Resource Summary Report

Generated by T1D on Jul 29, 2026

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

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

Resource Name: MGI: DNBSEQ-G400

Resource ID: SCR_017980

Alternate URLs: https://en.mgi-tech.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 T1D .

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) Immunopeptidomics 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.