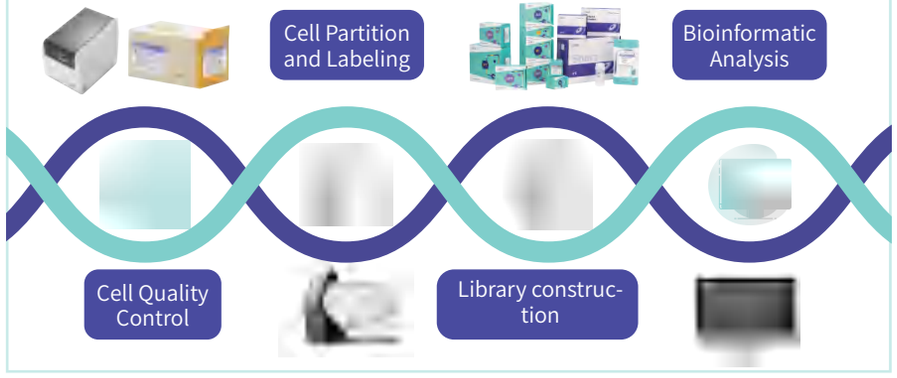
SeekGene BioSciences is a technology-driven platform dedicated to innovation and application in single-cell sequencing.
We advance single-cell multiomics technologies to unlock high-dimensional cellular insights and empower scientific discovery worldwide.

Vision	Technology-driven innovation to decode life' s unknowns
Values	Integrity · Rigor · Innovation · Simplicity

What We Deliver

- Innovative, Comprehensive Single-Cell Multiomics Solutions
- End-to-End, Reliable Platforms for Research



Follow our social media to stay ahead with latest advances in single-cell field

SEEKGENE

Mail: info@seekgene.com
Website: https//:www.seekgene.com

SEEKGENE

SeekOne™ DD Series Products

All-In-One:
Multi-Omics Single-Cell System

Decoding Unknown of Life with Novel Single-cell Technology

Mail: info@seekgene.com

- **20+**
  End-to-end innovative single-cell product solutions
  100+
  Granted invention patents and software copyrights

- **180+** publications enabled
  Total Impact Factor > **2,000**

- **20+ projects supported**
  Technology Innovation 2030,
  Beijing Natural Science Foundation, and related programs

- **270+** species, **2,800+** sample types validated
  20,000+ single-cell projects completed
  70,000+ samples processed for dissociation

- **1,000+** research institutions worldwide
  12+ laboratories across China

Company History

7 years	20+	70,000+
continuous innovation	products commercialized	samples processed

2015
Founded

2018
R&D program initiated

2020
Beijing headquarters established
SeekOne™ MM Single Cell Platform launched
SeekOne™ MM 3’ scRNA-seq solution launched
SeekSoul™ Tools bioinformatics software released

2021
Commercial operations initiated
Beijing and Shanghai laboratories established
Guangzhou and Chengdu laboratories established
SeekOne™ DD Single Cell Platform launched
SeekOne™ DD 3’ scRNA-seq solution launched

2022
Wuhan and Shenyang laboratories established
SeekOne™ MM Large-well scRNA-seq solution launched
SeekOne™ DD Immune Profiling solution launched
SeekOne™ DD scFAST-seq solution launched
SeekMate™ Tissue Dissociation reagents launched

2023
Tianjin and Shenzhen laboratories established
Selected for China National Key R&D Program (14th Five-Year Plan)
SeekMate Tinitan™ Fluorescence Cell Counter launched
SeekSoul™ Online cloud platform released
SeekSpace™ Single-Cell Spatial platform launched
SeekSpace™ Spatial scRNA-seq solution launched

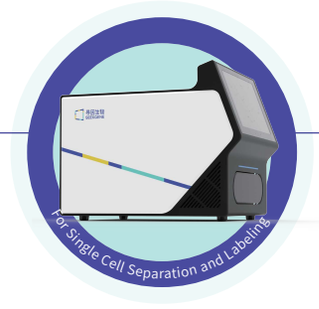
2024
Nanjing and Harbin laboratory established
Beijing Natural Science Foundation grant awarded
Approved for Science & Technology Innovation 2030 Program

2025
SeekOne™ DD FFPE scRNA-seq solution launched
SeekMate™ FFPE Dissociation solution launched
SeekOne™ DD scATAC + RNA-seq solution launched

2026
SeekOne™ DD scMethyl + RNA-seq solution launched
SeekOne™ DD scMLPSeq solution launched

SeekOne™ DD System - A Versatile Single Cell Platform

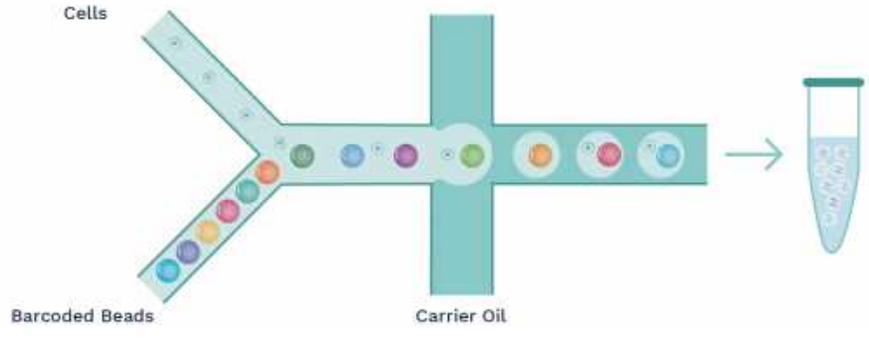
SeekOne™ DD System



- SeekSpace™ Spatial scRNA-seq (SeekSpace™ Single Cell Spatial Transcrip-tome-seq Kit)
- scMLPSeq (SeekOne™ DD Single Cell MLPSeq kit)
- scMethyl+RNA-seq (SeekOne™ DD Single Cell Multiome Methylation +RNA Kit)
- FFPE scRNA-seq (SeekOne™ DD FFPE Single Cell Transcrip-tome-seq Kit)
- scATAC+RNA-seq (SeekOne™ DD Single Cell Multiome ATAC + RNA Kit)
- Immune Profiling (SeekOne™ DD Single Cell 5' Transcrip-tome-seq and V(D)J Enrichment Kit)
- scFAST-seq (SeekOne™ DD Single Cell Full-length RNA Sequence Transcrip-tome-seq Kit)
- 3' scRNA-seq (SeekOne™ DD Single Cell 3' Transcrip-tome-seq Kit)

SeekOne™ Digital Droplet System

SeekOne™ Digital Droplet (SeekOne™ DD) System is an automated instrument for single cell partitioning, capture, and labeling based on the principle of microfluidics. In addition to general sample types, the DD system is particularly suitable for highly fragile cells, such as brain tissue, retinal tissue, and all tissues from aged individuals.



Specifications

- Size: 23.0×21.5×26.0 (cm)
- Weight: 7.25 Kg
- Cell size diameter of 5~40 μm
- High cell capture rates up to 65%
- Low doublet rates of as low as 0.3% for 1,000 cells
- Efficiently capture 500 - 60,000 cells / nuclei per channel
  Up to million cells / nuclei per run

Features

Efficient
Rapid generation of 150,000 droplets in 3 minutes

Stable
Equipped with temperature control system

Flexible
Single-chip per sample, flexibly run 1–8 samples

Cost-saving
Reusable Chip-P for empty channel, no chip waste

All-in-one
Compatible with all SeekOne™ DD reagent kits

User-friendly
One-touch UI, less operation

SeekOne™ DD Kits For Single Cell Library Construction

High - Efficiency
4.5 minutes run for 8 parallel samples.

Reliability
Validated across 270+ species, 2,800+ tissues, and 70,000+ samples.

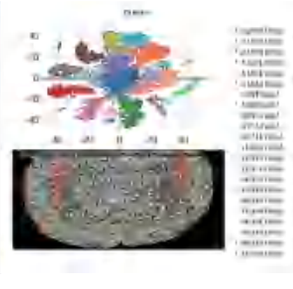
Broad Applications
Specialized reagent kits for oncology, immunology, development, virology, lncRNA, and other research fields.

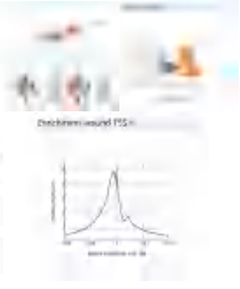
Full-chain Solution
End-to-end single-cell solutions, from cell labeling to bioinformatics analysis

Bioinformatic Analysis Tools

SeekGene offers specialized bioinformatics tools for single-cell and spatial data analysis, performing cell barcode extraction, genome alignment, and gene quantification to generate expression matrices for clustering and differential expression. The suite includes SeekSoul™ Tools (scRNA-seq), SeekSpace™ Tools (spatial), SeekArc™ Tools (ATAC + RNA multi-omics), and SeekSoul™ Methyl Tools (Methyl + RNA multi-omics) for complete workflow solutions.

SeekSoul™ Tools


SeekSpace™ Tools


SeekArc™ Tools

Accurate
Annotate cell using high UMI threshold + EmptyDrops method

Fast
Achieves faster processing speeds

Open-source
Open-source software, data compatible with SeekGene's proprietary platform and other platforms such as 10x

SeekOne™ DD Reagent Kits

Kits	Detection Information	Capture Principle	Sequencing Results	Read Length		Analysis Software	Acceptable Sample Type	Analysis Dimension	Research Purpose
SeekSpace™ Spatial scRNA-seq (SeekSpace™ Single Cell Spatial Transtriptome)	RNA: All mRNA, lnc RNA, viral RNA regardless of polyA tail	RNA: Semi-random primer	Coverage of full-length RNA sequences; Spatial localization	scRNA-seq Read 1：63 bp N7 Index：8 bp N5 Index：8 bp Read 2：150 bp	Spatial label-seq Read 1：63 bp N7 Index：8 bp N5 Index：8 bp Read 2：32 bp	SeekSpace™ Tools	OCT-embedded fresh frozen tissues	• Gene expression • SNP/InDel mutation • Gene fusion • Lnc & circle RNA regulation • Pathogen transcripts such as viral RNA • Alternative splicing • Spatial localization	True single-cell resolution Single cell gene expression, cell type identification and spatial location information
scMethyl+ RNA-seq (Single Cell Methylation + RNA Transcriptome)	RNA: mRNA Methylation: Whole-genome	RNA: TSO Methylation:TSO	RNA：5' ends of mRNA Methylation:Whole-genome DNA methylation sites	scRNA-seq Read 1: 29 bp A7 Index: 8 bp N5 Index: 8 bp Read 2: 90 bp	scMethyl-seq Read 1: 150 bp A7 Index: 8 bp N5 Index: 8 bp Read 2: 150 bp	SeekSoul™ Methyl Tools	Fresh samples; Frozen samples	• Gene expression • Whole-genome methylation levels • CNV • Epigenetic-transcriptional regulation associations	More comprehensive and deeper understanding of RNA mechanisms, regulation, and pathways, Atlas of DNA Methylation
scATAC+RNA-seq (Single Cell ATAC + RNA Transcriptome)	RNA: All mRNA, lncRNA, viral RNA regardless of polyA tail ATAC: open chromatin	RNA: Semi-random primer ATAC: Semi-random primer	Coverage of full-length RNA sequences; ATAC sequences	scRNA-seq Read1：29 bp N7 Index: 8 bp N5 Index: 8 bp Read2: 90 bp	scATAC-seq Read1: ⩾120bp A7 Index: 8 bp N5 Index: 8 bp Read2: ⩾50 bp	SeekArc™ Tools	Fresh samples; Frozen samples	• Gene expression • SNP/InDel mutation • Gene fusion • Lnc & circle RNA regulation • Pathogen transcripts such as viral RNA • Alternative splicing • Chromatin accessibility	More comprehensive and deeper understanding of RNA mechanisms, regulation, and pathways,Atlas of Chromatin Accessible Regions
scFAST-seq (Single Cell Full-length RNA Sequence Transcriptome)	RNA: All mRNA, lncRNA, viral RNA regardless of polyA tail	RNA: Semi-random primer	Coverage of full-length RNA sequences	Read1: 150 bp N7 Index: 8 bp N5 Index: 8 bp Read2: 150 bp		SeekSoul™ Tools	Fresh samples; Frozen samples	• Gene expression • SNP/InDel mutation • Gene fusion • Lnc & circle RNA regulation • Pathogen transcripts such as viral RNA • Alternative splicing	More comprehensive and deeper understanding of RNA mechanisms, regulation, and pathways
scMLPSeq (Single Cell Multiplex Ligation-based Probe)	RNA：Genes covered by the probe set	RNA：Targeted hybridization & ligation to designed probes	Genes covered by the probe set	Read1: 66 bp N7 Index: 8 bp N5 Index: 8 bp Read2: 50 bp		SeekSoul™ Tools	FFPE samples; Fixed cells/nuclei	• Gene expression	Answer key clinical questions through criteria-based patient selection
FFPE scRNA-seq (FFPE Single Cell RNA Transcriptome)	RNA: All mRNA, lncRNA, viral RNA regardless of polyA tail	RNA: Semi-random primer	Coverage of full-length RNA sequences	Read1: 150 bp N7 Index: 8 bp N5 Index: 8 bp Read2: 150 bp		SeekSoul™ Tools	FFPE samples	• Gene expression	Single cell gene expression and cell type identification for FFPE sample
Immune Profiling (5' scRNA-seq + V(D)J-seq)	RNA: RNA with polyA tails	RNA: TSO	5' ends of mRNA; V(D)J sequences	5' scRNA-seq Read1: 29 bp N7 Index: 8 bp N5 Index: 8 bp Read2: 90 bp	V(D)J-seq Read1: 29 bp N7 Index: 8 bp N5 Index: 8 bp Read2: 150 bp	SeekSoul™ Tools	Fresh samples	• Gene expression • TCR/BCR profiling	Immune receptor mapping, antigen specificity, immune cell diversity along with gene expression from a single cell
3' scRNA-seq (Single Cell 3' RNA Transcriptome)	RNA: RNA with polyA tails	RNA: Oligo dT	3' ends of mRNA	Read1: 29 bp N7 Index: 8 bp N5 Index: 8 bp Read2: 90 bp		SeekSoul™ Tools	Fresh samples; Frozen samples	• Gene expression	Single cell gene expression and cell type identification

Data Performance

SeekSpace™ Spatial scRNA-seq (SeekSpace™ Single Cell Spatial Transtriptome-seq)

Species	Sample Type	Estimated Number of Cells	Median Genes per Cell	Valid Barcodes	Sequencing Saturation	Reads Mapped to Genes	Total Genes Detected	Median UMI Counts per Cell
Homo	Brain	23,708	732	85.09%	71.64%	84.38%	25,841	1,317
	Breast Tumor	16,523	951	85.47%	38.90%	86.33%	29,015	1,327
	Prostate Tumor	19,501	798	89.53%	44.92%	92.04%	28,668	1,124
	Glioma	40,057	947	76.85%	42.98%	94.03%	31,260	1,316
	Eye	23,891	860	63.98%	31.18%	89.61%	31,334	1,195
	Testis	28,344	943	83.41%	40.56%	89.93%	34,789	1,219

scMethyl + RNA-seq (Single Cell Methylation + RNA Transtriptome-seq)

Species	Sample Type	Estimated Number of Cells	GEX Median Genes per Cell	C-T Conversion	CpG Coverage_Rate	Genome Coverage_Rate_of_Median_Cell	CPGs of_Median_Cell	Reads of_Median_Cell	Methylation RAW Data(G)	RNA RAW Data(G)
Homo	PBMC	2,195	1,076	99.68%	96.31%	1.46%	519,263	376,263	624	12
	Prostate Tumor	8,243	2,270	99.31%	96.30%	0.34%	108,221	84,901	522	104
	Cell Line (MDA-MB-231)	3,641	3,327	99.53%	95.52%	0.87%	319,731	225,676	484	42
Mouse	Brain	10,656	1,006	99.53%	96.18%	0.77%	175,559	166,228	1,070	112

scATAC+RNA-seq (Single Cell ATAC + RNA Transcriptome-seq)

Species	Sample Type	Estimated Number of Cells	ATAC Median High-quality Fragments per Cell	GEX Median Genes per Cell	TSS Enrichment Score	ATAC_Raw_Bases(G)	RNA_Raw_Bases(G)	ATAC_Fraction_of_High-Quality_Fragments_in_Cells	ATAC_Fraction_of_Transposition_Events_in_Peaks_in_Cells
Homo	Melanoma	9,996	15,197	1,827	5.2	245	70	78.9%	36.9%
	PBMC	10,580	8,976	2,120	10.9	120	100	65.9%	66.5%
	Embryonic leg	10,003	10,240	2,288	5.3	150	150	53.9%	34.2%
Mouse	Brain	15,152	8,865	2,290	16.1	140	140	78.4%	66.7%
	Testis	15,000	5,595	1,947	16.3	120	100	65.9%	70.8%
	Embryo	17,149	8,883	3,099	14.7	150	150	53.5%	62.2%

scFAST-seq (Single Cell Full-length RNA Sequence Transcriptome-seq)

Species	Sample Type	Estimated Number of Cells	Mean Reads per Cell	Median Genes per Cell	Valid Barcodes	Sequencing Saturation	Reads Mapped Confidently to Genome	Fraction Reads in Cells	Total Genes Detected	rRNA%	mtRNA%	lncRNA%
Homo	Brain	9,457	37,319	3,300	92.17%	66.93%	88.59%	93.87%	25,122	1.63%	0.36%	6.40%
	PBMC	13,382	36,923	3,529	88.83%	50.58%	79.73%	92.66%	28,944	3.29%	0.55%	6.33%
	Liver Tumor	13,616	33,567	2,161	90.46%	67.28%	82.84%	95.37%	30,368	3.34%	0.17%	7.11%
	Prostate Tumor	12,293	52,308	3,587	88.76%	62.50%	86.98%	93.38%	30,712	2.02%	0.22%	6.08%

scMLPSeq (Single Cell Multiplex Ligation-based Probe-seq)

Species	Sample Type	Sample QC Results	Estimated Number of Cells	Mean Reads per Cell	Median Genes per Cell	Fraction Reads in Cells	Sequencing Saturation	Total Genes Detected	Median UMI Counts per Cell
Homo	Cervical Cancer	PASS	10,032	7,397	906	68.24%	67.85%	18,501	1,131
	Cervical Cancer	RISK	9,324	8,753	905	69.22%	69.83%	18,533	1,014
	Liver Cancer	FAIL	12,647	11,371	1,050	63.30%	51.59%	18,525	2,107

FFPE scRNA-seq (FFPE Single Cell RNA Transcriptiome-seq)

Species	Sample Type	Estimated Number of Cells	Median Reads per Cell	Median Genes per Cell	Sequencing Saturation	Total Genes Detected	Median UMI Counts per Cell
Homo	Uterine Sarcoma	7,647	15,891	1,372	16.76%	29,901	2,270
	Gastric Tumor	10,112	42,112	1,808	51.21%	31,225	2,939
	Lymphoma	8,261	66,982	1,472	68.70%	32,102	2,465
	Lung Tumor	9,562	48,951	1,211	70.25%	32,100	1,797

Immune Profiling (5' scRNA-seq + V(D)J-seq)

5' scRNA-seq

Species	Sample Type	Estimated Number of Cells	Median Genes per Cell	Valid Barcodes	Sequencing Saturation	Reads Mapped Confidently to Transcriptome	Fraction Reads in Cells	Total Genes Detected
Homo	PBMC	12,717	2,464	94.44%	70.37%	82.51%	87.38%	28,256
	PBMC	11,314	2,015	95.40%	70.52%	90.53%	89.68%	27,213
Mouse	PBMC	13,148	1,850	94.64%	54.79%	88.30%	86.18%	23,609

TCR-seq

Species	Sample Type	Estimated Number of Cells	Cells With Productive V-J Spanning Pair	Valid Barcodes	Reads Mapped to Any V(D)J Gene	Median TRA UMIs per Cell	Median TRB UMIs per Cell
Homo	PBMC	5,191	74.15%	97.60%	94.20%	3	5
	PBMC	3,984	65.21%	98.40%	95.50%	2	3
Mouse	PBMC	3,040	62.80%	90.90%	90.80%	3	5

BCR-seq

Species	Sample Type	Estimated Number of Cells	Cells With Productive V-J Spanning Pair	Valid Barcodes	Reads Mapped to Any V(D)J Gene	Median IGH UMIs per Cell	Median IGK UMIs per Cell	Median IGL UMIs per Cell
Homo	PBMC	1,586	97.04%	97.70%	93.40%	12.5	14	11
	PBMC	1,028	85.31%	98.60%	94.60%	8	14	12
Mouse	PBMC	1,487	84.30%	98.70%	96.80%	8	19	4

3' scRNA-seq (Single Cell 3' RNA Transcriptome-seq)

Species	Sample Type	Estimated Number of Cells	Median Genes per Cell	Valid Barcodes	Sequencing Saturation	Reads Mapped Confidently to Transcriptome	Fraction Reads in Cells	Total Genes Detected
Homo	Glioma	12,730	3,839	94%	48%	92%	95%	29,777
	PBMC	10,685	3,439	94%	35%	91%	88%	24,118
Mouse	Retina	8,783	3,189	88%	71%	83%	91%	22,628
	Brain	9,354	2,413	90%	58%	88%	93%	21,779

Order SeekOne™ DD Products

Product	Product Code
SeekOne™ Digital Droplet System	M001A

Product	Product Code
SeekSpace™ Single Cell Spatial Transcriptome-seq Kit, 8 tests	K02501-08
SeekOne™ DD Single Cell Multiome Methylation + RNA Kit, 8 tests	K00901-08
SeekOne™ DD Single Cell Multiome ATAC + RNA Kit, 8 tests	K02901-08
SeekOne™ DD Single Cell Full-length RNA Sequence Transcriptome-seq Kit, 8 tests	K00801-08
SeekOne™ DD Single Cell MLPSeq Kit, 8 tests	K03201-08
SeekOne™ DD FFPE Single Cell Transcriptome-seq Kit, 8 tests	K02101-08
SeekOne™ DD Single Cell 5' Transcriptome-seq Kit, 8 tests	K00501-08
SeekOne™ DD Single Cell TCR Enrichment Kit (Human), 8 tests	K00601-08
SeekOne™ DD Single Cell BCR Enrichment Kit (Human), 8 tests	K00701-08
SeekOne™ DD Single Cell TCR Enrichment Kit (Mouse), 8 tests	K01101-08
SeekOne™ DD Single Cell BCR Enrichment Kit (Mouse), 8 tests	K01201-08
SeekOne™ DD Single Cell 3' Transcriptome-seq Kit, 8 tests	K00202-08

Analysis Software
SeekSoul™ Online
SeekSoul™ Tools
SeekArc™ Tools
SeekSpace™ Tools
SeekSoul™ Methyl Tools

Featured Publications

NO.	Title	Journal	Publication Time	Product	DOI
1	Single-cell spatial transcriptomics reveals potential molecular mechanisms of Abelmoschus manihot (L.) medic in treating diabetic kidney disease	*iMeta*	2025 Dec.	scFAST-seq	http://dx.doi.org/10.1002/imt2.70099
2	Single-cell nascent transcription reveals sparse genome usage and plasticity	*Cell*	2025 Nov.	scFAST-seq	https://doi.org/10.1016/j.cell.2025.09.003
3	N6-methyladenosine on L1PA governs the trans-silencing of LTRs and restrains totipotency in naive human embryonic stem cells	*Cell Stem Cell*	2025 Nov.	scFAST-seq	https://doi.org/10.1016/j.stem.2025.10.003
4	DNA replication fork speed acts as a pacer in cortical neurogenesis	*Nature Communications*	2025 Nov.	scFAST-seq	https://doi.org/10.1038/s41467-025-65269-y
5	Targeting AKR1B1 inhibits metabolic reprogramming to reverse systemic therapy resistance in hepatocellular carcinoma	*Signal Transduction and Targeted Therapy*	2025 Aug.	scFAST-seq	https://doi.org/10.1038/s41392-025-02321-9
6	Splicing diversity enhances the molecular classification of pituitary neuroendocrine tumors	*Nature Communications*	2025 Feb.	scFAST-seq	https://doi.org/10.1038/s41467-025-56821-x
7	The landscape of RNA-binding proteins in mammalianspermatogenesis	*Science*	2024 Aug.	scFAST-seq	https://doi.org/10.1126/science.adj8172
8	Programmable macrophage-polarizing nanoparticles for MRI-guided early detection and treatment of pulmonary metastases	*Journal of Nanobiotechnology*	2025 Oct.	SeekSpace Spatial scRNA-seq	https://doi.org/10.1186/s12951-025-03749-5
9	Integrative spatial multiomics analysis reveals regulatory mechanisms of VCAM1+ proximal tubule cells in lupus nephritis	*Annals of the Rheumatic Diseases*	2025 Aug.	SeekSpace Spatial scRNA-seq	https://doi.org/10.1016/j.ard.2025.08.015
10	Myogenic enhancer snatching promotes adipogenic differentiation during epigenetic reprogramming mediated by lineage-specific transcription factors	*Cellular and Molecular Life Sciences*	2025 Nov.	scATAC + RNA-seq	https://doi.org/10.1007/s00018-025-05901-8
11	Predictive factors for neoadjuvant combined immunotherapy in gastric adenocarcinoma: Focusing on the primitive enterocyte phenotype and PVR	*British Journal of Cancer*	2025 May.	FFPE scRNA-seq	https://doi.org/10.1038/s41416-025-03031-3
12	Oxygen/sulfate radicals-generating CaS2 O8 nanosonosensitizers induce PAN‐optosis and calcium overload for enhanced peritoneal metastasis immunotherapy	*Science Bulletin*	2025 Jun.	5' scRNA-seq + V(D)J-seq	https://doi.org/10.1016/j.scib.2025.03.015
13	Epitope-focused vaccine immunogens design using tailored horseshoe-shaped scaffold	*Journal of Nanobiotechnology*	2025 Feb.	5' scRNA-seq + V(D)J-seq	https://doi.org/10.1186/s12951-025-03200-9
14	Blockade of purine metabolism reverses macrophage immunosuppression and enhances anti-tumor immunity in non-small cell lung cancer	*Drug Resistance Updates*	2025 Jan.	5' scRNA-seq + V(D)J-seq	https://doi.org/10.1016/j.drup.2024.101175
15	miR-423-5p-enriched small extracellular vesicles drive periodontal regeneration via Sfrp2+ cell expansion	*Bioactive Materials*	2026 Apr.	3' scRNA-seq	https://doi.org/10.1016/j.bioactmat.2025.11.026
16	Autocrine ECM molecules establish MSC quiescence during incisor development by disrupting WNT ligand trafficking process	*Nature Communications*	2025 Nov.	3' scRNA-seq	https://doi.org/10.1038/s41467-025-65705-z
17	YY1 enhances HIF-1α stability in tumor-associated macrophages to suppress antitumor immunity of prostate cancer in mice	*Nature Communications*	2025 Jul.	3' scRNA-seq	https://doi.org/10.1038/s41467-025-61560-0
18	Dectin-1 facilitates lung fungal-mediated pulmonary fibrosis	*Immunity*	2025 Jul.	3' scRNA-seq	https://doi.org/10.1016/j.immuni.2025.05.007
19	Integrating microbial GWAS and single cell transcriptomics reveals associations between host cell populations and the gut microbiome	*Nature Microbiology*	2025 Apr.	3' scRNA-seq	https://doi.org/10.1038/s41564-025-01978-w
20	Single-cell and spatial RNA sequencing identify divergent microenvironments and progression signatures in early- versus late-onset prostate cancer	*Nature Aging*	2025 Apr.	3' scRNA-seq	https://doi.org/10.1038/s43587-025-00842-0
21	Constitutively active glucagon receptor drives high blood glucose in birds	*Nature*	2025 Mar.	3' scRNA-seq	https://doi.org/10.1038/s41586-025-08811-8
22	Nociceptor neurons promote PDAC progression and cancer pain by interaction with cancer-associated fibroblasts and suppression of natural killer cells	*Cell Research*	2025 Mar.	3' scRNA-seq	https://doi.org/10.1038/s41422-025-01098-4
23	Single-cell transcriptomics reveals novel chondrocyte and osteoblast subtypes and their role in knee osteoarthritis pathogenesis	*Signal Transduction and Targeted Therapy*	2025 Feb.	3' scRNA-seq	https://doi.org/10.1038/s41392-025-02136-8