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Ultra-High Resolution Refinement of Proteins: *Serratia Marcescens* Endonuclease at 0.92 Å. Sergey V. Lindeman, Mitch Miller, Pierre LeMagueres, Kurt L. Krause, Dept. of Biology and Biochemistry, Univ. of Houston, Houston, TX 77204.

Serratia endonuclease is a remarkable extracellular nuclease that is capable to cleaving DNA and RNA in both double and single-stranded forms at rates much faster than DNase I. Crystals of this protein in space group $P2_12_12$ contain almost 500 residues within the asymmetric unit, yet they diffract to beyond 1.0 Å. We present here our refinement of this protein at 0.92 Å based on image-plate data collected at DESY using cryocooling. We have an observation/parameter ratio of over 8 – not including restraints, and therefore independent refinement of well-ordered regions can be carried out. However, this crystal form displays strong pseudocentering that complicates the refinement process. In this presentation, we will focus on methods to handle pseudosymmetry, our experience with bond lengths and angles relative to standard protein restraint parameters, solvent structure, tautomer and isostere placement, and direct hydrogen visualization.

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