

# Adam M Phillippy

## List of Publications by Citations

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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	Versatile and open software for comparing large genomes. <i>Genome Biology</i> , <b>2004</b> , 5, R12	18.3	3485
153	Canu: scalable and accurate long-read assembly via adaptive -mer weighting and repeat separation. <i>Genome Research</i> , <b>2017</b> , 27, 722-736	9.7	2943
152	Evolution of genes and genomes on the Drosophila phylogeny. <i>Nature</i> , <b>2007</b> , 450, 203-18	50.4	1586
151	Mash: fast genome and metagenome distance estimation using MinHash. <i>Genome Biology</i> , <b>2016</b> , 17, 13218.3	18.3	1066
150	High throughput ANI analysis of 90K prokaryotic genomes reveals clear species boundaries. <i>Nature Communications</i> , <b>2018</b> , 9, 5114	17.4	1006
149	Nanopore sequencing and assembly of a human genome with ultra-long reads. <i>Nature Biotechnology</i> , <b>2018</b> , 36, 338-345	44.5	968
148	Interactive metagenomic visualization in a Web browser. <i>BMC Bioinformatics</i> , <b>2011</b> , 12, 385	3.6	959
147	The Harvest suite for rapid core-genome alignment and visualization of thousands of intraspecific microbial genomes. <i>Genome Biology</i> , <b>2014</b> , 15, 524	18.3	820
146	Hybrid error correction and de novo assembly of single-molecule sequencing reads. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 693-700	44.5	758
145	Fast algorithms for large-scale genome alignment and comparison. <i>Nucleic Acids Research</i> , <b>2002</b> , 30, 2478-83	24.3	684
144	Assembling large genomes with single-molecule sequencing and locality-sensitive hashing. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 623-30	44.5	650
143	MUMmer4: A fast and versatile genome alignment system. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1005944	3.44	556
142	GAGE: A critical evaluation of genome assemblies and assembly algorithms. <i>Genome Research</i> , <b>2012</b> , 22, 557-67	9.7	485
141	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , <b>2013</b> , 2, 10	7.6	461
140	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. <i>Nature Biotechnology</i> , <b>2019</b> , 37, 1155-1162	44.5	427
139	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. <i>Genome Research</i> , <b>2017</b> , 27, 849-864	9.7	365
138	Assemblathon 1: a competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , <b>2011</b> , 21, 2224-41	9.7	364

137	Genome sequence of the PCE-dechlorinating bacterium Dehalococcoides ethenogenes. <i>Science</i> , <b>2005</b> , 307, 105-8	33.3	363
136	Using MUMmer to identify similar regions in large sequence sets. <i>Current Protocols in Bioinformatics</i> , <b>2003</b> , Chapter 10, Unit 10.3	24.2	324
135	Single-molecule sequencing and chromatin conformation capture enable de novo reference assembly of the domestic goat genome. <i>Nature Genetics</i> , <b>2017</b> , 49, 643-650	36.3	323
134	One chromosome, one contig: complete microbial genomes from long-read sequencing and assembly. <i>Current Opinion in Microbiology</i> , <b>2015</b> , 23, 110-20	7.9	302
133	Reducing assembly complexity of microbial genomes with single-molecule sequencing. <i>Genome Biology</i> , <b>2013</b> , 14, R101	18.3	286
132	Genome sequence and rapid evolution of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A. <i>BMC Genomics</i> , <b>2008</b> , 9, 204	4.5	275
131	Telomere-to-telomere assembly of a complete human X chromosome. <i>Nature</i> , <b>2020</b> , 585, 79-84	50.4	269
130	Improved reference genome of <i>Aedes aegypti</i> informs arbovirus vector control. <i>Nature</i> , <b>2018</b> , 563, 501-507	50.4	235
129	Integrating Hi-C links with assembly graphs for chromosome-scale assembly. <i>PLoS Computational Biology</i> , <b>2019</b> , 15, e1007273	5	202
128	Genome assembly forensics: finding the elusive mis-assembly. <i>Genome Biology</i> , <b>2008</b> , 9, R55	18.3	200
127	The channel catfish genome sequence provides insights into the evolution of scale formation in teleosts. <i>Nature Communications</i> , <b>2016</b> , 7, 11757	17.4	173
126	De novo assembly of haplotype-resolved genomes with trio binning. <i>Nature Biotechnology</i> , <b>2018</b> ,	44.5	171
125	Comparative genome assembly. <i>Briefings in Bioinformatics</i> , <b>2004</b> , 5, 237-48	13.4	165
124	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , <b>2021</b> , 592, 737-746	56.4	161
123	MetAMOS: a modular and open source metagenomic assembly and analysis pipeline. <i>Genome Biology</i> , <b>2013</b> , 14, R2	18.3	150
122	Two new complete genome sequences offer insight into host and tissue specificity of plant pathogenic <i>Xanthomonas</i> spp. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 5450-64	3.5	146
121	HiCanu: accurate assembly of segmental duplications, satellites, and allelic variants from high-fidelity long reads. <i>Genome Research</i> , <b>2020</b> , 30, 1291-1305	9.7	145
120	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 1044-1053	44.5	143

119	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , <b>2020</b> , 9,	7.6	140
118	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> , <b>2011</b> , 108, 5027-32	11.5	130
117	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> , <b>2011</b> , 108, E1423-32	11.5	117
116	The complete sequence of a human genome.. <i>Science</i> , <b>2022</b> , 376, 44-53	33.3	107
115	Long-read, whole-genome shotgun sequence data for five model organisms. <i>Scientific Data</i> , <b>2014</b> , 1, 140045	8.2	106
114	Mercury: reference-free quality, completeness, and phasing assessment for genome assemblies. <i>Genome Biology</i> , <b>2020</b> , 21, 245	18.3	101
113	A robust benchmark for detection of germline large deletions and insertions. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 1347-1355	44.5	98
112	Canu: scalable and accurate long-read assembly via adaptive k-mer weighting and repeat separation		89
111	Strategic vision for improving human health at The Forefront of Genomics. <i>Nature</i> , <b>2020</b> , 586, 683-692	50.4	73
110	The structure, function and evolution of a complete human chromosome 8. <i>Nature</i> , <b>2021</b> , 593, 101-107	50.4	72
109	High-coverage sequencing and annotated assemblies of the budgerigar genome. <i>GigaScience</i> , <b>2014</b> , 3, 11	7.6	67
108	De novo assembly of the goldfish () genome and the evolution of genes after whole-genome duplication. <i>Science Advances</i> , <b>2019</b> , 5, eaav0547	14.3	66
107	Mash Screen: high-throughput sequence containment estimation for genome discovery. <i>Genome Biology</i> , <b>2019</b> , 20, 232	18.3	63
106	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> , <b>2016</b> , 113, E2114-23	11.5	63
105	Probing the pan-genome of <i>Listeria monocytogenes</i> : new insights into intraspecific niche expansion and genomic diversification. <i>BMC Genomics</i> , <b>2010</b> , 11, 500	4.5	62
104	Hawkeye: an interactive visual analytics tool for genome assemblies. <i>Genome Biology</i> , <b>2007</b> , 8, R34	18.3	62
103	An improved pig reference genome sequence to enable pig genetics and genomics research. <i>GigaScience</i> , <b>2020</b> , 9,	7.6	60
102	Transcriptomic responses of <i>Salmonella enterica</i> serovars Enteritidis and Typhimurium to chlorine-based oxidative stress. <i>Applied and Environmental Microbiology</i> , <b>2010</b> , 76, 5013-24	4.8	59

101	Molecular epidemiologic investigation of an anthrax outbreak among heroin users, Europe. <i>Emerging Infectious Diseases</i> , <b>2012</b> , 18, 1307-13	10.2	58
100	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> , <b>2011</b> , 12, 291	4.5	58
99	The complete sequence of a human genome		58
98	RefSeq database growth influences the accuracy of k-mer-based lowest common ancestor species identification. <i>Genome Biology</i> , <b>2018</b> , 19, 165	18.3	57
97	Comprehensive DNA signature discovery and validation. <i>PLoS Computational Biology</i> , <b>2007</b> , 3, e98	5	53
96	A fast adaptive algorithm for computing whole-genome homology maps. <i>Bioinformatics</i> , <b>2018</b> , 34, i748-i756	7.56	53
95	Strain-level metagenomic assignment and compositional estimation for long reads with MetaMaps. <i>Nature Communications</i> , <b>2019</b> , 10, 3066	17.4	51
94	Evolutionary superscaffolding and chromosome anchoring to improve <i>Anopheles</i> genome assemblies. <i>BMC Biology</i> , <b>2020</b> , 18, 1	7.3	51
93	Automated ensemble assembly and validation of microbial genomes. <i>BMC Bioinformatics</i> , <b>2014</b> , 15, 126	3.6	45
92	Telomere-to-telomere assembly of a complete human X chromosome		45
91	Weighted minimizer sampling improves long read mapping. <i>Bioinformatics</i> , <b>2020</b> , 36, i1111-i1118	7.2	45
90	HLA*LA-HLA typing from linearly projected graph alignments. <i>Bioinformatics</i> , <b>2019</b> , 35, 4394-4396	7.2	42
89	Hawkeye and AMOS: visualizing and assessing the quality of genome assemblies. <i>Briefings in Bioinformatics</i> , <b>2013</b> , 14, 213-24	13.4	41
88	Haplotype-resolved genomes provide insights into structural variation and gene content in Angus and Brahman cattle. <i>Nature Communications</i> , <b>2020</b> , 11, 2071	17.4	38
87	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> , <b>2019</b> , 20, 153	18.3	38
86	Complete Genome Sequence of the Quality Control Strain <i>Staphylococcus aureus</i> subsp. <i>aureus</i> ATCC 25923. <i>Genome Announcements</i> , <b>2014</b> , 2,		38
85	Towards complete and error-free genome assemblies of all vertebrate species		38
84	Extended haplotype phasing of de novo genome assemblies with FALCON-Phase		37

83	Variation in human chromosome 21 ribosomal RNA genes characterized by TAR cloning and long-read sequencing. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 6712-6725	20.1	36
82	A robust benchmark for germline structural variant detection		34
81	Insignia: a DNA signature search web server for diagnostic assay development. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, W229-34	20.1	31
80	Highly-accurate long-read sequencing improves variant detection and assembly of a human genome		29
79	Efficient de novo assembly of eleven human genomes using PromethION sequencing and a novel nanopore toolkit		29
78	Platypus and echidna genomes reveal mammalian biology and evolution. <i>Nature</i> , <b>2021</b> , 592, 756-762	50.4	28
77	Strains used in whole organism Plasmodium falciparum vaccine trials differ in genome structure, sequence, and immunogenic potential. <i>Genome Medicine</i> , <b>2020</b> , 12, 6	14.4	27
76	A chromosome-scale assembly of the major African malaria vector Anopheles funestus. <i>GigaScience</i> , <b>2019</b> , 8,	7.6	26
75	A Fast Approximate Algorithm for Mapping Long Reads to Large Reference Databases. <i>Journal of Computational Biology</i> , <b>2018</b> , 25, 766-779	1.7	26
74	Improved reference genome of the arboviral vector Aedes albopictus. <i>Genome Biology</i> , <b>2020</b> , 21, 215	18.3	26
73	Analysis of the Aedes albopictus C6/36 genome provides insight into cell line utility for viral propagation. <i>GigaScience</i> , <b>2018</b> , 7, 1-13	7.6	24
72	Efficient oligonucleotide probe selection for pan-genomic tiling arrays. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 293	3.6	23
71	A Fast Approximate Algorithm for Mapping Long Reads to Large Reference Databases. <i>Lecture Notes in Computer Science</i> , <b>2017</b> , 66-81	0.9	21
70	Effect of sequence depth and length in long-read assembly of the maize inbred NC358. <i>Nature Communications</i> , <b>2020</b> , 11, 2288	17.4	21
69	Integrated microbial survey analysis of prokaryotic communities for the PhyloChip microarray. <i>Applied and Environmental Microbiology</i> , <b>2010</b> , 76, 5636-8	4.8	21
68	The evolution of the natural killer complex; a comparison between mammals using new high-quality genome assemblies and targeted annotation. <i>Immunogenetics</i> , <b>2017</b> , 69, 255-269	3.2	19
67	Complete vertebrate mitogenomes reveal widespread repeats and gene duplications. <i>Genome Biology</i> , <b>2021</b> , 22, 120	18.3	19
66	Complete genomic and epigenetic maps of human centromeres.. <i>Science</i> , <b>2022</b> , 376, eabl4178	33.3	19

65	Reply to <del>Errors</del> in long-read assemblies can critically affect protein predictionS <i>Nature Biotechnology</i> , <b>2019</b> , 37, 127-128	44.5	18
64	Continuous chromosome-scale haplotypes assembled from a single interspecies F1 hybrid of yak and cattle. <i>GigaScience</i> , <b>2020</b> , 9,	7.6	18
63	A long read mapping method for highly repetitive reference sequences		18
62	Complete Closed Genome Sequences of Mannheimia haemolytica Serotypes A1 and A6, Isolated from Cattle. <i>Genome Announcements</i> , <b>2013</b> , 1,		17
61	Mercury: reference-free quality, completeness, and phasing assessment for genome assemblies		16
60	Extended haplotype-phasing of long-read de novo genome assemblies using Hi-C. <i>Nature Communications</i> , <b>2021</b> , 12, 1935	17.4	16
59	High-throughput ANI Analysis of 90K Prokaryotic Genomes Reveals Clear Species Boundaries		15
58	An improved pig reference genome sequence to enable pig genetics and genomics research		15
57	Reference genome and demographic history of the most endangered marine mammal, the vaquita. <i>Molecular Ecology Resources</i> , <b>2021</b> , 21, 1008-1020	8.4	15
56	Population genomics of the critically endangered kākāCell <i>Genomics</i> , <b>2021</b> , 100002		15
55	Mash Screen: High-throughput sequence containment estimation for genome discovery		14
54	Mash: fast genome and metagenome distance estimation using MinHash		13
53	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly		13
52	HiCanu: accurate assembly of segmental duplications, satellites, and allelic variants from high-fidelity long reads		13
51	Segmental duplications and their variation in a complete human genome		13
50	Single-molecule sequencing and conformational capture enable de novo mammalian reference genomes		12
49	Complete assembly of parental haplotypes with trio binning		12
48	New insights into mammalian sex chromosome structure and evolution using high-quality sequences from bovine X and Y chromosomes. <i>BMC Genomics</i> , <b>2019</b> , 20, 1000	4.5	12

47	Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies		12
46	Epigenetic patterns in a complete human genome.. <i>Science</i> , <b>2022</b> , 376, eabj5089	33.3	12
45	From telomere to telomere: The transcriptional and epigenetic state of human repeat elements.. <i>Science</i> , <b>2022</b> , 376, eabk3112	33.3	12
44	A complete reference genome improves analysis of human genetic variation.. <i>Science</i> , <b>2022</b> , 376, eabl3533	33.3	12
43	Segmental duplications and their variation in a complete human genome.. <i>Science</i> , <b>2022</b> , 376, eabj6965	33.3	12
42	Integrating Hi-C links with assembly graphs for chromosome-scale assembly		11
41	Assembling Large Genomes with Single-Molecule Sequencing and Locality Sensitive Hashing		10
40	The structure, function, and evolution of a complete human chromosome 8		10
39	Genomic analyses of a livestock pest, the New World screwworm, find potential targets for genetic control programs. <i>Communications Biology</i> , <b>2020</b> , 3, 424	6.7	10
38	Evolutionary and biomedical insights from a marmoset diploid genome assembly. <i>Nature</i> , <b>2021</b> , 594, 227-233	50.4	10
37	Merfin: improved variant filtering and polishing via k-mer validation		10
36	Complete Closed Genome Sequences of Three <i>Bibersteinia trehalosi</i> Nasopharyngeal Isolates from Cattle with Shipping Fever. <i>Genome Announcements</i> , <b>2014</b> , 2,		9
35	Draft Genome Sequences from a Novel Clade of Strains, Isolated from the International Space Station. <i>Genome Announcements</i> , <b>2017</b> , 5,		9
34	A Fast Approximate Algorithm for Mapping Long Reads to Large Reference Databases		9
33	Epigenetic Patterns in a Complete Human Genome		9
32	A complete reference genome improves analysis of human genetic variation		9
31	Complete genomic and epigenetic maps of human centromeres		8
30	MetaMaps B strain-level metagenomic assignment and compositional estimation for long reads		7



29	From telomere to telomere: the transcriptional and epigenetic state of human repeat elements		7
28	Long-read mapping to repetitive reference sequences using Winnowmap2.. <i>Nature Methods</i> , <b>2022</b> ,	21.6	7
27	The Human Pangenome Project: a global resource to map genomic diversity.. <i>Nature</i> , <b>2022</b> , 604, 437-446	50.4	7
26	Identification and Genomic Analysis of a Novel Group C Orthobunyavirus Isolated from a Mosquito Captured near Iquitos, Peru. <i>PLoS Neglected Tropical Diseases</i> , <b>2016</b> , 10, e0004440	4.8	5
25	Complete vertebrate mitogenomes reveal widespread gene duplications and repeats		5
24	RefSeq database growth influences the accuracy of k-mer-based species identification		5
23	Effect of Sequence Depth and Length in Long-read Assembly of the Maize Inbred NC358		5
22	The whale shark genome reveals patterns of vertebrate gene family evolution. <i>ELife</i> , <b>2021</b> , 10,	8.9	5
21	Complete Closed Genome Sequences of Four Mannheimia varigena Isolates from Cattle with Shipping Fever. <i>Genome Announcements</i> , <b>2014</b> , 2,		4
20	Standards recommendations for the Earth BioGenome Project.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2022</b> , 119,	11.5	4
19	StainedGlass: Interactive visualization of massive tandem repeat structures with identity heatmaps.. <i>Bioinformatics</i> , <b>2022</b> ,	7.2	4
18	Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies.. <i>Nature Methods</i> , <b>2022</b> ,	21.6	4
17	Genome Sequence of the Attenuated Carbosap Vaccine Strain of Bacillus anthracis. <i>Genome Announcements</i> , <b>2013</b> , 1,		3
16	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> , <b>2022</b> , 119,	11.5	3
15	A contiguous de novo genome assembly of sugar beet EL10 (Beta vulgaris L.)		3
14	Assignment of virus and antimicrobial resistance genes to microbial hosts in a complex microbial community by combined long-read assembly and proximity ligation		3
13	Strains used in whole organism Plasmodium falciparum vaccine trials differ in genome structure, sequence, and immunogenic potential		3
12	False gene and chromosome losses affected by assembly and sequence errors		3

11	The genomic structure of a human chromosome 22 nucleolar organizer region determined by TAR cloning. <i>Scientific Reports</i> , <b>2021</b> , 11, 2997	4.9	3
10	Merfin: improved variant filtering, assembly evaluation and polishing via k-mer validation.. <i>Nature Methods</i> , <b>2022</b> ,	21.6	3
9	Automated assembly of high-quality diploid human reference genomes		3
8	De Novo assembly of the goldfish ( <i>Carassius auratus</i> ) genome and the evolution of genes after whole genome duplication		2
7	Weighted minimizer sampling improves long read mapping		2
6	HLA*PRG:LA [HLA typing from linearly projected graph alignments		2
5	Analysis of the <i>Aedes albopictus</i> C6/36 genome provides insight into cell line adaptations to in vitro viral propagation		1
4	Reference genome and demographic history of the most endangered marine mammal, the vaquita		1
3	The whale shark genome reveals patterns of vertebrate gene family evolution		1
2	Haplotype-Resolved Cattle Genomes Provide Insights Into Structural Variation and Adaptation		1
1	Irreconcilable differences: divorcing geographic mutation and recombination rates within a global MRSA clone. <i>Genome Biology</i> , <b>2012</b> , 13, 181	18.3	