Resource Summary Report

Generated by FDI Lab - SciCrunch.org on May 4, 2025

Saphyr

RRID:SCR_017992
Type: Tool

Proper Citation

Saphyr (RRID:SCR_017992)

Resource Information

URL: https://bionano.com/saphyr-systems/

Proper Citation: Saphyr (RRID:SCR_017992)

Description: Whole genome imaging instrument by Bionano Genomics for high speed, high throughput structural variant detection and analysis with exceptional sensitivity and specificity. Detects structural variations ranging from 500 bp to megabase pairs in length. For mosaic samples or heterogeneous cancer samples, detects all types of structural variants down to 5% Variant Allele Fraction. Calls repeats and complex rearrangements.

Synonyms: BIONANO SAPHYR® GENOME IMAGING

Resource Type: instrument resource

Keywords: sequencing machine, hardware, high-throughput sequencing, instrument, equipment

Funding:

Availability: Restricted

Resource Name: Saphyr

Resource ID: SCR_017992

Alternate URLs: https://www.analogway.com/files/uploads/produit/download/user-manual-saphyr.pdf

Old URLs: https://bionanogenomics.com/products/saphyr/

Record Creation Time: 20220129T080338+0000

Record Last Update: 20250420T014846+0000

Ratings and Alerts

No rating or validation information has been found for Saphyr.

No alerts have been found for Saphyr.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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

Shukla H, et al. (2022) Near-chromosomal de novo assembly of Bengal tiger genome reveals genetic hallmarks of apex predation. GigaScience, 12.

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

Field MA, et al. (2020) Canfam_GSD: De novo chromosome-length genome assembly of the German Shepherd Dog (Canis lupus familiaris) using a combination of long reads, optical mapping, and Hi-C. GigaScience, 9(4).

Etherington GJ, et al. (2020) Sequencing smart: De novo sequencing and assembly approaches for a non-model mammal. GigaScience, 9(5).