

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 7, 2026

[bamova](#)

RRID:SCR_000510

Type: Tool

Proper Citation

bamova (RRID:SCR_000510)

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, software application, software resource, data processing software

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: 20260807T042511+0000

Ratings and Alerts

No rating or validation information has been found for bamova.

No alerts have been found for bamova.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.