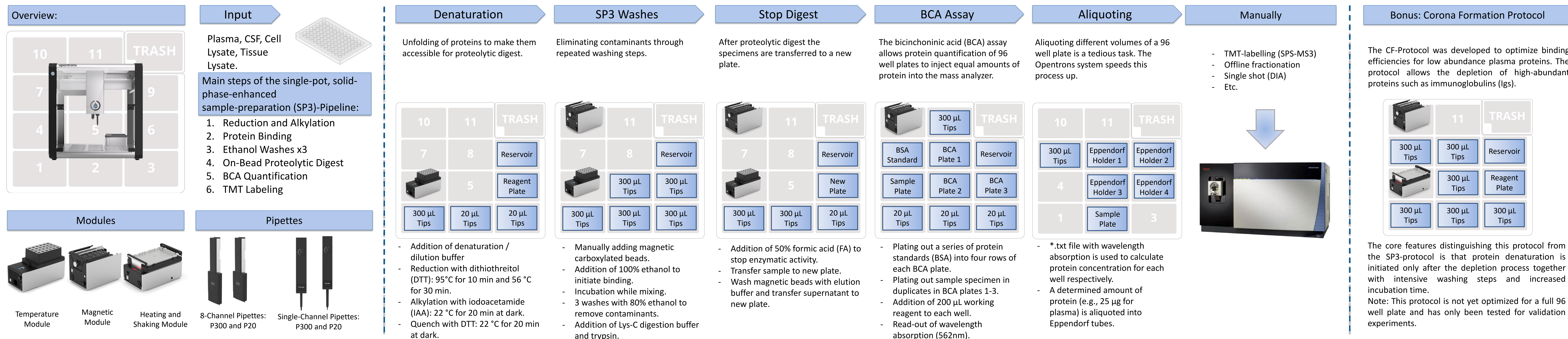


Building a universal proteomics sample preparation platform using low-cost liquid handling robotics and 3D-printing

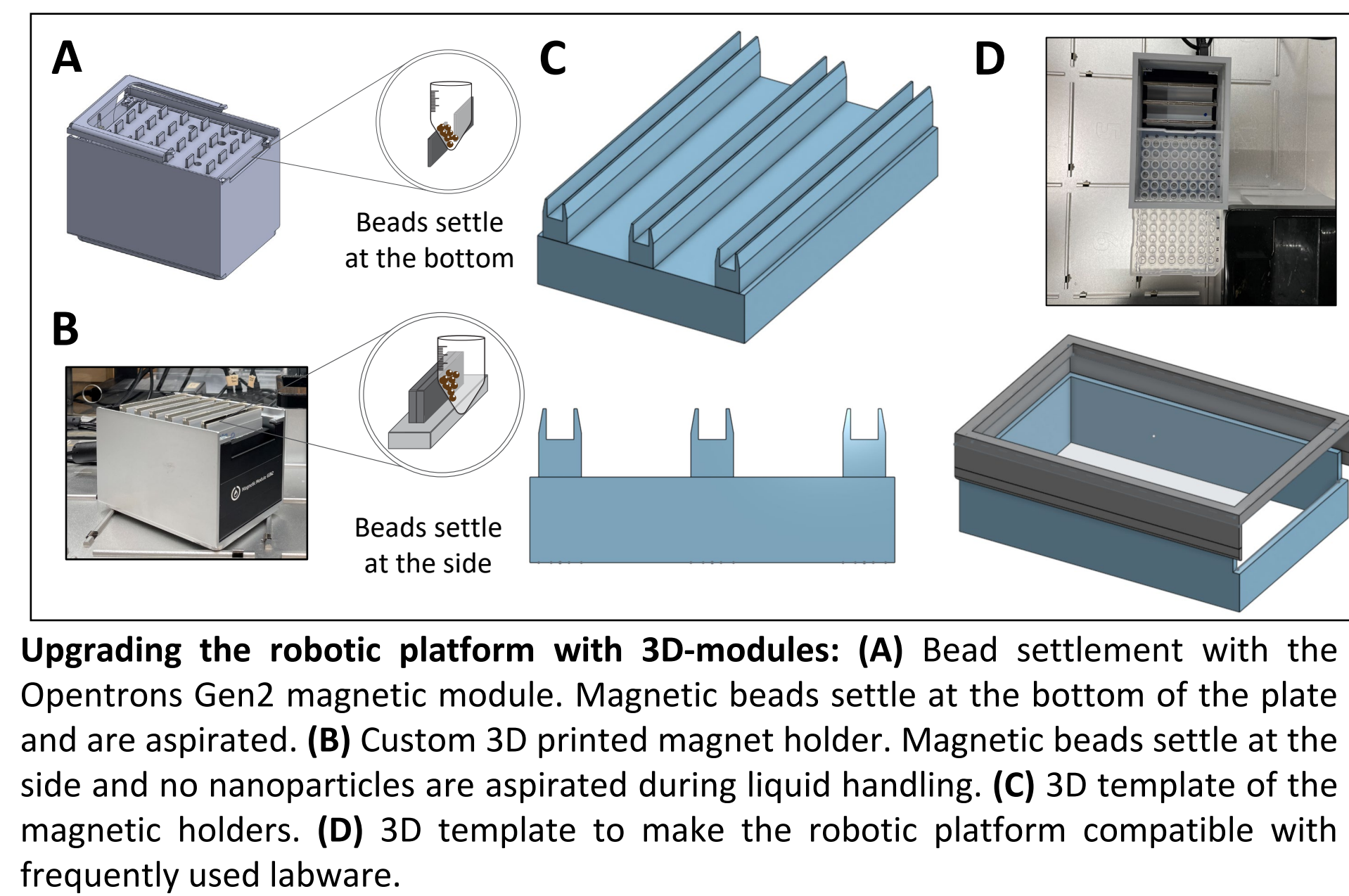
Benedikt C. Clemens, Eric F. Zaniewski, Johannes Kreuzer, Xcanda I. Herrera Lopez, Soroush Hajizadeh, Robert Morris, Wilhelm Haas



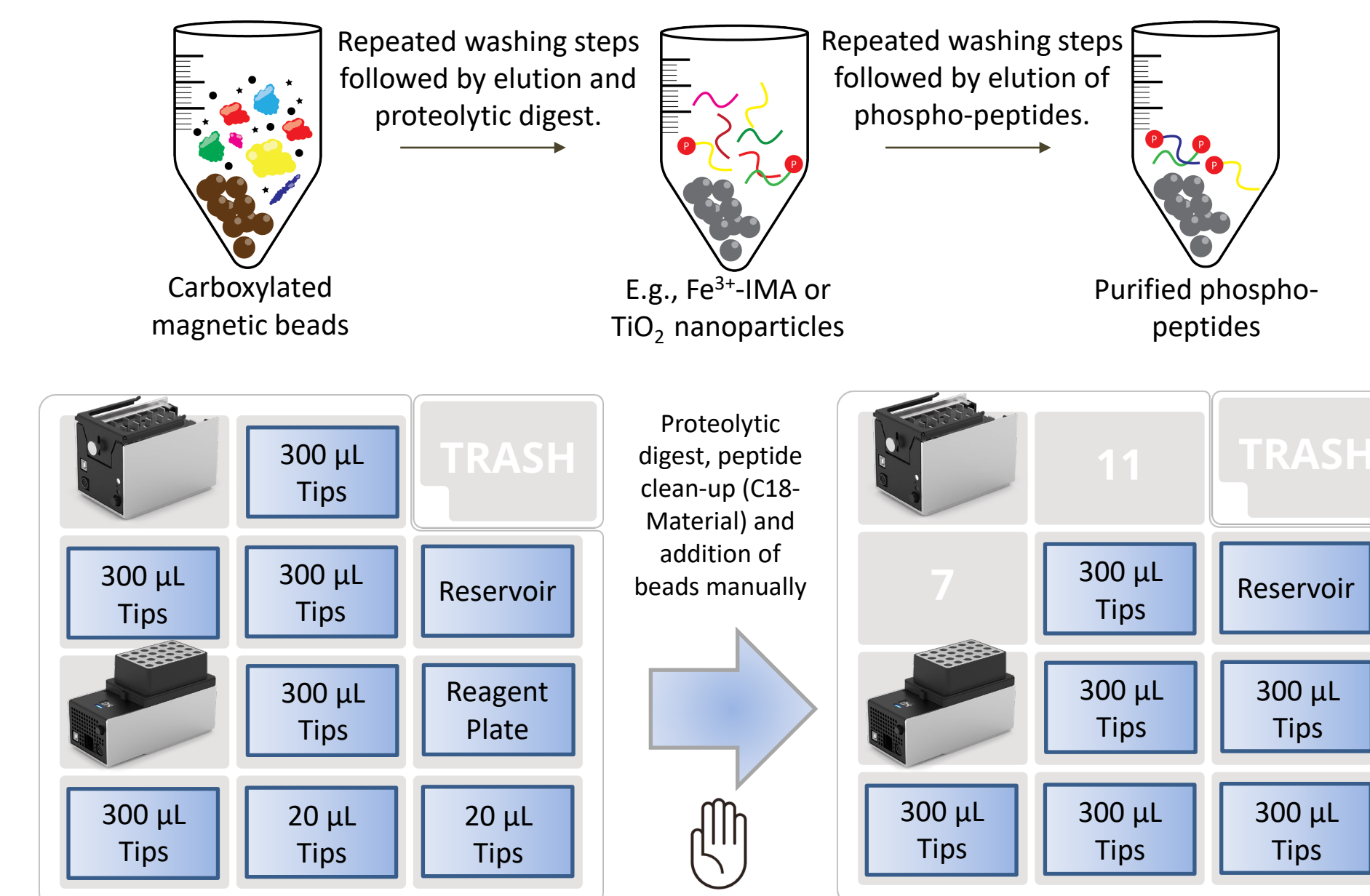
Introduction

Multiplexed proteomics through isobaric labeling and the combination of data-independent acquisition (DIA) methods with artificial intelligence (AI)-driven data analysis approaches have – over the last years – substantially increased the throughput of mass spectrometry-based proteomics. The developments have reached a point where the major costs in analyzing proteome samples are shifted from the required instrument time to sample preparation. Addressing this situation requires improvements in sample preparation processing that match those in mass spectrometry technology. Key features for these improvements are sample preparation automation that is highly versatile to cover needs across different applications and research groups as well as cost-effectiveness regarding hardware and consumables to attract wide-spread usage. We present such a platform based on Opentrons liquid handler robotics.

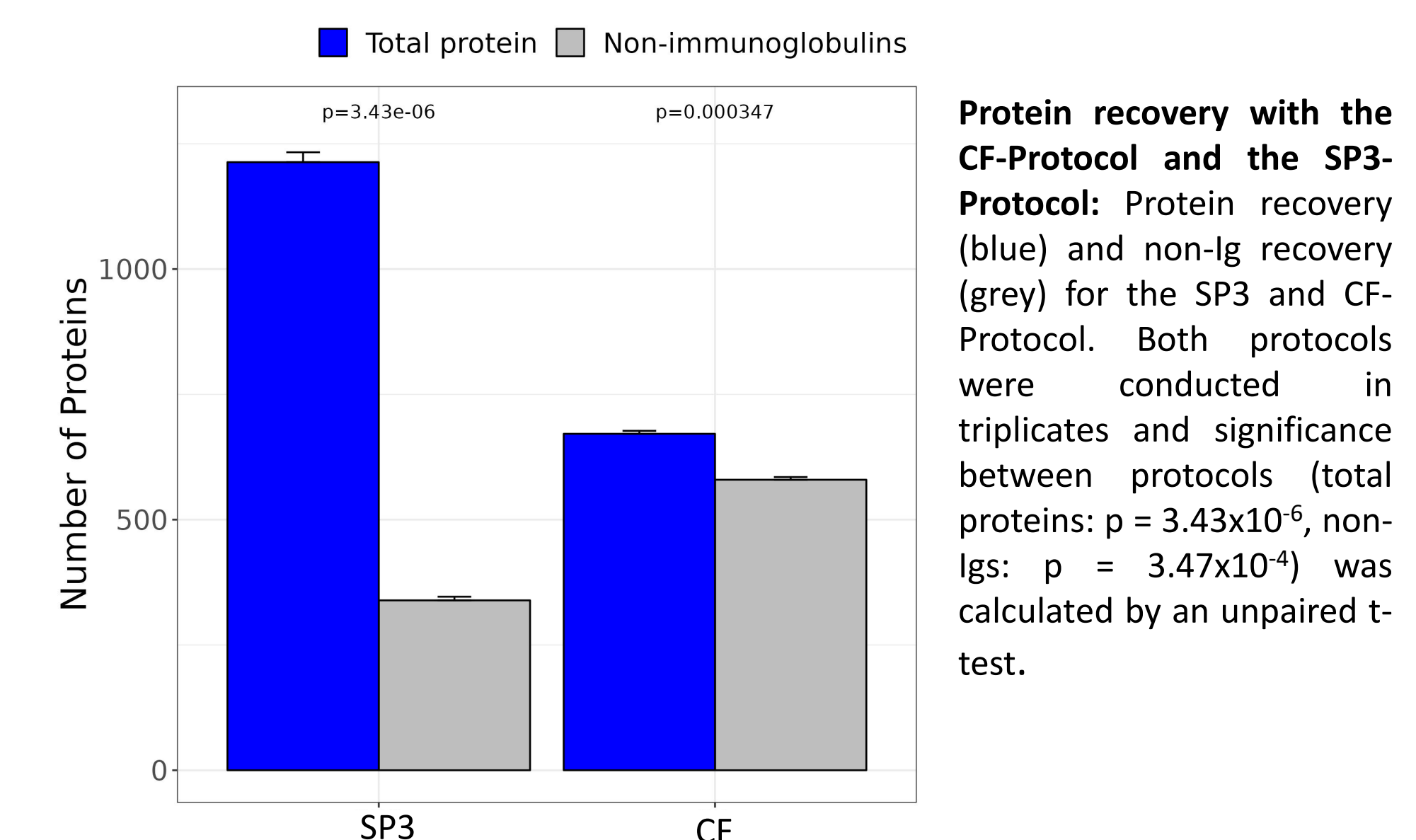
3D Design



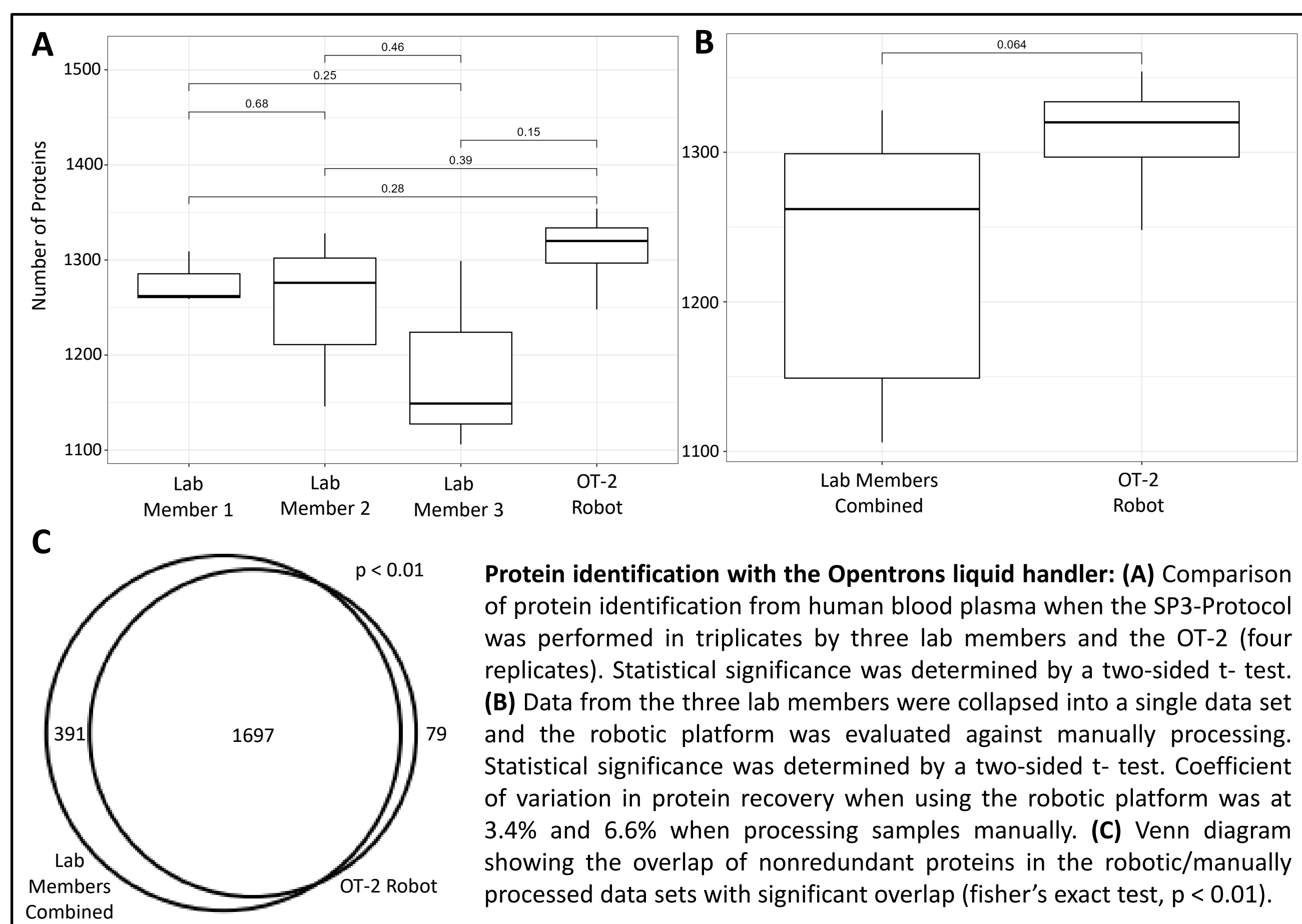
Set up for Phospho-Proteomics



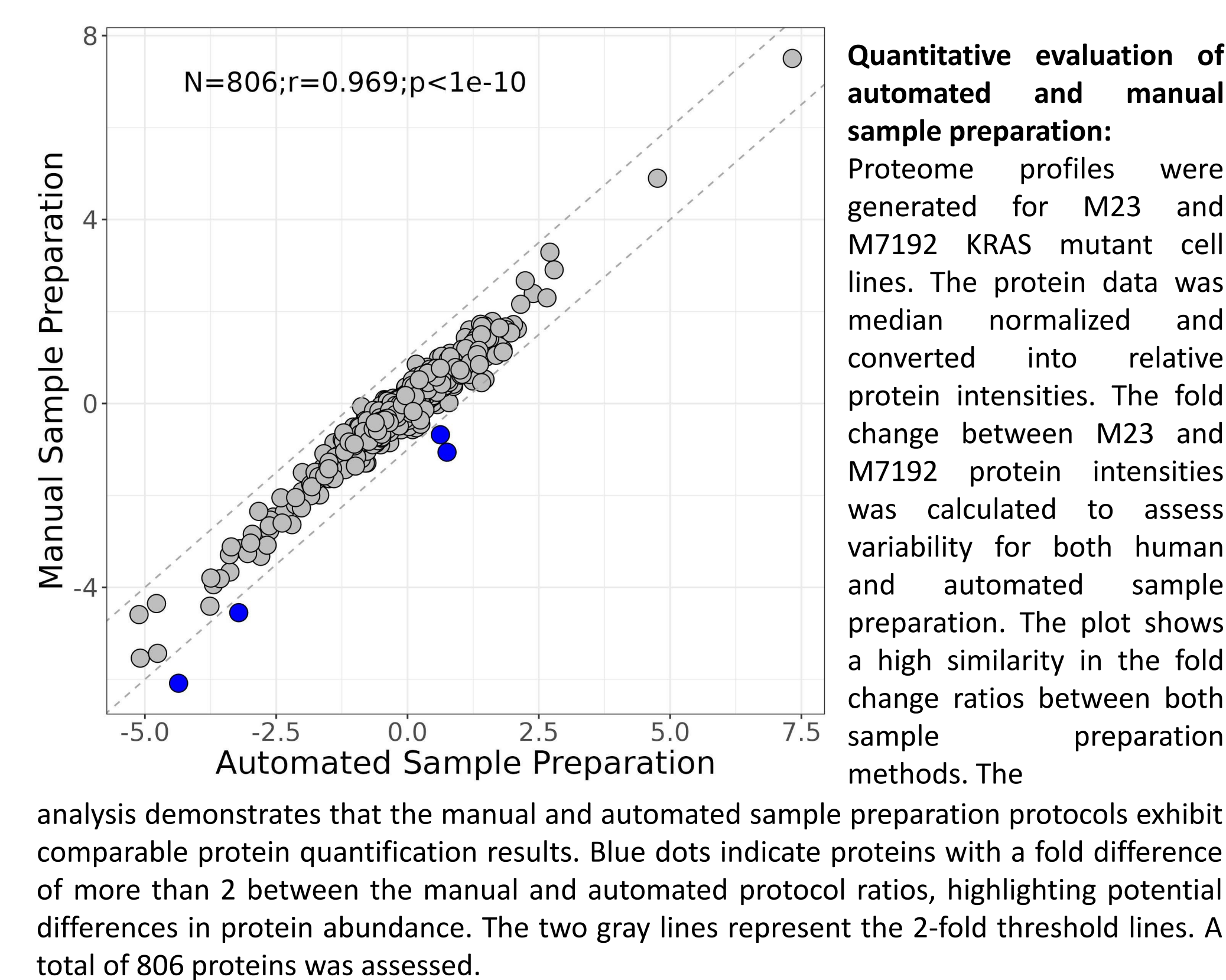
Corona-Formation Protocol



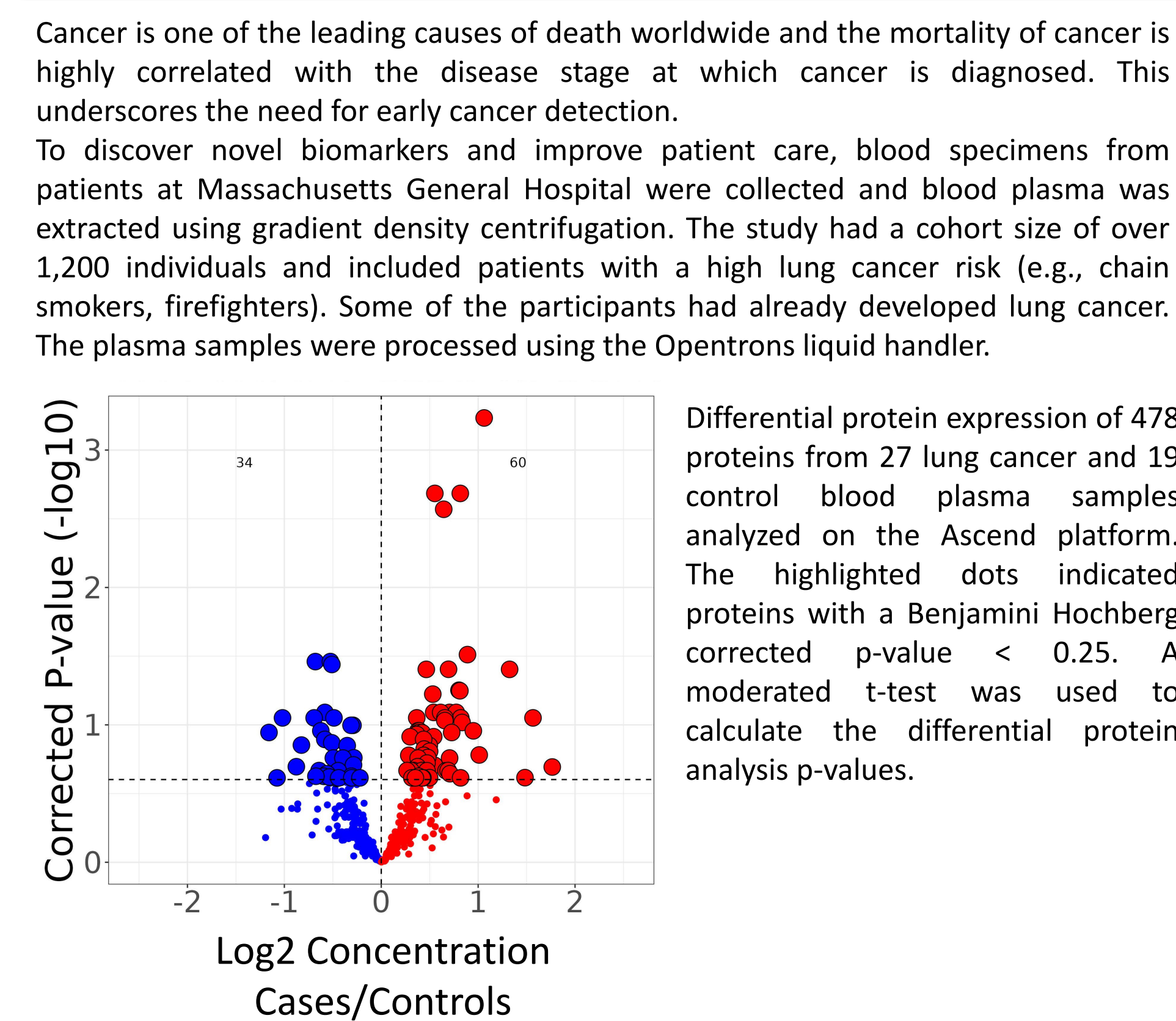
Automated vs Manual Preparation



Quantitative Evaluation



>1,200 Blood Plasma Samples



Benefits

Lab technician operating the Opentrons system		Lab technician alone
3x96 samples per day		1x96 samples per day
	Robot	Manually
Denaturation:	~ 2 hours	2 hours and 30 minutes
SP3-Washes:	1 hour 40 minutes	2 hours and 30 minutes
Stop Digest / Transfer:	25 minutes	35 minutes
BCA Assay:	1 hour	1 hour and 30 minutes
Aliquoting:	45 minutes	1 hour
Hands-on time:	1 hour	8 hours

References

1. Liu, X. et al. A Semiautomated Paramagnetic Bead-Based Platform for Isobaric Tag Sample Preparation. J Am Soc Mass Spectrom. 32(6):1519-1529 (2021).
2. Leuter, M. et al. R2-P2 rapid-robotic phosphoproteomics enables multidimensional cell signaling studies. Mol Syst Biol. (12): e9021 (2019).
3. Hughes, C.S. et al. Single-pot, solid-phase-enhanced sample preparation for proteomics experiments. Nat Protoc 14, 68–85 (2019).