Magnetic Separation device — a plate that can be hooked up to the Biomek instruments.

In January, PerkinElmer (Boston, Massachusetts) launched its modular and scalable JANUS Automated Workstation. "Many units can be configured at the time of sale," says Nance Hall, business unit leader for automation and liquid handling. "With JANUS, you can scale and change the system not only when you buy, but also in the future." Users can also program the selection of numerous dispense heads and formats. "It is as though you go into a kitchen and you are asked if you need a cup or a teaspoon," explains Hall. "In the kitchen you will use both." Likewise, the JANUS allows users to choose different tools automatically depending on the volume range and microplate densities.

Another popular choice among liquid handlers is the Freedom EVO automated liquid handler from Tecan in Durham, North Carolina. Others include the Sciclone ALH Workstation from Caliper Sciences (Hopkinton, Massachusetts), the BioCube System from Proteodyne (Windsor, Connecticut) and the 925 PC Workstation and GX-281 Liquid Handler from Gilson (Middleton, Wisconsin). "You can use over 300 standard racks and many more custom ones," says Gilson's spokesperson Greg Robinson.

Going large

For crystallization and other functional studies, a researcher needs more protein than is possible in 96-well plate format. For such purposes, a number of parallel-purification systems that can accommodate larger volumes of cells are starting to come onto the market.

PIERCE

Just swell: Pierce Biotechnology's SwellGel discs.

GE Healthcare's AKTAxpress is a fully automated chromatography system for purification of His- and GST-tagged proteins, yielding up to 50 mg of target protein. Affinity chromatography is the first step of all protocols, but as a second step it is possible to choose between desalting or gel filtration, and an ion-exchange step can be added too. Automatic tag removal is possible in all multi-step protocols.

Teledyne Isco (Lincoln, Nebraska) launched the BioOptix 10 last year, a ten-channel parallel-purification system for high-capacity protein purification with subsequent fraction collection. This means it can purify protein from ten different samples by ion exchange, affinity or size-exclusion chromatography. The instrument includes a high-capacity fraction collector (20 to 60 fractions per sample). Ten independently controlled pumps can be programmed with different gradient conditions for rapid identification of columns and conditions that give optimal results. "Instead of doing it sequentially, a process that can take 4–5 days, you can load different columns and run the instrument over lunch," says John Urh, product manager for chromatography

Another player in this arena, QIAGEN's BioRobot Protein LS System, has the capacity for the parallel purification of up to 24 large-scale cultures in less than three hours, and PerkinElmer's JANUS system can be configured for large-scale purification protocols.

New reagents and instruments have allowed researchers to set up pipelines for high-throughput protein production of a scale and capacity that match the needs of their individual labs. As a result of these advances, hundreds of proteins from different organisms have been purified and their structures and functions determined. But keeping abreast of this rapidly changing field will require ongoing innovation. "Several years ago everyone was talking about genomics, now the focus is on proteomics. More and more we are seeing research moving toward specific proteins," says PerkinElmer's Hall. "The challenge is trying to keep up with the technologies."

Laura Bonetta is a freelance writer based in the Washington DC area.

TARGET IDENTIFICATION

High-throughput protein-purification pipelines are becoming part of many proteomics efforts. But how to choose the targets to put through the pipeline? For those who want to focus on targets relevant to a disease-related process, it is important to catalogue where, when and to what extent a protein is expressed. Currently the main method for determining the protein complement of a given cell or tissue uses two-dimensional (2D) gel electrophoresis or liquid chromatography to resolve the proteins in the sample, and mass spectrometry to then identify the individual proteins. A problem with this approach is that it is difficult to identify rare proteins, because cell extracts are dominated by a few very abundant proteins.

Beckman Coulter has developed a number of innovations for protein fractionation to address this problem. "We first selectively remove the most abundant proteins from a sample," says Jerry Feitelson, marketing manager for the company. The ProteomeLab IgY-12 partitioning kits selectively remove the 12 most abundant proteins — albumins and immunoglobulins — from human/primate serum or plasma. These proteins make up 95% of the total protein expressed by cells. So removing them increases the chances of identifying proteins that are not highly expressed and are probably more interesting to researchers. The technology uses antibodies bound to inert beads, which are then packed in liquid-chromatography columns or, for smaller samples, spin columns. "The advantages of our reagents are the greater capacity, increased specificity and the ability to bind across species," says Feitelson. The enriched material can then be collected and further fractionated with the Beckman Coulter ProteomeLab PF 2D protein fractionation system. The instrument divides proteins in two dimensions: first, in a 2D gel, samples are separated by isoelectric focusing and size, and then automatically injected into a liquid-chromatography column. The process is fully automated. "One run takes ten hours, so you can do two in one day," says Feitelson. Detailed protein maps can be constructed for easy comparison between two samples using the Proteome Lab software suite. Interesting proteins can then be further analysed by cutting out the corresponding band, for example, and putting it into a mass spectrometer.

Pall Corporation has also introduced the Enchant Life Sciences kits for albumin depletion and immunoglobulin G purification. L.B.

H. DEWALD/BECKMAN COULTER