

X-ray crystallography in the era of high-quality predictions

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X-ray crystallography remains the most commonly used experimental method for determining protein structure. Yet, recently, a plethora of machine-learning approaches was introduced that solve almost completely some of the most difficult problems in structural biology. In my talk, I will discuss the recent advances in macromolecular crystallography and computational methods, highlighting the areas where experimental approaches are still indispensable as well as the tasks where the two methods complement each other very well. I will also provide examples where crystallography studies by Russian scientists were instrumental in obtaining important results [1–7].

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