

Resource Summary Report

Generated by [NIF](#) on Sep 16, 2026

[hypeR](#)

RRID:SCR_027229

Type: Tool

Proper Citation

hypeR (RRID:SCR_027229)

Resource Information

URL: <https://montilab.github.io/hypeR-docs/>

Proper Citation: hypeR (RRID:SCR_027229)

Description: Software R package that supports different types of gene set enrichment workflows. Offers multiple enrichment, visualization, and sharing methods in addition to novel features such as hierarchical geneset analysis and built-in markdown reporting.

Resource Type: software resource, software toolkit, source code

Defining Citation: [PMID:31498385](#)

Keywords: gene set enrichment workflows, hierarchical geneset analysis, built-in markdown reporting,

Funding: NIA 2U19AG023122;
William M. Wood Foundation

Availability: Free, Available for download, Freely available

Resource Name: hypeR

Resource ID: SCR_027229

License: GNU GPLv3

Record Creation Time: 20250723T062011+0000

Record Last Update: 20260912T200522+0000

Ratings and Alerts

No rating or validation information has been found for hypeR.

No alerts have been found for hypeR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Suresh V, et al. (2026) Modelling EWS::FLI1 protein fluctuations reveal determinants of tumor plasticity in Ewing sarcoma. EMBO molecular medicine, 18(2), 646.

Marstrand-Jørgensen AB, et al. (2025) Temporal glomerular gene expression dynamics during disease progression in a mouse model of hypertension-accelerated diabetic kidney disease. Animal models and experimental medicine, 8(12), 2115.

Dado T, et al. (2022) Hyperrealistic neural decoding for reconstructing faces from fMRI activations via the GAN latent space. Scientific reports, 12(1), 141.