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Celebrating the International Year of Crystallography

Introduction

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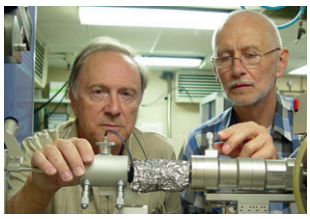
With this special issue, the *FEBS Journal* is joining the international community of structure-oriented enthusiasts in the celebration of IYCr2014, the UN-declared International Year of Crystallography, 2014. Unlike the major disciplines such as physics, chemistry and biology, crystallography is a timid and seemingly narrowly defined science. It is, however, extremely powerful through its literally structure-penetrating methodology and interdisciplinary intergrowth with virtually all other natural and life sciences. Crystallography evolved from an obscure mineralogy-related subject and only gained impetus with the discovery made by Max von Laue in 1912 that X-rays can be diffracted by crystals. In the hands of the father-and-son team of the Braggs in England, this discovery, extended by arcane mathematical theories, became a formidable tool for deciphering the atomic structure of matter. Starting off with the simplest chemical molecules and crystals, the method of X-ray crystallography was used to boldly attack also biological macromolecules, now planting its flag of victory in the domain of huge complexes, including viruses, biological machines and organelles.

In a spectacular synergism, crystallography and technology have fueled their own advances. It is not widely known that crystallographers were the first to apply electronic computers for massive calculations, as well as being skilled programmers and co-creators of the first software tools. Progress in biotechnology and other high-output methods for sample preparation has also been stimulated by crystallography. The most dramatic change happened, and is still happening, in the generation of powerful X-ray beams. Home sources that evolved from the original design by Röntgen are already being phased out and even the most powerful synchrotrons are now dwarfed by the looming X-ray free electron lasers. With brightness that makes our Sun look frighteningly pale, these sources will ultimately allow us to get rid of the final constraint: of the crystal.... Thus we are looking into crystallography without crystals, at nanometer scale and in femtosecond time. But the principle of diffraction holds, and the goal is still the same: to understand the processes of life through the elucidation of the atomic structure of matter, even when it is transient, dynamic or otherwise delicate.

This issue contains six review articles and 19 regular papers, all of them representing different aspects of the application of crystallography to structural biology. It opens with a brief history of macromolecular crystallography [1] written by the editors of this issue together with Zbyszek Dauter, Section Co-editor of *Acta Crystallographica D*. The review is focused on a family tree of crystallographers and their numerous achievements, mainly those that led to the award of Nobel Prizes. In order to show that progress is not always easy and predictable, an accompanying review by Dauter and Jaskolski shows that this history also had its downsides and that even the most brilliant scientists can miss proper conclusions or go astray in their work.

Although macromolecular crystallography is considered to be a mature discipline, new tools are still being developed and several papers reflect this aspect of macromolecular crystallography. Jingue Lu and Peter Sun [2] review the methods to generate heavy atom derivatives that are still needed in



Despite having permanent locations on different continents, Mariusz Jaskolski and Alex Wlodawer have been closely collaborating for over a quarter of a century. They both proudly call themselves crystallographers, even if such a designation might currently not be the most politically correct. Mariusz has worked on all aspects of small-molecule and macromolecular crystallography as professor at Adam Mickiewicz University and in the Institute of Bioorganic Chemistry of the Polish Academy of Sciences in Poznan, Poland. Alex formerly worked at the National Bureau of Standards (now NIST) and is currently at the National Cancer Institute in Frederick, MD, USA. He has contributed to the development of technical aspects of structural biology, such as the use of neutron and synchrotron radiation for proteins, as well as to structural elucidation of several headline macromolecules. Their collaborative projects, some initiated when Mariusz was a visiting scientist at the NCI, included structural characterization of retroviral proteases and integrases or anticancer proteins such as L-asparaginase. They have also been promoting education and understanding of crystallography through a series of didactic reviews.

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many structural studies. The group of Isabel Usón discusses their Arcimboldo method that uses small fragments from poor homology models to solve new crystal structures. John Tainer and his colleagues provide an analysis of the '*R* factor gap' that indicates the discrepancies between the model and the data from which it has been derived, whereas Andrew Karplus and coworkers [3] discuss conformation-dependent restraints in macromolecular refinement. The paper by Stefano Ricagno and his colleagues shows how structural information can be used for engineering proteins with desired properties.

In the next part of the issue, contributions from structural biology and other crystallography-related approaches have been arranged according to a leading structural theme. Several papers review or report structural discoveries that can influence the treatment of human diseases. Rolf Hilgenfeld reviews the field of the design of novel drugs for targeting SARS and MERS [4], whereas Borek *et al.* [5] discuss new findings regarding L-asparaginase, a protein used in the treatment of leukemia. A work from the laboratory of Matthias Bochtler analyzes an interesting case of the structure of an antimicrobial peptidase, lysostaphin, effective against *Staphylococcus aureus* and derived from another *Staphylococcus* species.

Crystallographic information is also used to illuminate enzymology, as shown in the paper by Xinhua Ji and his coworkers which presents a study of the bifunctional folate pathway [6]. Maria Armenia Carrondo and her colleagues describe the structure of a catalase from *Deinococcus radiodurans* and the group of Clemens Steegborn contributes a study aimed at explaining the structural basis of catalysis by adenylyl cyclase. Multiple crystal structures of fungal β-mannosidases are described in a paper by Igor Polikarpov and his colleagues. Structural dissection is also used to unravel other biological mechanisms, including transport phenomena. Ralf Ficner with coworkers review the allosteric aspects of nuclear transport [7] and Udo Heinemann and his group present the crystal structure of a protein involved in the regulation of a multimeric complex called transport protein particle [8]. Gergely Nagy, Ibolya Leveles and Beáta Vértessy [9] discuss preventive DNA repair called 'sanitizing', while work from George Phillips's laboratory explains molecular recognition promiscuity of a thermophilic enzyme.

Protein–ligand interactions are an important area of crystallographic scrutiny, as illustrated by work from the laboratory of Anthony Addlagatta that focuses on selectivity of inhibition of type I methionine aminopeptidase. Yet another paper, presented by Poul Nissen and his colleagues, analyzes the crystal structure of a complex membrane machine, ATPase, in the presence of different lipid molecules from its environment.

Finally, there is a collection of case studies reporting interesting structural observations on diversified subjects, ranging from saccharide sensors in a gut symbiont, presented by Wayne Hendrickson and colleagues [10], to deoxyribonucleoside regulator, presented by the laboratory of Pavlina Řezáčová, to a transcriptional regulator with a novel fold, discovered by Andrzej Joachimiak and his colleagues. Other papers included in this segment provide structural explanation of the redox properties of a laccase by Vlada Urlacher and colleagues or analyze the glycosylation pattern of a latex peroxidase (Gottfried Palm and colleagues).

This brief summary of the contents of this special issue clearly shows that macromolecular crystallography is very much alive and well during the International Year and that this discipline is still vibrant and evolving. We hope that this issue will provide interesting reading for a wide circle of readers with diversified appetite for exciting structural, methodological or historical aspects of structural biology in general and crystallography in particular.

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