

Multi-platform discovery of haplotype-resolved structure

Nature Communications

10, 1784

DOI: [10.1038/s41467-018-08148-z](https://doi.org/10.1038/s41467-018-08148-z)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Versatile Quality Control Methods for Nanopore Sequencing. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431986306.	0.6	1
2	Comparison of mitochondrial DNA variants detection using short- and long-read sequencing. <i>Journal of Human Genetics</i> , 2019, 64, 1107-1116.	1.1	8
3	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. <i>Nature Biotechnology</i> , 2019, 37, 1155-1162.	9.4	1,010
4	Goodbye reference, hello genome graphs. <i>Nature Biotechnology</i> , 2019, 37, 866-868.	9.4	19
5	A clinically validated whole genome pipeline for structural variant detection and analysis. <i>BMC Genomics</i> , 2019, 20, 545.	1.2	15
6	Long-read sequencing in human genetics. <i>Medizinische Genetik</i> , 2019, 31, 198-204.	0.1	12
7	Fully-sensitive seed finding in sequence graphs using a hybrid index. <i>Bioinformatics</i> , 2019, 35, i81-i89.	1.8	12
8	Large-scale mammalian genome rearrangements coincide with chromatin interactions. <i>Bioinformatics</i> , 2019, 35, i117-i126.	1.8	4
9	Genetic Variation, Comparative Genomics, and the Diagnosis of Disease. <i>New England Journal of Medicine</i> , 2019, 381, 64-74.	13.9	127
10	Joint inference and alignment of genome structures enables characterization of compartment-independent reorganization across cell types. <i>Epigenetics and Chromatin</i> , 2019, 12, 61.	1.8	4
11	Longshot enables accurate variant calling in diploid genomes from single-molecule long read sequencing. <i>Nature Communications</i> , 2019, 10, 4660.	5.8	156
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16	Clonal crops show structural variation role in domestication. <i>Nature Plants</i> , 2019, 5, 915-916.	4.7	4
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18	Mapping Genome Variants Sheds Light on Genetic and Phenotypic Differentiation in Chinese. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 226-228.	3.0	1

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20	VISOR: a versatile haplotype-aware structural variant simulator for short- and long-read sequencing. <i>Bioinformatics</i> , 2020, 36, 1267-1269.	1.8	29
21	SVIM: structural variant identification using mapped long reads. <i>Bioinformatics</i> , 2019, 35, 2907-2915.	1.8	173
22	One reference genome is not enough. <i>Genome Biology</i> , 2019, 20, 104.	3.8	58
23	High-coverage, long-read sequencing of Han Chinese trio reference samples. <i>Scientific Data</i> , 2019, 6, 91.	2.4	13
24	Haplotype-aware diplotyping from noisy long reads. <i>Genome Biology</i> , 2019, 20, 116.	3.8	43
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