Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

CIBERSORT

RRID:SCR_016955
Type: Tool

Proper Citation

CIBERSORT (RRID:SCR_016955)

Resource Information

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

Proper Citation: CIBERSORT (RRID:SCR_016955)

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, data analytics software, software application

Defining Citation: PMID:25822800

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

Funding: Doris Duke Charitable Foundation ;
Damon Runyon Cancer Research Foundation ;
B&J Cardan Oncology Research Fund ;
Ludwig Institute for Cancer Research ;
NCI U01 CA154969;
NIAID U19 AI090019;
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: 20260808T190517+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 1908 mentions in open access literature.

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

Lawal B, et al. (2026) IMIREG: a lineage-resolved regulon signature unveiling immune engagement archetypes and predicting immunotherapy response across diverse cancers. NPJ precision oncology, 10(1).

Garfinkle EAR, et al. (2026) Adjuvant personalized multivalent neoantigen DNA vaccination for MGMT unmethylated glioblastoma: a phase 1 trial. Nature cancer, 7(7), 1064.

Peng S, et al. (2026) AI-based pathomics model predicts regulatory T cell infiltration and radiotherapy response in IDH-wild-type glioblastoma. Frontiers in immunology, 17, 1817892.

Feng J, et al. (2026) Multiomics reveals fatty acid metabolism and immune remodeling in retinal artery occlusion. iScience, 29(7), 116445.

Wang X, et al. (2026) Clinicogenomic Characterization of Primary Sclerosing Cholangitis-Associated Biliary Tract Cancers. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(2), 363.

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

Huang C, et al. (2026) Survival Genie 2: a next-generation web server for targeted and single-cell-based survival analyses. Genome medicine, 18(1).

Belanger K, et al. (2026) Cancer-Associated Fibroblasts Promote Epithelial-Mesenchymal Transition and Classical to Basal Subtype Shift in Pancreatic Cancer. Cancer research, 86(14), 3604.

Altendorf L, et al. (2026) Molecular changes during AT/RT progression associated with epithelial-mesenchymal transition and extracellular matrix changes. Acta neuropathologica, 152(1).

Ni J, et al. (2026) PEAK1 promotes prostate cancer progression and docetaxel resistance by mediating the polarization of tumor-associated macrophages. European journal of medical research, 31(1), 41.

Dang J, et al. (2026) Podophyllotoxin sensitizes triple-negative breast cancer cells to CD47-targeted immunotherapy. Cell insight, 5(3), 100313.

Dong X, et al. (2026) Identification of glycometabolism-related genes for predicting the prognosis of patients with glioblastoma and its correlation with immune infiltration. Discover oncology, 17(1).

Li S, et al. (2026) Exploration of CD2 and CD3D as potential immune-related biomarkers for IORT in breast cancer treatment. Medicine, 105(18), e48367.

Gong T, et al. (2026) Integrative epitranscriptomic and transcriptomic characterization in human colorectal cancer. Journal of advanced research, 84, 323.

Zhang Y, et al. (2026) Identification of necrosis-related signature for predicting prognosis and immunotherapy response in gastric cancer. Translational cancer research, 15(1), 54.

Vryza P, et al. (2026) Predicting skin melanoma progression via LAG-3, TIGIT and HAVCR2. Functional & integrative genomics, 26(1).

Yu A, et al. (2026) A novel diagnostic model for HIV-HTN comorbidity: genomic discovery, clinical validation, and mechanistic elucidation. Frontiers in medicine, 13, 1781646.

Yamaguchi M, et al. (2026) Metabolomic and transcriptomic analyses identify metabolic alterations and immune suppression in ovarian cancer. Scientific reports, 16(1).

Qin M, et al. (2026) Development and validation of a novel senescence-associated gene signature for prediction of survival and endocrine-disrupting chemicals in bladder cancer. Discover oncology, 17(1).

Li L, et al. (2026) Pan-cancer analysis reveals DDIAS as a potential diagnostic biomarker, prognostic indicator, and tumor-immune correlate. Discover oncology, 17(1).