

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

BEAGLE

RRID:SCR_001789

Type: Tool

Proper Citation

BEAGLE (RRID:SCR_001789)

Resource Information

URL: <http://faculty.washington.edu/browning/beagle/beagle.html>

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Description: Software package for analysis of large-scale genetic data sets with hundreds of thousands of markers genotyped on thousands of samples. BEAGLE can * phase genotype data (i.e. infer haplotypes) for unrelated individuals, parent-offspring pairs, and parent-offspring trios. * infer sporadic missing genotype data. * impute ungenotyped markers that have been genotyped in a reference panel. * perform single marker and haplotypic association analysis. * detect genetic regions that are homozygous-by-descent in an individual or identical-by-descent in pairs of individuals. Beagle can also be used in conjunction with PRESTO, a program for fast and flexible permutation testing. PRESTO can compute empirical distributions of order statistics, analyze stratified data, and determine significance levels for one-stage and two-stage genetic association studies. BEAGLE is written in Java and runs on any computing platform with a Java version 1.6 interpreter (e.g. Windows, Unix, Linux, Solaris, Mac).

Abbreviations: BEAGLE

Synonyms: BEAGLE Genetic Analysis Software Package

Resource Type: software application, software resource

Defining Citation: [PMID:17924348](#), [PMID:17326099](#), [PMID:21310274](#), [DOI:10.1086/521987](#)

Keywords: gene, genetic, genomic, java, ms-windows, linux, unix, solaris, macos, identity by descent, genotype, haplotype

Availability: Free, Available for download, Freely available

Resource Name: BEAGLE

Resource ID: SCR_001789

Alternate IDs: nlx_154238, OMICS_00052, OMICS_00201

Alternate URLs: <https://sources.debian.org/src/beagle/>

Old URLs: <https://www.stat.auckland.ac.nz/%7Ebrowning/beagle/beagle.html>

License: GNU General Public License, v3 or newer

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260905T133225+0000

Ratings and Alerts

No rating or validation information has been found for BEAGLE.

No alerts have been found for BEAGLE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2377 mentions in open access literature.

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

Yang W, et al. (2026) Multi-omics reveals co-regulation of hepatic bile acid metabolism in laying hens by host genetics and the cecal Anaerostipes. Poultry science, 105(3), 106388.

Lu Q, et al. (2026) Genomic characterization and pathogenicity validation of Mycoplasma ovipneumoniae strains from diseased sheep: insights into potential pathogenic mechanisms of GSWW364. Veterinary research, 57(1).

Zhuang Z, et al. (2026) A new integrated genetic and transcriptomic approach for investigating DUX4 and DUX4C. Journal of human genetics, 71(6), 373.

Yuan Z, et al. (2026) Targeted expansion of a barley genebank core collection facilitates the discovery of disease resistance loci. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 139(1), 30.

Liu C, et al. (2026) Genome-Wide Association Study of Leukocyte Traits Reveals Candidate Genes Associated With Immunity in Holstein Cattle From Southern China. Veterinary medicine and science, 12(2), e70858.

Temple SD, et al. (2026) Multiple-testing corrections in case-control studies using identity-by-descent segments. American journal of human genetics, 113(3), 453.

Saha A, et al. (2026) HLA Class II Alleles Are Associated With Anti-Drug Antibodies in Ulcerative Colitis Patients Treated With Etrolizumab. *HLA*, 107(2), e70557.

Watson N, et al. (2026) Across-breed analyses of genome-wide association studies for stature and mammary gland morphology in cattle reveal pleiotropic effects of the Friesian POLLED haplotype. *Genetics, selection, evolution : GSE*, 58(1).

McClelland P, et al. (2026) A multi-ancestry genetic reference for the Quebec population. *Nature communications*, 17(1), 1319.

Reeve MP, et al. (2026) Genome-wide association analyses of autoimmune hypothyroidism reveal autoimmune and thyroid-specific contributions and an inverse relationship with cancer risk. *Nature genetics*, 58(3), 550.

Bakherad M, et al. (2026) Variation in Follicle-Stimulating Hormone Receptor Expression Is Associated with the Twinning Rate QTL Located on Bovine Chromosome 11 in Holstein Cattle. *Animals : an open access journal from MDPI*, 16(4).

Rowley E, et al. (2026) Genetic relatedness of Cambodian *Plasmodium falciparum* isolates is driven by geography and occupation. *medRxiv : the preprint server for health sciences*.

Haapaniemi H, et al. (2026) The genetic basis of dermatophytosis skin infection susceptibility. *Nature communications*, 17(1).

Salo V, et al. (2026) Genetic architecture of lumbar spinal stenosis. *Nature communications*, 17(1).

Telles-de-Deus J, et al. (2026) Evolution and spillover dynamics of yellow fever at the forest-urban interface in Brazil. *Nature microbiology*, 11(4), 877.

Ding J, et al. (2026) Profiling Peripheral Blood with an Optimized, Multiplexed, Single-cell Multiome Approach Supports an Insulin-driven Asthma Subtype. *bioRxiv : the preprint server for biology*.

Zhu R, et al. (2026) Enhancing genomic prediction for key production traits in chickens through ultrasound phenotyping and multi-model comparative analysis. *Journal of animal science and biotechnology*, 17(1).

Valverde G, et al. (2026) An ancient genome of *Streptococcus pyogenes* from a pre-Columbian Bolivian mummy. *Nature communications*, 17(1).

Bernini F, et al. (2026) An analysis of the genomic architecture of the worldwide Irish Wolfhound dogs. *Scientific reports*, 16(1).

Pfennig A, et al. (2026) Limited Selection on Neanderthal DNA in 30,780 Recently Admixed Genomes with African-like Ancestry. *Molecular biology and evolution*, 43(7).