

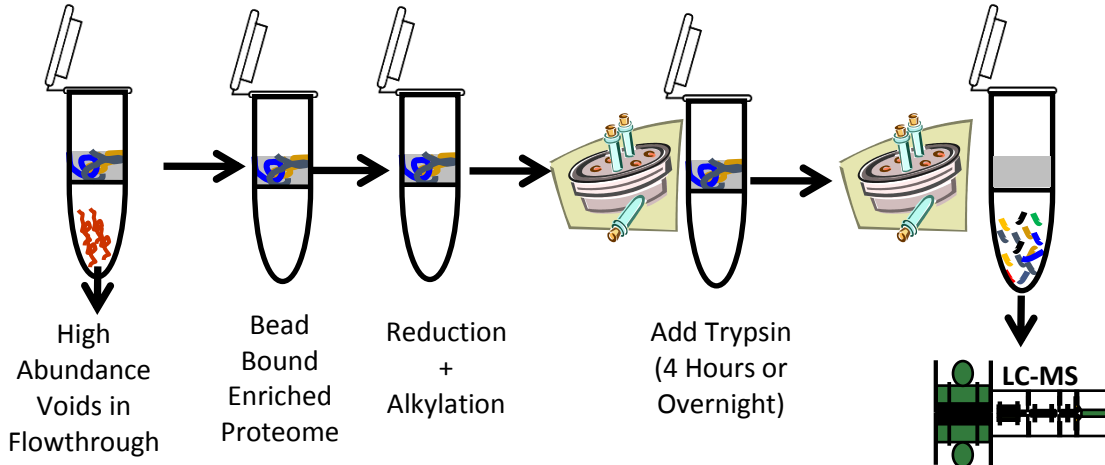


On-Bead Digestion Kits For LC-MS Proteomics

On-Bead Digestion

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

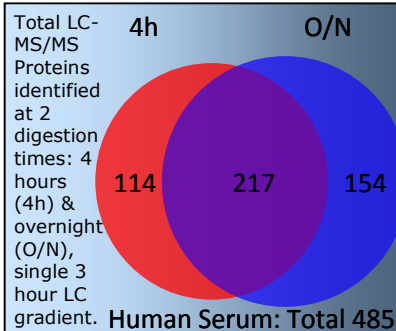
- Simple, reproducible workflows
- Equivalent or better than in-solution digestion
- Seamless to LC-MS, no desalting or C18 separations
- Unique proteolytic efficiencies
- Label, label-free & phospho/glyco compatible



AlbuVoid™ LC-MS On-Bead

Albumin depletion plus low abundance protein enrichment, coupled with optimized on-bead digestion protocols for LC-MS serum and plasma proteomics

- Seamless workflows
- Unique proteolytic efficiencies
- Label, label free compatible



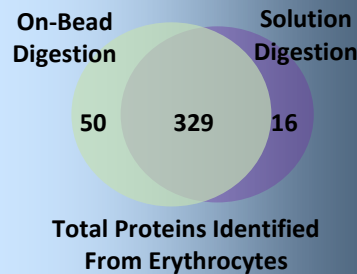
Product	Size	Item No.
AlbuVoid™ LC-MS On-Bead	5 Preps	AVB-MS05
AlbuVoid™ LC-MS On-Bead	10 Preps	AVB-MS10

Based on 50-100 µl serum preps

HemoVoid™ LC-MS On-Bead

Hemoglobin depletion plus low abundance protein enrichment, coupled with optimized on-bead digestion protocols for LC-MS erythrocyte & blood proteomics

- Seamless workflows
- Unique proteolytic efficiencies
- Label, label free compatible

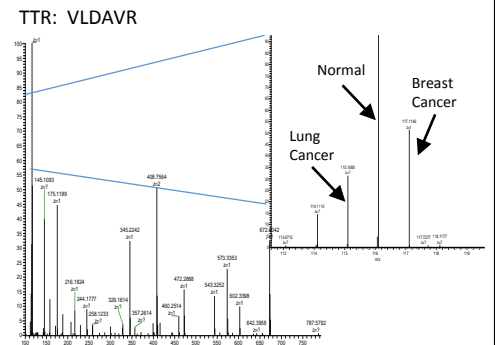
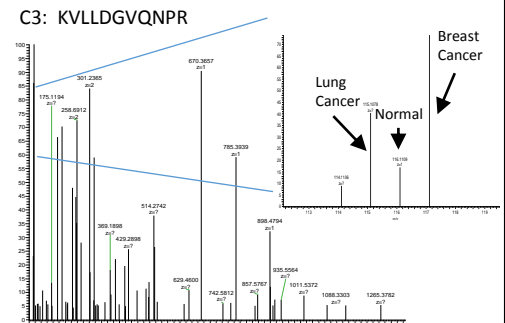


Product	Size	Item No.
HemoVoid™ LC-MS On-Bead	5 Preps	HVB-MS05
HemoVoid™ LC-MS On-Bead	10 Preps	HVB-MS10

Based on 100-200 µl erythrocytes

Quantitative Efficiency

Label or label-free



Isobaric (iTRAQ) labeled peptides from two representative proteins differentially quantified after **AlbuVoid™ LC-MS On-Bead**. On right, the MS2 spectral reporter ions magnified. Top: Complement C3, Bottom: Transthyretin (TTR)