

Resource Summary Report

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

rBiopaxParser

RRID:SCR_002744

Type: Tool

Proper Citation

rBiopaxParser (RRID:SCR_002744)

Resource Information

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

Proper Citation: rBiopaxParser (RRID:SCR_002744)

Description: A software package that provides a comprehensive set of functions for parsing, viewing and modifying BioPAX pathway data within R. At the moment BioPAX level 2 and level 3 are supported.

Synonyms: rBiopaxParser - Parses BioPax files and represents them in R

Resource Type: software resource

Defining Citation: [PMID:23274212](#)

Keywords: software package, mac os x, unix/linux, windows, data representation, bio.tools

Availability: Free, Freely available, Available for download

Resource Name: rBiopaxParser

Resource ID: SCR_002744

Alternate IDs: biotools:rbiopaxparser, OMICS_05211

Alternate URLs: <https://github.com/frankkramer/rBiopaxParser>,
<https://bio.tools/rbiopaxparser>

License: GNU General Public License, v2 or greater

Record Creation Time: 20220129T080215+0000

Record Last Update: 20260905T132453+0000

Ratings and Alerts

No rating or validation information has been found for rBiopaxParser.

No alerts have been found for rBiopaxParser.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Hammoud Z, et al. (2020) Multipath: An R Package to Generate Integrated Reproducible Pathway Models. *Biology*, 9(12).

Benis N, et al. (2019) High-level integration of murine intestinal transcriptomics data highlights the importance of the complement system in mucosal homeostasis. *BMC genomics*, 20(1), 1028.

Benis N, et al. (2016) Building pathway graphs from BioPAX data in R. *F1000Research*, 5, 2414.

Wachter A, et al. (2015) Decoding Cellular Dynamics in Epidermal Growth Factor Signaling Using a New Pathway-Based Integration Approach for Proteomics and Transcriptomics Data. *Frontiers in genetics*, 6, 351.