cpSRP is unique among SRPs in being devoid of RNA. cpSRP consists of an evolutionarily conserved 54-kDa subunit (cpSRP54) and an unique 43-kDa subunit (cpSRP43). cpSRP43 subunit has four-ankyrin repeat domain at the N terminus and a C-terminal chromo domain (CD). The C-terminal CD of cpSRP43 has been shown to provide interaction sites for the cpSRP54 subunit. In addition, the chromodomain in the cpSRP43 subunit is also believed to be important for the formation of the transit complex with LHCP. In this context, we embarked on the structural characterization of the C-terminal CD using a variety of biophysical techniques including multidimensional NMR spectroscopy. Far UV circular dichroism spectrum of CD shows that the backbone of the protein is predominantly in the helical conformation. 1H-15N HSQC spectrum of CD is well- dispersed suggesting that the protein is structured. Complete resonance assignments (1H, 15N and 13C) in CD have been accomplished using a variety of triple resonance experiments. Chemical shift index plots show that CD is an $\alpha + \beta$ protein. A detailed analysis of the three-dimensional solution structure of CD will be presented. The three-dimensional solution structure of CD provides valuable insights into the molecular mechanism underlying the post-translational transport and integration of LHCP on the thylakoid membrane.

1302-Pos

The PSI SGKB Technology Portal - An Online Database of Structural Genomics Technologies

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The Protein Structure Initiative (PSI) Structural Genomics KnowledgeBase (SGKB) technology portal is an online database of PSI-derived technologies. Information within the portal will be of use to scientists involved in all branches of molecular biology. Advances are described in all stages of the protein production pipeline, from initial target selection to cloning, expression, structure solution and structure analysis. Information is provided on robotics, high-throughput protocols, and software development.
The url for the website is: http//:technology.lbl.gov/portal/

1303-Pos

Protein Structure Initiative Material Repository (PSI-MR): A Resource of Structural Genomics Plasmids for the Biological Community

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The Protein Structure Initiative Material Repository (PSI-MR; http://psimr.asu.edu) provides centralized storage and distribution for the growing collection of more than 80,000 protein expression plasmids created by PSI researchers. These plasmids are an invaluable resource that allows the research community to dissect the biological function of proteins whose structures have been identified by the PSI. The plasmid annotation, which includes the full length sequence, vector information, and associated publications, is stored in a freely available, searchable database called DNASU (http://dnasu.asu.edu). Each PSI plasmid is also linked to a variety of additional resources, including the PSI Structural Genomics Knowledgebase (PSI-SGKB: http://kb.psi-structuralgenomics.org), which facilitates cross-referencing of a particular plasmid to protein annotations and experimental data. Nearly 16,000 PSI plasmid samples are currently available and can be requested directly though the website. The PSI-MR has also developed a novel strategy to avoid the most common concern encountered when distributing plasmids, namely the complexity of material transfer agreement (MTA) processing and the resulting delays this causes. It is in this context that we developed and successfully implemented the Expedited Process MTA, in which we created a network of institutions that agree to the terms of transfer in advance of a material request, thus eliminating the delay researchers would typically encounter while their institution is processing the MTA. Our hope is that by creating a repository of expression-ready plasmids and expediting the process for receiving these plasmids, we will help accelerate the accessibility and pace of scientific discovery.

1304-Pos

How to use the PSI Structural Genomics Knowledgebase to Enable Research

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The Protein Structure Initiative Structural Genomics Knowledgebase (PSI SGKB, URL: http://kb.psi-structuralgenomics.org) is a web resource designed to turn the products of the structural genomics and structural biology efforts into knowledge that can be used by the biological community to understand living systems and disease. We will present examples and demonstrate how to use the PSI SGKB to enable biological research. For example, a protein sequence or PDB ID search will provide a list of protein structures from the Protein Data Bank, associated biological descriptions (annotations), homology models, structural genomics protein target information, experimental protocols, and the ability to order available DNA clones. A text search will find technology reports and publications that were created by the PSI's high-throughput research efforts. Web tools that aid in bench top research, such as protein construct design, are also available. Created in collaboration with the Nature Publishing Group, the Structural Genomics Knowledgebase Gateway provides a research library, editorials about new research advances, news, and an events calendar also present a broader view of structural genomics and structural biology. The PSI SGKB is funded by the NIGMS.

1305-Pos

NIGMS PSI:Biology Initiative High-Throughput-Enabled Structural Biology

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The primary goal of the Protein Structure Initiative:Biology (PSI:Biology) to be funded by the National Institute of General Medical Sciences (NIGMS) is to apply high-throughput structural biology to important biological problems (http://www.nigms.nih.gov/Initiatives/PSI/psi biology/). This will be accomplished by establishing partnerships between centers for structure determination and biologists with interests in particular proteins or collections of proteins. The PSI:Biology network centers will include: 1) Centers for High-Throughput Structure Determination, 2) Centers for Membrane Protein Structure Determination, 3) the PSI:Materials Repository, and 4) the PSI:Biology Knowledgebase. The partnerships, established through Consortia for High-Throughput-Enabled Structural Biology Partnerships, will define targets for structure determination and provide funds for functional studies in the applicants' laboratories and for a portion of the cost for structure determination in the center. In addition to protein structures and models, the PSI:Biology network will generate and make available reagents and plasmids for expressed proteins to support functional studies in the research community. NIGMS encourages Partnership applications from biologists or groups of biologists with biological questions that will benefit from the determination of relevant protein structures. The PSI:Biology high-throughput approach will enable examination of families of proteins related to the target proteins, an approach that has proven highly successful in generating the first structure of a family member and then allowing many other family members to be modeled. Examples of current partnerships include using structural genomics, modeling and systems biology to generate a three-dimensional reconstruction of the central metabolic network of the bacterium, *Thermotoga maritima*, and the discovery of novel enzymatic mechanisms for the enoylase and amido hydrolase classes of enzymes. Additional opportunities for researchers to join the PSI:Biology network will be provided through ongoing and future program announcements. Researchers may also suggest proteins for structure determination through the PSI Community Nomination site at: http://cnt.psi-structuralgenomics.org/CNT/targetlogin.jsp.

1306-Pos

Technology Development Highlights Generated from the Center for Eukaryotic Structural Genomics

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The Center for Eukaryotic Structural Genomics (CESG) aims to be the leading center for developing and disseminating tested technologies to efficiently solve structures of eukaryotic proteins. We create, evaluate, and optimize innovative protocols for producing eukaryotic proteins in active forms. We seek to improve the efficiency of all stages from target selection-design to three-dimensional structure determination by X-ray crystallography or NMR spectroscopy, including development of bioinformatic techniques and LIMS tools. Using our protein production platform, we refine methods for improving the yield of structures from high-value targets, in particular proteins from humans and other vertebrates. CESG has a substantial outreach component; more than 400 targets from outside requestors have been accepted for study with a structure success rate of 5%, which compares favorably with the eukaryotic success rates for the