

Resource Summary Report

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PanglaoDB

RRID:SCR_022580

Type: Tool

Proper Citation

PanglaoDB (RRID:SCR_022580)

Resource Information

URL: <https://panglaodb.se/>

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Description: Database for exploration of single cell RNA sequencing experiments from mouse and human. Collects and integrate data from multiple studies and present them through unified framework.

Resource Type: data or information resource, database

Defining Citation: [PMID:30951143](#)

Keywords: single cell RNA sequencing experiments, mouse data, human data, single cell RNA sequencing

Funding: Karolinska Institutet/AstraZeneca Integrated Cardio Metabolic Centre ;
Fondation Leducq—Transatlantic PlaQOmics Network ;
Hjärt-och Lungfonden ;
Vetenskapsrådet

Availability: Free, Freely available

Resource Name: PanglaoDB

Resource ID: SCR_022580

Record Creation Time: 20220726T050157+0000

Record Last Update: 20260729T044538+0000

Ratings and Alerts

No rating or validation information has been found for PanglaoDB.

No alerts have been found for PanglaoDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 91 mentions in open access literature.

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

Huang L, et al. (2025) Comprehensive single-cell analysis of triple-negative breast cancer based on cDC1 immune-related genes: prognostic model construction and immunotherapy potential. *Discover oncology*, 16(1), 206.

Zhang X, et al. (2025) Expression of stearyl coenzyme a desaturase in neuronal cells facilitates pancreatic cancer progression. *Cancer cell international*, 25(1), 57.

Chen X, et al. (2025) Cross one single body 49 tissues single-cell transcriptome reveals detailed macrophage heterogeneity during pig pregnancy. *Frontiers in immunology*, 16, 1574120.

Balko J, et al. (2025) Peripheral blood gene expression signatures of systemic immunity predict tumor microenvironment biology and therapeutic response in breast cancer. *Research square*.

Qi Y, et al. (2025) Integrated eQTL-pQTL Mendelian randomization and single-cell sequencing reveal therapeutic targets in ovarian clear cell cancer. *Discover oncology*, 16(1), 1249.

Zheng Y, et al. (2025) Multiple data sets to explore the key molecules and mechanism of lymph node metastasis in gastric cancer. *Discover oncology*, 16(1), 606.

García-Rodríguez JL, et al. (2025) Cancer-associated fibroblasts shape the formation of budding cancer cells at the invasive front of human colorectal cancer. *Communications biology*, 8(1), 1345.

Zampieri C, et al. (2025) The urokinase receptor/uPAR is a major effector of p53 gain-of-function mutations in gemcitabine-treated pancreatic ductal adenocarcinoma. *The Journal of biological chemistry*, 301(9), 110561.

Lluch A, et al. (2025) Defective Olfactomedin-2 connects adipocyte dysfunction to obesity. *Nature communications*, 16(1), 7154.

Jelcic I, et al. (2025) T-bet+ CXCR3+ B cells drive hyperreactive B-T cell interactions in multiple sclerosis. *Cell reports. Medicine*, 6(3), 102027.

Li G, et al. (2025) Deciphering the Regulatory Networks of the Migrasome-Associated Cell Subpopulation in Heterotopic Ossification via Multi-Omics Analysis. *FASEB journal* : official publication of the Federation of American Societies for Experimental Biology,

39(12), e70749.

Yan H, et al. (2025) Integrated single-cell transcriptomics and Mendelian randomization identify neutrophil-associated biomarker genes in colorectal cancer. *Discover oncology*, 16(1), 1705.

Chakraborty S, et al. (2025) Unique epithelial proliferative transcriptomic signature in proton pump inhibitor-responsive pediatric eosinophilic esophagitis. *JCI insight*, 10(19).

Zhao G, et al. (2025) Integrating single-cell sequencing and clinical insights to explore malignant transformation in odontogenic keratocyst. *Computational and structural biotechnology journal*, 27, 1158.

Liu J, et al. (2025) Genetic liability to systemic inflammatory regulators is causally linked to COVID-19 diverse phenotypes: Insights from multi-omics association study and single-cell RNA sequencing analysis. *Medicine*, 104(34), e44089.

Shao XD, et al. (2025) Identification of promising lung cancer targets from human plasma proteins via Mendelian randomization. *Discover oncology*, 16(1), 1927.

Luo X, et al. (2025) Single-cell RNA sequencing identifies PD-L1 + mesenchymal stem cells with enhanced immunomodulatory capacity and alleviated the degree of ectopic new bone formation in ankylosing spondylitis. *Stem cell research & therapy*, 16(1), 684.

Dai L, et al. (2025) Spatial transcriptomics reveals prognostically LYZ+ fibroblasts and colocalization with FN1+ macrophages in diffuse large B-cell lymphoma. *Cancer immunology, immunotherapy : CII*, 74(4), 123.

Mair T, et al. (2025) The atypical KRASQ22K mutation directs TGF- β response towards partial epithelial-to-mesenchymal transition in patient-derived colorectal cancer tumoroids. *Molecular oncology*, 19(8), 2212.

Zagare A, et al. (2025) Deciphering shared molecular dysregulation across Parkinson's disease variants using a multi-modal network-based data integration and analysis. *NPJ Parkinson's disease*, 11(1), 63.