P.04.23.5

Acta Cryst. (2005). A**61**, C261

Opening of the Safety-belt Loop of Human Aldose Reductase

Marianna Biadene[a], Isabel Hazemann[b], Thomas R. Schneider[c], [a]*Department of Inorganic Chemistry, University of Goettingen, Germany.* [b]*IGBMC, Illkirch, France.* [c]*IFOM-The FIRC Institute of Molecular Oncology, Milano, Italy.* E-mail: marianna@shelx.uni-ac.gwdg.de

Aldose reductase (ALR2; EC 1.1.1.21) is a member of the aldo-keto reductase superfamily and it catalyzes the NADPH-dependent reduction of aldeydes to their corresponding alcohols. It is implicated in the polyol pathway and in diabetic complication.

The crystal structure of native aldose reductase has been determined to a resolution of 0.82 Å with a final R = 9.50 and R_{free} = 10.90 and a mean coordinate error for the fully occupied sites of the protein of 0.011 Å (from fully matrix inversion). The structure contains a large number of multiple conformations: 78 out of 316 residues were modeled in two conformations.

The overall structure folds into an eight-stranded α/β barrel with the active site located at the C-terminal end of the barrel and the $NADP^+$-binding site near the hydrophobic binding pocket [1]. The cofactor is held in place by the so-called 'safety-belt' (a loop between residue 216 and 227 of the canonical α/β barrel) [2].

The active site of the structure contains a citrate molecule in two conformations. One of the conformations stabilizes the closed position of the safety-belt, whereby the other permits the safety-belt to open. Due to the high resolution, the partially opened conformation of the safety-belt can be observed in the electron density.

[1] El-Kabbani O., Wilson D., Petrash J. M., Quiocho F. A., *Molecular Vision*, 1998, 4. [2] Wilson D.W., Bohren K.M., Gabbay K.H and Quiocho F.A., *Science*, 1992, **257**, 81.

Keywords: high-resolution refinement, active-site structure, loop modeling

P.04.23.6

Acta Cryst. (2005). A**61**, C261

Crystal Structure of *Caenorhabditis elegans* Spermidine Synthase: in Preparation

Veronica Tamu-Dufe[a], K. Lüersen[b], M-L. Eschbach[b], H. Haider[b], R.D. Walter[b], S. Al-Karadaghi[a], [a]*Department of Molecular Biophysics, Lund University, Sweden.* [b]*Department of Biochemistry, Bernhard Nocht Institute for Tropical Medicine, Hamburg,Germany.* E-mail: veronica.tamu_dufe@mbfys.lu.se

Caenorhabditis elegans (C.elegans) is a free living worm and a well established model organism to study general biological processes like development.

Consistent with reports on other organisms, growth of *C. Elegans* depends on polyamines. Polyamines such as putrescine, spermidine and spermineare aliphatic polycations, essential for regulation of cell proliferation and differentiation. Spermidine synthase isoneofthekey enzymes in the polyamine biosynthetic pathway.

This enzyme catalyzes the transfer of the aminopropyl group from decarboxylated S-adenosylmethionine to putrescine in the biosynthesis of spermidine.

Spermidine synthase from *C. Elegans* has been over-expressed in Escherichiacoli, purified by affinity chromatography and co-crystallized with putrescine, which is the substrate. The crystals diffract to 2.5Å and belong to the monoclinic P21 space group with unit cell dimensions, a=59.99, b=99.23, c=67.85Å and β=107.2°. The asymmetric unit contains two molecules. Model building and refinement are ongoing.

Keywords: *Caenorhabditis elegans*, polyamines, spermidine synthase

P.04.23.7

Acta Cryst. (2005). A**61**, C261

Structure of *Ralstonia solanacearum* Fucose Binding Lectin at 0.94Å Resolution

Edward Mitchell[1], Nikola Kostlánová[2], Nechama Gilboa-Garber[3], Stefan Oscarson[4], Michaela Wimmerová[2], Anne Imberty[5], [1]*ESRF, BP 220, F-38043 Grenoble, France.* [2]*National Centre for Biomolecular Research, Masaryk University, Kotlářska 2, 61137 Brno, Czech Republic.* [3]*Faculty of Life Sciences, Bar-Ilan University, Ramat-Gan 52900, Israel.* [4]*Department of Organic Chemistry, Arrhenius Laboratory, Stockholm University, S-106 91 Stockholm, Sweden.* [5]*CERMAV-CNRS, BP 53, F-38041, Grenoble, France.* E-mail: mitchell@esrf.fr

Ralstonia solanacearum is a soil-born bacterium belonging to the group of beta-proteobacteria. It is responsible for bacterial wilts in over 200 plants including potato, tomato and banana, and is capable of living for prolonged periods in soil, infecting hosts via the roots.

A 9.9 kDa fucose-binding lectin (RSL) has been found in *R. Solanacearum* extract. Ultra-high resolution diffraction data to 0.94Å data were collected from crystals of the recombinant RSL: α-methyl-fucose complex at ESRF, Grenoble. Superb phasing was obtained using the RSL:seleno-methyl fucoside complex, showing the crystals to contain three monomers, each of two 4-stranded β-sheets, with two sugar sites per monomer. The three monomers associate to form a 6-bladed β-propeller; the first time such an arrangement has been observed. ITC microcalorimetry and surface plasmon resonance studies are underway to define the fine specificity to fucosylated oligosaccharides present in plant cell walls, that may be the target for the lectin in soil.

Keywords: lectin crystallography, atomic resolution crystallography, synchrotron radiation crystallography

P.04.23.8

Acta Cryst. (2005). A**61**, C261

Crystal Structures of Ribosomal Protein L10 in Complex with L7/12 N-Terminal Domains

Mihaela Diaconu, Markus C. Wahl, *Max Planck Institute for Biophysical Chemistry, Göttingen, Germany.* E-mail: mdiacon@gwdg.de

The L7/12 stalk of the large ribosomal subunit comprises protein L10 and multiple copies of L7/12. It is involved in binding of translation factors and stimulation of factor-dependent GTP hydrolysis. The stalk is disordered in available crystal structures of ribosomes or 50S subunits. We have determined crystal structures of *Thermotoga maritima* L10 in complex with three L7/12 N-terminal domain (NTD) dimers. The structures are in agreement with a multitude of biochemical data. A globular NTD of L10 encompasses the binding region for 23S rRNA. A long C-terminal helix (α8) of L10 shows a modular design with consecutive binding sites for L7/12 dimers. L10 helix α8 assumes different positions with respect to the NTD in different crystal forms and thus constitutes a mobile platform for the attached L7/12 molecules. The number of L7/12 dimers varies with the length of L10 helix α8 in different species. The structure of the L7/12 NTD dimers agrees with one mode of dimerization observed in isolated L7/12. The hinge region of L7/12 can bind in α-helical form to the NTD in isolation but is displaced by L10 upon complex formation and becomes disordered. The organization of the complex supports its function in factor recruitment and GTPase activation.

Keywords: L10-L7/12 complex, L7/12 stalk, ribosome structure

P.04.24.1

Acta Cryst. (2005). A**61**, C261-C262

Comparative Study of Thrombin Binding of Potassium vs. Sodium

Christopher J. Carrell, A. O. Pineda, E. di Cera, F. S. Mathews, *Department of Biochemistry and Molecular Biophysics, Washington University School of Medicine, 660 S. Euclid St., Box 8231, St. Louis, Mo 63110*. E-mail: carrell@biochem.wustl.edu

Thrombin, a critical serine protease responsible for blood coagulation, is an allosteric enzyme that binds an alkali metal cation near the substrate-binding site. We have obtained a crystal structure to a resolution of 1.9 Å for the potassium-bound form of thrombin and compared it to the existing structure of sodium-bound thrombin.[1]