**Poster Presentation**

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## *When protein crystal dehydration helps*

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A typical protein crystal contains 30-60% solvent. For a naked crystal, this solvent is distributed between solvent shells, where water and solvent molecules make specific interactions with the crystalline protein, and solvent channels filled with disordered solvent molecules. This internal solvent map of the crystal can be modified by placing the crystal in a dehydrating environment. This may in turn induce changes to the crystal lattice and affect mosaicity, resolution and quality of diffraction data. A dehydrating environment can be generated around a crystal in several ways with various degrees of precision and complexity. In this study we have used the HC1 device (Maatel) to mount crystals an air stream of known relative humidity – a precise yet hassle-free approach to altering crystal hydration. We set out to analyse a range of different crystals to establish usable protocols that will allow one to explore to crystal hydration space, either by preparing samples before synchrotron beamtime or by undertaking the experiments during beamtime. Our results, considered in the light of the literature surrounding crystal dehydration, provide guidance for when dehydration can help diffraction.

**Keywords:** Protein crystals, Dehydration