

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	Canu: scalable and accurate long-read assembly via adaptive <i>k</i> -mer weighting and repeat separation. <i>Genome Research</i> , 2017, 27, 722-736.	5.5	5,620
2	Versatile and open software for comparing large genomes. <i>Genome Biology</i> , 2004, 5, R12.	9.6	4,989
3	High throughput ANI analysis of 90K prokaryotic genomes reveals clear species boundaries. <i>Nature Communications</i> , 2018, 9, 5114.	12.8	2,816
4	Mash: fast genome and metagenome distance estimation using MinHash. <i>Genome Biology</i> , 2016, 17, 132.	8.8	2,099
5	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	27.8	1,886
6	Interactive metagenomic visualization in a Web browser. <i>BMC Bioinformatics</i> , 2011, 12, 385.	2.6	1,617
7	Nanopore sequencing and assembly of a human genome with ultra-long reads. <i>Nature Biotechnology</i> , 2018, 36, 338-345.	17.5	1,443
8	The Harvest suite for rapid core-genome alignment and visualization of thousands of intraspecific microbial genomes. <i>Genome Biology</i> , 2014, 15, 524.	8.8	1,428
9	MUMmer4: A fast and versatile genome alignment system. <i>PLoS Computational Biology</i> , 2018, 14, e1005944.	3.2	1,412
10	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	12.6	1,222
11	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	27.8	1,139
12	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
13	Merqury: reference-free quality, completeness, and phasing assessment for genome assemblies. <i>Genome Biology</i> , 2020, 21, 245.	8.8	975
14	Hybrid error correction and de novo assembly of single-molecule sequencing reads. <i>Nature Biotechnology</i> , 2012, 30, 693-700.	17.5	946
15	Fast algorithms for large-scale genome alignment and comparison. <i>Nucleic Acids Research</i> , 2002, 30, 2478-2483.	14.5	931
16	Assembling large genomes with single-molecule sequencing and locality-sensitive hashing. <i>Nature Biotechnology</i> , 2015, 33, 623-630.	17.5	877
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	GAGE: A critical evaluation of genome assemblies and assembly algorithms. <i>Genome Research</i> , 2012, 22, 557-567.	5.5	597
20	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013, 2, 10.	6.4	582
21	Telomere-to-telomere assembly of a complete human X chromosome. <i>Nature</i> , 2020, 585, 79-84.	27.8	549
22	Integrating Hi-C links with assembly graphs for chromosome-scale assembly. <i>PLoS Computational Biology</i> , 2019, 15, e1007273.	3.2	509
23	Using MUMmer to Identify Similar Regions in Large Sequence Sets. <i>Current Protocols in Bioinformatics</i> , 2003, 00, Unit 10.3.	25.8	505
24	Assemblathon 1: A competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011, 21, 2224-2241.	5.5	443
25	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
26	Improved reference genome of <i>Aedes aegypti</i> informs arbovirus vector control. <i>Nature</i> , 2018, 563, 501-507.	27.8	426
27	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
28	Genome Sequence of the PCE-Dechlorinating Bacterium <i>Dehalococcoides ethenogenes</i> . <i>Science</i> , 2005, 307, 105-108.	12.6	402
29	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020, 9, .	6.4	380
30	Reducing assembly complexity of microbial genomes with single-molecule sequencing. <i>Genome Biology</i> , 2013, 14, R101.	9.6	378
31	De novo assembly of haplotype-resolved genomes with trio binning. <i>Nature Biotechnology</i> , 2018, 36, 1174-1182.	17.5	352
32	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
33	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
34	Genome assembly forensics: finding the elusive mis-assembly. <i>Genome Biology</i> , 2008, 9, R55.	9.6	248
35	A robust benchmark for detection of germline large deletions and insertions. <i>Nature Biotechnology</i> , 2020, 38, 1347-1355.	17.5	233
36	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

#	ARTICLE	IF	CITATIONS
37	The structure, function and evolution of a complete human chromosome 8. <i>Nature</i> , 2021, 593, 101-107.	27.8	221
38	Complete genomic and epigenetic maps of human centromeres. <i>Science</i> , 2022, 376, eabl4178.	12.6	204
39	Comparative genome assembly. <i>Briefings in Bioinformatics</i> , 2004, 5, 237-248.	6.5	193
40	Strategic vision for improving human health at The Forefront of Genomics. <i>Nature</i> , 2020, 586, 683-692.	27.8	192
41	The Human Pangenome Project: a global resource to map genomic diversity. <i>Nature</i> , 2022, 604, 437-446.	27.8	192
42	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
43	An improved pig reference genome sequence to enable pig genetics and genomics research. <i>GigaScience</i> , 2020, 9, .	6.4	187
44	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
45	Evolutionary superscaffolding and chromosome anchoring to improve <i>Anopheles</i> genome assemblies. <i>BMC Biology</i> , 2020, 18, 1.	3.8	177
46	MetAMOS: a modular and open source metagenomic assembly and analysis pipeline. <i>Genome Biology</i> , 2013, 14, R2.	9.6	174
47	Mash Screen: high-throughput sequence containment estimation for genome discovery. <i>Genome Biology</i> , 2019, 20, 232.	8.8	173
48	<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
49	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
50	From telomere to telomere: The transcriptional and epigenetic state of human repeat elements. <i>Science</i> , 2022, 376, eabk3112.	12.6	146
51	A complete reference genome improves analysis of human genetic variation. <i>Science</i> , 2022, 376, eabl3533.	12.6	144
52	Long-read, whole-genome shotgun sequence data for five model organisms. <i>Scientific Data</i> , 2014, 1, 140045.	5.3	138
53	Segmental duplications and their variation in a complete human genome. <i>Science</i> , 2022, 376, eabj6965.	12.6	130
54	Epigenetic patterns in a complete human genome. <i>Science</i> , 2022, 376, eabj5089.	12.6	118

#	ARTICLE	IF	CITATIONS
55	Weighted minimizer sampling improves long read mapping. <i>Bioinformatics</i> , 2020, 36, i111-i118.	4.1	116
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	A fast adaptive algorithm for computing whole-genome homology maps. <i>Bioinformatics</i> , 2018, 34, i748-i756.	4.1	110
58	Population genomics of the critically endangered kakapo. <i>Cell Genomics</i> , 2021, 1, 100002.	6.5	106
59	Strain-level metagenomic assignment and compositional estimation for long reads with MetaMaps. <i>Nature Communications</i> , 2019, 10, 3066.	12.8	98
60	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
61	HLA*LA€”HLA typing from linearly projected graph alignments. <i>Bioinformatics</i> , 2019, 35, 4394-4396.	4.1	88
62	Platypus and echidna genomes reveal mammalian biology and evolution. <i>Nature</i> , 2021, 592, 756-762.	27.8	85
63	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
64	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
65	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
66	Long-read mapping to repetitive reference sequences using Winnowmap2. <i>Nature Methods</i> , 2022, 19, 705-710.	19.0	80
67	Molecular Epidemiologic Investigation of an Anthrax Outbreak among Heroin Users, Europe. <i>Emerging Infectious Diseases</i> , 2012, 18, 1307-1313.	4.3	77
68	High-coverage sequencing and annotated assemblies of the budgerigar genome. <i>GigaScience</i> , 2014, 3, 11.	6.4	75
69	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
70	Complete vertebrate mitogenomes reveal widespread repeats and gene duplications. <i>Genome Biology</i> , 2021, 22, 120.	8.8	69
71	Hawkeye: an interactive visual analytics tool for genome assemblies. <i>Genome Biology</i> , 2007, 8, R34.	9.6	66
72	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

#	ARTICLE	IF	CITATIONS
73	Improved reference genome of the arboviral vector <i>Aedes albopictus</i> . <i>Genome Biology</i> , 2020, 21, 215.	8.8	65
74	Extended haplotype-phasing of long-read de novo genome assemblies using Hi-C. <i>Nature Communications</i> , 2021, 12, 1935.	12.8	64
75	Comprehensive DNA Signature Discovery and Validation. <i>PLoS Computational Biology</i> , 2007, 3, e98.	3.2	63
76	New advances in sequence assembly. <i>Genome Research</i> , 2017, 27, xi-xiii.	5.5	63
77	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
78	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
79	Automated ensemble assembly and validation of microbial genomes. <i>BMC Bioinformatics</i> , 2014, 15, 126.	2.6	60
80	A chromosome-scale assembly of the major African malaria vector <i>Anopheles funestus</i> . <i>GigaScience</i> , 2019, 8, .	6.4	56
81	Hawkeye and AMOS: visualizing and assessing the quality of genome assemblies. <i>Briefings in Bioinformatics</i> , 2013, 14, 213-224.	6.5	54
82	Reference genome and demographic history of the most endangered marine mammal, the vaquita. <i>Molecular Ecology Resources</i> , 2021, 21, 1008-1020.	4.8	54
83	Complete Genome Sequence of the Quality Control Strain <i>Staphylococcus aureus</i> subsp. <i>aureus</i> ATCC 25923. <i>Genome Announcements</i> , 2014, 2, .	0.8	53
84	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
85	Continuous chromosome-scale haplotypes assembled from a single interspecies F1 hybrid of yak and cattle. <i>GigaScience</i> , 2020, 9, .	6.4	46
86	Evolutionary and biomedical insights from a marmoset diploid genome assembly. <i>Nature</i> , 2021, 594, 227-233.	27.8	42
87	StainedGlass: interactive visualization of massive tandem repeat structures with identity heatmaps. <i>Bioinformatics</i> , 2022, 38, 2049-2051.	4.1	42
88	Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies. <i>Nature Methods</i> , 2022, 19, 687-695.	19.0	42
89	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
90	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

#	ARTICLE	IF	CITATIONS
91	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
92	Insignia: a DNA signature search web server for diagnostic assay development. <i>Nucleic Acids Research</i> , 2009, 37, W229-W234.	14.5	37
93	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
94	Balancing openness with Indigenous data sovereignty: An opportunity to leave no one behind in the journey to sequence all of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	33
95	Standards recommendations for the Earth BioGenome Project. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	33
96	Merfin: improved variant filtering, assembly evaluation and polishing via k-mer validation. <i>Nature Methods</i> , 2022, 19, 696-704.	19.0	30
97	The rise of a digital immune system. <i>GigaScience</i> , 2012, 1, 4.	6.4	29
98	Reply to "Errors in long-read assemblies can critically affect protein prediction". <i>Nature Biotechnology</i> , 2019, 37, 127-128.	17.5	29
99	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
100	Efficient oligonucleotide probe selection for pan-genomic tiling arrays. <i>BMC Bioinformatics</i> , 2009, 10, 293.	2.6	25
101	Integrated Microbial Survey Analysis of Prokaryotic Communities for the PhyloChip Microarray. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5636-5638.	3.1	24
102	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
103	Complete Closed Genome Sequences of <i>Mannheimia haemolytica</i> Serotypes A1 and A6, Isolated from Cattle. <i>Genome Announcements</i> , 2013, 1, .	0.8	19
104	The whale shark genome reveals patterns of vertebrate gene family evolution. <i>ELife</i> , 2021, 10, .	6.0	19
105	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
106	The genomic structure of a human chromosome 22 nucleolar organizer region determined by TAR cloning. <i>Scientific Reports</i> , 2021, 11, 2997.	3.3	13
107	Complete Closed Genome Sequences of Three <i>Bibersteinia trehalosi</i> Nasopharyngeal Isolates from Cattle with Shipping Fever. <i>Genome Announcements</i> , 2014, 2, .	0.8	9
108	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

#	ARTICLE	IF	CITATIONS
109	Complete Closed Genome Sequences of Four <i>Mannheimia varigena</i> Isolates from Cattle with Shipping Fever. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
110	Genome Sequence of the Attenuated Carbovap Vaccine Strain of <i>Bacillus anthracis</i> . <i>Genome Announcements</i> , 2013, 1, .	0.8	4
111	Krona: Interactive Metagenomic Visualization in a Web Browser. , 2013, , 1-8.		1
112	Irreconcilable differences: divorcing geographic mutation and recombination rates within a global MRSA clone. <i>Genome Biology</i> , 2012, 13, 181.	9.6	0