

# Sergey Koren

## List of Publications by Year in descending order

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Version: 2024-02-01

68  
papers

28,505  
citations

41344

49  
h-index

95266

68  
g-index

111  
all docs

111  
docs citations

111  
times ranked

29329  
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	Mash: fast genome and metagenome distance estimation using MinHash. <i>Genome Biology</i> , 2016, 17, 132.	8.8	2,099
3	Nanopore sequencing and assembly of a human genome with ultra-long reads. <i>Nature Biotechnology</i> , 2018, 36, 338-345.	17.5	1,443
4	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	12.6	1,222
5	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	27.8	1,139
6	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
7	Mercury: reference-free quality, completeness, and phasing assessment for genome assemblies. <i>Genome Biology</i> , 2020, 21, 245.	8.8	975
8	Assembly algorithms for next-generation sequencing data. <i>Genomics</i> , 2010, 95, 315-327.	2.9	957
9	Hybrid error correction and de novo assembly of single-molecule sequencing reads. <i>Nature Biotechnology</i> , 2012, 30, 693-700.	17.5	946
10	Assembling large genomes with single-molecule sequencing and locality-sensitive hashing. <i>Nature Biotechnology</i> , 2015, 33, 623-630.	17.5	877
11	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
12	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
13	GAGE: A critical evaluation of genome assemblies and assembly algorithms. <i>Genome Research</i> , 2012, 22, 557-567.	5.5	597
14	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013, 2, 10.	6.4	582
15	Telomere-to-telomere assembly of a complete human X chromosome. <i>Nature</i> , 2020, 585, 79-84.	27.8	549
16	Integrating Hi-C links with assembly graphs for chromosome-scale assembly. <i>PLoS Computational Biology</i> , 2019, 15, e1007273.	3.2	509
17	Aggressive assembly of pyrosequencing reads with mates. <i>Bioinformatics</i> , 2008, 24, 2818-2824.	4.1	498
18	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

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19	Improved reference genome of <i>Aedes aegypti</i> informs arbovirus vector control. <i>Nature</i> , 2018, 563, 501-507.	27.8	426
20	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
21	Hybrid assembly of the large and highly repetitive genome of <i>Aegilops tauschii</i> , a progenitor of bread wheat, with the MaSuRCA mega-reads algorithm. <i>Genome Research</i> , 2017, 27, 787-792.	5.5	382
22	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020, 9, .	6.4	380
23	Reducing assembly complexity of microbial genomes with single-molecule sequencing. <i>Genome Biology</i> , 2013, 14, R101.	9.6	378
24	De novo assembly of haplotype-resolved genomes with trio binning. <i>Nature Biotechnology</i> , 2018, 36, 1174-1182.	17.5	352
25	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
26	A robust benchmark for detection of germline large deletions and insertions. <i>Nature Biotechnology</i> , 2020, 38, 1347-1355.	17.5	233
27	The structure, function and evolution of a complete human chromosome 8. <i>Nature</i> , 2021, 593, 101-107.	27.8	221
28	Complete genomic and epigenetic maps of human centromeres. <i>Science</i> , 2022, 376, eabl4178.	12.6	204
29	Scaffolding of long read assemblies using long range contact information. <i>BMC Genomics</i> , 2017, 18, 527.	2.8	194
30	De Novo Assembly of a New <i>Solanum pennellii</i> Accession Using Nanopore Sequencing. <i>Plant Cell</i> , 2017, 29, 2336-2348.	6.6	192
31	An improved pig reference genome sequence to enable pig genetics and genomics research. <i>GigaScience</i> , 2020, 9, .	6.4	187
32	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
33	Evolutionary superscaffolding and chromosome anchoring to improve <i>Anopheles</i> genome assemblies. <i>BMC Biology</i> , 2020, 18, 1.	3.8	177
34	Mash Screen: high-throughput sequence containment estimation for genome discovery. <i>Genome Biology</i> , 2019, 20, 232.	8.8	173
35	A complete reference genome improves analysis of human genetic variation. <i>Science</i> , 2022, 376, eabl3533.	12.6	144
36	Segmental duplications and their variation in a complete human genome. <i>Science</i> , 2022, 376, eabj6965.	12.6	130

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37	Bambus 2: scaffolding metagenomes. <i>Bioinformatics</i> , 2011, 27, 2964-2971.	4.1	124
38	Epigenetic patterns in a complete human genome. <i>Science</i> , 2022, 376, eabj5089.	12.6	118
39	Weighted minimizer sampling improves long read mapping. <i>Bioinformatics</i> , 2020, 36, i111-i118.	4.1	116
40	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.	6.5	113
41	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
42	A fast adaptive algorithm for computing whole-genome homology maps. <i>Bioinformatics</i> , 2018, 34, i748-i756.	4.1	110
43	Strain-level metagenomic assignment and compositional estimation for long reads with MetaMaps. <i>Nature Communications</i> , 2019, 10, 3066.	12.8	98
44	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
45	HLA*LA€”HLA typing from linearly projected graph alignments. <i>Bioinformatics</i> , 2019, 35, 4394-4396.	4.1	88
46	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
47	Long-read mapping to repetitive reference sequences using Winnowmap2. <i>Nature Methods</i> , 2022, 19, 705-710.	19.0	80
48	Complete vertebrate mitogenomes reveal widespread repeats and gene duplications. <i>Genome Biology</i> , 2021, 22, 120.	8.8	69
49	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
50	Improved reference genome of the arboviral vector <i>Aedes albopictus</i> . <i>Genome Biology</i> , 2020, 21, 215.	8.8	65
51	Extended haplotype-phasing of long-read de novo genome assemblies using Hi-C. <i>Nature Communications</i> , 2021, 12, 1935.	12.8	64
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.	14.5	61
53	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
54	A chromosome-scale assembly of the major African malaria vector <i>Anopheles funestus</i> . <i>GigaScience</i> , 2019, 8, .	6.4	56

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55	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
56	Continuous chromosome-scale haplotypes assembled from a single interspecies F1 hybrid of yak and cattle. <i>GigaScience</i> , 2020, 9, .	6.4	46
57	De novo likelihood-based measures for comparing genome assemblies. <i>BMC Research Notes</i> , 2013, 6, 334.	1.4	43
58	Evolutionary and biomedical insights from a marmoset diploid genome assembly. <i>Nature</i> , 2021, 594, 227-233.	27.8	42
59	Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies. <i>Nature Methods</i> , 2022, 19, 687-695.	19.0	42
60	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
61	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
62	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
63	De novo assembly of the complex genome of <i>Nippostrongylus brasiliensis</i> using MinION long reads. <i>BMC Biology</i> , 2018, 16, 6.	3.8	35
64	Merfin: improved variant filtering, assembly evaluation and polishing via k-mer validation. <i>Nature Methods</i> , 2022, 19, 696-704.	19.0	30
65	Reply to "Errors in long-read assemblies can critically affect protein prediction". <i>Nature Biotechnology</i> , 2019, 37, 127-128.	17.5	29
66	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
67	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
68	De novo likelihood-based measures for comparing metagenomic assemblies. , 2013, , .		1