

Are you getting enough protein?

New ideas in proteomics and protein handling.

oMALDI source

Applied Biosystems www.appliedbiosystems.com

A new angle on proteomics

Applied Biosystems' new orthogonal matrix-assisted laser desorption ionization (oMALDI) source for the company's API QSTAR Pulsar Hybrid LC/MS/MS system features interchangeable MALDI and API ion sources and is compatible with tandem MS. With an oMALDI source, the QSTAR Pulsar system identifies proteins separated by one- or two-dimensional gel electrophoresis at the femtomole level by peptide mass fingerprinting of the protein digest or using sequence data from tandem mass spectra acquired by collision-induced dissociation of individual peptide precursor ions. Database search and acquisition of MS and MS/MS spectra can be combined inter-actively for more informative analytical data.

Reader Service No. 100

FluoroTect Green_{lys}

Promega

www.promega.com

In vitro translation labelling system

Based on a lysine-charged tRNA labelled at the epsilon position of the lysine with the fluorophore BODIPY, FluoroTect Green_{lys} allows for the fluorescent labelling and detection of proteins synthesized *in vitro*. Fluorescent lysine residues are incorporated into synthesized proteins during *in vitro* translation reactions, eliminating the need for radioactivity. There is no need to transfer, fix or dry gels.

Reader Service No. 101

ADV01

Cytoskeleton, Inc.

www.cytoskeleton.com

Bone up on protein measurement

This advanced protein assay reagent combines low protein-to-protein variance with a strong signal for a sensitive assay. A one-step procedure results in a change from green to blue recognized by measuring absorbance at 570–615 nm. ADV01 can be used to determine protein concentration in a buffer, biological fluid, tissue culture media or in combination with an activity assay to follow protein purification.

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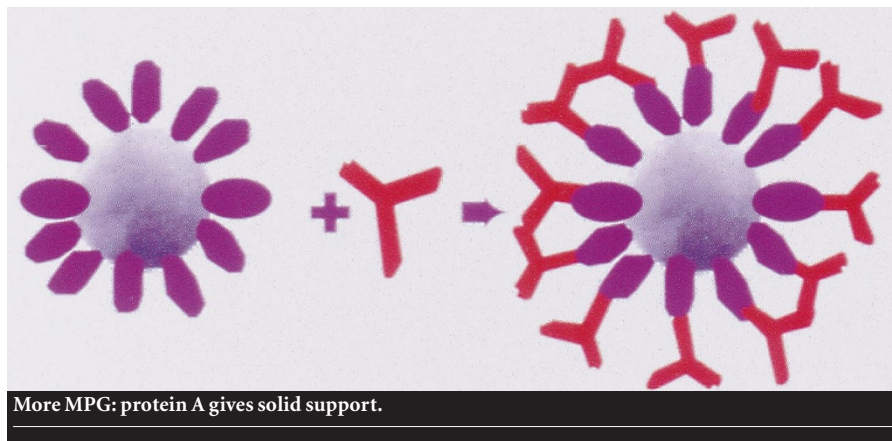
Magnetic protein A particles

CPG

www.cpg-biotech.com

Immunoassay and bioassay supports

Protein A covalently attached to magnetic porous glass (MPG) particles confers immunoglobulin binding properties similar to those of unconjugated protein A. Nominal binding capacity of 1 mg of particles is 40–75 µg



More MPG: protein A gives solid support.

immunoglobulin. MPG protein A particles can be used as solid supports in single or automated immunoassays and bioassays for separating unbound labelled tracer. They are suitable for small-scale affinity purifications or immunoprecipitation direct from ascites, serum, homogenates, lysates and culture supernatants for gel or other physical analyses. The particles can be regenerated up to 12 times and will continue to provide more than 90% of initial binding capacity.

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ArrayStat

Imaging Research www.imagingresearch.com

Inferential software

This genomics software package is designed to provide a comprehensive inferential statistical analysis of gene expression array data from a variety of file formats with as few as two replicates per spot. It can be used to identify statistically significant expression changes and poorly reproduced spots, and to determine the number of replicates required to reliably detect a desired fold change in gene expression. ArrayStat can be integrated with the ArrayVision quantification program.

Reader Service No. 104

OmniUltra

ThermoHybaid

www.thermoHybaid.com

Material gain

The injection-moulded polycarbonate used in this PCR plate is gamma irradiated for 100% sterility with no brittleness. The sealing characteristics of polycarbonate avoid the need for heated sealing solutions and the material is receptive to coatings for advanced protocols such as streptavidin for biotin-labelled PCR. The plate is designed for full robot compatibility. Samples are available from ThermoHybaid.

Reader Service No. 105

Proteomics catalogue

Pierce

www.piercenet.com

"Proteomics Connection", published this year

This free 60-page catalogue features products used in cell lysis, total protein determination, protein staining, western blot detection and protein-protein interaction analysis. It contains a resources section listing proteomics-related books and recent journal articles.

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These notes are compiled in the Nature office from information provided by the manufacturers.

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