

STRUCTURAL AND FUNCTIONAL GENOMICS

Guest Editorial

The genomic research explosion in the 1990s achieved several paradigm shifts in biology research. It provided almost complete catalogues of genes and proteins in different organisms, preparing the way for understanding the workings of biological systems. It simultaneously led to tremendous advances in technology. Finally, it showed that hypothesis-driven research and discovery-driven research are both valuable and complementary approaches to significant biological questions.

The term 'post-genomic era' hints that we now have a much harder task ahead of us. After completing the catalogues of components, we need to identify what individual components do and how they do it together. Many methodological advances will be required to be able to address these questions comprehensively. Some such new approaches are featured in this, the first Special Technical Feature of the *Australian Biochemist*. All three articles demonstrate the transition from cataloguing one state of a system to comparing and following the responses

to biological changes. Kamarinos and Waltham give us advice on how to use microarray technology and point out the common pitfalls. Attard *et al.* describe the powerful DIGE method and its use for monitoring differences in proteomic profiles between different functional states and different systems. Finally, Listwan *et al.* describe advances in high-throughput protein production for structural biology. Both expression profiling and proteomics are well suited to be integrated with structural biology as an extremely powerful approach to functional genomics, by combining methods that give insights into biochemical and cellular functions of proteins.

The methodology described in these papers can equally be applied to smaller scale projects and to more comprehensive applications. Therefore, although you may be a PhD student focusing on a specific action of just one gene or protein, the methodology described in these papers may be applicable to your problem, and hopefully you can access it in a lab nearby.

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