01.4-01 PROGRESS IN THE REFINEMENT OF THE STRUCTURE OF α-LYTIC PROTEASE AT 1.8 Å RESOLUTION. By M. Fujinaga, L.T.J. Delbaere* and M.N.G. James, MRC Group in Protein Structure and Function, Department of Biochemistry, University of Alberta, Edmonton, Alberta, T6G 2H7.

α-lytic protease is produced by the soil bacterium *Lysobacter enzymogenes*. It is a serine protease containing the active site sequence Asp-Ser-Gly as in the mammalian pancreatic serine proteases (Whitaker, D.R., Jurasek, L., and Roy, C. [1966] Biochem. Biophys. Res. Commun. 24:173-178; Whitaker, D.R., and Roy, C. [1967] Can. J. Biochem. 45:911-916). The comparison of the tertiary structure of α-lytic protease at 2.8 Å resolution with the structure of the pancreatic protease, elastase, had shown 55% topological equivalence of the α-carbons. For the structures of α-lytic protease and the bacterial serine protease, SGPA, the corresponding figure was 82% (Brayer, G.D., Delbaere, L.T.J., and James, M.N.G. [1979] J. Mol. Biol. 131:743-775).

The refinement of the structure of α-lytic protease at 1.8 Å resolution is being done with the restrained parameter least-squares procedure (Hendrickson, W.A., and Konnert, J.H. [1978] Proc. Madras Symp. on Biomol. Struct., Conform., Function, Evol., Pergamon, Oxford). The program has been modified by B. Furey for an array processor (Floating Point Systems AP190-L). At the time of writing of this abstract, the state of refinement was as follows. The standard R factor was 19.6% with 13638 reflections [I>2σ(I)]. There were 5960 variables which included positional and individual thermal parameters of the enzyme and 75 solvent molecules, and the occupancies of the solvent molecules. The r.m.s. deviation from ideal bond lengths was 0.029 Å while the corresponding value for angle distance was 0.038 Å.

The results of the preliminary comparisons of the structures of α-lytic protease with the refined structure of SGPA (Sielecki, A.R. et al. [1979] J. Mol. Biol. 134: 781-804), and with the 2.5 Å structure of elastase (L. Sawyer, personal communication) will be presented.

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01.4-02 STRUCTURE OF RIBONUCLEASE A: X-RAY AND NEUTRON REFINEMENT. By Alexander Wlodawer[+*], Richard Bott[*], and Lennart Sjölin[+*]; [+]National Measurement Laboratory, National Bureau of Standards, Washington, DC 20234, USA and [*]LMB, NIADDKD, National Institutes of Health, Bethesda, MD 20205, USA.

The crystal structure of monoclinic ribonuclease A ($P2_1$, a = 30.18 Å, b = 38.4 Å, c = 53.32 Å, β = 105.85°) has been refined with the X-ray data at 2.0 Å resolution. The final model contained, in addition to protein, 176 water sites of varying occupancy and a phosphate near the active site. The root-mean-square deviation of the interatomic bonds from ideality was 0.022 Å, and the crystallographic R = 0.159. Several parts of the polypeptide chain, particularly residues 16-24, were rebuilt several times using computer graphics. The "fragment ΔF" maps indicated the necessity of deleting one residue from this segment, and only after all solvents were properly placed, a compensating insertion nearby became visible.

This model was further refined with both X-ray and neutron structure amplitudes after hydrogen and deuterium atoms were appended in stereochemically feasible positions. Crystallographic R = .236 for the neutron data at 2.8 Å, and the refinement is being continued with the data extending to 2.0 Å. The system of hydrogen bonds in the vicinity of the active site was examined in detail. The residues Asp 121 - His 119 - phosphate - His 12 are connected by a sequence of hydrogen bonds, which may correspond to the situation existing in the presence of the substrate.

01.4-03 LOW-RESOLUTION (4.5Å) REFINEMENT OF THE IMMUNOGLOBULIN J539 Fab FRAGMENT. By Gerson H. Cohen, Laboratory of Molecular Biology, National Institute of Arthritis, Metabolism & Digestive Diseases, NIH, Bethesda, MD 20205, USA.

Using the reported solution for the low resolution structure of J539 (Navia, Segal, Padlan, Davies, Rao, Rudikoff & Potter, Proc. Natl. Acad. Sci. USA (1979), 76, 4071-4074), an immunoglobulin Fab fragment, we are applying the CORELS procedure (Sussman, Holbrook, Church & Kim, Acta Cryst. (1977), A33; 800-804) to obtain a suitable model for higher resolution refinement. After refining the six orientation parameters of the entire molecule as a rigid body, the molecule was subdivided first into variable and constant halves and then into its four domains. Subsequently, individual amino acids were treated without altering the side chain conformations.

The initial model used for this study was a rotated and slightly altered version of the refined McPC603 (Satow & Davies, unpublished). The progress of the refinement process will be presented.