

Microsymposium

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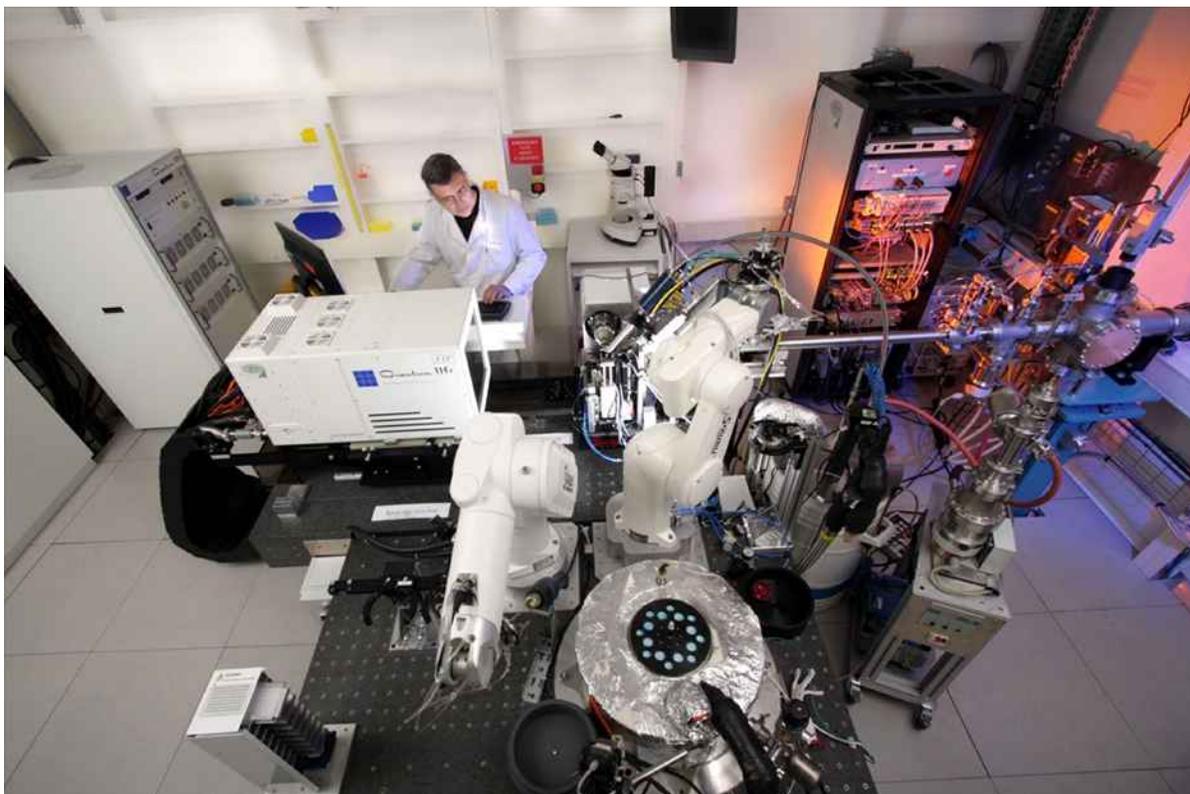
Progress of robotized systems for crystallography for beamlines and laboratories

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Development of 6-axis robotic arm based systems for protein crystallography automation is now expanding rapidly. From the seminal work accomplished on beamline FIP-BM30A (ESRF) in 2000' to the present developments, robot based systems significantly changed the crystallography experiment strategy. They open possibilities for new strategies, give a high flexibility to the experimental setup, and make automation and remote control much easier. The robotized platform on which are based our present developments, named G-Rob, plays as a fully integrated, multi-purpose automated and remotely controlled diffractometer for beamlines and laboratories. G-Rob integrates several functions: classical sample changer; goniometer for frozen samples or capillaries [1], including frozen sample transfer from a storage Dewar; crystallization trays handling for in situ screening and data collection on crystallization plates and microchips [2]; powder diffraction; beam monitoring; on line crystal fluorescence/absorption; crystal harvesting; Etc. Thanks to its tool changer, the robot arm can go automatically from one application to another. G-Rob can be easily upgraded with new functions. Several G-Rob systems, both at synchrotrons (ESRF, LNL, BNL) or as laboratory in-house systems (EPFL, CBS) are now available for the crystallography community. Among the last results obtained with G-Rob are: (i) Automated structure resolution at room temperature, for the analysis of protein dynamic; (ii) Automated structural screening for the fragment based drug design strategy. New functions are also under development, such as the remote controlled robotized crystal harvesting [3]. Such manipulations of individual crystals with the robot closes the gap for fully remote, and in the future fully automated, operation of crystallography pipeline.

[1] L Jacquamet, J Ohana, J Joly et al., *Acta Cryst. D*, 2004, 60, 888-894., [2] L Jacquamet, J Ohana, J Joly et al., *Structure*, 2004, 12, 1219-1225., [3] MY Heidari Khajepour, H Lebrette, X Vernede et al., *Acta D*, 2013, 69, 381-387.



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