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

Defining Citation: PMID:34791407

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

Funding:

Availability: Restricted

Resource Name: European Genome phenome Archive

Resource ID: SCR_004944

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

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

Record Creation Time: 20220129T080227+0000

Record Last Update: 20250403T060404+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 459 mentions in open access literature.

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

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.

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.

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

Te Aika B, et al. (2025) Aotearoa genomic data repository: An ?huru m?wai for taonga species sequencing data. Molecular ecology resources, 25(2), e13866.

Ziegler DV, et al. (2025) CDK4 inactivation inhibits apoptosis via mitochondria-ER contact remodeling in triple-negative breast cancer. Nature communications, 16(1), 541.

Subramanian DN, et al. (2025) Assessment of candidate high-grade serous ovarian carcinoma predisposition genes through integrated germline and tumour sequencing. NPJ genomic medicine, 10(1), 1.

Legebeke J, et al. (2025) Uplift of genetic diagnosis of rare respiratory disease using airway epithelium transcriptome analysis. Human molecular genetics, 34(2), 148.

Ganguli P, et al. (2025) Context-dependent effects of CDKN2A and other 9p21 gene losses during the evolution of esophageal cancer. Nature cancer, 6(1), 158.

Yap WS, et al. (2025) High-coverage whole-genome sequencing of a Jakun individual from the "Orang Asli" Proto-Malay subtribe from Peninsular Malaysia. Human genome variation, 12(1), 4.

Kim J, et al. (2025) Highly accurate Korean draft genomes reveal structural variation highlighting human telomere evolution. Nucleic acids research, 53(1).

Chen YC, et al. (2025) Multiomics Analysis Reveals Molecular Changes during Early Progression of Precancerous Lesions to Lung Adenocarcinoma in Never-Smokers. Cancer research, 85(3), 602.

Würth R, et al. (2025) Circulating tumor cell plasticity determines breast cancer therapy resistance via neuregulin 1-HER3 signaling. Nature cancer, 6(1), 67.

Chen T, et al. (2025) In-depth inference of transcriptional regulatory networks reveals NPM1 as a therapeutic ribosomal regulator in MYC-amplified medulloblastoma. NPJ precision oncology, 9(1), 10.

Giuliani KTK, et al. (2025) Human proximal tubular epithelial cell interleukin-1 receptor signalling triggers G2/M arrest and cellular senescence during hypoxic kidney injury. Cell death & disease, 16(1), 61.

Kim YH, et al. (2024) Integrative Multi-omics Analysis Reveals Different Metabolic Phenotypes Based on Molecular Characteristics in Thyroid Cancer. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(4), 883.

Iser F, et al. (2024) Cerebrospinal Fluid cfDNA Sequencing for Classification of Central Nervous System Glioma. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(14), 2974.

Rosenheim J, et al. (2024) SARS-CoV-2 human challenge reveals biomarkers that discriminate early and late phases of respiratory viral infections. Nature communications, 15(1), 10434.

Rediti M, et al. (2024) Identification of HER2-positive breast cancer molecular subtypes with

potential clinical implications in the ALTTO clinical trial. Nature communications, 15(1), 10402.

Fernandez-Mateos J, et al. (2024) Tumor evolution metrics predict recurrence beyond 10 years in locally advanced prostate cancer. Nature cancer, 5(9), 1334.

Iqbal MA, et al. (2024) Protocol for performing metabolic pathway-based subtyping of breast tumors. STAR protocols, 5(3), 103173.