

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

[ploidyNGS](#)

RRID:SCR_021320

Type: Tool

Proper Citation

ploidyNGS (RRID:SCR_021320)

Resource Information

URL: <https://github.com/diriano/ploidyNGS>

Proper Citation: ploidyNGS (RRID:SCR_021320)

Description: Open source software tool for visually exploring ploidy with Next Generation Sequencing data. Used to visualize and explore ploidy levels in newly sequenced genome, exploiting short read data. Allows identification of ploidy level of newly sequenced genome in visual way. Implemented in Python and R.

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

Defining Citation: [PMID:28383704](#)

Keywords: Visually exploring ploidy, Next Generation Sequencing, newly sequenced genome, exploiting short read data

Funding: Sao Paulo Research Foundation

Availability: Free, Available for download, Freely available

Resource Name: ploidyNGS

Resource ID: SCR_021320

License: GNU General Public License

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260815T182654+0000

Ratings and Alerts

No rating or validation information has been found for ploidyNGS.

No alerts have been found for ploidyNGS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Pevsner R, et al. (2026) Telomere-to-telomere genome assembly of Microsporidia sp. MB, a microsporidian symbiont of *Anopheles coluzzii* isolated from Burkina Faso. *BMC genomics*, 27(1).

Wi??niewska MM, et al. (2026) The genome sequence of the gastric gland parasite, *Cryptosporidium proliferans*. *iScience*, 29(5), 115597.

Colp MJ, et al. (2026) Genome Sequence Data Reveal Complex and Variable Ploidy in the Amoebozoan *Acanthamoeba castellanii*. *Genome biology and evolution*, 18(4).

Liang H, et al. (2025) Chromosome-level genomes of two Bracteacoccaceae highlight adaptations to biocrusts. *Nature communications*, 16(1), 1492.

Wang R, et al. (2024) Genetic characteristics of the diploid offsprings in potato Cooperation 88 induced by diploid donor IVP101. *Frontiers in plant science*, 15, 1486549.

Canales NA, et al. (2022) A highly contiguous, scaffold-level nuclear genome assembly for the fever tree (*Cinchona pubescens* Vahl) as a novel resource for Rubiaceae research. *GigaByte* (Hong Kong, China), 2022, gigabyte71.

Salas-Leiva DE, et al. (2021) Genomic analysis finds no evidence of canonical eukaryotic DNA processing complexes in a free-living protist. *Nature communications*, 12(1), 6003.

Rueda-Mejia MP, et al. (2021) Genome, transcriptome and secretome analyses of the antagonistic, yeast-like fungus *Aureobasidium pullulans* to identify potential biocontrol genes. *Microbial cell* (Graz, Austria), 8(8), 184.