

[s8a.m4.p3] Over-production, purification and preliminary X-ray crystallographic analysis of GlcV, the ATP-binding cassette of the glucose ABC transport system from *Sulfolobus solfataricus*. G. Verdon, S.V. Albers*, B.W. Dijkstra, A.J.M. Driessen*, A.-M.W.H. Thunnissen, *University of Groningen, Biophysical Chemistry, Dept. of Chemistry, Nijenborgh 4, 9747 AG Groningen and * Dept. of Microbiology, Kercklaan 30, 9751 NN Haren, The Netherlands.*
Keywords: ABC transport system, glucose, ATP-binding cassette.

In all living organisms, ABC transporters provide specific and active transport facilities to export or import a variety of molecules across cellular membranes. Their molecular organisation is based on two conserved components: a transmembrane channel and cytosolic ATP-hydrolysing modules providing the driving force needed for the translocation process. These components are often fused into a single polypeptide in export systems like, for example, those from the MDR (Multi-Drug Resistance) family. However some systems use individual proteins to build-up the transporter, while bacterial import systems display an additional membrane-bound substrate-binding subunit dedicated to nutrients uptake.

When cultured on a medium containing glucose as main carbon source, the hyperthermophilic *Sulfolobus solfataricus* expresses a very strong glucose-binding activity. The gene encoding this glucose-binding protein (GlcS) was found next to an operon containing three genes showing a high similarity with bacterial ABC importers: two integral membrane permeases (GlcT and GlcU) and GlcV as the molecular motor of the system.

GlcV was over-produced in *E. coli* and purified in large amounts using three chromatographic steps. Initial crystallisation screens and rounds of optimisation without ATP provided crystals diffracting to high resolution. Our progress toward the crystal structure of GlcV will be presented.

[s8a.m4.p4] Structural evidence for ligand specificity in the binding domain of the human Androgen receptor. P.M. Matias¹, R. Coelho¹, M. Thomaz^{1,2}, C. Peixoto², S. Macedo² and M.A. Carrondo¹, ¹*Instituto de Tecnologia Química e Biológica, Universidade Nova de Lisboa, Apartado 127, 2780 Oeiras, Portugal;* ²*Instituto de Biologia Experimental e Tecnológica, Apartado 12, 2780 Oeiras, Portugal.*
Keywords: human androgen receptor, human progesterone receptor, ligand binding domain.

The crystal structure of the human Androgen Receptor (hAR) in complex with the ligand metribolone (R1881) has been determined by the molecular replacement method and refined against 2.4 Å diffraction data, to R = 21.0% and R_{free} = 29.7%. The three-dimensional structure of the hAR LBD shows the typical nuclear receptor fold. The ligand interactions with the polypeptide chain were analysed and compared with those observed in the structures of the human Progesterone Receptor (hPR) complexed with progesterone. The change of two residues in the ligand binding pocket (LBP) between hPR and hAR was identified as the most likely source for the specificity of the R1881 ligand binding to hAR LBD.