

# Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

## LEON BIS

RRID:SCR\_021803

Type: Tool

### Proper Citation

LEON BIS (RRID:SCR\_021803)

### Resource Information

**URL:** <http://www.lbgi.fr/~julie/LEON-BIS>

**Proper Citation:** LEON BIS (RRID:SCR\_021803)

**Description:** Software tool for sequence alignments evaluation. Multiple alignment evaluation of sequence neighbours using Bayesian inference system. Used to distinguish sections in multiple sequence alignments that are conserved across whole family or within subfamilies, and should be useful for automatic, high-throughput genome annotations, 2D/3D structure predictions, protein-protein interaction predictions etc.

**Synonyms:** LEON-BIS

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

**Defining Citation:** [PMID:27387560](#)

**Keywords:** sequence alignments evaluation, distinguish sections, multiple sequence alignments, genome annotations, 2D/3D structure predictions, protein-protein interaction predictions

**Availability:** Free, Available for download, Freely available

**Resource Name:** LEON BIS

**Resource ID:** SCR\_021803

**Record Creation Time:** 20220129T080357+0000

**Record Last Update:** 20260815T042839+0000

### Ratings and Alerts

No rating or validation information has been found for LEON BIS.

No alerts have been found for LEON BIS.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Vanni C, et al. (2022) Unifying the known and unknown microbial coding sequence space. eLife, 11.