

A crystallization robot, unique in UPAT, is expected to provide new possibilities for crystallization trials (SEE-STRUCT module) and enhance efforts in Structure determination of proteins in crystals through X-ray diffraction.

Protein production and purification requires usually heavy efforts and loss of protein quantities. Therefore, pure protein is expensive and often hundreds of combinations of variables must be tried before a novel protein can be crystallized from solution. Manual methods for crystallization are slow and error-prone.

UPAT's Crystallization Robot provides the possibility for quick and accurate dispense of vapour diffusion drops from pre-dispensed reservoirs into sitting drop wells. Protein can be added at the same time using automated dispensing techniques. A suite of software includes packages for screening and optimization and provides easy-to-use interfaces for setting up screening experiments. Algorithms calculate and control pH for any number of buffer species. It can deliver more than 350 microbatch wells per hour, automatically covered with oil with no further requirement for sealing. This equipment will enhance the structural determination efforts of the SEE-DRUG initiatives, being integrated between the SEE-PROT/STRUCT/PHARM groups. With this tool a large number of proteins (either produced by the members of the SEE-DRUG project or by non-UPAT collaborators) will be tested for crystallization. Additionally, the dynamic information obtained by the NMR methodology will be used for the successful crystallization of proteins.

Successful crystals will be used in diffractometers in Athens or in European Synchrotrons facilities for high-resolution structure determination.