

# Resource Summary Report

Generated by [NIF](#) on Sep 19, 2026

## ObservableHQ

RRID:SCR\_016173

Type: Tool

### Proper Citation

ObservableHQ (RRID:SCR\_016173)

### Resource Information

**URL:** <https://beta.observablehq.com/>

**Proper Citation:** ObservableHQ (RRID:SCR\_016173)

**Description:** Web application for a code and text writing environment. It uses javascript and can be used to produce executable papers.

**Resource Type:** application programming interface, data access protocol, software resource, web application

**Keywords:** code, text, environment, writing, paper, research, journal, execute, programming, javascript

**Availability:** Open source, Freely available, Account required, Account required for full access

**Resource Name:** ObservableHQ

**Resource ID:** SCR\_016173

**License URLs:** <https://beta.observablehq.com/terms-of-service>

**Record Creation Time:** 20220129T080329+0000

**Record Last Update:** 20260912T195836+0000

### Ratings and Alerts

No rating or validation information has been found for ObservableHQ.

No alerts have been found for ObservableHQ.

### Data and Source Information

## Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Woitowich NC, et al. (2024) Analysis of NIH K99/R00 awards and the career progression of awardees. eLife, 12.

Woitowich NC, et al. (2023) Analysis of NIH K99/R00 Awards and the Career Progression of Awardees. bioRxiv : the preprint server for biology.

Martin DP, et al. (2022) Selection analysis identifies unusual clustered mutational changes in Omicron lineage BA.1 that likely impact Spike function. bioRxiv : the preprint server for biology.

Martin DP, et al. (2022) Selection Analysis Identifies Clusters of Unusual Mutational Changes in Omicron Lineage BA.1 That Likely Impact Spike Function. Molecular biology and evolution, 39(4).

Martin DP, et al. (2021) The emergence and ongoing convergent evolution of the N501Y lineages coincides with a major global shift in the SARS-CoV-2 selective landscape. medRxiv : the preprint server for health sciences.

Ortega DR, et al. (2020) Repurposing a chemosensory macromolecular machine. Nature communications, 11(1), 2041.

Torre D, et al. (2018) BioJupies: Automated Generation of Interactive Notebooks for RNA-Seq Data Analysis in the Cloud. Cell systems, 7(5), 556.