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AlbuSorb™ PLUS

Albumin + IgG Depletion From Serum or Plasma

- >400 µg total serum protein mass (> 85% Albumin, >85% IgG depleted) from 25 µl serum prep
- Affinity-type equivalence, virtually no cross-reactivity with other proteins
- Disposable, no column regeneration or cross-contamination
- Combines unique bead technology, not based on Blue-dye affinity, with optimized Protein A
- Mild conditions maintains structural integrity and simple transfer to secondary analysis
- Suitable for immunoassay, Western blot, 1 & 2D Electrophoresis, enzyme assay, LC-MS
- Tested species include human, sheep, bovine, rabbit, mouse, rat

Poly-electrolytes are polymers with repeating units of stationary charges. **AlbuSorb™** comes from a class of solid-phase, or surface-based, elastomeric poly-electrolytic surfaces that bind proteins through an empirically derived chemistry combining elements of polymer composition, cross-linking architecture and charge properties. AlbuSorb™ combines with an optimized immobilized Protein A to create **AlbuSorb™ PLUS**.

Unlike immuno-affinity, the surfaces utilized are disposable eliminating cycle to cycle variance and cross-contamination. **AlbuSorb™ PLUS** is supplied as a powder. Simply weigh, centrifuge and/or filter, and recover the {albumin + Immunoglobulin} - depleted serum in the supernatant.

Gel Image: SDS-PAGE non-reduced, Criterion™ Tris.HCl (Bio-Rad) 4-15%

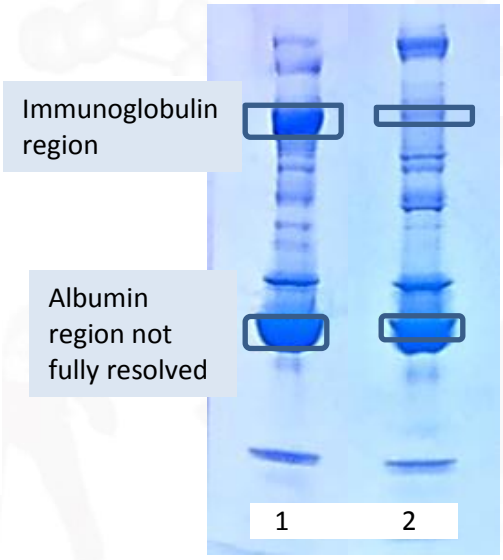
1: Human Serum Control (25 µl Serum + 250 µl Buffer)

2: **AlbuSorb™ PLUS** Flow-Through

Analysis by gel estimation & LC-MS Spectral Counts

Albumin <10%, 85+%+ removal

IG annotated <10%, 85+%+ removal



Product	Size	# Serum Preps	Item No.
AlbuSorb™ PLUS	20 preps	20, 25 µl Serum Samples	APK285-20
AlbuSorb™ PLUS	100 preps	100, 25 µl Serum Samples	APK285-100

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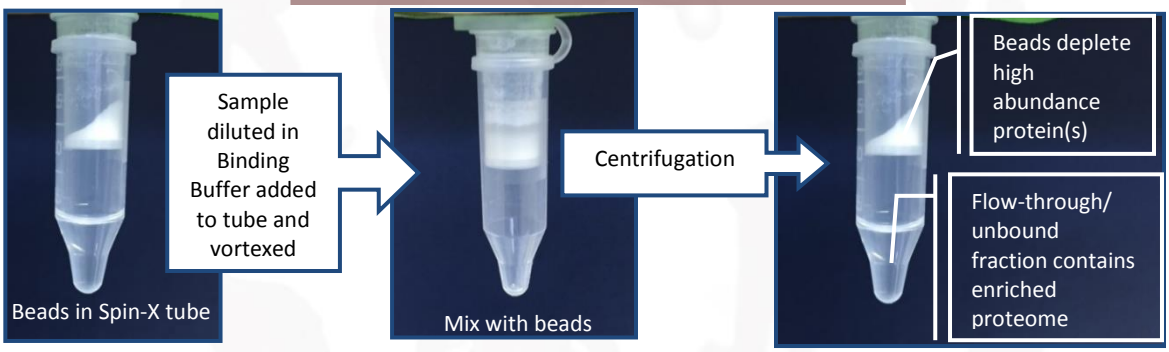
Items	Item No APK285-20	Item No APK285-100	Reagent
AlbuSorb™ PLUS	1.2 Gram	6.0 Gram	Supplied
Binding Buffer BB1 (0.05M K_2HPO_4 Dibasic, pH 7.5)	30 ml	150 ml	Supplied
Spin-X Filters	20	100	Supplied

Typical Performance	AlbuSorb™	AlbuSorb™ PLUS
Serum Sample Volume	25 µl	25 µl
Albumin Removal	>90%	>85%
Immunoglobulin Removal	-	>85%
Recovered Protein Mass	500-600 µg (Albumin depleted)	400-500 µg (Albumin + Ig depleted)
LC-MS/MS unique proteins (single 3 hr gradient)	350-400	350-400

SELECTIVE BINDING WORKFLOW



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PROTOCOL – Based on processing 25 µl Serum

For best results – the serum should be clear and free of colloidal material. We recommend first filtering through a 0.45 µm syringe-type filter before beginning the prep.

1. Weigh out 60 mg of **AlbuSorb™ PLUS** powder into the supplied microfuge spin-filters.

2. Add 400 µl of **Binding Buffer BB1** to condition the **AlbuSorb™ PLUS** powder. Shake it manually/ vortex for 3 min and then centrifuge for 2 minutes at 1,000 g's. Discard the filtrate.

3. Repeat step-2

4. As a requirement for albumin binding, add 250 µl of the **BB1 Buffer** and then add 25 µl of the serum to **Step 3**. Mix for 10 minutes on a rotating shaker.

5. Centrifuge for 4 minutes at 9,000 g's; **filtrate contains serum proteins depleted of albumin and Immunoglobulins.**

Note – when observing proteins on SDS-PAGE (4-15%), other high abundance proteins migrate to the same region as Albumin, and may not be fully resolved.

Scaleable and Versatile Protocol
The protocol can be scaled up or down proportionally to adjust for different serum volumes. The bead amount can be adjusted to accommodate more or less albumin removal.

References

Exosome
Chettimada, Sukrutha, et al. "Exosome markers associated with immune activation and oxidative stress in HIV patients on antiretroviral therapy." *Scientific Reports* 8.1 (2018): 7227.

Cerebrospinal Fluid
Gwenael Pottiez, Pawel Ciborowski. Proteomic Profiling of Cerebrospinal Fluid Expression Profiling In Neuroscience Neuromethods.2012;64:245-270

Synovial fluid
Happonen KE, Fürst CM, Saxne T et al. PRELP protein inhibits the formation of the complement membrane attack complex.Journal of Biological Chemistry.2012;287(11):8092-100

- **Serum**
Nelson K, Wilkinson, S. et al., High resolution accurate mass spectrometry-based proteomics in ecotoxicology: SWATH-MS to detect differentially expressed plasma proteins in the amphibian toxicological model *Xenopus laevis*. Poster: Conference: PRIMO20, May 2019

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Holmberg R, Refai E, Höög A.Lowering apolipoprotein CIII delays onset of type 1 diabetes. Proceedings of the National Academy of Sciences.2011;108(26):10685-9.

Tang MX, Ogawa K, Asamoto M. Effects of Nobiletin on PhIP-Induced Prostate and Colon Carcinogenesis in F344 Rats Nutrition and Cancer.2011;63(2):227-33

Holmberg, Rebecka Apolipoprotein CIII and Ljungan virus in diabetes 2010. Doctoral Thesis

Lu Q, Zheng X, McIntosh T Development of different analysis platforms with LC-MS for pharmacokinetic studies of protein drugs. Analytical Chemistry.2009;81(21):8715-23

Cell/Tissue Culture Media
"AlbuSorb™ worked very well for us. We removed at least 90% of the albumin from our 10% FBS conditioned medium samples", states Joseph Sucic, University of Michigan.

Urine
Zubiri, Irene, et al. Diabetic nephropathy induces changes in the proteome of human urinary exosomes as revealed by label-free comparative analysis. Journal of Proteomics (2013).

Patent
Berggren, Per Olaf, Yang, Shao-Nian. 2012. Methods For Treating And/Or Limiting Development Of Diabetes.U.S. Patent 20120328630 Kind Code: A1, filed June 25, 2012, and issued December 27, 2012.

CONTACT US

We welcome your questions and comments regarding our products.

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