

Resource Summary Report

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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: 20260817T040722+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 [dkNET](#) .

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.

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.

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).

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

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.

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

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

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).

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).

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.

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.

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.