



Numerical Computer Methods, Part D: Pt. D

(Methods in Enzymology)

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The aim of this volume is to brief researchers of the importance of data analysis in enzymology, and of the modern methods that have developed concomitantly with computer hardware. It is also to validate researchers' computer programs with real and synthetic data to ascertain that the results produced are what they expected.

Selected Contents: Prediction of protein structure; modeling and studying proteins with molecular dynamics; statistical error in isothermal titration calorimetry; analysis of circular dichroism data; model comparison methods



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