

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

BAMA

RRID:SCR_009071

Type: Tool

Proper Citation

BAMA (RRID:SCR_009071)

Resource Information

URL: <http://www.rni.helsinki.fi/~mjs/>

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Description: Software application to select a trait-associated subset of markers among many candidates. The program is based on Bayesian modeling/estimation and it suits for both quantitative and qualitative traits. It can handle bi- and multiallelic markers as well as applied in situations where part of the marker genotypes may be missing. As an output of the program, one obtains posterior estimate of number and positions of trait-associated markers. (entry from Genetic Analysis Software), THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: BAMA

Synonyms: Bayesian Analysis of Multilocus Association

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c, linux

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: BAMA

Resource ID: SCR_009071

Alternate IDs: nlx_154065

Record Creation Time: 20220129T080250+0000

Record Last Update: 20260731T042809+0000

Ratings and Alerts

No rating or validation information has been found for BAMA.

No alerts have been found for BAMA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 98 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Kang Z, et al. (2025) Estimation of total mediation effect for a binary trait in a case-control study for high-dimensional omics mediators†. *bioRxiv : the preprint server for biology*.

Walker ME, et al. (2025) Antibacterial macrocyclic peptides reveal a distinct mode of BamA inhibition. *Nature communications*, 16(1), 3395.

Chawana TD, et al. (2025) Pharmacokinetic interaction assessment of an HIV broadly neutralizing monoclonal antibody VRC07-523LS: a cross-protocol analysis of three phase 1 trials in people without HIV. *BMC immunology*, 26(1), 8.

Estelle DL, et al. (2025) Unstable laboratory Wolbachia strain w-Anga is negatively correlated with Plasmodium falciparum in wild malaria vectors. *Scientific reports*, 15(1), 17732.

Machin JM, et al. (2025) OmpA Specifically Modulates the Activity of Enzymes that Reside in the Crowded Bacterial Outer Membrane. *Journal of molecular biology*, 437(19), 169346.

Miller IG, et al. (2025) Influence of Distinct Maternal Cytomegalovirus-Specific Neutralizing and Fc Receptor-Binding Responses on Congenital Cytomegalovirus Transmission in HIV-Exposed Neonates. *Viruses*, 17(3).

Georgieva M, et al. (2025) Mutations in the essential outer membrane protein BamA contribute to Escherichia coli resistance to the antimicrobial peptide TAT-RasGAP317-326. *The Journal of biological chemistry*, 301(1), 108018.

Li Z, et al. (2025) Gut microbiota orchestrates skeletal muscle development and metabolism in germ-free and SPF pigs. *Frontiers in microbiology*, 16, 1615884.

Shi Q, et al. (2025) Bama pig is a suitable animal for studying laryngopharyngeal reflux disease. *Acta otorhinolaryngologica Italica : organo ufficiale della Societa italiana di otorinolaringologia e chirurgia cervico-facciale*, 45(1), 21.

Wang Z, et al. (2024) A minimum functional form of the Escherichia coli BAM complex constituted by BamADE assembles outer membrane proteins in vitro. *The Journal of biological chemistry*, 300(6), 107324.

Momeni M, et al. (2024) Targeting BamA, the essential component of the *Acinetobacter baumannii* β -barrel assembly machinery, hinders its ability to adhere to and invade human alveolar basal epithelial cell line. *Heliyon*, 10(14), e34371.

Miner MD, et al. (2024) Polytopic fractional delivery of an HIV vaccine alters cellular responses and results in increased epitope breadth in a phase 1 randomized trial. *EBioMedicine*, 100, 104987.

Spreng RL, et al. (2024) Identification of RTS,S/AS01 vaccine-induced humoral biomarkers predictive of protection against controlled human malaria infection. *JCI insight*, 9(19).

Li D, et al. (2024) Lipid scrambling is a general feature of protein insertases. *Proceedings of the National Academy of Sciences of the United States of America*, 121(17), e2319476121.

Walsh SR, et al. (2024) Safety and pharmacokinetics of VRC07-523LS administered via different routes and doses (HVTN 127/HPTN 087): A Phase I randomized clinical trial. *PLoS medicine*, 21(6), e1004329.

Levy Y, et al. (2024) Safety and immunogenicity of CD40.HIVRI.Env, a dendritic cell-based HIV vaccine, in healthy HIV-uninfected adults: a first-in-human randomized, placebo-controlled, dose-escalation study (ANRS VRI06). *EClinicalMedicine*, 77, 102845.

Guo X, et al. (2024) A deep learning-driven discovery of berberine derivatives as novel antibacterial against multidrug-resistant *Helicobacter pylori*. *Signal transduction and targeted therapy*, 9(1), 183.

Bishop SL, et al. (2024) Microbial Diversity Impacts Non-Protein Amino Acid Production in Cyanobacterial Bloom Cultures Collected from Lake Winnipeg. *Toxins*, 16(4).

Dos Santos TMA, et al. (2024) Native β -barrel substrates pass through two shared intermediates during folding on the BAM complex. *Proceedings of the National Academy of Sciences of the United States of America*, 121(42), e2409672121.

Sun D, et al. (2024) The discovery and structural basis of two distinct state-dependent inhibitors of BamA. *Nature communications*, 15(1), 8718.