Qian Zhao

CMI-P-32

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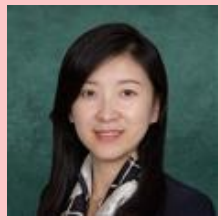

Research Keywords

Proteomics, Natural novel peptides, Mass spectrometry

Academic Career

B.S., 2007, Xi'an Jiaotong University; Ph.D.,2012, The University of Hong Kong(advisor: Dan Yang); Investigator, 2013-2014, Novartis Institutes for Biomedical Research; Postdoctoral Training, 2014-2016, University of California, San Francisco (advisor: Jack Taunton and Alma Burlingame); Research Assistant Professor, 2016-2017, Hong Kong Baptist University; Assistant Professor, 2017-2023, The Hong Kong Polytechnical University; Associate Professor, 2023-present, The Hong Kong Polytechnical University

Selected Publications

Proteogenomic Profiling Reveals Small ORFs and Functional Microproteins in Activated T Cells. Zhao. Q., et al. Mol. Cell. Proteomics. 2025 Jun;24(6):100914.

Enhanced Discovery of Alternative Proteins (AltProts) in Mouse Cardiac Development Using Data-Independent Acquisition (DIA) Proteomics. Anal. Chem. 2025, 97, 3, 1517–1527

An integrated approach for discovering non-canonical MHC-I peptides encoded by small open reading frames. Zhao. Q., et al. J Am Soc Mass Spectrom. 2021;32(9):2346-2357.

Imaging-Based High-Content Screening with Clickable Probes Identifies XPB Inhibitors. Zhao. Q., et al. Angew. Chem. 2025, e202505585.

Multiplexed Target Profiling with Integrated Chemical Genomics and Chemical Proteomics. Zhao. Q., et al. J. Med. Chem.,2024, 67(19), 17542-17550.

An optimized proteomics approach reveals novel alternative proteins in mouse liver development. Zhao. Q., et al. Mol. Cell. Proteomics.2022, 22(1), 100480.

Integrated Mass Spectrometry Reveals Celastrol as a Novel Catechol-O-methyltransferase Inhibitor. Zhao. Q., et al. ACS Chem Bio., 2022, 17(8), 2003-2009.

Why My Lab?

My lab can offer...

Our lab specializes in protein mass spectrometry analysis, ribosome sequencing and translation mapping, the construction of classical and non-classical immunopeptide databases with mass spectrometry identification, as well as the study of functional peptides encoded by small open reading frames (sORFs), assessing their biological significance. The lab is equipped with advanced instruments and an integrated mass spectrometry platform, including ultra-high resolution mass spectrometry (Thermo Scientific Orbitrap Fusion Lumos Mass Spectrometer), non-denaturing ion mobility-quadrupole time-of-flight mass spectrometry system (Synapt G2

HDMS), triple quadrupole mass spectrometry system (Xevo TQD), and matrix-assisted laser desorption ionization time-of-flight mass spectrometer (Autoflex speed), along with a well-established biochemical platform and data analysis platform.