

# UNIVERSITY OF MINNESOTA

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## CENTER FOR METABOLOMICS AND PROTEOMICS

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XXXX, 2022

XXX  
XXXXX  
XXXX

Dear XXX,

The Center for Metabolomics and Proteomics (CMSP) would be happy to collaborate with you on your proposed work titled “ ”. As per our discussion, our experienced team will work with you to optimize detection and quantification of peptides from your protein(s) of interest (XX, YY, ZZZ) using analytical scale liquid chromatography (LC) and mass spectrometry. We will also work with you or a member of your laboratory to be trained on our instrument methods and data analysis.

The CMSP offers a variety of mass spectrometry-based platforms for analysis of compounds relevant to your work. The CMSP is equipped with instrumentation for targeted, quantitative analysis of peptides and other molecules of interest using a SCIEX QTRAP 6500 LC-MS and multiple reaction monitoring (MRM) methods. We routinely carry out these types of targeted proteomic studies. In addition, the ThermoFisher Orbitrap Fusion LC-MS system in the CMSP provides sensitive and high-quality quantitative data for targeted proteomics using parallel reaction monitoring (PRM).

The CMSP also has access to necessary software to analyze quantitative proteomics data. The CMSP works closely with Research Computing at the University, where we have put in place software and infrastructure to analyze high throughput discovery metabolomics data. We have the Progenesis software package in place for quantifying and identifying metabolites of interest from this data.

We look forward to assisting you in this work and helping you to successfully achieve your aims.

Sincerely,



Timothy J. Griffin, Ph.D.  
Professor and Director, Center for Metabolomics and Proteomics