proteins are 0.097 GPa^{-1} and 0.076 GPa^{-1}, respectively. It may imply that SoIPMDH, which is from land bacteria, is more sensitive to pressure than SbIPMDH from extremophile.

The SoIPMDH structure shows a dimer that presents an internal hydrophobic cavity surrounded by Pro120, Lue121, Ile125, Lue232 and Lue258 at the dimer interface. Two structurally functional water molecules appeared in the cavity at a pressure of 470 MPa, while no such water molecule could be observed under atmospheric pressure. Previous published works assume that the pressure denaturation of proteins is induced by water penetration into the hydrophobic interior of proteins. Although concrete data are lacking, several theoretical and simulation studies support this theory [2]. The present observation is a direct evidence of the fact that water molecules do penetrate into the inner cavities of proteins under high pressure.

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Keywords: high-pressure protein crystallography, high-pressure adaptation, pressure denaturation

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Automation and remote control of the MX beamlines at the canadian light source

Pawel Grochulski,[a,b] Michel Fodje,[a,b] James Gorin,[a] Shaun Labiuk,[a] Kathryn Janzen[a] and Russ Berg,[a] [a]*Canadian Light Source, Saskatoon*. [b]*University of Saskatchewan, Saskatoon (Canada).* E-mail: Pawel.Grochulski@lightsource.ca

The Canadian Light Source (CLS) is a 2.9 GeV national synchrotron radiation facility located on the University of Saskatchewan campus in Saskatoon. The Canadian Macromolecular Crystallography Facility (CMCF) is composed of two beamlines, the small-gap in-vacuum undulator illuminated beamline 08ID-1 and a second bending magnet beamline, 08B1-1 [1]. Beamlines are equipped with very robust end-stations including on-axis visualization systems and Rayonix 300 CCD series detectors. They are each complemented with a Stanford automounter (SAM) which accepts SSRL type cassettes or universal pucks. MxDC, a beamline control system developed in-house, is integrated with a data processing module, AutoProcess, allowing full automation of data collection and data processing with minimal human intervention [2]. AutoProcess is based on XDS, Pointless, CCP4 and BEST packages. The system also allows remote control of experiments through interaction with a Laboratory Information Management System (LIMS) that was developed at the facility.

The CMCF provides service to more than 60 Principal Investigators in Canada and the United States. Up to 25% of the beam time is devoted to commercial users and the general user program is guaranteed up to 55% of the useful beam time and is run under a peer-review proposal system. The CMCF staff provides "Mail-In" crystallography service to the users with the highest scored proposals.

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New possibilities offered to crystallography by 6-axis robotic-arm based systems

Jean-Luc Ferrer,[a] Xavier Vernede,[a] Pierre Mazel,[c] Pierrick Rogues,[c] Florian Bouis,[a] Matthieu Privat,[b] Jean-Loup Rechatin,[b] Nathalie Larive,[c.] [a]*Institut de Biologie Structurale CEA-CNRS-UJF, Grenoble, France.* [b]*Irelec, Saint Martin d'Hères, France.* [c]*NatX-ray SAS, Grenoble, France.* E-mail: jean-luc.ferrer@ibs.fr

CATS and G-Rob systems were developed on protein crystallography beamline FIP-BM30A at the ESRF. CATS [1] is a high throughput reliable sample changer currently operating on the major synchrotrons worldwide (BESSY, SLS, DLS, APS, …) and commercialized by Irelec Company (www.irelec-alcen.com). G-Rob, also a 6-axis robotic arm based system, is a fully integrated device for crystallography beamlines (commercialized by Irelec) and laboratories (commercialized by NatX-ray company, www.natx-ray.com). G-Rob is an "all in one" system, since it integrates the following functions:

- sample changer,
- goniometer for frozen samples, capillaries, … [2],
- crystallization plates/micro-chips screening for *in situ* analysis of diffraction condition and data collection [3],
- beam monitoring.

G-Rob provides unique features. It is automated: thanks to its tool changer, it goes automatically from one application to another. CATS and G-Rob are also highly flexible: if a new application or a new sample format emerges in the community, a new tool can be designed to implement it. They are highly reliable systems, based on well-known, industrial quality equipments, with reduced maintenance.

Several G-Rob systems, both at synchrotrons or as laboratories in-house systems, are now available (ESRF, EPFL, …). The first system, in use on beamline FIP-BM30A, was made available to the research community in 2005 and up to now, users have expressed an unprecedented high degree of satisfaction. The crystallization plates screening capability for example appears to be a precious tool in several cases (crystals too small to be fished, or too fragile, of when there is no good cryoprotectant).

Several results obtained on FIP-BM30A are presented, such as *in situ* screening of membrane proteins, ribosome, high pressure protein diffraction, etc. Recent experiments demonstrated also the possibility of the automated structural screening for the Fragment Based Drug Design strategy: the same crystal was reproduced in presence of a library of fragments. Systematic *in situ* data collection has shown some of the fragments present in the active site, without having to manipulate the crystals individually. *In situ* data collection was also used recently to solve the structure of entire viruses (D Stuart et al.). All these experiments take advantage of a new sitting drop plate specially designed for *in situ* X-ray analysis. This plate was developed in collaboration between beamline FIP-BM30A at the ESRF (Grenoble, France) and Greiner BioOne. Movies are available on www.natx-ray.com

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Automated characterization of nanotube membranes of large Size By X-Ray scattering

P. Launois,[a] M. Huard,[a] D. Petermann,[a] J. Cambedouzou,[a] M. Mille,[b]