

Resource Summary Report

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CIBERSORT

RRID:SCR_016955

Type: Tool

Proper Citation

CIBERSORT (RRID:SCR_016955)

Resource Information

URL: <https://cibersort.stanford.edu/>

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Description: Software tool to provide an estimation of the abundances of member cell types in a mixed cell population, using gene expression data. Used for characterizing cell composition of complex tissues from their gene expression profiles, large scale analysis of RNA mixtures for cellular biomarkers and therapeutic targets.

Resource Type: software application, software resource, data analytics software

Defining Citation: [PMID:25822800](#)

Keywords: estimation, abundance, cell, type, mixed, population, gene, expression, data, tissue, complex, analysis, RNA, biomarker, therapeutic, target, bio.tools

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US Department of Defense ;
Siebel Stem Cell Institute ;
Thomas and Stacey Siebel Foundation

Availability: Not freely available for download or distribution, Available for non commercial users, Registration required

Resource Name: CIBERSORT

Resource ID: SCR_016955

Alternate IDs: biotools:CIBERSORT

Alternate URLs: <https://bio.tools/CIBERSORT>

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260805T044401+0000

Ratings and Alerts

No rating or validation information has been found for CIBERSORT.

No alerts have been found for CIBERSORT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1239 mentions in open access literature.

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

Mogi M, et al. (2026) Pan-cancer analysis of RNA expression signatures associated with cancer tissue architecture. British journal of cancer, 134(1), 141.

Yan C, et al. (2026) RAS/MEK/PI3K pathway inhibition augments response to CD40 agonism by targeting CD11b+ Bregs thereby overcoming melanoma PD1-resistance. Nature communications, 17(1), 162.

Luo B, et al. (2025) Resveratrol amplifies the anti-tumor effect of γ -PD-1 by altering the intestinal microbiome and PGD2 content. Gut microbes, 17(1), 2447821.

Yin A, et al. (2025) EFTUD2 is a promising diagnostic and prognostic indicator involved in the tumor immune microenvironment and glycolysis of lung adenocarcinoma. Frontiers in oncology, 15, 1499217.

Ma H, et al. (2025) Spatially Resolved Tumor Ecosystems and Cell States in Gastric Adenocarcinoma Progression and Evolution. Cancer discovery, 15(4), 767.

Shi J, et al. (2025) Identification of biomarkers for chronic renal fibrosis and their relationship with immune infiltration and cell death. Renal failure, 47(1), 2449195.

Wang S, et al. (2025) Ferroptosis-related genes participate in the microglia-induced neuroinflammation of spinal cord injury via NF- κ B signaling: evidence from integrated single-cell and spatial transcriptomic analysis. Journal of translational medicine, 23(1), 43.

Zhao Y, et al. (2025) The immune-related gene CD5 is a prognostic biomarker associated with the tumor microenvironment of breast cancer. Discover oncology, 16(1), 39.

Zhao B, et al. (2025) Exosome-related genes influence the progression of stroke through neuroinflammatory responses. *Frontiers in neurology*, 16, 1517588.

Lang T, et al. (2025) CYBB identified as a key immune hub gene linking lung cancer and atrial fibrillation. *Journal of cardiothoracic surgery*, 20(1), 262.

Chen J, et al. (2025) ALOX15B-based efferocytosis clusters: prognostic implications and immune cell infiltration in breast cancer. *Discover oncology*, 16(1), 1159.

Liu Y, et al. (2025) Exploration on the potential predictive value of regulator of G-protein signaling 2 in the efficacy of concurrent chemoradiotherapy on cervical squamous cell carcinoma. *CytoJournal*, 22, 53.

Ye C, et al. (2025) Comprehensive analysis of single-cell and bulk RNA sequencing data reveals an EGFR signature for predicting immunotherapy response and prognosis in pancreatic cancer. *Frontiers in immunology*, 16, 1604394.

Lu Y, et al. (2025) Signatures of tumor microenvironment-related genes and long noncoding RNAs predict poor prognosis in osteosarcoma. *PloS one*, 20(7), e0326876.

Xin P, et al. (2025) PCK1 as a potential hub gene in distinguishing lactate metabolism between rheumatoid arthritis and osteoarthritis. *PeerJ*, 13, e19661.

Chen JJ, et al. (2025) CD79A and GADD45A as novel immune-related biomarkers for respiratory syncytial virus severity in children: an integrated machine learning analysis and clinical validation. *Frontiers in immunology*, 16, 1609183.

Chen M, et al. (2025) CENPF as a Potential Biomarker Associated with the Immune Microenvironment of Renal Cancer. *Technology in cancer research & treatment*, 24, 15330338251330791.

Qian YY, et al. (2025) NR4A3 potentials M1-like macrophage polarization to facilitate anti-tumor immune responses in breast cancer. *NPJ breast cancer*, 11(1), 67.

Ji Y, et al. (2025) Shared pathogenesis in polycystic ovaries and rheumatoid arthritis: an analysis of key genes and pathways. *Frontiers in genetics*, 16, 1554139.

Zhang S, et al. (2025) RPA3 and RFC3 as biomarkers for myocardial infarction diagnosis under computed tomography angiography. *Medicine*, 104(26), e43087.