

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 [ASWG](#) .

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.

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.

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.

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.

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*.