

Sergey Koren

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.

100
papers

14,300
citations

43
h-index

111
g-index

111
ext. papers

21,961
ext. citations

19.7
avg, IF

6.7
L-index

#	Paper	IF	Citations
100	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
99	Mash: fast genome and metagenome distance estimation using MinHash. <i>Genome Biology</i> , 2016 , 17, 13218.3	18.3	1066
98	Nanopore sequencing and assembly of a human genome with ultra-long reads. <i>Nature Biotechnology</i> , 2018 , 36, 338-345	44.5	968
97	Assembly algorithms for next-generation sequencing data. <i>Genomics</i> , 2010 , 95, 315-27	4.3	764
96	Hybrid error correction and de novo assembly of single-molecule sequencing reads. <i>Nature Biotechnology</i> , 2012 , 30, 693-700	44.5	758
95	Assembling large genomes with single-molecule sequencing and locality-sensitive hashing. <i>Nature Biotechnology</i> , 2015 , 33, 623-30	44.5	650
94	GAGE: A critical evaluation of genome assemblies and assembly algorithms. <i>Genome Research</i> , 2012 , 22, 557-67	9.7	485
93	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013 , 2, 10	7.6	461
92	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
91	Aggressive assembly of pyrosequencing reads with mates. <i>Bioinformatics</i> , 2008 , 24, 2818-24	7.2	407
90	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
89	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
88	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
87	Reducing assembly complexity of microbial genomes with single-molecule sequencing. <i>Genome Biology</i> , 2013 , 14, R101	18.3	286
86	Telomere-to-telomere assembly of a complete human X chromosome. <i>Nature</i> , 2020 , 585, 79-84	50.4	269
85	Improved reference genome of <i>Aedes aegypti</i> informs arbovirus vector control. <i>Nature</i> , 2018 , 563, 501-507	50.4	235
84	Hybrid assembly of the large and highly repetitive genome of , a progenitor of bread wheat, with the MaSuRCA mega-reads algorithm. <i>Genome Research</i> , 2017 , 27, 787-792	9.7	208

83	Integrating Hi-C links with assembly graphs for chromosome-scale assembly. <i>PLoS Computational Biology</i> , 2019 , 15, e1007273	5	202
82	De novo assembly of haplotype-resolved genomes with trio binning. <i>Nature Biotechnology</i> , 2018 ,	44.5	171
81	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021 , 592, 737-746.	46.4	161
80	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
79	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
78	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020 , 9,	7.6	140
77	De Novo Assembly of a New Accession Using Nanopore Sequencing. <i>Plant Cell</i> , 2017 , 29, 2336-2348	11.6	138
76	The complete sequence of a human genome.. <i>Science</i> , 2022 , 376, 44-53	33.3	107
75	Bambus 2: scaffolding metagenomes. <i>Bioinformatics</i> , 2011 , 27, 2964-71	7.2	106
74	Mercury: reference-free quality, completeness, and phasing assessment for genome assemblies. <i>Genome Biology</i> , 2020 , 21, 245	18.3	101
73	A robust benchmark for detection of germline large deletions and insertions. <i>Nature Biotechnology</i> , 2020 , 38, 1347-1355	44.5	98
72	Scaffolding of long read assemblies using long range contact information. <i>BMC Genomics</i> , 2017 , 18, 527	4.5	90
71	Canu: scalable and accurate long-read assembly via adaptive k-mer weighting and repeat separation		89
70	The structure, function and evolution of a complete human chromosome 8. <i>Nature</i> , 2021 , 593, 101-107	50.4	72
69	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
68	Mash Screen: high-throughput sequence containment estimation for genome discovery. <i>Genome Biology</i> , 2019 , 20, 232	18.3	63
67	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
66	Metagenomic assembly through the lens of validation: recent advances in assessing and improving the quality of genomes assembled from metagenomes. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1140-1150	13.4	63

65	An improved pig reference genome sequence to enable pig genetics and genomics research. <i>GigaScience</i> , 2020 , 9,	7.6	60
64	The complete sequence of a human genome		58
63	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
62	A fast adaptive algorithm for computing whole-genome homology maps. <i>Bioinformatics</i> , 2018 , 34, i748-i756	7.5	53
61	Strain-level metagenomic assignment and compositional estimation for long reads with MetaMaps. <i>Nature Communications</i> , 2019 , 10, 3066	17.4	51
60	Evolutionary superscaffolding and chromosome anchoring to improve Anopheles genome assemblies. <i>BMC Biology</i> , 2020 , 18, 1	7.3	51
59	Telomere-to-telomere assembly of a complete human X chromosome		45
58	Weighted minimizer sampling improves long read mapping. <i>Bioinformatics</i> , 2020 , 36, i1111-i1118	7.2	45
57	HLA*LA-HLA typing from linearly projected graph alignments. <i>Bioinformatics</i> , 2019 , 35, 4394-4396	7.2	42
56	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
55	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
54	Towards complete and error-free genome assemblies of all vertebrate species		38
53	Extended haplotype phasing of de novo genome assemblies with FALCON-Phase		37
52	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
51	A robust benchmark for germline structural variant detection		34
50	De novo likelihood-based measures for comparing genome assemblies. <i>BMC Research Notes</i> , 2013 , 6, 334	2.3	33
49	Highly-accurate long-read sequencing improves variant detection and assembly of a human genome		29
48	Efficient de novo assembly of eleven human genomes using PromethION sequencing and a novel nanopore toolkit		29

47	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
46	A chromosome-scale assembly of the major African malaria vector Anopheles funestus. <i>GigaScience</i> , 2019 , 8,	7.6	26
45	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
44	Improved reference genome of the arboviral vector Aedes albopictus. <i>Genome Biology</i> , 2020 , 21, 215	18.3	26
43	Analysis of the Aedes albopictus C6/36 genome provides insight into cell line utility for viral propagation. <i>GigaScience</i> , 2018 , 7, 1-13	7.6	24
42	De novo assembly of the complex genome of Nippostrongylus brasiliensis using MinION long reads. <i>BMC Biology</i> , 2018 , 16, 6	7.3	22
41	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
40	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
39	Complete vertebrate mitogenomes reveal widespread repeats and gene duplications. <i>Genome Biology</i> , 2021 , 22, 120	18.3	19
38	Complete genomic and epigenetic maps of human centromeres.. <i>Science</i> , 2022 , 376, eabl4178	33.3	19
37	Reply to VErrors in long-read assemblies can critically affect protein predictionV <i>Nature Biotechnology</i> , 2019 , 37, 127-128	44.5	18
36	Continuous chromosome-scale haplotypes assembled from a single interspecies F1 hybrid of yak and cattle. <i>GigaScience</i> , 2020 , 9,	7.6	18
35	A long read mapping method for highly repetitive reference sequences		18
34	Merqury: reference-free quality, completeness, and phasing assessment for genome assemblies		16
33	Extended haplotype-phasing of long-read de novo genome assemblies using Hi-C. <i>Nature Communications</i> , 2021 , 12, 1935	17.4	16
32	An improved pig reference genome sequence to enable pig genetics and genomics research		15
31	Mash Screen: High-throughput sequence containment estimation for genome discovery		14
30	HiCanu: accurate assembly of segmental duplications, satellites, and allelic variants from high-fidelity long reads		13

29	Segmental duplications and their variation in a complete human genome		13
28	Complete assembly of parental haplotypes with trio binning		12
27	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
26	Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies		12
25	Epigenetic patterns in a complete human genome.. <i>Science</i> , 2022 , 376, eabj5089	33.3	12
24	A complete reference genome improves analysis of human genetic variation.. <i>Science</i> , 2022 , 376, eabl3533	33.3	12
23	Segmental duplications and their variation in a complete human genome.. <i>Science</i> , 2022 , 376, eabj6965	33.3	12
22	Integrating Hi-C links with assembly graphs for chromosome-scale assembly		11
21	Assembling Large Genomes with Single-Molecule Sequencing and Locality Sensitive Hashing		10
20	The structure, function, and evolution of a complete human chromosome 8		10
19	Improved <i>Aedes aegypti</i> mosquito reference genome assembly enables biological discovery and vector control		10
18	Evolutionary and biomedical insights from a marmoset diploid genome assembly. <i>Nature</i> , 2021 , 594, 227-233	50.4	10
17	Merfin: improved variant filtering and polishing via k-mer validation		10
16	Draft Genome Sequences from a Novel Clade of Strains, Isolated from the International Space Station. <i>Genome Announcements</i> , 2017 , 5,		9
15	A Fast Approximate Algorithm for Mapping Long Reads to Large Reference Databases		9
14	Epigenetic Patterns in a Complete Human Genome		9
13	A complete reference genome improves analysis of human genetic variation		9
12	Complete genomic and epigenetic maps of human centromeres		8

11	MetaMaps ▮ Strain-level metagenomic assignment and compositional estimation for long reads		7
10	Long-read mapping to repetitive reference sequences using Winnowmap2.. <i>Nature Methods</i> , 2022 ,	21.6	7
9	MetaCompass: Reference-guided Assembly of Metagenomes		6
8	Complete vertebrate mitogenomes reveal widespread gene duplications and repeats		5
7	Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies.. <i>Nature Methods</i> , 2022 ,	21.6	4
6	Merfin: improved variant filtering, assembly evaluation and polishing via k-mer validation.. <i>Nature Methods</i> , 2022 ,	21.6	3
5	Automated assembly of high-quality diploid human reference genomes		3
4	HLA*PRG:LA ▮ HLA typing from linearly projected graph alignments		2
3	De novo likelihood-based measures for comparing metagenomic assemblies 2013 ,		1
2	The whale shark genome reveals patterns of vertebrate gene family evolution		1
1	Haplotype-Resolved Cattle Genomes Provide Insights Into Structural Variation and Adaptation		1