

Resource Summary Report

Generated by SPARC SAWG on Jul 28, 2026

clustLasso

RRID:SCR_018820

Type: Tool

Proper Citation

clustLasso (RRID:SCR_018820)

Resource Information

URL: <https://gitlab.com/biomerieux-data-science/clustlasso>

Proper Citation: clustLasso (RRID:SCR_018820)

Description: Software R package to build predictive signatures of microbial phenotypes. Software package implementing cluster lasso approach.

Resource Type: software resource, software toolkit

Keywords: Predictive signatures, microbial phenotype, cluster lasso approach, build predictive signature, phenotype, data, bio.tools

Availability: Free, Freely available

Resource Name: clustLasso

Resource ID: SCR_018820

Alternate IDs: biotools:clustlasso

Alternate URLs: <https://bio.tools/clustlasso>

License: GNU GPL V2

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260725T191304+0000

Ratings and Alerts

No rating or validation information has been found for clustLasso.

No alerts have been found for clustLasso.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Jaillard M, et al. (2020) Interpreting k-mer-based signatures for antibiotic resistance prediction. GigaScience, 9(10).