

Resource Summary Report

Generated by [RRID](#) on Apr 8, 2025

Binder

RRID:SCR_016437

Type: Tool

Proper Citation

Binder (RRID:SCR_016437)

Resource Information

URL: <https://mybinder.org/>

Proper Citation: Binder (RRID:SCR_016437)

Description: Open-source web application for managing digital repositories. Allows to create custom computing environments that can be shared and used by many remote users. Turns a GitHub repository containing a collection of Jupyter Notebooks into a collection of interactive notebooks. With Binder, open those notebooks in an executable environment, making your code immediately reproducible by anyone, anywhere.

Resource Type: web application, storage service resource, data repository, service resource, software resource

Keywords: managing, digital, repository, Jupyter Notebook, interactive notebook, code, reproducible

Funding:

Availability: Open source, Freely available

Resource Name: Binder

Resource ID: SCR_016437

License: Public

Record Creation Time: 20220129T080330+0000

Record Last Update: 20250407T220334+0000

Ratings and Alerts

No rating or validation information has been found for Binder.

No alerts have been found for Binder.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 37 mentions in open access literature.

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

Sinha A, et al. (2025) The NeuroML ecosystem for standardized multi-scale modeling in neuroscience. *eLife*, 13.

Bayarri G, et al. (2024) Using interactive Jupyter Notebooks and BioConda for FAIR and reproducible biomolecular simulation workflows. *PLoS computational biology*, 20(6), e1012173.

Sipakov R, et al. (2024) Leveraging Quadratic Polynomials in Python for Advanced Data Analysis. *F1000Research*, 13, 490.

Padilla DK, et al. (2024) Preparing the Next Generation of Integrative Organismal Biologists. *Integrative and comparative biology*, 64(3), 1007.

Beránek J, et al. (2024) Analysis of metadynamics simulations by metadynminer.py. *Bioinformatics (Oxford, England)*, 40(10).

Moore J, et al. (2023) OME-Zarr: a cloud-optimized bioimaging file format with international community support. *bioRxiv : the preprint server for biology*.

Fabbris G, et al. (2023) Resonant inelastic x-ray scattering data for Ruddlesden-Popper and reduced Ruddlesden-Popper nickelates. *Scientific data*, 10(1), 174.

Rocca-Serra P, et al. (2023) The FAIR Cookbook - the essential resource for and by FAIR doers. *Scientific data*, 10(1), 292.

Moore J, et al. (2023) OME-Zarr: a cloud-optimized bioimaging file format with international community support. *Histochemistry and cell biology*, 160(3), 223.

Khanal P, et al. (2023) Gas7 Is a Novel Dendritic Spine Initiation Factor. *eNeuro*, 10(4).

de Vries SEJ, et al. (2023) Sharing neurophysiology data from the Allen Brain Observatory.

eLife, 12.

Stall S, et al. (2023) Journal Production Guidance for Software and Data Citations. *Scientific data*, 10(1), 656.

DuPre E, et al. (2022) Beyond advertising: New infrastructures for publishing integrated research objects. *PLoS computational biology*, 18(1), e1009651.

Bayarri G, et al. (2022) BioExcel Building Blocks Workflows (BioBB-Wfs), an integrated web-based platform for biomolecular simulations. *Nucleic acids research*, 50(W1), W99.

Gomes DGE, et al. (2022) Why don't we share data and code? Perceived barriers and benefits to public archiving practices. *Proceedings. Biological sciences*, 289(1987), 20221113.

Kolpakov F, et al. (2022) BioUML-towards a universal research platform. *Nucleic acids research*, 50(W1), W124.

Juavinett AL, et al. (2022) The next generation of neuroscientists needs to learn how to code, and we need new ways to teach them. *Neuron*, 110(4), 576.

Schniete JK, et al. (2021) ActDES - a curated Actinobacterial Database for Evolutionary Studies. *Microbial genomics*, 7(1).

Vuorre M, et al. (2021) Sharing and organizing research products as R packages. *Behavior research methods*, 53(2), 792.

Boudreau M, et al. (2021) On the open-source landscape of PLOS Computational Biology. *PLoS computational biology*, 17(2), e1008725.