

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

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: 20260808T190051+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 107 mentions in open access literature.

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

Wagner M, et al. (2026) The Genomics of Convergent Adaptation to Intertidal Gravel Beaches in Mediterranean Clingfishes. *Genome biology and evolution*, 18(3).

Brouwer M, et al. (2026) Integrating plant phenotypic and genotypic data in the AGENT project: a BrAPI service implementation. *Bioinformatics (Oxford, England)*, 42(5).

Lind BM, et al. (2026) CartograPlant: bridging genomic, phenotypic, and environmental data to advance plant resilience and eco-evolutionary insight. *Genetics*, 232(4).

Steensma MJ, et al. (2026) Deficiency in homozygous haplotypes reveals recessive lethal variants affecting fertility and viability in the Friesian horse. *BMC genomics*, 27(1).

Tello-Ruiz MK, et al. (2026) Adoption of Standard Reference SNP Identifiers in Agricultural Genomics for Interoperability and Data Reuse. *Scientific data*, 13(1).

Novoa-Bravo M, et al. (2026) Machine learning-based gait classification and genome-wide association identify a QTL for gait type in Colombian paso horses. *iScience*, 29(7), 116320.

Li H, et al. (2026) Genome-wide association study reveals the genetic architecture of drought tolerance in maize using yield-based resistance indices and transcriptomic evidence. *The plant genome*, 19(2), e70255.

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.

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.

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.

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

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.

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.

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

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

Tan J, et al. (2025) Long read Nanopore sequencing identifies precise breakpoints of a de novo paracentric inversion that disrupt the MEIS2 gene in a Chinese girl with syndromic developmental delay. *BMC pediatrics*, 25(1), 18.

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.

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

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), e11103.

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.