Resource Summary Report

Generated by NIF on Apr 23, 2025

GenABEL

RRID:SCR_001842
Type: Tool

Proper Citation

GenABEL (RRID:SCR_001842)

Resource Information

URL: http://www.genabel.org/packages/GenABEL

Proper Citation: GenABEL (RRID:SCR_001842)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on February 28,2023. R software library for genome-wide association analysis for quantitative, binary and time-till-event traits.

Synonyms: GenABEL package, R/GENABEL

Resource Type: software resource, software library, software toolkit

Defining Citation: PMID:17384015, DOI:10.1186/1471-2105-11-134, DOI:10.1093/bioinformatics/btm108

Keywords: r, genome-wide association, single nucleotide polymorphism

Funding: Centre for Medical Systems Biology; Netherlands ;
Netherlands Genomics Initiative ;
Netherlands Organisation for Scientific Research ;
Russian Foundation for Basic Research

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: GenABEL

Resource ID: SCR_001842

Alternate IDs: nlx_154328, OMICS_00234

Alternate URLs: http://mga.bionet.nsc.ru/~yurii/ABEL/GenABEL/, https://cran.r-project.org/web/packages/GenABEL/index.html, https://sources.debian.org/src/probabel/

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Ratings and Alerts

No rating or validation information has been found for GenABEL.

No alerts have been found for GenABEL.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 502 mentions in open access literature.

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

Liu Y, et al. (2025) Novel genetic variants in the NLRP3 inflammasome-related PANX1 and APP genes predict survival of patients with hepatitis B virus-related hepatocellular carcinoma. Clinical & translational oncology : official publication of the Federation of Spanish Oncology Societies and of the National Cancer Institute of Mexico, 27(2), 630.

Opmeer Y, et al. (2025) Polymyositis in Kooiker dogs is associated with a 39 kb deletion upstream of the canine IL21/IL2 locus. PLoS genetics, 21(1), e1011538.

Ban S, et al. (2024) Predicting the final metabolic profile based on the succession-related microbiota during spontaneous fermentation of the starter for Chinese liquor making. mSystems, 9(2), e0058623.

Lu G, et al. (2024) Potentially functional variants of INPP5D and EXOSC3 in immunity B cell-related genes are associated with non-small cell lung cancer survival. Frontiers in immunology, 15, 1440454.

Rebhun RB, et al. (2024) A variant in the 5'UTR of ERBB4 is associated with lifespan in Golden Retrievers. GeroScience, 46(3), 2849.

Murgiano L, et al. (2024) A naturally occurring canine model of syndromic congenital microphthalmia. G3 (Bethesda, Md.), 14(6).

Naake T, et al. (2024) Genome-wide association studies identify loci controlling specialized

seed metabolites in Arabidopsis. Plant physiology, 194(3), 1705.

Meng X, et al. (2024) Multi-ancestry genome-wide association study of major depression aids locus discovery, fine mapping, gene prioritization and causal inference. Nature genetics, 56(2), 222.

Ray NR, et al. (2024) Extended genome-wide association study employing the African genome resources panel identifies novel susceptibility loci for Alzheimer's disease in individuals of African ancestry. Alzheimer's & dementia : the journal of the Alzheimer's Association, 20(8), 5247.

Zhang W, et al. (2024) Host genetics and gut microbiota synergistically regulate feed utilization in egg-type chickens. Journal of animal science and biotechnology, 15(1), 123.

Akgun B, et al. (2024) Genome-wide association analysis and admixture mapping in a Puerto Rican cohort supports an Alzheimer disease risk locus on chromosome 12. Frontiers in aging neuroscience, 16, 1459796.

Patel JN, et al. (2024) Pharmacogenetic and clinical risk factors for bevacizumab-related gastrointestinal hemorrhage in prostate cancer patients treated on CALGB 90401 (Alliance). The pharmacogenomics journal, 24(2), 6.

Shore CJ, et al. (2024) Genetic effects on the skin methylome in healthy older twins. American journal of human genetics, 111(9), 1932.

Liu S, et al. (2024) Genetic variants of m6A modification genes are associated with survival of HBV-related hepatocellular carcinoma. Journal of cellular and molecular medicine, 28(16), e18517.

McAuley JB, et al. (2024) The Genetic Architecture of Recombination Rates is Polygenic and Differs Between the Sexes in Wild House Sparrows (Passer domesticus). Molecular biology and evolution, 41(9).

Tomar A, et al. (2024) Epigenetic inheritance of diet-induced and sperm-borne mitochondrial RNAs. Nature, 630(8017), 720.

Minnai F, et al. (2024) A genome-wide association study for survival from a multi-centre European study identified variants associated with COVID-19 risk of death. Scientific reports, 14(1), 3000.

Colombi D, et al. (2024) Population structure and identification of genomic regions associated with productive traits in five Italian beef cattle breeds. Scientific reports, 14(1), 8529.

Lu G, et al. (2024) Genetic variants of LRRC8C, OAS2, and CCL25 in the T cell exhaustion-related genes are associated with non-small cell lung cancer survival. Frontiers in immunology, 15, 1455927.

Shahbazi M, et al. (2023) Comprehensive association analysis of speech recognition thresholds after cisplatin-based chemotherapy in survivors of adult-onset cancer. Cancer medicine, 12(3), 2999.