

# Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 19, 2026

## [bamova](#)

RRID:SCR\_000510

Type: Tool

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### Proper Citation

bamova (RRID:SCR\_000510)

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### Resource Information

**URL:** <http://www.uwyo.edu/buerkle/software/bamova/>

**Proper Citation:** bamova (RRID:SCR\_000510)

**Description:** Software that implements a Bayesian Analysis of Molecular Variance and different likelihood models for three different types of molecular data (including two models for high throughput sequence data).

**Abbreviations:** bamova

**Resource Type:** data analysis software, data processing software, software application, software resource

**Defining Citation:** [PMID:21212231](#)

**Keywords:** mac os x, high throughput sequence

**Funding:** NSF 701757

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** bamova

**Resource ID:** SCR\_000510

**Alternate IDs:** OMICS\_01532

**License:** GNU General Public License, v3 or later

**Record Creation Time:** 20220129T080202+0000

**Record Last Update:** 20260919T194925+0000

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### Ratings and Alerts

No rating or validation information has been found for bamova.

No alerts have been found for bamova.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.