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## How well do we understand macromolecular crystals?

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R-values represent the discrepancy between our macromolecular models and the measured X-ray data; they typically are around 20%, clearly showing that something is amiss; our current models of macromolecular crystal structures seem to be lacking. A better understanding of the shortcomings in our current models (and methods) could be an important factor to solving the most difficult structures and to improving all others to obtain more biological information. But what causes this difference?

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