

Resource Summary Report

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BIMBAM

RRID:SCR_009129

Type: Tool

Proper Citation

BIMBAM (RRID:SCR_009129)

Resource Information

URL: <http://stephenslab.uchicago.edu/software.html>

Proper Citation: BIMBAM (RRID:SCR_009129)

Description: Software application (entry from Genetic Analysis Software)

Abbreviations: BIMBAM

Synonyms: Bayesian IMputation-Based Association Mapping

Resource Type: software application, software resource

Keywords: gene, genetic, genomic

Resource Name: BIMBAM

Resource ID: SCR_009129

Alternate IDs: nlx_154242

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260805T044217+0000

Ratings and Alerts

No rating or validation information has been found for BIMBAM.

No alerts have been found for BIMBAM.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 77 mentions in open access literature.

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

Huo Y, et al. (2025) Genome-wide association analysis and gene mining of flavonoids in *Xanthoceras sorbifolia*. Scientific reports, 15(1), 20808.

Tough RH, et al. (2025) Functionally-informed fine-mapping identifies genetic variants linking increased CHD1L expression and HIV restriction in monocytes. Scientific reports, 15(1), 2325.

Ranasinghe RW, et al. (2025) Biochemical and Genomic Underpinnings of Carotenoid Colour Variation Across a Hybrid Zone Between South Asian Flameback Woodpeckers. Molecular ecology, 34(19), e70084.

Ahmed SR, et al. (2024) Advancing crop improvement through GWAS and beyond in mung bean. Frontiers in plant science, 15, 1436532.

Wang Z, et al. (2024) Refine localizations of functional variants affecting eggshell color of Lueyang black-boned chicken in the SLCO1B3. Poultry science, 103(1), 103212.

Chen Q, et al. (2022) A new molecular mechanism supports that blue-greenish egg color evolved independently across chicken breeds. Poultry science, 101(12), 102223.

Sinclair-Waters M, et al. (2022) Dissecting the loci underlying maturation timing in Atlantic salmon using haplotype and multi-SNP based association methods. Heredity, 129(6), 356.

Yang Z, et al. (2021) Genome-Wide Association Study Using Whole-Genome Sequencing Identifies a Genomic Region on Chromosome 6 Associated With Comb Traits in Nandan-Yao Chicken. Frontiers in genetics, 12, 682501.

Wang Z, et al. (2021) Research Note: Fine mapping of sequence variants associated with body weight of Lueyang black-boned chicken in the CCKAR gene. Poultry science, 100(11), 101448.

Ahluwalia TS, et al. (2021) Genome-wide association study of circulating interleukin 6 levels identifies novel loci. Human molecular genetics, 30(5), 393.

Vilor-Tejedor N, et al. (2021) Multivariate Analysis and Modelling of multiple Brain endOphenotypes: Let's MAMBO! Computational and structural biotechnology journal, 19, 5800.

García-Fernández C, et al. (2021) GWAS of pod morphological and color characters in common bean. BMC plant biology, 21(1), 184.

Shang L, et al. (2020) Genetic Architecture of Gene Expression in European and African Americans: An eQTL Mapping Study in GENOA. American journal of human genetics, 106(4), 496.

Abuga KM, et al. (2020) Interferon-gamma polymorphisms and risk of iron deficiency and anaemia in Gambian children. Wellcome open research, 5, 40.

Xu Z, et al. (2020) Selection signature reveals genes associated with susceptibility loci affecting respiratory disease due to pleiotropic and hitchhiking effect in Chinese indigenous pigs. Asian-Australasian journal of animal sciences, 33(2), 187.

Su M, et al. (2020) Genomic analysis of variability in Delta-toxin levels between *Staphylococcus aureus* strains. PeerJ, 8, e8717.

Morton MJL, et al. (2019) Salt stress under the scalpel - dissecting the genetics of salt tolerance. The Plant journal : for cell and molecular biology, 97(1), 148.

Mozaffari SV, et al. (2019) Parent-of-origin effects on quantitative phenotypes in a large Hutterite pedigree. Communications biology, 2, 28.

Rito T, et al. (2019) Association of Leukotriene A4 Hydrolase with Tuberculosis Susceptibility Using Genomic Data in Portugal. Microorganisms, 7(12).

Chundru VK, et al. (2019) Examining the Impact of Imputation Errors on Fine-Mapping Using DNA Methylation QTL as a Model Trait. Genetics, 212(3), 577.