

## Cancer study leverages proteomics profiling to drive precision medicine advancements

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**A study spans 11 cancer research laboratories from across the world, including six Cancer Moonshot initiative facilities, and has been co-led by experts from the Inova Health System (VA, USA), ETH Zurich (Switzerland) and Thermo Fisher Scientific (CA, USA)**



In line with its commitment to delivering the promise of proteomics to improve human health, Thermo Fisher Scientific has participated in an international collaborative cancer study indicating that harmonized mass spectrometry platforms, in conjunction with standardized data acquisition procedures, optimize multi-center proteotype analyses to drive advancements in precision medicine.

Published last Friday in [Nature Communications](#), the groundbreaking study spans 11 cancer research laboratories from across the world, including six Cancer Moonshot initiative facilities, and has been co-led by experts from the Inova Health System (VA, USA), ETH Zurich (Switzerland) and Thermo Fisher Scientific (CA, USA). Importantly, the study has demonstrated the capability of Thermo Fisher's patented high resolution MS1-based quantitation data-independent acquisition (HRMS1-DIA) workflow to facilitate high throughput, and improved inter- and intra-laboratory reproducibility when run in a 24/7 operation mode.

"Bringing together scientists from across the globe in this grass-roots effort has denoted the ability to harmonize high-throughput quantitative proteomics at new depths with exquisite analytical rigor, including in minute quantities of tissue derived from laser microdissected formalin-fixed, paraffin-embedded archival cancer specimens," said Dr. Thomas Conrads, Senior Director of Women's Health Research in the Women's Service Line of Inova Health System and the affiliated Women's Health Integrated Research Center at Inova Health System. "This opens up the opportunity to conduct highly distributed, international cancer cohort studies rivaling genomics capabilities."

Designed for use with the Thermo Scientific Orbitrap mass spectrometers, the HRMS1-DIA workflow creates the potential to leverage proteomics profiling as a guiding tool, paving the way for the distributed multi-omic digitization of large clinical

specimen cohorts across multiple sites, as a prerequisite for turning molecular precision medicine into reality.

Thermo Fisher Scientific's presenting virtual seminar session at HUPO Connect 2020 from 19-22 October, on "Accelerating COVID Proteomics Research Using Tandem Mass Tags (TMT)". The session provided insight on 'Providing COVID-19 Clarity Using TMT Reagents for Precision Measurements' and 'TMT-Based Comparative Interactomics of SARS-CoV-2 and Coronavirus Non-Structural Protein Homologs to Identify Shared and Unique Host-Cell Dependencies'.

To join the conference; [HUPO Connect 2020](#)-ThermoFisher Presentation