

NuGel[™] bead formats support high throughput sample prep and automation

The "Omics" revolution has highlighted the need for new and different sample preparation separation processes to overcome the inefficiencies of conventional technologies. Biotech Support Group is a leading provider of proteomic depletion and enrichment products.

NuGel™ features:

- 50 µm porous silica bead that is passivated through a proprietary coating
- exceedingly fast filtration and settling characteristics,
- perfectly suited to high throughput and automation
- customizable formats
- not derived from immuno-affinity
- selective depletion of Albumin, Albumin & lgG, and Hemoglobin.

Optimization for specific applications can include bead amounts, sample volume loads, and cycle times. Functional integrity of all proteins is maintained, and downstream proteomic analysis can include LC-MS, immunoassays, cellular response and enzymatic assays.





Finally, INTip[™] SPE formats have been proven to be

compatible with most automation platforms, i.e., Integra, Hamilton, etc. As bloodderived samples for clinical proteomics progresses, simple, robust and reproducible sample preparation for targeted analysis will require consumable formats and compatibility with automation. This format fulfills this purpose.

Please inquire for price and availability.

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 **NuGeI™** 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/ASMSBSGD PXPoster.pdf



LC-MS Proteom Analysis of Seru (single 2 hr gradient)	nic ^{JM} Whole Blood Lysate Control	After NuGel™ HemogloBind™/ INTip™ SPE
Total Spectral Cou (Sp. Cts)	ints 14532	19054
Total Protein IDs Sp. Cts)	(≥2 306	420
# of Unique Prote IDs (≥2 Sp. Cts)	ein 27	134
# of Enriched Proteins ≥3X		47
# of Depleted Proteins (other th Hemoglobin subunits) ≥3X	nan 6	





INTip[™] SPE