009**, 4, e4524	3.7	53
21	Efficient sampling of parsimonious inversion histories with application to genome rearrangement in Yersinia. *Genome Biology and Evolution*, **2009**, 1, 153-64	3.9	13
20	Reordering contigs of draft genomes using the Mauve aligner. *Bioinformatics*, **2009**, 25, 2071-3	7.2	389
19	Lateral transfer of genes and gene fragments in prokaryotes. *Genome Biology and Evolution*, **2009**, 1, 429-38	3.9	54
18	Seevolution: visualizing chromosome evolution. *Bioinformatics*, **2009**, 25, 960-1	7.2	5
17	A novel heuristic for local multiple alignment of interspersed DNA repeats. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2009**, 6, 180-9	3	13
16	Phylogenetic and molecular analysis of hydrogen-producing green algae. *Journal of Experimental Botany*, **2009**, 60, 1691-702	7	53
15	Inferring genomic flux in bacteria. *Genome Research*, **2009**, 19, 306-17	9.7	26
14	Dynamics of genome rearrangement in bacterial populations. *PLoS Genetics*, **2008**, 4, e1000128	6	156
13	ASAP: a resource for annotating, curating, comparing, and disseminating genomic data. *Nucleic Acids Research*, **2006**, 34, D41-5	20.1	54
12	Genome-wide detection and analysis of homologous recombination among sequenced strains of Escherichia coli. *Genome Biology*, **2006**, 7, R44	18.3	60
11	GRIL: genome rearrangement and inversion locator. *Bioinformatics*, **2004**, 20, 122-4	7.2	38
10	ASAP, a systematic annotation package for community analysis of genomes. *Nucleic Acids Research*, **2003**, 31, 147-51	20.1	132
9	Critical Assessment of Metagenome Interpretation □ benchmark of computational metagenomics software		17

List of Publications

8	Effective online Bayesian phylogenetics via sequential Monte Carlo with guided proposals	1
7	Tutorial: Assessing metagenomics software with the CAMI benchmarking toolkit	1
6	Metagenomics Strain Resolution on Assembly Graphs	6
5	CAMISIM: Simulating metagenomes and microbial communities	3
4	bin3C : Exploiting Hi-C sequencing data to accurately resolve metagenome-assembled genomes (MAGs)	1
3	Trial by phylogenetics - Evaluating the Multi-Species Coalescent for phylogenetic inference on taxa with high levels of paralogy (Gonyaulacales, Dinophyceae)	3
2	Hackflex: low cost Illumina Nextera Flex sequencing library construction	9
1	Automated strain separation in low-complexity metagenomes using long reads	2