

Resource Summary Report

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INSDC

RRID:SCR_011967

Type: Tool

Proper Citation

INSDC (RRID:SCR_011967)

Resource Information

URL: <http://www.insdc.org/>

Proper Citation: INSDC (RRID:SCR_011967)

Description: International collaboration of the International Nucleotide Sequence Databases (INSD), DDBJ, ENA, and GenBank, maintained for over 18 years. Individuals submitting data to the international sequence databases should be aware of INSDC policy.

Abbreviations: INSDC

Synonyms: International Nucleotide Sequence Database Collaboration

Resource Type: portal, community building portal, data or information resource

Keywords: nucleotide sequence, FASEB list

Resource Name: INSDC

Resource ID: SCR_011967

Alternate IDs: OMICS_01653

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260728T043400+0000

Ratings and Alerts

No rating or validation information has been found for INSDC.

No alerts have been found for INSDC.

Data and Source Information

Usage and Citation Metrics

We found 214 mentions in open access literature.

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

Hanna SJ, et al. (2025) The Type 1 Diabetes T Cell Receptor and B Cell Receptor Repository in the AIRR Data Commons: a practical guide for access, use and contributions through the Type 1 Diabetes AIRR Consortium. *Diabetologia*, 68(1), 186.

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

Fischer L, et al. (2025) Recombinant Myxoma Virus in European Brown Hares, 2023-2024. *Emerging infectious diseases*, 31(8), 1608.

Vancaester E, et al. (2025) Ghosts of symbionts past: the hidden history of the dynamic association between filarial nematodes and their Wolbachia endosymbionts. *G3 (Bethesda, Md.)*, 15(12).

Righi E, et al. (2025) The BioGenome Portal: a web-based platform for biodiversity genomics data management. *NAR genomics and bioinformatics*, 7(1), lqaf020.

Dyer SC, et al. (2025) Ensembl 2025. *Nucleic acids research*, 53(D1), D948.

Suetsugu K, et al. (2025) Mycoheterotrophic continuum in rhizoctonia associations: genetic divergence and carbon acquisition variation among *Odontochilus* orchids. *Annals of botany*, 136(2), 407.

Damerow JE, et al. (2025) Opening doors to physical sample tracking and attribution in Earth and environmental sciences. *Scientific data*, 12(1), 1047.

Kim L, et al. (2025) Tier-based standards for FAIR sequence data and metadata sharing in microbiome research. *Nucleic acids research*, 53(15).

Valderrama B, et al. (2025) The South American MicroBiome Archive (saMBA): enriching the microbiome field by studying neglected populations. *Nature communications*, 16(1), 7371.

Elliott L, et al. (2025) wholeskim: Utilising Genome Skims for Taxonomically Annotating Ancient DNA Metagenomes. *Molecular ecology resources*, 25(8), e70001.

Islam S, et al. (2025) Commentary on "Preliminary Species Hypotheses" in *Entomological Taxonomy: A Global Data and FAIR Infrastructure Perspective*. *Biodiversity data journal*, 13, e141562.

Val-Calvo J, et al. (2025) Leveraging the subgenus category to address monophyletic genus over-splitting: illustration with recently proposed *Mycobacteriales* genera. *International journal of systematic and evolutionary microbiology*, 75(9).

, et al. (2025) A nuclear phylogenomic tree of grasses (Poaceae) recovers current classification despite gene tree incongruence. *The New phytologist*, 245(2), 818.

Formenti G, et al. (2025) Evaluation of sequencing reads at scale using rdeval. *bioRxiv : the preprint server for biology*.

Furlong J, et al. (2025) Automated Annotation and Validation of Human Respiratory Virus Sequences using VADR. *bioRxiv : the preprint server for biology*.

Jha N, et al. (2025) Gaia: An AI-enabled genomic context-aware platform for protein sequence annotation. *Science advances*, 11(25), eadv5109.

Formenti G, et al. (2025) Evaluation of sequencing reads at scale using rdeval. *Bioinformatics (Oxford, England)*, 41(9).

Heuermann MC, et al. (2025) White paper: standards for handling and analyzing plant pan-genomes. *F1000Research*, 14, 739.

Elko EA, et al. (2024) Recurrent SARS-CoV-2 mutations at Spike D796 evade antibodies from pre-Omicron convalescent and vaccinated subjects. *Microbiology spectrum*, 12(2), e0329123.