

Special Issue on Women in Proteomics

Lan Huang, Anne-Claude Gavin, and Jyoti S. Choudhary

Co-Editors for the Special Issue on Women in Proteomics:

Drs Lan Huang, Anne-Claude Gavin, and Jyoti Choudhary

This special issue celebrates the achievements and leadership of women in proteomics, highlighting their scientific excellence, innovation, and impact on the field. It features cutting-edge advances in proteomic technologies, including single-cell platforms, enrichment strategies, proteogenomics, and evolving methods for protein extraction, labeling, and molecular annotation. The issue also highlights multiomics and data-driven frameworks that help decode disease mechanisms, uncover diagnostic and/or therapeutic targets, and strengthen standards for proteome research. Together, these studies provide new insights into post-translational regulation, signaling networks, and cellular responses across diverse biological contexts, from cancer and infection to tissue microenvironments.

Featured Contributors to This Special Issue:

Keriann Backus (University of California, Los Angeles [UCLA], USA)

Dr Keriann Backus is an Associate Professor of Biological Chemistry and Chemistry & Biochemistry at UCLA and a leading innovator in quantitative chemoproteomics. She pioneered proteome-wide small-molecule screening strategies that have revealed ligands for traditionally “undruggable” classes of proteins like transcription factors. In this issue, her group contributes CySP3-96, a scalable, streamlined, and cost-effective sample-preparation platform for highly reproducible chemoproteomics studies.

Yu-Ju Chen (Academia Sinica, Taiwan)

Dr Yu-Ju Chen, Distinguished Research Fellow at Academia Sinica, pioneers ultrasensitive proteomics and post-translational modification omics to decode disease and enable translation. Her team integrated microfluidics into single-cell proteomics and reported the first single-cell phosphoproteomic landscape to advance therapy. She launched the Taiwan Cancer Moonshot to elucidate the pathogenesis of East Asian nonsmoking lung adenocarcinoma. Her group also developed a mass spectrometry (MS)-based assay to detect serum protein variants for early gastric cancer detection. In this issue, she describes a metal ion-enhanced zwitterionic hydrophilic interaction liquid chromatography StageTip strategy for concurrent N-glycoproteomic and phosphoproteomic profiling.

Ileana Cristea (Princeton University, USA)

Dr Ileana Cristea, the Henry L. Hillman Professor of Molecular Biology at Princeton University, is a pioneering leader

in integrating cutting-edge proteomics with virology to elucidate host defense mechanisms against human viruses. Her laboratory has contributed to the emergence of the research field of nuclear viral DNA sensing in immune response, to uncovering organelle remodeling and new organelle structure contacts during infections, to discovering antiviral factors for therapeutic interventions, and to characterizing a virus microenvironment. In this issue, she presents a review on proteomic characterization of intercellular communication in viruses.

Meng-Qiu Dong (National Institute of Biological Sciences, Beijing, China)

Dr Meng-Qiu Dong is a leading developer of MS tools for structural and functional proteomics. Trained with John R. Yates III at The Scripps Research Institute, she has led her lab at the National Institute of Biological Sciences laboratory since 2007. Working with collaborators, her lab has developed tools to advance cross-linking MS, including the pLink search engine and novel cross-linkers. In this issue, she contributes a global analysis of protein and small-molecule substrates of ubiquitin-like proteins.

Ying Ge (University of Wisconsin-Madison, USA)

Dr Ying Ge, Professor of Cell and Regenerative Biology and Chemistry at the University of Wisconsin-Madison, has made seminal contributions to top-down proteomics, enabling comprehensive analysis of proteoforms. Her group developed multiple novel technologies to advance top-down proteomics, including a photocleavable surfactant, chromatographic methods, nanomaterial-based enrichment strategies, and a versatile MASH software package. Her technologies have been well integrated with cardiac biology to understand heart disease and regeneration. In this issue, her group contributes a single-step protein extraction platform for lung extracellular matrix proteomics.

Tamar (Tami) Geiger (Weizmann Institute of Science, Israel)

Dr Tami Geiger is a Professor at the Department of Molecular Cell Biology, Weizmann Institute of Science. She conducts clinical proteomic research on breast cancer, melanoma, ovarian cancer, and colorectal cancer, emphasizing tumor-immune interactions, metabolic reprogramming, and integration with imaging technologies. In addition, she develops single-cell and spatial proteomic technologies. In this issue, she contributes an automated, high-throughput single-cell proteomics pipeline to enable deep, scalable profiling of tumor-associated macrophages.

Concha Gil (Complutense University of Madrid, Spain)

Dr Concha Gil is Professor of Microbiology and Director of the Proteomics Unit at Complutense University, Madrid, leading research on host–pathogen interactions and meta-proteomics of the human microbiota. She has extensive expertise in yeasts, particularly *Candida albicans*. Her current work focuses on the *C. albicans*–host interaction and on developing new strategies for diagnosing infectious diseases, using invasive candidiasis as a model. In this issue, she contributes a review on omics and multiomics-based diagnostics for invasive candidiasis.

Sandra Goetze (ETH Zurich, Switzerland)

Since 2014, Dr Sandra Goetze has conducted proteomics research at ETH Zurich, contributing to the development of MS-based methods for clinical and translational applications. In 2021, she became Chief Scientific Officer of the Clinical Proteotype Analysis Center and Coordinator of the Swiss Multi-Omics Center at ETH Zurich, providing strategic direction and scientific expertise to advance integrative multiomics research aimed at improving disease understanding, diagnosis, and treatment. In this issue, she presents a multiomics data analysis workflow for elucidating disease mechanisms in methylmalonic aciduria.

Lingjun Li (University of Wisconsin-Madison, USA)

Dr Lingjun Li is Vilas Distinguished Achievement Professor and Charles Melbourne Johnson Distinguished Chair in Pharmaceutical Sciences and Chemistry at the University of Wisconsin-Madison. She has pioneered innovative MS imaging and spatial omics technologies, including high-throughput single-cell MS imaging and tissue expansion MS imaging. Her innovations in isobaric chemical tagging (DiLeu, SUGAR, DeAla tags) have significantly advanced quantitative omics. Dr Li's contributions span neuro-peptidomics, glycoproteomics, lipidomics, and the development of the first citrullinome atlas. Here, she presents a proteome-wide investigation of proline hydroxylation in pancreatic ductal adenocarcinoma using the DiLeu labeling strategy.

Kathryn Lilley (University of Cambridge, UK)

Dr Kathryn Lilley is a Professor at the University of Cambridge and a world leader in subcellular omics. Her group has pioneered methods to study the dynamic subcellular locations of transcripts and proteins on a cell-wide scale, applicable to any sample. These methods supported by robust open-source informatics tools, have revealed cellular mechanisms overlooked by traditional proteomics workflows based on abundance changes. Recently, her lab has developed unbiased strategies to define the RNA-binding proteome, uncovering many noncanonical RNA-binding proteins. Her team reports here the global proteomics evidence for subcellular-specific antiferroptotic responses to ionizing radiation.

Sandra Orchard (European Molecular Biology Laboratory, European Bioinformatics Institute [EMBL-EBI], Germany)

Dr Sandra Orchard leads the Protein Function Content team at EMBL-EBI, with a strong background in protein annotation, particularly in molecular interactions, protein complexes, and protein kinases. Her team is responsible for the curation of UniProt and the Gene Ontology and also contributes to the IntAct molecular interaction database and the Complex Portal. She is active in multiple data standardization efforts, including the HUPO Proteomics Standards Initiative. Here, she reviews the broad impact of HUPO-PSI data standards on advancing proteomics tools, resources, and community practice.

Evangelia Petsalaki (European Molecular Biology Laboratory, European Bioinformatics Institute [EMBL-EBI], Germany)

Dr Evangelia Petsalaki, a group leader at EMBL-EBI, is a computational biologist. She has developed integrative tools, such as SELPHI (presented in this issue), PhosX, and phuEGO, to extract active signaling networks and infer kinase activities directly from phosphoproteomics data. By combining quantitative (phospho)proteomics with network-based inference, her research has uncovered mechanisms of drug resistance, immune regulation, and biomarkers for metabolic disease. She presents a data-driven approach for extracting human kinase–substrate relationships from multiomics datasets.

Tess Branon (Genentech, USA) and Namrata Udeshi (Broad Institute, USA)

Drs Tess Branon and Namrata Udeshi have made significant contributions to proximity labeling-based interactomics. Branon co-developed transformative proximity labeling technologies, including TurboID, during her training with Professor Alice Ting, enabling rapid, precise, and minimally disruptive mapping of protein interaction networks directly in living systems. As a principal scientist and interactomics group lead at Genentech, Branon continues to advance interactomic technologies to drive drug discovery and therapeutic research. Udeshi is Director of Research and Development in the Proteomics Platform at the Broad Institute of MIT and Harvard and has spent over two decades developing MS-based methods to study proteins including analysis of spatial proteomes, protein interactions, ubiquitination and beyond to understand cellular systems. Together, Branon and Udeshi co-senior authored this perspective on the scientific and collaborative forces driving the evolution of proximity labeling.

Hui Zhang (Johns Hopkins University, USA)

Dr Hui Zhang is a Professor at Johns Hopkins University and a leading expert in proteomics with seminal contributions to glycoproteomics and proteogenomics. She pioneered

foundational glycoproteomic technologies that enabled quantitative, site-specific characterization of glycosylation and helped establish glycoproteomics as a major branch of proteomic science. Her group has also driven large-scale proteogenomic studies across multiple cancer types to understand disease biology. In this issue, she presents a single-cell proteomic analysis of drug-resistant prostate cancer cells, uncovering molecular signatures linked to morphological changes.

Lihua Zhang (Dalian Institute of Chemical Physics, Chinese Academy of Sciences, China)

Dr Lihua Zhang is a Professor at Dalian Institute of Chemical Physics. Her work has significantly advanced the analytical aspects of proteomics. She has developed sample preparation methods to improve proteome analysis, including new materials to improve peptide and protein separation, and novel cross-linkers and *in vivo* cross-linking MS methods to decipher protein conformation and interactions on a large scale. In this issue, she introduces a negative-enrichment strategy for

profiling protein methylation by leveraging the complementary specificities of LysargiNase and trypsin.

Qian Zhao (The Hong Kong Polytechnic University, China)

Dr Qian Zhao is an Associate Professor at the Hong Kong Polytechnic University. She develops innovative technologies in chemical proteomics and peptidomics, establishing advanced platforms and synthetic probes to map drug targets, discover therapeutic candidates, and decode nascent proteomes. Her team has created workflows for MS-based discovery of microproteins, leading to the identification of thousands of previously unannotated species, and has introduced new methods for uncovering noncanonical immunopeptides. In this issue, she reveals novel small ORFs and functional microproteins in activated T cells.

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