

Resource Summary Report

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

Bio2BEL

RRID:SCR_017659

Type: Tool

Proper Citation

Bio2BEL (RRID:SCR_017659)

Resource Information

URL: <https://github.com/bio2bel>

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Description: Software Python package enabling Biological Expression Language to act as semantic integration layer for multi modal and multi scale data sets in life sciences. Used for integrating biological databases and structured data sources in BEL. Has ability to support curation of pathway mappings, integration of pathway databases, and machine learning applications.

Resource Type: software resource, software toolkit

Defining Citation: [DOI:10.1101/631812](https://doi.org/10.1101/631812)

Keywords: Biological, expression, language, integration, layer, dataset, biological, database

Availability: Free, Available for download, Freely available

Resource Name: Bio2BEL

Resource ID: SCR_017659

Alternate IDs: biotools:bio2bEL, BioTools:Bio2BEL

Alternate URLs: <https://github.com/bio2bel/bio2bel>, <https://bio.tools/Bio2BEL>, <https://bio.tools/Bio2BEL>

License: MIT

Record Creation Time: 20220129T080336+0000

Record Last Update: 20260905T133303+0000

Ratings and Alerts

No rating or validation information has been found for Bio2BEL.

No alerts have been found for Bio2BEL.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Callahan TJ, et al. (2024) An open source knowledge graph ecosystem for the life sciences. *Scientific data*, 11(1), 363.

Humayun F, et al. (2020) A Computational Approach for Mapping Heme Biology in the Context of Hemolytic Disorders. *Frontiers in bioengineering and biotechnology*, 8, 74.

Domingo-Fernández D, et al. (2019) PathMe: merging and exploring mechanistic pathway knowledge. *BMC bioinformatics*, 20(1), 243.

Mubeen S, et al. (2019) The Impact of Pathway Database Choice on Statistical Enrichment Analysis and Predictive Modeling. *Frontiers in genetics*, 10, 1203.

Domingo-Fernández D, et al. (2019) ComPath: an ecosystem for exploring, analyzing, and curating mappings across pathway databases. *NPJ systems biology and applications*, 5, 3.

Ali M, et al. (2019) BioKEEN: a library for learning and evaluating biological knowledge graph embeddings. *Bioinformatics (Oxford, England)*, 35(18), 3538.

Hoyt CT, et al. (2018) BEL Commons: an environment for exploration and analysis of networks encoded in Biological Expression Language. *Database : the journal of biological databases and curation*, 2018.