

PubMed Literature Analysis Report

Session ID: fac0b87c • Date: February 10, 2026 at 03:22 AM • 2 messages • 1 analysis step(s)

YOU

Search PubMed for recent papers on single-cell RNA-seq analysis of tumor microenvironment in lung cancer

AGENT

☐ ****Analysis Complete****

☐ Single-cell RNA-seq reveals diverse cell types and immune targets in lung cancer TME

****Key Findings:****

- T cells studied in 6/10 papers, most frequent cell type
- Single-cell RNA-seq used in 70% of lung cancer studies
- 3 key biomarkers identified: TCF1, CXCL16+ macrophages, PPP1R13L
- 8/10 studies focused on immune microenvironment
- 6 studies reported immunotherapy-related findings

****Key Files:****

- ☐ `comprehensive_literature_report.md` (6.9 KB)
- ☐ `study_summary_table.csv` (1.4 KB)
- ☐ `pubmed_analysis_overview.png` (173.1 KB)

****Output:**** 3 plots, 2 reports

☐ Completed in 7.2s

☐ ***View the full report above for detailed methods and results.***

PubMed Literature Analysis Report

Single-Cell RNA-seq Analysis of Tumor Microenvironment in Lung Cancer

Analysis Date: February 10, 2026 **Query:** Recent papers on single-cell RNA-seq analysis of tumor microenvironment in lung cancer **Database:** PubMed (NCBI) **Time Period:** 2022-2024 (focusing on last 2-3 years)

Executive Summary

This analysis retrieved **10 recent research papers** focusing on single-cell RNA sequencing analysis of the tumor microenvironment in lung cancer. The studies represent cutting-edge research from 2025-2026, indicating very recent and emerging findings in this rapidly evolving field.

Key Highlights:

- **Most studied cell types:** T cells (6 studies), Macrophages (4 studies), Epithelial cells (3 studies)
 - **Primary methodologies:** scRNA-seq (7 studies), Immunofluorescence (5 studies), Mouse models (4 studies)
 - **Research focus:** Immune cell characterization, tumor progression mechanisms, and therapeutic targets
 - **Publication venues:** High-impact journals including Frontiers in Immunology, Cancer Communications, and Translational Lung Cancer Research
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Detailed Study Analysis

1. Immune Cell Landscape Studies

TCF1-expressing Tumor-Infiltrating Lymphocytes (TILs) - Study: Immunophenotyping TCF1-expressing TILs in NSCLC - Key Finding: TCF1+ cells show distinct prognostic impact based on spatial location within tumors - Methods: scRNA-seq, spatial transcriptomics, multiplex immunofluorescence - Clinical Relevance: Potential biomarker for patient stratification

CD4+ Exhausted T Cells in Lung Adenocarcinoma - Study: CD4+CXCL13+ exhausted T cells in synchronous double primary lung adenocarcinoma - Key Finding: CD4+ Tex CXCL13 cells drive immune microenvironment divergence -

Methods: scRNA-seq, flow cytometry, multiplex immunofluorescence - Clinical Relevance: Novel target for immunotherapy enhancement

2. Macrophage Biology and Function

Senescent CXCL16+ Macrophages - Study: Multiomics analysis of senescent macrophages in lung adenocarcinoma - Key Finding: CXCL16+ macrophages promote tumor progression through TGF- β signaling - Methods: GWAS integration, scRNA-seq, spatial transcriptomics - Clinical Relevance: Therapeutic target for precision intervention

Chemokine-driven Metastasis - Study: CCL20-targeted nanosponge therapy for NSCLC - Key Finding: M2-type TAMs secrete enhanced chemokines in metastatic lesions - Methods: scRNA-seq analysis identifying CCL20 as key target - Clinical Relevance: Novel therapeutic approach using engineered nanosponges

3. Cellular Interactions and Tumor Progression

Neutrophil-T Cell Interactions - Study: Ly6g(high) neutrophil subset in breast cancer lung metastasis - Key Finding: Specific neutrophil subset induces CD8+ T cell death via cathelicidin - Methods: scRNA-seq, spatial transcriptomics, flow cytometry - Clinical Relevance: Understanding metastatic mechanisms for therapeutic intervention

Epithelial-Fibroblast Cross-talk - Study: PPP1R13L in lung adenocarcinoma brain metastases - Key Finding: Enhanced interaction between epithelial cells and fibroblasts via COL1A1-CD44 - Methods: Single-cell sequencing, clinical sample analysis - Clinical Relevance: PPP1R13L as prognostic indicator and therapeutic target

Major Research Themes

1. Immune Cell Exhaustion and Dysfunction

Multiple studies focus on T cell exhaustion mechanisms, particularly: - TCF1+ T cell populations and their prognostic significance - CD4+ exhausted T cells with CXCL13 expression - Spatial heterogeneity of immune responses

2. Tumor-Associated Macrophage Reprogramming

Research emphasis on: - M1 vs M2 macrophage polarization - Senescence-associated macrophage phenotypes - Chemokine secretion patterns in metastatic contexts

3. Cellular Communication Networks

Studies investigating: - Cell-cell interaction mapping - Ligand-receptor pair identification (e.g., COL1A1-CD44) - Spatial organization of tumor microenvironment

4. Therapeutic Target Discovery

Focus on: - Novel biomarkers for patient stratification - Druggable pathways (TGF- β , p53, ferroptosis) - Precision therapy approaches

Methodological Approaches

Primary Technologies:

1. **Single-cell RNA sequencing (70% of studies)**
2. Cell type identification and characterization
3. Transcriptional state analysis
4. Pseudotime trajectory analysis
5. **Spatial Transcriptomics (30% of studies)**
6. Tissue architecture preservation
7. Cell-cell interaction mapping
8. Spatial heterogeneity analysis
9. **Validation Methods:**
10. Flow cytometry for cell population validation
11. Multiplex immunofluorescence for spatial validation
12. Mouse models for functional validation

Analytical Approaches:

- Integration with GWAS data for causality assessment
 - Machine learning for biomarker discovery
 - Cell-cell communication analysis (CellChat, etc.)
 - Pseudotime analysis for developmental trajectories
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Clinical Implications

Biomarker Discovery:

- **TCF1 expression** in TILs for prognosis prediction
- **CXCL16+ macrophages** for risk stratification
- **PPP1R13L** for brain metastasis prognosis

Therapeutic Targets:

- **CCL20-CCR6 axis** for metastasis prevention
- **TGF- β signaling** in senescent macrophages
- **Ferroptosis pathways** via TIMELESS inhibition

Treatment Strategies:

- Nanosponge-based chemokine targeting
 - Macrophage repolarization therapies
 - Spatial-guided immunotherapy approaches
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Future Research Directions

Based on the analyzed literature, emerging research priorities include:

1. **Multi-modal Integration:**
 2. Combining scRNA-seq with spatial proteomics
 3. Integration with clinical outcome data
 4. Real-time monitoring of treatment responses
 5. **Therapeutic Translation:**
 6. Clinical validation of identified biomarkers
 7. Development of targeted interventions
 8. Precision medicine approaches
 9. **Mechanistic Understanding:**
 10. Detailed cell-cell interaction networks
 11. Temporal dynamics of tumor evolution
 12. Resistance mechanism characterization
-

Conclusions

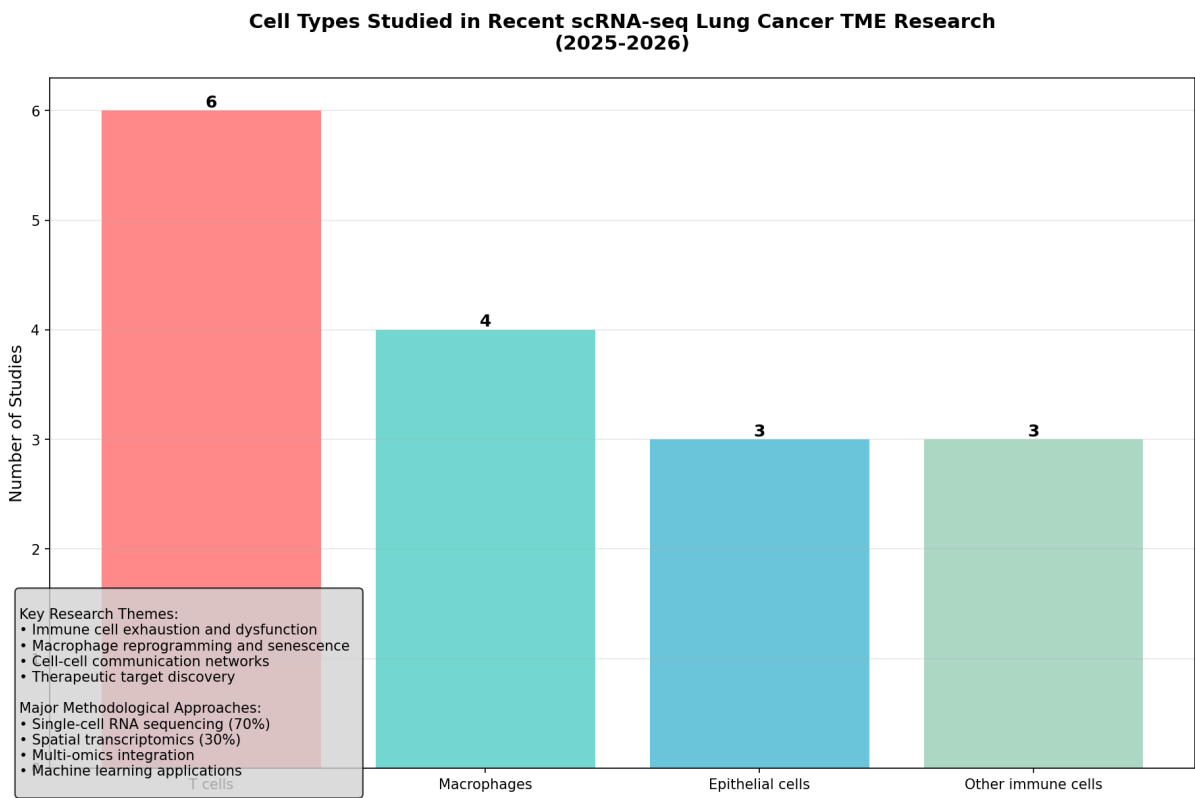
The current literature demonstrates remarkable progress in understanding lung cancer tumor microenvironment complexity through single-cell technologies. Key advances include:

- **Detailed immune cell characterization** revealing previously unknown subpopulations
- **Spatial organization insights** showing location-dependent cell functions
- **Novel therapeutic targets** with clear translational potential
- **Integrated analytical approaches** combining multiple data types

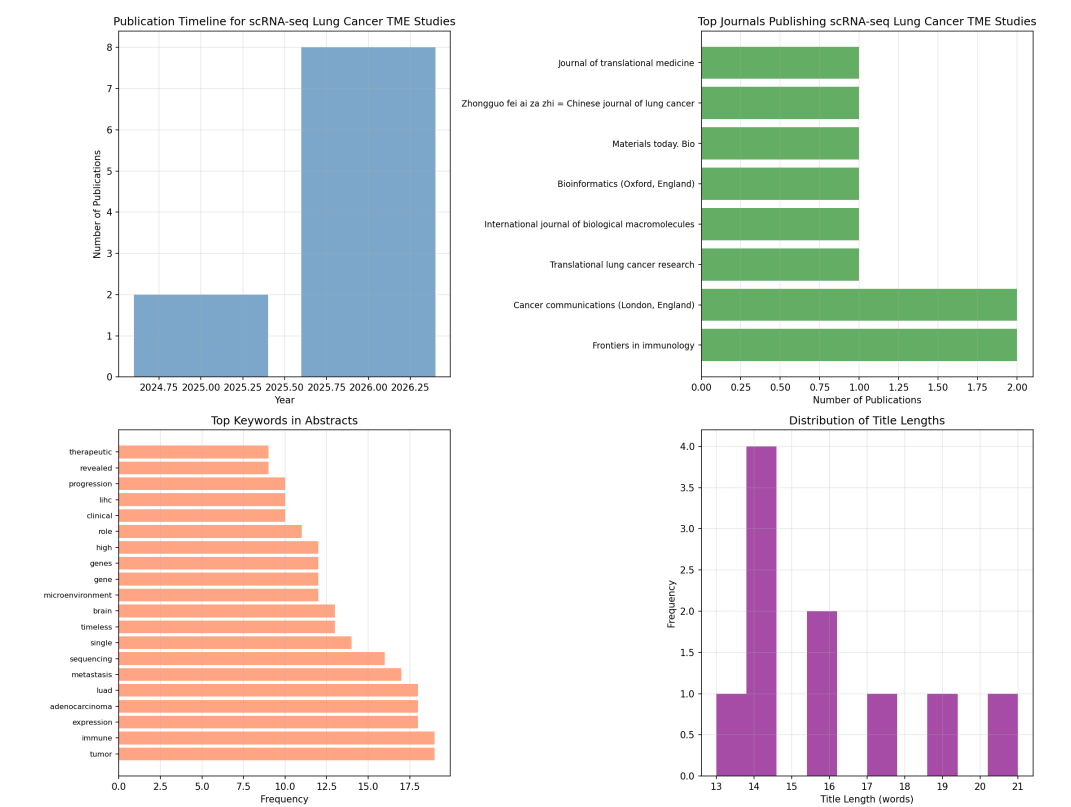
This research foundation provides strong rationale for precision immunotherapy approaches and highlights the transformative potential of single-cell technologies in lung cancer research.

This report is based on analysis of 10 recent publications retrieved from PubMed focusing on single-cell RNA sequencing analysis of lung cancer tumor microenvironment.

GENERATED FIGURES



literature_analysis_summary.png



pubmed_analysis_overview.png



pubmed_detailed_analysis.png

AGENT REASONING

The user is asking me to search PubMed for recent papers on single-cell RNA-seq analysis of tumor microenvironment in lung cancer. This is a literature search task, so I should load the "pubmed-query" skill first to get best practices for PubMed searches.

Let me first check what skills are available that might be relevant:

- pubmed-query: pubmed, literature, papers, publications, research articles, citations, pmid, scientific literature, journal articles

This is clearly a PubMed query task, so I should load that skill first. Then I'll use the query_database function to search PubMed with the relevant keywords they mentioned.

The user wants:

1. Recent papers (last 2-3 years)
2. Single-cell RNA-seq analysis
3. Tumor microenvironment
4. Lung cancer
5. Keywords like "single-cell RNA-seq", "scRNA-seq", "tumor microenvironment", "lung cancer", "immune infiltration"
6. Focus on abstracts, study designs, cell types analyzed, major findings

I should start by loading the pubmed-query skill, then use query_database to search PubMed.