

10 YEARS OF PROTEIN POLYCRYSTALLOGRAPHY

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A simulation of a protein powder diffraction pattern was stunning in the apparent amount of information that was seen. A subsequent experiment on met-myoglobin showed a powder diffraction pattern from essentially perfect polycrystalline material that showed very little sample broadening; the peak widths were essentially limited by the instrument resolution. The challenge was to make use of this in protein structure analysis. This talk will recall some of those early experiments and data analyses, as well as an overview of some current progress and future possibilities.

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