Resource Summary Report

Generated by SPARC SAWG on Aug 7, 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, DOI: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 SPARC SAWG .

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.

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

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.

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).

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.

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.

Lin Y, et al. (2022) Allele-specific regulatory effects on the pig transcriptome. 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 Q, et al. (2022) Chromosome-level genome assembly of goose provides insight into the adaptation and growth of local goose breeds. GigaScience, 12.

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

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.

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.

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.