isomorphous replacement and anamolous scattering from
a single mercuric iodide derivative (Freymann, Metcalf,
Turner and Wiley, unpublished). The electron density
map indicates a rod-shaped dimer, with a core of four
80 Å long alpha-helices.

The human histocompatability antigen HLA-A2 is active
in tissue graft rejection and immunological recognition
during surveillance by "T-killer" cells. The papain-
solubilized HLA is a 2 chain structure (46,000 daltons),
which is purified from human tissue culture cells.
This is a technically challenging problem as the
crystals are very thin plates. X-ray data to 2.8 Å
resolution for the native and a platinum tetrachloride
derivative were collected at the EMBL synchrotron out-
station in Hamburg from crystals 10-30 microns thick.
Three platinum sites have been determined from the
three-dimensional difference Patterson (Bjorkman,
Bennett and Wiley, unpublished). An antigenically
distinct HLA, A28, forms an isomorphous crystal.
Further progress in this analysis will be discussed.

02.X−8   THE STRUCTURE OF NEURAMINIDASE. By P.M.
Colman, J.N. Varghese and W.G. Laver, CSIRO Division of
Protein Chemistry, Parkville 3052, Australia and
Australian National University, Canberra, Australia.

The three dimensional structure of the N2 subtype of
influenza neuraminidase has been determined by a com-
bination of the multiple isomorphous replacement method
in one crystal form with noncrystallographic symmetry
averaging in a second crystal form where two copies of
the polypeptide are found in the asymmetric unit. The
two crystal types used are of neuraminidases from
naturally occurring field isolates from 1957 and 1967
with sequence homology of ~90%. Neuraminidase was
liberated from the viral membrane by pronase digestion.

The chain folding has revealed a new class of tertiary
structure in which six twisted β sheets, all with 'W'
topology, are arranged like the blades of a propeller
to form one of the four subunits of the enzyme. Four of
the five potential glycosylation sequences carry carbo-
hydrate. One of these oligosaccharides is involved in
stabilisation of the circularly symmetric tetramer.

The enzyme active centre has been identified by
difference Fourier analysis of sialic acid soaked
crystals. The binding site is in a cavity on that
surface of the tetramer distal to the viral membrane,
and near the corners of the box shaped tetramer. The
cavity is lined with nine acidic groups, six basic groups
and three hydrophobic groups which are strictly conserved
in amino acid sequences of neuraminidases both within
and between subtypes of influenza.

Sites of field strain sequence variation have been mapped
on to the structure and reveal a nearly continuous
surface of variation encircling the catalytic cavity.

02.X−9   STRUCTURES OF SEVERAL BINDING PROTEINS
INVOLVED IN ACTIVE TRANSPORT AND CHEMOTAXIS. by F.A.
Quiocho, N.K. Vyas, J.W. Pflugrath, M.A. Saper, and M.N.
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Binding proteins located in the periplasm of Gram-
negative bacteria are essential components of osmotic-
shock sensitive active transport and chemotaxis. The
following binding proteins have been solved in our labo-
ratory at the resolution indicated: L-arabinose-binding
protein (1.7 Å), sulfate-binding protein (2.0 Å),
leucine, isoleucine, valine-binding protein (2.8 Å), and
the D-galactose-binding protein (2.5 Å). With the ex-
ception of the amino acid binder, each structure has
been solved with bound ligand. The arabinose- and
sulfate-binding proteins have been refined by restrained
least squares method to R-factors of 13.7% and 14.0%,
respectively. Despite lack of significant sequence
homology, these proteins have a high degree of overall
structural similarity; all four proteins are elongated
and composed of two globular domains with a central β-
pleated sheet sandwiched between helices. As a group
these proteins are unusual since each domain is folded
from two separate polypeptide chain segments. These
proteins have a common ligand binding site located in
the cleft between the two domains. The interaction of
L-arabinose and sulfate with respective receptor protein
revealed novel features. Either α- or β-L-arabinose is
bound in the same site of the binding protein, and all
sugar hydroxyls and ring oxygen in both anomers form
identical extensive networks of hydrogen-bonds with side
chain residues. The sulfate bound to the sulfate-
binding protein forms hydrogen-bonds with seven residues
none of which are charged; three of these residues are
peptide NH from the N-termini of three helices. The
bound arabinose or sulfate is inaccessible to the bulk
solvent. (Research supported by NIH, NSF and the Robert
A. Welch Foundation.)

02.X−10   THE STRUCTURE OF GLYCOLATE OXIDASE
FROM SPINACH. By Y. Lindqvist and C.-I. Bränden,
Department of Chemistry and Molecular Biology, Swedish
University of Agricultural Sciences, S-750 07 Uppsala,
Sweden.

Glycolate oxidase is one of the key enzymes in the photo-
respiration of plants, where it oxidizes glycolate to glyoxy-
late. It is a flavin enzyme using FMN as cofactor. Struc-
ture determination of glycolate oxidase from spinach to 5.5
Å resolution showed (Y. Lindqvist & C.I. Bränden, J. Mol.
Biol. (1980) 143, 201-211) that two thirds of the electron
density could be interpreted as eight αβ-units wound up as
a barrel as in triose-phosphate-isomerase (D.C. Phillips,
M.J.E. Sternberg, J.M. Thornton & I.A. Wilson J. Mol. Biol.
(1978) 119, 329-351). The data have been extended to 2.5 Å
resolution and an electron density map based on two heavy
atom derivatives $Hg(CN)_4{}^{2-}$ and $Pt(NH_3)_2Cl_2$ was calcu-
lated. From this map it was possible to build in the β -
strands and some of the helices of the αβ-barrel but
several helices were poorly defined. For density not be-
longing to the αβ-barrel it was not possible to trace the
main chain. Since our platinum derivative did not con-
tribute much to the phasing we had in actual fact SIR
phases. We therefore tried the ISIR-ISAS program package
written by Bi-Cheng Wang (Acta Cryst A, in press). This
program defines a protein-solvent boundary from the map,
flattens the solvent and after backtransformation of the
filtered map combines the phases using Sim weighting. This
is done in several iterative cycles. The result on our data
was striking and gave a map where the helices of the αβ -
barrel can now be clearly defined and additional helices in
the extra density regions have been identified. We are
presently building a model on a graphics display and the
result of this work will be presented.