Resource Summary Report

Generated by RRID on Apr 28, 2025

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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NCI T32 CA09302;
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: 20250428T054027+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 1098 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Wang S, et al. (2025) Ferroptosis-related genes participate in the microglia-induced neuroinflammation of spinal cord injury via NF-?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.

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.

Zheng G, et al. (2025) Spatial and Single-Cell Transcriptomics Unraveled Spatial Evolution of Papillary Thyroid Cancer. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(2), e2404491.

Zheng Z, et al. (2025) Peripheral blood RNA biomarkers can predict lesion severity in

degenerative cervical myelopathy. Neural regeneration research, 20(6), 1764.

Chen K, et al. (2025) Habitat radiomics based on CT images to predict survival and immune status in hepatocellular carcinoma, a multi-cohort validation study. Translational oncology, 52, 102260.

Qin X, et al. (2025) The roles of STAT1, CASP8, and MYD88 in the care of ischemic stroke. Medicine, 104(4), e41396.

Zhang Y, et al. (2025) Bioinformatics analysis of ferroptosis-related hub genes and immunoinfiltration in myocardial ischemia/reperfusion following heart transplantation. BMC cardiovascular disorders, 25(1), 16.

Lu X, et al. (2025) Cellular Senescence in Hepatocellular Carcinoma: Immune Microenvironment Insights via Machine Learning and In Vitro Experiments. International journal of molecular sciences, 26(2).

Xie Y, et al. (2025) Identification of a metabolic-immune signature associated with prognosis in colon cancer and exploration of potential predictive efficacy of immunotherapy response. Clinical and experimental medicine, 25(1), 46.

Cai H, et al. (2025) Prognostic assessment of early-stage liver cirrhosis induced by HCV using an integrated model of CX3CR1-associated immune infiltration genes. Scientific reports, 15(1), 1771.

Fan Y, et al. (2025) Single-cell RNA-seq analysis reveals microenvironmental infiltration of myeloid cells and pancreatic prognostic markers in PDAC. Discover oncology, 16(1), 81.

Burdett NL, et al. (2024) Timing of whole genome duplication is associated with tumor-specific MHC-II depletion in serous ovarian cancer. Nature communications, 15(1), 6069.

D'Angelo SP, et al. (2024) Biomarker Analyses Investigating Disease Biology and Associations with Outcomes in the JAVELIN Merkel 200 Trial of Avelumab in Metastatic Merkel Cell Carcinoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(19), 4352.

Mu M, et al. (2024) Targeting Ferroptosis-Elicited Inflammation Suppresses Hepatocellular Carcinoma Metastasis and Enhances Sorafenib Efficacy. Cancer research, 84(6), 841.

Umeda M, et al. (2024) A new genomic framework to categorize pediatric acute myeloid leukemia. Nature genetics, 56(2), 281.

Liu H, et al. (2024) Identifying molecular subtypes and tumor microenvironment infiltration signatures in kidney renal clear cell carcinoma based on stemness-associated disulfidptosis genes by integrating machine learning, single-cell analyses and experimental validation. Heliyon, 10(4), e26094.

Zhang MQ, et al. (2024) Fatty acid metabolism-related lncRNAs are potential biomarkers for survival prediction in clear cell renal cell carcinoma. Medicine, 103(8), e37207.

Huang J, et al. (2024) Comprehensive analysis reveals the prognostic and immunogenic characteristics of DNA methylation regulators in lung adenocarcinoma. Respiratory research, 25(1), 74.

Ye Q, et al. (2024) PANoptosis-like death in acute-on-chronic liver failure injury. Scientific reports, 14(1), 392.