Structure of the GH76 α-mannanase homolog, BT2949, from the gut symbiont Bacteroides thetaiotaomicron


A high-resolution structure of a noncanonical α-mannanase relevant to human health and nutrition has been solved via heavy-atom phasing of a selenomethionine derivative.

Serial crystallography

In cellulo serial crystallography of alcohol oxidase crystals inside yeast cells


The application of serial femtosecond crystallography to naturally occurring peroxisomal protein crystals within yeast cells is described. The concept of utilizing peroxisomes for the production of protein nanocrystals is outlined.

Serial femtosecond crystallography: the first five years

I. Schlichting

The advent of hard X-ray free-electron lasers has opened a new chapter in macromolecular crystallography. Recent results, developments and prospects of serial femtosecond crystallography are outlined.

Three-dimensional coherent X-ray diffractive imaging of whole frozen-hydrated cells


Since its first experimental demonstration in 1999, coherent diffractive imaging (CDI) has been applied to image a broad range of samples using advanced synchrotron radiation, X-ray free-electron lasers, high-harmonic generation and electrons. Here, the experimental demonstration of cryogenic CDI for quantitative three-dimensional imaging of whole frozen-hydrated cells is reported. As a proof of principle, the three-dimensional mass density of the sub-cellular organization of a Neospora caninum cell is determined based on its natural contrast.

Native sulfur/chlorine SAD phasing for serial femtosecond crystallography


Sulfur SAD phasing facilitates the structure determination of diverse native proteins using femtosecond X-rays from free-electron lasers via serial femtosecond crystallography.

Towards time-resolved serial crystallography in a microfluidic device


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Crystallization in the 21st century

M. Y. Hawkes

The field of crystallization, which has had a major impact on the sciences in the last 100 years, is continuing to provide new insights into structure-function relationships and drug discovery. Structure-function-dynamics will become an integrated theme for many studies as we transition from the "benevolent tyranny" of crystal structure determination to the "cruelty" of functional analyses.

Methods and instrumentation


This review provides an overview of the current state of the art in methods and instrumentation for crystallization, focusing on microfluidic devices and high-throughput screens.

Cryocryogen induced X-ray diffraction imaging of biological samples at SACU: a convergent approach with cryo-electron and light microscopy

K. Takakura and K. Yonemasu

This paper describes a novel cryogenic approach for X-ray diffraction imaging of biological samples at SACU, combining cryo-electron and light microscopy to enhance structural information.

The Macromolecular Neutron Diffraction Facility MaNDi at the Spallation Neutron Source

L. Crozier et al.

The Macromolecular Neutron Diffraction Facility MaNDi at the Spallation Neutron Source is described, showcasing its capabilities for neutron diffraction experiments.

Structure determination of an integral membrane protein at room temperature from crystals in situ


This paper presents a method for determining the structure of an integral membrane protein at room temperature from crystals collected in situ.

Analysis of crystallization data in the Protein Data Bank

M. Deatherage, A. P. Polo, E. A. Brown, F. Angyan, P. D. C. Cooper

This paper discusses the analysis of crystallization data in the Protein Data Bank, offering insights into the design and optimization of crystallization experiments.

Protocols for macromolecular model building and refinement into electron cryo-microscopy reconstructions


A description of new protocols for model building and refinement using electron cryo-microscopy reconstructions.

An overview of heavy atom derivatization of protein crystals

A. C. P. Will, J. J. Baker, B. A. McCammon

This review summarizes the methods and strategies for heavy atom derivatization of protein crystals.

Lessons from ten years of crystallization experiments at the SGC

M. Brown, T. Krojer, F. Garman

This paper presents lessons learned from ten years of crystallization experiments at the SGC, focusing on practical guidelines for the design of screening experiments.

Tools for macromolecular model building and refinement into electron cryo-microscopy reconstructions

A. Brazil, J. P. H. Brazil, K. A. Notcutt, J. Tom, E. E. S. K. Muthukumar

A description of new tools for macromolecular model building and refinement using electron cryo-microscopy reconstructions.

Proteins and complexes

Three-dimensional structures of two heavily N-glycosylated Aspergillus sp. family GH1 j-1,2-galactosidases

J. A. Regin et al.

The 3D structures of two industrially important family GH1 j-1,2-galactosidases from Aspergillus niger and Aspergillus flavus are described, highlighting the use of these enzymes in the production of biofuels.

Crystal structure of FhuD at 1.6 A resolution: a ferrichrome-binding protein from E. coli


The crystal structure of FhuD at 1.6 A resolution is presented, revealing insights into the ferrichrome-binding mechanism.

Structure determination of an integral membrane protein at room temperature from crystals in situ


This paper presents a method for determining the structure of an integral membrane protein at room temperature from crystals collected in situ.

A comprehensive review of the lipid cubic phase or bicontinuous cubic lattice (LBC) as a cryoprotectant environment

M. A. R. Michael, B. A. McCammon

A comprehensive review of the lipid cubic phase or bicontinuous cubic lattice (LBC) as a cryoprotectant environment is provided, highlighting its applications in structural biology.

Viruses and pathogens

Molecular architecture of the nucleoprotein C-terminal domain from the Ebola and Marburg viruses


Crystal structures of the C-terminal domain of the nucleoprotein (NP) from the Marburg and Ebola viruses are presented, offering insights into the viral replication process.

Complete epitopes for vaccine design derived from a crystal structure of the broadly neutralizing antibodies PGT128 and BANC195 in complex with HIV-1 Env trimers


The crystal structure of the broadly neutralizing antibodies BANC195 and PGT128 bound to an HIV-1 Env trimers is presented, facilitating the development of new vaccine candidates.