

Solution of the Structure of the Doubled c-Axis Variant of T_3R_3 Zinc Human Insulin Complex from Powder Diffraction Data

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Introduction: Grinding of T_3R_3 zinc human insulin complex results in the formation of a doubled c-axis variant (T_3R_3DC) with the rhombohedral lattice constants $a=81.275\text{\AA}$ and $c=73.024\text{\AA}$ and the space group R3. Over a few days this material reverts to the previously known R3 structure with $a=81.084\text{\AA}$ and $c=37.537\text{\AA}$. In this work the transition was discovered and the structural change elucidated from an analysis of high resolution X-ray powder diffraction data.

Methods and Materials: Powder diffraction data were collected over the range 1.0° - 13.0° in 0.002° steps at $\lambda=0.700233(1)\text{\AA}$ for the T_3R_3 complex and 1.0° - 25.0° in 0.005° steps at $\lambda=1.401107(1)\text{\AA}$ for the T_3R_3DC form. Indexing of both powder patterns was achieved using the CRYSFIRE (R. Shirley, private communication) suite of programs and structure solution and refinement using the GSAS package.

Results: The structure of the T_3R_3DC variant is shown in **Figure 1** and results from a shear-induced dehydration of alternate T_3R_3 pairs and is accompanied by rotations of 17.2° and 9.5° of the two T_3R_3 complexes with respect to their orientations in the original T_3R_3 structure.

Conclusions: In summary, we have demonstrated that it is possible to solve and refine a protein crystal structure from powder diffraction data by employing a molecular replacement technique and a combined stereochemical restraint and Rietveld refinement. The relative ease with which this was done here suggests that this approach can be employed, for example, to examine structural changes in a series of protein derivatives in which the structure of one member is known from a single crystal study.

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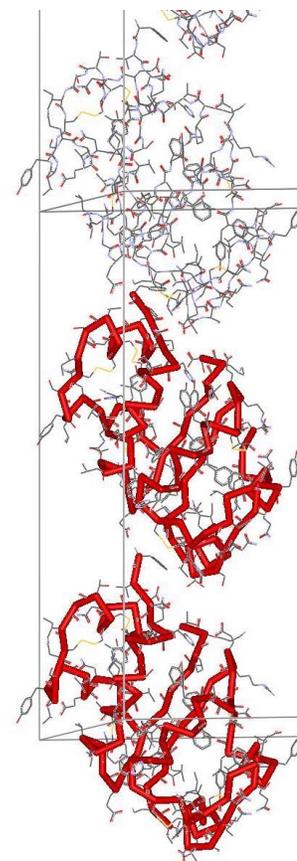


Figure 1. A packing diagram of three TR complexes stacked along the crystallographic c-axis in T_3R_3DC . A C_α trace is shown in red for the two complexes that comprise the unique crystallographic unit and the unit cell edges are also marked.