

Resource Summary Report

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MGI: DNBSEQ-G400

RRID:SCR_017980

Type: Tool

Proper Citation

MGI: DNBSEQ-G400 (RRID:SCR_017980)

Resource Information

URL: https://en.mgitech.cn/products/instruments_info/2/

Proper Citation: MGI: DNBSEQ-G400 (RRID:SCR_017980)

Description: Sequencer developed by MGI Tech Co. Ltd. Next generation sequencing platform. Its sequencing principle relies on DNB and cPAS technologies also used in previous version of BGISEQ-500 device, but reagents for MGISEQ-2000 are refined and platform utilizes updated software. Built with new chip system that can flexibly support variety of different sequencing models.

Abbreviations: Restricted

Synonyms: MGISEQ-2000

Resource Type: instrument resource

Defining Citation: [DOI:10.1101/577080](https://doi.org/10.1101/577080)

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

Resource Name: MGI: DNBSEQ-G400

Resource ID: SCR_017980

Alternate URLs: <https://en.mgitech.com//Uploads/Temp/file/20220616/62aacd2432d7b.pdf>

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260725T190842+0000

Ratings and Alerts

No rating or validation information has been found for MGI: DNBSEQ-G400.

No alerts have been found for MGI: DNBSEQ-G400.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Naktang C, et al. (2025) Chromosome-level assemblies of two hexaploid bamboos, *Thyrsostachys oliveri* and *Thyrsostachys siamensis*, provide a foundation for functional and comparative genomics studies. *GigaScience*, 14.

Ishikawa R, et al. (2025) Immunohistochemical and molecular evolutionary features of jejunoileal adenocarcinoma unveiled through comparative analysis with colorectal adenocarcinoma. *Neoplasia* (New York, N.Y.), 66, 101180.

Micoli G, et al. (2025) Decoding the Genomic and Functional Landscape of Emerging Subtypes in Ovarian Cancer. *Cancer discovery*, 15(11), 2262.

Yoshimura T, et al. (2025) High-Throughput Drug Screening of Clear Cell Ovarian Cancer Organoids Reveals Vulnerability to Proteasome Inhibitors and Dinaciclib and Identifies AGR2 as a Therapeutic Target. *Cancer research communications*, 5(6), 1018.

Ishino T, et al. (2025) Immunopectidomics combined with full-length transcriptomics uncovers diverse neoantigens. *Cell reports*, 45(1), 116781.

Zhang Y, et al. (2024) A trade-off in evolution: the adaptive landscape of spiders without venom glands. *GigaScience*, 13.

Bai M, et al. (2024) The telomere-to-telomere (T2T) genome of *Peucedanum praeruptorum* Dunn provides insights into the genome evolution and coumarin biosynthesis. *GigaScience*, 13.

Souza-Borges CH, et al. (2024) De novo assembly and characterization of a highly degenerated ZW sex chromosome in the fish *Megaleporinus macrocephalus*. *GigaScience*, 13.

Santos R, et al. (2024) Low-coverage whole genome sequencing for a highly selective cohort of severe COVID-19 patients. *GigaByte* (Hong Kong, China), 2024, gigabyte127.

Zhang H, et al. (2022) Genomes and demographic histories of the endangered *Bretschneidera sinensis* (Akaniaceae). *GigaScience*, 11.

Kudo KI, et al. (2022) ?Np63? transcriptionally represses p53 target genes involved in the radiation-induced DNA damage response : ?Np63? may cause genomic instability in epithelial stem cells. *Radiation oncology* (London, England), 17(1), 183.

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

Xu M, et al. (2021) Accurate haplotype-resolved assembly reveals the origin of structural variants for human trios. *Bioinformatics* (Oxford, England), 37(15), 2095.