Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 15, 2025

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

Funding:

Availability: GNU General Public License, v2 or greater

Resource Name: rBiopaxParser

Resource ID: SCR_002744

Alternate IDs: biotools:rbiopaxparser, OMICS_05211

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

Record Creation Time: 20220129T080215+0000

Record Last Update: 20250410T064922+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 FDI Lab - SciCrunch.org.

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.