## Gehrke Proteomics Center

More info: <https://research.missouri.edu/gehrke-proteomics-center>

The Charles W. Gehrke Proteomics Center offers researchers the resources to generate qualitative and quantitative data on proteins linked to growth and disease in plants, animals, and humans. Using the center’s mass spectrometers and other equipment, scientists isolate, separate, and identify proteins. The information they gain is useful not only in understanding disease mechanism, but also in discovering new drugs and treatments. Insight into protein interaction networks can be obtained using pull-downs of fusion proteins or immunoprecipitation followed by mass spectrometry. These data advance discovery in a wide variety of fields including agriculture, biology, protein biochemistry, molecular biology, analytical chemistry, and bioinformatics.

The center is approximately 2,300 square feet in the Bond Life Sciences Center and is equipped with state-of-the-art equipment for protein extraction and advanced mass spectrometry. The center offers three main areas of analyses: global quantitative proteomics, intact mass analyses, and targeted quantitation of individual proteins or peptides.

For global analyses, center employees extract protein from frozen tissue or cell lysates using SOPs, and following trypsin digestion, identify peptides using an NSF-MRI-funded Bruker timsTOF-Pro instrument. The center has in-house licenses of software for protein identification and quantitation including PEAKS XPro, Spectronaut, and Proteome Discoverer. The center provides validated lists of proteins changing in abundance under the conditions examined.

Intact mass and accurate mass analyses (e.g., of synthetic therapeutic peptides, recombinant proteins, or oligonucleotides) are conducted using Agilent QTOF or ThermoScientific LTQ Orbitrap instruments. This approach can be used to confirm fidelity of synthesis or stoichiometry of protein or DNA labeling, for example.

Targeted quantitation of peptides (e.g., phosphorylation site stoichiometry) or proteins (e.g., disease biomarkers) is conducted using LCM-MRM on a Thermo Scientific Quantiva QQQ instrument and Skyline software. Known biomarkers of disease can be quantified in 10s to 100s of samples using this technique, with increased specificity compared to ELISA or Westerns.

The center emphasizes its full-service aspect by always involving staff and investigators throughout sample analyses. Center employees facilitate experimental design, data analysis, manuscript figure/methods preparation, grant application figures, methods, and facilities description preparation.