Tertiary structure combines regular secondary structures and loops (coil)

Bovine carboxypeptidase A
Tertiary structures may contain common patterns, or motifs, of secondary structures (= supersecondary structures)
Some ‘folds’ are built up from smaller motifs
Other folds are not built up from smaller motifs

Sperm whale myoglobin, the first protein structure to be determined
Multiple folds may combine as domains of a tertiary structure

Domains:
- independently folding units
- (often with distinct functions)

Protein:
Glyceraldehyde-3-phosphate dehydrogenase (GAPDH), an enzyme of glycolysis
There are ~1,000 different protein folds, which can be classified by structure and homology

*For example:* **CATH** – a system for categorizing protein folds (at the level of domains)

- **Class** – general description of predominant secondary structures (α, β, α/β)
- **Architecture** – arrangement of secondary structure elements
- **Topology** – connectivity of secondary structure elements
- **Homologous superfamily** – evolutionary relationship
Class: folds can be grouped by predominant secondary structure(s)
**Architecture**: arrangement of $2^\text{o}$ structures

**Topology**: connectivity of $2^\text{o}$ structures

These $\beta$-barrels have similar architecture… but different topology
There are ~1,000 different protein folds, which can be classified by structure and homology.

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Protein structure is conserved more than sequence

c-type cytochromes from different species have little sequence similarity
Quaternary structure combines multiple subunits, often in a symmetric arrangement

Oligomeric protein, multimeric protein, oligomer, multimer (if large, protein complex):
Protein composed of multiple polypeptide chains
*Ex: hemoglobin tetramer*

Subunit:
One polypeptide chain of an oligomer
*Ex: α₁ subunit*

Protomer:
Repeating structural unit
*Ex: one αβ dimer*
Virus capsids are generally highly symmetric.

Icosahedral symmetry (rotational symmetry)
Virus capsids are generally highly symmetric.