

Resource Summary Report

Generated by [NIF](#) on Sep 10, 2026

drug perturbation Gene Set Enrichment Analysis

RRID:SCR_025351

Type: Tool

Proper Citation

drug perturbation Gene Set Enrichment Analysis (RRID:SCR_025351)

Resource Information

URL: https://github.com/sxf296/drug_targeting

Proper Citation: drug perturbation Gene Set Enrichment Analysis (RRID:SCR_025351)

Description: Software tool to detect phenotypically relevant drug targets through unique transcriptomic enrichment that emphasizes biological directionality of drug-derived gene sets. Exploratory tool to screen for possible drug targeting molecules.

Abbreviations: dpGSEA

Resource Type: software resource, source code

Defining Citation: [DOI:10.1186/s12859-020-03929-0](https://doi.org/10.1186/s12859-020-03929-0)

Keywords: detect phenotypically relevant drug targets, drug-derived gene sets, transcriptomic enrichment,

Funding: NHLBI T32HL007567;
NIAID P30AI036219

Availability: Free, Available for download, Freely available

Resource Name: drug perturbation Gene Set Enrichment Analysis

Resource ID: SCR_025351

Record Creation Time: 20240521T053244+0000

Record Last Update: 20260905T133456+0000

Ratings and Alerts

No rating or validation information has been found for drug perturbation Gene Set Enrichment Analysis.

No alerts have been found for drug perturbation Gene Set Enrichment Analysis.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Ismail J, et al. (2026) Single-cell transcriptomics reveal altered B cell responses and T cell senescence in geriatric non-responders to COVID-19 mRNA vaccination. iScience, 29(5), 115730.

Kachroo P, et al. (2025) DNA-methylation markers associated with lung function at birth and childhood reveal early life programming of inflammatory pathways. bioRxiv : the preprint server for biology.