

DOCTORAL CANDIDATE: Trung Tran
DEGREE: Philosophiae Doctor
FACULTY: Faculty of Mathematics and Natural Sciences
DEPARTMENT: Bioscience
AREA OF EXPERTISE: Proteomics
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DISSERTATION TITLE: *Quantitative proteome analyses of phosphorylated proteins and alternative splice variants in human cell lines and urine*

Doctoral candidate MSc Trung Tran at the Department of Bioscience has been working intensively in developing methods to study phosphorylation in human cell lines and urine samples of prostate cancer patients. He has established a general workflow to reproducibly enrich and identify phosphopeptides (peptides with additional phosphate group(s) on them) in samples with different complexity. Several thousand phosphopeptides could be identified in human cell lines. Using 1 ml urine from patients with prostate cancer, hundreds of phosphopeptides were repetitively identified while most other studies used around 50 ml. This result has proved the effectiveness of this workflow. It is relatively easy to implement in a large-scale manner and has been implemented at the proteomics core facility at the Department of Biosciences. Two customized databases have also been developed to identify peptides that are specific for alternative splice variants which aids in identifying and studying the diversity of proteins through alternative splicing. These databases provide the experimental data to prove the existence of different alternative splice variants which generate different forms of proteins. Moreover, the databases can easily be implemented in general proteomics workflow. Trung has also established a two-point quantification method to determine the absolute amount of targeted peptides with better quality control than the traditional one-point quantification approach. This method is significantly less expensive compared to the common one-point quantification method using AQUA peptides. Hence, it could be practically applied for the absolute quantification of multiple proteins.