

Title: **Work with proteins: purification, stabilization and crystallization**

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The aim of this practical final degree work has been the achieving of stable protein crystals to perform a characterization of the structure of the proteins under study by crystallographic techniques.

In the laboratory of Proteolysis of the Institute of Molecular Biology of Barcelona (IBMB), the technique used to determine the structure of proteins is the diffraction of Synchrotron radiation (X-Ray) and for this technique it is necessary to get crystal proteins.

The crystallization of proteins has gained relevance due to its fundamental role in the structural determination, since the knowledge of its structure allows us to know mechanisms of action of the protein, redesign it to give it new functions and / or design new drugs. The production of high quality crystals has always been a bottleneck for the structural determination of the proteins.

For the realization of crystallization experiments, the protein samples were concentrated to carry out the technique of vapor diffusion. The pure P5 protein was extracted and purified from the overexpressed cells supplied by the collaborating laboratory of the project. The diffraction of crystals was carried out at the premises of the European Synchrotron Radiation Facility (Grenoble) and the ALBA Synchrotron (Barcelona). The problem of the phases could be solved by means of molecular replacement and to make the model of the structure of the P1 protein.

Keywords: Protein, crystals, diffraction, structural determination.