Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

Liver cell atlas

RRID:SCR_023627
Type: Tool

Proper Citation

Liver cell atlas (RRID:SCR_023627)

Resource Information

URL: https://www.livercellatlas.org

Proper Citation: Liver cell atlas (RRID:SCR_023627)

Description: Portal to search liver single cell RNA-sequencing datasets. Datasets for expression of genes or proteins (when CITE-seq was performed). To search for gene enter the official gene name. To search for protein please click to see specific names to use for different markers included.

Resource Type: atlas, data or information resource

Keywords: liver single cell RNA-sequencing data, liver cell, RNA-sequencing data, gene expression, protein, dataset,

Availability: Free, Freely available

Resource Name: Liver cell atlas

Resource ID: SCR_023627

Record Creation Time: 20230527T050216+0000

Record Last Update: 20260912T200221+0000

Ratings and Alerts

No rating or validation information has been found for Liver cell atlas.

No alerts have been found for Liver cell atlas.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 41 mentions in open access literature.

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

Yu D, et al. (2026) Single-cell atlas of hepatitis C virus inoculated tree shrew liver reveals immune activation, metabolic reprogramming, and persistent inflammation. EBioMedicine, 123, 106080.

Zhao L, et al. (2026) Iturin derived from Bacillus modulates lipid and glucose metabolism while mitigating the progression of MASLD. iScience, 29(4), 115470.

Sano A, et al. (2026) Endothelial cell glycogen synthase kinase 3? promotes lipotoxic endotheliopathy and liver inflammation in MASH. JCI insight, 11(12).

Balasubramani S, et al. (2026) Affinity Proteomics-Based Non-Invasive Detection of Clinically Significant Liver Disease. Alimentary pharmacology & therapeutics, 64(1), 74.

Severeid PE, et al. (2026) Factor VIII originates primarily from anatomically distinct subsets of liver sinusoidal endothelial cells. Blood advances, 10(8), 2867.

Breinig M, et al. (2026) Integrated in vivo combinatorial functional genomics and spatial transcriptomics of tumours to decode genotype-to-phenotype relationships. Nature biomedical engineering, 10(1), 125.

Fuster-Martínez I, et al. (2026) Hypoxia in MASLD: a spatial determinant of the pathogenesis. Trends in molecular medicine.

Calligaris M, et al. (2026) iRhom2 regulates HMGB1 secretion to modulate inflammation and hepatocyte senescence in an in vitro model of ischemia-reperfusion injury. Cell death & disease, 17(1), 7.

Fritzsche S, et al. (2026) Strawberry Notch 1 Acts as a Transcriptional Regulator Driving Oncogenic Programs in Liver Carcinogenesis. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(20), e07238.

Hong H, et al. (2025) Characterizing Kupffer Cell Production of CD5 Antigen-Like and Its Function on Regulating Migration of Natural Killer T Cells. The American journal of pathology, 195(10), 1839.

Lehrich BM, et al. (2025) Precision targeting of ?-catenin induces tumor reprogramming and immunity in hepatocellular cancers. Nature communications, 16(1), 5009.

Saris J, et al. (2025) Peritoneal resident macrophages constitute an immunosuppressive environment in peritoneal metastasized colorectal cancer. Nature communications, 16(1), 3669.

Gill R, et al. (2025) Gc inhibition preserves insulin sensitivity and reduces body weight without loss of muscle mass. JCI insight, 10(23).

Wu Y, et al. (2025) Cross-level Cross-Scale Inference and Imputation of Single-cell Spatial Proteomics. Research square.

Örd T, et al. (2025) Single-cell to pre-clinical evaluation of Trem2, Folr2, and Slc7a7 as macrophage-associated biomarkers for atherosclerosis. Cardiovascular research, 121(16), 2503.

Nataraj K, et al. (2025) Androgen Effects on Alcohol-induced Liver Fibrosis Are Controlled by a Notch-dependent Epigenetic Switch. Cellular and molecular gastroenterology and hepatology, 19(1), 101414.

Chen R, et al. (2025) A comprehensive benchmarking for spatially resolved transcriptomics clustering methods across variable technologies, organs, and replicates. iMeta, 4(6), e70084.

Chen H, et al. (2025) Integrative genome-wide analysis unveils the genetic landscape of gallstone disease and highlights novel loci with therapeutic potential. BMJ open gastroenterology, 12(1).

Dall M, et al. (2025) Hepatocyte dedifferentiation in 2D culture reveals extensive transcriptomic and proteomic rewiring. Hepatology communications, 9(11).

Ou Z, et al. (2025) Spatiotemporal Transcriptomic Profiling Reveals the Dynamic Immunological Landscape of Alveolar Echinococcosis. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(18), e2405914.