

Resource Summary Report

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ARACNE

RRID:SCR_002180

Type: Tool

Proper Citation

ARACNE (RRID:SCR_002180)

Resource Information

URL: <http://wiki.c2b2.columbia.edu/califanolab/index.php/Software/ARACNE>

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Description: An algorithm, using microarray expression profiles, to scale up to the complexity of regulatory networks in mammalian cells, yet general enough to address a wider range of network deconvolution problems. This method uses an information theoretic approach to eliminate the vast majority of indirect interactions typically inferred by pairwise analysis.

Abbreviations: ARACNE

Synonyms: Algorithm for the Reconstruction of Accurate Cellular Networks

Resource Type: software resource, software application

Defining Citation: [PMID:16723010](#)

Keywords: cellular network, cellular, network, microarray, expression profile, deconvolution, regulatory network

Availability: Free, Freely available

Resource Name: ARACNE

Resource ID: SCR_002180

Alternate IDs: OMICS_01851

Record Creation Time: 20220129T080212+0000

Record Last Update: 20260801T191044+0000

Ratings and Alerts

No rating or validation information has been found for ARACNE.

No alerts have been found for ARACNE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 157 mentions in open access literature.

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

Li JJ, et al. (2026) NSD2 targeting reverses plasticity and drug resistance in prostate cancer. *Nature*, 649(8095), 216.

Yu Q, et al. (2025) Causal genes identification of giant cell arteritis in CD4+ Memory t cells: an integration of multi-omics and expression quantitative trait locus analysis. *Inflammation research : official journal of the European Histamine Research Society ... [et al.]*, 74(1), 3.

Moakley DF, et al. (2025) Reverse engineering neuron-type-specific and type-orthogonal splicing-regulatory networks using diverse cellular transcriptomes. *Cell reports*, 44(7), 115898.

Khayer N, et al. (2025) A dynamic co-expression approach reveals Gins2 as a potential upstream modulator of HNSCC metastasis. *Scientific reports*, 15(1), 3322.

Wang J, et al. (2025) A multi-omic approach implicates novel protein dysregulation in post-traumatic stress disorder. *Genome medicine*, 17(1), 43.

Jeong S, et al. (2025) Aggressive serous ovarian cancer subtype defined by high centrality lncRNA profiles and master transcription factors. *Scientific reports*, 15(1), 20631.

Ripperger TJ, et al. (2025) Early, adjuvant-responsive epigenetic programs in B cells imprint subsequent plasma cell survival and the duration of humoral immunity. *bioRxiv : the preprint server for biology*.

Yin J, et al. (2025) Cross-cohort integrative multi-omics analysis of cancer essential gene ATP6V0B to dissect functional characteristics and clinical implications in breast cancer. *World journal of surgical oncology*, 24(1), 8.

López-Sánchez P, et al. (2025) Patient-specific gene co-expression networks reveal novel subtypes and predictive biomarkers in lung adenocarcinoma. *NPJ systems biology and applications*, 11(1), 44.

Qian F, et al. (2025) Network analysis of master regulators associated with invasive phenotypes in multiple myeloma. *Frontiers in cell and developmental biology*, 13, 1586870.

Pavel A, et al. (2025) Comparing gene-gene co-expression network approaches for the analysis of cell differentiation and specification on scRNAseq data. Computational and structural biotechnology journal, 27, 2747.

Li BI, et al. (2025) The regulatory architecture of the primed pluripotent cell state. Nature communications, 16(1), 3351.

Li X, et al. (2025) CircMAN1A2 Levels Determine GBM Susceptibility to TMZ in a Pathway Involving TEP1- and KEAP1-Mediated NRF2 Degradation Leading to Ferroptosis. CNS neuroscience & therapeutics, 31(7), e70489.

Valenti G, et al. (2025) Regulatory network analysis of Dclk1 gene expression reveals a tuft cell-ILC2 axis that inhibits pancreatic tumor progression. Cell reports, 44(6), 115734.

Fiorentino J, et al. (2024) Prediction of protein-RNA interactions from single-cell transcriptomic data. Nucleic acids research, 52(6), e31.

Galindez G, et al. (2024) Inference of differential gene regulatory networks using boosted differential trees. Bioinformatics advances, 4(1), vbae034.

Anglada-Girotto M, et al. (2024) Disentangling the splicing factor programs underlying complex molecular phenotypes. bioRxiv : the preprint server for biology.

Moakley DF, et al. (2024) Reverse engineering neuron type-specific and type-orthogonal splicing-regulatory networks using single-cell transcriptomes. bioRxiv : the preprint server for biology.

Song KJ, et al. (2024) Proteogenomic analysis reveals non-small cell lung cancer subtypes predicting chromosome instability, and tumor microenvironment. Nature communications, 15(1), 10164.

Logan R, et al. (2024) Sex-specific Concordance of Striatal Transcriptional Signatures of Opioid Addiction in Human and Rodent Brains. Research square.