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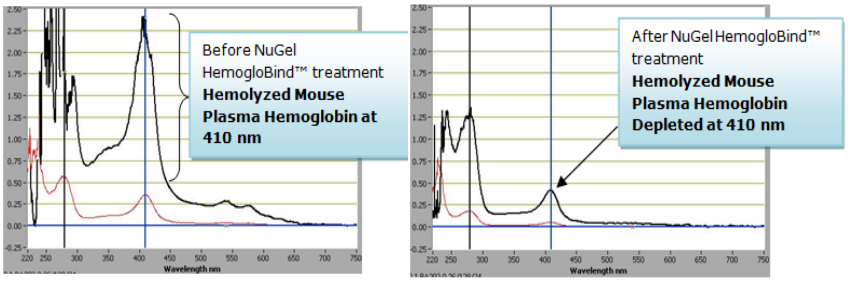
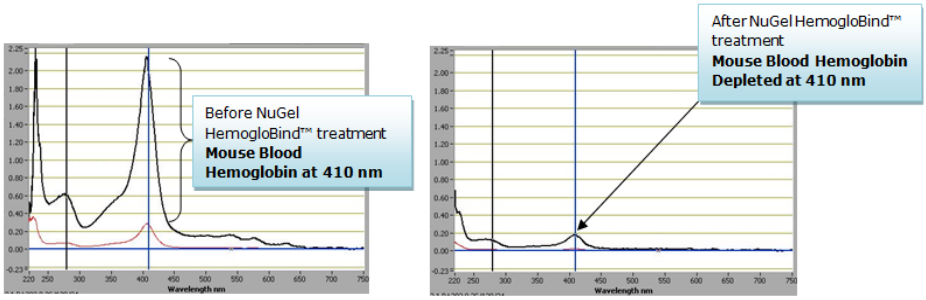
NuGel-HemogloBind™

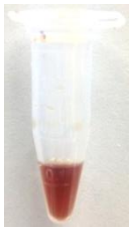
Hemoglobin Removal with NuGel™ Dry-Bead Format

- Has a high degree of specificity for hemoglobin binding up to 10 mg/ml
- Removes hemoglobin from any species blood including human, mouse, rat, sheep, bovine, goat, etc
- Removes hemoglobin from clarified organ/tissue lysates.
- Hemoglobin removal from red blood cell lysate for proteomics and biomarker drug discovery
- The flow through fractions (hemoglobin depleted) retain their enzymatic and biological activity
- Compatible with LC-MS, activity-based profiling and proteomic investigations
- Validated in the automation compatible high-throughput DPX Technologies XTR tip format

NuGel™ Hemoglobind™ is a modified version of suspension HemogloBind™, engineered for increased stability and improved installation for high-throughput formats. It is based on NuGel™ silica (50 microns in size, 1000Å) covalently bound to elastomeric polyelectrolytes. Comparable to selection properties of suspension HemogloBind™, at recommended quantities, >95% of hemoglobin can be removed with very high selectivity.







Hemolyzed Mouse Plasma before Treatment with NuGel

NuGel HemogloBind™

Hemolyzed Mouse Plasma after Treatment with NuGel HemogloBind

Diluted Hemolyzed Mouse Plasma Before Treatment

NuGel HemogloBind™

Diluted Hemolyzed Mouse Plasma After Treatment

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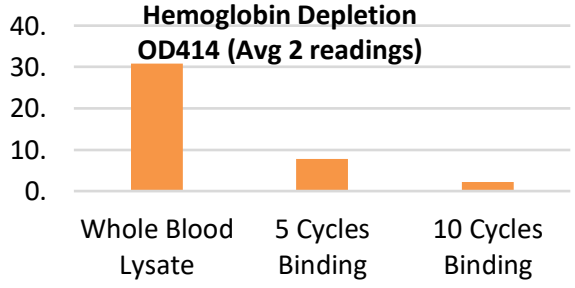
LC-MS data from NuGel™ HemogloBind™ installed within the high-throughput DPX Technologies XTR tip format

Representative Enriched Proteins after NuGel HemogloBind (Uniprot ID)	Description	Sp. Cts control	Sp. Cts after
sp|P01023|A2MG_HUMAN	Alpha-2-macroglobulin	376	896
sp|P04114|APOB_HUMAN	Apolipoprotein B-100	280	660
sp|P02751-1|FINC_HUMAN	Fibronectin	120	248
sp|P43652|AFAM_HUMAN	Afamin	23	54
sp|P11277|SPTB1_HUMAN	Spectrin beta chain	32	130
sp|P02549|SPTA1_HUMAN	Spectrin alpha chain	39	163
sp|P04003|C4BPA_HUMAN	C4b-binding protein alpha chain	15	50
sp|P08697|A2AP_HUMAN	Alpha-2-antiplasmin	19	48
sp|Q06033|ITIH3_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H3	14	43
sp|P02730|B3AT_HUMAN	Band 3 anion transport protein	42	110
sp|P05543|THBG_HUMAN	Thyroxine-binding globulin	7	27
sp|P09871|C1S_HUMAN	Complement C1s subcomponent	9	34
sp|O75882|ATRN_HUMAN	Attractin	4	18
sp|P16157|ANK1_HUMAN	Ankyrin-1	18	73
sp|P04406|G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase	28	61
sp|P02750|A2GL_HUMAN	Leucine-rich alpha-2-glycoprotein	4	13
sp|P62258|1433E_HUMAN	14-3-3 protein epsilon	11	51
sp|P20742|PZP_HUMAN	Pregnancy zone protein	7	36
tr|G3V1D3|G3V1D3_HUMAN	Dipeptidyl peptidase 3	9	42
tr|C9JIF9|C9JIF9_HUMAN	Acyl-peptide hydrolase	11	38
sp|P15169|CBPN_HUMAN	Carboxypeptidase N catalytic chain	2	14
sp|P05160|F13B_HUMAN	Coagulation factor XIII B chain	1	13
sp|P16452|EPB42_HUMAN	Protein 4.2	5	38
sp|Q13630|FCL_HUMAN	GDP-L-fucose synthase	8	33
sp|P09960|LKHA4_HUMAN	Leukotriene A-4 hydrolase	9	28
sp|P22314-2|UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1	8	28
sp|P07900|HS90A_HUMAN	Heat shock protein HSP 90-alpha	3	28
sp|P12955|PEPD_HUMAN	Xaa-Pro dipeptidase	3	23
sp|P23142|FBLN1_HUMAN	Fibulin-1	4	19
sp|P25786|PSA1_HUMAN	Proteasome subunit alpha type-1	2	25
sp|P31946|1433B_HUMAN	14-3-3 protein beta/alpha	4	18
sp|P45974|UBP5_HUMAN	Ubiquitin carboxyl-terminal hydrolase 5	2	20
sp|Q6XQN6|PNCB_HUMAN	Nicotinate phosphoribosyltransferase	3	17
sp|P09211|GSTP1_HUMAN	Glutathione S-transferase P	5	15
sp|P61970|NTF2_HUMAN	Nuclear transport factor 2	4	15
tr|F6TLX2|F6TLX2_HUMAN	Glyoxalase domain-containing protein 4	4	15
sp|P07996|TSP1_HUMAN	Thrombospondin-1	nd	19
sp|P28070|PSB4_HUMAN	Proteasome subunit beta type-4	4	15
sp|P00488|F13A_HUMAN	Coagulation factor XIII A chain	1	16
sp|P21980|TGM2_HUMAN	Protein-glutamine gamma-glutamyltransferase 2	1	14
sp|Q14974|IMB1_HUMAN	Importin subunit beta-1	nd	14
sp|P53396|ACLY_HUMAN	ATP-citrate synthase	1	13
sp|P06132|DCUP_HUMAN	Uroporphyrinogen decarboxylase	1	13
tr|B3KQV6|B3KQV6_HUMAN	Serine/threonine-protein phosphatase 2A	nd	10

LC-MS Proteomic Analysis of Serum (single 2 hr gradient)	Whole Blood Lysate Control	After NuGel™ HemogloBind™/ INTip™
Total Spectral Counts (Sp. Cts)	**14532**	**19054**
Total Protein IDs (≥2 Sp. Cts)	**306**	**420**
# of Unique Protein IDs (≥2 Sp. Cts)	**27**	**134**
# of Enriched Proteins ≥3X		**47**
# of Depleted Proteins (other than Hemoglobin subunits) ≥3X	**6**	



From a poster report describing NuGel™ HemogloBind™ installed within the high-throughput DPX Technologies XTR tip format. For full poster report, go to: https://www.biotechsupportgroup.com/v/vspfiles/templates/257/pdf/ASMSBSGDPXPoster.pdf

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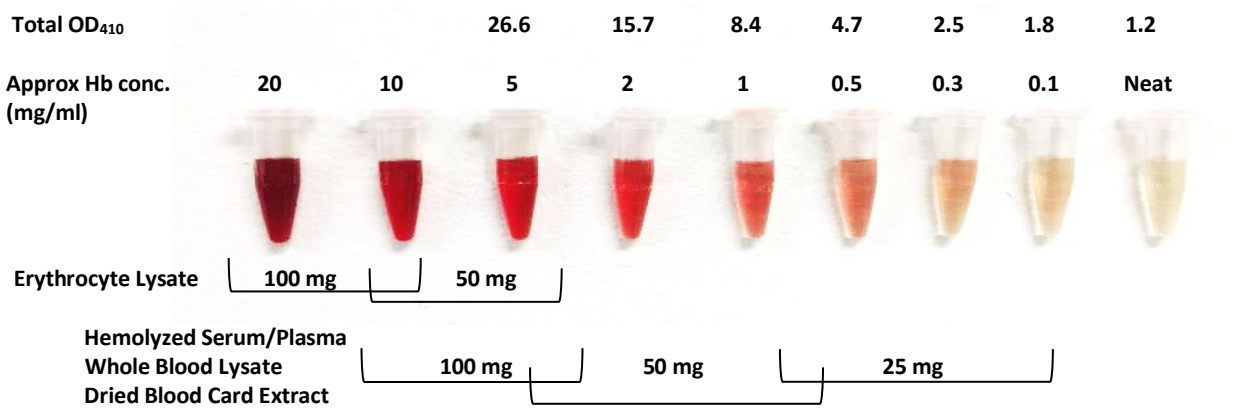
Product	Size	Total Sample Processed	Product Code
NuGel-HemogloBind™	25 preps	500µl of blood or 5 ml of Hemolyzed Serum or Plasma	NP-HO-T25
NuGel-HemogloBind™	50 preps	1 ml of blood or 10 ml of Hemolyzed Serum or Plasma	NP-HO-T50
NuGel-HemogloBind™	5 preps	100µl of blood or 1 ml of Hemolyzed Serum or Plasma	Included in HemoTrial™ kit (HTK-05)
NuGel-HemogloBind™	5 preps	100µl of blood or 1 ml of Hemolyzed Serum or Plasma	Included in HemogloBind™ Trial kit (HB145K)

Items Required	5 Prep	25 Prep	50 Prep	Reagent
NuGel-HemogloBind™ beads	0.25 gram	1.25 grams	2.5 gram	Supplied
Hemoglobin Binding Buffer (HB) 0.05M K_2HPO_4 pH 6.5	3 ml	15 ml	30 ml	Supplied
Spin-filter / tube assemblies	5	25	50	Supplied

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

Guidelines for determining the quantity of NuGel™ HemogloBind™ to sample. Use this chart to estimate the amount of Hemoglobin in samples containing mostly Hemoglobin (i.e., lysed erythrocytes) or mostly serum/plasma proteins (i.e., hemolyzed serum). Adjust bead amounts as necessary to optimize for investigative goals.

NuGel™ HemogloBind™ bead amounts (mgs/prep) are based on 200 µl sample volumes



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PROTOCOL – To Treat Whole Blood (10-20 µl) Sample

1. **BEAD CONDITIONING.** Weigh out 50 mg of **NuGel-HemogloBind™** beads in a Spin-filter tube. Add 200 µl of **Hemoglobin Binding Buffer (HB)** to the beads. Vortex or mix well for 2 minutes at room temperature. Centrifuge for 4 minutes at 5,000-10,000 rpm (2,000-8,000xg). Discard the filtrate.
2. **SAMPLE CONDITIONING.** In a separate microfuge tube, add 200-400 µl of **Hemoglobin Binding Buffer (HB)** and 10-20 µl of blood sample. Vortex for 3 minutes.
3. **SAMPLE PROCESSING.** Add sample from step 2 to conditioned beads from step 1.
4. Vortex or mix well for 10 minutes at room temperature followed by centrifugation for 4 minutes at 5,000-10,000 rpm (2,000-8,000xg).
5. Collect the filtrate which contains the hemoglobin depleted sample suitable for further analysis; the retained material contains the hemoglobin removed.

PROTOCOL – To Treat Hemolyzed Serum/Plasma (200 µl) Sample

1. **BEAD CONDITIONING.** Weigh out 50 mg of **NuGel-HemogloBind™** beads in a Spin-filter. Add 400 µl Hemoglobin Binding Buffer. Vortex or mix well for 2 minutes at room temperature. Centrifuge for 4 minutes at 5,000-10,000 rpm (2,000-8,000xg). Discard the filtrate.
2. **SAMPLE PROCESSING.** Add 200 µl Hemolyzed sample to the conditioned beads.
3. Vortex or mix well for 10 minutes at room temperature followed by centrifugation for 4 minutes at 5,000-10,000 rpm (2,000-8,000xg) rpm.
4. Collect the filtrate which contains the hemoglobin depleted sample suitable for further analysis; the retained material contains the hemoglobin removed.

Scaleable and Versatile Protocol

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

Desorption of Bound Hemoglobin

For purification and/or analysis of hemoglobin, 100 mM Tris-Borate, pH 9, will facilitate desorption of hemoglobin bound to **NuGel™ HemogloBind™**.

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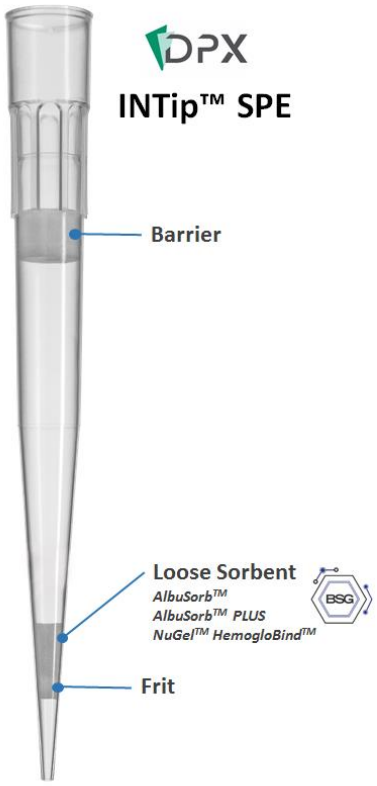
Validated in the high-throughput XTR tip format

The XTR tip format improves ease of use and scalability to process multiple samples in parallel, utilizing 96-well plates and automated liquid handlers. INTip™ SPE formats have been proven to be compatible with most automation platforms, i.e., Integra, Hamilton, etc. The **NuGel™ HemogloBind™** beads are loosely contained inside the XTR tips for a dispersive functionality that maximizes depletion efficacy.

A poster report is downloadable at:
https://www.biotechsupportgroup.com/v/vspfiles/templates/257/pdf/ASMSBSGDPXPoster.pdf

Please inquire for price and availability.



Selection of HemogloBind ™ Reference Applications

Hemolyzed Serum Analyses
Krishna, Neel K., and Kenji Cunnion. "Derivative Peptide Compounds and Methods of Use." U.S. Patent Application No. 15/192,934. http://www.freepatentsonline.com/y2016/0376322.html

The patent application describes synthetic peptide compounds for therapy and diagnostics of complement-mediated diseases, such as inflammatory diseases, autoimmune diseases, and microbial and bacterial infections and non-complement-mediated diseases, such cystic fibrosis and various acute diseases. The invention describes Peptide Inhibitors of Complement C1. In the example description, the patent states "Due to large amounts of hemolysis in the latter time points and the associated optical interference in bilirubin analysis, all the samples were pre-treated with HemogloBind™ (Biotech Support Group, NJ) prior to analysis with the Bilirubin Assay Kit."

Hemolyzed Serum Exosome Analyses
Nishida-Aoki, Nao, et al. "Disruption of Circulating Extracellular Vesicles as a Novel Therapeutic Strategy against Cancer Metastasis." *Molecular Therapy* 25.1 (2017): 181-191.

http://dx.doi.org/10.1016/j.ymthe.2016.10.009
The researchers report on a novel strategy of therapeutic antibody treatment to target cancer-derived EVs and inhibit the metastasis of breast cancer in a mouse model. The article states "Hemoglobin was accumulated with HemogloBind™ beads…EVs in the sera were concentrated by ultracentrifugation…".

Red Cell Lysates

Hojo-Souza NS, de Azevedo PO, de Castro JT, Teixeira-Carvalho A, Lieberman J, et al. (2020) Contributions of IFN-γ and granulysin to the clearance of Plasmodium yoelii blood stage. PLOS Pathogens 16(9): e1008840. https://doi.org/10.1371/journal.ppat.1008840

The authors investigated how Plasmodium infection induces MHC-I expression on Retics. In addition, whether granulysin helps control Plasmodium infection *in vivo* has not been studied. To remove interferences associated with Hemoglobin, the article states, "For western blot analysis, erythroblasts pellets were resuspended in RIPA Buffer (Sigma)…. The Retics were treated with HemogloBind …".

Dziekan, Jerzy Michal, et al. "Cellular thermal shift assay for the identification of drug–target interactions in the Plasmodium falciparum proteome." Nature Protocols (2020): 1-41.

The cellular thermal shift assay (CETSA) protocol presents a comprehensive strategy for the identification of drug targets. CETSA enables proteome-wide target screening for unmodified antimalarial compounds with undetermined mechanisms of action, providing quantitative evidence about direct drug–protein interactions. The experimental workflow involves treatment of *P. falciparum*–infected erythrocytes with a compound of interest, heat exposure to denature proteins, soluble protein isolation, enzymatic digestion, peptide labeling with tandem mass tags, offline fractionation, and liquid chromatography–tandem mass spectrometry (LC-MS) analysis. The article states "**The intact-cell CETSA protocol features a HemogloBind- based sample processing step, which provides a relatively fast, reliable and inexpensive method to deplete >90% of hemoglobin from processed intact-cell samples. As a result, it leads to a 40-50% increase in the number of peptide spectrum matches (PSMs) for *P. falciparum* and non-hemoglobin human proteins.".**

Nguyen, Anthony T., et al. "UBE2O remodels the proteome during terminal erythroid differentiation." *Science* 357.6350 (2017): eaan0218.

This 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, which were then vortexed for another 10 min at room temperature followed by 4 min of centrifugation at 10000 x *g*. The supernatants, which contain hemoglobin-depleted sample, were … processed for TMT quantification.".

Whole Blood Lysates

Kaneko, Tomonori, et al. " System-wide hematopoietic and immune signaling aberrations in COVID-19 revealed by deep proteome and phosphoproteome analysis. " Research Square preprint (2021).

The author's goals were to gain systems-level insights into SARS-CoV-2 pathogenesis. For that, they compared the blood proteome and phosphoproteome of ICU patients with or without SARS-CoV-2 infection, and healthy control subjects by quantitative mass spectrometry. To remove the highly abundant amount of Hemoglobin, the article states "Hemoglobin was depleted from PBMC whole cell lysate samples according to HemogloBind ™ manufacturer instruction with modifications."

Lahut, Suna, et al. "Blood RNA biomarkers in prodromal PARK4 and REM sleep behavior disorder show role of complexin-1 loss for risk of Parkinson's disease." *Disease Models & Mechanisms* (2017): dmm-028035. http://dmm.biologists.org/lookup/doi/10.1242/dmm.028035

The authors studied blood samples from a new large pedigree with *SNCA* gene duplication (PARK4 mutation), to identify effects of SNCA gain-of-function as potential disease biomarkers. The article states "For protein extraction from the EDTA tubes, 300 µl blood were lysed with equal amount of 1% SDS-RIPA buffer [50 mM Tris-HCl (pH 8.0), 150 mM NaCl, 1 mM EDTA, 1 mM EGTA, 1% Igepal CA-630 (Sigma), 0.5% sodium deoxycholate, 0.1% SDS, 1 mM PMSF and one tablet Complete Protease Inhibitor Cocktail (Roche)] and sonicated for 10 sec. The blood lysates were rotated at 4 °C for 30 min and centrifuged at 4 °C for 30 min. The supernatants were depleted in hemoglobin content using a commercial kit (HemogloBind™) following the manufacturer's instructions".

Chalásová, Katarína, et al. "Transketolase Activity but not Thiamine Membrane Transport Change in Response to Hyperglycaemia and Kidney Dysfunction." *Experimental and Clinical Endocrinology & Diabetes* (2017). https://www.thieme-connect.com/products/ejournals/abstract/10.1055/s-0043-115009

Diabetic kidney disease, a common complication of both type 1 and type 2 diabetes, is associated with significant morbidity and mortality, and represents the most common cause of chronic kidney disease. The study hypothesized that protective pentose

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phosphate pathway action in diabetes might be compromised by limited intracellular availability of an active transketolase cofactor thiamine diphosphate (TDP). To evaluate the levels of thiamine transporter proteins in whole blood, t he article states " For protein isolation, whole blood aliquots were lysed with water and haemoglobin was removed using HemogloBind™ (Biotech Support Group) according to manufacturer's instructions…".

Hemoglobin Isolation and Derivative Analysis
Yamagishi, Yoshikazu, Hirotaro Iwase, and Yasumitsu Ogra. "Post-Mortem Changes of Methomyl in Blood with Hemoglobin." Chemical Research in Toxicology.

In this study, the researchers considered specific methomyl hemoglobin adducts detected by liquid chromatography quadrupole time-of-flight mass spectrometry (LC-Q/TOF-MS). To help isolate Hemoglobin, the article states "Hb was separated with HemogloBind in accordance with the manufacturer's instructions." The authors conclude that one Hemoglobin derivative, the W-adduct could be used as a biomarker of methomyl poisoning.

Tissue Lysates, LC-MS Proteomics
Heather E. McKiernan, Phillip B. Danielson, Catherine O. Brown, Masha Signaevsky, Christian G. Westring and Kevin M. Legg, Developmental Validation of a Multiplex Proteomic Assay for the Identification of Forensically Relevant Biological Fluids, Forensic Science International, (2021) https://www.sciencedirect.com/science/article/pii/S0379073821002280?via%3Dihub

The aim of this study was to validate a multiplex proteomic assay for the identification of target peptide fragments by multiple reaction monitoring on a triple quadrupole mass spectrometer originating from tissue-specific proteins. The article states "If samples contained excessive quantities of hemolyzed red blood cells, four volumes of HemogloBind™ were added." The authors conclude that the mass spectrometry-based workflow offers significant advantages compared to existing serological methods.

C Wan, B Borgeson, S Phanse, F Tu, K Drew, G Clark, et al. Panorama of ancient metazoan macromolecular complexes. Nature Volume:525, Pages:339–344 Date published:(17 September 2015). doi:10.1038/nature14877.

HemogloBind™, contributed to this rigorous examination of protein complexes. When our products (**HemogloBind™ & NRicher™ 6**) were used as a pretreatment step in the overall workflow, twice the number of observations and annotations became possible. Furthermore, this study demonstrated the importance of a key feature implicit to all of our products; that is the maintenance of functional and structural integrity after separations.

Species Agnostic – Applications to Different Species
D'Alessandro, Angelo, et al. "Hematologic and systemic metabolic alterations due to Mediterranean type II G6PD deficiency in a novel murine model." *bioRxiv* (2021).

To generate a more accurate model of Glucose 6 phosphate dehydrogenase deficiency, the human sequence for a severe form of G6PD deficiency (Med -) was knocked into the murine G6PD locus and confirmed by Western blot. The article states "Briefly, RBCs were washed 3 times PBS, followed by transfer of one part washed RBCs into three parts water, followed by end over end rotation for 5 min at room temperature to lyse the RBCs. Lysed RBCs were then mixed 1:1 with HemogloBind™, followed by end over end rotation for 10 min at room temperature. HemogloBind™ and bound hemoglobin were pelleted by centrifugation, and supernatants subjected to an additional hemoglobin depletion with HemogloBind™. Supernatants were used for western blotting."

Southwell, Rebecca Marie, Kenneth Sherlock, and Matthew Baylis. "Cross-sectional study of British wild deer for evidence of Schmallenberg virus infection." Veterinary Record (2020).

The purpose of this study was to survey wild deer across Great Britain for recent evidence of Schmallenberg virus (SBV). Postmortem blood samples were tested for SBV antibodies. Because of the presence of Hemoglobin interference in many samples, the article states "**In order to avoid poor quality samples yielding false ELISA results, 59 samples estimated to have above 50mg/dL and less than 250mg/dL haemoglobin concentration, according to their colour, were selected for treatment with HemogloBind™** (Biotech Support Group, New Jersey, USA).".

Snider, Thomas H., Christina M. Wilhelm, Michael C. Babin, Gennady E. Platoff Jr, and David T. Yeung. "Assessing the therapeutic efficacy of oxime therapies against percutaneous organophosphorus pesticide and nerve agent challenges in the Hartley guinea pig."The Journal of Toxicological Sciences 40, no. 6 (2015): 759-775.

Clinical signs of cholinesterase inhibitor toxicity can be measured from blood cholinesterase [Acetylcholinesterase (AChE) and butyrylcholinesterase (BChE)] activity utilizing a modified Ellman's method. Biotech Support Group's unique solid-phase polymer for

hemoglobin depletion, was used for pretreatment. The article states "Briefly, whole blood samples were treated with HemogloBind™ which interferes with the ChE activity assay due to spectral overlap."

Craig, J. R., et al. "A comparison of the anatomical and gastrointestinal functional development between gilt and sow progeny around birth and weaning." *Journal of animal science* (2019).

Gilt progeny (GP) often have restricted growth performance and health status in comparison to sow progeny (SP) from birth. To better understand underlying mechanisms, the study aimed to compare differences in growth and development between GP and SP in the first 24 h after birth and in the peri-weaning period. Because serum samples were quite hemolysed after collection and processing, it became necessary to use HemogloBind™ to allow for better detection of IgG by ELISA. The article states "As per the manufacturer's instructions, 250 µL of Hemoglobind was added to 250 µL of hemolyzed serum…

Parvathi S. Kumar, Haree K. Pallera, Pamela S. Hair, Magdielis Gregory Rivera, Tushar A. Shah, Alice L. Werner,Frank A. Lattanzio, Kenji M. Cunnion, and Neel K. Krishna. Peptide inhibitor of complement C1 modulates acute intravascular hemolysis of mismatched red blood cells in rats.TRANSFUSION Volume 00, May 2016. doi:10.1111/trf.13674.

In brief, the study evaluated the role of a peptide inhibitor of complement C1 (PIC1) in an animal model of acute intravascular hemolysis in both prevention and rescue scenarios. The authors state "To remove free Hb that may cause optical interference in bilirubin analysis, we treated all the samples with Hb depletion from hemolyzed serum/plasma (HemogloBind). Bilirubin concentration was then measured with a Bilirubin Assay Kit (Sigma-Aldrich, St. Louis, MO)."

Blood Substitutes

Juriasingani, Smriti, et al. "Evaluating the Effects of Subnormothermic Perfusion with AP39 in a Novel Blood-Free Model of Ex Vivo Kidney Preservation and Reperfusion." *International Journal of Molecular Sciences* 22.13 (2021): 7180.

This study evaluated whether adding hydrogen sulfide donor AP39 to Hemopure, a blood substitute, during subnormothermic perfusion improves kidney outcomes. Because of the added Hemopure, the article states, "Most of the urine samples collected were heavily pigmented, due to the presence of hemoglobin from the Hemopure, which prevented the use of conventional urinalysis methods. A 1:3 dilution of urine in Hemoglobind (Biotech Support Group, Monmouth Junction, NJ, USA) allowed us to obtain clearer urine samples after 10 min of vigorous shaking and centrifugation at 12,000× *g*."

For a full list of Hemoglobin Removal References, visit:
https://www.biotechsupportgroup.com/References-s/138.htm#hemoglobin-depletion

Related Separations, Enrichment/Depletion & Sample Prep - All Product Categories (https://www.biotechsupportgroup.com/Products-a-z_a/258.htm)
Hemoglobin Removal (https://www.biotechsupportgroup.com/Articles.asp?ID=452)
Albumin & IgG Removal (https://www.biotechsupportgroup.com/Articles.asp?ID=451)
Lipid Removal and Clarification (https://www.biotechsupportgroup.com/Articles.asp?ID=456)
Sample Prep – Liquid Biopsy (https://www.biotechsupportgroup.com/Articles.asp?ID=457)
Sample Prep – Glyco, Virus, Kinase, Aqueous Protein Crash/Metabolomics (https://www.biotechsupportgroup.com/Articles.asp?ID=453)
Sample Prep – Mass Spectrometry (https://www.biotechsupportgroup.com/Articles.asp?ID=432)
Sample Prep – Genomics (https://www.biotechsupportgroup.com/Articles.asp?ID=455)

CONTACT US

We welcome your questions, comments and concerns regarding our products.

Call 732-274-2866, Monday – Friday 9am-6pm EST.
Email sales@biotechsupportgroup.com
Mail 1 Deer Park Drive, Suite M, Monmouth JCT, NJ 08852, USA