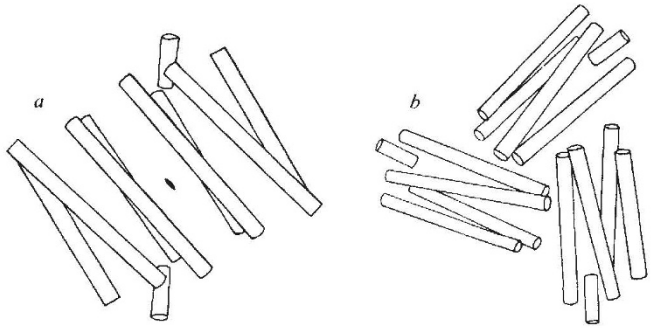
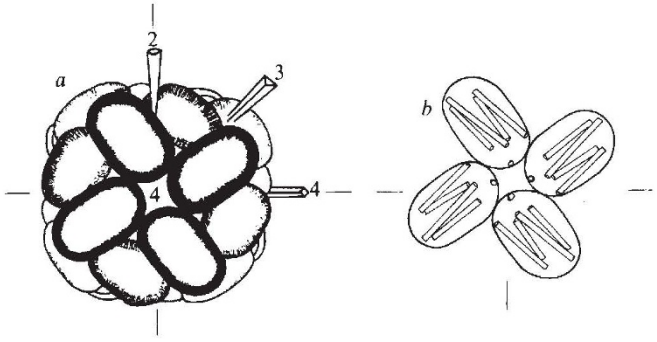


Fig. 3 Schematic views of apoferritin subunits, showing local packing around *a*, molecular twofold axes, *b*, molecular threefold axes. Only helical regions are shown. The helical rods from neighbouring subunits related by molecular dyads overlap along most of their lengths, and give a system of eight nearly parallel rods. A symmetrical dimer is thus suggested as a stable intermediate in the assembly of the protein shell. Probable inter-helical connections suggest that chain directions alternate so that neighbouring helices are antiparallel. Subunits related by molecular threefold axes have their helices nearly perpendicular and there is less inter-subunit contact than around the twofold axes.

(Fig. 1*a*). The Cd^{2+} ion pairs are bound roughly half way along the extended BC loop. Four loops and two Cd^{2+} ions participate in the double intermolecular bridge.

Not used in the structure determination, but found in separate isomorphous replacement studies are Tb^{3+} ions on the inner surface of the shell. The major site (Fig. 1*a*) is close to the twofold axis at a radius of 41.6 Å and only 4.3 Å from its symmetry-related pair. The Tb^{3+} sites which probably involve carboxyl groups[15], are of special relevance to ferritin formation. Our mechanism for the catalytic action of apoferritin in the oxidation of Fe(II), which gives it the power to accumulate Fe(III), becoming ferritin, involves sites for Fe(II)-oxidation and heteronucleation of hydrous ferric oxide[8]. Tb^{3+} ions inhibit iron uptake by apoferritin, and may bind at Fe-binding sites.

Fig. 4 Schematic drawings of the subunit arrangement in an apoferritin molecule viewed down a fourfold axis. *a*, Complete molecule showing some of its symmetry axes. *b*, Subunits related by a fourfold axis. Subunits approximate to cylinders or ellipsoids with length (approximately 55 Å) about twice their diameter (approximately 27 Å), although the shell is rather more smooth than these shapes suggest. Each subunit is in contact with five neighbours, although the contacts are of only three different types around the three different symmetry axes (as in Figs 4*b* and 3*a*, and 3*b*). The four major helices present in each subunit have their axes roughly parallel to the long axes of the subunits as drawn schematically in *b*. The interactions between subunits making the symmetrical tetramer seen in *b*, are less extensive than those in the symmetrical dimer and trimer of Fig. 3*a* and *b*. Compare with Fig. 1*c*.



The presence of a double site suggests the possibility of a cooperative two-electron transfer to oxygen from two close Fe(II), giving two Fe(III), which is followed by the formation of an oxo-bridge by elimination of protons from bound water molecules. Here again we can compare the structure with that of myohaemerythrin[13], in which each subunit contains a pair of Fe atoms 3.44 ± 0.05 Å apart, which reversibly binds oxygen. This Fe–Fe pair is set well within the subunit, whereas in apoferritin the Tb^{3+} ions belong to different subunits and lie on the inner surface of the protein shell.

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Erratum

In the letter 'Subgenomic, cellular Rous sarcoma virus RNAs contain oligonucleotides from the 3′ half and the 5′ terminus of virion RNA' by P. Mellon & P. H. Duesberg, *Nature* **270**, 631, lines 32–35 of paragraph 4 should be deleted. In the last line of paragraph 4 the numbers 6 and 3 should be underlined.

Corrigendum

In the letter 'On melting icebergs' by H. E. Huppert & J. S. Turner, *Nature* **271**, 46, in the first line for 'their' read 'suitable'.