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Dear Editorial Board,

We are pleased to submit our manuscript, *“mspms: A Comprehensive R Package and Graphic Interface for Multiplex Substrate Profiling by Mass Spectrometry Analysis,”* for consideration in *PLOS Computational Biology*.

Our work introduces mspms, a novel, open-source R package designed to streamline and democratize the analysis of multiplex substrate profiling by mass spectrometry (MSP-MS) data. Following rigorous benchmarking using ground-truth substrate specificities for cathepsins A-D, we show that mspms reliably captures substrate specificities across a broad range of proteases. With its robust functionality and user-friendly design, mspms fills a critical need in proteomics, offering researchers a powerful tool to accelerate the study of proteolytic enzymes and their roles in health and disease.

The mspms package has been officially accepted into the Bioconductor ecosystem following an independent peer-review process. This ensures seamless compatibility with established analytical pipelines. The package also features an intuitive graphical user interface, making it accessible to researchers regardless of their programming expertise. These capabilities are tailored to support several popular modern proteomics workflows, broadening its appeal and usability across a wide range of researchers.

Given *PLOS Computational Biology’s* focus on advancing methods and applications in proteomics and systems biology, we believe our work is an excellent fit for your journal. By combining open-source software with reproducible workflows, mspms supports the journal’s mission to promote innovative tools that benefit the global proteomics community. This work also contributes to broader goals in systems biology by enabling the integration of MSP-MS data to uncover deeper insights into biological systems and their regulatory networks.

All authors have approved the manuscript for submission. We confirm that this work has not been published or submitted elsewhere, and we have no conflicts of interest to disclose.

Thank you for considering our manuscript. We look forward to the opportunity to share mspms with the proteomics community through *PLOS Computational Biology*

Sincerely,

Charlie Bayne

On behalf of all authors