Resource Summary Report

Generated by PRECISE-TBI on Aug 1, 2026

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, data repository, storage service resource, data access protocol, service resource, data set, software resource, web service

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: 20260801T042559+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 605 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

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).

Nteliopoulos G, et al. (2026) Identification of actionable targets using DEPArray-based sorting of pure carcinoma and stromal populations from formalin-fixed paraffin-embedded tissues followed by shallow whole-genome sequencing. The Journal of pathology, 268(1), 13.

Elias R, et al. (2025) Clear-Cell Renal Cell Carcinoma Molecular Subtypes Differ by African and European Genetic Similarity. Cancer research communications, 5(5), 743.

Umeda M, et al. (2025) Fusion oncoproteins and cooperating mutations define disease phenotypes in NUP98-rearranged leukemia. medRxiv : the preprint server for health sciences.

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

Wick W, et al. (2025) Molecularly matched targeted therapies plus radiotherapy in glioblastoma: the phase 1/2a N2M2 umbrella trial. Nature medicine.

Bulduk BK, et al. (2025) High frequency of mitochondrial DNA rearrangements in the peripheral blood of adults with intellectual disability. Journal of intellectual disability research : JIDR, 69(2), 137.

Zhi D, et al. (2025) Proxy panels enable privacy-aware outsourcing of genotype imputation. Genome research, 35(2), 326.

Moreno Rueda LY, et al. (2025) Single-cell analysis of neoplastic plasma cells identifies myeloma pathobiology mediators and potential targets. Cell reports. Medicine, 6(2), 101925.

Guo S, et al. (2025) A deconvolution framework that uses single-cell sequencing plus a small benchmark data set for accurate analysis of cell type ratios in complex tissue samples. Genome research, 35(1), 147.

Erickson A, et al. (2025) Clonal phylogenies inferred from bulk, single cell, and spatial transcriptomic analysis of epithelial cancers. PloS one, 20(1), e0316475.

Kogai H, et al. (2025) Broad-Spectrum Efficacy of CEACAM6-Targeted Antibody-Drug Conjugate with BET Protein Degrader in Colorectal, Lung, and Breast Cancer Mouse Models. Molecular cancer therapeutics, 24(3), 392.

Hollander JF, et al. (2025) Serially Quantifying TERT Rearrangement Breakpoints in ctDNA Enables Minimal Residual Disease Monitoring in Patients with Neuroblastoma. Cancer research communications, 5(1), 167.

Ungvari Z, et al. (2025) Senescence-related genes as prognostic indicators in breast cancer survival. GeroScience, 47(3), 2995.

Mazziotta F, et al. (2025) A phase I/II trial of WT1-specific TCR gene therapy for patients with acute myeloid leukemia and active disease post-allogeneic hematopoietic cell transplantation: skewing towards NK-like phenotype impairs T cell function and persistence. Nature communications, 16(1), 5214.

Lee BS, et al. (2025) NXPE1 alters the sialoglycome by acetylating sialic acids in the human colon. Nature communications, 16(1), 4912.

Mogire RM, et al. (2025) OSBPL11 is an African-specific locus associated with 25-hydroxyvitamin D concentrations and cardiometabolic health. medRxiv : the preprint server for health sciences.

Groenendijk A, et al. (2025) Gene Expression Analysis of (Paired) Primary and Relapsed Wilms Tumor Samples to Unravel the Underlying Factors Driving Tumor Recurrence. Cancer medicine, 14(11), e70969.

Vinsland E, et al. (2025) Cell atlas of the developing human meninges reveals a dura origin of meningioma. bioRxiv : the preprint server for biology.