# **Resource Summary Report**

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# **Cirrocumulus**

RRID:SCR\_021646 Type: Tool

### **Proper Citation**

Cirrocumulus (RRID:SCR\_021646)

### **Resource Information**

URL: https://cirrocumulus.readthedocs.io/en/stable/

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**Description:** Web interactive visualization tool for large scale single cell genomics data.Interactive web application for exploring million scale single cell datasets. Can be hosted on Google App Engine application for collaborative use or can be run in standalone mode on personal computer. Consists of client side component implemented in JavaScript and server component implemented in Python. Client uses React to manage state and WebGL to visualize variables on 2D/3D embeddings in performant manner. Server component consists of functions to manage datasets, slice variables from dataset stored in PARQUET, Zarr or H5AD formats.

Resource Type: web application, software resource

**Keywords:** large scale single cell genomics data, exploring million scale single cell datasets, visualize variables, manage datasets

#### Funding:

Availability: Free, Available for download, Freely available

Resource Name: Cirrocumulus

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Alternate URLs: https://github.com/klarman-cellobservatory/cirrocumulus/blob/413898061f1c48350071d200f043cc43104dd04f/docs/index.rst Record Creation Time: 20220129T080356+0000

Record Last Update: 20250407T220623+0000

## **Ratings and Alerts**

No rating or validation information has been found for Cirrocumulus.

No alerts have been found for Cirrocumulus.

### Data and Source Information

Source: <u>SciCrunch Registry</u>

## **Usage and Citation Metrics**

We have not found any literature mentions for this resource.