

Resource Summary Report

Generated by [RRID](#) on Sep 10, 2026

[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>

Proper Citation: ARACNE (RRID:SCR_002180)

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 application, software resource

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: 20260905T133226+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 163 mentions in open access literature.

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

García-Cortés D, et al. (2026) Loss of long-range co-expression is a common feature in cancer. NPJ systems biology and applications, 12(1).

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

Safranek CW, et al. (2026) Simulated evaluation of large language model stepwise diagnostic reasoning with real-world chest pain encounters and Bayesian networks. BMC medical informatics and decision making, 26(1).

Anglada-Girotto M, et al. (2026) Exon inclusion signatures enable accurate estimation of splicing factor activity. Nature communications, 17(1).

Ager CR, et al. (2026) Neoadjuvant Fc-enhanced anti-CTLA-4 targets Tregs to augment androgen deprivation in high-risk prostate cancer: A randomized phase I trial. Cell reports. Medicine, 7(3), 102638.

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.

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.

Hegde A, et al. (2025) Machine learning methods for gene regulatory network inference. Briefings in bioinformatics, 26(5).

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.

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.

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.

Shahsavari M, et al. (2025) Gene regulatory and co-expression networks reveal novel hub genes and regulatory mechanisms in rapeseed (*Brassica napus* L.) under drought stress. *Scientific reports*, 16(1), 3470.

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.

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.