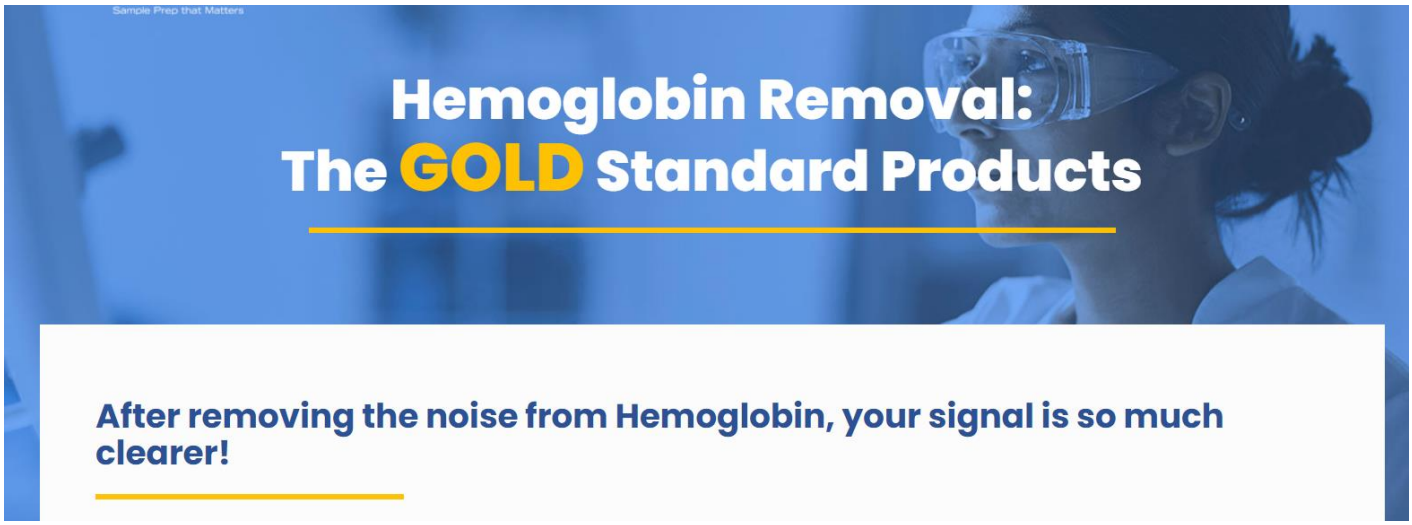
BIOTECH SUPPORT GROUP

Sample Prep that Matters



After removing the noise from Hemoglobin, your signal is so much clearer!

HemoVoid™

Removes Hemoglobin from erythrocyte and whole blood lysates, enriching the low abundance proteome

LEARN MORE

HemogloBind™

Engineered for high degree of selectivity to avoid cross reacting with most common serum components.

LEARN MORE

HemoVoid™ LC-MS On-Bead

Depletion plus low abundance protein enrichment with optimized on-bead digestion for LC-MS erythrocyte & whole blood

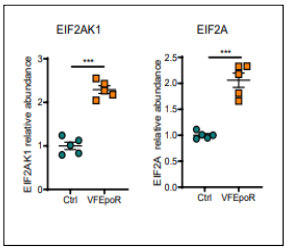
NuGel™ HemogloBind™

Similar performance properties to HemogloBind suspension, but supplied in dry powder format.

For more information on all of our Hemoglobin Removal products, visit:

https://www.biotechsupportgroup.com/Hemoglobin-Removal-s/312.htm

BSG's Hemoglobin Removal Products in LC-MS Proteomic Analysis



Liu, Wenli, et al. "Erythroid lineage Jak2 V617F expression promotes atherosclerosis through erythrophagocytosis and macrophage ferroptosis." *The Journal of Clinical Investigation* (2022).
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. … Samples were first digested with LysC in HVWB (from kit) with protease: protein ratio 1:100 overnight at 37 °C and then with trypsin in HVWB (from kit) with protease: protein ratio 1:30."

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 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 article describes methods to digest the HemoVoid™ bead-bound proteome, greatly simplifying the workflow for LC-MS/MS analysis.

Lange, Philipp F., et al. "Annotating N termini for the human proteome project: N termini and Nα-acetylation status differentiate stable cleaved protein species from degradation remnants in the human erythrocyte proteome." *Journal of proteome research* 13.4 (2014): 2028-2044.
The article describes a goal of the Chromosome-centric Human Proteome Project to identify all human protein species. With 3,844 proteins annotated as "missing" this is challenging. Enucleated and largely void of internal membranes and organelles, 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 1369 human erythrocyte natural and neo-N-termini and 1234 proteins. From the **HemoVoid™ treated, hemoglobin-depleted soluble fraction, 778 proteins were identified, 171 of which were not represented in either the soluble non-depleted fraction or the membrane fraction**.

Nguyen, Anthony T., et al. "UBE2O remodels the proteome during terminal erythroid differentiation." *Science* 357.6350 (2017)
The mechanisms that drive reticulocyte transition to red blood cell in terminally differentiating cells remain largely unclear. During reticulocyte maturation, the proteome is remodeled through the programmed elimination of most generic constituents of the cell, in parallel with abundant synthesis of hemoglobin. The study used multiplexed quantitative proteomics to identify candidate substrates of UBE2O, an E2 (ubiquitin-conjugating) enzyme, in an unbiased and global manner. Because of the overly abundant presence of Hemoglobin, selective depletion of Hemoglobin was necessary. The article states "Reticulocytes were lysed by vortexing for 5 minutes at room temperature… An additional 10 bed vol of **Hemoglobind™ suspension was added to the samples, …were … processed for TMT quantification**.".

A complete list of Hemoglobin Removal references can be found on our website at:
https://www.biotechsupportgroup.com/References-s/138.htm#hemoglobin-depletion