

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 18, 2026

Nebula

RRID:SCR_001516

Type: Tool

Proper Citation

Nebula (RRID:SCR_001516)

Resource Information

URL: <http://nebula.curie.fr/>

Proper Citation: Nebula (RRID:SCR_001516)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 23,2022. Web portal that allows users to analyze ChIP-seq data., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: Nebula - A web-server for advanced ChIP-seq data analysis

Resource Type: data access protocol, data analysis software, data processing software, sequence analysis software, software application, software resource, web service

Defining Citation: [PMID:22829625](#)

Keywords: web portal, chip-seq data, online analysis tool

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Nebula

Resource ID: SCR_001516

Alternate IDs: OMICS_00424

Record Creation Time: 20220129T080208+0000

Record Last Update: 20260912T195526+0000

Ratings and Alerts

No rating or validation information has been found for Nebula.

No alerts have been found for Nebula.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

Wu Y, et al. (2025) Association of ten VEGF family genes with Alzheimer's disease endophenotypes at single cell resolution. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 21(2), e14419.

Fries LE, et al. (2025) Single-Cell RNA-Seq Reveals Adventitial Fibroblast Alterations during Mouse Atherosclerosis. *bioRxiv : the preprint server for biology*.

Chin WL, et al. (2025) Coupling of response biomarkers between tumor and peripheral blood in patients undergoing chemoimmunotherapy. *Cell reports. Medicine*, 6(1), 101882.

Read DF, et al. (2024) Single-cell analysis of chromatin and expression reveals age- and sex-associated alterations in the human heart. *Communications biology*, 7(1), 1052.

Lee H, et al. (2024) Pseudobulk with proper offsets has the same statistical properties as generalized linear mixed models in single-cell case-control studies. *Bioinformatics (Oxford, England)*, 40(8).

Dilly J, et al. (2024) Mechanisms of Resistance to Oncogenic KRAS Inhibition in Pancreatic Cancer. *Cancer discovery*, 14(11), 2135.

Gan S, et al. (2024) Dynamic changes of the immune microenvironment in the development of gastric cancer caused by inflammation. *Molecular therapy. Oncology*, 32(3), 200849.

Nechanitzky R, et al. (2024) CaSSiDI: novel single-cell "Cluster Similarity Scoring and Distinction Index" reveals critical functions for PirB and context-dependent Cebpb repression. *Cell death and differentiation*, 31(3), 265.

Mathys H, et al. (2024) Single-cell multiregion dissection of Alzheimer's disease. *Nature*, 632(8026), 858.

Teo AYY, et al. (2024) Best practices for differential accessibility analysis in single-cell epigenomics. *Nature communications*, 15(1), 8805.

Gerayeli FV, et al. (2024) Single-cell sequencing reveals cellular landscape alterations in the airway mucosa of patients with pulmonary long COVID. *The European respiratory journal*, 64(5).

Ostrem BEL, et al. (2024) Fetal brain response to maternal inflammation requires microglia. *Development (Cambridge, England)*, 151(10).

Reis-de-Oliveira G, et al. (2024) OmicScope unravels systems-level insights from quantitative proteomics data. *Nature communications*, 15(1), 6510.

Simmons SK, et al. (2023) Mostly natural sequencing-by-synthesis for scRNA-seq using Ultima sequencing. *Nature biotechnology*, 41(2), 204.

Boocock J, et al. (2023) Single-cell eQTL mapping in yeast reveals a tradeoff between growth and reproduction. *bioRxiv : the preprint server for biology*.

Ramsden H, et al. (2023) Nanoscale Cathodoluminescence and Conductive Mode Scanning Electron Microscopy of van der Waals Heterostructures. *ACS nano*, 17(12), 11882.

Gandal MJ, et al. (2022) Broad transcriptomic dysregulation occurs across the cerebral cortex in ASD. *Nature*, 611(7936), 532.

Straeten F, et al. (2022) Integrated single-cell transcriptomics of cerebrospinal fluid cells in treatment-naïve multiple sclerosis. *Journal of neuroinflammation*, 19(1), 306.

Khorsand P, et al. (2021) Nebula: ultra-efficient mapping-free structural variant genotyper. *Nucleic acids research*, 49(8), e47.

He L, et al. (2021) NEBULA is a fast negative binomial mixed model for differential or co-expression analysis of large-scale multi-subject single-cell data. *Communications biology*, 4(1), 629.