

**Macromolecular crystallography (MC)** is a most important research area nowadays, providing essential information to many research areas, such as Medicine and Drug Development. As an example, while studying a certain protein target related with a specific disease, the extensive analysis of the protein crystal structure can provide molecular clues for the development of specific drugs which will define novel therapeutic strategies. MC can also have applications on bio- and nanotechnological areas, being important, for instance, for protein design, where starting from a known protein structure, a new molecule is designed by making calculated variations aimed at a specific function. The Macromolecular Crystallography Unit at ITQB is organized into four different Laboratories: Structural Genomics, Structural Biology, Industry and Medicine Applied Crystallography and Membrane Protein Crystallography. Different projects are currently under way in our unit (<http://xtal.itqb.unl.pt>) and the methodologies used can be summarized into five stages: gene cloning, protein expression, purification and crystallization, structure determination, refinement and analysis. For some projects, the target proteins are cloned, expressed and purified within the Unit, whereas for others the purified protein is supplied by other research Laboratories, either from ITQB or outside, within the framework of collaboration projects. Our main goal is to obtain the crystal structure of the protein targets under study, in order to be able to understand the molecular processes in which the proteins take part.