Resource Summary Report

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European Genome phenome Archive

RRID:SCR_004944
Type: Tool

Proper Citation

European Genome phenome Archive (RRID:SCR_004944)

Resource Information

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

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Description: Web service for permanent archiving and sharing of all types of personally identifiable genetic and phenotypic data resulting from biomedical research projects. The repository allows you to explore datasets from numerous genotype experiments, supplied by a range of data providers. The EGA''s role is to provide secure access to the data that otherwise could not be distributed to the research community. The EGA contains exclusive data collected from individuals whose consent agreements authorize data release only for specific research use or to bona fide researchers. Strict protocols govern how information is managed, stored and distributed by the EGA project. As an example, only members of the EGA team are allowed to process data in a secure computing facility. Once processed, all data are encrypted for dissemination and the encryption keys are delivered offline. The EGA also supports data access only for the consortium members prior to publication.

Abbreviations: EGA

Synonyms: , The European Genome-phenome Archive, The European Genome-phenome Archive (EGA), EGA

Resource Type: data or information resource, web service, software resource, data access protocol, data set, service resource, storage service resource, data repository

Defining Citation: PMID:34791407

Keywords: phenomenon, trait, sequence, genotype, experiment, case-control, population, family study, snp, cnv, phenotype, genomic, gold standard, bio.tools

Availability: Restricted

Resource Name: European Genome phenome Archive

Resource ID: SCR_004944

Alternate IDs: BioTools:ega, biotools:ega, r3d100011242, OMICS_01028, nlx_91316

Alternate URLs: https://ega-archive.org/, https://bio.tools/ega, https://bio.tools/ega, https://doi.org/10.17616/R3W619

Record Creation Time: 20220129T080227+0000

Record Last Update: 20260808T185829+0000

Ratings and Alerts

No rating or validation information has been found for European Genome phenome Archive.

No alerts have been found for European Genome phenome Archive.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 787 mentions in open access literature.

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

Tosi M, et al. (2026) A multi-omics study on monozygotic twins discordant for amyotrophic lateral sclerosis and literature review underline a potential role for innate immunity and epigenetic dysregulation in disease mechanisms. Neurological sciences : official journal of the Italian Neurological Society and of the Italian Society of Clinical Neurophysiology, 47(3), 230.

Georgiou G, et al. (2026) Integrative Network Analysis of Single-Cell RNA Findings and a Priori Knowledge Highlights Gene Regulators in Multiple Myeloma Progression. International journal of molecular sciences, 27(2).

Jaratlerdsiri W, et al. (2026) A catalogue of early diverged contemporary human genome variation reveals distinct Khoe-San populations. Nature communications, 17(1).

Ek M, et al. (2026) Long-read genome sequencing enhances diagnostics of pediatric neurological disorders. Genome medicine, 18(1), 12.

Bettoni F, et al. (2026) Liquid-based genomic profiling in high-risk localized prostate cancer. Frontiers in urology, 6, 1789586.

Gan J, et al. (2026) Cell Death Index Predicts Sepsis Outcomes and Highlights Necroptosis as a Therapeutic Target. Journal of inflammation research, 19, 577930.

El Makhzen N, et al. (2026) CFTR gene variant detection in moroccan individuals via nanopore long-read sequencing. Frontiers in genetics, 17, 1769093.

Cao H, et al. (2026) Ethnic-specific effects of the LILRB2-LILRB5 locus and newly identified risk loci for Alzheimer's disease in the East Asian population. Alzheimer's & dementia : the journal of the Alzheimer's Association, 22(2), e71219.

Vlachos G, et al. (2026) Functional footprints of homologous recombination deficiency in prostate cancer revealed by ctDNA fragmentation and transcription factor accessibility. British journal of cancer.

Chong AS, et al. (2026) Tracing the molecular route to progression in miRNA-biogenesis-defective thyroid lesions. JCI insight, 11(3).

Fang H, et al. (2026) PLOD2 promotes proliferation, migration and invasion of colorectal cancer cells via PI3K-AKT-GSK3?? signaling pathway. Scientific reports, 16(1).

Borda V, et al. (2026) Unraveling the genetic landscape and admixture dynamics of urban populations across Peru. Communications biology, 9(1).

Miglierina E, et al. (2026) DIS3 licenses B cells for plasma cell differentiation in humans. Cellular & molecular immunology, 23(1), 31.

Rychlicka-Buniowska E, et al. (2026) Loss of Y chromosome in Alzheimer's patients co-occurs with somatic mutations beyond CHIP drivers. Life science alliance, 9(2).

Zhu L, et al. (2026) A Circulating GPNMB-Based Multimodal Model Integrates Tumor-Immune Crosstalk to Predict Immunotherapy Response in Esophageal Cancer. Cancer discovery, 16(7), 1360.

Larrea-Sebal A, et al. (2026) Blood proteomics: insights from public data. Genome biology, 27(1).

Blas M, et al. (2026) Evaluation of ensilication technology for ambient DNA preservation. NAR molecular medicine, 3(1), ugag011.

Inayat H, et al. (2026) Integrative multi-cohort analysis of DNA methylation profiles for pancreatic ductal adenocarcinoma biomarker discovery and prognosis. Frontiers in bioinformatics, 6, 1808516.

Radulovich N, et al. (2026) Preclinical Combination Targeting VEGF and PI3K in a Rare, Aggressive Mixed Endometrial Carcinoma: An Applied Case Report. Cancer research communications, 6(4), 832.

Pospich R, et al. (2026) Staphylococcus aureus serine protease-like protein B elicits a type 1/type 2 immune response in atopic dermatitis patients. Frontiers in immunology, 17, 1798583.