



AlbuVoid™ Albumin Depletion Kit

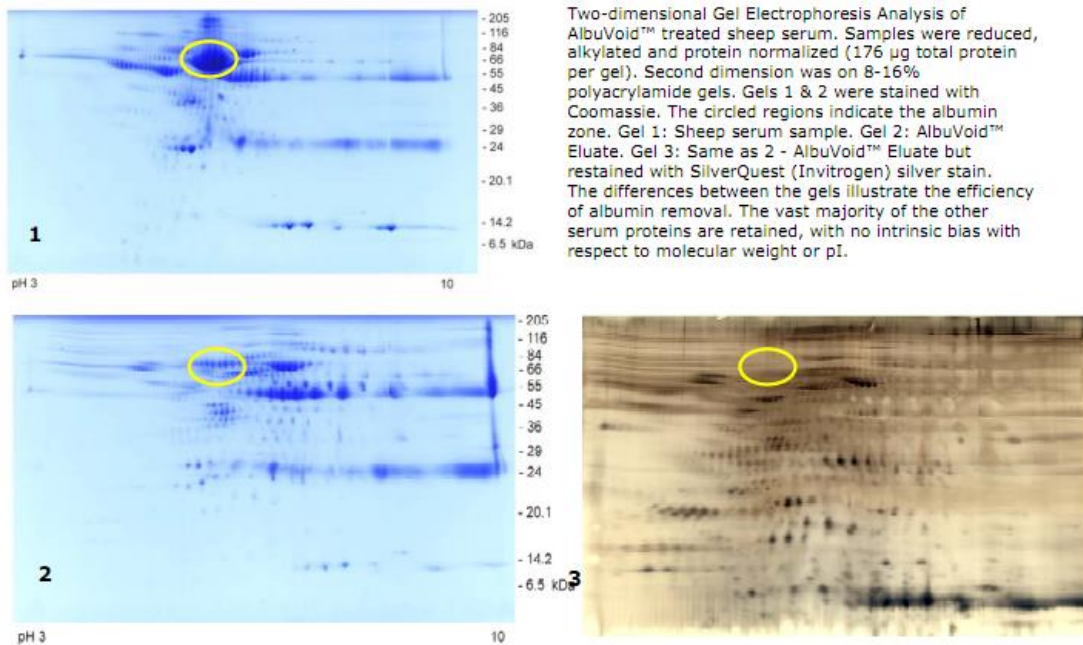
Albumin Depletion Plus Low Abundance Serum Protein Enrichment

- Albumin voids in flow-through >95%, with <30 minute bind/wash/elute protocol
- Low abundance enrichment equivalent or better than hexa-peptides or immuno-affinity
- Disposable, cost-effective, no column regeneration or cross-contamination
- Mild elution maintains tertiary structure and simple transfer to secondary analysis
- The eluted fractions retain their enzymatic and biological activity
- Works for all species tested including human, sheep, bovine, goat, rat, mouse, and calf.
- No molecular weight or pI bias
- On-bead protocols improve workflow and efficiency

AlbuVoid™ is an albumin depletion reagent kit. It removes albumin from serum and plasma samples while concentrating low abundance proteins. The **AlbuVoid™** protocol uses mild buffers; the protocol conditions are so gentle that native enzyme activity is retained in elution fractions.

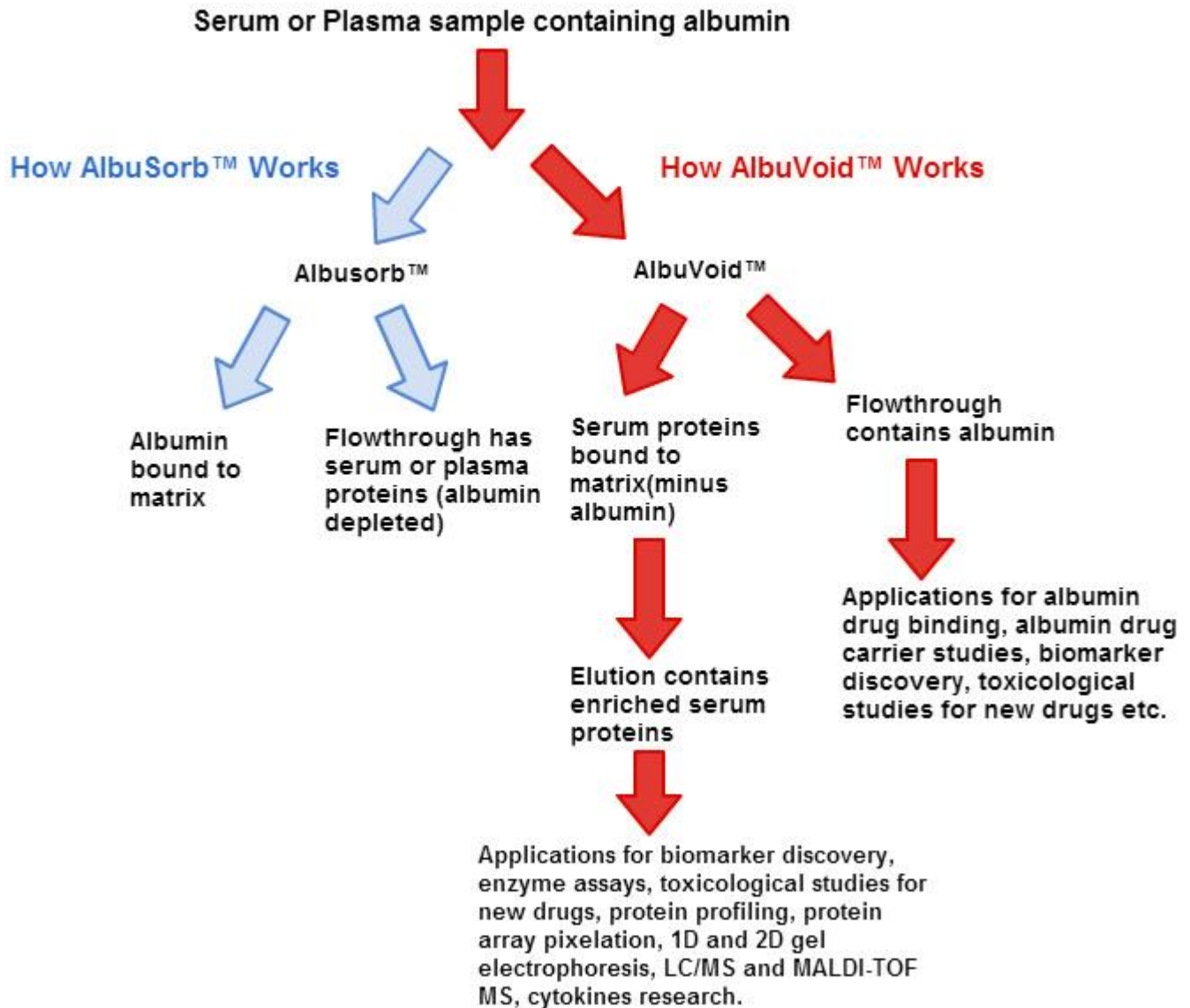
AlbuVoid™ does not bind albumin. The low abundance proteins which bind to **AlbuVoid™**, are eluted off without the albumin. Consequently, the low abundance serum proteins are enriched. It is ideal for applications involving discovery and targeted proteomics, enzyme assays, toxicological studies for new drugs, protein profiling, protein arrays, 1D and 2D gel electrophoresis, LC-MS, and cytokines research.

AlbuVoid™ derives from a silica-based library of individual mixed-mode polymeric ligands. The library was designed to facilitate weak binding of proteins, allowing for rapid elution from the matrix without any foreknowledge of the variety of proteins contained in the starting sample. Because of its specialized voiding properties, **AlbuVoid™** depletes high abundance proteins in serum like albumin while improving the resolution of less abundant serum proteins.





Depletion of albumin using Albusorb™ or Albuvoid™



Product	Size	Total samples processed	Item No.	Price
AlbuVoid™	5 Preps	5 x 200 µl samples	AVK-05	\$235
AlbuVoid™	10 Preps	10 x 200 µl samples	AVK-10	\$345
AlbuVoid™	50 Preps	50 x 200 µl samples	AVK-50	\$950

Note: Please contact sales@biotechsupportgroup.com for prices in bulk quantities.



Items Required	5 Prep	10 Prep	50 Prep	Reagent
AlbuVoid™	0.25 gram	0.5 gram	2.5 grams	Supplied
Binding Buffer AVBB, PH 6.0	6 ml	12 ml	60 ml	Supplied
Wash Buffer AVWB, PH 7.0	6 ml	12 ml	60 ml	Supplied
Elution Buffer AVEB, PH 9.8	6 ml	12 ml	60 ml	Supplied
SpinX Centrifuge tube filters	5	10	50	Supplied

PROTOCOL – Based on processing 200 µl Serum

1. Weigh out 50 mg of **AlbuVoid™** matrix in a spin-tube (0.45µ SpinX centrifuge tube filter from Corning).
2. Add 250 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 200 µl of **AVBB** and 200 µl of the **Serum**. Vortex for 10 min and then centrifuge for 4 minutes at 10,000 rpm.
5. Remove the albumin enriched supernatant (Flow-Through) **FT**.
6. To the pellet add 500 µl 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. **The bead is now enriched with albumin depleted proteins. For LC-MS sample preparation, an on-bead digestion protocol can be applied (protocol follows on next page). Otherwise proceed to the next step.**
8. To the pellet add 400 µl of **Elution Buffer AVEB**. Vortex for 10 min and centrifuge for 4 minutes at 10,000 rpm. Remove the filtrate as elution (albumin depleted proteins). The protein eluate is ready for further functional or LC-MS analysis.

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.



Suggested On-Bead Digestion Protocol

- ❖ After the final wash steps from step 7, add 100 µl of 10 mM DTT solution to the beads for complete immersion, mix and incubate at 60°C for ½ hour.
- ❖ After cooling, add 100 µl of 50 mM iodoacetamide to the DTT/bead suspension, mix and incubate in the dark for 1 hour.
- ❖ Centrifuge at 5000xg (medium setting, not max) for 3 mins, and discard supernatant.
- ❖ On-bead digestion is done by adding 200 µl of a 0.125 µg/µL (or calculated to a user preferred ratio – typically 50-100:1 w:w, protein:trypsin) of MS-grade Trypsin to the beads. Digest overnight at 37°C.
- ❖ Centrifuge at 5000xg (medium setting, not max) for 3 mins, and retain peptide filtrate.
- ❖ To further extract remaining peptides, add 200 µl of 10% solution of formic acid to the beads.
- ❖ Incubate for 15 minutes at 37°C, centrifuge at 5000xg (medium setting, not max) for 3 mins, and add this volume to the first volume.
- ❖ Reduce to final volume using a SpeedVac.

References:

Serum

[Serum Profiling Making Mark on Predictive Medicine](#)

Vicki Glaser. Genetic Engineering & Biotechnology News. 2011;31(7):1-55.

Plasma

Espes, Daniel, Joey Lau, and Per-Ola Carlsson. "[Increased circulating levels of betatrophin in individuals with long-standing type 1 diabetes.](#)" Diabetologia(2013): 1-4.

Patents

Narain, Niven Rajin, Rangaprasad Sarangarajan, and Vivek K. Vishnudas. "[INTERROGATORY CELL-BASED ASSAYS AND USES THEREOF.](#)" U.S. Patent No. 20,120,258,874. 11 Oct. 2012.

Cell Culture

Narain, Niven Rajin, Rangaprasad Sarangarajan, Vivek K. Vishnudas, and Michael Andrew Kiebish. "[USE OF MARKERS IN THE IDENTIFICATION OF CARDIOTOXIC AGENTS AND IN THE DIAGNOSIS AND MONITORING OF CARDIOMYOPATHY AND CARDIOVASCULAR DISEASE.](#)" U.S. Patent 20,140,100,128, issued April 10, 2014.

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.

[AlbuVoid™](#) abstract entitled "[Improved proteomic enrichment and workflow strategies](#)", poster board 089 presented at US HUPO 2014



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