



WEIZMANN INSTITUTE OF SCIENCE

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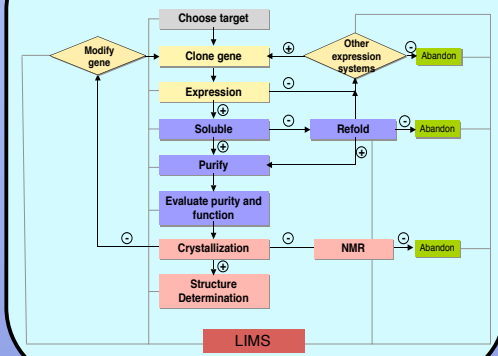
Background

The 3D structure of biological macromolecules is a key element in understanding biological processes and plays a central role in the discovery of new lead drugs. Till now, less than 5% of the unique structures of human proteins have been determined. Therefore, there is a need to facilitate the process involved in determining structures of proteins based on genomic data. The Weizmann Structural Proteomics Center located in the Dept. of Structural Biology at the Weizmann Institute of Science, has been selected by the Ministry of Science & Technology to be the Israel Structural Proteomics Center (ISPC). It is a member of the Structural Proteomics in Europe (SPINE) consortium and receives support from the Divadol Foundation.

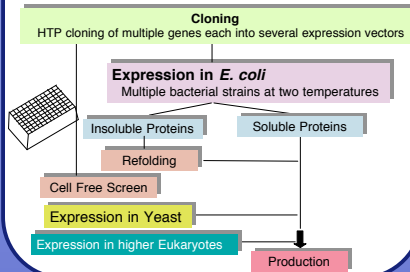
Goals of ISPC

To develop HTP methodologies for cloning, expression, purification, crystallization and structure determination of **proteins related to human health and disease**.

HTP Structural Proteomics

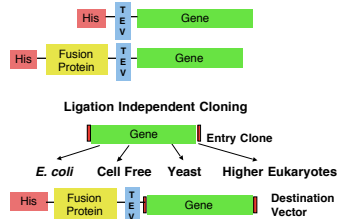


Protein Production at the ISPC

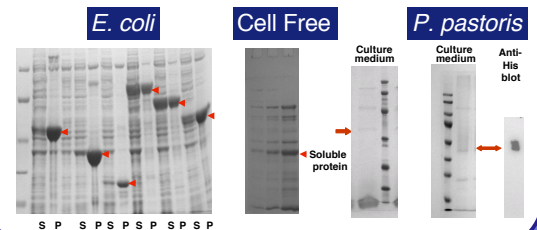


Cloning

Engineering unique expression vectors for the ISPC



Expression Systems



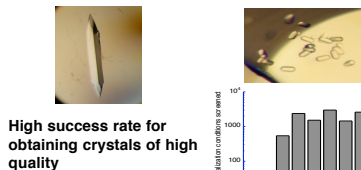
Protein Purification

Purification using AKTA 3D

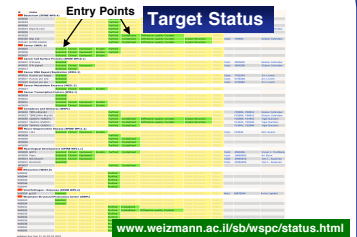
- Three steps of purification starting with capture by affinity tag
- Removal of tag by TEV cleavage
- Final Ni column to remove His-TEV and uncleaved protein
- Protein Concentration
- Crystallization

Crystallization

Screening is carried out using a Douglas Instruments IMPAX 1-5 robot which employs the batch method under oil.



Bioinformatics tools



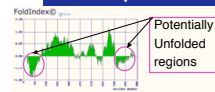
SeqAlert

SeqAlert® is a sequence alerting service that will periodically compare your sequence(s) against sequences from determined 3D structures, or structures being determined at PDB, and TargetDB, the database of target sequences from worldwide structural genomics projects.

Start a new search: Please enter the protein sequence (or sequences, separated by empty lines) in FASTA format, and the email where you want the results. Click on the "new request" button.

bioportal.weizmann.ac.il/salrtb/main

Does a protein fold?

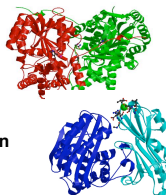


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Structure Determination

8 structures solved in 2003

Human aspartate aminotransferase (GOT1)



Elucidating the 'hot spots' of interactions between TEM mutant and BLIP