

Resource Summary Report

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European Variation Archive (EVA)

RRID:SCR_017425

Type: Tool

Proper Citation

European Variation Archive (EVA) (RRID:SCR_017425)

Resource Information

URL: <https://www.ebi.ac.uk/eva/>

Proper Citation: European Variation Archive (EVA) (RRID:SCR_017425)

Description: Open access database of all types of genetic variation data from all species. Users can download data from any study, or submit their own data to archive. You can also query all variants by study, gene, chromosomal location or dbSNP identifier using our Variant Browser.

Abbreviations: EVA

Synonyms: EVA, European Variation Archive

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

Keywords: Collection, genetic, variation, data, chromosomal, location, dbSNP, bio.tools

Availability: Free, Freely available

Resource Name: European Variation Archive (EVA)

Resource ID: SCR_017425

Alternate IDs: biotools:eva

Alternate URLs: <https://bio.tools/eva>

Record Creation Time: 20220129T080335+0000

Record Last Update: 20260729T044435+0000

Ratings and Alerts

No rating or validation information has been found for European Variation Archive (EVA).

No alerts have been found for European Variation Archive (EVA).

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 89 mentions in open access literature.

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

Smith JR, et al. (2025) Standardized pipelines support and facilitate integration of diverse datasets at the Rat Genome Database. Database : the journal of biological databases and curation, 2025.

Santin A, et al. (2025) Normal hearing function genetics: have you heard all about it? An integrated approach of genome-wide association studies and transcriptome-wide association studies in three Italian cohorts. Frontiers in genetics, 16, 1522338.

Murgiano L, et al. (2025) Two genes, one culprit - a functional candidate validation of a SPATA7 deletion in dogs with day blindness/retinal degeneration. PLoS genetics, 21(12), e1011961.

Shin JW, et al. (2025) High-quality phased genome assemblies of line-bred Korean Hanwoo cattle. Scientific data, 12(1), 1807.

Zhou X, et al. (2025) Novel human single-domain antibodies exert potent anti-tumor activity by targeting EGF-like repeat epitope of EpCAM. Frontiers in pharmacology, 16, 1530268.

Sigurðardóttir H, et al. (2025) Genetic influence of a STAU2 frameshift mutation and RELN regulatory elements on performance in Icelandic horses. Scientific reports, 15(1), 11641.

Murgiano L, et al. (2025) GTPBP2 in-frame deletion in canine model with non-syndromic progressive retinal atrophy. Scientific reports, 15(1), 6079.

Poutougnigni Matenchi Y, et al. (2025) Genomic diversity of Cameroonian Gudali and Gudali-cross cattle. Scientific reports, 15(1), 15066.

Fernandez-Ciruelos B, et al. (2025) Novel antimicrobial 3-phenyl-4-phenoxy pyrazole derivatives target cell wall lipid intermediates with low mammalian cytotoxicity. Scientific reports, 15(1), 35646.

Fanelli A, et al. (2024) The K9 lymphoma assay allows a genetic subgrouping of canine lymphomas with improved risk classification. Scientific reports, 14(1), 18687.

Kattenberg JH, et al. (2024) Population genomic evidence of structured and connected *Plasmodium vivax* populations under host selection in Latin America. *Ecology and evolution*, 14(3), e111103.

Ko BS, et al. (2024) A brief guide to analyzing expression quantitative trait loci. *Molecules and cells*, 47(11), 100139.

Ramirez-Ramirez AR, et al. (2024) Using ddRADseq to assess the genetic diversity of in-farm and gene bank cacao resources in the Baracoa region, eastern Cuba, for use and conservation purposes. *Frontiers in plant science*, 15, 1367632.

Cozzi P, et al. (2024) SMARTER-database: a tool to integrate SNP array datasets for sheep and goat breeds. *GigaByte (Hong Kong, China)*, 2024, gigabyte139.

Zhang L, et al. (2024) FishSNP: a high quality cross-species SNP database of fishes. *Scientific data*, 11(1), 286.

Ortega F, et al. (2024) Identification of QTLs involved in destemming and fruit quality for mechanical harvesting of New Mexico pod-type green chile. *Frontiers in plant science*, 15, 1357986.

Gazola AA, et al. (2024) Precision oncology platforms: practical strategies for genomic database utilization in cancer treatment. *Molecular cytogenetics*, 17(1), 28.

Hirahara L, et al. (2024) Association of high disease activity and serum IL-6 levels with the incidence of inflammatory major organ events in Behçet disease: a prospective registry study. *Frontiers in immunology*, 15, 1354969.

Botchway PK, et al. (2024) Genotypic and phenotypic characterisation of three local chicken ecotypes of Ghana based on principal component analysis and body measurements. *PloS one*, 19(8), e0308420.

Skarp S, et al. (2024) Novel Genetic Variants Associated with Primary Myocardial Fibrosis in Sudden Cardiac Death Victims. *Journal of cardiovascular translational research*, 17(6), 1229.