Resource Summary Report

Generated by RRID on Apr 28, 2025

GENIE3

RRID:SCR_000217
Type: Tool

Proper Citation

GENIE3 (RRID:SCR_000217)

Resource Information

URL: http://www.montefiore.ulg.ac.be/~huynh-thu/software.html

Proper Citation: GENIE3 (RRID:SCR_000217)

Description: An algorithm for the inference of gene regulatory networks from expression data.

Abbreviations: GENIE3

Resource Type: software resource

Defining Citation: PMID:20927193

Keywords: javascript, bio.tools

Funding:

Resource Name: GENIE3

Resource ID: SCR_000217

Alternate IDs: biotools:genie3, OMICS_01683

Alternate URLs: https://bio.tools/genie3

Record Creation Time: 20220129T080200+0000

Record Last Update: 20250420T013934+0000

Ratings and Alerts

No rating or validation information has been found for GENIE3.

No alerts have been found for GENIE3.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Wang W, et al. (2024) Identification of hypoxic macrophages in glioblastoma with therapeutic potential for vasculature normalization. Cancer cell, 42(5), 815.

Tasis A, et al. (2024) Single-Cell Analysis of Bone Marrow CD8+ T Cells in Myeloid Neoplasms Reveals Pathways Associated with Disease Progression and Response to Treatment with Azacitidine. Cancer research communications, 4(12), 3067.

Li CY, et al. (2022) The sage genome provides insight into the evolutionary dynamics of diterpene biosynthesis gene cluster in plants. Cell reports, 40(7), 111236.

Cebrian-Silla A, et al. (2021) Single-cell analysis of the ventricular-subventricular zone reveals signatures of dorsal and ventral adult neurogenesis. eLife, 10.

Dibaeinia P, et al. (2020) SERGIO: A Single-Cell Expression Simulator Guided by Gene Regulatory Networks. Cell systems, 11(3), 252.

Kang Y, et al. (2018) NetProphet 2.0: mapping transcription factor networks by exploiting scalable data resources. Bioinformatics (Oxford, England), 34(2), 249.

Desai JS, et al. (2017) Improving Gene Regulatory Network Inference by Incorporating Rates of Transcriptional Changes. Scientific reports, 7(1), 17244.

Hu Y, et al. (2016) A machine learning approach for the identification of key markers involved in brain development from single-cell transcriptomic data. BMC genomics, 17(Suppl 13), 1025.

Huynh-Thu VA, et al. (2010) Inferring regulatory networks from expression data using tree-based methods. PloS one, 5(9).