

Adam M Phillippy

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8609623/publications.pdf>

Version: 2024-02-01

112
papers

46,272
citations

15504

65
h-index

22832

112
g-index

174
all docs

174
docs citations

174
times ranked

45509
citing authors

#	ARTICLE	IF	CITATIONS
1	Balancing openness with Indigenous data sovereignty: An opportunity to leave no one behind in the journey to sequence all of life. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	33
2	Standards recommendations for the Earth BioGenome Project. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	33
3	StainedGlass: interactive visualization of massive tandem repeat structures with identity heatmaps. Bioinformatics, 2022, 38, 2049-2051.	4.1	42
4	Merfin: improved variant filtering, assembly evaluation and polishing via k-mer validation. Nature Methods, 2022, 19, 696-704.	19.0	30
5	Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies. Nature Methods, 2022, 19, 687-695.	19.0	42
6	Epigenetic patterns in a complete human genome. Science, 2022, 376, eabj5089.	12.6	118
7	Complete genomic and epigenetic maps of human centromeres. Science, 2022, 376, eabl4178.	12.6	204
8	From telomere to telomere: The transcriptional and epigenetic state of human repeat elements. Science, 2022, 376, eabk3112.	12.6	146
9	A complete reference genome improves analysis of human genetic variation. Science, 2022, 376, eabl3533.	12.6	144
10	The complete sequence of a human genome. Science, 2022, 376, 44-53.	12.6	1,222
11	Segmental duplications and their variation in a complete human genome. Science, 2022, 376, eabj6965.	12.6	130
12	Long-read mapping to repetitive reference sequences using Winnowmap2. Nature Methods, 2022, 19, 705-710.	19.0	80
13	The Human Pangenome Project: a global resource to map genomic diversity. Nature, 2022, 604, 437-446.	27.8	192
14	Reference genome and demographic history of the most endangered marine mammal, the vaquita. Molecular Ecology Resources, 2021, 21, 1008-1020.	4.8	54
15	The genomic structure of a human chromosome 22 nucleolar organizer region determined by TAR cloning. Scientific Reports, 2021, 11, 2997.	3.3	13
16	The structure, function and evolution of a complete human chromosome 8. Nature, 2021, 593, 101-107.	27.8	221
17	Evolutionary and biomedical insights from a marmoset diploid genome assembly. Nature, 2021, 594, 227-233.	27.8	42
18	Extended haplotype-phasing of long-read de novo genome assemblies using Hi-C. Nature Communications, 2021, 12, 1935.	12.8	64

#	ARTICLE	IF	CITATIONS
19	Complete vertebrate mitogenomes reveal widespread repeats and gene duplications. <i>Genome Biology</i> , 2021, 22, 120.	8.8	69
20	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	27.8	1,139
21	The whale shark genome reveals patterns of vertebrate gene family evolution. <i>ELife</i> , 2021, 10, .	6.0	19
22	Population genomics of the critically endangered kakapo. <i>Cell Genomics</i> , 2021, 1, 100002.	6.5	106
23	Platypus and echidna genomes reveal mammalian biology and evolution. <i>Nature</i> , 2021, 592, 756-762.	27.8	85
24	Strains used in whole organism <i>Plasmodium falciparum</i> vaccine trials differ in genome structure, sequence, and immunogenic potential. <i>Genome Medicine</i> , 2020, 12, 6.	8.2	61
25	Evolutionary superscaffolding and chromosome anchoring to improve <i>Anopheles</i> genome assemblies. <i>BMC Biology</i> , 2020, 18, 1.	3.8	177
26	Weighted minimizer sampling improves long read mapping. <i>Bioinformatics</i> , 2020, 36, i111-i118.	4.1	116
27	Genomic analyses of a livestock pest, the New World screwworm, find potential targets for genetic control programs. <i>Communications Biology</i> , 2020, 3, 424.	4.4	26
28	Strategic vision for improving human health at The Forefront of Genomics. <i>Nature</i> , 2020, 586, 683-692.	27.8	192
29	Telomere-to-telomere assembly of a complete human X chromosome. <i>Nature</i> , 2020, 585, 79-84.	27.8	549
30	Improved reference genome of the arboviral vector <i>Aedes albopictus</i> . <i>Genome Biology</i> , 2020, 21, 215.	8.8	65
31	Mercury: reference-free quality, completeness, and phasing assessment for genome assemblies. <i>Genome Biology</i> , 2020, 21, 245.	8.8	975
32	HiCanu: accurate assembly of segmental duplications, satellites, and allelic variants from high-fidelity long reads. <i>Genome Research</i> , 2020, 30, 1291-1305.	5.5	440
33	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. <i>Nature Biotechnology</i> , 2020, 38, 1044-1053.	17.5	344
34	Effect of sequence depth and length in long-read assembly of the maize inbred NC358. <i>Nature Communications</i> , 2020, 11, 2288.	12.8	39
35	A robust benchmark for detection of germline large deletions and insertions. <i>Nature Biotechnology</i> , 2020, 38, 1347-1355.	17.5	233
36	An improved pig reference genome sequence to enable pig genetics and genomics research. <i>GigaScience</i> , 2020, 9, .	6.4	187

#	ARTICLE	IF	CITATIONS
37	Haplotype-resolved genomes provide insights into structural variation and gene content in Angus and Brahman cattle. <i>Nature Communications</i> , 2020, 11, 2071.	12.8	84
38	Continuous chromosome-scale haplotypes assembled from a single interspecies F1 hybrid of yak and cattle. <i>GigaScience</i> , 2020, 9, .	6.4	46
39	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020, 9, .	6.4	380
40	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. <i>Nature Biotechnology</i> , 2019, 37, 1155-1162.	17.5	1,010
41	Assignment of virus and antimicrobial resistance genes to microbial hosts in a complex microbial community by combined long-read assembly and proximity ligation. <i>Genome Biology</i> , 2019, 20, 153.	8.8	66
42	Strain-level metagenomic assignment and compositional estimation for long reads with MetaMaps. <i>Nature Communications</i> , 2019, 10, 3066.	12.8	98
43	De novo assembly of the goldfish (<i>Carassius auratus</i>) genome and the evolution of genes after whole-genome duplication. <i>Science Advances</i> , 2019, 5, eaav0547.	10.3	182
44	Mash Screen: high-throughput sequence containment estimation for genome discovery. <i>Genome Biology</i> , 2019, 20, 232.	8.8	173
45	Integrating Hi-C links with assembly graphs for chromosome-scale assembly. <i>PLoS Computational Biology</i> , 2019, 15, e1007273.	3.2	509
46	Reply to “Errors in long-read assemblies can critically affect protein prediction”. <i>Nature Biotechnology</i> , 2019, 37, 127-128.	17.5	29
47	A chromosome-scale assembly of the major African malaria vector <i>Anopheles funestus</i> . <i>GigaScience</i> , 2019, 8, .	6.4	56
48	HLA*LA”HLA typing from linearly projected graph alignments. <i>Bioinformatics</i> , 2019, 35, 4394-4396.	4.1	88
49	New insights into mammalian sex chromosome structure and evolution using high-quality sequences from bovine X and Y chromosomes. <i>BMC Genomics</i> , 2019, 20, 1000.	2.8	21
50	Nanopore sequencing and assembly of a human genome with ultra-long reads. <i>Nature Biotechnology</i> , 2018, 36, 338-345.	17.5	1,443
51	Analysis of the <i>Aedes albopictus</i> C6/36 genome provides insight into cell line utility for viral propagation. <i>GigaScience</i> , 2018, 7, 1-13.	6.4	51
52	A Fast Approximate Algorithm for Mapping Long Reads to Large Reference Databases. <i>Journal of Computational Biology</i> , 2018, 25, 766-779.	1.6	41
53	Improved reference genome of <i>Aedes aegypti</i> informs arbovirus vector control. <i>Nature</i> , 2018, 563, 501-507.	27.8	426
54	High throughput ANI analysis of 90K prokaryotic genomes reveals clear species boundaries. <i>Nature Communications</i> , 2018, 9, 5114.	12.8	2,816

#	ARTICLE	IF	CITATIONS
55	A fast adaptive algorithm for computing whole-genome homology maps. <i>Bioinformatics</i> , 2018, 34, i748-i756.	4.1	110
56	RefSeq database growth influences the accuracy of k-mer-based lowest common ancestor species identification. <i>Genome Biology</i> , 2018, 19, 165.	8.8	111
57	De novo assembly of haplotype-resolved genomes with trio binning. <i>Nature Biotechnology</i> , 2018, 36, 1174-1182.	17.5	352
58	Variation in human chromosome 21 ribosomal RNA genes characterized by TAR cloning and long-read sequencing. <i>Nucleic Acids Research</i> , 2018, 46, 6712-6725.	14.5	61
59	MUMmer4: A fast and versatile genome alignment system. <i>PLoS Computational Biology</i> , 2018, 14, e1005944.	3.2	1,412
60	Single-molecule sequencing and chromatin conformation capture enable de novo reference assembly of the domestic goat genome. <i>Nature Genetics</i> , 2017, 49, 643-650.	21.4	600
61	The evolution of the natural killer complex; a comparison between mammals using new high-quality genome assemblies and targeted annotation. <i>Immunogenetics</i> , 2017, 69, 255-269.	2.4	40
62	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. <i>Genome Research</i> , 2017, 27, 849-864.	5.5	728
63	New advances in sequence assembly. <i>Genome Research</i> , 2017, 27, xi-xiii.	5.5	63
64	A Fast Approximate Algorithm for Mapping Long Reads to Large Reference Databases. <i>Lecture Notes in Computer Science</i> , 2017, , 66-81.	1.3	36
65	Canu: scalable and accurate long-read assembly via adaptive k -mer weighting and repeat separation. <i>Genome Research</i> , 2017, 27, 722-736.	5.5	5,620
66	Draft Genome Sequences from a Novel Clade of <i>Bacillus cereus</i> <i>Sensu Lato</i> Strains, Isolated from the International Space Station. <i>Genome Announcements</i> , 2017, 5, .	0.8	14
67	Mash: fast genome and metagenome distance estimation using MinHash. <i>Genome Biology</i> , 2016, 17, 132.	8.8	2,099
68	Radical remodeling of the Y chromosome in a recent radiation of malaria mosquitoes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2114-23.	7.1	92
69	The channel catfish genome sequence provides insights into the evolution of scale formation in teleosts. <i>Nature Communications</i> , 2016, 7, 11757.	12.8	231
70	Identification and Genomic Analysis of a Novel Group C Orthobunyavirus Isolated from a Mosquito Captured near Iquitos, Peru. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004440.	3.0	9
71	Assembling large genomes with single-molecule sequencing and locality-sensitive hashing. <i>Nature Biotechnology</i> , 2015, 33, 623-630.	17.5	877
72	One chromosome, one contig: complete microbial genomes from long-read sequencing and assembly. <i>Current Opinion in Microbiology</i> , 2015, 23, 110-120.	5.1	413

#	ARTICLE	IF	CITATIONS
73	Long-read, whole-genome shotgun sequence data for five model organisms. Scientific Data, 2014, 1, 140045.	5.3	138
74	Complete Genome Sequence of the Quality Control Strain <i>Staphylococcus aureus</i> subsp. <i>aureus</i> ATCC 25923. Genome Announcements, 2014, 2, .	0.8	53
75	The Harvest suite for rapid core-genome alignment and visualization of thousands of intraspecific microbial genomes. Genome Biology, 2014, 15, 524.	8.8	1,428
76	High-coverage sequencing and annotated assemblies of the budgerigar genome. GigaScience, 2014, 3, 11.	6.4	75
77	Automated ensemble assembly and validation of microbial genomes. BMC Bioinformatics, 2014, 15, 126.	2.6	60
78	Complete Closed Genome Sequences of Three <i>Bibersteinia trehalosi</i> Nasopharyngeal Isolates from Cattle with Shipping Fever. Genome Announcements, 2014, 2, .	0.8	9
79	Complete Closed Genome Sequences of Four <i>Mannheimia varigena</i> Isolates from Cattle with Shipping Fever. Genome Announcements, 2014, 2, .	0.8	6
80	MetAMOS: a modular and open source metagenomic assembly and analysis pipeline. Genome Biology, 2013, 14, R2.	9.6	174
81	Hawkeye and AMOS: visualizing and assessing the quality of genome assemblies. Briefings in Bioinformatics, 2013, 14, 213-224.	6.5	54
82	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. GigaScience, 2013, 2, 10.	6.4	582
83	Genome Sequence of the Attenuated Carbosap Vaccine Strain of <i>Bacillus anthracis</i> . Genome Announcements, 2013, 1, .	0.8	4
84	Complete Closed Genome Sequences of <i>Mannheimia haemolytica</i> Serotypes A1 and A6, Isolated from Cattle. Genome Announcements, 2013, 1, .	0.8	19
85	Reducing assembly complexity of microbial genomes with single-molecule sequencing. Genome Biology, 2013, 14, R101.	9.6	378
86	Krona: Interactive Metagenomic Visualization in a Web Browser. , 2013, , 1-8.		1
87	Irreconcilable differences: divorcing geographic mutation and recombination rates within a global MRSA clone. Genome Biology, 2012, 13, 181.	9.6	0
88	The rise of a digital immune system. GigaScience, 2012, 1, 4.	6.4	29
89	Molecular Epidemiologic Investigation of an Anthrax Outbreak among Heroin Users, Europe. Emerging Infectious Diseases, 2012, 18, 1307-1313.	4.3	77
90	GAGE: A critical evaluation of genome assemblies and assembly algorithms. Genome Research, 2012, 22, 557-567.	5.5	597

#	ARTICLE	IF	CITATIONS
91	Hybrid error correction and de novo assembly of single-molecule sequencing reads. <i>Nature Biotechnology</i> , 2012, 30, 693-700.	17.5	946
92	Two New Complete Genome Sequences Offer Insight into Host and Tissue Specificity of Plant Pathogenic <i>Xanthomonas</i> spp. <i>Journal of Bacteriology</i> , 2011, 193, 5450-5464.	2.2	189
93	Interactive metagenomic visualization in a Web browser. <i>BMC Bioinformatics</i> , 2011, 12, 385.	2.6	1,617
94	Genomic comparison of multi-drug resistant invasive and colonizing <i>Acinetobacter baumannii</i> isolated from diverse human body sites reveals genomic plasticity. <i>BMC Genomics</i> , 2011, 12, 291.	2.8	80
95	Assemblathon 1: A competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011, 21, 2224-2241.	5.5	443
96	Complex microbiome underlying secondary and primary metabolism in the tunicate- <i>Prochloron</i> symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E1423-32.	7.1	146
97	<i>Bacillus anthracis</i> comparative genome analysis in support of the Amerithrax investigation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5027-5032.	7.1	152
98	Probing the pan-genome of <i>Listeria monocytogenes</i> : new insights into intraspecific niche expansion and genomic diversification. <i>BMC Genomics</i> , 2010, 11, 500.	2.8	74
99	Integrated Microbial Survey Analysis of Prokaryotic Communities for the PhyloChip Microarray. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5636-5638.	3.1	24
100	Transcriptomic Responses of <i>Salmonella enterica</i> Serovars Enteritidis and Typhimurium to Chlorine-Based Oxidative Stress. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5013-5024.	3.1	82
101	Insignia: a DNA signature search web server for diagnostic assay development. <i>Nucleic Acids Research</i> , 2009, 37, W229-W234.	14.5	37
102	Efficient oligonucleotide probe selection for pan-genomic tiling arrays. <i>BMC Bioinformatics</i> , 2009, 10, 293.	2.6	25
103	Genome sequence and rapid evolution of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A. <i>BMC Genomics</i> , 2008, 9, 204.	2.8	327
104	Genome assembly forensics: finding the elusive mis-assembly. <i>Genome Biology</i> , 2008, 9, R55.	9.6	248
105	Comprehensive DNA Signature Discovery and Validation. <i>PLoS Computational Biology</i> , 2007, 3, e98.	3.2	63
106	Hawkeye: an interactive visual analytics tool for genome assemblies. <i>Genome Biology</i> , 2007, 8, R34.	9.6	66
107	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	27.8	1,886
108	Genome Sequence of the PCE-Dechlorinating Bacterium <i>Dehalococcoides ethenogenes</i> . <i>Science</i> , 2005, 307, 105-108.	12.6	402

#	ARTICLE	IF	CITATIONS
109	Comparative genome assembly. Briefings in Bioinformatics, 2004, 5, 237-248.	6.5	193
110	Versatile and open software for comparing large genomes. Genome Biology, 2004, 5, R12.	9.6	4,989
111	Using MUMmer to Identify Similar Regions in Large Sequence Sets. Current Protocols in Bioinformatics, 2003, 00, Unit 10.3.	25.8	505
112	Fast algorithms for large-scale genome alignment and comparison. Nucleic Acids Research, 2002, 30, 2478-2483.	14.5	931