

MS03 Crystallization and biophysical characterization

MS3-05

Nucleation and reproducibility in protein crystallization assisted by the crystallophore
E. Girard¹, Z. Alsalman¹, A. Robin², S. Engilberge¹, A. Roux³, F. Riobé³, O. Maury³

¹Univ. Grenoble Alpes, CEA, CNRS, IBS - Grenoble (France), ²European Molecular Biology Laboratory - Grenoble (France), ³Univ. Lyon, ENS de Lyon, CNRS UMR 5182, Université Claude Bernard Lyon 1, Laboratoire de Chimie - Lyon (France)

Abstract

Obtaining crystals remains the major hurdle encountered by bio-crystallographers in their race to get new high-quality structures. The crystallophore, Xo4, is a family of nucleating and phasing molecules based on lanthanide complexes. Tb-Xo4 was the first molecule of this family to be described [1].

Tb-Xo4 crystallization properties will be first described through results obtained on more than fifteen proteins and will show that Tb-Xo4 is an efficient tool as:

- (i) Tb-Xo4 increases the number of crystallization conditions by promoting unique ones [1,2]
- (ii) The crystalline forms promoted by the crystallophore bypass crystal defects often encountered by crystallographers such as low-resolution diffracting samples or crystals with twinning [3]
- (iii) Crystals can be obtained from enriched fractions containing several proteins, contrary to the dogma that crystallization can only be promoted from pure protein sample [3] leading to the structure determination of a protein complex [4].
- (iv) Even more unexpected, the crystallophore is able to induce nucleation directly from the protein solution, as exemplified by the crystallization of hen egg white lysozyme in water [5].

Then, we will focus on the crystallization reproducibility, a prerequisite and particular issue in structure-based drug design. Reproducibility is largely improved with the crystallophore. This will be illustrated by results with three different proteins obtained in the framework of a collaborative project with the High throughput Crystallization Platform (HTX-lab) at EMBL-Grenoble, the Polyvalan startup (<https://crystallophore.fr>) and Edelris company (<https://www.edelris.com>).

Altogether, crystallophore is an efficient solution for protein crystallization and structure determination in the bio-crystallographer toolbox.

Authors acknowledge financial supports from the Fondation Maison de la Chimie, Agence Nationale de la Recherche (ANR Ln23-13-BS07-0007-01) and Region Auvergne Rhône Alpes (programs Xo4-2.0 and Crysfrag).

References

- [1] Engilberge, S., Riobé, F., Di Pietro, S., Lassalle, L., Coquelle, N., Arnaud, C.-A., Pitrat, D., Mulatier, J.-C., Madern, D., Breyton, C., Maury, O. & Girard, E. (2017). *Chem. Sci.* 8, 5909–5917.
- [2] Jiang, T., Roux, A., Engilberge, S., Alsalman, Z., Di Pietro, S., Franzetti, B., Riobé, F., Maury, O. & Girard, E. (2020). *Crystal Growth & Design.* 20, 5322–5329.
- [3] Engilberge, S., Wagner, T., Santoni, G., Breyton, C., Shima, S., Franzetti, B., Riobé, F., Maury, O. & Girard, E. (2019). *Journal of Applied Crystallography.* 52, 722–731.
- [4] Vögeli, B., Engilberge, S., Girard, E., Riobé, F., Maury, O., Erb, T. J., Shima, S. & Wagner, T. (2018). *Proceedings of the National Academy of Sciences.* 115, 3380–3385.
- [5] de Wijn, R., Rollet, K., Engilberge, S., McEwen, A. G., Hennig, O., Betat, H., Mörl, M., Riobé, F., Maury, O., Girard, E., Bénas, P., Lorber, B. & Sauter, C. (2020). *Crystals.* 10, 65.