



University of Groningen

Solution Structure of E. coli IIBcellobiose of the PEP-dependent PTS

AB, E.; Scheek, R.M.; Robillard, G.T.

IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

Document Version Publisher's PDF, also known as Version of record

Publication date: 1996

Link to publication in University of Groningen/UMCG research database

Citation for published version (APA):

AB, E., Scheek, R. M., & Robillard, G. T. (1996). Solution Structure of E. coli IIBcellobiose of the PEPdependent PTS.

Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

The publication may also be distributed here under the terms of Article 25fa of the Dutch Copyright Act, indicated by the "Taverne" license. More information can be found on the University of Groningen website: https://www.rug.nl/library/open-access/self-archiving-pure/taverneamendment.

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Downloaded from the University of Groningen/UMCG research database (Pure): http://www.rug.nl/research/portal. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.

Download date: 04-06-2022

A1 3D structures: experimental determination

3D RECONSTRUCTION OF BOVINE PAPILLOMAVIRUS VISUALIZED AT 9Å

P-A1-05

B.L. TRUS^{1,3}, H.L. GREENSTONE², R.B.S. RODEN². J.T. SCHILLER²AND F.P. BOOY³

¹ DCRT-CBEL; ² NCI-LCO; ³ NIAMS-LSB; NIH, Bethesda, MD 20892, USA

Purpose: We have been using bovine papillomavirus (BPV) to extend the resolution of 3D density maps reconstructed from cryo-micrographs with a view to visualising protein domains and ultimately tertiary structure.BPV has a diameter of ~ 600 Å, a T number of 7, and two shell proteins (L1 and L2) in a ratio of 30:1(1).

Methods: Micrographs were recorded on a Philips EM400RT using a modified Gatan cooling holder, digitized on a Perkin Elmer 1010MG, preprocessed and reconstructed as described (2). Origin and orientational refinement ensued to high precision (3).

Results: Resolution of the 3D reconstruction from ~200 images was assessed by FRC coefficients (4) using the 2-sigma curve as the threshold for meaningful signal and a new method based on the spectral signal-to-noise ratio (5). Two independent reconstructions compared well by FRC (6) and DPR (7).

Conclusions: The 3D reconstruction was statistically significant to 9Å resolution by all criteria applied. Features are seen in greater detail at increasing resolution. The button of density at the center of the 5-fold pentons may mark the location of the minor capsid protein L2.

References: (1) Baker et al. (1991) Biophys. J. 60: 1445 (2) Newcomb et al. (1993) J. Mol. Biol. 232: 499-511. (3) Baker and Cheng (1996) J.Struct. Biol. 116: 120-130. (4) Conway et al. (1993) Struc. Biol. 111: 222-233.

(5) Unser et al. (1996) manuscript in submission.(6) Saxton, and Baumeister (1982) J. Microscopy 127: 7

(7) Frank et al. (1981) Science 214: 1353

P-A1-07

SOLUTION CONFORMATION OF [PRO 7,13] αA-CONOTOXIN PIVA

KIM S-M, HWANG K-J, KIM S-K, SHON K-J, GRAY WR, OLIVERA BM, RIVIER J, HAN K-H.

Biomolecular Structure R.U., KRIBB(KOR), Dept. of Physiology and Biophysics, Case Western Reserve Univ.(USA), Dept. of Biology, Univ. of Utah (USA), Clayton Lab. for Peptide Biology, Salk Inst.(USA)

Purpose: An approach to the study of ligandrecpetor interactions is to investigate the highresolution structures of various ligands which are molecules of less complexity than the receptor, while systematically collecting relevant information regarding ligand-receptor interactions.

Methods: NMR experiments were performed in a phase-sensitive mode using a Varian UNITY 500 spectrometer at 14°C and 25°C. Calculation of structures were done using distance-geometry and back-calculation of NOESY spectrum using 324 NOE restraints.

Results: The final set of the 12 best structure: had an average backbone rms deviation of 0.95Å and back calculation of experimental NOE spectrum had provided 49 new NOE restraints and yielded the R-factors of R_s=0.641 and R.=0.157.

Conclusions: The solution structure of [Pro 7,13] aA-conotoxin P_{IVA} should provide a framework for structure function strudies for the entire aA family of conotoxins and determin for acetylcholine receptor-targeted conotoxins.

SECONDARY STRUCTURE OF HUMAN SEMINAL PLASMA PROSTATIC INHIBIN: BIOPHYSICAL STUDY RASTOGI VK, CHARY KVR, GOVIL G.

Tata Institute of Fundamental Research, Mumbai, (IN)

Purpose: Prostatic Inhibin (HSPI) protein (M_r = 10.4 kDa) has been isolated from human seminal plasma to study the three-dimensional structure.

Methods: CD, fluorescence and 2D NMR experiments have been carried out in aqueous solution at different pH and temperature.

Results & Conclusions: CD measurements revealed that HSPI has a rigid and ordered structure. Fluorescence studies showed that both the tryptophans in the protein are in hydrophobic core. Analysis of NMR spectra has enabled us to identify and assign nearly all spin systems. NMR studies revealed that the protein predominantly adopts anti-parallel B-sheet conformation. No α -helical segments are present. The segments C42-Y43-E44-T45 and S88-V89-S90-E91 are found to adopt type II βturns.

P-A1-08

Solution Structure of E. coli enzyme IIBeal of the PEP-dependent PTS

AB E, SCHEEK RM, ROBILLARD GT. GBB/BIOSON, University of Groningen, Groningen (NL) Purpose: Determination of the 3D solution structure of enzyme IIBodiobies (IIBod), the central catalytic domain in posphoenolpyruvatedependent phosphotransferase system for cellobiose. Enzyme IIB is phosphorylated at Cys10 by enzyme IIA and in turn phosphorylates the carbohydrate cellobiose after transport through the membrane.

Methods: Heteronuclear triple-resonance 3D NMR experiment were performed in order to obtain the resonance assignments and obtain NOE information. Distance geometry and molecular dynamics calculations were performed in to obtain a cluster of structures. In order to simplify the assignment of NOE resonances, we used ambiguous restraints during the MD calculation.

Results: Using app. 2000 NOE intensities a cluster of 32 structures was obtained with an rms deviation of C° positions of 1.3 Å. Conclusions: Enzyme IIB consists of a central four-stranded parallel β -sheet, and 5 α -helices which flank the sheet on both sides. The catalytic residue Cys10 is positioned at the end of the first \$-strand just before a flexible loop which probably constitutes the phophorylgroup binding loop.