

**Table 4** Examples of common protein folds.

	Fold	Schematic	Description	Comments	Examples
All α	four-helix bundle		Helix–turn–helix motifs. Comprise four antiparallel helices with short connecting loops.	Polar side-chains on exposed surfaces interact with the aqueous environment; hydrophobic residues are towards the centre.	myohaemerythrin, uteroglobin, ferritin (pdb file 1h96)
	globin fold		Usually 6–8 α helices. Variable arrangements. Two C-terminal helices adopt a helix–turn–helix conformation; remaining helices pack with greater angles between their axes ($\sim 50^\circ$).	Helices wrap around an active site (e.g. a haem molecule).	myoglobins (e.g. pdb file 1azi), haemoglobins (e.g. pdg 1gzx), phycocyanins
All β	up-and-down β barrels		Antiparallel β sheet with β meander connections wraps around to form a barrel structure.	The inner surface of the barrel is rich in hydrophobic side-chains.	retinol binding protein (carries retinol, which is hydrophobic, inside the barrel) (pdb file 1aqb)

**Table 4** (continued) Examples of common protein folds.

	Fold	Schematic	Description	Comments	Examples
	Greek key barrels		Greek key motifs wrap around to form a barrel structure.	The inner surface of the barrel is rich in hydrophobic side-chains.	prealbumin (pdb file 1bmz), gamma crystallin (eye lens)
α/β	α/β barrels		Parallel β strands alternate with parallel α helices and these components are linked by surface loops. (Thus helices are antiparallel to strands.) The β strands are arranged on the inside, forming the barrel shape, with α helices around the outside of the barrel.	The inner surface of the barrel is rich in hydrophobic side-chains. The loops between the C-terminus of the β strands and the N-terminus of the α helices form active sites and ligand binding sites.	The α/β barrel structure is common in enzymes of the glycolytic pathway, oxidases, isomerases and hydrolases. Example: triose phosphate isomerase (pdb file 1tim)
	α/β sheet		Alternate α and β components with connecting loops, as in the α/β barrel. β strands are hydrogen-bonded to each other and form a β sheet and the helices are alternately above and below the plane of this sheet.	This arrangement often creates a crevice at the C-terminal edge of the sheet, and it is here that substrates bind.	flavodoxin (redox protein) (pdb file 1ahn)

**Table 4** (continued) Examples of common protein folds.

	Fold	Schematic	Description	Comments	Examples
α/β	Rossmann fold	<p>top view</p>	Two $\beta\alpha\beta\alpha\beta$ units. Mostly parallel β strands connected via loops with helices. Helices run antiparallel to β strands.	This motif is also known as a dinucleotide binding fold.	Different dehydrogenases have variations on this type of fold, e.g. the NAD binding domain of glyceraldehydes 3-phosphate dehydrogenase (an enzyme of the glycolytic pathway) (pdb file 4gpd)