

**Recent trends and developments in modern biomolecular crystallography**

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Amazing technical and instrumental advances in robotic automation, concurrent miniaturization, and remote instrumentation access have removed much of the procedural and logistic tedium of protein structure determination via biomolecular crystallography. However, in most steps - from expression and crystallization to model refinement and ligand docking - the expectations and the level of difficulty of chosen targets have at least kept pace with the technical advances. Numerous conceptual and technical challenges which need human ingenuity and skill remain - particularly in protein preparation, crystallization, crystal handling, and implementation of fully autonomous robotics in structure determination pipelines.