Resource Summary Report

Generated by T1D on Aug 2, 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: data or information resource, database

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: 20260801T190923+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 T1D .

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

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.

Pangrácová M, et al. (2025) Extended longevity of termite kings and queens is accompanied by extranuclear localization of telomerase in somatic organs and caste-specific expression of its isoforms. Insect science, 32(2), 364.

Castonguay-Paradis S, et al. (2025) The Human Fecal Endocannabinoidome Mediator Profile Is Mainly Defined by the Fecal Microbiota and Diet. The Journal of clinical endocrinology and metabolism, 110(3), 739.

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.

Gaikwad KB, et al. (2025) Computational approaches for identifications of altered ion channels in keratoconus. Eye (London, England), 39(1), 145.

Tao F, et al. (2025) Insight into the composition and differentiation of endophytic microbial communities in kernels via 368 maize transcriptomes. Journal of advanced research, 71, 5.

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

Burbrink FT, et al. (2025) The genetic origins of species boundaries at subtropical and temperate ecoregions in the North American racers (Coluber constrictor). Heredity, 134(2), 87.

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

Ngan WY, et al. (2025) A more significant role for insertion sequences in large-scale rearrangements in bacterial genomes. mBio, 16(1), e0305224.

Sánchez-Serna G, et al. (2025) Less, but More: New Insights From Appendicularians on Chordate Fgf Evolution and the Divergence of Tunicate Lifestyles. Molecular biology and evolution, 42(1).

Salas-López M, et al. (2025) Human Milk Archaea Associated with Neonatal Gut Colonization and Its Co-Occurrence with Bacteria. Microorganisms, 13(1).

Ren X, et al. (2025) Genomic and Metabolomic Analyses of Streptomyces albulus with Enhanced ?-Poly-l-lysine Production Through Adaptive Laboratory Evolution. Microorganisms, 13(1).

Márquez-Sanz R, et al. (2025) The Establishment of a Terrestrial Macroalga Canopy Impacts Microbial Soil Communities in Antarctica. Microbial ecology, 88(1), 4.

Das BK, et al. (2025) Exploring microbial players for metagenomic profiling of carbon cycling bacteria in sundarban mangrove soils. Scientific reports, 15(1), 4784.

Boukhatem A, et al. (2025) Promoting the recovery of soil health in As and Sb-polluted soils: new evidence from the biochar-compost option. Environmental science and pollution research international, 32(2), 559.

Huang M, et al. (2025) Goose multi-omics database: A comprehensive multi-omics database for goose genomics. Poultry science, 104(3), 104842.

Mulenga M, et al. (2025) Revolutionizing colorectal cancer detection: A breakthrough in microbiome data analysis. PloS one, 20(1), e0316493.

Chandrasekaran P, et al. (2025) The intestinal microbiome and metabolome discern disease severity in cytotoxic T-lymphocyte-associated protein 4 deficiency. Microbiome, 13(1), 51.