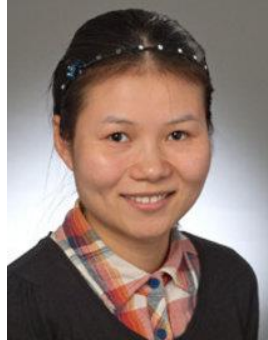# Multiplexed quantitative site-specific N-glycoproteomics method development and applications

Pan Fang

Soochow University

Regulation of protein N-glycosylation is essential in human cells. However, large-scale, accurate, and site-specific quantification of glycosylation is still technically challenging. We introduced SugarQuant, an integrated mass spectrometry-based pipeline comprising protein aggregation capture (PAC)-based sample preparation, multi-notch MS3 acquisition (Glyco-SPS-MS3) and a data-processing tool (GlycoBinder) that enables confident identification and quantification of intact glycopeptides in complex biological samples. We apply SugarQuant to identify and quantify more than 5,000 unique glycoforms in Burkitt's lymphoma cells, and determine site-specific glycosylation changes that occurred upon inhibition of fucosylation at high confidence. We further demonstrated the implementation of FAIMS in SugarQuant provided the most accuracy and precision for glycoproteomics.

Brief introduction:

Dr. Pan Fang received her doctoral degree from Fudan University in 2017. She then worked as a postdoctoral researcher in Max planck institute for biophysical chemistry in Germany for three years (2017-2020). Her main research focus is mass spectrometry based glycoproteomics. She then worked on drug target deconvolution as a senior research engineer in Karolinska institutet. From October 2021, she started independent research as a group leader in Soochow University.