Automation in protein crystallography: advances and new frontiers.



Workshop on Synthetic Biology and Robotics

February 24th, 2011 - São Paulo, Brazil





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Structural Biology in a Nutschell



Steps in protein crystallization and analysis

- Protein Production
- Crystalization
- X-Ray data collection
- Diffraction data Refinement







Rational Drug Design



Enzyme Catalysis



Protein Folding



and more ...



Rational Drug Design



Enzyme Catalysis



Protein Folding



and more ...



Cloning







Fermentation





Purification



Rational Drug Design



Enzyme Catalysis



Protein Folding



and more ...

Protein Crystallization: manual





(A) Equilibration proceeds through vapor phase



(B) Drop volume decreases, increasing concentration of both precipitant and protein

Crystallization by Vapour Difusion

Protein Crystallization: manual









Typical experiment:

2 to 3µl protein
>6 mg/mL
2 to 3µl crystallization solution
300 to 500 µl crystallization solution in well
Initial screening:
300 – 500 conditions
i.e. 3.6 to 6 g of pure protein !!!!!



Protein Crystallization: mountig











Protein Crystallization: aligning





Protein Crystallization: Diffraction data collection





Refinment/interpretation



Research lab. scale

Data Collection and Refinement

Large Scale (Structural Genomics)

Large Scale (Structural Genomics)

The long-term goal of the NYSGRC is to determine the 10,000 plus three-dimensional protein structures envisaged by the National Institute of General Medical Sciences Protein Structure Initiative.

The specific aims are:

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- Identify target protein sequences for structural genomics
- Develop high-throughput E.coli expression of soluble target proteins
- Develop high-throughput production of target proteins
- Develop high-throughput biophysical characterization of target proteins
- Develop high-throughput crystallization of target proteins
- Develop efficient experimental strategies for MAD crystallography
- Develop high-throughput synchrotron data collection with target protein crystals
 - Develop and use an Internet-based computational pipeline for protein crystallography
 - Develop high-throughput molecular replacement tools for crystallography
 - Develop high-throughput comparative modeling for structural genomics
 - Develop efficient annotation and dissemination of protein structures and models
 - Develop an Internet-based "web-book" for use by the NYSGRC

Structural Genomes

Center for Eukaryotic Structural Genomics

Develop the methodologies and technology necessary for high-throughput, genome scale, eukaryotic protein production, characterization and structure determination, focusing on proteins from Arabidopsis.

Joint Center for Structural Genomics

Develop technology and structural studies of human and C. elegans proteins involved in signal transduction.

Midwest Center for Structural Genomics

Develop robotic technology and synchorotron-based X-ray cyrstallography methods; structural studies of archaea, bacteria and eukarya proteins.

Northeast Structural Genomics Consortium

Develop technology; analyze complementarity of NMR and crystallographic methods; and structural studies of roundworm, fly and human proteins.

Southeast Collaboratory for Structural Genomics

Develop automated NMR and crystallographic structure determination; structural studies of Pyrococcus furiosus, C. elegans and human proteins.

Structural Genomics of Pathogenic Protozoa

Develop technologies and structure determination of proteins from major global pathogenic protozoa, Leishmania major, Trypanosoma brucei, Trypanosoma cruzi and Plasmodium falciparum.

TB Structural Genomics Consortium

Develop technology and structural study of Mycobacterium tuberculosis proteins.

Project Description Flow Diagrams Contact Information Consortium Members Diseases Under Investigation * Chagas' Disease [American Trypanosomiasis] * African Sleeping Sickness [African Trypanosomiasis] * Leishmaniasis * Malaria Target Organisms * Trypanosoma cruzi * Trypanosoma brucei * Leishmania spp. * Plasmodium falciparum * (Plasmodium vivax) Send Suggestions for Protein Targets Genome Status SGPP Progress 3-D Structures Structures w/Ligands Papers by SGPP Related Links/Resources Employment Opportunities SGPP News Articles Feedback on SGPP web site

STRUCTURAL GENOMICS OF PATHOGENIC PROTOZOA

Click to see status of SGPP Targets MSGPP Targets CHTSB Targets

Structural Genomics Method Development **Discovery of New Folds** Medicinal Drug Design

Supported by:

This website is no longer being actively updated. For further progress please see SGPP's successors:

MSGPP Medical Structural Genomics of Pathogenic Protozoa

CHTSB Center for High-Throughput Structural Biology

Structural Genomics of Pathogenic Protozoa Target Selection Scheme

STRUCTURAL GENOMICS OF PATHOGENIC PROTOZOA

FLOW DIAGRAMS

Structural Genomics of Pathogenic Protozoa - Flow Diagram

SGPP Target Status - Page 1 of 1391

<<first <previous <all> next> last>>

Search in title • * for

Last updated May 22, 2007 *title: SGPP ID, source, original source ID, updated ID if known, protein name, function, PDB ID, tags;

aa_seq, nt_seq: amino acid or nucleotide sequence - exact match only

Targets are sorted by progress. See all targets, 15 targets per page, nucleotide sequences, amino acid sequences or XML.

Target				³ Status									
¹ Organism & Target ID	²Src	Database Identifier	Cloned	Ex- press- ed	Solu- ble	Puri- fied	Cry Screen- ing	stals Growth Lab	Diffr. Qual. Xtals	Diffrac- tion Data,Å	Xtal Struc- ture	In PDB	
Lmaj004091AAA	Gd	LmjF30.0810	+	+	+	+	+	+	+	1.9	+	1xtp	
Lmaj004144AAA	Gd	LmjF30.1890	+	+	+	+	+	+	+	1.7	+	1y63	
Lmaj005461AAB	Gd	LmjF32.0700	+	+	+	+	+	+	+	2.0	+	lyf9	
Lmaj007771BAB	Gd	LmjF23.0050	+	+	+	+	+	+	+	2.0	+	2hqj	
Lmaj008024AAA	Gd	LmjF01.0480	+	+	+	+	+	+	+	2.1	+	lsvv	
Lmaj01134AAC	Gd	LmjF13.1460	+	+	+	+	+	+	+	1.95	+	lylx	
Pfal000304AAA	Ρ	PF10_0225	+	+	+	+	+	+	+	2.1	+	2f84	
Pfal004331AAA	Ρ	MAL13P1.257	+	+	+	+	+	+	+	2.2	+	lzso	
Pfal004546AAA	Ρ	MAL6P1.148	+	+	+	+	+	+	+	2.2	+	1y13	
Pfal005984AAA	Ρ	PF11_0208	+	+	+	+	+	+	+	2.6	+	1xq9	
Pfal006645AAA	Ρ	PF13_0349	+	+	+	+	+	+	+	3.05	+	1 xiq	
Pfal007201AAA	Ρ	PF14_0545	+	+	+	+	+	+	+	2.9	+	1syr	
Pfal007254AAA	Ρ	PF14_0598	+	+	+	+	+	+	+	2.5	+	2b4r	
Pfal008421AAA	Р	PFE0660c	+	+	+	+	+	+	+	1.8	+	1sq6	
Pfal008434AAA	Ρ	PFE0730c	+	+	+	+	+	+	+	2.9	+	2f8m	

Target				³ Status									
10 recention for				Ex-			Crystals		Diffr.	Diffrac-	Xtal		
Target ID	² Src	Database Identifier	Cloned	press-	Solu-	Puri-	Screen-	Growth	Qual. Xtals	tion Data Å	Struc-	In	
			\square	eu	Die	neu	mg	Lab		2		TDD	
Tbru019101AAA	Gd	Tb09.211.3420	+	+	+	+	+	+	+	2.5	+	3bnw	
Tcru019078AAA	Gd	Tc00.1047053510339.50	+	+	+	+	+	+	+	2.8	+	3bwb	
Pfal000066AAA	Ρ	PF10_0022	+	+	+	+	+	+	+	2.8			
Pfal006821AAA	Р	PF14_0164	+	+	+	+	+	+	+	3.5			
Lmaj010130AAA	Gd	LmjF10.0560	+	+	+	+	+	+	+	2.0			
Lbra003107AAA		LbrM25.2080	+	+	+	+	+	+	+				
Lmaj002537AAA	Gd	LmjF16.0230	+	+	+	+	+	+	+	2.8			
Lmaj004542AAA	Gd	LmjF31.0560	+	+	+	+	+	+	+	2.1			
Lmaj004655AAA	Gd	LmjF31.2410	+	+	+	+	+	+	+				
Lmaj00521AAA	Gd	LmjF32.2980	+	+	+	+	+	+	+	3.8			
Lmaj00592AAA	Gd	LmjF23.0360	+	+	+	+	+	+	+	3.0			
Lmaj00847AAA	Gd	LmjF14.1370	+	+	+	+	+	+	+				
Lmaj00884AAA	Gd	LmjF14.0240	+	+	+	+	+	+	+	1.9	+	3ksv	
Lmaj01188AAA	Gd	LmjF04.0070	+	+	+	+	+	+	+	3.1			
Pviv005676AAA	Ρ	Pv111245	+	+	+	+	+	+	+	3.3	+	2pgf	

Rational Drug Design

Enzyme Catalysis

Protein Folding

and more ...

Targets for Drug Action

Proteins

> 98% farmaceuticals

- Nucleic Ácids
- Lipids (membranes)
- sugars

< 2% farmaceuticals

The "druggable" genome

revisão por A.L.Hopkins & C.R.Groom, Nature Reviews Drug Discovery, 2002, vol.1,#9, pp 727-730

 = of the ~30000 genes in the human genome capable of expressing a proteins and binding to a small molecule (Drug).

Estimated number of drug targets

Paradime in strcuture based drug design

A good inhibitor should have a significant structural and chemical comlemetarity to the target receptor.

Structure based drug target design

Estratégia (1)

Estratégia (2)

Crystal structure of T.cruzi GAPDH in complex with natural product competitive

T.cruzi GAPDH-Chalepin complex

Space grown crystals

T.cruzi native GAPDH T.cruzi GAPDH-Chalepin complex

Structure-based design of modified natural products derivatives

Chalepin at *T.cruzi* GAPDH active site

Compound SCG001

Thank you