

# 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	Merfin: improved variant filtering, assembly evaluation and polishing via k-mer validation. Nature Methods, 2022, 19, 696-704.	19.0	30
2	Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies. Nature Methods, 2022, 19, 687-695.	19.0	42
3	Epigenetic patterns in a complete human genome. Science, 2022, 376, eabj5089.	12.6	118
4	Complete genomic and epigenetic maps of human centromeres. Science, 2022, 376, eabl4178.	12.6	204
5	A complete reference genome improves analysis of human genetic variation. Science, 2022, 376, eabl3533.	12.6	144
6	The complete sequence of a human genome. Science, 2022, 376, 44-53.	12.6	1,222
7	Segmental duplications and their variation in a complete human genome. Science, 2022, 376, eabj6965.	12.6	130
8	Long-read mapping to repetitive reference sequences using Winnowmap2. Nature Methods, 2022, 19, 705-710.	19.0	80
9	The structure, function and evolution of a complete human chromosome 8. Nature, 2021, 593, 101-107.	27.8	221
10	Evolutionary and biomedical insights from a marmoset diploid genome assembly. Nature, 2021, 594, 227-233.	27.8	42
11	Extended haplotype-phasing of long-read de novo genome assemblies using Hi-C. Nature Communications, 2021, 12, 1935.	12.8	64
12	Complete vertebrate mitogenomes reveal widespread repeats and gene duplications. Genome Biology, 2021, 22, 120.	8.8	69
13	Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.	27.8	1,139
14	Strains used in whole organism Plasmodium falciparum vaccine trials differ in genome structure, sequence, and immunogenic potential. Genome Medicine, 2020, 12, 6.	8.2	61
15	Evolutionary superscaffolding and chromosome anchoring to improve Anopheles genome assemblies. BMC Biology, 2020, 18, 1.	3.8	177
16	Weighted minimizer sampling improves long read mapping. Bioinformatics, 2020, 36, i111-i118.	4.1	116
17	Telomere-to-telomere assembly of a complete human X chromosome. Nature, 2020, 585, 79-84.	27.8	549
18	Improved reference genome of the arboviral vector Aedes albopictus. Genome Biology, 2020, 21, 215.	8.8	65

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19	Merqury: reference-free quality, completeness, and phasing assessment for genome assemblies. <i>Genome Biology</i> , 2020, 21, 245.	8.8	975
20	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
21	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
22	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
23	A robust benchmark for detection of germline large deletions and insertions. <i>Nature Biotechnology</i> , 2020, 38, 1347-1355.	17.5	233
24	An improved pig reference genome sequence to enable pig genetics and genomics research. <i>GigaScience</i> , 2020, 9, .	6.4	187
25	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
26	Continuous chromosome-scale haplotypes assembled from a single interspecies F1 hybrid of yak and cattle. <i>GigaScience</i> , 2020, 9, .	6.4	46
27	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020, 9, .	6.4	380
28	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
29	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
30	Strain-level metagenomic assignment and compositional estimation for long reads with MetaMaps. <i>Nature Communications</i> , 2019, 10, 3066.	12.8	98
31	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
32	Mash Screen: high-throughput sequence containment estimation for genome discovery. <i>Genome Biology</i> , 2019, 20, 232.	8.8	173
33	Integrating Hi-C links with assembly graphs for chromosome-scale assembly. <i>PLoS Computational Biology</i> , 2019, 15, e1007273.	3.2	509
34	Reply to "Errors in long-read assemblies can critically affect protein prediction". <i>Nature Biotechnology</i> , 2019, 37, 127-128.	17.5	29
35	A chromosome-scale assembly of the major African malaria vector <i>Anopheles funestus</i> . <i>GigaScience</i> , 2019, 8, .	6.4	56
36	HLA*LA"HLA typing from linearly projected graph alignments. <i>Bioinformatics</i> , 2019, 35, 4394-4396.	4.1	88

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37	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
38	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
39	Nanopore sequencing and assembly of a human genome with ultra-long reads. <i>Nature Biotechnology</i> , 2018, 36, 338-345.	17.5	1,443
40	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
41	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
42	Improved reference genome of <i>Aedes aegypti</i> informs arbovirus vector control. <i>Nature</i> , 2018, 563, 501-507.	27.8	426
43	A fast adaptive algorithm for computing whole-genome homology maps. <i>Bioinformatics</i> , 2018, 34, i748-i756.	4.1	110
44	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
45	De novo assembly of haplotype-resolved genomes with trio binning. <i>Nature Biotechnology</i> , 2018, 36, 1174-1182.	17.5	352
46	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
47	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
48	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
49	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
50	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
51	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
52	Canu: scalable and accurate long-read assembly via adaptive k-mer weighting and repeat separation. <i>Genome Research</i> , 2017, 27, 722-736.	5.5	5,620
53	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
54	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

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55	Scaffolding of long read assemblies using long range contact information. BMC Genomics, 2017, 18, 527.	2.8	194
56	Mash: fast genome and metagenome distance estimation using MinHash. Genome Biology, 2016, 17, 132.	8.8	2,099
57	Radical remodeling of the Y chromosome in a recent radiation of malaria mosquitoes. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2114-23.	7.1	92
58	Assembling large genomes with single-molecule sequencing and locality-sensitive hashing. Nature Biotechnology, 2015, 33, 623-630.	17.5	877
59	One chromosome, one contig: complete microbial genomes from long-read sequencing and assembly. Current Opinion in Microbiology, 2015, 23, 110-120.	5.1	413
60	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. GigaScience, 2013, 2, 10.	6.4	582
61	De novo likelihood-based measures for comparing genome assemblies. BMC Research Notes, 2013, 6, 334.	1.4	43
62	De novo likelihood-based measures for comparing metagenomic assemblies. , 2013, , .		1
63	Reducing assembly complexity of microbial genomes with single-molecule sequencing. Genome Biology, 2013, 14, R101.	9.6	378
64	GAGE: A critical evaluation of genome assemblies and assembly algorithms. Genome Research, 2012, 22, 557-567.	5.5	597
65	Hybrid error correction and de novo assembly of single-molecule sequencing reads. Nature Biotechnology, 2012, 30, 693-700.	17.5	946
66	Bambus 2: scaffolding metagenomes. Bioinformatics, 2011, 27, 2964-2971.	4.1	124
67	Assembly algorithms for next-generation sequencing data. Genomics, 2010, 95, 315-327.	2.9	957
68	Aggressive assembly of pyrosequencing reads with mates. Bioinformatics, 2008, 24, 2818-2824.	4.1	498