Charlie Bayne

*Biomedical Science Graduate Student*

[chnayne@health.ucsd.edu](mailto:chnayne@health.ucsd.edu)

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Dear Editorial Board,

My coauthors and I are pleased to submit our manuscript entitled **“mspms: a R package and graphical interface for the analysis of multiplex protease substrate profiling data”** for consideration in *GigaScience.* This paper introduces a novel, open-source R package designed to enhance the analysis of data produced using the multiplex protease profiling by mass spectrometry (MSP-MS) assay. Specifically, this package is utilized to analyze the substrate specificities of cathepsins A-D in the manuscript.

**Summary of the Manuscript:**

Traditional methods for analyzing MSP-MS data face challenges related to reproducibility, flexibility, and usability. Our mspms R package addresses these challenges by providing a comprehensive software solution that includes a well-structured application programing interface, extensive documentation, and an intuitive graphical user interface. The manuscript details the technical aspects of the package and demonstrates its application through the analysis of MSP-MS data to determine the substrate specificity of four well-characterized enzymes, cathepsins A-D. We validate the effectiveness of our analytical approach by comparing our findings with the established literature, confirming consistent results for all enzymes profiled.

**Why *GigaScience*?:**

We believe *GigaScience* is the ideal venue for our manuscript due to the journal’s emphasis on high quality research that prioritizes reproducibility, usability, and utility. The open-access model and global reach of *GigaScience* aligns with our goal to make the "mspms” package widely available to the research community.

We have no conflicts of interest to declare, all of the authors have approved the manuscript for submission, and the content within has not been published, or submitted for publication elsewhere.

Thank you for considering our manuscript for publication. We look forward to the opportunity to share our research with the scientific community through *GigaScience*.

Sincerely,

Charlie Bayne