

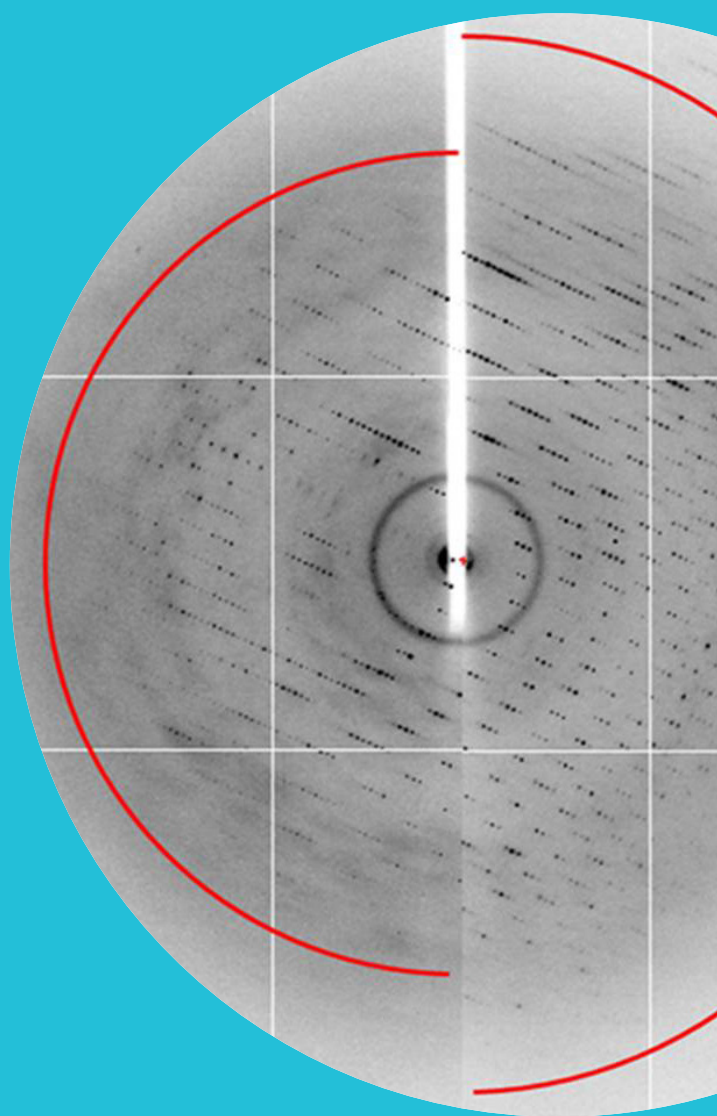


## CASE STUDY

# HC1: a user-friendly device for crystal dehydration

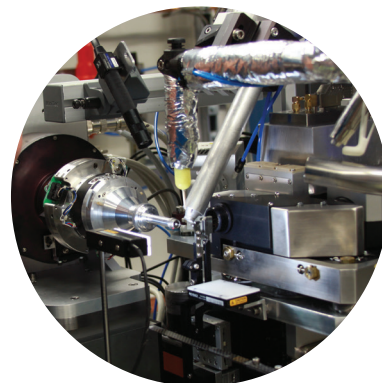
Investigating the 3D structure of macromolecules by X-ray crystallography requires the production of high quality crystals, and yet this step remains a tedious and empirical task.

Weak packing and high solvent content are among the most frequent factors causing a negative impact on the acquisition of suitable diffraction images. It is, therefore, useful to develop post-crystallisation methods to enhance crystal quality.



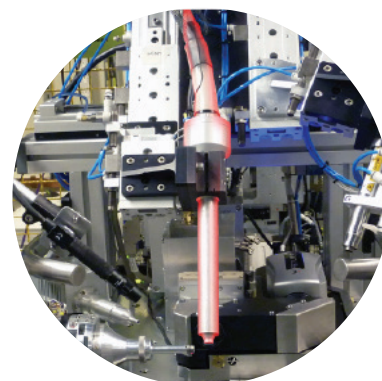
## The Challenge

Crystal dehydration is a technique reported, in some cases, to improve crystal diffraction properties. Upon modulation of the solvent content, a crystal may experience significant changes in one or more of the following parameters; space group, unit cell, mosaic spread, spot profile and resolution limit. This process is, however, challenging to control manually and it can be difficult to reproduce the original observation.



## The Solution

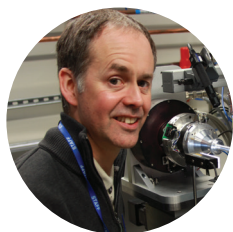
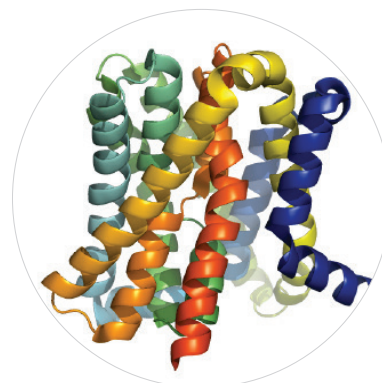
The HC1 device is ideally suited to handle dehydration projects without the need for manual manipulation. It operates by delivering an air stream of carefully controlled relative humidity to the sample, adjusting the solvent content within the crystal. Thanks to its design, it fits all MX beamlines at Diamond and enables the user to correlate precise relative humidity ratios with observed diffraction images.



## The Benefits

Simple and straightforward to use, the HC1 device allows the user to define a reproducible dehydration protocol within a reasonable timeframe. Mounted on any MX beamline, the system provides a real-time feedback about the impact of dehydration on crystal diffraction properties.

In combination with the sample changer, it is easy to condition and freeze samples for upcoming data collections. The HC1 device can also help to fully understand a crystal system, optimise cryo-conditions or compensate damage effects generated by soaking.



**“In determining the structure of a bacterial homologue of a bile acid transporter we saw that, by dehydrating our crystals, their diffraction limit improved from 4Å to 2Å. We were able to do this very efficiently and reproducibly with the HC1 device at Diamond. The increase in the resolution was highly beneficial in the refinement and analysis of the structure.”** [Dr Alex Cameron, Imperial College London / Membrane Protein Laboratory](#)



## For further information

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