



# Redefining ORNL's Suite of Protein Analysis Technologies by Adding Flexibility, Analytical Capacity, and Biological Utility



- **Purpose:**

- Because of the immense challenges associated with analyzing proteins at the proteomic and at the protein complex level, we have to constantly refine our technologies and the accompanying workflows.
- For the analysis of protein complexes, one of the most important areas of research is developing tags that are both efficient for affinity isolation and compatible with downstream mass spectrometry analysis.
- As we increase throughput, we must establish a series of protein/peptide QA/QC standards so that we can be assured that our instruments and workflows are operating properly.
- Since the output from these mass spectrometric analyses require extensive algorithmic analysis, we must work closely with our colleagues developing bioinformatic workflows and new algorithms

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