How to deal with Pathological Crystals of Macromolecules

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Although macromolecular crystallography is rapidly becoming largely routine due to advances in the methods of data collection, structure solution and refinement, difficult cases are still common. We have recently completed a number of structure determinations that utilized less than perfect crystals and these cases exemplify various difficulties faced by protein crystallographers. The structure of the proteolytic domain of *Archaeoglobus fulgidus* Lon was solved with crystals that contained superimposed orthorhombic and monoclinic lattices in a seemingly single crystal. Another, hexagonal crystal form exhibited unusually large degree of non-isomorphism that was not apparent in the analysis of the unit cell parameters. Crystals of the *A. fulgidus* Rio1 kinase exhibited both pseudosymmetry and twinning that masked the problems during analysis of intensity distribution. We will discuss the ways of identifying the observed phenomena and the approaches to solving and refining macromolecular stuctures if only less than perfect crystals are available.

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