structure was refined to 2.2Å resolution with R=0.212 and R(free)=0.256; the cell parameters are *a*=47.2Å, *b*=58.6Å, *c*=43.4Å, α=95.3°, β=103.2°, γ=93.6°. Details on each of the structural determinations and results will be discussed.

PS04.15.31 METAL-BINDING IN SUPERANTIGENS. E.M. Schad[1], M.Dohlsten[2], Per Björk[2], L.A. Svensson[1]. Molecular Biophysics, Chemical Center, Lund University, P.O. Box 124, 221 00 Lund, Sweden[1], Pharmacia Oncology Immunology, Lund, Sweden[2].

One of the most striking aspects of the structure of SEA is the unusual octahedral metal-coordination geometry. In addition, SEA displays a N-terminal coordination to the metal-ion (Schad et al., 1995). The coordinating residues of Zn^{2+} are the same ligands as those found for Cd^{2+} including the N-terminal coordination. The unusual ligand coordination by the N-terminal serine residue observed is comparable to the coordination found in the structure of phospholipase C (Hough et al., 1989; Hansen et al., 1992). In SEA, the metal-ion is coordinated by a primary bidentate formed by ligands His 225 and Asp 227. These two ligands are separated by a short spacer that according to Vaillee & Auld (1990) provides localized and overall stabilization to the protein. A longer spacer provided by His 187 donates flexibility to the coordination site. It should be noted that zinc binding proteins commonly have a tetrahedral geometry with this short spacer-long spacer ligand composition (Vallee & Auld, 1990). Alanine substitution of His 225 and Asp 227 resulted in a more than 1000fold reduced MHC class II binding affinity, whereas the His 187 mutation displayed only a 100-fold reduced binding affinity (Abrahmsen et al., 1995). This suggests that modification of the short spacer bidentate formed by His 225 and Asp 227 severely affects the MHC class II binding to domain II. In contrast, mutations of the longer spacer His 187 have less of an effect on the other metal ligands in retaining significant MHC class II binding in this region. This is further supported by the varying temperature factors observed in the metal coordination site mentioned previously.

PS04.15.32 CRYSTAL STRUCTURE OF THE MHC CLASS IB MOLECULE H2-M3 WITH FOUR DIFFERENT FORMYLATED-PEPTIDES. San Tai Shen[a], Chyung-Ru Wang[b], Kirsten Fischer Lindahl[b,c], Johann Deisenhofer[a,b], Dept. of Biochemistry[a], Howard Hughes Medical Institute[b], Dept. of Microbiology[c], University of Texas Southwestern Medical Center, Dallas, Texas 75235-9050

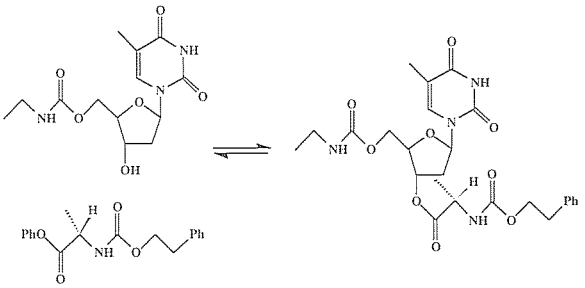
H2-M3 is a major histocompatibility complex (MHC) Ib molecule of mouse with a 10^4-fold preference for binding N-formylated peptides. H2-M3 associates with β2-microglobulin (β2m) to present a polymorphic endogenous peptide derived from the mitochondrially encoded ND1 protein to CD^{8+} cytotoxic T cells. The crystal structure of H2-M3 with a bound formylated 9-mer peptide derived from rat ND1 protein was solved in our laboratory (Wang C-R *et al.*, Cell, 70: 215-223, 1995). The overall structure of H2-M3 resembles MHC class Ia, such as HLA-A2 or H2-Kb, but the peptide-binding groove is different. The formyl group is coordinated by His-9 and a bound water molecule, and the side chain of the polymorphic residue which determines the antigen specificity of the bound peptide is buried.

To examine whether there is any conformational change in the MHC-peptide complex depending on the identity of the polymorphic residue, we intend to cocrystallize H2-M3 with each of four ND1 7-mer peptides that differ in the polymorphic residue (Ire, Ala, Val, and Thr). We have used molecular replacement to solve the crystal structures of H2-M3 bound with two of these peptides. The crystal strcuture determinations for the other two are still on progress.

PS04.15.33 CRYSTAL STRUCTURE OF AN AMINOACYLATION CATALYTIC ANTIBODY. Ben Spiller*, B.D. Santarsiero, Linda Hsieh, Raymond Stevens, Department of Molecular and Cell Biology, University of California, Berkeley CA 94720 USA

Many hydrolytic catalytic antibodies have made by raising antibodies against phosphate esters. Bimolecular addition reactions go through the same transition states as hydrolysis reactions and, with appropriate leaving groups, can be catalyzed by antibodies raised against phosphate esters.

Here, the first high resolution crystal structure of an antibody that catalyzes an addition reaction, aminoacylation, is presented. This antibody catalyzes the reaction shown. The antibody was generated by immunization with a transition state analog in which the reactive carbon ester is replaced by a phosphate ester with a phenol leaving group.



The FAB fragment was crystallized in space group $P4_32_12$ with cell parameters a=60, c= 281. Data were collected on an RaxisII and the structure was determined to 2.6 Angstroms by molecular replacement.

The aminoacylation catalytic antibody is amongst the fastest catalytic antibodies, with K_{cat}/K_m equal to 5.4×10^4 M^{-1} min^{-1}(the uncatalyzed rate is 2.6×10^{-4} M^{-1} min^{-1}). Remarkably, the antibody binds hapten with a K_d of 240 pM while K_m's for acyl acceptor and donor are 770uM and 260uM respectively. Thus the transition state analog is bound six orders of magnitude more tightly than the ground state. The antibody efficiently transfers an acyl group to an alcohol in aqueous solution.

PS04.15.34 STRUCTURE AND COMPARISON OF HIV-1 GP120 PEPTIDES IN COMPLEX WITH HIV-1 NEUTRALIZING FABS. R. L. Stanfield, J. B. Ghiara, J. M. Rini, E. A. Stura, A. C. Satterthwait, I. A. Wilson, The Scripps Research Institute, 10666 N. Torrey Pines Road, La Jolla, CA 92037

Crystal structures have been determined for three different HIV-1 neutralizing antibody Fab fragments in complex with several linear and cyclic peptides. The Fabs were all raised against the same 40-amino acid disulfide linked peptide, corresponding in sequence to the principal neutralizing determinant (PND) loop from HIV-1 gp120 (MN isolate). The complexes studied include Fab 50.1 (MN specific) with linear peptide, Fab 59.1 (broadly specific) with two linear peptides, and Fab 58.2 (potent and broadly specific) in complex with one linear and three cyclic peptides. The three different antibodies recognize overlapping epitopes on the PND loop (50.1-CKRIHIGPG, 59.1-HIGPGRAFYT, 58.2-RIHIGPGRAFY). The peptides bound to 50.1 and 59.1 are very similar, but differ from peptides bound to 58.2 around the GPGR region. Information from the early Fab- peptide complex structures has been used in the design of constrained peptides. These peptides have an Aib (α-aminoisobutyric acid) residue in the place of an Ala residue involved in a helical turn. The Aib containing