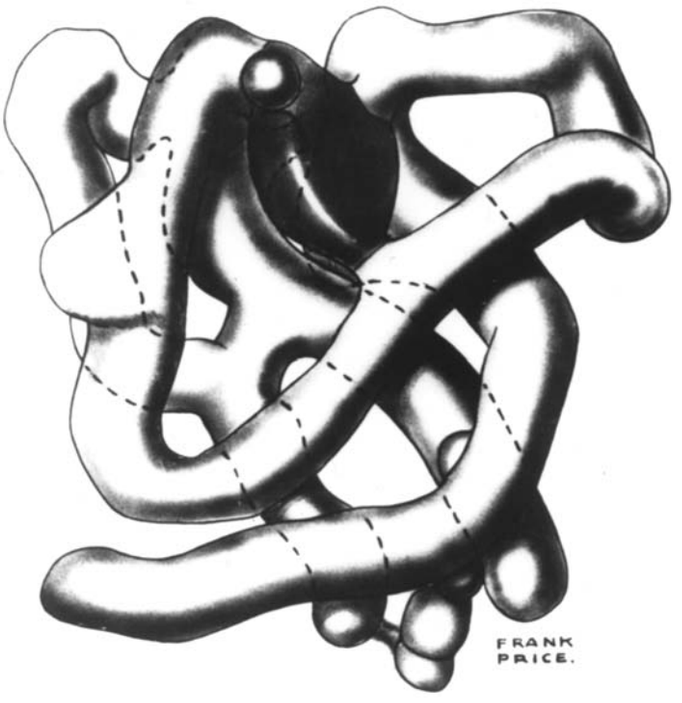

Fig. 1.2.5.1. A model of the myoglobin molecule at 6 Å resolution. Reprinted with permission from Bodo *et al.* (1959). Copyright (1959) Royal Society of London.

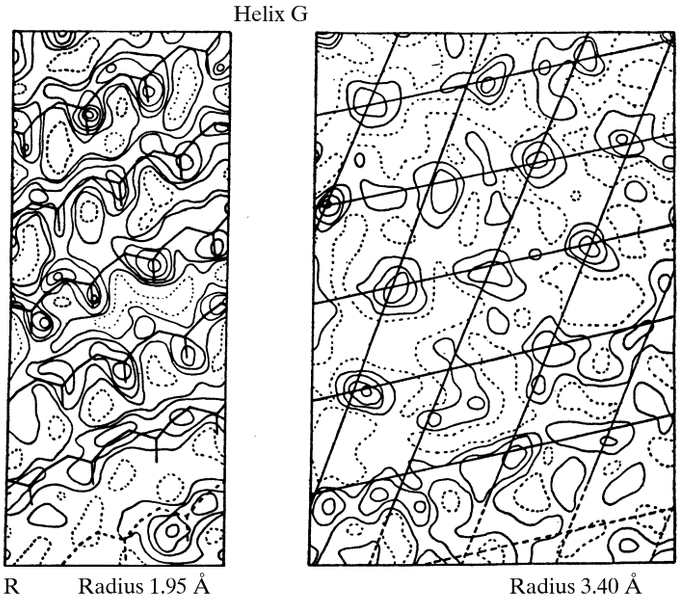

Fig. 1.2.5.2. Cylindrical sections through a helical segment of a myoglobin polypeptide chain. (*a*) The density in a cylindrical mantle of 1.95 Å radius, corresponding to the mean radius of the main-chain atoms in an α-helix. The calculated atomic positions of the α-helix are superimposed and roughly correspond to the density peaks. (*b*) The density at the radius of the β-carbon atoms; the positions of the β-carbon atoms calculated for a right-handed α-helix are marked by the superimposed grid (Kendrew & Watson, unpublished). Reprinted with permission from Perutz (1962). Copyright (1962) Elsevier Publishing Co.

6 Å-resolution map of myoglobin (Bluhm *et al.*, 1958). EDSAC2 came on-line in 1958 and was the computer on which all the calculations were made for the 5.5 Å map of haemoglobin (Cullis *et al.*, 1962) and the 2.0 Å map of myoglobin. It was the tool on which many of the now well established crystallographic techniques were initially developed. By about 1960, the home-built, one-of-a-kind machines were starting to be replaced by commercial machines. Large mainframe IBM computers (704, 709 *etc.*), together with FORTRAN as a symbolic language, became available.

1.2.5. The first protein structures (1957 to the 1970s)

By the time three-dimensional structures of proteins were being solved, Linderström-Lang (Linderström-Lang & Schellman, 1959) had introduced the concepts of 'primary', 'secondary' and 'tertiary' structures, providing a basis for the interpretation of electron-density maps. The first three-dimensional protein structure to be solved was that of myoglobin at 6 Å resolution (Fig. 1.2.5.1) in 1957 (Kendrew *et al.*, 1958). It clearly showed sausage-like features which were assumed to be α-helices. The iron-containing haem group was identified as a somewhat larger electron-density feature. The structure determination of haemoglobin at 5.5 Å resolution in 1959 (Cullis *et al.*, 1962) showed that each of its two independent chains, α and β, had a fold similar to that of myoglobin and, thus, suggested a divergent evolutionary process for oxygen transport molecules. These first protein structures were mostly helical, features that could be recognized readily at low resolution. Had the first structures been of mostly β structure, as is the case for pepsin or chymotrypsin, history might have been different.

The absolute hand of the haemoglobin structure was determined using anomalous dispersion (Cullis *et al.*, 1962) in a manner similar to that used by Bijvoet. This was confirmed almost immediately when a 2 Å-resolution map of myoglobin was calculated in 1959 (Kendrew *et al.*, 1960). By plotting the electron density of the α-helices on cylindrical sections (Fig. 1.2.5.2), it was possible to see not only that the Pauling prediction of the α-helix structure was accurately obeyed, but also that the C_β atoms were consistent with *laevo* amino acids and that all eight helices were right-handed on account of the steric hindrance that would occur between the C_β atom and carbonyl oxygen in left-handed helices.

The first enzyme structure to be solved was that of lysozyme in 1965 (Blake *et al.*, 1965), following a gap of six years after the excitement caused by the discovery of the globin structures. Diffusion of substrates into crystals of lysozyme showed how substrates bound to the enzyme (Blake, Johnson *et al.*, 1967), which in turn suggested a catalytic mechanism and identified the essential catalytic residues.

From 1965 onwards, the rate of protein-structure determinations gradually increased to about one a year: carboxypeptidase (Reeke *et al.*, 1967), chymotrypsin (Matthews *et al.*, 1967), ribonuclease (Kartha *et al.*, 1967; Wyckoff *et al.*, 1967), papain (Drenth *et al.*, 1968), insulin (Adams *et al.*, 1969), lactate dehydrogenase (Adams *et al.*, 1970) and cytochrome *c* (Dickerson *et al.*, 1971) were early examples. Every new structure was a major event. These structures laid the foundation for structural biology. From a crystallographic point of view, Drenth's structure determination of papain was particularly significant in that he was able to show an amino-acid sequencing error where 13 residues had to be inserted between Phe28 and Arg31, and he showed that a 38-residue peptide that had been assigned to position 138 to 176 needed to be transposed to a position between the extra 13 residues and Arg31.

The structures of the globins had suggested that proteins with similar functions were likely to have evolved from a common precursor and, hence, that there might be a limited number of protein folding motifs. Comparison of the active centres of chymotrypsin and subtilisin showed that convergent evolutionary pathways could exist (Drenth *et al.*, 1972; Kraut *et al.*, 1972).

references