Native Fab NQ10 X-ray intensities were measured on a four circle diffractometer to 4.5 Å resolution. Two heavy atom derivatives were obtained using UDP-acetate at different concentrations. An electron density map at 6 Å resolution clearly revealed the molecular boundaries. Using a rigid body refinement program and the three-dimensional structure of Fab D1.3, a model was fitted to the electron density map showing the traces of the light and heavy chains. The model was refined to 4.5 Å resolution. Measurement of intensities to higher resolution and further refinement of the model are currently underway. The latest progress in the structure determination will be reviewed.

Radically different variable domain interactions were observed in antibody light- and heavy-chain domains crystallized from either distilled water or from 1.5 M ammonium sulfate. Light chains are characterized by an amino-terminal variable domain and a carboxyl-terminal constant domain linked by an extended peptide. We had previously determined the structure of light-chain dimer Loc in a crystal form obtained from ammonium sulfate (G.-Chang, et al., 1983, Biochemistry 22, 4890). The two variable domains form a very unusual antigen binding site consisting of a protrusion with a groove on each side. We have now determined the crystal structure of Loc as crystallized from distilled water. At present, the R = 35% for 3.5 Å data. In this structure, the association of the two variable domains forms a cavity that resembles the "conventional" antigen binding site that was observed in the Hcg protein. The association of the constant domains is very similar in the two crystal forms. Two independent hinge-bending motions are required to convert the structure observed in one crystal form to that observed in the other form. Work supported by the U. S. Department of Energy under contract no. W-31-109-ENG-38.

CRYSTALLIZATION AND CRYSTALLOGRAPHIC STUDY OF DIG LIVER NADH-CYTOCHROME b5 REDUCTASE. By K. Kimi1, S. Kaidi2, H. N. Ramaial3, P. Iyennagi4, K. Kobayashi5, and K. Hayashi5, 1Department of Applied Chemistry, Faculty of Engineering, Osaka University, Suita, Osaka 565, 2Institute of Basic Medical Sciences, University of Tsukuba, McPherson, Thorny, 305, and 3Institute of Scientific and Industrial Research, Osaka University, Takatsuki, Osaka 567, JAPAN

NADH-cytochrome b5 reductase (EC 1.6.2.2) catalyzes to reduce cytochrome b5 in an electron-transport chain from NADH to a terminal oxidase desaturase in the endoplasmic reticulum. The enzyme is an amphipathic membrane-bound flavoprotein with a single subunit containing one molecule of FAD. The protein molecule consists of a large, hydrophilic catalytic domain and a smaller, hydrophobic membrane-binding domain. We have crystallized the following two forms of this enzyme from pig liver microsomes: the intact molecule (32kDa) solubilized by a detergent (Triton N-101) and the catalytic domain (30kDa) solubilized by a protease (cathepsin D). Crystals have been grown from polyethylene glycol solutions by the vapour diffusion method. The crystals of the intact enzyme are large enough (2.5 x 1.5 x 1.5 mm) and belong to the orthorhombic space group P212121; with unit-cell dimensions of a = 87.1, b = 73.2, c = 69.0 Å. The asymmetric unit contains one protein molecule, the V4 value being 2.6 Å²/Da. X-ray diffraction patterns extend to 2.0 Å resolution. Data collection of native crystals and search for heavy-atom derivatives are currently underway.