

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

## [eisa](#)

RRID:SCR\_012883

Type: Tool

### Proper Citation

eisa (RRID:SCR\_012883)

### Resource Information

**URL:** <http://www.bioconductor.org/packages/release/bioc/html/eisa.html>

**Proper Citation:** eisa (RRID:SCR\_012883)

**Description:** A biclustering method; it finds correlated blocks (transcription modules) in gene expression (or other tabular) data.

**Abbreviations:** eisa

**Synonyms:** eisa - Expression data analysis via the Iterative Signature Algorithm

**Resource Type:** software resource

**Keywords:** bio.tools

**Availability:** Free

**Resource Name:** eisa

**Resource ID:** SCR\_012883

**Alternate IDs:** OMICS\_01801, biotools:eisa

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

**Record Creation Time:** 20220129T080313+0000

**Record Last Update:** 20260905T132729+0000

### Ratings and Alerts

No rating or validation information has been found for eisa.

No alerts have been found for eisa.

## Data and Source Information

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

## Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Pitoy A, et al. (2024) Isatuximab-dexamethasone-pomalidomide combination effects on serum M protein and PFS in myeloma: Development of a joint model using phase I/II data. CPT: pharmacometrics & systems pharmacology, 13(12), 2087.

Munz N, et al. (2021) Exon-Intron Differential Analysis Reveals the Role of Competing Endogenous RNAs in Post-Transcriptional Regulation of Translation. Non-coding RNA, 7(2).