

# Long-read sequence assembly of the gorilla genome

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Citation Report

#	ARTICLE	IF	CITATIONS
1	The Complete Chloroplast Genome Sequence of the Medicinal Plant <i>Swertia mussotii</i> Using the PacBio RS II Platform. <i>Molecules</i> , 2016, 21, 1029.	1.7	53
2	Contiguous and accurate <i>de novo</i> assembly of metazoan genomes with modest long read coverage. <i>Nucleic Acids Research</i> , 2016, 44, gkw654.	6.5	329
3	Towards integration of population and comparative genomics in forest trees. <i>New Phytologist</i> , 2016, 212, 338-344.	3.5	31
4	Evolution and demography of the great apes. <i>Current Opinion in Genetics and Development</i> , 2016, 41, 124-129.	1.5	27
5	Reading the Underlying Information From Massive Metagenomic Sequencing Data. <i>Proceedings of the IEEE</i> , 2016, , 1-15.	16.4	12
6	Human adaptation and evolution by segmental duplication. <i>Current Opinion in Genetics and Development</i> , 2016, 41, 44-52.	1.5	157
7	Phased diploid genome assembly with single-molecule real-time sequencing. <i>Nature Methods</i> , 2016, 13, 1050-1054.	9.0	1,658
8	The population genomics of rhesus macaques ( <i>Macaca mulatta</i> ) based on whole-genome sequences. <i>Genome Research</i> , 2016, 26, 1651-1662.	2.4	101
9	Genome sequence and analysis of the Japanese morning glory <i>Ipomoea nil</i> . <i>Nature Communications</i> , 2016, 7, 13295.	5.8	138
10	Short tandem repeats, segmental duplications, gene deletion, and genomic instability in a rapidly diversified immune gene family. <i>BMC Genomics</i> , 2016, 17, 900.	1.2	25
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15	Single-molecule sequencing and chromatin conformation capture enable <i>de novo</i> reference assembly of the domestic goat genome. <i>Nature Genetics</i> , 2017, 49, 643-650.	9.4	600
16	An improved assembly and annotation of the allohexaploid wheat genome identifies complete families of agronomic genes and provides genomic evidence for chromosomal translocations. <i>Genome Research</i> , 2017, 27, 885-896.	2.4	464
17	Contrasting evolutionary genome dynamics between domesticated and wild yeasts. <i>Nature Genetics</i> , 2017, 49, 913-924.	9.4	340
18	Resolving Multicopy Duplications <i>de novo</i> Using Polyploid Phasing. <i>Lecture Notes in Computer Science</i> , 2017, 10229, 117-133.	1.0	22

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20	Recent advances in sequence assembly: principles and applications. <i>Briefings in Functional Genomics</i> , 2017, 16, 361-378.	1.3	14
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22	Structural Variation Shapes the Landscape of Recombination in Mouse. <i>Genetics</i> , 2017, 206, 603-619.	1.2	51
23	Advantages of genome sequencing by long-read sequencer using SMRT technology in medical area. <i>Human Cell</i> , 2017, 30, 149-161.	1.2	144
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35	MECAT: fast mapping, error correction, and de novo assembly for single-molecule sequencing reads. <i>Nature Methods</i> , 2017, 14, 1072-1074.	9.0	357
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40	Contributions of <i>Zea mays</i> subspecies <i>mexicana</i> haplotypes to modern maize. <i>Nature Communications</i> , 2017, 8, 1874.	5.8	102
41	Genome Sequence of <i>Roseovarius mucosus</i> Strain SMR3, Isolated from a Culture of the Diatom <i>Skeletonema marinoi</i>. <i>Genome Announcements</i> , 2017, 5, .	0.8	7
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52	Hybrid de novo genome assembly and centromere characterization of the gray mouse lemur ( <i>Microcebus murinus</i> ). <i>BMC Biology</i> , 2017, 15, 110.	1.7	53
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88	Structural Variants in Ancient Genomes. Population Genomics, 2018, , 375-391.	0.2	1
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129	Population Genetics and Savanna Monkeys. , 2019, , 81-100.		0
130	Population Genetic Structure of Vervet Monkeys in South Africa. , 2019, , 101-106.		0
131	Behavioral Ecology of Savanna Monkeys. , 2019, , 109-126.		1
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133	Biological Complexity in Primate Sociality and Health. , 2019, , 133-140.		0
134	Predation and Food Competition in Vervet Monkeys ( <i>Chlorocebus pygerythrus</i> ). , 2019, , 141-151.		0
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141	Ethnoprimateology and Savanna Monkeys. , 2019, , 235-243.		1
142	Exploring Caribbean Green Monkeys ( <i>Chlorocebus sabaues</i> ) through an Ethnoprimateological Lens. , 2019, , 244-254.		0
143	Vervet Monkeys ( <i>Chlorocebus pygerythrus</i> ), Chimpanzees ( <i>Pan troglodytes</i> ), and Humans ( <i>Homo</i> ) Tj ETQq1 1 0.784314 rgBT 6Overloc		
146	Short communication: Identification of the pseudoautosomal region in the Hereford bovine reference genome assembly ARS-UCD1.2. <i>Journal of Dairy Science</i> , 2019, 102, 3254-3258.	1.4	18
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156	Iso-Seq Allows Genome-Independent Transcriptome Profiling of Grape Berry Development. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 755-767.	0.8	79
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161	Porous Zero-Mode Waveguides for Picogram-Level DNA Capture. <i>Nano Letters</i> , 2019, 19, 921-929.	4.5	22
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164	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.	3.2	113
165	Comprehensive evaluation of non-hybrid genome assembly tools for third-generation PacBio long-read sequence data. <i>Briefings in Bioinformatics</i> , 2019, 20, 866-876.	3.2	86
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169	Prospects for sociogenomics in avian cooperative breeding and parental care. <i>Environmental Epigenetics</i> , 2020, 66, 293-306.	0.9	2
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171	The design and construction of reference pangenome graphs with minigraph. <i>Genome Biology</i> , 2020, 21, 265.	3.8	195
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