Resource Summary Report

Generated by NIF on Apr 16, 2025

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/

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

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

Funding:

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: 20250416T063822+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 81 mentions in open access literature.

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

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.

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.

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.

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

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.

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.

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.

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.

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

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.

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.

Carvalho CM, et al. (2023) Germline Mutations Landscape in a Cohort of the State of Minas Gerais, Brazil, in Patients Who Underwent Genetic Counseling for Gynecological and Breast Cancer. Revista brasileira de ginecologia e obstetricia : revista da Federacao Brasileira das Sociedades de Ginecologia e Obstetricia, 45(2), 74.

Liu Y, et al. (2023) Identification of genetic associations and functional SNPs of bovine KLF6 gene on milk production traits in Chinese holstein. BMC genomic data, 24(1), 72.

Lourenço RA, et al. (2023) BRCA1 VUS: A functional analysis to differentiate pathogenic from benign variants identified in clinical diagnostic panels for breast cancer. Molecular medicine reports, 28(1).

Le Clercq LS, et al. (2023) Birds of a feather flock together: a dataset for Clock and Adcyap1 genes from migration genetics studies. Scientific data, 10(1), 787.

Peterson KA, et al. (2023) Whole genome analysis for 163 gRNAs in Cas9-edited mice reveals minimal off-target activity. Communications biology, 6(1), 626.

Mukhopadhyay A, et al. (2023) TLR4 and MD2 variation among horses with differential TNF? baseline concentrations and response to intravenous lipopolysaccharide infusion. Scientific reports, 13(1), 1486.

Maksimov MO, et al. (2023) A novel quantitative trait locus implicates Msh3 in the propensity for genome-wide short tandem repeat expansions in mice. Genome research, 33(5), 689.

Hu ZL, et al. (2022) Bringing the Animal QTLdb and CorrDB into the future: meeting new challenges and providing updated services. Nucleic acids research, 50(D1), D956.