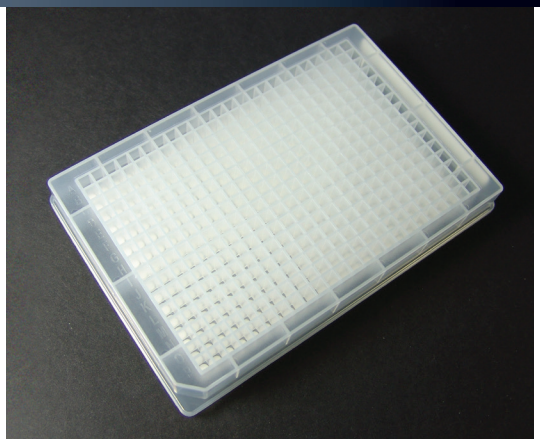
384-Well Protein Desalting Plate

2025

Analytical offers a unique new product, a 384-Well Protein Desalting Plate. This high-throughput product removes salts and buffers for downstream application prior to MS analysis.

Mass Spectrometry (MS) based proteomics is extensively used for the evaluation of posttranslational modifications and characterization of proteins by peptide mass fingerprinting. Salts and buffers are commonly used during isolation and stabilization of proteins. However, many of these salts and buffers may have adverse effects on protein function or stability, or interfere with downstream applications, hence must be removed. Also, many of these salts and buffers have a deleterious effect on Matrix-Assisted Laser Desorption Ionization (MALDI) and Electro Spraylonization Mass Spectrometry (ESI-MS), hence must be removed.



Cat. No.	Description	Qty
384DP140	384-Well Protein Desalting Plate	Each

Features and Advantages:

- **384-Well plate with size exclusion resin**
- **Removes urea and other salts from protein samples**

High-throughput format allows simultaneous handling of 384 samples for desalting proteins by centrifugation.

Experimental Data:

Protein recovery was >85% and desalting efficiency was >99% (5-20 L of 1 mg/ml BSA containing 1M NaCl was loaded). When loading 5L sample, adding 10-15L stacker of buffer/water is required for better protein recovery.

General Protocol:

STEP 1	Remove the storage buffer by centrifugation at 300 x g for 2 minutes.
STEP 2	Equilibrate the resin by adding 50L of buffer or water and centrifuge at 300 x g for 2 minutes and repeat the step.
STEP 3	Add 5-20 L of sample and centrifuge at 300 x g for 2 minutes.

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