

Resource Summary Report

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Long Ranger

RRID:SCR_018925

Type: Tool

Proper Citation

Long Ranger (RRID:SCR_018925)

Resource Information

URL: <https://support.10xgenomics.com/genome-exome/software/pipelines/latest/what-is-long-ranger>

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Description: Software tool as set of analysis pipelines that processes Chromium sequencing output to align reads and call and phase SNPs, indels, and structural variants by 10x Genomics.

Resource Type: data analysis software, data processing software, software application, software resource, software toolkit

Keywords: Analysis pipelines, process chromium sequencing output, align reads, call SNPs, phase SNPs, indel, structural variant, 10x Genomics

Availability: Restricted

Resource Name: Long Ranger

Resource ID: SCR_018925

License: <https://support.10xgenomics.com/genome-exome/software/downloads/latest>

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260905T132844+0000

Ratings and Alerts

No rating or validation information has been found for Long Ranger.

No alerts have been found for Long Ranger.

Data and Source Information

Usage and Citation Metrics

We found 14 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Azam S, et al. (2025) Advancing the Indian cattle pangenome: characterizing non-reference sequences in *Bos indicus*. *Journal of animal science and biotechnology*, 16(1), 21.

Robb TJ, et al. (2023) Complex Patterns of Genomic Heterogeneity Identified in 42 Tumor Samples and ctDNA of a Pulmonary Atypical Carcinoid Patient. *Cancer research communications*, 3(1), 31.

Kanamori S, et al. (2022) Draft genome of six Cuban Anolis lizards and insights into genetic changes during their diversification. *BMC ecology and evolution*, 22(1), 129.

Winter S, et al. (2022) A Chromosome-Scale Genome Assembly of the Okapi (*Okapia johnstoni*). *The Journal of heredity*, 113(5), 568.

Catania T, et al. (2022) A functionally conserved STORR gene fusion in *Papaver* species that diverged 16.8 million years ago. *Nature communications*, 13(1), 3150.

Knudsen S, et al. (2022) FIND-IT: Accelerated trait development for a green evolution. *Science advances*, 8(34), eabq2266.

Peel E, et al. (2021) A reference genome for the critically endangered woylie, *Bettongia penicillata ogilbyi*. *GigaByte (Hong Kong, China)*, 2021, gigabyte35.

Wang Y, et al. (2021) Comprehensive identification of somatic nucleotide variants in human brain tissue. *Genome biology*, 22(1), 92.

Zhang JY, et al. (2021) Using de novo assembly to identify structural variation of eight complex immune system gene regions. *PLoS computational biology*, 17(8), e1009254.

Brandies PA, et al. (2020) The first *Antechinus* reference genome provides a resource for investigating the genetic basis of semelparity and age-related neuropathologies. *GigaByte (Hong Kong, China)*, 2020, gigabyte7.

Long HK, et al. (2020) Loss of Extreme Long-Range Enhancers in Human Neural Crest Drives a Craniofacial Disorder. *Cell stem cell*, 27(5), 765.

Zhang L, et al. (2020) De novo diploid genome assembly for genome-wide structural variant detection. *NAR genomics and bioinformatics*, 2(1), lqz018.

Legeai F, et al. (2020) Genomic architecture of endogenous ichnoviruses reveals distinct evolutionary pathways leading to virus domestication in parasitic wasps. *BMC biology*, 18(1), 89.

Hiltunen M, et al. (2019) Maintenance of High Genome Integrity over Vegetative Growth in the Fairy-Ring Mushroom *Marasmius oreades*. *Current biology* : CB, 29(16), 2758.