

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/

Proper Citation: MGI: DNBSEQ-T7 (RRID:SCR_017981)

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: 20260829T182538+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 [nidm-terms](#) .

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

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).

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.

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.

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 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.

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.