Short supply

Improving proteomic techniques will tackle questions in cell biology, signal transduction and clinical research. But workers with the key knowledge in protein biochemistry, mass spectrometry and bioinformatics are hard to find, says Kendall Powell.

Overwhelmed: like many in proteomics, John Bergeron is finding it hard to recruit the skills he needs to deal with the outpouring of protein data.

John Bergeron is being swamped. His team feeds peptide after peptide, isolated from a range of cellular components, into the lab's mass spectrometer, which in turn churns out reams of data. The researchers then scramble to use this information to identify new proteins and the cellular processes in which they are involved. Even though only a quarter or so of the proteins are identified, Bergeron says that his group at McGill University in Montreal, Canada, can barely keep up. Bergeron's experience is not unique — he, along with colleagues in North America and Europe, is finding it difficult to find qualified scientists to help tame the outpouring of protein data.

Proteomics — loosely defined as the study of all of the proteins expressed in an organ, tissue or cell at a given time — presents a challenge vastly more complex than cataloguing genomes. But two sets of papers published last year hint at the scientific rewards and professional opportunities that the field can provide. One showed intricate protein–protein interaction maps from yeast (A.-C. Gavin *et al. Nature* **415**, 141–147 and Y. Ho *et al. Nature* **415**, 180–183; 2002); the other revealed a promising diagnostic marker for ovarian cancer (E. F. Petricoin *et al. Lancet* **359**, 572–577; 2002).

These efforts symbolize two areas ripe for growth in proteomics — the study of protein interactions and pathways, and the search for clinical biomarkers. To take on such projects, research centres need scientists with a thriving proteomics plan for key biological questions and an understanding of how technologies might be used to answer them. In particular, there is a pressing need for mass spectrometrists who can dream up new tools or strategies but who are also classically trained protein biochemists, so that they understand the underlying chemistry of protein separation, identification and characterization.

So where will such scientists come from? Joël Vandekerckhove at Ghent University in Belgium says that across Europe the number of chemistry graduates, a subset of whom will have both the protein-chemistry education and the mass-spectrometry experience

needed for proteomics, is shrinking. Instead of hundreds of graduates, many chemistry departments now produce just a few dozen each year. And many of these tend to head for careers in the pharmaceutical industry. In the United States, 15% fewer biochemistry doctorates were awarded in 2001 compared with 1993, according to a survey by the National Science Foundation.

ACADEMIC SHORTFALL

As a result, recruiting postdocs into academia can be tough, says Simon Gaskell, director of mass spectrometry at the University of Manchester Institute of Science and Technology, UK. "Anyone who can spell mass spectrometry and proteomics can get a job in industry — and probably at 50% higher pay," he says. An increasingly popular way to get a PhD in the field is to work in industry while doing a thesis part-time, he adds.

"Mass spectrometry can be a pretty lucrative environment," says David Muddiman, co-director of the Mayo Proteomics Research Center in Rochester, Minnesota. Students can make up to US\$100,000 a year if they take an analytical chemistry job in industry after graduating, he explains. There are not nearly enough mass-spectrometry groups producing students who really understand the technology, he adds.

Although Muddiman agrees that new technology can take on loads never achieved before — such as his new mass spectrometer, which has a resolution 60 times greater than more conventional models — he cautions against falling in love with a particular technique. "Almost anyone can learn to run a machine like it's a stove and cook a bowl of soup," he says. "But those people are going to be in trouble in 5–10 years." Only mass spectrometrists with a fundamental understanding of the field can move proteomics along by developing the next generation of machines.

Protein bioinformaticians, whose skills include programming and database management, may be the hardest to recruit into academia, as these skills are

Technology is key to proteomics, but researchers should be wary of becoming over-enamoured with equipment, says David Muddiman.

APPLIED BIOSYSTEMS

Reverse migration

Traditionally, scientists move from academia into industry. But in proteomics, there are signs that the traffic is changing direction.

Take Martin Latterich, the former director of proteomics at biotech firm Illumina in San Diego, who will become an associate professor at McGill University in Montreal, Canada, later this year.

Latterich is returning to the challenges of basic proteomics research — an area in which

Illumina is cutting back.

His move signals a change in academic institutions, which are now embracing proteomics technologies that have been proved effective by industry.

Latterich is not unique. Ruedi Aebersold, a proteomics pioneer at the Institute for Systems Biology in Seattle, Washington, says that he has received applications from more researchers in industry than he can possibly employ. **K.P.**

much in demand in industry — although there are signs that skilled people from industry are flowing back into academia if their company has foundered (see ‘Reverse migration’, above). As a result, both academic centres and funding agencies allow for higher salary ranges.

While proteomic experts jockey for limited human resources, they all agree that there is room for almost any technical or biological background in the burgeoning field — especially if you can bring a little of both. Because proteins drive all of life’s machinery and represent the vast majority of therapeutic targets, proteomics will be answering questions in basic and clinical research far into the future.

“Even if someone doesn’t want to specialize in proteomics, it’s good to pick up the skills and way of thinking,” says Matthias Mann, a functional-genomics researcher at the University of Southern Denmark in Odense. Mann’s lab illustrates how many skills are needed for a good proteomics lab. Chemists, engineers, biologists and computational experts are organized into either instrumentation or experimentation groups, and these maintain constant contact with each other (see ‘The protein hit squad’, right).

COORDINATED APPROACH

The willingness to work in a team is a prerequisite for scientists who want to work on some of the largest public research efforts in proteomics — perhaps the area in which the most exciting professional and scientific opportunities lie. To try to coordinate these efforts internationally, the Human Proteome Organisation has outlined five initial goals for researchers, including defining the human serum and liver proteomes and standardizing known protein antibodies. The National Heart, Lung, and Blood Institute launched ten proteomics centres around the United States in 2002 with a total funding of \$157 million over seven years.

European resources are also flowing into centres such as the Swedish Human Proteome Resource, a four-year research programme worth 60 million

Swedish kronor (US\$7.6 million) per year. And Britain’s Leukaemia Research Fund set up a proteomics facility at UMIST to give leukaemia researchers access to proteomics experts such as Gaskell who can help them to design cutting-edge projects.

But today’s hot topic is tomorrow’s status quo. Even though last year’s papers on yeast protein–protein interactions and diagnostic markers for ovarian cancer showed promise, the field will have to keep proving it can meet the substantial challenges that lie ahead: perfecting protein arrays to match the quality of DNA arrays, designing better information platforms, and pushing the strategies for identifying complex protein mixtures even further. Because of these new challenges and the ongoing large projects, there should be ample opportunities in proteomics for the foreseeable future — but the best jobs may go to people with a combination of an understanding of biochemistry as well as a background in engineering or computation.

Kendall Powell is a science writer based in Broomfield, Colorado.

Human Proteome Organisation

♦ www.hupo.org

Mayo Proteomics Research Center

♦ www.mayo.edu/research/mprc

Leukaemia Research Fund proteomics facility

♦ www.lrf.umist.ac.uk

Human Proteome Resource

♦ www.biotech.kth.se/molbio/hpr

Genome Canada

♦ www.genomecanada.ca

All together now: Matthias Mann sees integrated teamwork as essential in the proteomics laboratory.

The protein hit squad

People who want to work in Simon Hubbard’s protein bioinformatics group at the University of Manchester Institute of Science and Technology, UK, simply can’t fit the “geeky” stereotype of the computational wizard, he says. This is because his team spends its time designing software to help researchers query public database information in new ways or predict genes from organisms without completed genomes. So everyone must be willing to communicate with a

range of scientists. Apart from programmers, they must also be databank curators, liaison officers to the experimental proteome scientists, and software test pilots.

In fact, Hubbard says that the best part of his job is sitting down with experimental scientists and helping them to identify their proteins. Starting out with a mass of raw data that could represent hundreds of different peptides adds a level of challenge to the job not seen with genomic sequence data, he adds. **K.P.**