



Protein Structure Prediction (Methods in Molecular Biology)

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This book covers elements of both the data-driven comparative modeling approach to structure prediction and also recent attempts to simulate folding using explicit or simplified models. Despite the unsolved mystery of how a protein folds, advances are being made in predicting the interactions of proteins with other molecules. Also rapidly advancing are the methods for solving the inverse folding problem, the problem of finding a sequence to fit a structure.

This book focuses on the various computational methods for prediction, their successes and their limitations, from the perspective of their most well known practitioners.

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