

Resource Summary Report

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European Nucleotide Archive (ENA)

RRID:SCR_006515

Type: Tool

Proper Citation

European Nucleotide Archive (ENA) (RRID:SCR_006515)

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: ENA, European Nucleotide Archive

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

Defining Citation: [PMID: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: EMBL ;
Wellcome Trust ;
European Union

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

Resource Name: European Nucleotide Archive (ENA)

Resource ID: SCR_006515

Alternate IDs: OMICS_01029, r3d100010527, nif-0000-32981

Alternate URLs: <http://www.ebi.ac.uk/embl/>, <https://doi.org/10.17616/R3HW3J>

Record Creation Time: 20220129T080236+0000

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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 1272 mentions in open access literature.

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

Krueger T, et al. (2025) Exo-Tox: Identifying Exotoxins from secreted bacterial proteins. BioData mining, 18(1), 52.

Zacharias NM, et al. (2025) Differential Efficacy of Bevacizumab and Erlotinib in Preclinical Models of Renal Medullary Carcinoma and Fumarate Hydratase-Deficient Renal Cell Carcinoma. *Molecular cancer therapeutics*.

Liu X, et al. (2025) Increasing Stemness Drives Prostate Cancer Progression, Plasticity, Therapy Resistance and Poor Patient Survival. *bioRxiv : the preprint server for biology*.

Ma T, et al. (2025) Pan-Cancer Analyses Refine the Single-Cell Portrait of Tumor-Infiltrating Dendritic Cells. *Cancer research*, 85(19), 3596.

Lin GT, et al. (2025) Combining Apatinib and Oxaliplatin Remodels the Immunosuppressive Tumor Microenvironment and Sensitizes Desert-Type Gastric Cancer to Immunotherapy. *Cancer research*, 85(11), 2117.

Rebelo AR, et al. (2025) One day in Denmark: whole-genome sequence-based analysis of *Escherichia coli* isolates from clinical settings. *The Journal of antimicrobial chemotherapy*, 80(4), 1011.

Horsfield ST, et al. (2025) Optimizing nanopore adaptive sampling for pneumococcal serotype surveillance in complex samples using the graph-based GNASty algorithm. *Genome research*, 35(4), 1025.

Wang L, et al. (2025) Bile-Liver phenotype: Exploring the microbiota landscape in bile and intratumor of cholangiocarcinoma. *Computational and structural biotechnology journal*, 27, 1173.

Tommasi A, et al. (2025) Fifteen millennia of human mitogenome evolution in Sicily. *Science advances*, 11(46), eady1674.

Thoenen L, et al. (2025) Synthetic communities of maize root bacteria interact and redirect benzoxazinoid metabolism. *mSphere*, 10(9), e0015925.

Freick M, et al. (2025) Trisomy 26 in a Holstein calf with disorders of sex development. *Animal genetics*, 56(1), e13489.

Thirumoorthy TP, et al. (2025) Recent emergence of cephalosporin-resistant *Salmonella* Typhi in India due to the endemic clone acquiring IncFIB(K) plasmid encoding blaCTX-M-15 gene. *Microbiology spectrum*, 13(5), e0087524.

Gy I, et al. (2025) The arabidopsis GyraseB3 contributes to transposon silencing by promoting histone deacetylation. *Nucleic acids research*, 53(18).

Zhou Q, et al. (2025) Characterizing DNA recognition preferences of transcription factors using global couplings and high-throughput sequencing. *Nucleic acids research*, 53(12).

Ouancharee W, et al. (2025) Predominance of hypervirulent ST283 and genetic diversity of levofloxacin resistance in multidrug-resistant, hypervirulent *Streptococcus agalactiae* in Thailand. *Journal of medical microbiology*, 74(3).

Wasimuddin , et al. (2025) Component specific responses of the microbiomes to common chemical stressors in the human food chain. *Environmental microbiome*, 20(1), 43.

Riccioni G, et al. (2025) Molecular diversity patterns and introgression in alpine and Northern European populations of Arctic charr (*Salvelinus alpinus*). *Scientific reports*, 15(1), 41306.

Nitaramorn N, et al. (2025) Experimental models of liver-stage malaria: Progress, gaps, and challenges. *PLoS pathogens*, 21(12), e1013796.

Juma MA, et al. (2025) Genomic detection of Panton-Valentine Leucocidins encoding genes, virulence factors and distribution of antiseptic resistance determinants among Methicillin-resistant *S. aureus* isolates from patients attending regional referral hospitals in Tanzania. *BMC medical genomics*, 18(1), 14.

Boulling A, et al. (2025) A bovine model of rhizomelic chondrodysplasia punctata caused by a deep intronic splicing variant in the GNPAT gene. *Genetics, selection, evolution : GSE*, 57(1), 23.