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## HemoVoid™

### *Hemoglobin Depletion Plus Low Abundance Protein Enrichment For Erythrocyte Lysate Proteomics*

- Hemoglobin voids in flow-through >98%, with <30 minute bind/wash/elute protocol
- Hemoglobin removal from red cell lysates for RBC proteomics
- Hemoglobin removal from hemolyzed serum
- Low abundance protein and enzyme enrichment
- Disposable, cost-effective
- Mild elution maintains tertiary structure and simple transfer to secondary analysis
- Species agnostic, validated on human, sheep, bovine, goat, fish, etc.
- The eluted fractions retain their enzymatic and biological activity

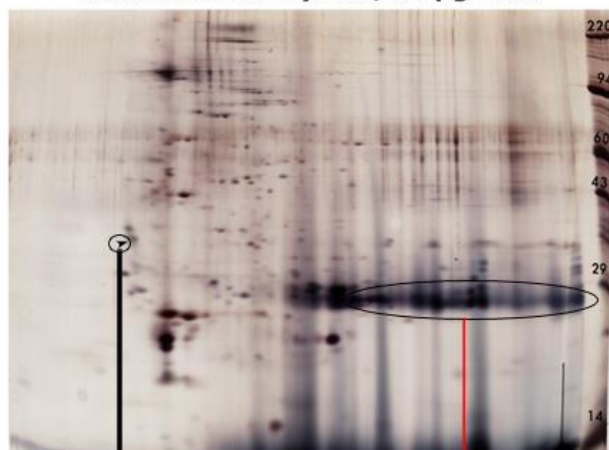
HemoVoid™, a silica-based protein enrichment matrix, removes hemoglobin from erythrocyte lysate samples while concentrating low abundance, and/or low molecular weight proteins. The HemoVoid™ protocol uses mild buffers; the protocol conditions are so gentle that native enzyme activity is retained in elution fractions.

HemoVoid™ derives from a silica-based library of individual mixed-mode ligand combinations (ionic, hydrophobic, aromatic, polymer). 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. HemoVoid™ depletes hemoglobin from red cell lysates while enriching the less abundant blood proteins.



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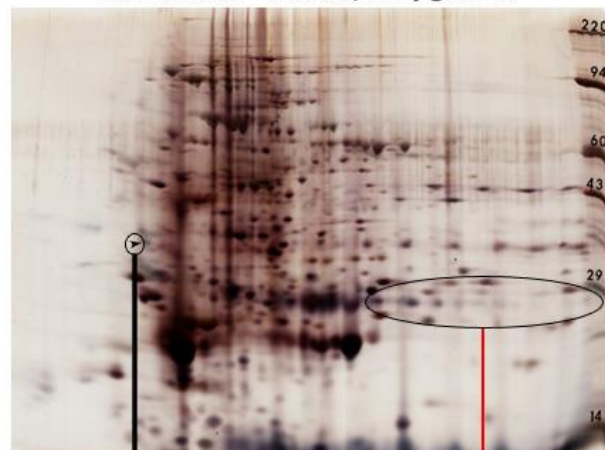
**Red Blood Cell Lysate, 50 µg Load**



IEF Internal standard,  
pI 5.2

Hemoglobin  
Subunits  
Region

**HemoVoid™ Eluate, 50 µg Load**



IEF Internal Standard,  
pI 5.2

Hemoglobin  
Subunits  
Region

**Materials and Methods.** IEF Dimension: 2% pH [3.5 - 10.0] carrier ampholines were employed in 2mm glass tubes for focusing. Size dimension: Each IEF tube gel was sealed to a 10% acrylamide slab gel. After electrophoresis, proteins were fixed and silver stained. Molecular weight reference standards are represented on the far right side of each image.

**Results and Discussion.** When comparing the two gel images, the HemoVoid™ eluate (right) has been severely depleted of Hemoglobin. The remainder of the red cell proteins are substantially enriched (visualized) and are better resolved in the HemoVoid™ eluate. Many more proteins are detectable after HemoVoid™ treatment with extensive protein coverage across both dimensions.

Product	Size	Total samples processed	Item No.
HemoVoid™	10 Preps	10 x 300 µl	HVK-10
HemoVoid™	50 Preps	50 x 300 µl	HVK-50
HemoVoid™	100 Preps	100 x 300 µl	HVK-100

**NOTE: Please contact [sales@biotechsupportgroup.com](mailto:sales@biotechsupportgroup.com) for prices in bulk quantities.**



Items Required	5 Prep	10 Prep	50 Prep	100 Prep	Item
HemoVoid™ beads	0.25 gram	0.5 gram	2.5 grams	5.0 grams	Supplied
Binding Buffer HVBB (0.05M HEPES, pH 6.0)	4 ml	8 ml	40 ml	80 ml	Supplied
Wash Buffer HVWB (0.05M HEPES, pH 7.0)	8 ml	15 ml	75 ml	150 ml	Supplied
Elution Buffer HVEB (0.25M Tris + 0.5M NaCl, pH 9-10)	2 ml	3 ml	15 ml	30 ml	Supplied
Spin-filter & tube assemblies	5	10	50	100	Supplied

**Additional Spin-Filters (low protein binding, 0.45 µm filter element) can be purchased separately, please inquire.**

## PROTOCOL – Based on processing 300 µl Red Cell Lysate

Notes:

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

The centrifugation time may vary, adjust as necessary to get complete filtration through the beads.

The protocol can be scaled up or down proportionally to adjust for different volumes. The bead amount can be adjusted to accommodate more or less hemoglobin removal.

- 1. BEAD CONDITIONING.** Weigh out 50 mg of **HemoVoid™** beads in a spin-filter. Add 250 µl of **Binding Buffer HVBB**. Vortex or mix thoroughly for 5 minutes at room temperature followed by centrifugation for 2 minutes at 5,000-10,000 rpm (2,000-8,000xg). Discard the filtrate. Repeat step-1.
- 2. SAMPLE PROCESSING.** Add 300 µl of **HVBB** to beads followed by 300 µl of the **Sample** to the beads. Vortex or mix thoroughly for 10 min and then centrifuge for 4 minutes at 5,000-10,000 rpm (2,000-8,000xg).
3. Remove the filtrate as Flow-Through, containing the unbound Hemoglobin.
4. To the beads, add 500 µl of **Wash Buffer HVWB**. Vortex or mix well for 5 min and centrifuge for 4 minutes at 5,000-10,000 rpm (2,000-8,000xg). Remove the filtrate as **Wash**. Repeat Step-4, 2 times.

**The HemoVoid™ beads contain the enriched Hemoglobin-depleted sub-proteome. As an option for LC-MS sample preparation, the bead assisted on-bead digestion protocol (BASP™) is provided, see box on next page. To elute the bound proteins, continue to step 5.**

- 5. BEAD ELUTION.** To the beads, add 300 µl of **Elution Buffer HVEB**. Vortex or mix thoroughly for 10 min and centrifuge for 4 minutes at 10,000 rpm. Remove the filtrate as **Elution**. The Hemoglobin-depleted eluate sub-proteome (0.25M Tris + 0.5M NaCl, pH 9.0-10.0) is suitable for further analysis.



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### Bead Assisted Sample Prep (BASP™), also known as on-bead digestion

6. Using **Wash Buffer AVWB**, prepare to 10mM of DTT concentration, and add 200 µl to the beads and vortex for 10 minutes and incubate for 30 minutes at 60C.
7. Cool the samples to RT, add suitable volume of Iodoacetamide to 20mM and incubate in the dark for 45 minutes
8. Centrifuge at 5,000-10,000 rpm (2,000-8,000xg) for 5 minutes, and discard filtrate. Rinse the bottoms of the spin-filter tubes with 500 µl of 50% ACN, **Wash Buffer AVWB** twice, to remove any traces of the filtrate.
9. Add 16 µg trypsin in 200 µl **Wash Buffer AVWB** to the beads and keep at 37°C for a minimum 4 hours to maximum overnight. Overnight is recommended to start with. In select targeted circumstances, 2 hours may be sufficient.
10. Centrifuge at 5,000-10,000 rpm (2,000-8,000xg) for 5 minutes, and retain digested peptides filtrate.
11. To further extract remaining peptides, add 300 µL 10% formic acid, vortex 10 min, centrifuge at 5,000-10,000 rpm (2,000-8,000xg) for 5 mins., and add this volume to the first volume.
12. Total is about 500µl. Prepare to desired final concentration. Store at -80°C until LC-MS/MS.

### Selection of HemoVoid™ Reference Applications

#### Red Blood Cells (RBC) Lysates

[Liu, Wenli, et al. "Erythroid lineage Jak2 V617F expression promotes atherosclerosis through erythrophagocytosis and macrophage ferroptosis." \*The Journal of Clinical Investigation\* \(2022\).](#)

To investigate whether selective erythroid Jak2VF expression promotes atherosclerosis, the study used hyperlipidemic Erythropoietin Receptor Cre mice that express Jak2VF in the erythroid lineage (VFEpoR mice). To explore underlying defects promoting oxidative changes in Jak2VF Red Blood Cells (RBC), unbiased proteomics profiling was conducted. The article states "...**haemoglobin removal and on-bead digestion, ...was based on the protocol in HemoVoid kit...**" The proteomic data showed a prominent increase in EIF2AK1 (also known as heme-regulated inhibitor, HRI) and EIF2A (Left), consistent with increased oxidative stress.

[Jing, Lun, et al. "PROTEOMIC ANALYSIS IDENTIFIED LBP AND CD14 AS KEY PROTEINS IN BLOOD/BIPHASIC CALCIUM PHOSPHATE MICROPARTICLE INTERACTIONS." \*Acta Biomaterialia\* \(2021\).](#)

In a LC-MS/MS proteomic study, the authors compared the differentially expressed blood proteins (plasma and blood cell proteins) and the deregulated signaling pathways of osteogenic and fibrogenic blood composites. The article describes use of HemoVoid™ for depletion of Hemoglobin prior to LC-MS analysis, "each composite material or 4 blood clots were pooled into 3ml of cooled lysis buffer [HEPES 50mM (pH 7.4); NaCl 150mM; EDTA 20mM (pH 8); CHAPS 1%; DTT 1mM; Protease and Phosphatase inhibitor cocktail]. ...The supernatants were collected, and hemoglobin depleted using several HemoVoid™ columns (Biotech Support Group). When indicated, albumin was also partially removed using AlbuVoid™ depletion reagent kit (Biotech Support Group) following the manufacturer's instructions." **From these enrichment steps, the investigators found respectively 80 and 92 proteins differentially expressed between blood clot and BCP 80-200 or BCP 200-500 blood composites.**

[Bollenbach, Alexander, et al. "GC-MS and LC-MS/MS pilot studies on the guanidine \(NG\)-dimethylation in native, asymmetrically and symmetrically NG-dimethylated arginine-vasopressin peptides and proteins in human red blood cells." \*Journal of Chromatography B\* \(2020\): 122024.](#)



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The study aimed to report the identity, biological activity and concentration of *NG*-methylated proteins by using GC-MS and LCMS/MS approaches. The article states "we included in our method the use of HemoVoid™ to remove specifically most erythrocytic hemoglobin and to improve the SDS-PAGE separation of proteins for further processing. **The HemoVoid™, ... allowed removal of erythrocytic hemoglobin to a large extent from the hemolysate.** ... removal of hemoglobin by this technique enabled an effective separation by SDS-PAGE and isolation of bands....".

Rosin-Arbesfeld, Rina, and Ronen SIMAN-TOV. "[Article of manufacture and methods for increasing survival of red blood cells.](#)" U.S. Patent Application No. 15/739,857.

The patent application describes an ex - vivo method of increasing survival of red blood cells (RBCs). The method comprises contacting the RBCs with an activator of the non - canonical Wnt pathway, which results in actin polymerization, thereby increasing survival of RBCs. The invention's description states "The Haemolysates were enriched with over 95 % hemoglobin. For hemoglobin depletion, the hemoglobin depletion kit of HemoVoid ... was used". Upon depletion of hemoglobin, a reduction in cytoplasmic actin levels was observed.

Nemkov, Travis, et al. "[Hypoxia modulates the purine salvage pathway and decreases red blood cell and supernatant levels of hypoxanthine during refrigerated storage.](#)" *haematologica* 103.2 (2018): 361-372.

The goal of this study was to use proteomics in part to understand hypoxanthine catabolism *in vivo* for stored red blood cells. It is still unclear whether accumulation of hypoxanthine in stored red blood cell units is clinically relevant for transfused recipients. The article states "Proteomic analyses of RBC membranes and cytosols were performed...RBC cytosolic proteins were depleted of hemoglobin using HemoVoid™ (Biotech Support Group, Monmouth Junction, NJ, USA), ...".

Cortese-Krott, Miriam M., et al. "Identification of a soluble guanylate cyclase in RBCs: preserved activity in patients with coronary artery disease." *Redox Biology* (2017).  
<http://www.sciencedirect.com/science/article/pii/S2213231717306535>

In brief, the authors aimed to investigate whether RBCs carry a functional soluble guanylate cyclase (sGC) signalling pathway and to address whether this pathway is compromised in coronary artery disease. The article states "**Using a commercial resin (HemoVoid™), which removes hemoglobin... and allows enrichment of soluble cytoplasmic proteins, we established a procedure that allows fast and reliable preparation of hemoglobin-free cell lysates from as little as 1-2 ml blood.** In those samples, expression and activity of the cGMP-generating sGC, cGMP-hydrolyzing PDE5 and cGMP-transducing PKG was assessed by enzymatic assays and Western blot analysis".

Feliciano, Amélia, et al. "Evening and morning alterations in Obstructive Sleep Apnea red blood cell proteome." *Data in Brief* (2017). <http://dx.doi.org/10.1016/j.dib.2017.01.005>

Using proteomics-based evaluation of red blood cells (RBC), the authors identified differentially abundant proteins associated with Obstructive Sleep Apnea Syndrome (OSA). The article states "RBC cytoplasmic fraction depleted of hemoglobin, using HemoVoid™ system, were analyzed by two-dimensional fluorescence difference gel electrophoresis (2D-DIGE), the 2D image software-based analyzed and relevant differentially abundant proteins identified by mass spectrometry (MS)".

Philipp F Lange, Pitter F Huesgen, Karen Nguyen, and Christopher M Overall. "[Annotating N termini for the Human Proteome Project: N termini and N<sub>α</sub>-acetylation status differentiate stable cleaved protein species from degradation remnants in the human erythrocyte proteome](#)". *J. Proteome Research.*, Just Accepted Manuscript • DOI: 10.1021/pr401191w • 21 Feb 2014

The article describes a goal of the Chromosome-centric Human Proteome Project to identify all human protein species. Enucleated, erythrocytes are simple yet proteomically challenging cells due to the high hemoglobin content (about 97% by mass) and wide dynamic range of protein concentrations that impedes protein identification. Using a N-terminomics procedure called TAILS, the authors identified from the **HemoVoid™ treated, soluble fraction, 778 proteins were identified, 171 of which were not represented in either the soluble non-depleted fraction or the membrane fraction.**

### RBCs in Parkinson's Disease

Klatt, Stephan, et al. "[Optimizing red blood cell protein extraction for biomarker quantitation with mass spectrometry.](#)" *Analytical and Bioanalytical Chemistry* (2020): 1-14.

The article describes the advantage of HemoVoid™ in detection of low abundance proteins when comparing their amounts (in percent) between four alternative extraction conditions, stating "... Most peptides, following HemoVoid™ extraction, showed ion abundances ranging between 1.00E+5 and 1.00E+6 (31%). In comparison to this, fewer peptides (10–23%) were within





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this range following extraction with all other protocols". With respect to potential biomarkers for Parkinson's Disease, the article states "For example, PRDX6 accounts for 0.4% of the total ion abundance after DOC (deoxycholate) extraction, whereas **following HV (HemoVoid™) extraction, this increases to 8%, a 20-fold enrichment**". The authors conclude that the HemoVoid™ method significantly reduces the concentration of hemoglobin, resulting in an increased signal-to noise of the remaining red cell proteins. The article describes methods to digest the HemoVoid™ bead-bound proteome, greatly simplifying the workflow for LC-MS/MS analysis.

Elhadi, Suaad Abd, et al. "[α-Synuclein in blood cells differentiates Parkinson's disease from healthy controls.](#)" *Annals of Clinical and Translational Neurology*.

The goal of this study was to determine whether blood cells expressing α-Synuclein can differentiate Parkinson's disease (PD) from healthy controls. Two proteoforms - P-Ser129 α-Syn (phosphorylated pathological form in Lewy bodies) and Oxidized α-Syn levels are observed in blood cells, but both at considerably lower concentration than total α-Syn, so the extremely high abundance of hemoglobin interferes with their analysis. To compensate, the article states for P-Ser129 α-Syn & Oxidized α-Syn detection by immunoassay, "followed from hemoglobin clearance with HemoVoid kit (Biotech Support Group)".

### Species Agnostic – Applications in non-human samples

Puente-Marin, Sara, et al. "[In Silico Functional Networks Identified in Fish Nucleated Red Blood Cells by Means of Transcriptomic and Proteomic Profiling.](#)" *Genes* 9.4 (2018): 202.

Nucleated red blood cells (RBCs) of fish have, in the last decade, been implicated in several immune-related functions, such as antiviral response, phagocytosis or cytokine-mediated signaling. Label-free shotgun proteomic analyses were carried out for in silico functional pathway profiling of rainbow trout RBCs. The article states "The cytosolic fraction, approximately 300 μL, was depleted of hemoglobin using HemoVoid™ kit (Biotech Support Group, Monmouth Junction, NJ, USA), in accordance with the manufacturer's instructions".

Nombela I, Puente-Marin S, Chico V et al. [Identification of diverse defense mechanisms in trout red blood cells in response to VHSV halted viral replication](#) *F1000Research* 2017, 6:1958 (doi: [10.12688/f1000research.12985.1](#))

The objective of this study was to determine the immune response and mechanisms of fish RBCs against viruses targeting other cells or tissues. The article states "a new proteomic analysis method was carried out that combines fractionation into cytosolic and membrane fractions, haemoglobin removal of the cytosolic fraction, protein digestion, pH reversed-phase peptide fractionation and finally LC ESI-MS/MS analysis of each of the fractions... Briefly, the haemoglobin of the cytosolic fraction was removed using a column of HemoVoid™ kit (Biotech Support Group, Monmouth Junction, NJ), following the manufacturer instructions".

**For a full list of Hemoglobin Removal References, visit:**

<https://www.biotechsupportgroup.com/References-s/138.htm#hemoglobin-depletion>

### RELATED SAMPLE PREP PRODUCTS:

#### Albumin & IgG Removal products:

<https://www.biotechsupportgroup.com/Albumin-Removal-s/307.htm>

#### Lipid Removal Reagent and Clarification products:

<https://www.biotechsupportgroup.com/Lipid-Removal-s/316.htm>

## CONTACT US

**We welcome your questions and comments regarding our products.**

Call 732-274-2866, 800-935-0628 (North America) Mon – Fri 9am-6pm EST.  
Email [sales@biotechsupportgroup.com](mailto:sales@biotechsupportgroup.com)