

Resource Summary Report

Generated by [RRID](#) on Aug 4, 2026

[NCBI BioProject](#)

RRID:SCR_004801

Type: Tool

Proper Citation

NCBI BioProject (RRID:SCR_004801)

Resource Information

URL: <http://www.ncbi.nlm.nih.gov/bioproject>

Proper Citation: NCBI BioProject (RRID:SCR_004801)

Description: Database of biological data related to a single initiative, originating from a single organization or from a consortium. A BioProject record provides users a single place to find links to the diverse data types generated for that project. It is a searchable collection of complete and incomplete (in-progress) large-scale sequencing, assembly, annotation, and mapping projects for cellular organisms. Submissions are supported by a web-based Submission Portal. The database facilitates organization and classification of project data submitted to NCBI, EBI and DDBJ databases that captures descriptive information about research projects that result in high volume submissions to archival databases, ties together related data across multiple archives and serves as a central portal by which to inform users of data availability. BioProject records link to corresponding data stored in archival repositories. The BioProject resource is a redesigned, expanded, replacement of the NCBI Genome Project resource. The redesign adds tracking of several data elements including more precise information about a project's scope, material, and objectives. Genome Project identifiers are retained in the BioProject as the ID value for a record, and an Accession number has been added. Database content is exchanged with other members of the International Nucleotide Sequence Database Collaboration (INSDC). BioProject is accessible via FTP.

Synonyms: NCBI BioProject Database, BioProject

Resource Type: database, data or information resource

Defining Citation: [PMID:22139929](#)

Keywords: genome sequencing, sequencing, genotype, phenotype, sequence variant, epigenetic, data set, genome, assembly, annotation, mapping, cellular organism, gene mapping, gene expression, biological tag, gene rearrangement, genetic algorithm, genetic code, genetic genealogy, gold standard, bio.tools

Funding: NLM

Availability: Free, Freely available

Resource Name: NCBI BioProject

Resource ID: SCR_004801

Alternate IDs: r3d100013330, nlx_143909, biotools:bioproject

Alternate URLs: <http://www.ncbi.nlm.nih.gov/genomeprj>, <https://bio.tools/bioproject>, <https://doi.org/10.17616/R31NJMS2>

Old URLs: <http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?CMD=search&DB=genomeprj>

Record Creation Time: 20220129T080226+0000

Record Last Update: 20260805T044113+0000

Ratings and Alerts

No rating or validation information has been found for NCBI BioProject.

No alerts have been found for NCBI BioProject.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13968 mentions in open access literature.

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

Chatenoud H, et al. (2025) Metabolic comparison of minimally to noninvasive urogenital sample types for studying gynecologic health: A pilot study. *iScience*, 28(7), 112938.

Bleve A, et al. (2025) ROR?? Bridges Cancer-Driven Lipid Dysmetabolism and Myeloid Immunosuppression. *Cancer discovery*, 15(7), 1505.

Su X, et al. (2025) Single or Combined Supplementation of Rhodotorula Yeast Culture and Bacillus Subtilis Enhances Intestinal Barrier Function in Yellow-Feathered Broilers. *Veterinary sciences*, 12(6).

Trutschel L, et al. (2025) Sulfide Oxidation Products Support Microbial Metabolism at Interface Environments in a Marine-Like Serpentinizing Spring in Northern California. *Geobiology*, 23(4), e70026.

Kharrat L, et al. (2025) Large-Scale Genomic Analysis of CpG-Mediated Immunogenicity in Bacteriophages and a Novel Predictive Risk Index. *bioRxiv : the preprint server for*

biology.

Huang J, et al. (2025) Phylogenomic relationships and species delimitation of *Cotoneaster* ser. *Pannosi*, ser. *Buxifolii*, and related taxa. *Frontiers in plant science*, 16, 1575925.

Tran L, et al. (2025) Impact of peripheral circadian misalignment and alcohol on the resiliency of intestinal barrier and microbiota. *Gut microbes*, 17(1), 2509281.

Liu M, et al. (2025) Alterations of the Enteric Virome in Vogt-Koyanagi-Harada Disease. *Investigative ophthalmology & visual science*, 66(6), 15.

Salazar-Hamm PS, et al. (2025) Phylogenetic and ecological drivers of the avian lung mycobiome and its potentially pathogenic component. *Communications biology*, 8(1), 634.

Zhu J, et al. (2025) Neutrophil infiltration and microglial shifts in sepsis induced preterm brain injury: pathological insights. *Acta neuropathologica communications*, 13(1), 79.

Kobayashi Y, et al. (2025) Physiological and Genomic Characterization of Oligotrophic *Nitrobacter* Isolated from a Forest Soil in Japan. *Microbes and environments*, 40(2).

Lo Presti A, et al. (2025) Exploring the genetic diversity of the 3' untranslated region (UTR) of Dengue virus. *Virology journal*, 22(1), 197.

Shen NE, et al. (2025) Insights From Amniotic and Umbilical Cord Mesenchymal Stem Cells in Wound Healing. *Journal of cellular and molecular medicine*, 29(12), e70679.

Sun W, et al. (2025) Effects of dietary glycerol, vitamin C and niacinamide supplementation on liver of growing-finishing pigs. *Frontiers in veterinary science*, 12, 1620128.

Gutiérrez-Larruscain D, et al. (2025) Phylogenomic Evidence of Fire Regime Changes: The Case of a Resprouting Juniper. *Ecology letters*, 28(7), e70169.

Ge S, et al. (2025) A cis-natural antisense RNA regulates alternative polyadenylation of *SISPX5* under Pi starvation in tomato. *Nature communications*, 16(1), 7981.

Feng H, et al. (2025) A non-classical PUF family protein in oomycetes functions as a pre-rRNA processing regulator and a target for RNAi-based disease control. *PLoS pathogens*, 21(7), e1013379.

Cai Y, et al. (2025) Comprehensive Analyses of PANoptosome with Potential Implications in Cancer Prognosis and Immunotherapy. *Biochemical genetics*, 63(1), 331.

Johnson BD, et al. (2025) Sensitivity of transcriptomics: Different samples and methodology alter conclusions in Gulf pipefish (*Syngnathus scovelli*). *The Journal of heredity*, 116(2), 139.

Lin H, et al. (2025) Metagenome-based diversity and functional analysis of culturable microbes in sugarcane. *Microbiology spectrum*, 13(1), e0198224.