

# Protein folds and fold-space

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With the number of known protein folds potentially approaching completion, the problems associated with their systematic classification are evaluated. It is argued that it will be difficult, if not impossible, to find a general metric based on pairwise comparison that will provide a satisfactory classification. It is suggested that some progress may be made through comparison against a library of idealised 'template' folds but a proper solution can only be attained if this includes a model of the underlying evolutionary processes. These processes are considered with examples of some unexpected relationships among folds.