

# Resource Summary Report

Generated by [NIF](#) on Oct 20, 2026

## BARS

RRID:SCR\_009123

Type: Tool

---

### Proper Citation

BARS (RRID:SCR\_009123)

---

### Resource Information

**URL:** <http://wpicr.wpic.pitt.edu/WPICCompGen/bars.htm>

**Proper Citation:** BARS (RRID:SCR\_009123)

**Description:** Software application that is a statistical method that bridges the gap between single-locus and haplotype-based tests of association. It is based on the non-parametric regression techniques embodied by Bayesian Adaptive Regression Splines. (entry from Genetic Analysis Software), THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

**Abbreviations:** BARS

**Synonyms:** Bayesian Adaptive Regression Splines

**Resource Type:** software application, software resource

**Keywords:** gene, genetic, genomic, r, linux, bio.tools

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

**Resource Name:** BARS

**Resource ID:** SCR\_009123

**Alternate IDs:** nlx\_154204, biotools:bars, nlx\_154228, SCR\_009106

**Alternate URLs:** <https://bio.tools/bars>

**Record Creation Time:** 20220129T080251+0000

**Record Last Update:** 20261017T202723+0000

---

### Ratings and Alerts

No rating or validation information has been found for BARS.

No alerts have been found for BARS.

---

## Data and Source Information

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

---

## Usage and Citation Metrics

We have not found any literature mentions for this resource.