Resource Summary Report

Generated by RRID on May 16, 2025

BioNano Irys system

RRID:SCR_016754
Type: Tool

Proper Citation

BioNano Irys system (RRID:SCR_016754)

Resource Information

URL: https://bionanogenomics.com/wp-content/uploads/2017/01/30047-Irys-User-Guide.pdf

Proper Citation: BioNano Irys system (RRID:SCR_016754)

Description: System by BioNano Genomics (formerly BioNanomatrix) which provides optical next generation mapping (NGM). Used for sequence assembly and structural variation analysis. Provides Scaffold Bionano genome mapping data with sequencing data to improve assembly contiguity, reduce sequencing coverage needed, and automatically correct errors in sequencing based assemblies.

Resource Type: instrument resource

Keywords: instrument, Irys, system, BioNano Genomics, BioNanomatrix, optical, next, generation, mapping, sequence, assembly, structural, variation, analysis, data,

Funding:

Availability: Commercially available

Resource Name: BioNano Irys system

Resource ID: SCR_016754

Alternate URLs: https://bionanogenomics.com/wp-content/uploads/2017/01/2016-Irys-System-Brochure.pdf

Old URLs: https://bionanogenomics.com/technology/genome-assembly/

Record Creation Time: 20220129T080332+0000

Record Last Update: 20250420T014818+0000

Ratings and Alerts

No rating or validation information has been found for BioNano Irys system.

No alerts have been found for BioNano Irys system.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 34 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Cahn J, et al. (2024) MaizeCODE reveals bi-directionally expressed enhancers that harbor molecular signatures of maize domestication. Nature communications, 15(1), 10854.

Shen F, et al. (2023) Comparative genomics reveals a unique nitrogen-carbon balance system in Asteraceae. Nature communications, 14(1), 4334.

Zhang W, et al. (2023) Genome architecture and diverged selection shaping pattern of genomic differentiation in wild barley. Plant biotechnology journal, 21(1), 46.

He Q, et al. (2023) A graph-based genome and pan-genome variation of the model plant Setaria. Nature genetics, 55(7), 1232.

Wang H, et al. (2022) A Chromosome-level assembly of the Japanese eel genome, insights into gene duplication and chromosomal reorganization. GigaScience, 11.

Xu Z, et al. (2022) Genome sequence of Gossypium anomalum facilitates interspecific introgression breeding. Plant communications, 3(5), 100350.

Palmada-Flores M, et al. (2022) A high-quality, long-read genome assembly of the endangered ring-tailed lemur (Lemur catta). GigaScience, 11.

Li Y, et al. (2021) Subtelomeric assembly of a multi-gene pathway for antimicrobial defense compounds in cereals. Nature communications, 12(1), 2563.

Nath S, et al. (2021) Improved contiguity of the threespine stickleback genome using long-read sequencing. G3 (Bethesda, Md.), 11(2).

Yan L, et al. (2021) Genome assembly of primitive cultivated potato Solanum stenotomum

provides insights into potato evolution. G3 (Bethesda, Md.), 11(10).

Cui F, et al. (2021) The genome of the warm-season turfgrass African bermudagrass (Cynodon transvaalensis). Horticulture research, 8(1), 93.

Paritosh K, et al. (2021) A chromosome-scale assembly of allotetraploid Brassica juncea (AABB) elucidates comparative architecture of the A and B genomes. Plant biotechnology journal, 19(3), 602.

Liu Y, et al. (2021) De Novo Sequencing and High-Contiguity Genome Assembly of Moniezia expansa Reveals Its Specific Fatty Acid Metabolism and Reproductive Stem Cell Regulatory Network. Frontiers in cellular and infection microbiology, 11, 693914.

Li J, et al. (2021) A new duck genome reveals conserved and convergently evolved chromosome architectures of birds and mammals. GigaScience, 10(1).

Wang J, et al. (2021) A high-quality chromosome-scale assembly of the centipedegrass [Eremochloa ophiuroides (Munro) Hack.] genome provides insights into chromosomal structural evolution and prostrate growth habit. Horticulture research, 8(1), 201.

Hu Y, et al. (2021) Genome assembly and population genomic analysis provide insights into the evolution of modern sweet corn. Nature communications, 12(1), 1227.

Chapman LM, et al. (2020) A crowdsourced set of curated structural variants for the human genome. PLoS computational biology, 16(6), e1007933.

Shao F, et al. (2020) Chromosome-level genome assembly of the female western mosquitofish (Gambusia affinis). GigaScience, 9(8).

Xie J, et al. (2020) A chromosome-scale reference genome of Aquilegia oxysepala var. kansuensis. Horticulture research, 7(1), 113.

Delmore K, et al. (2020) The evolutionary history and genomics of European blackcap migration. eLife, 9.