Título: Protein Structure Prediction

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The prediction of the three-dimensional structure of a protein from its amino acid sequence is a problem faced by an increasing number of biological scientists. This book provides a practical guide to making these predictions by reviewing strategies of different computer modeling algorithms and highlighting the degree of confidence attributed to them. Also in the volume are descriptions of the following: the principles of protein folding; sequence homology and motif searches; prediction of secondary structure; homology modeling; modeling of antibody combining sites; tertiary fold recognition; modeling of transmembrane proteins; ab initio prediction; protein-ligand docking simulations; and the use of molecular mechanics and dynamics.