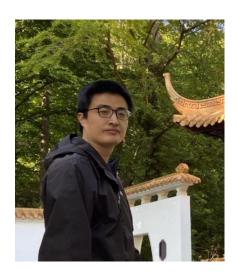Title:
Towards flexible and comprehensive glycopeptide analysis with pGlyco Series

Abstract:
I believe Glycoproteomics is becoming one of the most general extensions of proteomics after phosphoproteomics. In recent years, we have developed glycan-first glycopeptide search engine series called pGlyco for both N/O-glycopeptide identification. Additional to peptide part analysis, pGlyco more focuses on glycan part search and quality control. For glycan identification, pGlyco3, the newest version of pGlyco, mainly supports glycan structure database search with built-in or user-defined glycan structures. This feature allows us to analyze glycans with customized modifications. We also provide the glycan database-free search named pGlycoNovo in pGlyco3 as an experimental feature. pGlyco3 integrates a site-specific glycan localization (SSGL) algorithm — pGlycoSite to fast and accurately localize glycans by using ETD/EThcD spectra. All these modules enable flexible and comprehensive analyses of glycopeptides. But there are still a lot of issues in terms of both 'wet' and 'dry' experiments, I will also discuss about possible future developments in pGlyco3 in this talk.

个人简介
曾文锋，博士，本科毕业于西安电子科技大学软件工程专业（2006-2010），博士毕业于中国科学院计算技术研究所的 pFind 实验室（2010-2017）。之后在中科院计算所担任助理研究员（2017-2020）。目前在德国 Max-Planck Institute of Biochemistry, Matthias Mann 实验室做博士后研究工作。主要研究兴趣集中在糖蛋白质搜索引擎的开发和机器学习/深度学习方法在蛋白质组学的应用。以第一作者或者通讯作者身份在 Nature Methods, Nature Communications, Cell Systems 和 Analytical Chemistry 等高水平杂志发表文章十余篇。主要工作有有糖肽搜索引擎 pGlyco 系列和基于深度学习的谱图预测算法 pDeep 系列。目前 pGlyco 系列软件累计现在已经达到 1000 余次，是糖蛋

白质组学领域最受欢迎的软件之一，已经成为国内外一些实验室的主要糖肽鉴定工具。