

Microsymposium

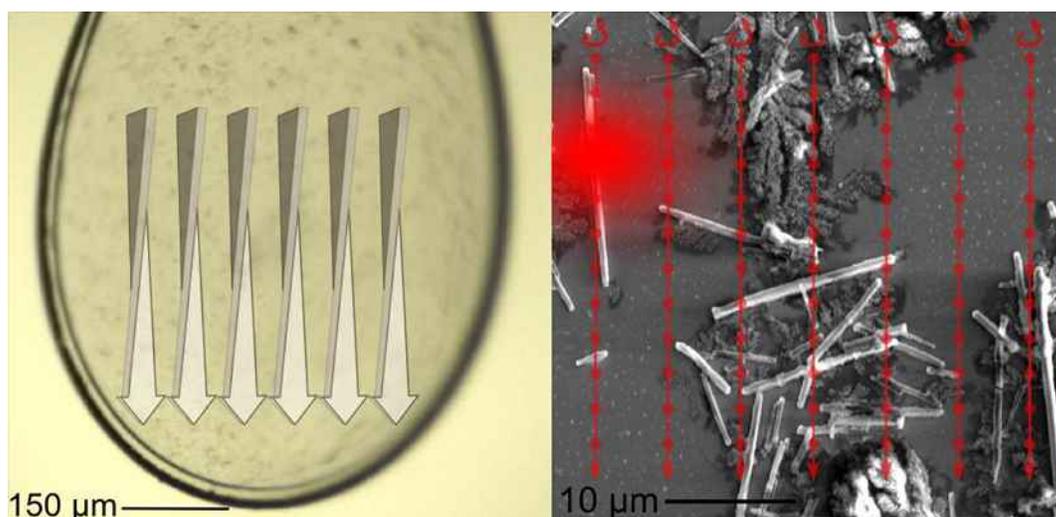
MS22.O03

Serial crystallography using synchrotron radiation - novel strategies for microcrystallography

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Protein crystallography continues to be one of the most frequently used techniques to obtain structural information of biomacromolecules to atomic resolution. Since protein crystals of delicate target systems are often limited in size, one of the main goals in the design of modern beamlines is the construction of highly intense X-ray beams with small focal size to obtain high resolution diffraction images of microcrystals. However, this development has led to the situation, that the full intensity of the beam can destroy a protein crystal within fractions of a second. Therefore often only a small number of diffraction patterns can be obtained from one single crystal. Here we describe the adaptation of the serial crystallography approach, which has first been developed at X-ray Free-Electron Lasers (Chapman et al. 2011) to the usage of a microfocus synchrotron beamline, using a standard cryogenic loop for sample delivery. We proved this concept with in vivo grown cathepsinB microcrystals (TbCatB, Koopmann et al. 2012, Redecke et al. 2013) (average of 9 μm^3), a medically and pharmaceutically relevant protein, involved in the life cycle of *T. brucei*. In these experiments it was possible to show that serial crystallography enables the utilization and outcome of the above described bottlenecks and features of modern 3rd generation synchrotron microfocus beamlines. Our strategy exploits the combination of a micron-sized X-ray beam, high precision diffractometry and shutterless data acquisition with a pixel-array detector. By combining the data of 80 TbCatB crystals, it was possible to assemble a dataset to 3.0 Å resolution. The data allow the refinement of a structural model that is consistent with that previously obtained using FEL radiation, providing mutual validation.

[1] Cornelius Gati, Gleb Bourenkov, Marco Klinge, Dirk Rehders, Francesco Stellato, Dominik Oberthür, Oleksandr Yefanov, Benjamin P Sommer, Stefan Mogk, Michael Duszynski, Christian Betzel, Thomas R Schneider, Henry N Chapman and Lars Redecke. (2014). *IUCrJ* 2, [2] Redecke, L., Nass, K., DePonte, D.P., White, T.A., Rehders, D., Barty, A., Stellato, F., Liang, M., Barends, T.R., Boutet, S., Williams, G.J., Messerschmidt, M., Seibert, M.M., Aquila, A., Arnlund, D., Bajt, S., Barth, T., Bogan, M.J., Caleman, C., Chao, [3] Chapman, H.N., Fromme, P., Barty, A., White, T.A., Kirian, R.A., Aquila, A., Hunter, M.S., Schulz, J., DePonte, D.P., Weierstall, U., Doak, R.B., Maia, F.R., Martin, A.V., Schlichting, I., Lomb, L., Coppola, N., Shoeman, R.L., Epp, S.W., Hartmann, R., Rol



Keywords: Serial crystallography, Protein microcrystallography, In vivo grown microcrystals