

Resource Summary Report

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BioC Java Library

RRID:SCR_014777

Type: Tool

Proper Citation

BioC Java Library (RRID:SCR_014777)

Resource Information

URL: <http://bioc.sourceforge.net>

Proper Citation: BioC Java Library (RRID:SCR_014777)

Description: An interchange format to represent, store and exchange data and annotations in a standardized manner.

Resource Type: source code, software resource

Keywords: interoperability, source code, interchange format, represent data, store data, exchange data, annotations

Availability: Available for download

Resource Name: BioC Java Library

Resource ID: SCR_014777

Record Creation Time: 20220129T080322+0000

Record Last Update: 20260729T044332+0000

Ratings and Alerts

No rating or validation information has been found for BioC Java Library.

No alerts have been found for BioC Java Library.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 27 mentions in open access literature.

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

Vollmar M, et al. (2024) Dataset from a human-in-the-loop approach to identify functionally important protein residues from literature. *Scientific data*, 11(1), 1032.

Caronni N, et al. (2021) TIM4 expression by dendritic cells mediates uptake of tumor-associated antigens and anti-tumor responses. *Nature communications*, 12(1), 2237.

Consonni M, et al. (2021) Human T cells engineered with a leukemia lipid-specific TCR enables donor-unrestricted recognition of CD1c-expressing leukemia. *Nature communications*, 12(1), 4844.

Teschendorff AE, et al. (2020) EPISCORE: cell type deconvolution of bulk tissue DNA methylomes from single-cell RNA-Seq data. *Genome biology*, 21(1), 221.

Bertolio R, et al. (2019) Sterol regulatory element binding protein 1 couples mechanical cues and lipid metabolism. *Nature communications*, 10(1), 1326.

Chen W, et al. (2019) Single-cell landscape in mammary epithelium reveals bipotent-like cells associated with breast cancer risk and outcome. *Communications biology*, 2, 306.

Barravecchia I, et al. (2019) MICAL2 is expressed in cancer associated neo-angiogenic capillary endothelia and it is required for endothelial cell viability, motility and VEGF response. *Biochimica et biophysica acta. Molecular basis of disease*, 1865(9), 2111.

Mavrikaki M, et al. (2019) Sex-Dependent Changes in miRNA Expression in the Bed Nucleus of the Stria Terminalis Following Stress. *Frontiers in molecular neuroscience*, 12, 236.

Arroyo J, et al. (2018) Incorporation of Carbon Nanofillers Tunes Mechanical and Electrical Percolation in PHBV:PLA Blends. *Polymers*, 10(12).

Fiore A, et al. (2018) Induction of immunosuppressive functions and NF- κ B by FLIP in monocytes. *Nature communications*, 9(1), 5193.

Bergmaier P, et al. (2018) Choice of binding sites for CTCFL compared to CTCF is driven by chromatin and by sequence preference. *Nucleic acids research*, 46(14), 7097.

Kwon D, et al. (2018) ezTag: tagging biomedical concepts via interactive learning. *Nucleic acids research*, 46(W1), W523.

Murugesan G, et al. (2017) BCC-NER: bidirectional, contextual clues named entity tagger for gene/protein mention recognition. *EURASIP journal on bioinformatics & systems biology*, 2017(1), 7.

Aydin F, et al. (2017) Automatic query generation using word embeddings for retrieving passages describing experimental methods. *Database : the journal of biological databases and curation*, 2017.

Venkatesan A, et al. (2016) SciLite: a platform for displaying text-mined annotations as a means to link research articles with biological data. Wellcome open research, 1, 25.

Przybył P, et al. (2016) Text mining resources for the life sciences. Database : the journal of biological databases and curation, 2016.

Calabria E, et al. (2016) Aging: a portrait from gene expression profile in blood cells. Aging, 8(8), 1802.

D'haene E, et al. (2016) Identification of long non-coding RNAs involved in neuronal development and intellectual disability. Scientific reports, 6, 28396.

Fu X, et al. (2015) Supporting the annotation of chronic obstructive pulmonary disease (COPD) phenotypes with text mining workflows. Journal of biomedical semantics, 6, 8.

Aibar S, et al. (2015) Analyse multiple disease subtypes and build associated gene networks using genome-wide expression profiles. BMC genomics, 16 Suppl 5(Suppl 5), S3.