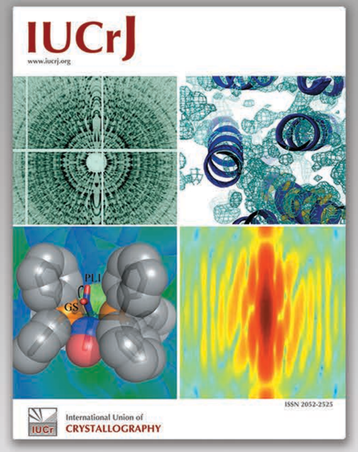

Now accepting papers in cryoEM

*"We are delighted to announce that three of the world leaders in cryoEM – Richard Henderson (MRC, Cambridge), Sriram Subramaniam (NIH, Bethesda) and Werner Kühlbrandt (MPIBP, Frankfurt) – are joining the editorial board of **IUCrJ**. We urge the cryoEM community to make this premier journal of IUCr their natural home, sharing advances and results to the widest community of structural scientists"*

– Samar Hasnain, Editor-in-Chief, U. Liverpool, UK

"There has been a quantum leap in the power of single particle cryoEM due to recent improvements in microscopes, detectors and computer programs. It is entirely appropriate that the IUCr should become the home for cryoEM in the same way as it has nurtured X-ray and other crystallographies since its foundation in 1948. CryoEM and X-ray crystallography are both diffraction techniques with similar underlying concepts and intellectual framework"

– Richard Henderson, MRC, Cambridge, UK

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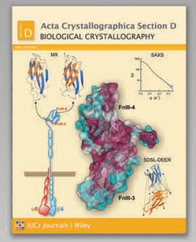
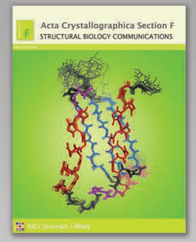
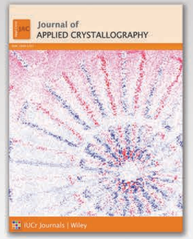
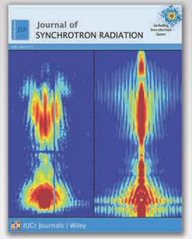
Key IUCrBio journals



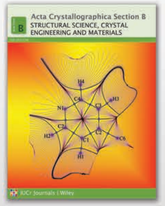


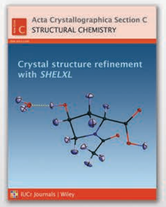
Enabling technologies

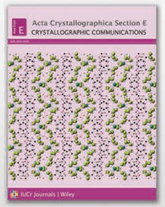




Other IUCr journals







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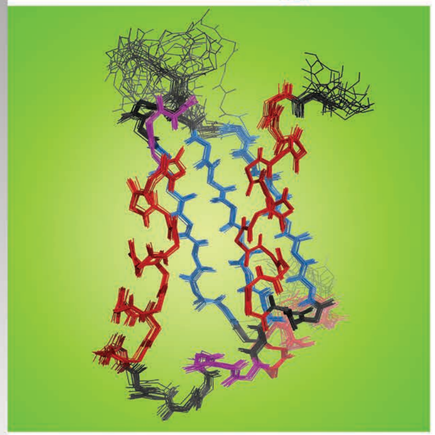
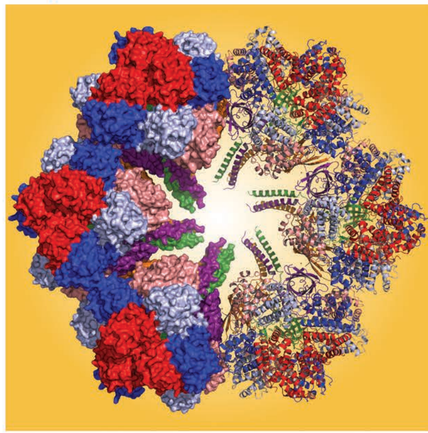
IUCrBio

Structural biology from IUCr journals





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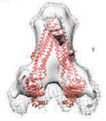
Health and disease processes

Acta Cryst. (2015). D**71**, 1725–1735
http://dx.doi.org/10.1107/S1399004715010676

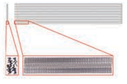


Three-dimensional structure of the human breast cancer resistance protein (BCRP/ABCG2) in an inward-facing conformation

M. F. Rosenberg, Z. Bikadi, E. Hazai, T. Starborg, L. Kelley, N. E. Chayen, R. C. Ford and Q. Mao

The first three-dimensional structure of human ABCG2 in the absence of nucleotides and transported substrates has been determined at 2.0 nm resolution. In this state, ABCG2 is in an inward-facing conformation.

Acta Cryst. (2015). D**71**, 882–895
http://dx.doi.org/10.1107/S1399004715001674

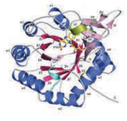


The architecture of amyloid-like peptide fibrils revealed by X-ray scattering, diffraction and electron microscopy

A. E. Langkilde, K. L. Morris, L. C. Serpell, D. I. Svergun and B. Vestergaard

The aggregation process and the fibril state of an amyloidogenic peptide suggest monomer addition to be the prevailing mechanism of elongation and a model of the peptide packing in the fibrils has been obtained.

Acta Cryst. (2015). F**71**, 547–552
http://dx.doi.org/10.1107/S2053230X15000886

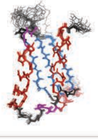


Recombinant production, crystallization and crystal structure determination of dihydroorotate dehydrogenase from *Leishmania (Viannia) braziliensis*

R. A. G. Reis, E. Lorenzato, V. C. Silva and M. C. Nonato

The crystal structure of *L. (V.) braziliensis* dihydroorotate dehydrogenase, a potential target for drug development against cutaneous leishmaniasis, is reported.

Acta Cryst. (2015). F**71**, 514–521
http://dx.doi.org/10.1107/S2053230X1402799X

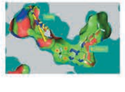


Solution-state NMR structure of the putative morphogene protein BolA (PFE0790c) from *Plasmodium falciparum*

G. W. Buchko, A. Yee, A. Semesi, P. J. Myler, C. H. Arrowsmith and R. Hui

Parasitic protozoans of the *Plasmodium* genus are responsible for malaria, a disease that kills approximately one child every minute in Africa and ~2000 people per day worldwide. Here, the solution structure of the 84-residue BolA protein PFE0790c from the deadliest *Plasmodium* species, *P. falciparum*, is reported.

Acta Cryst. (2015). F**71**, 485–499
http://dx.doi.org/10.1107/S2053230X15004987

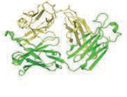


Three-dimensional structures in the design of therapeutics targeting parasitic protozoa: reflections on the past, present and future

W. G. J. Hol

A review and historical perspective covering the many different aspects of antiparasitic drug discovery, in particular targeting protists, is presented. The key role of structural studies in the process is highlighted and specific high-profile examples are given.

Acta Cryst. (2015). F**71**, 145–148
http://dx.doi.org/10.1107/S2053230X14027599



Structure of the apo anti-influenza CH65 Fab

P. S. Lee, A. J. Arnell and I. A. Wilson

The crystal structure of anti-influenza antibody CH65 at 1.70 Å resolution reveals that the affinity-matured antibody evolved to preconfigure the antibody loops to increase binding affinity to the hemagglutinin.

Lipid cubic phase technology

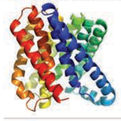
Acta Cryst. (2015). D**71**, 1238–1256
http://dx.doi.org/10.1107/S1399004715005210

In meso in situ serial X-ray crystallography of soluble and membrane proteins

C.-Y. Huang, V. Olieric, P. Ma, E. Panepucci, K. Diederichs, M. Wang and M. Caffrey

A method for performing high-throughput *in situ* serial X-ray crystallography with soluble and membrane proteins in the lipid cubic phase is described. It works with microgram quantities of protein and lipid (and ligand when present) and is compatible with the most demanding sulfur SAD phasing.

Acta Cryst. (2015). D**71**, 1228–1237
http://dx.doi.org/10.1107/S139900471500423X

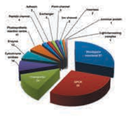


Structure determination of an integral membrane protein at room temperature from crystals *in situ*

D. Axford, J. Foadi, N.-J. Hu, H. G. Choudhury, S. Iwata, K. Beis, G. Evans and Y. Alguel

The structure determination of an integral membrane protein using synchrotron X-ray diffraction data collected at room temperature directly in vapour-diffusion crystallization plates (*in situ*) is demonstrated.

Acta Cryst. (2015). F**71**, 3–18
http://dx.doi.org/10.1107/S2053230X14026843

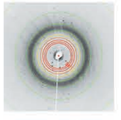


A comprehensive review of the lipid cubic phase or *in meso* method for crystallizing membrane and soluble proteins and complexes

M. Caffrey

A comprehensive and up-to-date review of the lipid cubic phase or *in meso* method for crystallizing membrane and soluble proteins and complexes is reported. Recent applications of the method for *in situ* serial crystallography at X-ray free-electron lasers and synchrotrons are described.

IUCrJ (2015). **2**, 168–176
http://dx.doi.org/10.1107/S2052252514026487



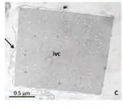
Lipidic cubic phase serial millisecond crystallography using synchrotron radiation

P. Nogly *et al.*

This article describes the structure determination of a membrane protein by serial injection of microcrystals in lipidic cubic phases into a synchrotron microfocus beam. The method is discussed with respect to serial femtosecond crystallography at free-electron lasers.

XFEL diffraction and imaging

Acta Cryst. (2015). F**71**, 929–937
http://dx.doi.org/10.1107/S2053230X15011450

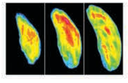


In vivo protein crystallization in combination with highly brilliant radiation sources offers novel opportunities for the structural analysis of post-translationally modified eukaryotic proteins

M. Duszenko, L. Redecke, C. N. Mudogo, B. P. Sommer, S. Mogk, D. Oberthuer and C. Betzel

In vivo formation of protein crystals and their isolation and structural analysis by novel highly brilliant XFEL and synchrotron-radiation sources is described.

IUCrJ. (2015). **2**
http://dx.doi.org/10.1107/S205225251501235X



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

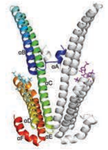
J. A. Rodriguez *et al.*

The first experimental demonstration of cryogenic coherent diffractive imaging for quantitative three-dimensional imaging of whole frozen-hydrated cells is reported.

On the cover of this leaflet (clockwise from top left): putative morphogene protein BolA (PFE0790c) from *Plasmodium falciparum* [*Acta Cryst.* (2015). F**71**, 514–521]; giant haemoglobin from *Glossoscolex paulistus* [*Acta Cryst.* (2015). D**71**, 1257–1271]; a simulation of Sirius, the new Brazilian Synchrotron Light Source, with (inset) the actual building under construction.

Structural biology

Acta Cryst. (2015). D**71**, 494–504
http://dx.doi.org/10.1107/S1399004714027114

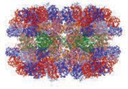


Interaction of the amyloid precursor protein-like protein 1 (APLP1) E2 domain with heparan sulfate involves two distinct binding modes

S. O. Dahms, M. C. Mayer, D. Roeser, G. Multhaup and M. E. Than

Two X-ray structures of APLP1 E2 with and without a heparin dodecasaccharide are presented, revealing two distinct binding modes of the protein to heparan sulfate. The data provide a mechanistic explanation of how APP-like proteins bind to heparan sulfates and how they specifically recognize nonreducing structures of heparan sulfates.

Acta Cryst. (2015). D**71**, 1257–1271
http://dx.doi.org/10.1107/S1399004715005453



The structure of the giant haemoglobin from *Glossoscolex paulistus*

J. F. Ruggiero Bachega, F. Vasconcelos Maluf, B. Andi, H. D'Muniz Pereira, M. Falsarella Carazzollea, A. M. Orville, M. Tabak, J. Brandão-Neto, R. C. Garratt and E. Horjales Reboredo

The structure of the giant haemoglobin from *G. paulistus* was determined.

IUCrJ (2014). **1**, 429–438
http://dx.doi.org/10.1107/S2052252514021113

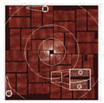
Binding site asymmetry in human transthyretin: insights from a joint neutron and X-ray crystallographic analysis using perdeuterated protein

M. Haupt, M. P. Blakeley, S. J. Fisher, S. A. Mason, J. B. Cooper, E. P. Mitchell and V. T. Forsyth

A neutron crystallographic study of perdeuterated transthyretin reveals important aspects of the structure relating to its stability and its propensity to form fibrils, as well as evidence of a single water molecule that affects the symmetry of the two binding pockets.

Serial crystallography

IUCrJ (2014). **1**, 95–100
http://dx.doi.org/10.1107/S2052252514001444

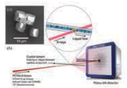


Femtosecond X-ray diffraction from two-dimensional protein crystals

M. Frank *et al.*

Bragg diffraction achieved from two-dimensional protein crystals using femtosecond X-ray laser snapshots is presented.

IUCrJ (2014). **1**, 204–212
http://dx.doi.org/10.1107/S2052252514010070

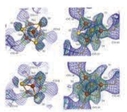


Room-temperature macromolecular serial crystallography using synchrotron radiation

F. Stellato *et al.*

The room-temperature structure of lysozyme is determined using 40000 individual diffraction patterns from micro-crystals flowing in liquid suspension across a synchrotron microfocus beamline.

J. Synchrotron Rad. (2015). **22**, 225–238
http://dx.doi.org/10.1107/S1600577515002349



Indications of radiation damage in ferredoxin microcrystals using high-intensity X-FEL beams

K. Nass *et al.*

High-dose serial femtosecond crystallography experiments were performed on microcrystals of the metalloprotein ferredoxin. Indications of radiation damage to the two [4Fe–4S] clusters are observed.