

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 resource, software application, 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: 20260801T042803+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 [PRECISE-TBI](#) .

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 ?-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.

Gao L, et al. (2025) Identification of m6A methyltransferase-related WTAP and ZC3H13 predicts immune infiltrates in glioblastoma. Scientific reports, 15(1), 4412.

Cheng Z, et al. (2025) Vitamin A family suppresses periodontitis by restoring mitochondrial metabolic reprogramming in macrophages through JAK-STAT pathway. Frontiers in genetics, 16, 1505933.

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.

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

Zhang Z, et al. (2025) Exploration of the clinical prognostic model of BRCA based on PCAT7. *Frontiers in oncology*, 15, 1580858.

Rodríguez-Moreno JF, et al. (2025) Treatment Efficacy and Molecular Dynamics of Neoadjuvant Durvalumab and Olaparib in Resectable Urothelial Bladder Cancer: The NEODURVARIB Trial. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(9), 1644.

Zhou S, et al. (2025) Integration of multi-omics data to unveil the molecular landscape and role of piRNAs in early-onset colorectal cancer. *BMC medicine*, 23(1), 250.

Zhu K, et al. (2025) An energy metabolism-related signature relevant to the tumor immune microenvironment in HNSCC. *Discover oncology*, 16(1), 806.

Jiang Y, et al. (2025) HDAC6 facilitates LUAD progression by inducing EMT and enhancing macrophage polarization towards the M2 phenotype. *NPJ precision oncology*, 9(1), 150.

Liu Z, et al. (2025) Identification of m5C RNA modification-related gene signature for predicting prognosis and immune microenvironment-related characteristics of heart failure. *Hereditas*, 162(1), 83.

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.

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