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Macromolecular Crystallography – Quo vadis?

Thursday, 15 September 2022 08:45 (1 hour)

Macromolecular Crystallography with X-rays (MX) had its beginnings in the 50's and 60's of the last century. Since then, the method has become ever more powerful by enormous technological progress in the production of samples, growth of crystals, production of X-rays, instrumentation for data collection, computer programs, and data bases. MX has produced the major fraction of the high-resolution structural information on biological macromolecules available to us today.

With the recent resolution revolution in cryo-electron microscopy and the latest breakthroughs in protein structure prediction, the landscape of methods supporting structural biology is changing. I will discuss this changing landscape and expose current and future opportunities in static and time-resolved macromolecular crystallography, in particular with respect to its use in the field of structural enzymology.

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