Oral presentation

A generic cross-seeding approach to protein crystallization

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Obtaining diffraction-quality crystals is the rate-limiting step in biological macromolecular X-ray crystallography. Here, an innovative approach that increases the yield of useful protein crystals is presented. The approach is based on the preparation of a mixture that integrates a multitude of different protein crystal fragments. The fragments represent a heterogeneous set of nanotemplates that can potentially promote the crystal nucleation of proteins unrelated to the proteins initially employed to prepare the fragments. We added our generic cross-seeding mixture to a sample of human retinoblastoma binding protein 9 before proceeding with crystallisation assays. A novel crystal from was readily obtained and the corresponding structure solved at 1.2 Å resolution.