Sergey Koren

List of Publications by Year in Descending Order

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	Merfin: improved variant filtering, assembly evaluation and polishing via k-mer validation.. *Nature Methods*, **2022**,	21.6	3
99	Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies.. *Nature Methods*, **2022**,	21.6	4
98	Epigenetic patterns in a complete human genome.. *Science*, **2022**, 376, eabj5089	33.3	12
97	Complete genomic and epigenetic maps of human centromeres.. *Science*, **2022**, 376, eabl4178	33.3	19
96	A complete reference genome improves analysis of human genetic variation.. *Science*, **2022**, 376, eabl3533	33.3	12
95	The complete sequence of a human genome.. *Science*, **2022**, 376, 44-53	33.3	107
94	Segmental duplications and their variation in a complete human genome.. *Science*, **2022**, 376, eabj6965	33.3	12
93	Long-read mapping to repetitive reference sequences using Winnowmap2.. *Nature Methods*, **2022**,	21.6	7
92	The structure, function and evolution of a complete human chromosome 8. *Nature*, **2021**, 593, 101-107	50.4	72
91	Evolutionary and biomedical insights from a marmoset diploid genome assembly. *Nature*, **2021**, 594, 227-233	50.4	10
90	Extended haplotype-phasing of long-read de novo genome assemblies using Hi-C. *Nature Communications*, **2021**, 12, 1935	17.4	16
89	Complete vertebrate mitogenomes reveal widespread repeats and gene duplications. *Genome Biology*, **2021**, 22, 120	18.3	19
88	Towards complete and error-free genome assemblies of all vertebrate species. *Nature*, **2021**, 592, 737-746	50.4	161
87	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. *Nature Biotechnology*, **2020**, 38, 1044-1053	44.5	143
86	Effect of sequence depth and length in long-read assembly of the maize inbred NC358. *Nature Communications*, **2020**, 11, 2288	17.4	21
85	A robust benchmark for detection of germline large deletions and insertions. *Nature Biotechnology*, **2020**, 38, 1347-1355	44.5	98
84	An improved pig reference genome sequence to enable pig genetics and genomics research. *GigaScience*, **2020**, 9,	7.6	60

83	Haplotype-resolved genomes provide insights into structural variation and gene content in Angus and Brahman cattle. *Nature Communications*, **2020**, 11, 2071	17.4	38
82	Continuous chromosome-scale haplotypes assembled from a single interspecies F1 hybrid of yak and cattle. *GigaScience*, **2020**, 9,	7.6	18
81	Strains used in whole organism Plasmodium falciparum vaccine trials differ in genome structure, sequence, and immunogenic potential. *Genome Medicine*, **2020**, 12, 6	14.4	27
80	Evolutionary superscaffolding and chromosome anchoring to improve Anopheles genome assemblies. *BMC Biology*, **2020**, 18, 1	7.3	51
79	Weighted minimizer sampling improves long read mapping. *Bioinformatics*, **2020**, 36, i111-i118	7.2	45
78	Telomere-to-telomere assembly of a complete human X chromosome. *Nature*, **2020**, 585, 79-84	50.4	269
77	Improved reference genome of the arboviral vector Aedes albopictus. *Genome Biology*, **2020**, 21, 215	18.3	26
76	Merqury: reference-free quality, completeness, and phasing assessment for genome assemblies. *Genome Biology*, **2020**, 21, 245	18.3	101
75	HiCanu: accurate assembly of segmental duplications, satellites, and allelic variants from high-fidelity long reads. *Genome Research*, **2020**, 30, 1291-1305	9.7	145
74	De novo assembly of the cattle reference genome with single-molecule sequencing. *GigaScience*, **2020**, 9,	7.6	140
73	Integrating Hi-C links with assembly graphs for chromosome-scale assembly. *PLoS Computational Biology*, **2019**, 15, e1007273	5	202
72	Reply to \Errors in long-read assemblies can critically affect protein prediction\ *Nature Biotechnology*, **2019**, 37, 127-128	44.5	18
71	A chromosome-scale assembly of the major African malaria vector Anopheles funestus. *GigaScience* , **2019**, 8,	7.6	26
70	HLA*LA-HLA typing from linearly projected graph alignments. *Bioinformatics*, **2019**, 35, 4394-4396	7.2	42
69	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. *Nature Biotechnology*, **2019**, 37, 1155-1162	44.5	427
68	Assignment of virus and antimicrobial resistance genes to microbial hosts in a complex microbial community by combined long-read assembly and proximity ligation. *Genome Biology*, **2019**, 20, 153	18.3	38
67	Strain-level metagenomic assignment and compositional estimation for long reads with MetaMaps. *Nature Communications*, **2019**, 10, 3066	17.4	51
66	De novo assembly of the goldfish () genome and the evolution of genes after whole-genome duplication. *Science Advances*, **2019**, 5, eaav0547	14.3	66

65	Mash Screen: high-throughput sequence containment estimation for genome discovery. *Genome Biology*, **2019**, 20, 232	18.3	63
64	New insights into mammalian sex chromosome structure and evolution using high-quality sequences from bovine X and Y chromosomes. *BMC Genomics*, **2019**, 20, 1000	4.5	12
63	Metagenomic assembly through the lens of validation: recent advances in assessing and improving the quality of genomes assembled from metagenomes. *Briefings in Bioinformatics*, **2019**, 20, 1140-1150	13.4	63
62	Nanopore sequencing and assembly of a human genome with ultra-long reads. *Nature Biotechnology*, **2018**, 36, 338-345	44.5	968
61	Analysis of the Aedes albopictus C6/36 genome provides insight into cell line utility for viral propagation. *GigaScience*, **2018**, 7, 1-13	7.6	24
60	A Fast Approximate Algorithm for Mapping Long Reads to Large Reference Databases. *Journal of Computational Biology*, **2018**, 25, 766-779	1.7	26
59	De novo assembly of the complex genome of Nippostrongylus brasiliensis using MinION long reads. *BMC Biology*, **2018**, 16, 6	7.3	22
58	Improved reference genome of Aedes aegypti informs arbovirus vector control. *Nature*, **2018**, 563, 501-507	50.4	235
57	A fast adaptive algorithm for computing whole-genome homology maps. *Bioinformatics*, **2018**, 34, i748-i756	7.5	53
56	RefSeq database growth influences the accuracy of k-mer-based lowest common ancestor species identification. *Genome Biology*, **2018**, 19, 165	18.3	57
55	De novo assembly of haplotype-resolved genomes with trio binning. *Nature Biotechnology*, **2018**,	44.5	171
54	Variation in human chromosome 21 ribosomal RNA genes characterized by TAR cloning and long-read sequencing. *Nucleic Acids Research*, **2018**, 46, 6712-6725	20.1	36
53	Hybrid assembly of the large and highly repetitive genome of , a progenitor of bread wheat, with the MaSuRCA mega-reads algorithm. *Genome Research*, **2017**, 27, 787-792	9.7	208
52	Single-molecule sequencing and chromatin conformation capture enable de novo reference assembly of the domestic goat genome. *Nature Genetics*, **2017**, 49, 643-650	36.3	323
51	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. *Genome Research*, **2017**, 27, 849-864	9.7	365
50	A Fast Approximate Algorithm for Mapping Long Reads to Large Reference Databases. *Lecture Notes in Computer Science*, **2017**, 66-81	0.9	21
49	Canu: scalable and accurate long-read assembly via adaptive -mer weighting and repeat separation. *Genome Research*, **2017**, 27, 722-736	9.7	2943
48	De Novo Assembly of a New Accession Using Nanopore Sequencing. *Plant Cell*, **2017**, 29, 2336-2348	11.6	138

47   Scaffolding of long read assemblies using long range contact information. *BMC Genomics*, **2017**, 18, 527   4.5   90

46   Draft Genome Sequences from a Novel Clade of Strains, Isolated from the International Space Station. *Genome Announcements*, **2017**, 5,   9

45   Mash: fast genome and metagenome distance estimation using MinHash. *Genome Biology*, **2016**, 17, 132   18.3   1066

44   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   11.5   63

43   Assembling large genomes with single-molecule sequencing and locality-sensitive hashing. *Nature Biotechnology*, **2015**, 33, 623-30   44.5   650

42   One chromosome, one contig: complete microbial genomes from long-read sequencing and assembly. *Current Opinion in Microbiology*, **2015**, 23, 110-20   7.9   302

41   Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. *GigaScience*, **2013**, 2, 10   7.6   461

40   De novo likelihood-based measures for comparing genome assemblies. *BMC Research Notes*, **2013**, 6, 334   2.3   33

39   De novo likelihood-based measures for comparing metagenomic assemblies **2013**,   1

38   Reducing assembly complexity of microbial genomes with single-molecule sequencing. *Genome Biology*, **2013**, 14, R101   18.3   286

37   GAGE: A critical evaluation of genome assemblies and assembly algorithms. *Genome Research*, **2012**, 22, 557-67   9.7   485

36   Hybrid error correction and de novo assembly of single-molecule sequencing reads. *Nature Biotechnology*, **2012**, 30, 693-700   44.5   758

35   Bambus 2: scaffolding metagenomes. *Bioinformatics*, **2011**, 27, 2964-71   7.2   106

34   Assembly algorithms for next-generation sequencing data. *Genomics*, **2010**, 95, 315-27   4.3   764

33   Aggressive assembly of pyrosequencing reads with mates. *Bioinformatics*, **2008**, 24, 2818-24   7.2   407

32   Assembling Large Genomes with Single-Molecule Sequencing and Locality Sensitive Hashing   10

31   Canu: scalable and accurate long-read assembly via adaptive k-mer weighting and repeat separation   89

30   A Fast Approximate Algorithm for Mapping Long Reads to Large Reference Databases   9

LIST OF PUBLICATIONS