

Resource Summary Report

Generated by [kravitz2](#) on Aug 4, 2026

BGI: BGISEQ-500

RRID:SCR_017979

Type: Tool

Proper Citation

BGI: BGISEQ-500 (RRID:SCR_017979)

Resource Information

URL: <https://en.mgitech.cn/Uploads/Temp/file/20191231/5e0b086c38d24.pdf>

Proper Citation: BGI: BGISEQ-500 (RRID:SCR_017979)

Description: Desktop sequencer developed by BGI. Using DNA nanoball and combinational probe anchor synthesis developed from Complete Genomics sequencing technologies, it generates short reads at large scale. BGI/MGI Sequencer.

Resource Type: instrument resource

Defining Citation: [DOI:10.1093/gigascience/giy144](https://doi.org/10.1093/gigascience/giy144), [DOI:10.1101/786962](https://doi.org/10.1101/786962)

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

Availability: Restricted

Resource Name: BGI: BGISEQ-500

Resource ID: SCR_017979

Old URLs: <https://www.bgi.com/global/company/careers/bgi-launches-its-desktop-sequencer-bgiseq-500/>

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260801T190552+0000

Ratings and Alerts

No rating or validation information has been found for BGI: BGISEQ-500.

No alerts have been found for BGI: BGISEQ-500.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 25 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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

Chen H, et al. (2025) Chromosome-level genome assembly of *Pinus massoniana* provides insights into conifer adaptive evolution. *GigaScience*, 14.

Jonckheere S, et al. (2025) Development and validation of a high-throughput screening pipeline of compound libraries to target EMT. *Cell death and differentiation*.

Shen X, et al. (2024) Exploring the cobia (*Rachycentron canadum*) genome: unveiling putative male heterogametic regions and identification of sex-specific markers. *GigaScience*, 13.

Hillen H, et al. (2024) A Novel Irreversible TEAD Inhibitor, SWTX-143, Blocks Hippo Pathway Transcriptional Output and Causes Tumor Regression in Preclinical Mesothelioma Models. *Molecular cancer therapeutics*, 23(1), 3.

Xu Y, et al. (2024) Kinship analysis and pedigree reconstruction by RAD sequencing in cattle. *GigaByte (Hong Kong, China)*, 2024, 1.

Kumar S, et al. (2023) Evolution of Resistance to Irinotecan in Cancer Cells Involves Generation of Topoisomerase-Guided Mutations in Non-Coding Genome That Reduce the Chances of DNA Breaks. *International journal of molecular sciences*, 24(10).

Chen S, et al. (2023) Epigenetically Downregulated Breast Cancer Gene 2 through Acetyltransferase Lysine Acetyltransferase 2B Increases the Sensitivity of Colorectal Cancer to Olaparib. *Cancers*, 15(23).

Liu B, et al. (2023) The genome assembly and annotation of the many-banded krait, *Bungarus multicinctus*. *GigaByte (Hong Kong, China)*, 2023, gigabyte82.

Peterson ND, et al. (2023) Non-canonical pattern recognition of a pathogen-derived metabolite by a nuclear hormone receptor identifies virulent bacteria in *C. elegans*. *Immunity*, 56(4), 768.

Vad-Nielsen J, et al. (2023) Genome-wide epigenetic and mRNA-expression profiling followed by CRISPR/Cas9-mediated gene-disruptions corroborate the MIR141/MIR200C-ZEB1/ZEB2-FGFR1 axis in acquired EMT-associated EGFR TKI-resistance in NSCLC cells. *Translational lung cancer research*, 12(1), 42.

Wang J, et al. (2022) Chromosome-level genome assembly of the Pacific geoduck *Panopea generosa* reveals major inter- and intrachromosomal rearrangements and substantial expansion of the copine gene family. *GigaScience*, 12.

Lin Y, et al. (2022) Allele-specific regulatory effects on the pig transcriptome. *GigaScience*, 12.

Zhao Q, et al. (2022) Chromosome-level genome assembly of goose provides insight into the adaptation and growth of local goose breeds. *GigaScience*, 12.

Kim HS, et al. (2022) LT1, an ONT long-read-based assembly scaffolded with Hi-C data and polished with short reads. *GigaByte* (Hong Kong, China), 2022, gigabyte51.

Zhao H, et al. (2022) Dynamic Alteration of the Gut Microbiota Associated with Obesity and Intestinal Inflammation in Ovariectomy C57BL/6 Mice. *International journal of endocrinology*, 2022, 6600158.

Zhou M, et al. (2022) Circadian signatures of anterior hypothalamus in time-restricted feeding. *F1000Research*, 11, 1087.

Kim HM, et al. (2021) Comparative analysis of 7 short-read sequencing platforms using the Korean Reference Genome: MGI and Illumina sequencing benchmark for whole-genome sequencing. *GigaScience*, 10(3).

Wang Q, et al. (2021) Linking gut microbiome to bone mineral density: a shotgun metagenomic dataset from 361 elderly women. *GigaByte* (Hong Kong, China), 2021, gigabyte12.

Zhang R, et al. (2021) Chromosome-level genome assembly of the humpback puffer, *Tetraodon palembangensis*. *GigaByte* (Hong Kong, China), 2021, gigabyte17.