extend and deepen understanding of protein structure, protein evolved by evolution and natural selection. For the first time, protein crystallography. Protein engineering provides a means to our own powers of understanding.

The catalytic function of an enzyme is a particularly sensitive property, because enzyme kinetic parameters can be interpreted in terms of free energy changes during the catalytic process. A change in these parameters, caused by engineering a single amino-acid change, gives a direct measure of a change in the free energy of interaction at some point in the catalytic process. 'Calorimetry' of individual hydrogen bonds and other specific interactions is possible. Larger changes, involving whole sections of chain or domains, can also be studied; similarly the energy of quaternary interaction between protein monomers can be changed.

These interpretations rely on assumptions about the structure of the factitious mutant which can be checked cryocrystallographically. Many small changes produce molecules which crystallise isomorphously with the wild-type enzyme. More radical changes will result in altered crystal structures which can be solved by molecular replacement techniques.

Protein engineering can be used to assist crystallography, by the elimination of a mobile domain or a site of glycosylation to produce better crystals, or by introduction of specific amino acids to provide sites for heavy atoms. Work on tyrosyl-tRNA synthetase (with A.R. Fersht and G. Winter) is used to illustrate these points. Some of the possible useful applications of protein engineering are discussed.

For decades x-ray photons were thought of as being of far less use in surface crystallography than electrons or ions. Their comparatively low interaction cross section with atoms was the main reason for this judgement. The availability of highly intense synchrotron radiation sources, however, has drastically changed this situation. Techniques which were formerly only reserved for bulk studies, such as kinematical diffraction and diffuse scattering, have become applicable for surfaces as well and there are in addition even ways to study in a continuous fashion the geometry change from surface to bulk by adding to the diffraction process the additional feature of total external reflection. Besides standard x-ray techniques new experimental approaches were also found and developed such as surface x-ray absorption spectroscopy and x-ray interference fields created by dynamical Bragg diffraction. These methods make use of information which is available in inelastic scattering channels of the photon-matter interaction. Characteristic fluorescence photons and Auger electrons are measured often in combination with the elastically scattered photons. In many applications, the low cross section can be applied advantageously. For example, the kinematical theory can be used for x-ray diffraction studies. Because of the large penetration depth, interfaces which are covered by an epitelial layer or by a liquid can also be investigated.

A comprehensive review of the present status of x-ray surface crystallography will be presented.