

Resource Summary Report

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DNA DataBank of Japan (DDBJ)

RRID:SCR_002359

Type: Tool

Proper Citation

DNA DataBank of Japan (DDBJ) (RRID:SCR_002359)

Resource Information

URL: <http://www.ddbj.nig.ac.jp>

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Description: Maintains and provides archival, retrieval and analytical resources for biological information. Central DDBJ resource consists of public, open-access nucleotide sequence databases including raw sequence reads, assembly information and functional annotation. Database content is exchanged with EBI and NCBI within the framework of the International Nucleotide Sequence Database Collaboration (INSDC). In 2011, DDBJ launched two new resources: DDBJ Omics Archive and BioProject. DOR is archival database of functional genomics data generated by microarray and highly parallel new generation sequencers. Data are exchanged between the ArrayExpress at EBI and DOR in the common MAGE-TAB format. BioProject provides organizational framework to access metadata about research projects and data from projects that are deposited into different databases.

Abbreviations: DDBJ

Synonyms: DNA DataBank of Japan (DDBJ), DNA DataBank of Japan, DDBJ, DNA Data Bank of Japan, DDBJ - DNA Data Bank of Japan

Resource Type: data or information resource, data repository, database, service resource, storage service resource

Defining Citation: [PMID:26578571](#), [PMID:25477381](#)

Keywords: nucleotide sequence, genome, dna, dna database, dna research, nucleotide, phylogenetics, protein, sequence, protein binding, gene expression, gene, genetics, nucleoid, genomics, protein binding, gold standard, bio.tools, FASEB list

Funding: Japanese Ministry of Education Culture Sports Science and Technology MEXT

Availability: Free, Freely available,

Resource Name: DNA DataBank of Japan (DDBJ)

Resource ID: SCR_002359

Alternate IDs: OMICS_01644, biotools:ddbj, nif-0000-02740, r3d100010218

Alternate URLs: <https://bio.tools/ddbj>, <https://doi.org/10.17616/R3M01R>

Record Creation Time: 20220129T080213+0000

Record Last Update: 20260905T132447+0000

Ratings and Alerts

No rating or validation information has been found for DNA DataBank of Japan (DDBJ).

No alerts have been found for DNA DataBank of Japan (DDBJ).

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 709 mentions in open access literature.

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

Wu C, et al. (2026) Complete genome sequence of *Paenibacillus polymyxa* 19197, an endophytic bacterium isolated from the morel mushroom *Morchella importuna*. Microbiology resource announcements, 15(3), e0117125.

Ohse K, et al. (2026) Genetic analysis of *Mycobacterium abscessus* reveals genomic diversity linked to global plasmid distribution. iScience, 29(4), 115150.

Zhou T, et al. (2026) Integrated Transcriptomics and Experimental Validation Reveal That Ellagic Acid Alleviates Fuchs Endothelial Corneal Dystrophy via PLA2/NF- κ B Signaling. Investigative ophthalmology & visual science, 67(1), 31.

Wu S, et al. (2026) Environmental DNA (eDNA) Technology in Biodiversity and Ecosystem Health Research: Advances and Prospects. Ecology and evolution, 16(1), e72891.

Kettongruang S, et al. (2026) Diversity and Plant Growth-Promoting Potential of Duckweed-Associated Bacteria on *Wolffia globosa* Biomass Production and Nutritional Quality. Environmental microbiology reports, 18(2), e70312.

Yamamoto S, et al. (2026) Dorsoventral-mediated Shh induction is required for axolotl limb regeneration. eLife, 14.

Seto J, et al. (2026) Food poisoning from raw horse meat contaminated with Shiga toxin-producing *Escherichia coli* O157 linked to nationwide spread of closely related strains,

Japan, 2023. Microbiology spectrum, 14(5), e0411525.

Hong P, et al. (2026) Molecular characterization of *Moniezia expansa* (Rudolphi, 1810) (Cestoda: Anoplocephalidae) from a captive common eland (*Tragelaphus oryx*) in Taiwan. International journal for parasitology. Parasites and wildlife, 29, 101220.

Ara T, et al. (2026) DDBJ update in 2025: system integration for global data-sharing including pathogen surveillance. Nucleic acids research, 54(D1), D106.

Ito K, et al. (2026) In vitro comparative analysis of steamed wood and other lignocellulosic substrates on ruminal fermentation and microbiota. Frontiers in veterinary science, 13, 1750760.

Yu S, et al. (2026) A new *Isospora* species (Apicomplexa: Eimeriidae) from Taiwan Blue Magpie (*Urocissa caerulea*) (Passeriformes: Corvidae) with the first complete corvid coccidian mitogenome. International journal for parasitology. Parasites and wildlife, 30, 101246.

Wassel MA, et al. (2026) Tetrodotoxin (TTX) reshapes the functional potential of the gut microbiome in juvenile tiger pufferfish (*Takifugu rubripes*) across salinity gradients. Animal microbiome, 8(1).

Furudate K, et al. (2025) Spatial colocalization and molecular crosstalk of myofibroblastic CAFs and tumor cells shape lymph node metastasis in oral squamous cell carcinoma. PLoS genetics, 21(9), e1011791.

Ueda S, et al. (2025) Divergent and subnucleus-specific gene expression responses to chronic stress hormone exposure in the amygdala. Frontiers in molecular neuroscience, 18, 1659846.

Cannon EKS, et al. (2025) Guidelines for gene and genome assembly nomenclature. Genetics, 229(3).

Quainoo DK, et al. (2025) Genetic insights for enhancing conservation strategies in captive and wild Asian elephants through improved non-invasive DNA-based individual identification. PloS one, 20(5), e0320480.

Huang C, et al. (2025) *Nicotiana benthamiana* VASCULAR-RELATED NAC-DOMAIN7-2 (NbVND7-2) has a role in xylem formation during interfamilial grafting. Journal of experimental botany, 76(8), 2207.

Chatanga E, et al. (2025) Mitogenomics of the tropical bont tick *Amblyomma variegatum* reveals vertical and horizontal transmission of *Rickettsia africae*. PLoS neglected tropical diseases, 19(10), e0013610.

Kobayashi Y, et al. (2025) CqHKT1 and CqSOS1 mediate genotype-dependent Na⁺ exclusion under high salinity conditions in quinoa. Frontiers in plant science, 16, 1597647.

Yasuoka K, et al. (2025) Genome Analysis of Japanese *Yersinia pseudotuberculosis* Strains Isolated From Kawasaki Disease Patients and Other Sources and Their Phylogenetic Positions in the Global *Y. pseudotuberculosis* Population. Microbiology and immunology, 69(3), 182.