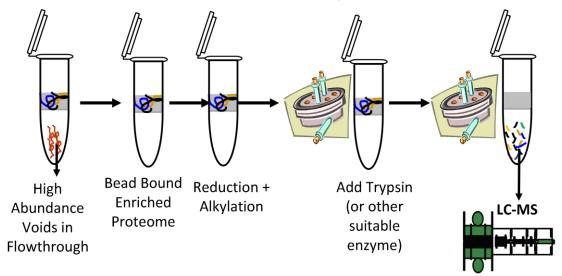


AlbuVoid™

Albumin Depleted, On-Bead Digestion Method

Workflow for On-Bead Digestion

High Abundance Depletion + Digestion Efficiency + Simple Workflows = Better LC-MS Output



- •Simple, reproducible workflows
- •Equivalent or better than in-solution digestion
- •Seamless to LC-MS, no desalting or C18 separations



PROTOCOL For On Bead Digestion Using AlbuVoid™ Based On Processing 50 - 100 µl Serum

Albumin Depleted On Bead Protein Enrichment

- 1. Weigh out 25 mg of **AlbuVoid™** beads in a spin-tube (0.45μ SpinX centrifuge tube filter from Corning).
- 2.Add 125 µl of **Binding Buffer AVBB.** Vortex for 5 minutes at room temperature followed by centrifugation at 3000 rpm. Discard the supernatant.
- 3.Repeat step-2
- 4.Condition by adding 100 μ l of AVBB and 50-100 μ l of the Serum. Centrifuge for 5 minutes at 10,000 rpm. Add clarified sample to the AlbuVoidTM beads in step 3. Vortex for 10 minutes and then centrifuge for 5 min. at 10,000 rpm.
- 5. Remove the albumin enriched supernatant (Flow-Through) FT.
- 6. To the pellet add 250 μ l of **Wash Buffer AVWB.** Vortex for 5 min and centrifuge for 4 minutes at 10,000 rpm. Remove the soup as **Wash.**
- 7. Repeat Step-6.

On-Bead Digestion Protocol

- 8. After the final wash steps from Step 7 from the enrichment, add 10 μ L 100mM DTT + 90 μ L **Wash Buffer AVWB**, vortex 10 min, incubate ½ hr at 60 °C.
- 9.After cooling, add 20µl 200mM Iodoacetamide, and 80 µL **Wash Buffer AVWB**, incubate in dark for 45 min at room temp.
- 10.Centrifuge at 10,000 rpm (microfuge max setting) for 5 minutes, and discard supernatant.
- 11.Add 40 μ L Sequencing-grade trypsin (0.4 μ g/ μ l, in 50mM acetic acid) + 60 μ L **Wash Buffer AVWB** to the beads. Digest overnight at 37°C or other optimized time period.
- 12. Centrifuge at 10,000 rpm (microfuge max setting) for 5 minutes, and retain peptide filtrate.
- 13.To further extract remaining peptides, add 150 μ L 10% formic acid, vortex 10 min, centrifuge at 10,000 rpm (microfuge max setting) for 5 mins., and add this volume to the first volume.
- 14. Total is about 250µl. Prepare to desired final concentration. Store at -80 °C until LC-MS/MS.

Note:

- The protocol can be scaled up or down proportionally to adjust for different serum volumes. The surface amount can be adjusted to accommodate more or less albumin removal.
- We have 0.45µ SpinX centrifuge tube filters. If required can be ordered separately.



References:

Serum

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On-Bead Digestion Protocols For LC-MS Proteomic Workflows

New on-bead digestion for LC-MS applications for proteomic studies

US HUPO 2014. Frontiers in Proteomics: Advancing Biology through Technology and Computation.

<u>AlbuVoid™</u> abstract entitled "<u>Improved proteomic enrichment and workflow strategies</u>", poster board 089 presented at US HUPO 2014

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