the base of the I 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 cl protein from an individual (BRE) with amyloidosis was purified to homogeneity and crystallized using the determined amino acid sequence. The DNA construct sequence coding for the precursor of the amyloid fibril subunit protein.

The data sets were reindexed and Laue checks of BRE was purified to homogeneity and crystallized using the determined amino acid sequence. The DNA construct sequence coding for 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 cl protein from an individual (BRE) with amyloidosis was purified to homogeneity and crystallized using the determined amino acid sequence.

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 faces and locate potential regions on the protein surface suitable for mutagenesis studies aimed at modulating the crystal packing and growth properties of the protein.

This work is supported by NIH grant DDC49655.