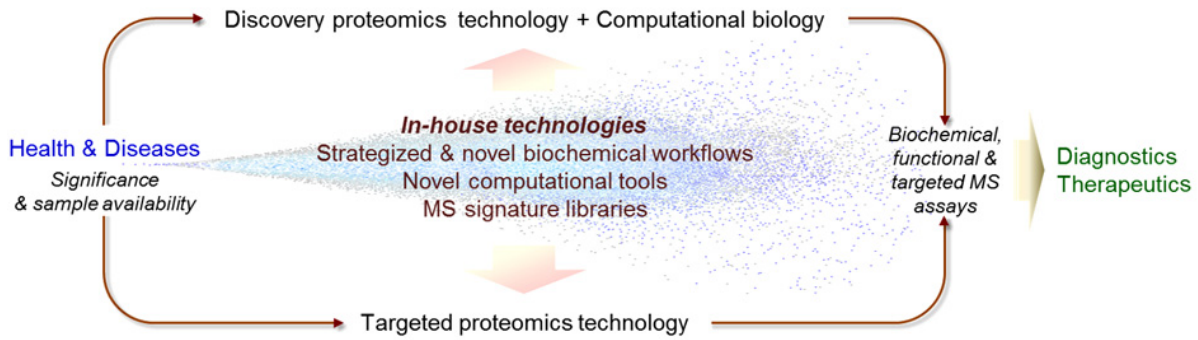
Research

Proteomics Mass Spectrometry in Health and Diseases

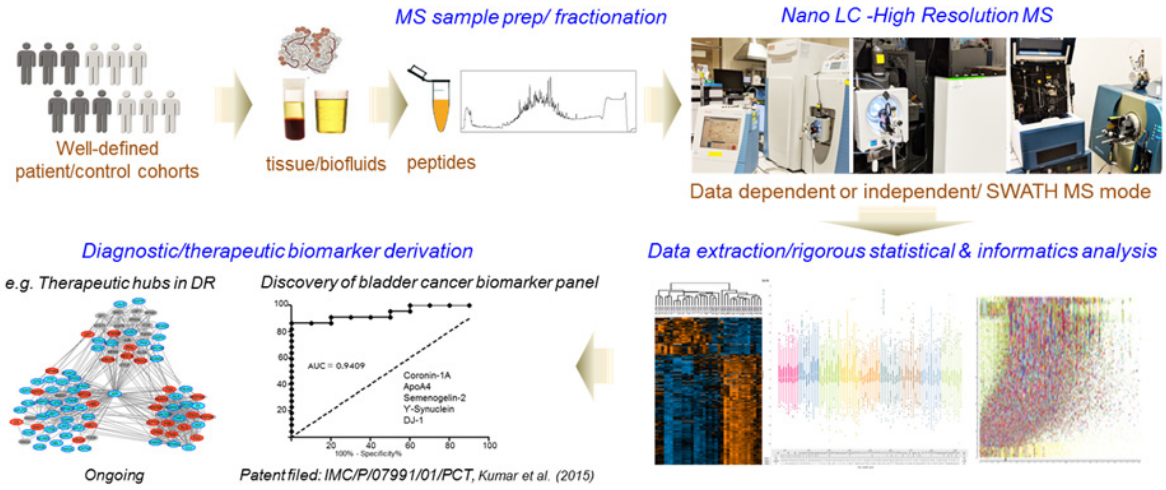
Proteomics mass spectrometry (MS) is the forefront technology for studying proteotype, the state of a proteome associated with a specific phenotype. Over the last decade, we have fully established this powerful technology including strategized pipelines for proteotype studies through proteome profiling (Swa *et al.* 2012 & 2015, Gunaratne *et al.* 2013, Alli Shaik *et al.* 2014, Ng *et al.* 2015), interactomes (Gunaratne *et al.* 2011, Coffill *et al.* 2012, Dong *et al.* 2016) and post-translational modifications (Alli Shaik *et al.* 2016 & 2017, Ho *et al.* 2015). Apart from discovery proteomics, our group also focuses on developing targeted proteomics applications (Wee *et al.* 2019). Currently we hold several translational and clinical research projects, and collaborate with international and national institutes, government agencies, hospitals and industry partners.



Our group focuses on 2 main research themes:

1. Disease biomarker discovery: Proteins orchestrate key biological events within the cell and any aberrant wiring in the complex protein-protein network often manifests itself in pathological conditions such as cancer. Identification of unique molecular signatures from haywire protein networks is important in early detection, precise diagnostics and targeted therapeutics of several disease conditions. Our group employs deep proteomics strategies to capture protein markers in dysregulated molecular pathways. We screen clinical samples including biofluids to identify deregulated protein clusters and subject them to advanced computational tools for reconstruction of biological networks to reveal druggable targets and prognostic markers that are clinically relevant. One of our main research interests is to dissect breast cancer heterogeneity and develop liquid biopsy approaches for early diagnosis, prognosis and patient stratifications. The other ongoing research projects in this line include chronic kidney disease (CKD), hepatitis B viral (HBV) infection, diabetic retinopathy (DR) and heart failure (HF) where our group leads in biomarker discovery and protein therapeutic target identification. We have already identified promising biomarker panels for bladder cancer and

CKD (urine), breast cancer (tissue) as well as DR, HF and HBV (blood). In addition to conventional biochemical tools for biomarker validation, we also establish and use in-house targeted MS assays as part of the work under our technology development theme.



2. Technology development: Applications of proteomics MS have traditionally been focusing on expression and post-translational (e.g. phosphorylation, acetylation and ubiquitination) profiling. In our group, we push the limits of this state-of-art MS technology in interrogating, tracking and validating molecular events. One such clinical application is the prototype we developed for single-shot flavivirus diagnosis (Wee *et al.* 2019). Other technology development projects include novel SWATH MS applications for tracking signalling pathways (in collaboration with SCIEX), development of novel screening tools (in collaboration with SFA), and biochemical approaches and advanced computational tools for next generation biomarker discovery.