

FEBS practical crystallization courses since 2004

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Structural genomics, the high-throughput structure determination of proteins encoded by a given genome depends to a large extent on the availability of crystals for X-ray diffraction. Obtaining crystals suitable for X-ray diffraction analysis is still the least understood step in the determination of protein structures by biocrystallography methods because the technique relies a lot on a trial-and-error approach. The success of the common trial-and-error experiments is not predictable yet even more rational approaches have been developed in the past few years, and prospects for the science of crystallogenes are relatively good.

Many of the new approaches are based on an improved theoretical insight into the processes of nucleation and crystal growth. However, what became apparent in recent years is a gap between these new developments and the willingness of young students and postdocs to absorb them. This is mainly due to the need to understand the thermodynamics and kinetics of the physical-chemical processes governing crystallization, a matter not easily digestible. Experience shows that a majority of students tends to rather spend many months with trial-and-error experiments than choose the more demanding approaches involving determination of phase diagrams, etc.

Our biennially organized practical crystallization courses (<http://febs.img.cas.cz>) supported by FEBS and Instruct as well as by many other companies supplying products for protein crystallization have been designed to help overcome this and to bring over the message of the benefits of more rational approaches to macromolecular crystallization. To achieve this goal, a number of prominent experts in the field as teachers and tutors have been invited for each course. The first lecture and practical crystallization course FEBS AC04-13 was organized in October 2004. Since this date and thanks to the FEBS (www.febs.org) we are glad that we were able to make a long tradition of these successful courses, which are quite different from other established courses in protein crystallization. During each course new trends and other methods are discussed and hereby the whole range of structural methods is always covered. The main aim and big advantage of these courses is a healthy mixture of advanced discussions of the theory and of laboratory experiments.

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