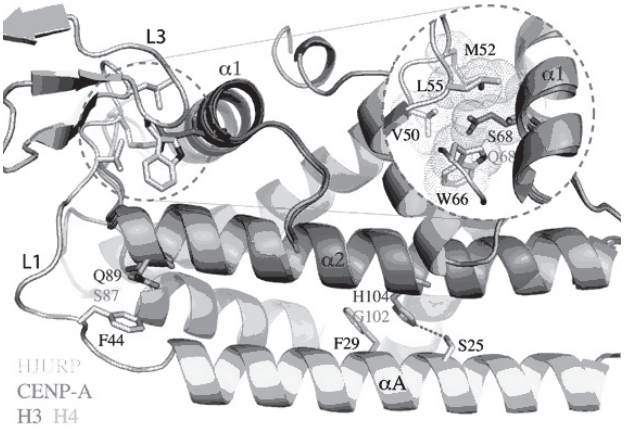

Structure of human CENP-A-H4-HJURP Complex

Keywords: centromere, CENP-A, histone chaperone

MS.16.1

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Engineering immunity against HIV-1 using designed antibody constructs

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Despite decades of effort, no current vaccine elicits neutralizing antibodies at concentrations blocking HIV-1 infection. In addition to structural features of HIV's envelope spike that facilitate antibody evasion, we proposed that the low density and limited lateral mobility of HIV spikes impedes bivalent binding by antibodies via inter-spike cross-linking [1]. In addition, molecular modeling suggested that bivalent binding within a single trimeric spike (intra-spike cross-linking) is also unlikely for antibodies directed against most protein epitopes. The resulting predominantly monovalent binding minimizes avidity and thereby high affinity binding and potent neutralization, thus expanding the range of HIV mutations permitting antibody evasion. In this talk, I will review our efforts to create high avidity anti-HIV protein reagents for use in gene therapy and/or passive immunization. One class of reagents is based upon a naturally-occurring dimeric form of 2G12, a neutralizing antibody that recognizes carbohydrates on the gp120 portion of the HIV spike. 2G12 monomers use both Fabs in an unusual domain-swapped (Fab)2 unit to recognize a constellation of carbohydrates on gp120. We have shown that dimerization of 2G12 leads to enhanced potency against HIV-1 strains that are sensitive to 2G12 monomers and neutralization of strains that are resistant to 2G12 monomers [2]. Thus carbohydrate-binding reagents are a logical starting point for engineering novel bivalent and multivalent antibody architectures capable of intra-spike cross-linking. Another class of engineered reagents we're working on involves fusion of the first two domains of the host receptor CD4 to the variable regions of an antibody recognizing the CD4-induced (CD4i) co-receptor binding site on gp120. We designed, expressed, purified, and tested the neutralization potencies of CD4-CD4i antibody reagents with different architectures, antibody combining sites, and linkers [3]. Implications of a crystal structure of a clade C gp120/CD4/CD4i Fab complex that demonstrates auto-reactive binding between the CD4i antibody and CD4 [4] will also be discussed.

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Keywords: antibodies, HIV-1, gp120

MS.16.2

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The multiple personalities of transthyretin

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The human plasma protein transthyretin (TTR) is a soluble protein that functions as transport protein for thyroxin. At certain conditions however the normally tetrameric protein dissociates and forms structurally less defined monomeric or dimeric species that are prone to aggregate and form fibrils/amyloids leading to disease — familial amyloidotic polyneuropathy (FAP, type I). One of our aims is to characterize in detail the structural changes in the TTR protein that lead to amyloid formation and disease [1], [2].

To prevent transthyretin fibril formation, one rather successful approach is to stabilize the native state structure, thereby reducing the protein's ability to form the misfolded intermediate structures needed to form fibrils [3]. Even though a number of stabilizing compounds have been found [4], [5], it is still desirable to find new and more structurally diverse scaffolds, and for those reasons we have initiated a fragment-based lead generation campaign [6] using human transthyretin as target protein. In this presentation, we will review our experiences and some of the results observed.

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Keywords: folding, drug design, stability

MS.16.3

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Structural biology and medicinal chemistry in neglected diseases of poverty

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Parasitic diseases are a major global cause of illness, morbidity, long-term disability, and death, with severe medical and psychological

consequences for millions of men, women and children. Despite the high prevalence of parasitic diseases worldwide, in most cases their treatment is inadequate, generating an urgent demand for new antiparasitic drugs. However, in addition to the traditional challenges involved in the complex process of drug discovery and development, there is the hurdle of the lack of investments in this field. This situation is especially problematic in de novo drug discovery, regarded as a high risk and costly process. Therefore, strategies that allow high quality hit identification rate as well as reduction in drug discovery costs are extremely useful in this field. The biology of parasitic organisms has been continuously studied in detail, providing a solid base for the selection of relevant molecular targets for drug discovery. Virtual screening strategies, including the use of both ligand- and structure-based methods, have been employed in the search for new inhibitors of relevant therapeutic targets related to parasitic diseases. More recently, the combination of computational and experimental techniques has been explored as a useful approach for the identification of high quality hits. This talk outlines the progresses and applications of the combined approach of protein structure determination followed by *in vitro* and *in silico* screening strategies for the discovery of innovative chemotherapy agents for a variety of neglected diseases of poverty, highlighting the challenges, limitations, and future perspectives in medicinal chemistry. We will conclude by reviewing our work on Chagas disease, with both ligand- and structure based drug design strategies, resulting in promising new leads and drug candidates.

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Keywords: trypanosome cruzi, schistosoma mansoni, drug candidates

MS.16.4

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X-ray microdiffraction reveals structural features of amyloid deposits *in situ*

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Amyloidoses, including Alzheimer's disease, belong to emerging public health problems in Western countries. All amyloidoses share the same morphologic, structural, and tinctorial properties consisting of insoluble fibrils stained by specific dyes, a fibrillar aspect in electron microscopy and a typical cross-β folding in X-ray diffraction pattern.

Most studies aiming at deciphering the amyloid structure rely on fibres generated *in vitro,* or extracted from tissues using protocols, which may modify their intrinsic structure. Therefore, *in situ* fine architecture of the deposits remains unknown.

Here, we present the first study, carried out on paraffin-embedded and frozen human renal tissue sections, aiming at revealing the structural features of amyloid fibrils in deposit without any possible structure modification induced by extraction [1]. To this end, we used synchrotron-based microdiffraction, which is the unique technique that gives access to micron-sized spatial resolution. This allowed detecting variations at the micron-scale in the fibres molecular structure. Hence, fibres orientation could be followed along a glomerulus and a variation inside and around the whole glomerulus unit could be monitored.

We further show that the *in situ* fibres in amyloid deposits are partly folded into cross-β sheets exhibiting a diffraction feature at 4.7 Å as *in vitro*-formed fibres. This validates the structural data from extracted fibres and strengthens the use of this diffraction signal as a main criterion of fibrils formation *in vitro*. We provide the experimental conditions for detecting the characteristic 4.7Å reflexion inside tissue cuts. Working on the tissue gives access to intrinsic information about the molecules, we thereby show a correlation between the position inside the glomerulus and the amyloid fibres partial orientation.

Materials and Methods. Experiments were performed at ESRF beamline ID13 using a 2 µm beam diameter. The samples consisted in 40 µm thick tissue slices.

These results are of highest importance to understand amyloid deposit formation and spark interest to investigate tissues. Given the possibility to access to the intrinsic structural parameters such as the fibre orientation or fibre size, relevant information about *in situ* mechanisms and conditions of deposits formation will become available with potential diagnostic and therapeutic consequences.

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Keywords: in situ X-ray structure imaging, cross-β folding, amyloidosis, fiber diffraction

MS.16.5

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Insights into the Food-Poisoning toxin, *Clostridium perfringens* enterotoxin

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Clostridium perfringens enterotoxin (CPE) is a major cause of antibiotic-associated and sporadic diarrhoea, it is also a major cause of food-poisoning [1]. The toxin is the second most common cause of hospital-acquired enteric disease, after *Clostridium difficile*. CPE is a 319-residue protein produced by type A or C isolates of *C. perfringens* and can be chromosome or plasmid located [2]. CPE is a pore-forming toxin that acts by forming pores in intestinal epithelial cells [3]. The toxin has been shown to form a number of complexes with claudin, and perhaps occludin, at the tight junctions of CaCo-2 cell cultures [4]. The exact composition of these complexes continues to be a matter for discussion. However, it appears CPE forms a small complex (of around 90 kDa on initial binding to membrane), followed by a larger pre-pore complex and finally the largest complex, the active pore form.

We present the X-ray crystallographic structure of CPE determined to 2.7 Å resolution. The fold of the protein reveals an expected homology to the HA-3 haemagluttinin from *Clostridium botulinum* and unexpected homology to the Aerolysin-like family of beta-pore-forming proteins. We have shown CPE to be a trimer in several different crystal forms, by Electron Microscopy and also in solution. The trimer has the characteristics of a biologically-significant oligomer, but does not form a pore, and the previously identified claudin-binding cleft [5] is unoccluded and oriented in a single plane on one side of the molecule. Residues previously associated with forming a membrane-inserted beta-hairpin [6] are folded in a small helix at the centre of the complex. However, Aerolysin-like pore-forming toxins are normally hexameric or heptameric and there is evidence to support a hexameric pore for CPE.

In this presentation we will discuss the homology between CPE