

Resource Summary Report

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MGI: DNBSEQ-T7

RRID:SCR_017981

Type: Tool

Proper Citation

MGI: DNBSEQ-T7 (RRID:SCR_017981)

Resource Information

URL: https://en.mgitech.cn/products/instruments_info/5/

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Description: Sequencer can generate 1-6Tb of high quality data per day, for wide range of applications including Whole Genome Sequencing, Deep Exome Sequencing, Epigenome Sequencing, Transcriptome Sequencing, and targeted panel projects. Powered by DNBSEQ™ Technology, DNBSEQ-T7 makes sequencing more efficient and productive with advances in biochemical, fluidics, and optical systems. Detection and characterization of copy number variants based on whole-genome sequencing by MGI platforms.

Resource Type: instrument resource

Defining Citation: [DOI:10.1101/786962](https://doi.org/10.1101/786962)

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

Availability: Restricted

Resource Name: MGI: DNBSEQ-T7

Resource ID: SCR_017981

Alternate URLs: <https://en.mgitech.com//Uploads/Temp/file/20230619/648fc032e4af9.pdf>

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260808T190056+0000

Ratings and Alerts

No rating or validation information has been found for MGI: DNBSEQ-T7.

No alerts have been found for MGI: DNBSEQ-T7.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

Tao Y, et al. (2026) TENT5A Maintains MYC mRNA Stability to Enhance Osteosarcoma Stemness. *Cancer research*, 86(9), 2161.

Mu H, et al. (2025) Methionine intervention induces PD-L1 expression to enhance the immune checkpoint therapy response in MTAP-deleted osteosarcoma. *Cell reports. Medicine*, 6(3), 101977.

Hwang T, et al. (2025) Comprehensive whole-genome sequencing reveals origins of mutational signatures associated with aging, mismatch repair deficiency and temozolomide chemotherapy. *Nucleic acids research*, 53(1).

Liu F, et al. (2025) The telomere-to-telomere gapless genome of grass carp provides insights for genetic improvement. *GigaScience*, 14.

Guang X, et al. (2025) Telomere-to-telomere African wild rice (*Oryza longistaminata*) reference genome reveals segmental and structural variation. *GigaScience*, 14.

Chen M, et al. (2025) The genome of *Hippophae salicifolia* provides new insights into the sexual differentiation of sea buckthorn. *GigaScience*, 14.

Bian C, et al. (2025) Telomere-to-telomere chromosome-scale genome assemblies of black and golden koi carp variants support construction of an ancient karyotype of Cypriniformes. *GigaScience*, 14.

Ren L, et al. (2025) Genomes reveal pervasive distant hybridization in nature among cyprinid fishes. *GigaScience*, 14.

Jiang M, et al. (2025) The telomere-to-telomere gap-free reference genome and taxonomic reassessment of *Siniperca roulei*. *GigaScience*, 14.

Zhang Y, et al. (2025) Immune Dysregulation and Endometrial Receptivity Impairment in Women with Repeated Implantation Failure and Dyslipidemia. *The Journal of clinical endocrinology and metabolism*.

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.

Wang H, et al. (2024) The genomes of *Dahlia pinnata*, *Cosmos bipinnatus*, and *Bidens alba* in tribe Coreopsideae provide insights into polyploid evolution and inulin biosynthesis. *GigaScience*, 13.

Yang YX, et al. (2024) The chromosome-level genome assembly of an endangered herb *Bergenia scopulosa* provides insights into local adaptation and genomic vulnerability under climate change. *GigaScience*, 13.

Wang YS, et al. (2024) Chromosome-level genome assemblies of two littorinid marine snails indicate genetic basis of intertidal adaptation and ancient karyotype evolved from bilaterian ancestors. *GigaScience*, 13.

Su R, et al. (2024) Near telomere-to-telomere genome assembly of Mongolian cattle: implications for population genetic variation and beef quality. *GigaScience*, 13.

Choi SY, et al. (2024) *Bdellovibrio svalbardensis* sp. nov., a newly described predator isolated from Svalbard, Norway. *International journal of systematic and evolutionary microbiology*, 74(1).

Yu Y, et al. (2024) Association between the skin microbiome and lichen striatus hypopigmentation: *Cutibacterium acnes* as a potential cause. *Journal of the European Academy of Dermatology and Venereology : JEADV*, 38(9), 1776.

Chandrasegaran P, et al. (2023) Modelling host- *Trypanosoma brucei gambiense* interactions in vitro using human induced pluripotent stem cell-derived cortical brain organoids. *F1000Research*, 12, 437.

Shin U, et al. (2023) A heterozygous mutation in *UBE2H* in a patient with developmental delay leads to an aberrant brain development in zebrafish. *Human genomics*, 17(1), 44.

Zhang K, et al. (2023) Comparative and population genomics of buckwheat species reveal key determinants of flavor and fertility. *Molecular plant*, 16(9), 1427.