

Resource Summary Report

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Protein Structure Initiative

RRID:SCR_002161

Type: Tool

Proper Citation

Protein Structure Initiative (RRID:SCR_002161)

Resource Information

URL: <http://www.structuralgenomics.org/>

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Description: The Structural Genomics Project aims at determination of the 3D structure of all proteins. It also aims to reduce the cost and time required to determine three-dimensional protein structures. It supports selection, registration, and tracking of protein families and representative targets. This aim can be achieved in four steps : -Organize known protein sequences into families. -Select family representatives as targets. -Solve the 3D structure of targets by X-ray crystallography or NMR spectroscopy. -Build models for other proteins by homology to solved 3D structures. PSI has established a high-throughput structure determination pipeline focused on eukaryotic proteins. NMR spectroscopy is an integral part of this pipeline, both as a method for structure determinations and as a means for screening proteins for stable structure. Because computational approaches have estimated that many eukaryotic proteins are highly disordered, about 1 year into the project, CESG began to use an algorithm. The project has been organized into two separate phases. The first phase was dedicated to demonstrating the feasibility of high-throughput structure determination, solving unique protein structures, and preparing for a subsequent production phase. The second phase, PSI-2, has focused on implementing the high-throughput structure determination methods developed in PSI-1, as well as homology modeling and addressing bottlenecks like modeling membrane proteins. The first phase of the Protein Structure Initiative (PSI-1) saw the establishment of nine pilot centers focusing on structural genomics studies of a range of organisms, including *Arabidopsis thaliana*, *Caenorhabditis elegans* and *Mycobacterium tuberculosis*. During this five-year period over 1,100 protein structures were determined, over 700 of which were classified as unique due to their 30% sequence similarity with other known protein structures. The primary goal of PSI-1 was to develop methods to streamline the structure determination process, resulted in an array of technical advances. Several methods developed during PSI-1 enhanced expression of recombinant proteins in systems like *Escherichia coli*, *Pichia pastoris* and insect cell lines. New streamlined approaches to cell cloning, expression and protein purification were also introduced, in which robotics and software platforms were integrated into the protein

production pipeline to minimize required manpower, increase speed, and lower costs. The goal of the second phase of the Protein Structure Initiative (PSI-2) is to use methods introduced in PSI-1 to determine a large number of proteins and continue development in streamlining the structural genomics pipeline. Currently, the third phase of the PSI is being developed and will be called PSI: Biology. The consortia will propose work on substantial biological problems that can benefit from the determination of many protein structures
Sponsors: PSI is funded by the U.S. National Institute of General Medical Sciences (NIGMS),

Synonyms: PSI

Resource Type: data or information resource, portal, topical portal

Keywords: elegans, escherichia, eukaryotic, expression, arabidopsis, biology, bottleneck, caenorhabditis, cell, clone, coli, crystallography, genomic, homology, insect, membrane, myobacterium, nmr, organism, pastoris, pichia, protein, purification, sequence, spectroscopy, structural, structure, thaliana, tuberculosis, x-ray

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Ratings and Alerts

No rating or validation information has been found for Protein Structure Initiative.

No alerts have been found for Protein Structure Initiative.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.