

# UNIVERSITY OF MINNESOTA

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## CENTER FOR METABOLOMICS AND PROTEOMICS

Timothy J. Griffin, Professor and Director  
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XXX XX, 2022

XXXXX, PhD  
XX  
XX  
XX

Dear XXX:

I am writing in support of your grant application titled “XXXXX.” My research interests are in the area of developing and applying mass spectrometry-based methodologies for the analysis of proteins and proteomes. Your experiments include powerful approaches for investigating XXXX which will undoubtedly reveal crucial discoveries about XXXX..

The Department of Biochemistry, Molecular Biology and Biophysics at the University of Minnesota has established the Center for Metabolomics and Proteomics (CMSP) core facility equipped with leading-edge mass spectrometric instrumentation. I serve as Faculty Director of CMSP. Relevant to your work, the facility is equipped with a Thermo Eclipse Orbitrap mass spectrometer. This instrument is a recent generation of Orbitrap mass spectrometers, which has a significant improvement of throughput and sensitivity. This instrument is ideal for maximizing protein identification and quantification using both labeled (e.g. TMT) and unlabeled methods in cell and tissue samples. It also provides exquisite sensitivity and accuracy for characterizing a wide variety of protein post-translational modifications (PTMs), as well as induced modifications to proteins on interest. The Eclipse can also do targeted validation analysis of proteins of interest via parallel reaction monitoring. In addition, we have a Thermo Orbitrap Fusion instrument, and QTrap 6500 for targeted proteomic studies, if needed in the course of this work.

Our staff at the facility includes PhD level scientists with many years of experience in MS and bioinformatics. They will provide expertise in choosing the methods and preparing samples and acquiring data. Recently developed software tools along with state-of-the-art instrumentation will provide the infrastructure necessary for success. We also work extensively with the Office of Information Technology to develop and maintain bioinformatic infrastructure necessary for data management and analysis, and thus the necessary tools are already in place to enable interpretation of the mass spectrometry data.

In summary, I am in full support of your well-thought out and impactful work, and the objectives

of your proposal. I am excited to lend my expertise to help in this work, as well as the resources available in the CMSP.

Sincerely,

A handwritten signature in black ink, appearing to read 'T. Griffin', with a stylized flourish at the end.

Timothy J. Griffin, Ph.D.  
Professor, Biochemistry, Molecular Biology and Biophysics  
Faculty Director, CMSP