

Oral Contributions

[MS39-05] **I am a protein crystal: get me out of here!** Elspeth F. Garman

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A critical step in the macromolecular crystallographic experiment is the journey that the hard won crystal must make from the crystallisation drop to the goniometer, in order that diffraction data can be collected. The experimenter has a pivotal role to play in manipulating the crystal so that it survives this journey in as good a state as possible. The effects on the ultimate data quality (and thus the electron density map) of small details in the harvesting [1] and cryocooling protocols [2,3] are frequently underestimated. By thinking about the impact of each stage of handling, degradation of the crystal, caused by ‘over handling’ and by the use of inappropriate or anecdotal cryocooling practices, can be minimised. This contribution will highlight the aspects to be considered, and give some pointers on how the results might be optimised once a crystal has been grown and the best possible diffraction data are required.

[1] Garman, E.F. & Murray, J.M.. *Acta Cryst.* (2003) D59, 1903–1913

[2] Garman, E.F. & Schneider, T.R J. *Appl. Cryst.* (1997) 30, 211-237

[3] Garman, E.F. *Acta Cryst.* (1999). D55, 1641-1653

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