

Resource Summary Report

Generated by SPARC SAWG on Aug 11, 2026

DoRothEA

RRID:SCR_027126

Type: Tool

Proper Citation

DoRothEA (RRID:SCR_027126)

Resource Information

URL: <https://bioconductor.org/packages/release/data/experiment/html/dorothea.html>

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Description: Software R package for storing the regulons. Gene regulatory network containing signed transcription factor (TF) - target gene interactions. DoRothEA regulons, the collection of TF and its transcriptional targets, were curated and collected from different types of evidence for both human and mouse. Confidence level was assigned to each TF-target interaction based on number of supporting evidence.

Resource Type: software toolkit, software resource

Keywords: Gene regulatory network, storing regulons, signed transcription factor, transcription factors collection, transcriptional targets collection, human, mouse

Availability: Free, Available for download, Freely available

Resource Name: DoRothEA

Resource ID: SCR_027126

Alternate URLs: <https://github.com/saezlab/dorothea/>

License: GNU GPL v3

Record Creation Time: 20250702T060923+0000

Record Last Update: 20260810T040923+0000

Ratings and Alerts

No rating or validation information has been found for DoRothEA.

No alerts have been found for DoRothEA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 32 mentions in open access literature.

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

Lawal B, et al. (2026) IMIREG: a lineage-resolved regulon signature unveiling immune engagement archetypes and predicting immunotherapy response across diverse cancers. NPJ precision oncology, 10(1).

Tickman BI, et al. (2026) The response to kidney injury is epigenetically regulated through the activation of bivalent genes. American journal of physiology. Renal physiology, 330(2), F238.

Wang Y, et al. (2025) Genetic and Multi-Omics Insights Into Monocyte Pantothenate-Mediated Protection in Acute Respiratory Distress Syndrome. Journal of cellular and molecular medicine, 29(19), e70812.

Grillo-Risco R, et al. (2025) A comprehensive transcriptional reference for severity and progression in spinal cord injury reveals novel translational biomarker genes. Journal of translational medicine, 23(1), 160.

Fan G, et al. (2025) The co-location of MARCO+ tumor-associated macrophages and CTSE+ tumor cells determined the poor prognosis in intrahepatic cholangiocarcinoma. Hepatology (Baltimore, Md.), 82(1), 25.

Dai L, et al. (2025) Spatial transcriptomics reveals prognostically LYZ+ fibroblasts and colocalization with FN1+ macrophages in diffuse large B-cell lymphoma. Cancer immunology, immunotherapy : CII, 74(4), 123.

Chen HX, et al. (2025) Huangqi decoction ameliorated intestinal barrier dysfunction via regulating NF- κ B signaling pathway in slow transit constipation model mice. World journal of gastrointestinal surgery, 17(5), 106000.

Hu Y, et al. (2025) Accurate Transcription Factor Activity Inference to Decipher Cell Identity from Single-Cell Transcriptomic Data with MetaTF. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(23), e10745.

Huang J, et al. (2025) FAHD1-mediated pyruvate metabolism in hepatocellular carcinoma: Multi-omics and causal genetic evidence. HGG advances, 6(4), 100494.

Eskandarian Boroujeni M, et al. (2025) Integrative multi-omics analysis of IFN γ -induced macrophages and atherosclerotic plaques reveals macrophage-dependent STAT1-driven transcription in atherosclerosis. Frontiers in immunology, 16, 1590953.

Horn S, et al. (2025) IL-1 protects from fatal systemic candidiasis in mice by inhibiting oxidative phosphorylation and hypoxia. Nature communications, 16(1), 2626.

Woods PS, et al. (2025) HIF-1 regulates mitochondrial function in bone marrow-derived macrophages but not in tissue-resident alveolar macrophages. *Scientific reports*, 15(1), 11574.

Cetin-Atalay R, et al. (2025) Sustained hypoxia but not intermittent hypoxia induces HIF-1 ? transcriptional response in human aortic endothelial cells. *Molecular omics*, 21(1), 19.

Fan C, et al. (2025) PIEZO1 gain-of-function mutation drives cardiomyopathy by disrupting myocardial lipid homeostasis besides iron overload. *Science advances*, 11(46), eady9242.

Chang H, et al. (2025) Single-cell transcriptomics reveals immune remodeling of the murine lung microenvironment following chronic house dust mite exposure. *Frontiers in immunology*, 16, 1652539.

Brummel K, et al. (2025) Spatiotemporal Immune Landscape and Long-term Immune Memory in POLE-Mutant Endometrial Cancer at the Single-Cell Level. *Cancer immunology research*, 13(12), 1911.

Shin KWD, et al. (2024) ATF4 and mTOR regulate metabolic reprogramming in TGF-?-treated lung fibroblasts. *bioRxiv : the preprint server for biology*.

Croizer H, et al. (2024) Deciphering the spatial landscape and plasticity of immunosuppressive fibroblasts in breast cancer. *Nature communications*, 15(1), 2806.

Yashar WM, et al. (2024) Predicting transcription factor activity using prior biological information. *iScience*, 27(3), 109124.

Li H, et al. (2024) Immunometabolic alterations in type 2 diabetes mellitus revealed by single-cell RNA sequencing: insights into subtypes and therapeutic targets. *Frontiers in immunology*, 15, 1537909.