

CRELUX partners with Eyen to advance 3D cryo-electron microscopy into industrial drug discovery applications

▶ SPOTLIGHT TECHNOLOGY: 3D Cryo-Electron Microscopy now at CRELUX

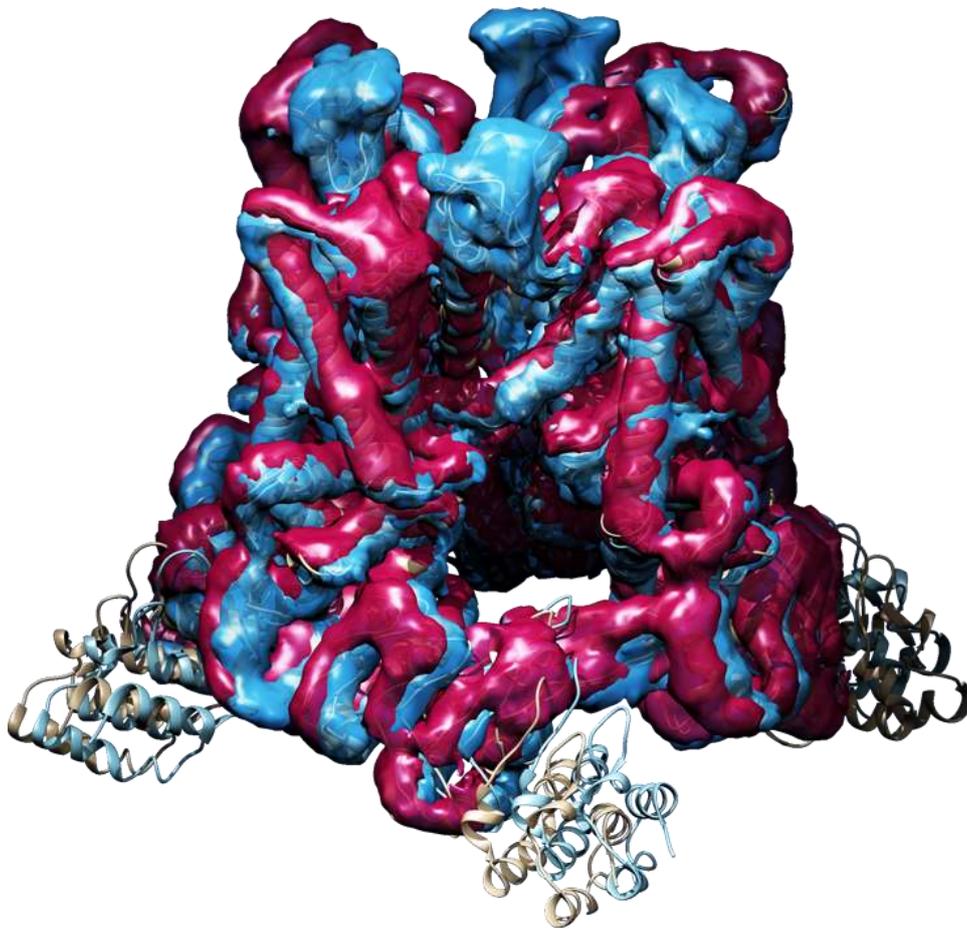


Figure: 3D CryoEM structure of a membrane protein (courtesy of Eyen)

The structure of membrane proteins can be resolved to quasi-atomic resolution, widening the range of feasible targets. Here, 3.4Å resolution of mammalian transient receptor potential channel was resolved. Cao et al., Nature (2013) 504, pp. 113-118, emd-5776, emd-5777

CRELUX is now collaborating with Eyen on 3D cryo-electron microscopy – an emerging structure determination technique that significantly improves our understanding of biological systems. It complements existing atomic-resolution approaches like X-ray crystallography by providing in-situ context within large complexes as well as access to structures of difficult to crystallize multi-domain proteins, antibodies or integral membrane proteins.

3D Cryo EM perfectly matches the technologies already established at CRELUX and can be easily integrated in our workflow. CRELUX's proprietary expression tools for the production of protein complexes with up to 10 different subunits enable access to large proteins at the highest quality available. The combination of CRELUX's protein expertise with Eyen's access to high end equipment like the K2 Summit camera makes Cryo EM a valuable option in the structure solution of large macromolecules.

To learn more about Eyen and Cryo3D electron microscopy also visit our partner's website at: <http://www.eyen.se>

Typical workflow comprises:

1. **Generation of high quality protein** solution of the target of interest (performed by CRELUX or provided by the client): Make use of our Prime Protein service.
2. **Cryogenic sample preparation:** Small amounts are prepared and flash-frozen to form an amorphous ice phase that preserves native, solution-like conditions.
3. **Electron microscope imaging:** An advanced transmission electron microscope is used to take high resolution 2D images of the vitrified sample in a low-exposure mode.
4. **Computational 3D reconstruction:** Iterative computational procedures are used to aggregate the 2D images into a 3D structure. Several protocols like electron tomography, single particle analysis, or sub-volume averaging are used.
5. **Analysis and interpretation:** The 3D models are verified and analyzed. Technological advances are making atomic resolution of large proteins possible.



▶ NEWS

CRELUX receives 800 000 euros funding from the EU Horizon 2020 program to identify novel marine compounds for treatment of age-related diseases in the project TASCAR.

Read more <http://www.crelux.com/news-1/#news> and www.tasctmar.eu



 **MEET us at**

RICT, July 1-3, Avignon, France

Discovery on Target, September 22-24, Boston, USA

Bio Europe, November 4-6, Munich, Germany

PSDI, November 8-10, Munich/Tegernsee, Germany

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