

Resource Summary Report

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DOSE

RRID:SCR_027408

Type: Tool

Proper Citation

DOSE (RRID:SCR_027408)

Resource Information

URL: <https://bioconductor.org/packages/release/bioc/html/DOSE.html>

Proper Citation: DOSE (RRID:SCR_027408)

Description: Software R package for disease ontology semantic and enrichment analysis.

Abbreviations: DOSE

Synonyms: Disease Ontology Semantic and Enrichment, Disease Ontology Semantic and Enrichment (DOSE)

Resource Type: software resource, software toolkit

Defining Citation: [PMID:25677125](#)

Keywords: disease ontology, semantic and enrichment analysis,

Funding: National Natural Science Foundation of China

Availability: Free, Available for download, Freely available

Resource Name: DOSE

Resource ID: SCR_027408

License: Artistic-2.0

Record Creation Time: 20250910T060301+0000

Record Last Update: 20260829T183506+0000

Ratings and Alerts

No rating or validation information has been found for DOSE.

No alerts have been found for DOSE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Rossini R, et al. (2026) Loss of multilevel 3D genome organization during breast cancer progression. *Genome research*, 36(1), 20.

Wasserer S, et al. (2024) Characterization of High and Low IFNG-Expressing Subgroups in Atopic Dermatitis. *International journal of molecular sciences*, 25(11).

Fang K, et al. (2024) Exploring the microRNA-mRNA regulatory network associated with solasonine in bladder cancer. *Translational andrology and urology*, 13(5), 812.

Polakkattil BK, et al. (2024) Methylome-wide and meQTL analysis helps to distinguish treatment response from non-response and pathogenesis markers in schizophrenia. *Frontiers in psychiatry*, 15, 1297760.

Lisowski P, et al. (2024) Mutant huntingtin impairs neurodevelopment in human brain organoids through CHCHD2-mediated neurometabolic failure. *Nature communications*, 15(1), 7027.

Tomasova K, et al. (2024) Telomere length as a predictor of therapy response and survival in patients diagnosed with ovarian carcinoma. *Heliyon*, 10(13), e33525.

Rossini R, et al. (2023) Multi-level 3D genome organization deteriorates during breast cancer progression. *bioRxiv : the preprint server for biology*.

Su Q, et al. (2022) Prioritizing potential circRNA biomarkers for bladder cancer and bladder urothelial cancer based on an ensemble model. *Frontiers in genetics*, 13, 1001608.

Want MY, et al. (2021) Inhibition of WHSC1 Allows for Reprogramming of the Immune Compartment in Prostate Cancer. *International journal of molecular sciences*, 22(16).

Nojima Y, et al. (2020) Metabolomic analysis of fibrotic mice combined with public RNA-Seq human lung data reveal potential diagnostic biomarker candidates for lung fibrosis. *FEBS open bio*, 10(11), 2427.

Swindell WR, et al. (2018) GM604 regulates developmental neurogenesis pathways and the expression of genes associated with amyotrophic lateral sclerosis. *Translational neurodegeneration*, 7, 30.

Marnetto D, et al. (2014) Genome-wide identification and characterization of fixed human-specific regulatory regions. *American journal of human genetics*, 95(1), 39.