

<<蛋白质计算机模拟>>

图书基本信息

书名 : <<蛋白质计算机模拟>>

13位ISBN编号 : 9787561529676

10位ISBN编号 : 7561529678

出版时间 : 2008-2

出版时间 : 厦门大学出版社

作者 : 周麟祥, 帅建伟

页数 : 325

版权说明 : 本站所提供之下载的PDF图书仅提供预览和简介, 请支持正版图书。

更多资源请访问 : <http://www.tushu007.com>

<<蛋白质计算机模拟>>

内容概要

This textbook covers a course of computer simulation of proteins for science major students , It consists of two knowledge blocks : Molecular Dynamics (MD) and Full Electron Structure Calculation of Proteins. We shall also discuss two main subjects: Knock-off Proteins and Protein-Lig and Interactions. However we shall not discuss the folding dynamics of proteins. These are discussed in "Cluster-Linux-Parallel Calculation System".

The Full Electron Structure Calculation of Proteins is one of the new features of this textbook. We assume the readers have the basic knowledge of computer languages , proteins and physics. Still , information on Unix , TCL and Python are included briefly in this textbook as a refreshing exercise. The keystone of this textbook is to elaborate the computer simulation of proteins. Therefore , merely reading this textbook is not enough. The students must practice all the problem examples on computers while studying. Otherwise , the students will not understand the topics discussed in this textbook.

<<蛋白质计算机模拟>>

作者简介

周麟祥，物理学教授。
1939年12月生，原籍浙江嘉兴。
1960年毕业于厦门大学物理系。
1993-1997年任美国林肯大学客座教授。
曾在厦门大学任教。
目前在复旦大学物理系主要从事蛋白质分子动力学和全电子结构的计算机模拟研究工作。

帅建伟，物理学教授。
1968年6月生，原籍四川。
1995年毕业于厦门大学物理系。
1996-2007年在香港、日本、德国、美国任职。
2007年回国前，在美国加州大学Irvine分校工作。
现在厦门大学物理系任闽江学者特聘教授，从事生物系统计算机模拟的研究工作。

<<蛋白质计算机模拟>>

书籍目录

PREFACEPART PRIOR KNOWLEDGEChapter 1 EDITING AND MANAGING FILE1.1 LOGIN AND LOGOUT1.1.1 Login and Logout1.1.2 File and Command1.1.3 Set Up1.2 EDITOR vi1.2.1 Login and Logout1.2.2 Two Statuses1.2.3 Command1.3 MANAGING FILE1.3.1 Login/Logout1.3.2 Create/Delete1.3.3 List/Read1.3.4 Editing File1.3.5 Grep/Find1.3.6 Check1.3.7 Encode1.3.8 Crypt1.3.9 Tar1.3.10 Compress1.3.11 Symbols1.3.12 Echo1.3.13 Awk ' {...}' (Aho, Weinberger and Kernighan) 1.3.14 Print1.3.15 Calculator bc1.3.16 Format ConvertingChapter 2 ENVIRONMENT2.1 KERNEL AND SHELL2.1.1 Three Layers: User-shell-kernel2.1.2 Four Kinds of Shells2.1.3 Shell Tree and Top-level Directories2.2 FILEPERMISSION2.2.1 Permission2.2.2 Change Mode2.2.3 Default Perrussion in the cshrc File2.3 CUSTOMIZING ENVIRONMENT2.3.1 User's Environment Files2.3.2 How to Edit Environment Files2.3.3 Set Up in .cshrc File2.4 INTERNET IN UNIX SYSTEM2.4.1 Internet Program in Unix2.4.2 Email2.4.3 FTP2.4.4 Telnet2.5 MANAGING SYSTEM2.6 CUSTOMIZING NET SERVER2.6.1 Three Commands2.6.2 SevenFilesChapter 3 SHELL SCRIPT3.1 WHATISSCRIPT3.2 SHELL SCRIPT LANGUAGE3.2.1 Shell Variable3.2.2 Operator3.2.3 Control3.2.4 Function3.2.5 1103.2.6 Access to Database or Another Shell ScriptChapter 4 COMPILING, DEBUG AND RUNNING4.1 COMPIILING A SIMPLE SOURCE CODE4.1.1 Compiling Process4.1.2 Compiling Command and Its Options4.2 MAKEFILE AND COMMAND:MAKE4.2.1 The Static Library and Dynamic Library.....PART PROTEIN MOLECULAR DYNAMICS

PART FULL ELECTRON STRUCTURE CALCULATION OF PROTEIN

Answer for Some Programs

INDEX

REFERENCES

<<蛋白质计算机模拟>>

版权说明

本站所提供下载的PDF图书仅提供预览和简介，请支持正版图书。

更多资源请访问:<http://www.tushu007.com>