

Resource Summary Report

Generated by [nidm-terms](#) on Aug 9, 2026

Chinese Genome Sequence Archive

RRID:SCR_025826

Type: Tool

Proper Citation

Chinese Genome Sequence Archive (RRID:SCR_025826)

Resource Information

URL: <https://ngdc.cncb.ac.cn/gsa/>

Proper Citation: Chinese Genome Sequence Archive (RRID:SCR_025826)

Description: Public archive of raw sequence data in National Genomics Data Center as part of the China National Center for Bioinformation. GSA accepts worldwide data submissions, performs data curation and quality control for all submitted data. Provides data storage and sharing services.

Abbreviations: GSE

Synonyms: Genome Sequence Archive Family, , Genome Sequence Archive

Resource Type: database, data or information resource

Defining Citation: [PMID:34400360](#)

Keywords: Chinese National Genomics Data Center, raw sequence data, data storage and sharing,

Funding: National Key R and D Program of China ;
Strategic Priority Research Program of Chinese Academy of Sciences ;
Genomics Data Center Construction of Chinese Academy of Sciences ;
National Natural Science Foundation of China ;
International Partnership Program of the Chinese Academy of Sciences

Resource Name: Chinese Genome Sequence Archive

Resource ID: SCR_025826

Alternate IDs: r3d100012342

Alternate URLs: <https://doi.org/10.17616/R3094D>

Record Creation Time: 20241001T053245+0000

Record Last Update: 20260808T190733+0000

Ratings and Alerts

No rating or validation information has been found for Chinese Genome Sequence Archive.

No alerts have been found for Chinese Genome Sequence Archive.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1805 mentions in open access literature.

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

Ding C, et al. (2026) Glioblastoma-Secreted C1QL1 Orchestrates Tumor Microtube Expansion and Neural Synaptic Pruning to Drive Malignant Synapse Formation and Recurrence. *Cancer discovery*, 16(6), 1176.

Nigri J, et al. (2026) Myofibroblasts Induce Neuroplasticity to Promote Pancreatic Inflammation and Cancer Progression. *Cancer discovery*, 16(5), 1014.

Tao T, et al. (2026) Copy-Number Aberrations in Circulating Tumor DNA Enable Diagnosis and Risk Stratification of Pediatric Neuroblastic Tumors. *Cancer research communications*, 6(1), 36.

Wang Q, et al. (2026) Serglycin Drives LAG3+ Treg Differentiation and Immunosuppression in Gastric Cancer. *Cancer research*, 86(10), 2395.

Chen Z, et al. (2026) Targeting TPX2-dependent lineage plasticity by CDK4/6 inhibition reverses therapy resistance in neuroendocrine bladder carcinoma. *Cell reports. Medicine*, 7(4), 102712.

Zhang JT, et al. (2026) LAMPAD: An Integrated Circulating Tumor DNA-Based Model for Predicting Potential Cure in Patients With Resected NSCLC. *Journal of thoracic oncology : official publication of the International Association for the Study of Lung Cancer*, 103729.

Zeng Y, et al. (2026) Endophyte *Acrocalymma vagum* establishes the holobiont with rice to attract beneficial microorganisms and promote disease resistance. *Journal of advanced research*, 79, 161.

Wang Y, et al. (2026) TREM2-Mediated Cholesterol Efflux in Macrophages Inhibits Anti-Tumor Immunity via Limitation of CD4+ T and NK Cells. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(5), e06995.

Mei H, et al. (2026) Integrin α v β 8-mediated TGF- β 1 activation regulates the sustained response in immune thrombocytopenia after TPO-RA withdrawal. *Blood*, 147(7), 783.

Ma Q, et al. (2026) Single-Cell Sequencing Reveals Circadian Sensitivity of Noise-Induced Hearing Loss Mediated by Macrophage-Driven NLRP3 Inflammasome Activation. *Neuroscience bulletin*, 42(2), 319.

He Y, et al. (2026) Single-Cell Transcriptome and Microbiome Profiling Uncover Ileal Immune Impairment in Intrauterine Growth-Retarded Piglets. *Current pharmaceutical design*, 32(8), 617.

Zhao Y, et al. (2026) The transcription factor ANAC017 links mitochondrial retrograde signaling with the ubiquitin-proteasome system to control mitochondrial function in *Arabidopsis*. *Plant communications*, 7(2), 101667.

Fan S, et al. (2026) Metatranscriptomic analyses of gut bacterial and viral communities in the critically endangered Yangtze finless porpoise (*Neophocaena asiaeorientalis asiaeorientalis*) under distinct environments. *Animal microbiome*, 8(1).

Ren X, et al. (2026) Integrating network pharmacology and transcriptomics to reveal the therapeutic effect of Long Mu Ning Xin Decoction on attention-deficit/hyperactivity disorder by regulating cAMP and PI3K/AKT pathways. *Frontiers in pharmacology*, 17, 1744709.

Wang Z, et al. (2026) Multiple active-sites editing of adenylation domains of *srfA* operon for constructing diverse surfactin lipopeptide. *Communications biology*, 9(1), 126.

Wang L, et al. (2026) Site-specific HPV18 integration facilitates cervical carcinogenesis through metabolic reprogramming-induced dysfunction of the SpHK1/S1P/S1PR1 pathway. *Cell death & disease*, 17(1), 24.

Zhao C, et al. (2026) Effect of crop rotation and crop succession on microorganisms and yield of tobacco rhizosphere soil. *BMC microbiology*, 26(1), 129.

Peng D, et al. (2026) Potyviruses recruit host eIF4A3 to block m6A-mediated RNA decay by steric hindrance of viral RNA methylation in plants. *Nucleic acids research*, 54(1).

Liu Y, et al. (2026) C/EBP- β -regulated complement hyperactivation in spleen of SFTSV-infected mice: A clue to targeted complement therapy. *PLoS pathogens*, 22(4), e1014144.

Jiang ZY, et al. (2026) U2AF1 modulates alternative exon selection and guards zygotic splicing activation in mouse preimplantation embryogenesis. *Cellular and molecular life sciences : CMLS*, 83(1).