Message from the Chair

Dear Proteomics and Metabolomics Division member,

With the 2017 AACC annual meeting fast approaching, I am excited to share information about the Division-sponsored events taking place at the annual meeting as well as numerous other events featuring proteomics and metabolomics.

This year, our annual Division luncheon will be replaced by the **Mass Spectacular** event (details below). This will be a dinner and networking event on August 1st starting at 7 pm. This is shaping up to be an amazing night and something you won't want to miss!

Proteomics and metabolomics is increadibly well represented in this year's annual meeting program; several events are highlighted below and there are many more great workshops, brown bags and symposium to be found in the program.

At this time, I would like to acknowledge new (and returning) members of our **division leadership**: Drs Danni Li (secretary), Alex Rai (treasurer), Zahra Shajani Yi (member at large) and Ashley Beasley Green (awards chair). On behalf of the entire division, I would also like to thank all of our outgoing leadership including members of the executive: Dr. Michael Bennett (past-president and current AACC president) and Dr. Jerry Yeo (treasurer). We greatly appreciate your service to the Division!

Sincerely,

Mari DeMarco, PhD DABCC FACB
Chair, Proteomics and Metabolomics Division

Proteomics & Metabolomics at the 2017 Annual Meeting

Division-Sponsored Events & Symposia

Mass Spectacular
Date/Time: Tuesday, August 1, 7–11 p.m.
Location: Marriott Marquis San Diego Marina

Sponsored by the Proteomics and Metabolomics Division & MS[3] Division

Members of the Proteomics and Metabolomics Division are invited to this awards ceremony, dinner, and celebration. This special event will take the place of our usual division luncheon. The night will include an update on our division, upcoming elections and awards ceremony. MS[3] Division poster abstracts and contributions will also be presented. The evening will conclude with live music, networking, and a raffle.

Registration is only $10 for both AACC members and non-members and includes dinner, a drink and a raffle ticket. To register go to the **online registration** and select "Add Sessions" and search for "Mass Spectacular"

Symposium

Tuesday, August 1, 2:30-5:00 PM

33212 MALDI-TOF Mass Spectrometry: Not Just for Clinical Microbiology Labs Anymore

This session will provide an introduction to MALDI-TOF mass spectrometry applications in clinical chemistry laboratories. This session uses an interactive approach to discuss the application of MALDI-TOF MS, combined with emerging technologies, for qualitative and quantitative investigation of biomarkers (peptides, proteins, DNA) and drugs of abuse.

Even More Proteomics and Metabolomics at the Annual Meeting!

Brown Bags

Tuesday, August 1, 7:30-8:30am/12:30-1:30pm

43102/53202 MALDI-TOF Mass Spectrometry and Its Applications in Laboratory Medicine

Symposia

Monday, July 31, 2:30-4:00pm

32222 Invited Oral Abstracts: Emerging Technologies

Wednesday, August 2, 10:30-12:00pm

75102 Introduction to Translational and Clinical Metabolomics for Personalized Medicine

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Research Highlights

2017 Division Abstract Award – Winner

Claire Knezevic, PhD

Development of Multiplexed Mass Spectrometry-based Assays for Urine Biomarkers of Aggressive Prostate Cancer

This year's Proteomics and Metabolomics Division abstract award goes to Dr. Claire Knezevic, PhD, Clinical Chemistry Fellow at Johns Hopkins School of Medicine, for her abstract: "Development of Multiplexed Mass Spectrometry-based Assays for Urine Biomarkers of Aggressive Prostate Cancer." Meet Dr. Knezevic and learn more about her research by attending her poster session on Wednesday August 2nd from 12:30-1:30 PDT pm at the 69TH AACC Annual Scientific Meeting & Clinical Lab Expo in the Sails Pavilion of the San Diego Convention Center.
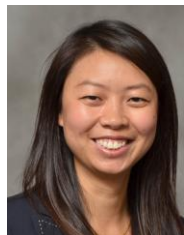
2016 Division Abstract Award – Winner

Ventzi Hristova, PhD

Biomarker Discovery by Proteomic Analysis of Ubiquitin Modification in Ovarian Cancer Cells

Cancer biomarker discovery has primarily focused on mutations at the nucleotide level that translate into abnormal protein conformation and function. However, the impact of impaired protein post-translational modifications (PTMs) on cell signaling and the utility of PTMs as disease markers are receiving increased attention. One such type of PTM, ubiquitination, occurs through a complex series of enzymatic steps that lead to addition of a single ubiquitin molecule or a poly-ubiquitin chain. The complexity of ubiquitination has limited the current understanding of how impaired ubiquitin PTM relates to cancer. In an effort to discover potential cancer biomarkers by assessing

ubiquitin PTM, Dr. Hristova focused her study on an ovarian cancer model and the identification of substrates that are covalently modified with either mono or poly-ubiquitin. Proteomic analysis by SILAC LC-MS/MS was used to characterize the ubiquitinome of SKOV-3 ovarian cancer cells and distinguish substrates modified for degradation vs. non-degradation signaling. In turn, the global ubiquitination pattern and specific ubiquitin PTM sites was used to identify oncoproteins with altered ubiquitin modification in their cancer model that represent potential disease biomarkers.

2016 Division Abstract Award – Honorable Mention

Danni Li, PhD DABCC

Molecular identity of prognostic biomarkers for Alzheimer's disease revealed

Alzheimer's disease is the leading cause of dementia in the elderly. In the letter published by Mapstone et al. in Nature Medicine, it was reported that a panel of plasma phospholipids that predicted cognitively normal adults who later progressed to either mild cognitive impairment or dementia due to Alzheimer's disease. However, a triple quadruple mass spectrometer was used, which generally lacks the mass accuracy and resolution needed to distinguish fatty acid moieties of phospholipids. The objective of Dr. Li's study was to determine fatty acid molecular components of 7 predictive phospholipids using a high-resolution accurate mass liquid chromatography tandem mass spectrometry (LC-MS/MS). The team used a plasma pool made from participants with normal cognition, mild cognitive impairment, and dementia and characterized the pool using a high resolution mass spectrometer. MS and MS/MS data were obtained at 120,000 and 30,000 mass resolving power, respectively. In the analysis, the fatty acid moiety of these predictive phospholipids was identified, enabling development of quantitative methods to measure these putative prognostic biomarkers in Alzheimer's disease.

Register for the Mass Spectacular event at the annual meeting to learn about the latest activities in the division, opportunities to become more involved with the division, upcoming division leadership elections and our 2017 award winners.