



Proteomics Ponders Prime Time

Improved technologies for tracking thousands of proteins at once have spawned talk of a full-scale project to reveal all the proteins in each tissue—but the price tag would be daunting

AMSTERDAM, THE NETHERLANDS—He's too polite to come right out and say it, but Amos Bairoch thinks that much of the data generated by proteomics groups over the past decade is junk. Following the completion of the human genome project, proteomics labs set out to survey all the proteins expressed in different cells and tissues, in essence, putting meat on the bone of the genome. Mass spectrometers and other tools turned out gigabytes of data that purported to identify large numbers of proteins and fed them to Bairoch, who heads Swiss-Prot, a massive database that houses the latest findings on proteins of all stripes. Today, most of those data are ignored, Bairoch says, because the readings were too imprecise to make positive identifications. Throughout the years, many casual observers of the field dismissed proteomics as a waste of time and money. "People thought [the technology] was ready 10 years ago. But they didn't see good results and got disenchanted," Bairoch says.

Today, however, Bairoch's databases and others like them are filling up with terabytes

of information that he calls "much better." The upshot: Proteomics is finally coming of age. With the help of better instrumentation and refined techniques, the top proteomics labs can identify and quantify more than 6000 distinct proteins from individual cells and tissues at a time. Now that these labs can cast such a wide net, many proteomics researchers say the time is ripe to undertake a full-scale human proteome project (HPP) to survey the landscape of proteins present in dozens of different human tissues. If successful, such a project would reveal which proteins are actually expressed in different types of cells and tissues, and at what levels, and the network of proteins they communicate with. That knowledge could offer researchers innumerable insights into how organisms convert their genetic blueprint into life and perhaps lead to breakthroughs in biology and medicine. "We are at the point where we can talk about doing this in 8 to 10 years," says Mathias Uhlen, a microbiologist and proteomics expert at the Royal Institute of Technology in Stockholm, Sweden.

It's not just talk. Uhlen and other proteomics leaders gathered here last month to weigh plans for an HPP and to sound out representatives of science funding agencies that would need to pony up the hundreds of millions—if not billions—of dollars needed to pull it off. Most of the responses suggested that tight science budgets make a new megasized international science project unlikely anytime soon. Nevertheless, even without a coordinated international HPP, the field is moving so fast that "it's happening already," says Matthias Mann, a proteomics expert at the Max Planck Institute of Biochemistry in Martinsried, Germany.

Spotted history

Many researchers probably assume an international proteome effort started years ago. The availability of the human genome sequence in 2001 told researchers how many proteins are likely to be out there and the exact sequence of amino acids they should look for. The race was on, amid plenty of hype. "Everyone was interested in proteomes," says Mann.

But there were problems, lots of them. For starters, proteins are chemically far more heterogeneous and complex than DNA and RNA. It was relatively easy for researchers to

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