

While most textbooks on bioinformatics focus on algorithms and treat protein structure prediction only superficially, this course book assumes a novel and unique focus. Adopting a didactic approach, the author explains all the current methods in terms of their reliability, limitations and user-friendliness. She provides practical examples to help first-time users become familiar with the possibilities and pitfalls of computer-based structure prediction, making this a must-have for students and researchers.

With a Foreword by Arthur Lesh.



Anna Tramontano was trained as a physicist but she soon became fascinated by the complexity of biology and by the promises of computational biology. After a post-doctoral period at UCSF, she joined the Biocomputing Programme of the EMBL in Heidelberg. In 1990 she moved back to Italy to work in the Merck Research Laboratories near Rome. A few years ago, she returned to the academic world as a Chair Professor of Biochemistry in "La Sapienza" University in Rome where she continues to pursue her scientific interests on protein structure prediction and analysis in the Department of Biochemical Sciences. She is a member of the European Molecular Biology Organization, the Scientific Council of Institute Pasteur – Fondazione Cenci Bolognetti, and the organizing Committee of the Critical Assessment of Techniques for Protein Structure Prediction (CASP) initiative. She was awarded the prize for Natural Sciences of the Italian Government, the "Marotta Prize" of the Italian National Academy of Science and the Minerva Prize for Scientific Research. She has published more than one hundred scientific articles in the field of Bioinformatics and Computational Biology.

