Robotic chain for the 2D crystallization of membrane proteins

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To understand protein functions at a molecular level, high-resolution structures are an invaluable tool for soluble as well as for membrane proteins. Although many structures can be obtained using X-ray diffraction, electron crystallography has recently proven to yield high quality structures in the field of membrane proteins. The two techniques are similar in some aspects, but the information that they provide are complementary, since the conformation of the protein in 3D and 2D crystals is the result of different environments. The importance of electron crystallography for elucidating the structure of membrane proteins arises from the fact that the environment of the 2D crystals is more similar to the native environment of the protein and, thus, the structure determined by means of 2D crystallography is thought to be closer to the native one.

Obtaining good quality crystals, large enough to yield high-resolution information is a bottleneck in the structural determination by electron microscopy on 2D crystals. Whereas 3D crystallization robots are very popular and widely used, automatic systems available to perform 2D crystallization trials are much rarer. Usually, a large number of parameters have to be tested to find conditions in which the protein forms 2D ordered arrays and to optimize them.

We are designing a robotic chain for the 2D crystallization of membrane proteins (Cracam) which allows to test many different 2D crystallization conditions.