

Medium throughput Protein Crystallography: Limiting Steps in the Pipeline

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The Structural Proteomics IN Europe (SPINE) project was the first EC funded structural genomic project. Its aim was to foster the high throughput determination of proteins relevant to human health. The major bottleneck was recognised to be the expression of soluble and stable proteins in sufficient amounts for crystallization, and this has proved to be true. The pipeline will be briefly summarized and the success rate for a set of proteins described. The presentation will concentrate on a set of targets from *Bacillus anthracis* from the SPINE partner groups in York and Oxford. A number of targets were selected using bioinformatics tools and put through the expression pipeline.

While only a small part of SPINE funds was allocated to crystallographic software, a number of scientists have recently been contributing to automation developments. Recent experience on applying these to SPINE targets will be described and bottlenecks indicated.

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