Mobley CV Highlights:

Excellence in research and service are the primary focuses

Excellence in Service: Mass Spectrometry Proteomics Shared Facility (MSP-SF)

Chronologic development

2006 – Developed a cutting-edge clinical proteomics facility *"de-novo"* with focus on prostate cancer biomarker discovery using cutting-edge multi-dimensional protein identification technologies (MudPIT), with high-level informatics tools including 7-high speed servers and overseen by a full time IT staff member recruited from Vanderbilt.

2007 – Initiated the first Comprehensive Cancer Center (CCC), Clinical Proteomics Shared Facility

2009 – Expanded Facility to a single campus wide mass spectrometry/ proteomics Shared Facility (MSP-SF).

Current overview

The current facility is extremely well equipped, and well-funded (bringing in > $600K direct costs/ annually), with focus on clinical-based discovery projects driven by various high-end informatics applications.

High-end MS and informatics tools acquired in part through collaborations; LTQ Velos Pro Orbitrap (Thermo), NanoHPLC stack (Agilent), Mass Hunter (Agilent) Refiner MS (Genedata), ProteoIQ (Dr.'s Ron Orlando and James Attwood; now owned by Premier Biosoft), and Metacore (in collaboration with Genego) – all used in our daily workflow to carry out data pre-processing, statistics, and systems biology that make the facility highly successful and competitive.

Basic Metrics; We analyze over 4000 samples annually, we have served over 200 PI's, and my group has worked collaboratively with dozens of investigators to support projects that include targeted and global proteomics, through funded mechanisms that include PPG's, UO1's, Centers, RO1's, and the UAB Pancreatic SPORE that together represent nearly $100 million in total funding. In addition, we currently support ~50 grant submissions annually, by generating pilot data, incorporating methods, consulting on experimental design, generating letters of support, and generating grant specific NIH biosketches.

Technology overview: we regularly analyze biological specimens using any number of quantification approaches, including; label-free, metabolic labels using stable isotope labeling of amino acids in cell culture (SILAC) or in mice (SILAM – we now offer control 15N specimens to all UAB faculty), or alternatively labeled with isobaric tags using iTRAQ (isotope tagged for relative and absolute quantification) or TMT (tandem mass tag) technologies. Of note, we also offer analysis of flash frozen (FF) and formalin fixed paraffin embedded specimens (FFPE), and our workflow includes targeted AQUA technologies and global PTM quantification.
Excellence in Research:

Research Interest(s)

My group's current focus include: 1) the identification of tissue specific and clinically relevant markers of prostate, breast, and pancreatic cancer by way of in-depth proteomics analysis of human biological fluids, tissue specimens, and exosomes, 2) the development of pathway specific stable isotope putative peptide library's derived empirically from prostate and pancreatic cancer related studies in mice and humans, 3) the use of high-level informatics to combine various –omics datasets for use in translational studies of diseases. In this context, my laboratory is currently studying genomic and proteomic datasets generated from both genetically engineered mice and human patients presenting with early stage vs. late stage disease. All of this work required a great deal of methods refinement and development.

Academic Positions, Associations, & Responsibilities

I am the Director of the UAB MSP-SF. I have held eight academic positions over the last fifteen years at University of Massachusetts Medical School, Vanderbilt University, and UAB. I currently hold five academic positions that include the Structural Biology Theme. I am an active member of eight Centers at UAB. I have held professional consultant positions for two companies, and have served on eight academic committees (external and internal). I have been a thesis committee member for six graduate students. I have been an ad hoc reviewer on numerous occasions for 18 separate journals, and I'm an associate editor for two journals.

Research Presentations & Publications with Metrics

I have been an invited speaker 39 times; at local functions (UAB, Southern Research, & Hudson Alpha) 21 times, with 13 invited presentations at national events, and five invited presentations at international sites. I have over 25 published abstracts (national & regional meetings), have published 55 peer reviewed manuscripts with one additional currently in review, and another five ready to submit within the next month. Of these manuscripts, 36 have been sited >10 times, with 2034 citations within those 36, and I have 14 manuscripts with >50 citations each. My I10-index score is 36, and my H-index score is presently 41. A number of these manuscripts have been published with high to medium impact factor levels including [Journal name & (I.F.)]; Cancer Cell (27), PNAS (10), Mol Cell Prot (9), Hum Mol Gen (7), Mol Cell Biol, (6), Mol Ther (6), J Immunol (6), JBC (5), J Lipid Res (5), J Prot Res (5), J Bio Chem (5), Plos One (4), Proteomics (4), J Mol Bio (4).

Research Funding

I have been awarded funds through nearly two dozen grants since arriving at UAB in 2006, including three training fellowships (not listed on CV). Currently, I am funded on five active NIH grants that cover my salary by over 90 percent (~95% currently), with additional coverage to 99 percent to be compensated by my MSP-SF chargeback account. I have four grants that are in review, three of which I am Co-I, and one where I am Co-PI.

Excellence in Teaching:

I have been mentor and/or co-mentor to 31 people; high school students, undergraduates, residents, medical students, graduate students, postdoctoral fellows, staff, Clinical Fellows, a Research Instructor, and an Assistant Professor.

I have presented a campus wide “Lunch and Learn” series with focus on proteomics applications, and have taught a number of *ad hoc classes in Mass Spectrometry*, Toxico-Proteomics, Clinical Proteomics, and Computational Biology. I teach monthly open-door sessions in my laboratory on experimental laboratory techniques.

I have provided short courses, tutorials, and seminars to investigators throughout the UAB community to forward basic information regarding proteomics applications, and to describe the services, methodologies and technologies available within the MSP-SF.

Ad-hoc instrument and software training sessions are given, and is intended to familiarize users who are new to mass spectrometry, and to provide cross-training for Facility staff.

I’m currently planning a translational/ clinical proteomics and informatics course that I have organized from the above interactions over the past few years.