Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 14, 2025

BioSample Database at EBI

RRID:SCR_004856
Type: Tool

Proper Citation

BioSample Database at EBI (RRID:SCR_004856)

Resource Information

URL: http://www.ebi.ac.uk/biosamples/

Proper Citation: BioSample Database at EBI (RRID:SCR_004856)

Description: Database that aggregates sample information for reference samples (e.g. Coriell Cell lines) and samples for which data exist in one of the EBI""s assay databases such as ArrayExpress, the European Nucleotide Archive or PRoteomics Identificates DatabasE. It provides links to assays for specific samples, and accepts direct submissions of sample information. The goals of the BioSample Database include: # recording and linking of sample information consistently within EBI databases such as ENA, ArrayExpress and PRIDE; # minimizing data entry efforts for EBI database submitters by enabling submitting sample descriptions once and referencing them later in data submissions to assay databases and # supporting cross database queries by sample characteristics. The database includes a growing set of reference samples, such as cell lines, which are repeatedly used in experiments and can be easily referenced from any database by their accession numbers. Accession numbers for the reference samples will be exchanged with a similar database at NCBI. The samples in the database can be queried by their attributes, such as sample types, disease names or sample providers. A simple tab-delimited format facilitates submissions of sample information to the database, initially via email to biosamples (at) ebi.ac.uk. Current data sources: * European Nucleotide Archive (424,811 samples) * PRIDE (17,001 samples) * ArrayExpress (1,187,884 samples) * ENCODE cell lines (119 samples) * CORIELL cell lines (27,002 samples) * Thousand Genome (2,628 samples) * HapMap (1,417 samples) * IMSR (248,660 samples)

Abbreviations: BioSD

Synonyms: BioSamples database, BioSamples, BioSamples Database at EBI, BioSample Database at the EBI, EBI BioSample Database, BioSample Database, BioSD at EBI, BioSD - BioSample Database

Resource Type: database, data or information resource

Defining Citation: PMID:22096232

Keywords: cell line, cell, nucleotide, sequencing, proteomics, peptide, protein, genomics, gene expression, biological sample, molecular, sequence, structure, cell line, topical portal, aggregator, gold standard, bio.tools

Funding: European Molecular Biology Laboratory; Heidelberg; Germany ;
European Union FP7 HEALTH-F4-2010-241669;
European Union FP7 HEALTH-F4-2007-201413

Availability: The community can contribute to this resource, Acknowledgement requested

Resource Name: BioSample Database at EBI

Resource ID: SCR_004856

Alternate IDs: biotools:biosamples, nlx_143930, OMICS_01025

Alternate URLs: https://bio.tools/biosamples

Record Creation Time: 20220129T080226+0000

Record Last Update: 20250412T054922+0000

Ratings and Alerts

No rating or validation information has been found for BioSample Database at EBI.

No alerts have been found for BioSample Database at EBI.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Leng D, et al. (2023) Comprehensive Analysis of Tumor Microenvironment Reveals Prognostic ceRNA Network Related to Immune Infiltration in Sarcoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 29(19), 3986.

Breeze CE, et al. (2022) Integrative analysis of 3604 GWAS reveals multiple novel cell type-specific regulatory associations. Genome biology, 23(1), 13.

Courtot M, et al. (2022) BioSamples database: FAIRer samples metadata to accelerate research data management. Nucleic acids research, 50(D1), D1500.

Alexandre PA, et al. (2021) Chromatin accessibility and regulatory vocabulary across indicine cattle tissues. Genome biology, 22(1), 273.

Massa AT, et al. (2020) Genome-Wide Histone Modifications and CTCF Enrichment Predict Gene Expression in Sheep Macrophages. Frontiers in genetics, 11, 612031.

Courtot M, et al. (2019) BioSamples database: an updated sample metadata hub. Nucleic acids research, 47(D1), D1172.

Schmid B, et al. (2019) Generation of a set of isogenic, gene-edited iPSC lines homozygous for all main APOE variants and an APOE knock-out line. Stem cell research, 34, 101349.

Kurtz A, et al. (2018) A Standard Nomenclature for Referencing and Authentication of Pluripotent Stem Cells. Stem cell reports, 10(1), 1.

Bush SJ, et al. (2017) Integration of quantitated expression estimates from polyA-selected and rRNA-depleted RNA-seq libraries. BMC bioinformatics, 18(1), 301.

Toribio AL, et al. (2017) European Nucleotide Archive in 2016. Nucleic acids research, 45(D1), D32.

Moschen S, et al. (2016) Network and biosignature analysis for the integration of transcriptomic and metabolomic data to characterize leaf senescence process in sunflower. BMC bioinformatics, 17 Suppl 5(Suppl 5), 174.

Malladi VS, et al. (2015) Ontology application and use at the ENCODE DCC. Database : the journal of biological databases and curation, 2015.

Faulconbridge A, et al. (2014) Updates to BioSamples database at European Bioinformatics Institute. Nucleic acids research, 42(Database issue), D50.

Bota M, et al. (2012) Combining collation and annotation efforts toward completion of the rat and mouse connectomes in BAMS. Frontiers in neuroinformatics, 6, 2.