Resource Summary Report

Generated by dkNET on May 19, 2025

tRanslatome

RRID:SCR_012810
Type: Tool

Proper Citation

tRanslatome (RRID:SCR_012810)

Resource Information

URL: http://www.bioconductor.org/packages/release/bioc/html/tRanslatome.html

Proper Citation: tRanslatome (RRID:SCR_012810)

Description: Detection of differentially expressed genes (DEGs) from the comparison of two biological conditions among different levels of gene expression, using several statistical methods: Rank Product, t-test, SAM, Limma, ANOTA, DESeq, edgeR.

Abbreviations: tRanslatome

Synonyms: tRanslatome - Comparison between multiple levels of gene expression

Resource Type: software resource

Defining Citation: PMID:24222209

Funding:

Availability: Free

Resource Name: tRanslatome

Resource ID: SCR_012810

Alternate IDs: OMICS_01316

Record Creation Time: 20220129T080312+0000

Record Last Update: 20250420T014620+0000

Ratings and Alerts

No rating or validation information has been found for tRanslatome.

No alerts have been found for tRanslatome.

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 dkNET.

Etna MP, et al. (2021) Genome-Wide Gene Expression Analysis of Mtb-Infected DC Highlights the Rapamycin-Driven Modulation of Regulatory Cytokines via the mTOR/GSK-3? Axis. Frontiers in immunology, 12, 649475.

Brina D, et al. (2015) eIF6 coordinates insulin sensitivity and lipid metabolism by coupling translation to transcription. Nature communications, 6, 8261.