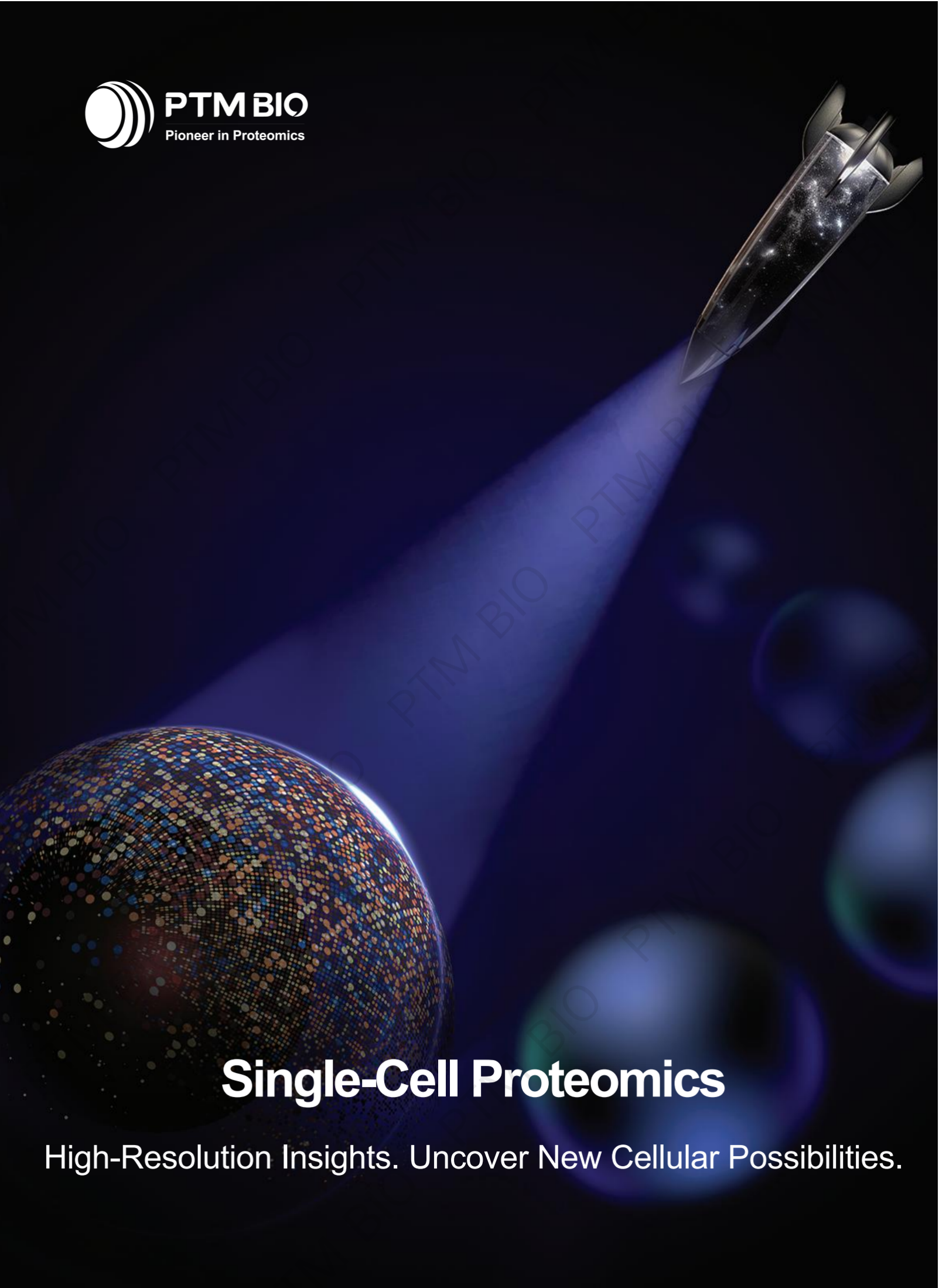


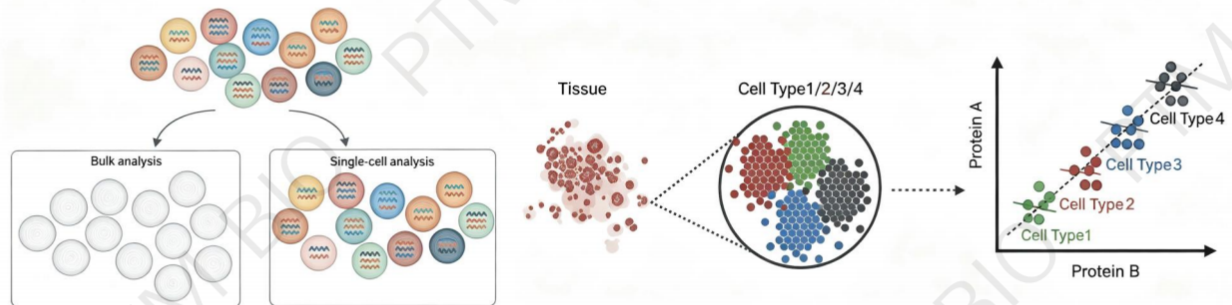


Single-Cell Proteomics

High-Resolution Insights. Uncover New Cellular Possibilities.

Single-Cell Proteomics

A Powerful Tool for High-Resolution Dissection of Biological Mechanisms



nature

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Single-cell proteomics takes centre stage

nature methods

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Focus | 10 March 2023

Focus on single-cell proteomics

nature methods

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Year in review 2023

[nature methods](#) 21, 1–2 (2024) | [Cell article](#)

Single-cell proteomics is also a rapidly growing field. In case you missed it, we recommend you check out our [Focus on single-cell proteomics](#), which includes a number of pieces, both technical and opinion-driven, regarding the current state of the field and what may be in store for the future. This Focus included a standout news piece¹ covering this fast-moving area of

Emerging at the Research Frontier

A 10-Article Special Feature in Nature Methods

Rapidly Gaining Attention Across the Research Community

Single-Cell Proteomics: From an Emerging Frontier to a Rapidly Growing Research Focus

An Integrated Single-Cell Proteomics Workflow

An Innovative Solution for Single-Cell Proteomics

Four Cutting-Edge Platforms Powering a New Level of Performance

•Cell Sorting Platform:

An industry-leading, fully integrated automated sorting workflow designed for gentle sample handling.

•Sample Preparation Platform:

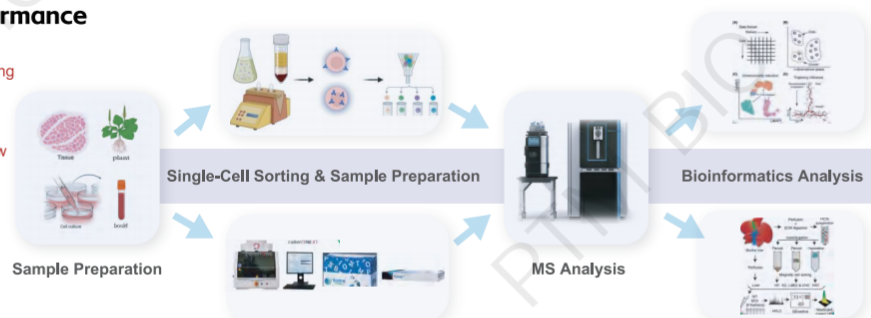
A proprietary single-cell sample preparation workflow developed by PTM BIO for streamlined and efficient processing.

•Mass Spectrometry Platform:

A high-performance proteomics platform for ultra-sensitive protein detection.

•Bioinformatics Platform:

A purpose-built single-cell bioinformatics platform developed by PTM BIO to enable deeper biological insights.



Research Areas

Tumor heterogeneity, cell differentiation, reproductive development, immune regulation, plant heterogeneity, stress responses, and more

Single-Cell Multi-Omics Profiling

Single-Cell Transcriptomics
↕
Single-Cell Proteomics

Integrated Data Analysis

Construct cellular atlases, identify distinct cell types, and characterize changes in cell-type composition and abundance
Integrate cell-type information with protein expression data

Biological Validation

Molecular validation at the RNA and protein levels

Four Integrated Platforms. Deeper Insights into the Single-Cell Proteomic Landscape.



Quality Assurance

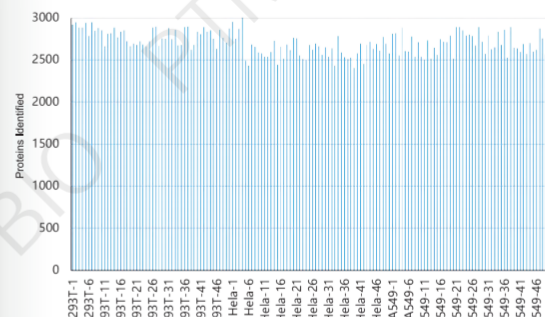
High-Quality Proteomics Data

Deep Proteome Coverage

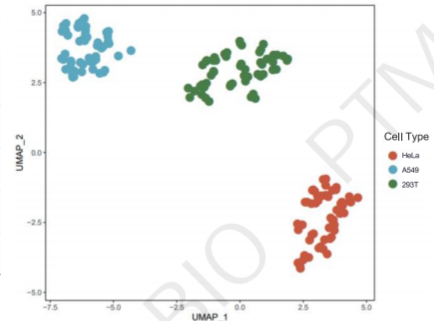
Robust Performance

High Reproducibility

Clear Cell-Type Separation



150 single cells analyzed. Mean proteins identified per cell: 2,728; cumulative proteins identified: 3,600.



Clear separation of distinct cell types

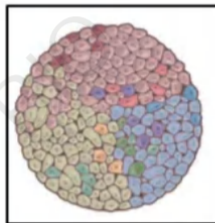
Research Applications

Broad Applications for Precise Biological Insights

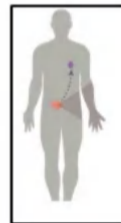
Single-cell proteomics provides foundational, high-resolution molecular information for investigating cellular heterogeneity, constructing detailed proteomic maps, and characterizing protein networks across cell populations. It plays an essential role in diverse research areas, including tumor heterogeneity, cell differentiation, cell-cycle regulation, reproductive development, neurodevelopment, and immune regulation. PTM BIO supports eight key application areas:



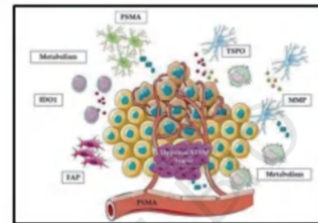
High-Resolution Tissue and Organ Proteomic Atlases



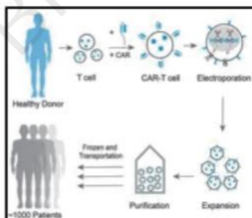
Tumor Heterogeneity and Drug Resistance



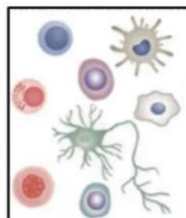
Circulating Tumor Cell (CTC) Analysis



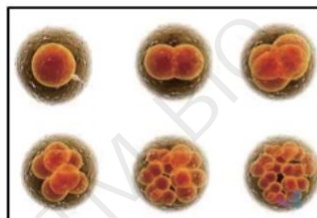
Immunology and Immuno-Oncology



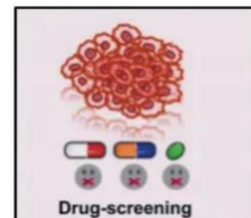
Cell Therapy Characterization



Neuroscience Research



Reproductive Biology Research



High-Throughput Drug Screening

Representative Studies

Single-Cell Proteomics Reveals Early Differentiation Mechanisms in Human HSPCs

Mapping early human blood cell differentiation using single-cell proteomics and transcriptomics

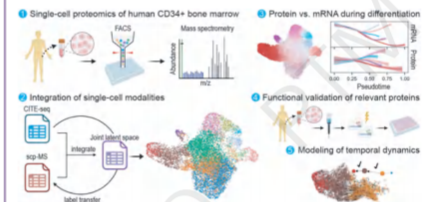
Science

Study Objective: To characterize differentiation mechanisms in the human hematopoietic system using single-cell proteomics.

Samples: HSPCs isolated from the bone marrow of six healthy donors.

Key Findings:

- (1) 2,506 HSPCs analyzed, with >2,900 proteins identified, establishing the first large-scale single-cell proteomic atlas of human HSPCs.
- (2) Integrated proteomic and transcriptomic data improved prediction of cell differentiation trajectories.
- (3) Low protein–mRNA correlation in HSCs highlighted unique protein-level regulatory information captured by single-cell proteomics.
- (4) The scProtVelo model was developed to infer differentiation direction from translational dynamics.



Single-Cell Proteomics Resolves Lineage Specification During Early Mouse Embryogenesis

Deciphering lineage specification during early embryogenesis in mouse gastruloids using multilayered proteomics

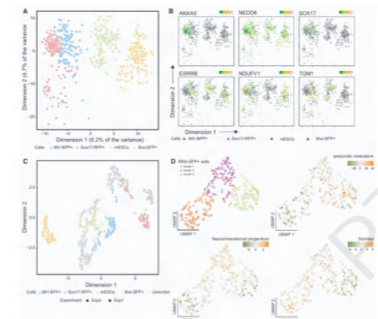
Cell
Stem Cell

Study Objective: Single-cell proteomics analyses enable the characterization of lineage-specific transcriptional programs during early mammalian embryonic development.

Samples: mESC-derived gastruloids containing SOX17-RFP+ endodermal, BRA-GFP+ mesodermal, MT1-BFP+ ectodermal, and undifferentiated cells.

Key Findings:

- (1) 560 cells quantified, with an average of 1,541 proteins per cell and 675 significantly differentially abundant proteins.
- (2) Analysis of 363 BRA-GFP+ cells identified three subpopulations corresponding to NMPs, somites, and presomitic mesoderm.



Single-Cell Proteomics Uncovers Molecular Mechanisms Underlying Oocyte Aging

Multi-omics analysis reveals translational landscapes and regulations in mouse and human oocyte aging

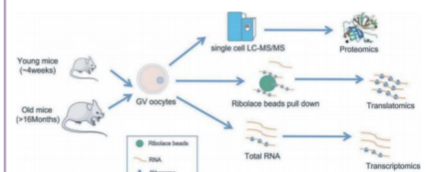
Advanced
Science

Study Objective: To investigate mechanisms underlying age-related declines in oocyte quality and developmental competence.

Samples: GV-stage oocytes from 4-week-old and 16-month-old female mice.

Key Findings:

- (1) Approximately 1,200 proteins were identified per oocyte.
- (2) Translatomic changes showed greater concordance with proteomic changes than transcriptomic changes in aged oocytes.
- (3) Translational dysregulation was associated with progesterone-mediated oocyte maturation, homologous recombination, and oocyte meiosis.



Selected Publications Supported by PTM BIO Services

Title	Journal
Metabolic regulation of gene expression by histone lactylation	<i>Nature</i> (IF=48.5)
Disordered methionine metabolism in MTAP/CDKN2A-deleted cancers leads to dependence on PRMT5	<i>Science</i> (IF=45.8)
Single-cell chromatin modification profiling reveals increased epigenetic variations with aging	<i>Cell</i> (IF=42.5)
Global profiling of O-GlcNAcylated and/or phosphorylated proteins in hepatoblastoma	<i>Signal Transduction and Targeted Therapy</i> (IF=52.7)
TRIM31 facilitates K27-linked polyubiquitination of SYK to regulate antifungal immunity	<i>Signal Transduction and Targeted Therapy</i> (IF=52.7)
VAV2 is required for DNA repair and implicated in cancer radiotherapy resistance	<i>Signal Transduction and Targeted Therapy</i> (IF=52.7)
Phosphoproteomics reveals therapeutic targets of esophageal squamous cell carcinoma	<i>Signal Transduction and Targeted Therapy</i> (IF=52.7)
Direct phosphorylation and stabilization of MYC by Aurora B kinase promote T-cell leukemogenesis	<i>Cancer Cell</i> (IF=44.5)
Increased glucose metabolism in TAMs fuels O-GlcNAcylation of lysosomal Cathepsin B to promote cancer metastasis and chemoresistance	<i>Cancer Cell</i> (IF=44.5)
Acquired semi-squamatization during chemotherapy suggests differentiation as a therapeutic strategy for bladder cancer	<i>Cancer Cell</i> (IF=44.5)
Short-chain enoyl-CoA hydratase mediates histone crotonylation and contributes to cardiac homeostasis	<i>Cell Research</i> (IF=25.9)
Landscape of the regulatory elements for lysine 2-hydroxyisobutyrylation pathway	<i>Cell Research</i> (IF=25.9)
Global profiling of crotonylation on non-histone proteins	<i>Cell Research</i> (IF=25.9)
Lysine 2-hydroxyisobutyrylation of NAT10 promotes cancer metastasis in an ac4C-dependent manner	<i>Circulation</i> (IF=38.6)



Email: service@ptm-biolab.com

Tel: +86 400-100-1145

Website: <https://ptmbio.com>

PTM BIO Co., Inc