



HemoVoid[™] Hemoglobin Variant Enrichment From Blood

Purification & Enrichment Of Hemoglobin From Blood For Hemoglobin Variant Research

- Hemoglobin enrichment from fresh or frozen blood and dried blood spot/blood card etc.
- Enriched hemoglobin voids in flow-through >98% pure, with <30 minute bind/wash/elute protocol
- Disposable, cost-effective and high-throughput.
- Mild buffer condition maintains tertiary structure and simple transfer to secondary analysis
- Enriches hemoglobin from diverse species including human, sheep, mouse, goat, rat, etc.
- Enriched/purified hemoglobin can be studied for variant research and other research applications.
- Eluted fractions contains hemoglobin depleted proteins which can be used for LC-MS, proteomic studies

Product	Size	Blood sample processed	Item No.		
HemoVoid™ Hemoglobin Enrichment Kit	10 Preps	500 μ l of Blood Sample	HBV-10		
HemoVoid™ Hemoglobin Enrichment Kit	50 Preps	2500 μl of Blood Sample	HBV-50		
NOTE: Please contact sales@biotechsupportgroup.com for prices in bulk amount.					

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Items Required	10 Prep	50 Prep	Reagent
HemoVoid™	0.5 gram	2.5 grams	Supplied
Binding Buffer HVBB, PH 6.0	12 ml	60 ml	Supplied
Wash Buffer HVWB, PH 7.0	3 ml	15 ml	Supplied
Elution Buffer HVEB, PH 9.8	3 ml	15 ml	Supplied
SpinX Centrifuge tube filters	10	50	Supplied





Hemovoid[™] Protocol For Hemoglobin Enrichment From Blood Samples For Hemoglobin Variant (HbS, HbE, HbC, HbD, HbF, HbA1c, Thalassemia, etc.) Research

Based On Processing 50 µl Blood Sample

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

- 1. Weigh out 50 mg of **HemoVoid**[™] matrix into the supplied SpinX filter.
- Add 300 µl of Binding Buffer HVBB to the SpinX Filter. Vortex or mix well for 5 minutes at room temperature followed by centrifugation at 3000 rpm. Discard the supernatant.
- 3. Repeat step-2
- 4. Add 300 μl of **HVBB** and 50 μl of the **blood sample.** Vortex for 10 min and then centrifuge for 2 minutes at 5000 rpm. Pippet off the supernatant and discard the pellet.
- 5. Add the supernatant (step 4) to the equilibrated surface (step 3). Vortex for 10 min and then centrifuge for 2 minutes at 5000 rpm. Remove the filtrate as Flow-Through **FT** which contains enriched hemoglobin and is ready for further analysis.

Note: If using RBC Lysate, add additional **Binding Buffer HVBB** (1:1 ratio of RBC Lysate to HVBB). Then continue from Step 4.

- 6. To the pellet, add 300 μl of **Wash Buffer HVWB.** Vortex or mix well for 5 min and centrifuge for 2 minutes at 5000 rpm. Remove the filtrate as **Wash** which contains residual enriched hemoglobin and is ready for **hemoglobin variant** analysis. Note: If necessary, Wash and Flow-Through can be mixed.
- 7. To the pellet, add 300 µl of Elution Buffer HVEB. Vortex or mix well for 10 min and centrifuge for 2 minutes at 5000 rpm. Remove this filtrate as Hemoglobin depleted blood protein. The elution contains hemoglobin depleted protein. This elution is now ready for further analysis.
- 8. **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 hemoglobin removal.





Related HemoVoid™ References

Human Red Blood Cells (RBC)

<u>HemoVoid™ On Bead Digestion Application Work On RBC</u> by Irene Granlund, *Umeå University*

Red Blood Cells, Plasmodium extracts

Machado, Patrícia Isabel Pires. *Pyruvate kinase and glucose-6-phosphate dehydrogenase deficiencies and their association with malaria–population genetics and proteomic studies*. Diss. Universidade do Porto, 2013.

Walpurgis, Katja, et al. "<u>Effects of gamma irradiation and 15 days of subsequent ex vivo</u> storage on the cytosolic red blood cell proteome analyzed by 2D DIGE and Orbitrap <u>MS</u>." *PROTEOMICS-Clinical Applications* (2013).

P. Falciparum Clone 3D7 Cultured In Human Erythrocytes

Lasonder E, Green JL, Camarda G, Talabani H, Holder AA, Langsley G, Alano P. <u>The</u> <u>Plasmodium falciparum schizont phospho-proteome reveals extensive phosphatidylinositol</u> <u>and cAMP-Protein Kinase A signalling</u>. J Proteome Research. 2012;

Red Blood Cell Lysate

Barasa, Benjamin, and Monique Slijper. "<u>Challenges for red blood cell biomarker discovery</u> <u>through proteomics</u>." *Biochimica et Biophysica Acta (BBA)-Proteins and Proteomics* 1844.5 (2014): 1003-1010.

Lange, Philipp F., Pitter F. Huesgen, Karen Nguyen, and Christopher M. Overall. "<u>Annotating</u> <u>N termini for the Human Proteome Project: N termini and Na-acetylation status differentiate</u> <u>stable cleaved protein species from degradation remnants in the human erythrocyte</u> <u>proteome</u>." *Journal of proteome research* (2014).

Katja Walpurgis, Maxie Kohler, Andreas Thomas et al.<u>Validated hemoglobin-depletion</u> approach for red blood cell lysate proteome analysis by means of 2D-PAGE and Orbitrap <u>MS</u>.Electrophoresis.2012;

Mizukawa, B., George, A., Pushkaran, S. et al. <u>Cooperating G6PD mutations associated with</u> <u>severe neonatal hyperbilirubinemia and cholestasis</u>.Pediatric Blood Cancer.2011;56: 840-842.

Sudha Neelam, David G Kakhniashvili, Stephan Wilkens et al. <u>Functional 20S proteasomes</u> <u>in mature human red blood cells</u> Experimental Biology and Medicine.2011;236:580-591



CONTACT US

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