

Resource Summary Report

Generated by [kravitz2](#) on Sep 2, 2026

CancerSEA

RRID:SCR_026155

Type: Tool

Proper Citation

CancerSEA (RRID:SCR_026155)

Resource Information

URL: <http://biocc.hrbmu.edu.cn/CancerSEA/>

Proper Citation: CancerSEA (RRID:SCR_026155)

Description: Database that aims to comprehensively explore distinct functional states of cancer cells at the single-cell level. Provides functional state-associated PCG/lncRNA repertoires across all cancers, in specific cancers, and in individual cancer single-cell datasets. Provides interface for comprehensively searching, browsing, visualizing and downloading functional state activity profiles of cancer single cells and corresponding PCGs/lncRNAs expression profiles.

Synonyms: Cancer Single-cell State Atlas

Resource Type: data or information resource, database

Defining Citation: [PMID:30329142](#)

Keywords: cancer single cells, PCGs/lncRNAs expression profiles, distinct functional states of cancer cells, single-cell level, searching, browsing, visualizing and downloading, functional state activity profiles,

Funding: National High Technology Research and Development Program of China ; National Natural Science Foundation of China

Availability: Free, Freely available

Resource Name: CancerSEA

Resource ID: SCR_026155

Record Creation Time: 20241210T053256+0000

Record Last Update: 20260829T183420+0000

Ratings and Alerts

No rating or validation information has been found for CancerSEA.

No alerts have been found for CancerSEA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 202 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Bai W, et al. (2026) CCL14, identified by multi-omics approach, serves as a novel indicator of disease severity and progression in lymphangioleiomyomatosis. Orphanet journal of rare diseases, 21(1), 59.

Chen J, et al. (2026) Tumor Electric Field Therapy Inhibits TGF- β /C1R Signaling Axis-Driven Epithelial-Mesenchymal Transition in Glioblastoma. CNS neuroscience & therapeutics, 32(1), e70738.

Qin Q, et al. (2026) Glutamine-driven upregulation of NPDC1 promotes colorectal cancer progression through PI3K/AKT signaling. Journal of translational medicine, 24(1), 268.

Liu J, et al. (2026) Spatial transcriptomics and single-cell analyses reveal the role of the cisplatin-resistant gene panel in NSCLC progression and the tumor microenvironment, identifying LOXL2 as a potential therapeutic target. Cancer cell international, 26(1).

Wang L, et al. (2026) MiR-551b-5p deficiency associates with malignant phenotypes in gastric cancer: potential mediation by TRAF6. BMC gastroenterology, 26(1).

Dong W, et al. (2026) Comprehensive Integrated Single-Cell and Spatial Transcriptomics Unveil the Dynamic Landscape of Betel Nut-Associated Oral Mucosal Carcinogenesis and Its Tumor Microenvironment. MedComm, 7(6), e70796.

Dong M, et al. (2026) Single-cell transcriptomics profiling elucidates RBP-driven metastatic signaling pathways in ER+ breast cancer. iScience, 29(6), 116155.

Zhu X, et al. (2026) Bioinformatic analysis and experimental validation of the function of mitogen-activated protein kinase in esophageal cancer. Discover oncology, 17(1).

Sun Z, et al. (2026) Comprehensive pan-cancer analysis and experimental verification of the roles of SCP2 in colon adenocarcinoma. BMC cancer, 26(1), 208.

Huang X, et al. (2026) Comprehensive bioinformatic analysis reveals TRPM4 as a biomarker for pan-cancer progression and macrophage infiltration. Discover oncology, 17(1).

Wang W, et al. (2026) Diverse roles of SERPINE1 in regulating cellular proliferation and invasion. *International journal of oncology*, 68(5).

Zhai X, et al. (2026) Pan-cancer characterization of POSTN and its clinical and microenvironmental associations in ER+ breast cancer. *Scientific reports*, 16(1).

Tang J, et al. (2026) Development and validation of an immune-related diagnostic signature for breast cancer bone metastasis. *Scientific reports*, 16(1).

Xu R, et al. (2026) Comprehensive pan-cancer analysis of FSCN1 as a marker for prognosis and immunity. *Discover oncology*, 17(1).

Zhan X, et al. (2026) Construction of a novel risk model for esophageal squamous cell carcinoma associated with purinergic signaling pathways and chemoradiotherapy sensitivity genes. *Frontiers in medicine*, 13, 1746281.

Guo S, et al. (2026) Integrative Multi-Omics and Pan-Cancer Analyses Identify CCL20 as a Prognostic Biomarker with Therapeutic Relevance in Esophageal Cancer. *Biomedicines*, 14(5).

Li S, et al. (2026) Alternative splicing events show high prognostic values and indicate potential core genes in acute myeloid leukemia. *Clinical and experimental medicine*, 26(1), 143.

Liu H, et al. (2026) OSBPL2-mediated lipid metabolism alteration governs lung cancer stem cells properties. *Stem cell research & therapy*, 17(1).

Zhang W, et al. (2026) Pro-tumourigenic effects of DCAF13 on the progression of colorectal cancer. *Oncology letters*, 31(4), 145.

Fan W, et al. (2026) Pan-cancer analysis reveals FOLH1 as a prognostic biomarker and immune modulator in human tumors. *Translational cancer research*, 15(3), 180.