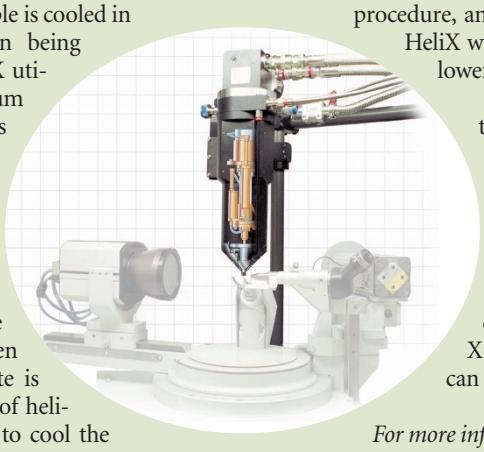
72. Matsuo, H., Kupce, E., Li, H. & Wagner, G. Use of Selective C alpha pulses for improvement of HN(CA)CO-D and HN(COCA)NH-D experiments. *J. Magn. Reson. Ser. B* **111**, 194–198 (1996).
73. Clubb, R. T., Thanabal, V. & Wagner, G. A new 3D HN(CA)HA experiment for obtaining fingerprint H^N -H^a cross peaks in ^{15}N- and ^{13}C-labeled proteins. *J. Biomol. NMR* **2**, 203–210 (1992).
74. Grzesiek, S. & Bax, A. Correlating backbone amide and side chain resonances in larger proteins by multiple relayed triple resonance NMR. *J. Am. Chem. Soc.* **114**, 6291–6293 (1992).
75. Palmer, A. G. I., Cavanagh, J., Byrd, R. A. & Rance, M. Sensitivity improvement in three-dimensional heteronuclear correlation NMR spectroscopy. *J. Magn. Reson.* **96**, 416–424 (1992).
76. Neri, D., Szyperski, T., Otting, G., Senn, H. & Wuthrich, K. Stereospecific nuclear magnetic resonance assignments of the methyl groups of valine and leucine in the DNA-binding domain of the 434 repressor by biosynthetically directed fractional ^{13}C labeling. *Biochemistry* **28**, 7510–7516 (1989).
77. Brunger, A. T. Crystallography and NMR system. *Acta Crystallogr.* **D54**, 905–921 (1998).
78. Brünger, A. T. *X-PLOR manual* (Yale University, New Haven, Connecticut; 1993).
79. Laskowski, R. A., Rullmannn, J. A., MacArthur, M. W., Kaptein, R. & Thornton, J. M. AQUA and PROCHECK-NMR: programs for checking the quality of protein structures solved by NMR. *J. Biomol. NMR* **8**, 477–486 (1996).
80. Carson, M. J. Ribbons 2.0. *J. Appl. Crystallogr.* **24**, 958–961 (1991).
81. Nicholls, A., Sharp, K. A. & Honig, B. Protein folding and association: insights from the interfacial and thermodynamic properties of hydrocarbons. *Struct. Funct. Genet.* **11**, 281–296 (1991).

product review

Oxford Cryosystems has announced the launch of the Oxford HeliX, the first commercially available helium system for X-ray crystallography in which the crystal sample is cooled in an open flow gas stream rather than being enclosed by windows. The Oxford HeliX utilizes helium gas, not liquid, from a helium cylinder and cools it to temperatures as low as 28 K. This is achieved by using a integrated two stage closed cycle cooler and a patented gas delivery system. Other benefits of the Oxford HeliX include: temperature stability of 0.3 K, reduction of helium gas consumption to 7.5 l min^{-1}, a push button temperature controller that is simple to use, and proven mechanical reliability. The low flow rate is designed to minimize the consumption of helium while still providing sufficient flow to cool the sample and eliminate the possibility of ice formation.

Oxford Cryosystems is the home of the nitrogen gas Cryostream Cooler, a popular flow nitrogen system. The design of that system has helped to make the difficult task of low temperature X-ray data collection a more routine procedure, and now the development of the Oxford HeliX will allow routine data collection at even lower temperatures.



The Oxford HeliX is useful for any crystallographer wishing to collect X-ray data below nitrogen temperatures where an open flow gas stream is essential. Experiments in which this would be useful include charge density studies, where lower temperatures offer enhanced data quality, and the cooling of biological samples in intense X-ray sources, where lower temperatures can increase the life time of the crystal.

For more information on the Oxford HeliX, contact:
Oxford Cryosystems
www.OxfordCryosystems.co.uk
email: info@OxfordCryosystems.co.uk

Molecular Structure Corporation has developed the first commercially available xenon derivatization flash cooling device, the Cryo-Xe-Siter. A critical step in X-ray crystallographic structure determination of a macromolecule is the preparation of heavy atom derivatives of the crystal. The noble gas xenon binds to hydrophobic sites and can serve as the needed heavy atom derivative. However, a major challenge to the widespread use of xenon has been the technical difficulty of preparing the derivatized crystals. Now, with the the Cryo-Xe-Siter, xenon derivatives of protein crystals can be produced easily — and at cryogenic temperatures.

The unique two-chamber design allows a protein crystal to reach equilibrium in the xenon atmosphere, at pressures up to 300 p.s.i. The crystal is then flash frozen while still under pressure. The Cryo-Xe-Siter accommodates popular pin mounts and has a small chamber to minimize xenon consumption. It is easy to use and safe to operate.

For more information on the Cryo-Xe-Siter, contact:
Molecular Structure Corporation
tel. 281 363 1033
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http://www.msc.com/