European Nucleotide Archive (ENA)

RRID:SCR_006515
Type: Tool

Proper Citation

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Resource Information

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

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**Description:** Public archive providing a comprehensive record of the world's nucleotide sequencing information, covering raw sequencing data, sequence assembly information and functional annotation. All submitted data, once public, will be exchanged with the NCBI and DDBJ as part of the INSDC data exchange agreement. The European Nucleotide Archive (ENA) captures and presents information relating to experimental workflows that are based around nucleotide sequencing. A typical workflow includes the isolation and preparation of material for sequencing, a run of a sequencing machine in which sequencing data are produced and a subsequent bioinformatic analysis pipeline. ENA records this information in a data model that covers input information (sample, experimental setup, machine configuration), output machine data (sequence traces, reads and quality scores) and interpreted information (assembly, mapping, functional annotation). Data arrive at ENA from a variety of sources including submissions of raw data, assembled sequences and annotation from small-scale sequencing efforts, data provision from the major European sequencing centers and routine and comprehensive exchange with their partners in the International Nucleotide Sequence Database Collaboration (INSDC). Provision of nucleotide sequence data to ENA or its INSDC partners has become a central and mandatory step in the dissemination of research findings to the scientific community. ENA works with publishers of scientific literature and funding bodies to ensure compliance with these principles and to provide optimal submission systems and data access tools that work seamlessly with the published literature. ENA is made up of a number of distinct databases that includes the EMBL Nucleotide Sequence Database (Embl-Bank), the newly established Sequence Read Archive (SRA) and the Trace Archive. The main tool for downloading ENA data is the ENA Browser, which is available through REST URLs for easy programmatic use. All ENA data are available through the ENA Browser. Note: EMBL Nucleotide Sequence Database (EMBL-Bank) is entirely included within this resource.

**Abbreviations:** ENA

**Synonyms:** European Nucleotide Archive, ENA

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

**Defining Citation:** [PMID:20972220](https://www.ncbi.nlm.nih.gov/pubmed/20972220)

**Keywords:** analysis, bioinformatics, dna, nucleotide, sequencing, web service, rna, molecular biology, nucleotide sequence, protein, gene expression, gene, genome, biochemistry, molecular structure, metabolite, protein binding, chemogenomics, gold standard

**Funding Agency:** EMBL, Wellcome Trust, European Union

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

**Resource Name:** European Nucleotide Archive (ENA)
Ratings and Alerts

No rating or validation information has been found for European Nucleotide Archive (ENA).

No alerts have been found for European Nucleotide Archive (ENA).

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1161 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Carús-Cadavieco M, et al. (2023) Cognitive decline in diabetic mice predisposed to Alzheimer's disease is greater than in wild type. Life science alliance, 6(6).

Pagnossin D, et al. (2023) Streptococcus canis genomic epidemiology reveals the potential for zoonotic transfer. Microbial genomics, 9(3).


Oggenfuss U, et al. (2023) Recent transposable element bursts are associated with the proximity to genes in a fungal plant pathogen. PLoS pathogens, 19(2), e1011130.

Nyerki E, et al. (2023) correctKin: an optimized method to infer relatedness up to the 4th degree from low-coverage ancient human genomes. Genome biology, 24(1), 38.


Cook DR, et al. (2022) Aberrant Expression and Subcellular Localization of ECT2 Drives Colorectal Cancer Progression and Growth. Cancer research, 82(1), 90.


Drews F, et al. (2022) Broad domains of histone marks in the highly compact Paramecium macronuclear genome. Genome research, 32(4), 710.

Salo M, et al. (2022) Sulfate-reducing bioreactors subjected to high sulfate loading rate or acidity: variations in microbial consortia. AMB Express, 12(1), 95.