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For forty years we have known the essential ingredients for protein folding - an amino acid sequence, and water. But the problem of predicting the three-dimensional structure from its sequence has eluded computational biologists even in the age of supercomputers and high throughput structural genomics. Despite the unsolved mystery of how a protein folds, advances are being made in predicting the interactions of proteins with other molecules, such as small ligands, nucleic acids or other proteins. Protein Structure Prediction focuses on the various computational methods for prediction, their successes and their limitations, from the perspective of their most well-known practitioners. Leaders in the field provide insights into template-based methods of prediction, structure alignment and indexing, protein features prediction, and methods for de novo structure prediction. Protein Structure Prediction is a cutting-edge text that all researchers in the field should have in their libraries