Proteomics and genomics
Catching function in action
Editorial overview

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A major interest of Jörg is the establishment and sensible use of high-throughput analysis processes – with some emphasis on array-based assays – for the understanding and evaluation of the complex molecular interactions in living organisms.

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Proteomics and genomics are a closely related pair in biological research, both performed in pursuit of a comprehensive understanding of the complex molecular functioning of a living cell. While the older sister, genomics, is well established, the younger brother, proteomics, is still busy finding his way through the pitfalls of adolescence, but is growing fast and is eventually bound to overtake his sister in size. In real terms, the two areas are not only related but actually much dependent on each other. For once, the results complement each other. Only by such aggregation of knowledge from seemingly different fields will a sensible interpretation of the complex matter of global molecular functioning become possible. Second, the technical approaches taken to acquire knowledge are, at least to some extent, rather similar in kind and are inspiring matching procedures in the other respective field. In this issue of *Current Opinion in Chemical Biology*, we have assembled articles that give an overview of the current state of tools and techniques in the area of functional analysis and their contributions to the advancement of biology and medicine.

The first few articles deal with aspects of functional interpretation of nucleic acid sequences, an essential task once the complete basic sequence structure of the genomes of various organisms is known. Camargo, de Souza, Brentani and Simpson (pp 13–16) point out that the definition of the catalog of protein-coding regions is not simply done upon completion of the sequence but requires additional experimental information. One means to such an end is large-scale mutagenesis followed by a detailed discription of the mutated organisms, a procedure reported by Beckers and de Angelis (pp 17–23) for their quest for defining many gene functions in mice. Remm and Metspalu (pp 24–30) and Lechner, Lathrop and Gut (pp 31–38) then describe their methods for large-scale genotyping single nucleotide polymorphisms (SNPs) and elaborate on the usefulness of SNPs for disease-gene detection and pharmacogenetics — the study of how genetic differences influence the variability in patients' responses to drugs.

In the only article dealing purely with theoretical considerations — although based on experimental evidence produced by others, of course — Copley, Letunic and Bork (pp 39–45) deliberate on the evolutionary processes shaping genomes and thus proteins because of different functional demands in different species.

The paper by Lilley, Razzaq and Dupree (pp 46–50) reviews the usefulness of two-dimensional gel-electrophoresis for protein analysis and provides an insight into recent technical advances. Mouradian (pp 51–56) describes an alternative separation technique, which could provide the means for a faster and more convenient isolation of individual proteins, although the 'old-fashioned' gel might not give way that easily.

For the study of protein–protein interactions, two-hybrid analysis has become a procedure of choice. Uetz (pp 57–62) reports that a combination of arraying technique and two-hybrid processes provides a convenient and efficient system, making the individual clones better identifiable and accessible. Important to all types of protein analysis could be the advancement in labelling techniques. Patton and Beechem (pp 63–69) inform on dichromatic fluorescence protein-labelling technologies that could facilitate multiplexed and quantitative analyses in proteomics.

Mirzabekov and Kolchinsky (pp 70–75) contribute the first article of this issue about protein microarrays. They discuss various aspects critical to the production of protein and — as a special case within this field — antibody arrays, a subject extended to the problems related to the application of this technology by the article of Joos, Stoll and Templin (pp 76–80). Wilson and Nock (pp 81–85) report on their experience in using protein arrays for expression profiling as well as binding and enzymatic assays. Weinberger, Dalmasso and Fung (pp 86–91) use the array technology in order to fractionate complex samples by retentate chromatography, while detection is accomplished by SELDI time-of-flight mass spectrometry.

Rodi, Makowski and Kay (pp 92–96) present results on the use of phage-display libraries for the mapping of protein–protein and protein–drug interactions. Such libraries, however, also have wider implications, such as being used in array-based analyses. Mousses, Kallioniemi, Kauraniemi and Kallioniemi (pp 97–101) use cell and tissue microarrays for functional and potentially clinical validation of molecular targets. Gilbert and Albala (pp 102–105) review methods for the expression of individual proteins in largely increased numbers.

Finally, Foury and Kucej (pp 106–111) take the biogenesis of yeast mitochondria as an example for a discussion of the extent to which yeast can act as a model system for human.

Hopefully, the tools, techniques and ideas presented in all these articles will be as inspiring and stimulating to the readers as they were to us personally. We wish to thank all of the contributing authors and to acknowledge the editorial staff of Elsevier Science for their support and input to this issue of *Current Opinion in Chemical Biology*.