the base of the J helix. The distinct atomic shifts of invariant Asp 169 away from the active site may prevent interactions between its main chain amide and the pyrimidine of the 5-fluoro-2'-deoxyuridylate inhibitor and between the Asp 169 side chain and the quinazoline ring of the cofactor. These movements could explain the decreased sensitivity of the mutant enzyme to 5-fluoro-2'-deoxyuridylate inhibition.

PS04.17.37 STRUCTURAL COMPARISON OF AMYLOIDOGENIC LIGHT CHAIN DIMER IN TWO CRYSTAL FORMS WITH NONAMYLOIDOGENIC COUNTERPARTS. Norbert Schormann and Merrill D. Benson, Dept. of Medicine, Indiana University School of Medicine, Indianapolis, IN 46202; USA.

In the majority of cases, immunocyte-derived amyloid light chain (AL) (primary) amyloidosis is associated with a nonmalignant expansion of a single plasma cell clone. The monoclonal immunoglobulin (IG) light chain product of the plasma cell clone is the precursor of the amyloid fibril subunit protein.

To investigate structural factors in amyloid fibril formation an attempt has been made to compare the variable region of amyloid proteins with nonamyloid light chain proteins with the goal of developing a structural model for the polymerization or aggregation process of IG light chain proteins.

A κI protein from an individual (BRE) with amyloidosis was completely characterized at the primary structure level. The DNA sequence coding for the variable segment of the κI light chain (κI V_L) was amplified by PCR from the patient's bone marrow DNA using the determined amino acid sequence. The DNA construct was used to express the recombinant κI V_L protein in vitro. Protein BRE was purified to homogeneity and crystallized using ammonium sulfate as precipitant. Two distinct crystal forms were obtained (Crystal form I: monoclinic, space group $P2_1$, with a=82.37Å, b=77.75Å, c=82.23Å, ß=119.97°; crystal form II: orthorhombic, space group $C222_1$, with a=82.04Å, b=142.11Å, c=77.86Å).

An effort was made to verify the original Laue group assignment, since both space groups are lower symmetry subgroups of hexagonal space group $P6_122$. The data sets were reindexed and processed using older R-Axis processing software and the newer BioteX program package. Reindexing trials and Laue checks of 'merge files' from different indexing solutions for crystal form I showed unambigously that the crystal system is correctly assigned as monoclinic. This structure was refined to 2Å. In the case of crystal form II, differences in R_{sym} and R_{merge} between indexing solutions were not as pronounced to discriminate against the hexagonal crystal system. In addition to refining the structure of BRE II in space group $C222_1$ to 1.8Å, we therefore included refinement in two possible hexagonal space groups ($P6_1$ and $P6_122$, with a=b=82.05Å, c=77.87Å, γ=120°).

The structures of both crystal forms were compared to each other and to nonamyloidogenic light chain dimers with special emphasis on domain-domain interactions. Models for amyloid fibril formation in AL amyloidosis are discussed.

PS04.17.38 STRUCTURE SOLUTION OF SOME C-REACTIVE PROTEINS. Annette K. Shrive, David Holden, Allison Metcalfe, Dean A.A. Myles, Margaret Hopkins, Ian D. Glover, David Hoole[1], Anne C. Bloomer[2] and Trevor J. Greenhough*, Dept. of Physics, and [1]Biological Sciences, Keele University, Keele, Staffs, ST5 5BG, UK. [2]MRC Laboratory of Molecular Biology, Hills Road, Cambridge CB2 2QH, UK. * and CCLRC Daresbury Laboratory, Warrington WA4 4AD, UK

C-reactive protein (CRP) is a member of the pentraxin family, a conserved, phylogenetically ancient super-family of oligomeric calcium-binding proteins exhibiting high sequence homologies, often forming a cyclic pentameric assembly. Studies centred at Keele have produced the structure of Ca-free rat CRP and Ca-bound human CRP, with the structure solution of Ca-free human CRP and CRP from *Limulus polyphemus* in progress.

Human CRP is a trace plasma protein of unknown biological function that is expressed dramatically as part of the acute-phase response and as such is used almost universally as a clinical test for infection and inflammation. The generation of a pentameric model from the pentraxin serum amyloid P (SAP) has finally provided the structure solution for both the rat and human crystals. The Ca-bound human structure contains a crystal contact where the calcium-binding loop from one protomer coordinates into the calcium site of a protomer in a symmetry related pentamer, revealing the mode of binding of the principal ligand phosphocholine (PC). A striking structural cleft, on the pentameric face opposite to the PC binding site, suggests an important functional role, perhaps in complement activation.

Rat CRP, in contrast to human CRP with which it shares 65% sequence identity, is a normal component of serum, is glycosylated, has been reported to contain a disulphide-linked dimer, and exhibits comparable affinities for phosphoethanolamine (PE) and PC. Native data to 3.3Å, from a single cryocooled small crystal, and the rebuilt pentameric SAP model have provided the structure solution. Conformational changes with respect to human SAP seen in human CRP are also present in rat CRP. The proposed disulphide linkages and PC/PE binding are discussed.

PS04.17.39 CRYSTAL PACKING INTERACTIONS IN STREPTAVIDIN CRYSTALS. Ronald E. Stenkamp, Stefanie Freitag, Isolde Le Trong, Ashutosh Chilkoti and Patrick S. Stayton, Dept. of Biological Structure and Center for Bioengineering, University of Washington, Seattle, WA 98195

The high-affinity streptavidin-biotin interaction is widely used in biotechnologies such as bioseparations and diagnostics. This interaction makes streptavidin and biotin prime candidates for structural and functional studies of protein-ligand interactions, but streptavidin's ability to crystallize in a number of three- dimensional and two-dimensional crystal forms [1,2,3,4,5] might also provide a mechanism for the design of biomaterials with specific inter-molecular spacings and orientations. For example, streptavidin is being investigated as a potential two-dimensional crystalline substrate for electron microscopic studies of other biological macromolecules. To provide a basis for the design of mutated streptavidin molecules with different packing characteristics, we are examining the crystal packing interactions in the various crystal forms available to date. We will determine which residues are most commonly involved in the inter-tetramer interfaces and locate potential regions on the protein surface suitable for mutagenesis studies aimed at modulating the crystal packing and growth properties of the protein.

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