

Adam M Phillippy

List of Publications by Year in Descending Order

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Version: 2024-04-10

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

154 papers	25,093 citations	57 h-index	158 g-index
174 ext. papers	37,093 ext. citations	18.3 avg, IF	7.13 L-index

#	Paper	IF	Citations
154	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,	11.5	3
153	Standards recommendations for the Earth BioGenome Project.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	4
152	StainedGlass: Interactive visualization of massive tandem repeat structures with identity heatmaps.. <i>Bioinformatics</i> , 2022 ,	7.2	4
151	Merfin: improved variant filtering, assembly evaluation and polishing via k-mer validation.. <i>Nature Methods</i> , 2022 ,	21.6	3
150	Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies.. <i>Nature Methods</i> , 2022 ,	21.6	4
149	Epigenetic patterns in a complete human genome.. <i>Science</i> , 2022 , 376, eabj5089	33.3	12
148	Complete genomic and epigenetic maps of human centromeres.. <i>Science</i> , 2022 , 376, eabl4178	33.3	19
147	From telomere to telomere: The transcriptional and epigenetic state of human repeat elements.. <i>Science</i> , 2022 , 376, eabk3112	33.3	12
146	A complete reference genome improves analysis of human genetic variation.. <i>Science</i> , 2022 , 376, eabl3533	33.3	12
145	The complete sequence of a human genome.. <i>Science</i> , 2022 , 376, 44-53	33.3	107
144	Segmental duplications and their variation in a complete human genome.. <i>Science</i> , 2022 , 376, eabj6965	33.3	12
143	Long-read mapping to repetitive reference sequences using Winnowmap2.. <i>Nature Methods</i> , 2022 ,	21.6	7
142	The Human Pangenome Project: a global resource to map genomic diversity.. <i>Nature</i> , 2022 , 604, 437-446	50.4	7
141	The structure, function and evolution of a complete human chromosome 8. <i>Nature</i> , 2021 , 593, 101-107	50.4	72
140	Evolutionary and biomedical insights from a marmoset diploid genome assembly. <i>Nature</i> , 2021 , 594, 227-233	50.4	10
139	Extended haplotype-phasing of long-read de novo genome assemblies using Hi-C. <i>Nature Communications</i> , 2021 , 12, 1935	17.4	16
138	Complete vertebrate mitogenomes reveal widespread repeats and gene duplications. <i>Genome Biology</i> , 2021 , 22, 120	18.3	19

137	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021 , 592, 737-746	46.4	161
136	Reference genome and demographic history of the most endangered marine mammal, the vaquita. <i>Molecular Ecology Resources</i> , 2021 , 21, 1008-1020	8.4	15
135	The genomic structure of a human chromosome 22 nucleolar organizer region determined by TAR cloning. <i>Scientific Reports</i> , 2021 , 11, 2997	4.9	3
134	The whale shark genome reveals patterns of vertebrate gene family evolution. <i>ELife</i> , 2021 , 10,	8.9	5
133	Population genomics of the critically endangered kudu. <i>Cell Genomics</i> , 2021 , 100002		15
132	Platypus and echidna genomes reveal mammalian biology and evolution. <i>Nature</i> , 2021 , 592, 756-762	50.4	28
131	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. <i>Nature Biotechnology</i> , 2020 , 38, 1044-1053	44.5	143
130	Effect of sequence depth and length in long-read assembly of the maize inbred NC358. <i>Nature Communications</i> , 2020 , 11, 2288	17.4	21
129	A robust benchmark for detection of germline large deletions and insertions. <i>Nature Biotechnology</i> , 2020 , 38, 1347-1355	44.5	98
128	An improved pig reference genome sequence to enable pig genetics and genomics research. <i>GigaScience</i> , 2020 , 9,	7.6	60
127	Haplotype-resolved genomes provide insights into structural variation and gene content in Angus and Brahman cattle. <i>Nature Communications</i> , 2020 , 11, 2071	17.4	38
126	Continuous chromosome-scale haplotypes assembled from a single interspecies F1 hybrid of yak and cattle. <i>GigaScience</i> , 2020 , 9,	7.6	18
125	Strains used in whole organism Plasmodium falciparum vaccine trials differ in genome structure, sequence, and immunogenic potential. <i>Genome Medicine</i> , 2020 , 12, 6	14.4	27
124	Evolutionary superscaffolding and chromosome anchoring to improve Anopheles genome assemblies. <i>BMC Biology</i> , 2020 , 18, 1	7.3	51
123	Weighted minimizer sampling improves long read mapping. <i>Bioinformatics</i> , 2020 , 36, i111-i118	7.2	45
122	Genomic analyses of a livestock pest, the New World screwworm, find potential targets for genetic control programs. <i>Communications Biology</i> , 2020 , 3, 424	6.7	10
121	Strategic vision for improving human health at The Forefront of Genomics. <i>Nature</i> , 2020 , 586, 683-692	50.4	73
120	Telomere-to-telomere assembly of a complete human X chromosome. <i>Nature</i> , 2020 , 585, 79-84	50.4	269

119	Improved reference genome of the arboviral vector <i>Aedes albopictus</i> . <i>Genome Biology</i> , 2020 , 21, 215	18.3	26
118	Mercury: reference-free quality, completeness, and phasing assessment for genome assemblies. <i>Genome Biology</i> , 2020 , 21, 245	18.3	101
117	HiCanu: accurate assembly of segmental duplications, satellites, and allelic variants from high-fidelity long reads. <i>Genome Research</i> , 2020 , 30, 1291-1305	9.7	145
116	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020 , 9,	7.6	140
115	Integrating Hi-C links with assembly graphs for chromosome-scale assembly. <i>PLoS Computational Biology</i> , 2019 , 15, e1007273	5	202
114	Reply to Errors in long-read assemblies can critically affect protein predictionS <i>Nature Biotechnology</i> , 2019 , 37, 127-128	44.5	18
113	A chromosome-scale assembly of the major African malaria vector <i>Anopheles funestus</i> . <i>GigaScience</i> , 2019 , 8,	7.6	26
112	HLA*LA-HLA typing from linearly projected graph alignments. <i>Bioinformatics</i> , 2019 , 35, 4394-4396	7.2	42
111	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. <i>Nature Biotechnology</i> , 2019 , 37, 1155-1162	44.5	427
110	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	18.3	38
109	Strain-level metagenomic assignment and compositional estimation for long reads with MetaMaps. <i>Nature Communications</i> , 2019 , 10, 3066	17.4	51
108	De novo assembly of the goldfish () genome and the evolution of genes after whole-genome duplication. <i>Science Advances</i> , 2019 , 5, eaav0547	14.3	66
107	Mash Screen: high-throughput sequence containment estimation for genome discovery. <i>Genome Biology</i> , 2019 , 20, 232	18.3	63
106	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	4.5	12
105	Nanopore sequencing and assembly of a human genome with ultra-long reads. <i>Nature Biotechnology</i> , 2018 , 36, 338-345	44.5	968
104	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	7.6	24
103	A Fast Approximate Algorithm for Mapping Long Reads to Large Reference Databases. <i>Journal of Computational Biology</i> , 2018 , 25, 766-779	1.7	26
102	MUMmer4: A fast and versatile genome alignment system. <i>PLoS Computational Biology</i> , 2018 , 14, e1005944	34.4	556

101	Improved reference genome of <i>Aedes aegypti</i> informs arbovirus vector control. <i>Nature</i> , 2018 , 563, 501-507	50.4	235
100	High throughput ANI analysis of 90K prokaryotic genomes reveals clear species boundaries. <i>Nature Communications</i> , 2018 , 9, 5114	17.4	1006
99	A fast adaptive algorithm for computing whole-genome homology maps. <i>Bioinformatics</i> , 2018 , 34, i748-i756	17.5	53
98	RefSeq database growth influences the accuracy of k-mer-based lowest common ancestor species identification. <i>Genome Biology</i> , 2018 , 19, 165	18.3	57
97	De novo assembly of haplotype-resolved genomes with trio binning. <i>Nature Biotechnology</i> , 2018 ,	44.5	171
96	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	20.1	36
95	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	36.3	323
94	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	3.2	19
93	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	9.7	365
92	A Fast Approximate Algorithm for Mapping Long Reads to Large Reference Databases. <i>Lecture Notes in Computer Science</i> , 2017 , 66-81	0.9	21
91	Canu: scalable and accurate long-read assembly via adaptive -mer weighting and repeat separation. <i>Genome Research</i> , 2017 , 27, 722-736	9.7	2943
90	Draft Genome Sequences from a Novel Clade of Strains, Isolated from the International Space Station. <i>Genome Announcements</i> , 2017 , 5,		9
89	The channel catfish genome sequence provides insights into the evolution of scale formation in teleosts. <i>Nature Communications</i> , 2016 , 7, 11757	17.4	173
88	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	4.8	5
87	Mash: fast genome and metagenome distance estimation using MinHash. <i>Genome Biology</i> , 2016 , 17, 132	18.3	1066
86	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	11.5	63
85	Assembling large genomes with single-molecule sequencing and locality-sensitive hashing. <i>Nature Biotechnology</i> , 2015 , 33, 623-30	44.5	650
84	One chromosome, one contig: complete microbial genomes from long-read sequencing and assembly. <i>Current Opinion in Microbiology</i> , 2015 , 23, 110-20	7.9	302

83	High-coverage sequencing and annotated assemblies of the budgerigar genome. <i>GigaScience</i> , 2014 , 3, 11	7.6	67
82	Automated ensemble assembly and validation of microbial genomes. <i>BMC Bioinformatics</i> , 2014 , 15, 126	3.6	45
81	Complete Closed Genome Sequences of Three Bibersteinia trehalosi Nasopharyngeal Isolates from Cattle with Shipping Fever. <i>Genome Announcements</i> , 2014 , 2,		9
80	Complete Closed Genome Sequences of Four Mannheimia varigena Isolates from Cattle with Shipping Fever. <i>Genome Announcements</i> , 2014 , 2,		4
79	Long-read, whole-genome shotgun sequence data for five model organisms. <i>Scientific Data</i> , 2014 , 1, 140045	8.2	106
78	Complete Genome Sequence of the Quality Control Strain Staphylococcus aureus subsp. aureus ATCC 25923. <i>Genome Announcements</i> , 2014 , 2,		38
77	The Harvest suite for rapid core-genome alignment and visualization of thousands of intraspecific microbial genomes. <i>Genome Biology</i> , 2014 , 15, 524	18.3	820
76	MetAMOS: a modular and open source metagenomic assembly and analysis pipeline. <i>Genome Biology</i> , 2013 , 14, R2	18.3	150
75	Hawkeye and AMOS: visualizing and assessing the quality of genome assemblies. <i>Briefings in Bioinformatics</i> , 2013 , 14, 213-24	13.4	41
74	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013 , 2, 10	7.6	461
73	Genome Sequence of the Attenuated Carbozap Vaccine Strain of Bacillus anthracis. <i>Genome Announcements</i> , 2013 , 1,		3
72	Complete Closed Genome Sequences of Mannheimia haemolytica Serotypes A1 and A6, Isolated from Cattle. <i>Genome Announcements</i> , 2013 , 1,		17
71	Reducing assembly complexity of microbial genomes with single-molecule sequencing. <i>Genome Biology</i> , 2013 , 14, R101	18.3	286
70	Irreconcilable differences: divorcing geographic mutation and recombination rates within a global MRSA clone. <i>Genome Biology</i> , 2012 , 13, 181	18.3	
69	Molecular epidemiologic investigation of an anthrax outbreak among heroin users, Europe. <i>Emerging Infectious Diseases</i> , 2012 , 18, 1307-13	10.2	58
68	GAGE: A critical evaluation of genome assemblies and assembly algorithms. <i>Genome Research</i> , 2012 , 22, 557-67	9.7	485
67	Hybrid error correction and de novo assembly of single-molecule sequencing reads. <i>Nature Biotechnology</i> , 2012 , 30, 693-700	44.5	758
66	Two new complete genome sequences offer insight into host and tissue specificity of plant pathogenic Xanthomonas spp. <i>Journal of Bacteriology</i> , 2011 , 193, 5450-64	3.5	146

65	Interactive metagenomic visualization in a Web browser. <i>BMC Bioinformatics</i> , 2011 , 12, 385	3.6	959
64	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	4.5	58
63	Assemblathon 1: a competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011 , 21, 2224-41	9.7	364
62	Complex microbiome underlying secondary and primary metabolism in the tunicate-Prochloron symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, E1423-32	11.5	117
61	Bacillus anthracis 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, 5027-32	11.5	130
60	Integrated microbial survey analysis of prokaryotic communities for the PhyloChip microarray. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 5636-8	4.8	21
59	Transcriptomic responses of <i>Salmonella enterica</i> serovars Enteritidis and Typhimurium to chlorine-based oxidative stress. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 5013-24	4.8	59
58	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	4.5	62
57	Insignia: a DNA signature search web server for diagnostic assay development. <i>Nucleic Acids Research</i> , 2009 , 37, W229-34	20.1	31
56	Efficient oligonucleotide probe selection for pan-genomic tiling arrays. <i>BMC Bioinformatics</i> , 2009 , 10, 293	3.6	23
55	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	4.5	275
54	Genome assembly forensics: finding the elusive mis-assembly. <i>Genome Biology</i> , 2008 , 9, R55	18.3	200
53	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007 , 450, 203-18	50.4	1586
52	Comprehensive DNA signature discovery and validation. <i>PLoS Computational Biology</i> , 2007 , 3, e98	5	53
51	Hawkeye: an interactive visual analytics tool for genome assemblies. <i>Genome Biology</i> , 2007 , 8, R34	18.3	62
50	Genome sequence of the PCE-dechlorinating bacterium <i>Dehalococcoides ethenogenes</i> . <i>Science</i> , 2005 , 307, 105-8	33.3	363
49	Comparative genome assembly. <i>Briefings in Bioinformatics</i> , 2004 , 5, 237-48	13.4	165
48	Versatile and open software for comparing large genomes. <i>Genome Biology</i> , 2004 , 5, R12	18.3	3485

47	Using MUMmer to identify similar regions in large sequence sets. <i>Current Protocols in Bioinformatics</i> , 2003 , Chapter 10, Unit 10.3	24.2	324
46	Fast algorithms for large-scale genome alignment and comparison. <i>Nucleic Acids Research</i> , 2002 , 30, 2478-83	24.2	684
45	De Novo assembly of the goldfish (<i>Carassius auratus</i>) genome and the evolution of genes after whole genome duplication		2
44	Assembling Large Genomes with Single-Molecule Sequencing and Locality Sensitive Hashing		10
43	Mash: fast genome and metagenome distance estimation using MinHash		13
42	Single-molecule sequencing and conformational capture enable de novo mammalian reference genomes		12
41	Canu: scalable and accurate long-read assembly via adaptive k-mer weighting and repeat separation		89
40	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly		13
39	A Fast Approximate Algorithm for Mapping Long Reads to Large Reference Databases		9
38	Analysis of the <i>Aedes albopictus</i> C6/36 genome provides insight into cell line adaptations to in vitro viral propagation		1
37	Weighted minimizer sampling improves long read mapping		2
36	HiCanu: accurate assembly of segmental duplications, satellites, and allelic variants from high-fidelity long reads		13
35	Merquy: reference-free quality, completeness, and phasing assessment for genome assemblies		16
34	Towards complete and error-free genome assemblies of all vertebrate species		38
33	Reference genome and demographic history of the most endangered marine mammal, the vaquita		1
32	Complete vertebrate mitogenomes reveal widespread gene duplications and repeats		5
31	The structure, function, and evolution of a complete human chromosome 8		10
30	A contiguous de novo genome assembly of sugar beet EL10 (<i>Beta vulgaris</i> L.)		3

29	A long read mapping method for highly repetitive reference sequences	18
28	High-throughput ANI Analysis of 90K Prokaryotic Genomes Reveals Clear Species Boundaries	15
27	Integrating Hi-C links with assembly graphs for chromosome-scale assembly	11
26	Complete assembly of parental haplotypes with trio binning	12
25	RefSeq database growth influences the accuracy of k-mer-based species identification	5
24	Extended haplotype phasing of de novo genome assemblies with FALCON-Phase	37
23	MetaMaps B strain-level metagenomic assignment and compositional estimation for long reads	7
22	HLA*PRG:LA HLA typing from linearly projected graph alignments	2
21	Assignment of virus and antimicrobial resistance genes to microbial hosts in a complex microbial community by combined long-read assembly and proximity ligation	3
20	Highly-accurate long-read sequencing improves variant detection and assembly of a human genome	29
19	Mash Screen: High-throughput sequence containment estimation for genome discovery	14
18	A robust benchmark for germline structural variant detection	34
17	An improved pig reference genome sequence to enable pig genetics and genomics research	15
16	Strains used in whole organism <i>Plasmodium falciparum</i> vaccine trials differ in genome structure, sequence, and immunogenic potential	3
15	The whale shark genome reveals patterns of vertebrate gene family evolution	1
14	Efficient de novo assembly of eleven human genomes using PromethION sequencing and a novel nanopore toolkit	29
13	Haplotype-Resolved Cattle Genomes Provide Insights Into Structural Variation and Adaptation	1
12	Telomere-to-telomere assembly of a complete human X chromosome	45

11	Effect of Sequence Depth and Length in Long-read Assembly of the Maize Inbred NC358	5
10	False gene and chromosome losses affected by assembly and sequence errors	3
9	Segmental duplications and their variation in a complete human genome	13
8	The complete sequence of a human genome	58
7	Epigenetic Patterns in a Complete Human Genome	9
6	From telomere to telomere: the transcriptional and epigenetic state of human repeat elements	7
5	A complete reference genome improves analysis of human genetic variation	9
4	Complete genomic and epigenetic maps of human centromeres	8
3	Merfin: improved variant filtering and polishing via k-mer validation	10
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1	Automated assembly of high-quality diploid human reference genomes	3