

## Preface

Protein modules are seen as autonomously functioning and/or folding units of protein sequence. Such modules are identified and grouped into families based on either similarity of sequence, three-dimensional structure or biological function. With the near completion of the human genome, life sciences are at the verge of a new age, often referred to as the '*post genomic era*'. The future task will be to ascribe a biological function to the newly identified protein sequences. Precise annotations of modules or functional motifs present in a given protein will significantly facilitate this process by assisting in the design of experimental approaches to meaningful and relevant experiments.

The first international EURESCO conference on *Functional Protein Modules*, held in Seefeld, Austria in October 2001 highlighted the importance of structural, functional and cell biological characterization of conserved regions of protein sequences for the future of proteomics and functional genomics. While the simplistic view of protein modules is one of a '*molecular LEGO*', the clear message from this past meeting is that nature is more ordered and rather engages in '*molecular SCRABBLE*'. While both information from sequence and structure data mining helps in ascribing, with a certain probability, the function(s) of a given protein module, the biological function of a module within the context of the entire protein can be predicted with much less certainty. Thus, the 71 participants of the meeting reached the consensus that more information is required from all sources, embracing *in silico* data mining, X-ray crystallography, NMR analysis, and also molecular and cell biological investigations. Only in

this way can we start to understand the use of individual 'letters' (modules) for constructing a 'word' (protein), to eventually interpret whole 'sentences' (biological processes).

This special issue compiles contributions from a number of participants from the Seefeld meeting and is complemented by reviews from colleagues whose views have helped shape our current understanding of protein domains. As for the Seefeld conference, the initial spark for this issue came from Matti Saraste, who was convinced that the time is right to come together and unify ideas and concepts and to dedicate a special issue to this theme. We all missed Matti at the meeting and we will continue to miss his scientific input and enthusiasm, and most of all, his personality, in the future. All authors of this issue responded with ebullience to the initial idea – little did we know that our contribution would be a legacy to a colleague, whose foresight and vision opened the doors for a field of scientific research, which unites scientists from different fields in a common goal.

Thanks Matti!

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