Bead Assisted Mass Spectrometry (BAMS™) Enables Effectively Instantaneous Transformation of MS1 Peak Lists to Quantitative Pathway Reports

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ABSTRACT

High throughput proteomics broadly rely on multi-dimensional separation methods producing tons of mass spectrometric data and a resulting multiplicity of peaks. Bead Assisted Mass Spectrometry (BAMS™) is a quantitatively stable policy of interest among mass spectrometers without a single or multiple bead (beads). BAMS™ is immediately achieved by beads, combined with the spatial separation of the immobilized mass spectrometric instrument. The BAMS™ instrument is a quantitative analysis and a single BAMS™ instrument produces a matrix dependent throughput. This method is based on the principle of immuno-affinity achieved by the beads, combined with the spatial separation of the immobilized mass spectrometric instrument. The BAMS™ instrument is a quantitative analysis and a single BAMS™ instrument produces a matrix dependent throughput. This method is based on the principle of immuno-affinity achieved by the beads, biotinylated with a specific antibody. Beads are treated with several wash buffers to remove total soluble fraction. The total soluble fraction is desalted over 360 mg SEP PAK Classic C18 columns (Waters, Richmond, VA, USA) and eluted into the pico-well using a matrix sprayer. Peptide elution and direct, MALDI MS measurement of the target peptide. Targeted MS/MS acquisition is performed using the manufacturer’s recommended protocol (LysC, AspN, GluC, ArgC, Promega and NEB). The resulting RAW data folder is consolidated into a simple text-based .ms1 peak list file using the well-known extraction program. The .ms1 peak list file is uploaded to a server and never leaves the user’s computer. The data is never uploaded to a server and never leaves the user’s computer.

METHODS

Figure 1. BAMS Workflow for Targeted Proteomics Applications.

RESULTS

Figure 2. Bead Assisted Mass Spectrometry (BAMS™) Enables Effectively Instantaneous Transformation of MS1 Peak Lists to Quantitative Pathway Reports.

CONCLUSIONS

The targeted nature of Bead Assisted Mass Spectrometry yields raw MALDI MS data sets that are not uploaded to a server and never leave the user’s computer.

ACKNOWLEDGEMENTS

The research described in this paper was developed with support from North Shore InnoVentures (https://nsiv.org/), its corporate sponsors and the Massachusetts Life Science Center (http://www.masslifesciences.com/) for grant support.

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REFERENCES

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