

Proteomic & Genomic Sample Preparation & Enrichment

BEOTECH **SUPPORT** GROUP

Sample Prep that Matters

PROTEOMICS SAMPLE PREP

ALBUMIN DEPLETION

HEMOGLOBIN DEPLETION

LOW ABUNDANCE ENRICHMENT

CLASS SPECIFIC ENRICHMENT

FUNCTIONAL PROTEOMICS

CHEMICAL PROTEOMICS

GENOMICS SAMPLE PREP

Biotech Support Group LLC

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Sample Prep that Matters

Our Mission

We are dedicated to create new methods and applications to drive efficient workflows and better data quality for all proteomic and biomarker analyses.

Technology Platforms

The "omics" revolution demanded new and different sample prep separations that were not efficiently performed by conventional technologies. For years the protein separations toolkit was limited to liquid chromatography and gel electrophoresis. While effective for many applications, such tools were not efficient for "omics" sample preparation, when throughput, economy and simplicity were required. Furthermore, these same separation tools most often denatured proteins which limited there use in applications which required the measurement of function, structure or bio-activity.

NuGel™ Silica Surface Chemistry

Through a proprietary polymer coating, 50 µm porous silica beads are crosslinked and passivated. From this NuGel™ platform chemistry, a library of bead architectures have been created. Each bead chemistry in the library presents a mixed-mode interaction; combining elements of ionic, aliphatic and aromatic hydrophobicity, and polymeric characteristics. One can think of these binding interactions in different terms; as general non-specific protein adsorbents, or as bead matrices with weak affinity or imperfect fit interactions. In this way, their binding behavior is very different from classical high affinity binding which demands near perfect fits. When conditions support protein binding saturation, progressive displacement allows the beads to bias for or against certain proteins. So in this manner, all derivative NuGel™ products were empirically characterized to meet the needs of the application; for example, HemoVoid™ to selectively void (not bind) hemoglobin while capturing the majority of the remaining low abundance proteome on the bead. NuGel™ bead products are supplied as dry powders, and NuGel™ based kits include all necessary buffers to meet the application requirements.

Polymers & Metallic Oxides

Along with the NuGel™ based products, ProCipitate™, and related products Viraffinity™, and HemogloBind™ come from a family of acid-alcohol elastomeric co-polymers. These polymers are synthesized in unique ways to have separation characteristics like salts and solvents, but with the mechanical advantages of solid-phases: simple removal of the bound macromolecules with no carryover of the solute, and adaptability to filtration, centrifugation, and automation. Two metallic oxide based products, Cleanascite™ and KinaSorb™, are also featured in the catalog. Polymer & metallic oxide based products are supplied as liquid suspensions.

While selective protein binding is the focus of the surface chemistries, many of our products crossover to other "omic" fields, finding applications in genomics and DNA isolation, and metabolomics.

The BSG Advantage

All of our products have these 4 common features and collective advantages:

Consumable

Cost-effective, not derived from biologicals



- No specialized instruments or HPLC
- Economical surface chemistries, not derived from biologicals
- No regeneration, so no prep to prep variability
- Simple, fast microfuge bind/wash/elute protocols

Enrichment / Depletion

Diverse strategies, species agnostic



- Products support strategies for both enrichment of low abundance proteomes, or depletion of high abundance proteins
- Species agnostic, not derived from biologicals

On-Bead Digestion

Efficient workflows, quality LC-MS/MS data



- Simple, reproducible workflows
- Equivalent or better than in-solution digestion
- Seamless to LC-MS, no desalting or C18 separations
- Unique proteolytic efficiencies

Functional Integrity Maintained throughout all separations



- Mild buffer conditions maintains native structure with retained enzymatic, functional & bio-activities
- Supports enzyme biomarker assays
- Functional & Chemical Proteomics
- Structural & activity-probe Proteomics
- Top-down & ArrayBridge PEP Proteomics

Page Contents

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Products are for research use only.



Albumin Removal Kits Enrichment of Low Abundance Serum/Plasma Proteins

AlbuVoid™

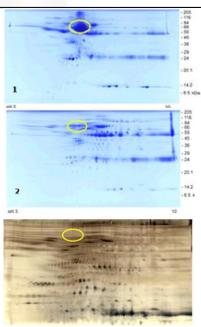
Selectively Voids Albumin, Binds Low Abundance Proteome

- Albumin voids in flow->95%
- Transferrin voids >99%
- <30 minute protocol
- Low abundance enrichment equivalent or better than hexapeptides or antibodies
- On-bead digestion protocols, efficient LC-MS workflows
- Disposable, costeffective, no column regeneration or cross-contamination
- Mild elution maintains native structure with retained enzymatic, functional & bio-activities
- Species agnostic

| Product | Size | Item No. |
|-----------|----------|----------|
| AlbuVoid™ | 5 Preps | AVK-05 |
| AlbuVoid™ | 10 Preps | AVK-10 |
| AlbuVoid™ | 50 Preps | AVK-50 |

Based on 100-200 µl serum preps

| 2DE analysis of | |
|-------------------------------|---|
| AlbuVoid [™] treated | |
| sheep serum. | |
| Samples were | |
| reduced, alkylated | |
| and total protein | |
| normalized. The | |
| circled regions | |
| indicate the | |
| albumin zone. Gel | |
| 1: Sheep serum | |
| sample. Gel2: | |
| AlbuVoid™ Eluate. | |
| Gel 3: Same as 2 - | |
| AlbuVoid™ Eluate | |
| but restained with | |
| SilverQuest | |
| (Invitrogen) silver | |
| stain. The | |
| differences betwee | n |
| the gels illustrate | |
| the efficiency of | |
| albumin removal, | |
| with no intrinsic pI | |
| or MW bias. | |
| | |



| Typical Performance | |
|--------------------------------------|------------|
| Serum Sample Volume | 100-200 µl |
| Albumin Removal | >95%* |
| LC-MS unique proteins | 400-600 |
| LC-MS unique peptides | 3000-5000 |
| Total Low Abundance Protein Recovery | >95%* |

^{*} Estimates based on SDS-PAGE visualization combined with Total Protein Assay.

AlbuVoid™ LC-MS On-Bead

Albumin depletion plus low abundance protein enrichment coupled with optimized on-bead digestion protocols for LC-MS serum and plasma proteomics

- Seamless workflows, unique proteolytic efficiencies
- Label, label free & glycocompatible
- See page 5 for more information and ordering

AlbuTrial™ Kit

Don't know which one to try? Try both. AlbuTrialTM kit is a combination of AlbuSorbTM and AlbuVoidTM with respective buffers.

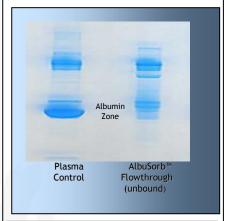
| Product | Item # |
|-------------------|-----------|
| AlbuTrial™ Kit | AVS-05 |

The Kit includes:

- 1 Gram **AlbuSorb**™ beads +
- 5 Preps **AlbuVoid™**

AlbuSorb™ Selectively Binds Albumin

- Removes 30 mg albumin/ml, >90%
- Economical small ligand surface architecture (not dye-based), bio-affinity performance
- Consumable, cost-effective, no column regeneration or cross-contamination
- Species agnostic
- Compatible with
 - o LC-MS
 - o Chemical
 - Functional proteomics



| Product | Size | Item No. | | |
|--|------|----------|--|--|
| AlbuSorb™ | 1 gm | A185-1 | | |
| AlbuSorb™ | 6 gm | A185-6 | | |
| 1 gm processes 20 preps, 25 µl serum samples | | | | |

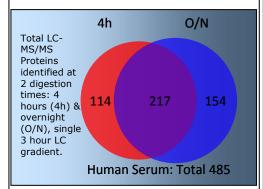


On-Bead Digestion Kits For LC-MS Proteomics

AlbuVoid™ LC-MS On-Bead

Albumin depletion plus low abundance protein enrichment coupled with optimized on-bead digestion protocols for LC-MS serum and plasma proteomics

- Seamless workflows
- Unique proteolytic efficiencies
- · Label, label free compatible



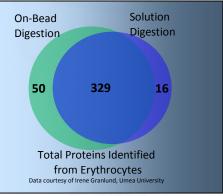
| Product | Size | Item No. |
|-------------------------------|-------------|----------|
| AlbuVoid™ LC-MS On-Bead | 5 Preps | HVB-MS05 |
| AlbuVoid™ LC-MS On-Bead | 10 Preps | HVB-MS10 |

Based on 50-100 µl serum preps

HemoVoid™ LC-MS On-Bead

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

- Seamless workflows
- Unique proteolytic efficiencies
- Label, label free compatible

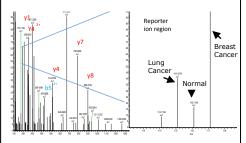


| Product | Size | Item No. | |
|--|------------|----------|--|
| HemoVoid™ LC-MS On- Bead | 5 Preps | HVB-MS05 | |
| HemoVoid™ LC-MS On- Bead 10 Preps HVB-MS1 | | | |
| Based on 100-200 µl erythrocyte | | | |

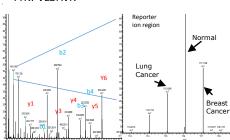
Quantitative Efficiency

Label or label-free

C3: KVLLDGVQNPR



TTR: VLDAVR



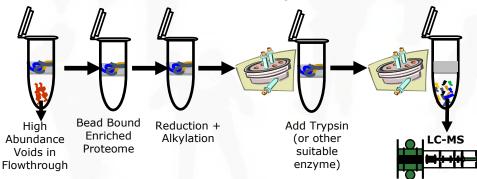
Isobaric (ITRAQ) labeled peptides from two representative proteins observed to be differentially quantified. On the right, the peptide features from the MS2 spectral profile, are magnified to illustrate the differences in reporter intensities between the three sera enriched with AlbuVoid™ and onbead digested. Top: Complement Component 3 (C3), Bottom: Transthyretin (TTR).

On-Bead Digestion

Efficient workflows, quality LC-MS/MS data

• Simple, reproducible workflows • Equivalent or better than in-solution digestion • Seamless to LC-MS, no desalting or C18 separations • Unique proteolytic efficiencies • Label, label-free & phospho/glyco compatible

High Abundance Depletion + Unique Digestion Efficiencies + Simple Workflows = Better LC-MS Output





Hemoglobin Depletion and/or Enrichment

HemoVoid™

Hemoglobin Depletion For Erythrocyte Proteomics

- Hemoglobin voids in flow-through >98%
- depletion from heavily hemolyzed serum, whole blood and dried blood spot (DBS) card
- Low abundance protein and enzyme enrichment
- Consumable, cost-effective
- Mild elution maintains native structure with retained enzymatic, functional and bioactivities
- Species agnostic
- Compatible with LC-MS, activity-probe profiling and virtually all proteomic analyses



2DE Comparison. Red circles indicate the Hemoglobin subunits region. The HemoVoid™ eluate (bottom) 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 proteome coverage across both dimensions.

| Product | Size | Item No. | |
|-----------|-----------|----------|--|
| HemoVoid™ | 10 Preps | HVK-10 | |
| HemoVoid™ | 50 Preps | HVK-50 | |
| HemoVoid™ | 100 Preps | HVK-100 | |

Based on 300 µl preps

HemoVoid™ LC-MS On-Bead

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

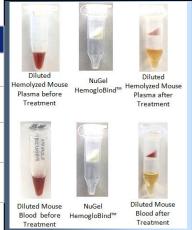
- Seamless workflows, unique proteolytic efficiencies
- Label, label free & phospho- compatible
- See page 5 for more information and ordering

HemogloBind™ & NuGel™ HemogloBind™ Removes Hemoglobin Interference

- Highly specific for hemoglobin binding
- depletion from hemolyzed serum and whole blood
- applicable to hemoglobin variant analysis
- Functional integrity maintained with simple transfer to post-treatment interrogations
- Species and tissue agnostic
- supports biomarker tests

| Product | Size | Item No. | |
|------------------------|-------------|-------------------|--|
| HemogloBind™ | 15 ml | H0145 -15 | |
| HemogloBind™ | 50 ml | H0145 -50 | |
| NuGel™ HemogloBind™ | 25 Preps | NP- HO- T25 | |
| NuGel™ HemogloBind™ | 50 Preps | NP- HO- T50 | |

1:1 v:v ratio HemogloBind™ suspension processes up to 10 mg/ml hemolyzed serum



Hemoglobin Removal Trial Kits

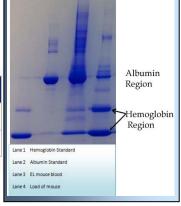
| Product | Size | Item No. |
|---------------------------|---|---------------|
| HemoTrial™ Kit | 5 ml HemogloBind™ + 5 Preps NuGel™ HemogloBind™ + 5 Preps HemoVoid™ | HTK-05 |
| HemogloBind™ Trial Kit | 5 ml HemogloBind™ + 5 Preps NuGel™ HemogloBind™ | HB145K -05 |

HemoVoid™ Blood Card Kit

The HemoVoid™ Blood Card kit substantially reduces hemoglobin interference from dried blood spot card protein analytes

| Product | Size | Item No. |
|------------|-------|-------------|
| HemoVoid™ | 10 | HVBC |
| Blood Card | Preps | -10 |
| HemoVoid™ | 50 | HVBC |
| Blood Card | Preps | -50 |

Based on 0.5" dried blood spot, ~ 15 µl whole blood



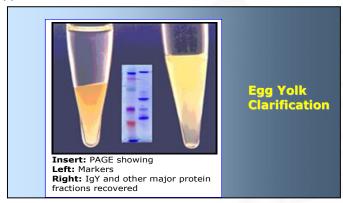


Sample Preparation

Cleanascite™

Lipid Adsorption & Clarification

- Effectively replaces chlorinated/fluorinated hydrocarbons (eg. freon)
- Workflows for antibodies, proteins, nucleic acids, proteoglycans, and most serum analytes
- Ideal for clarifying ascites, serum, cell & tissue culture, and organ homogenates
- · Clarifies bile and saliva
- · Extensively cited in journal articles
- Extends the life of membrane and chromatographic apparatus.



| Product | Quantity (ml) | Process Volume (ml)* | Item No. |
|--------------|------------------|-------------------------|------------|
| Cleanascite™ | 10 | 40 | X2555-10 |
| Cleanascite™ | 50 | 200 | X2555-50 |
| Cleanascite™ | 100 | 400 | X2555-100 |
| Cleanascite™ | 500 | 2000 | X2555-500 |
| Cleanascite™ | 1000 | 4000 | X2555-1000 |

^{*}Based on typical v:v ratio.

Surfactaway™ Triton Removal & Surfactaway™ SDS Removal

- Removes >99% detergent
- Very selective, virtually no cross-reactivity with other proteins
- Simple, just pipette, centrifuge and discard pellet
- Economical unique surface technology, not based on hydrophobic chromatography

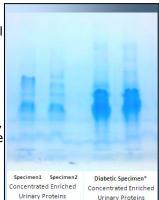
| Product | Quantity (ml) | # of preps* | Item No. |
|--------------------------------|------------------|----------------|-----------|
| Surfactaway™ Triton Removal | 30 | 120 | SA890-30 |
| Surfactaway™ Triton Removal | 250 | 1000 | SA890-250 |
| Surfactaway™ SDS Removal | 30 | 120 | SA645-30 |
| Surfactaway™ SDS Removal | 250 | 1000 | SA645-250 |

^{*}Based on typical v:v ratio.

UPCK™ Kit

Urine Protein Enrichment & Concentration

- Linearly scaleable, unlike ultrafiltration
- Alternative to solvent/alcohol precipitation
- On-bead digestion protocols
- <60 min. bind, wash and elute protocol
- Applicable to >1 & 2 DE > LC-MS > microarrays



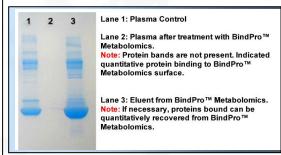
 The eluted fractions retain their enzymatic and biological activity

| Product | # of Preps | Item No. | | |
|------------------------------|------------|----------|--|--|
| UPCK™ Kit | 10 | UPCK-10 | | |
| UPCK™ Kit | 25 | UPCK-25 | | |
| Based on 10 ml urine samples | | | | |

BindPro™ & BindPro™ Metabolomics

Aqueous Protein Removal & Enrichment of Metabolites & Analytes

- Serum and plasma protein removal, >95%
- Aqueous protein crash
- < 30 minute protocol</p>
- Applicable for drug binding/screening and metabolomics



| Qty | Item No. |
|-----------|---------------------------|
| 15 Preps* | BPM55-15 |
| 50 Preps* | BPM55-50 |
| 15 ml | BP355-15 |
| 50 ml | BP355-50 |
| | 15 Preps* 50 Preps* 15 ml |

*Based on 20-30 µl serum

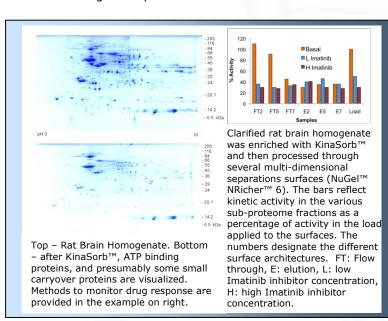
Class Specific Enrichment



KinaSorb™

Kinase (& ATP binding proteins) enrichment reagent

- Non-covalent immobilization of phosphate group with optimal nucleotide orientation & specificity
- Enrichment 3-5X, binding protein recoverable, ~200 μg
- 60 minute, scaleable protocol compatible with functional assays, electrophoresis and LC-MS
- Phosphatase activity & cyclic nucleotide phosphodiesterase (PDE) activity not detectable
- Improves protein normalization when comparing heterogeneous tissues
- On-bead digestion protocols for LC-MS IDs



| Product | # of preps | Item No. | | |
|---|------------|----------|--|--|
| KinaSorb™ 10 | 10 | KE785-10 | | |
| KinaSorb™ 50 | 50 | KE785-50 | | |
| Based on 100 µl tissue homogenate preps | | | | |

Viraffinity™ / ViraPrep™ Kits

Virus Enrichment & Purification

- Purifies whole infectious non-enveloped virus, isolates antigenic virions
- Enriches for viral proteins and nucleic acids
- No ultracentrifugation

| Product | Size | Item No. |
|------------------|-----------------------------|----------|
| Viraffinity™ | 15 ml suspension reagent | V1062-15 |
| ViraPrep™ Mammal | For 40 ml cell culture | VPM-40 |
| ViraPrep™ Lambda | For 5, 150 mm plate lysates | VLK-05 |

NuGel™ PBA & NuGel™ PBA Kit

Glycoprotein Enrichment Using Phenyl Boronic Acid

- Enriches heterogeneous sets of glycoprotein's, N-linked & O-linked
- Consumable, no column regeneration
- Species and tissue agnostic
- Sorbitol elution; compatible with functional assays, electrophoresis and LC-MS
- Binds biomolecules containing 1,2 cis-diol groups
- Chemically derived, ideal for glycoproteomic applications
- NuGel[™] polymer coating, porous silica based
- Supplied as bead only (dry powder) or as kit (includes all binding and elution buffers)

| Sample Type | %Glycoprotein (Sorbitol Elution) |
|----------------|----------------------------------|
| | |
| Mouse Plasma | 33 |
| Rat Serum | 44 |
| Sheep Serum | 18 |
| Bovine Serum | 40 |
| Bovine Brain | 9 |
| Homogenate | |

| Product | Qty | Item No. |
|----------------|--------------|----------|
| NuGel™ PBA Kit | 10 Preps* | NGPBA-10 |
| NuGel™ PBA Kit | 50 Preps* | NGPBA-50 |
| NuGel™ PBA | 5 Grams | NPBA-05 |
| NuGel™ PBA | 10 Grams | NPBA-10 |

Based on 50 µl serum preps

Functional & Chemical Proteomics



Functional & Top-down Proteomics

Building sequence/structure/function relationships

The continuum of protein conformations attributable to post-translational modification and non-covalent interactions produces important functions that cannot be directly or linearly correlated to protein abundance. Thus, functional annotation complements sequence annotation, but relies in part, on the functional or structural features of intact, non-denatured proteins. While the terminology can often overlap, chemical, and activity or structure-based proteomics can be considered a subset of functional proteomics.

The NuGel™ based NRicher™ product line supports all functional, chemical and top-down proteomic applications. The functional and structural integrity are always preserved upon separations with NRicher™ products. So functional protein attributes, as when the same or similar underlying sequence can have multiple conformations and functions, or when different sequences cross-over in function, are now open to investigation. Those aspiring to sift through these biological complexities can apply NRicher™ products to:

- Annotate multi-functional subproteomes
- Survey drug-interaction protein promiscuity
- Elucidate conformational variants
- Identify phenotypic biomarkers

NuGel™ NRicher™ Mx Chemical Displacement Proteomics

- Enrich proteomes with weak binding
- Displace bound proteins with small compounds or substrates
- Identify compound interacting proteomes with LC-MS
- Composite of the **NRicher™** 6 mixed mode beads

| Protein Description | Caffeine | Imatinib | Neg.Cont. |
|-------------------------------|----------|----------|-----------|
| Hemoglobin subunit beta-1 | 87 | 550 | 53 |
| Glucose-6-phosphate isomerase | 192 | 459 | 76 |
| Malate dehydrogenase | 117 | 356 | 35 |
| transketolase | 72 | 160 | 24 |
| Cytochrome c, somatic | 47 | 123 | 3 |
| Succinyl-CoA:3-ketoacid | | | |
| coenzyme A transferase | 69 | 122 | 19 |
| Transgelin | 0 | 84 | 0 |
| Annexin A2 | 26 | 66 | 0 |
| fumarate hydratase | 17 | 42 | 2 |
| annexin A3 | 5 | 36 | 0 |
| glutathione reductase | 9 | 36 | 0 |

A partial list of LC-MS/MS identification and spectral counts demonstrate Imatinib interaction (displaced) proteins from a common tissue homogenate, using CCDP. Caffeine was employed as a nonspecific control compound, negative control was the final wash buffer.

| Product | # of preps* | Item No. | |
|--------------------|-------------|----------|--|
| NuGel™ NRicher™ Mx | 5 | SR610-5 | |
| NuGel™ NRicher™ Mx | 25 | SR610-25 | |

^{*}Based on processing 0.5-1.0 mg total protein

NuGel™ NRicher™ 6 Functional proteomics and enrichment kit

- 12 differentiated subproteomes, 6 flow-through fractions, and 6 elution fractions
- Uncompromised functional and structural attributes
- Compare functional molecular profiles for biomarker discovery
- Enrich low abundance functional biomarkers for sequence and structural annotation
- Kit includes 6 mixed mode bead chemistries per prep
- Top-down proteomics

| Product | # of preps* | Item No. |
|-----------------------------|-------------|----------|
| NuGel™ NRicher™ 6 | 10 | SRPRO-10 |
| NuGel™ NRicher™ 6 | 50 | SRPRO-50 |
| *Based on processing ~1.0 n | | |

Nricher™ 6 Beads A, B, C, L, N, R Functional Activity Profile Normal Serum (upper panel) vs. Colon Cancer Serum (Lower Panel) A B C L N R A B C

PEP Functional Activity Analysis, courtesy of ArrayBridge (St. Louis, MO). 25 µl serum was load volume for all bead separations. Modified SDS-PAGE was employed for size separation and electroeluted into the wells. After addition of refolding solution, each well was monitored for Hexokinase activity using beef extract for cascade enzymes; NADP reduction being the final reporting measurement. The circled regions are activities up-regulated after substraction of background. The observed activities show a different pattern for each of the 6 NRicher™ beads and generally a feature pattern distinguishing the normal from the colon cancer sera



NuGel™

Polymer Coated Silica Affinity Matrices for Ligand Immobilization

| Product Name | Matrix Reactive Group | Ligand Reactive Group | Immobilization Conditions | Quantity (Grams) | Item No. |
|--------------------------|--------------------------------|-------------------------------------|--|---------------------|-------------|
| NuGEL™ Poly- Epoxy | Terminal Epoxy | Amino | Direct Coupling | 25 | NPEY -25 |
| NuGEL™ Poly- Amine | Terminal Amine | Carboxylic Acid, Carbohydrate | Carbodiiamide reaction, or NaIO ₄ derived Aldehyde | 25 | NPAM -25 |
| NuGEL™ Poly- Aldehyde | Terminal Aldehyde | Amino | Direct Coupling | 25 | NPAY -25 |
| NuGEL™ Poly- Hydroxy | Terminal Glycol | Amino | Carbodiimidazole mediated reaction | 25 | NPHX -25 |
| NuGEL™ Poly- Carboxy | Terminal Carboxylic Acid | Amino | Carbodiiamide mediated reaction | 25 | NPCY -25 |

NuGel™'s unique surface passivation can be applied to any porous silica, particle size or quantity for custom manufacture of ion-exchange, hydrophobic interaction, affinity chromatography or HPLC. Please inquire.

Genomics / DNA Isolation

Genomic Sample Preparation Products Especially Suitable for BACs and Multiplex SNPs

ProCipitate™ & ProPrep™ Kits

Superior Substitute to Phenol/Chloroform for DNA Isolation

- Used throughout the Human Genome Sequencing Project*
- Removes protein contaminants & leaves DNA unbound
- Improves yield of DNA over alternative bind and elute systems
- ProCipitate[™] supports the ProPrep[™] line of application specific kits

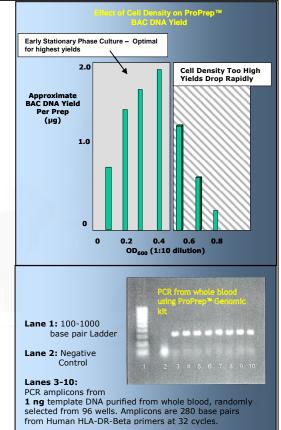
| Sample Size | ProCipitate™ Typical Usage |
|---|-------------------------------|
| 10 ml Yeast Culture Genomic DNA | 1-2 ml |
| Whole Blood Genomic DNA | 250 μl |
| 4 mm Plant Leaf | 100-200 μl |
| 2 ml culture BAC Preps | 80 μl |
| 250 μl culture Plasmid Preps 20 μl | |
| 200 ml Large Scale BAC Preps 5 ml | |
| Dried Blood Card (or ~ 15 μl Whole Blood) | 250 μl |

| Product | Size | Item No. |
|-------------------------------|-----------|-----------|
| ProCipitate™ | 30 ml | P0050-30 |
| ProCipitate™ | 100 ml | P0050-100 |
| ProPrep™ BAC Mini¹ | 100 preps | PMK-100 |
| ProPrep™ Genomic ² | 100 preps | PPG-100 |

- 1) Based on 2 ml BAC cultures
- 2) Based on 50 µl whole blood

J M Kelley; C E Field; M B Craven; D Bocskai; U J Kim; S D Rounsley; D Adams. High Throughput Direct End Sequencing of BAC Clones. Nucleic

Acids Research.1999.15;27(6):1539-1546



D C Bruce; M O Mundt; K K McMurry; L J Meincke; D L Robinson; N A Doggett; L L Deaven. BAC Library End Sequencing in Support of Whole Genome Assemblies DOE Joint Genome Institute and Center for Human Genome Studies, Los Alamos National Laboratory, Research Abstracts from the DOE Genome Contractor-Grantee Workshop IX (2002)

Distributors for Asia Pacific

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China



China



China



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