

Resource Summary Report

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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 toolkit, software resource, software library

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/>

Record Creation Time: 20220129T080209+0000

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 506 mentions in open access literature.

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

Huang M, et al. (2025) Goose multi-omics database: A comprehensive multi-omics database for goose genomics. Poultry science, 104(3), 104842.

Kiser JN, et al. (2025) Validation of loci and genes associated with fertility in Holstein cows using gene-set enrichment analysis-SNP and genotype-by-sequencing. BMC genomics, 26(1), 174.

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.

Zhu B, et al. (2025) Multiple strategies association revealed functional candidate FASN gene for fatty acid composition in cattle. Communications biology, 8(1), 208.

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).

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.

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.

Naake T, et al. (2024) Genome-wide association studies identify loci controlling specialized seed metabolites in Arabidopsis. *Plant physiology*, 194(3), 1705.

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.

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.

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.

Strath LJ, et al. (2024) Differential DNA methylation profiles of Alzheimer's disease-related genomic pathways in the blood of cognitively-intact individuals with and without high impact chronic pain. *Journal of Alzheimer's disease reports*, 8(1), 1549.

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.

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).

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.

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

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.