β-sheets in α/β-barrels shows that in these molecules McLachlan's equations do apply and that they can be used to help understand the principles governing such structures.

Knowledge of conserved features of α/β-barrels helped in what is probably the most successful attempt so far to predict the three-dimensional structure of a protein from its amino-acid sequence. Crawford *et al.*[9] used standard algorithms to predict the secondary structures in ten homologous sequences of the α-subunit of tryptophan synthase. They averaged the results for homologous positions and recognized the features of an α/β-barrel. This, together with other data, allowed them to predict a model with the correct overall fold. The secondary-structure assignments for all nine helices and six of the eight β-strands are close to those which were later found in the crystal structure[9].

Evolutionary relationships between proteins can be argued on the basis of the similarities in their sequences, structures and the geometries of their active sites. Most of the α/β-barrels have little or no similarity in their amino-acid sequences, and so discussions of their evolutionary relationships have mainly involved questions of structure[2]. Proteins that have diverged from a common ancestor have structural differences that increase with the number of amino-acid substitutions[11]. The main elements of secondary structure and the active-site peptides retain their fold but may shift relative to each other. For two homologous proteins, the structural differences in *these* regions, expressed in terms of the root mean square (r.m.s.) difference in the position of main-chain atoms, Δ (Å), are related to sequence differences by the approximate equation $\Delta = 0.40e^{1.87H}$, where H is the proportion of non-identical amino-acid residues[11]. Surface loops and peripheral elements of secondary structure may have quite different folds and no sequential homology.

Before the sequence of spinach glycolate was determined, Branden *et al.*[7] compared the structure of its α/β-barrel with that of yeast flavocytochrome b_2. The two proteins use the coenzyme FMN to oxidize small α-hydroxy acids. For the 320 residues that have the same fold, the r.m.s. difference in position is 1.6 Å. This implies[7,11] a sequence identity of 30–50 per cent. The recently determined sequence of glycolate oxidase[12] has 33 per cent of its residues identical to those in flavocytochrome b_2.

The two α/β-barrels in *N*-(5′-phosphoribosyl) anthranilate isomerase-indole-3-glycerol-phosphate synthase catalyse two consecutive reactions in the biosynthesis of tryptophan. Both α/β-barrels consist of about 200 residues. For the 185 residues that have the same fold in the two domains, r.m.s. difference in position is 2.17 Å and the sequence identity is 10.3 per cent[4]. The close fit of these values to the equation implies the descent of the two domains from a common ancestor.

Normally, the use of the equation requires atomic coordinates that have been well refined with high-resolution data. Lebioda and Stec in their paper in this issue[2] use an approach that overcomes this requirement. An ideal α/β-barrel has 8-fold symmetry (see Fig. 2), but real α/β-barrels have large local deviations from ideal symmetry. Proteins descended from a common ancestor might be expected to share to some extent the same local deviations. Hence the proper superposition of their structures: first strand of one structure on the first strand of the other structure, and so on, should produce a better fit than improper superpositions: first strand on one structure on second strand of the other structure, and so on. Previously, Lebioda *et al.*[13] used such calculations to show that the α/β-barrels of TIM, pyruvate kinase and KDPG aldolase are probably not descended from a common ancestor. In their new work[2], Lebioda and Stec show that enolase and pyruvate kinase, which catalyse two consecutive reactions in the glycolytic pathway, probably do share a common ancestor. Their conclusion is supported by similarities in the geometry of the active sites.

It is clear that some α/β-barrels with very little similarity in amino-acid sequence are descended from a common ancestor. But the similarities in the structures of the other α/β-barrels almost certainly arise from the stringent requirements of this fold — requirements that are not yet clearly understood. □

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Enter the Chinese dragons

British Museum (Natural History)

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***Shunosaurus* is one of six magnificent dinosaurs from China on display at the British Museum (Natural History) in London from 17 June until 31 January 1989. By virtue of its unsurpassed Mesozoic record, China is "the most important dinosaur region in the world" says Angela Milner, who excavated in China in 1982 with other researchers from the museum. The six skeletons show a good cross-section of the riches of Chinese dinosaurs, from the Triassic prosauropod *Lufengosaurus* to the Upper Cretaceous hadrosaur *Tsintaosaurus*. Others include the 2.5-metre-tall carnosaur *Gasosaurus*, the stegosaur *Tuojiangosaurus* and the 30-tonne sauropod *Mamenchisaurus*, which had the longest neck of any animal known. The fossils have travelled 7,000 miles by courtesy of the Institute of Vertebrate Palaeontology and Palaeoanthropology in Beijing. A four-year joint research programme between the institute and palaeontologists in Canada is currently unearthing dinosaurs in the Gobi Desert, many of which are previously undiscovered species.** Henry Gee