CORAL 384-Well Protein Desalting Plate

Mass Spectrometry (MS) based proteomics is extensively used for the evaluation of post-translational 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. Orochem offers a unique new product, CORAL 384-Well Protein Desalting Plate. This high-throughput product removes salts and buffers for downstream application prior to MS analysis.

Features and Advantages:

- 384-Well plate with size exclusion resin. (Provisional patent)
- Removes urea and other salts from protein samples.

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

General Protocol:

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

Experimental Data:

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

CORAL 384-Well protein desalting plate, catalog#OCPDSSP384