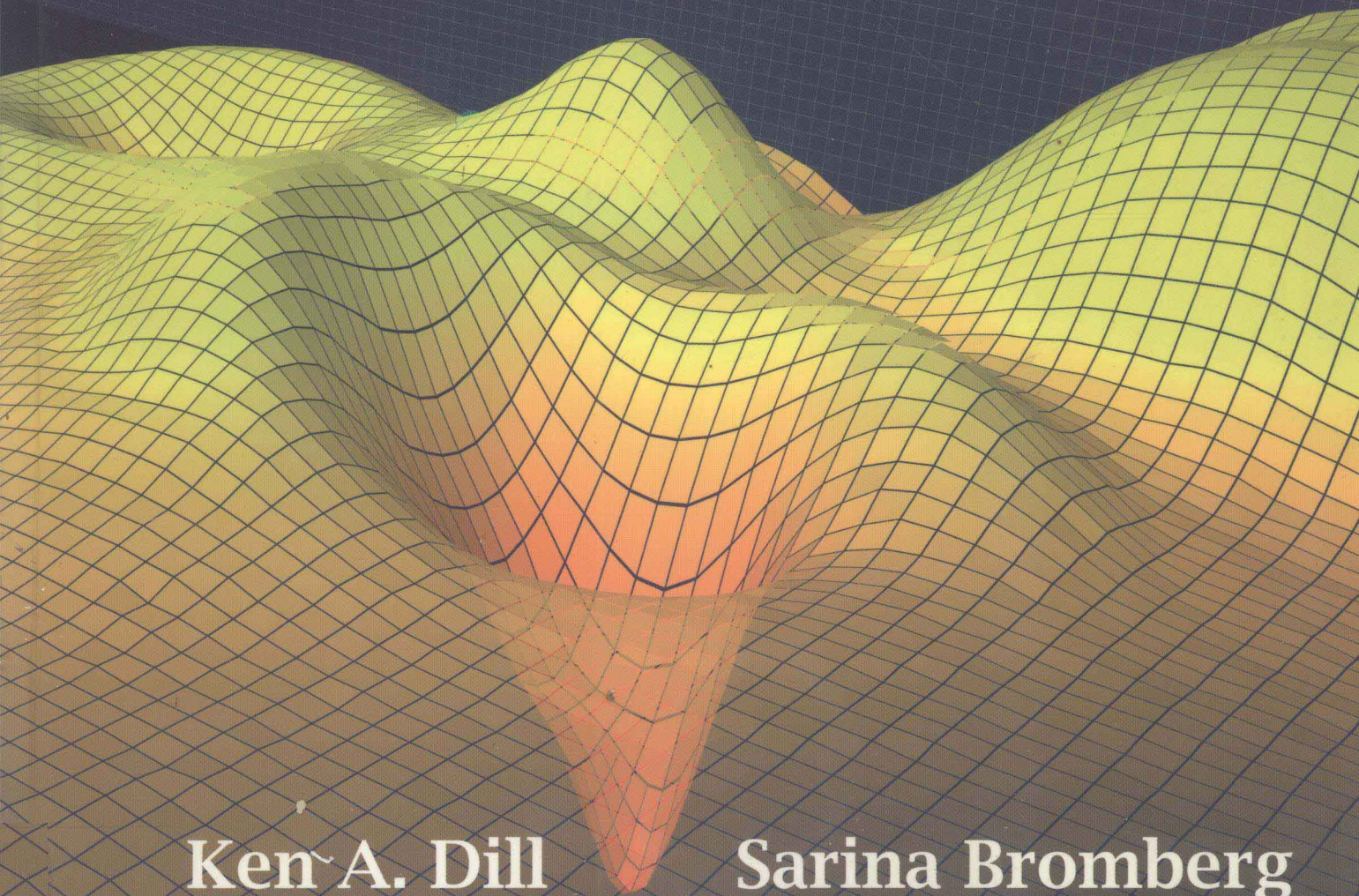


Molecular Driving Forces

Statistical Thermodynamics
in Chemistry and Biology

Ken A. Dill

Sarina Bromberg



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With the assistance of Dirk Stigter on the Electrostatics chapters

Figure Acknowledgements

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Table Acknowledgements

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Library of Congress Cataloging-in-Publication Data

Dill, Ken A.

Molecular driving forces: statistical thermodynamics in chemistry and biology / Ken A. Dill, Sarina Bromberg

p. cm.

Includes bibliographical references and index.

ISBN 0-8153-2051-5

1. Statistical thermodynamics. I. Bromberg, Sarina. II. Title.

QC311.5 .D55 2002

536'.7-dc21

2001053202

Published by Garland Science, a member of the Taylor & Francis Group
29 West 35th Street, New York, NY 10001-2299, USA
11 New Fetter Lane, London EC4P 4EE, UK

Printed in the United States of America

15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

Molecular Driving Forces

**Statistical Thermodynamics
in Chemistry and Biology**

About the Authors

Ken A. Dill is Professor of Pharmaceutical Chemistry and Biophysics at the University of California, San Francisco. He received his undergraduate training at Massachusetts Institute of Technology, his PhD from the University of California, San Diego, and did postdoctoral work at Stanford. A researcher in biopolymer statistical mechanics and protein folding, he has been the President of the Biophysical Society and received the Hans Neurath Award from the Protein Society in 1998.

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Dedicated to Austin, Peggy, Jim, Jolanda, Tyler, and Ryan

Preface

What forces drive atoms and molecules to bind, to adsorb, to dissolve, to permeate membranes, to undergo chemical reactions, and to undergo conformational changes? This is a textbook on statistical thermodynamics. It describes the forces that govern molecular behavior. Statistical thermodynamics uses physical models, mathematical approximations, and empirical laws that are rooted in the language of *entropy*, *distribution function*, *energy*, *heat capacity*, *free energy*, and *partition function*, to predict the behaviors of molecules in physical, chemical, and biological systems.

This text is intended for graduate students and advanced undergraduates in physical chemistry, biochemistry, bioengineering, polymer and materials science, pharmaceutical chemistry, chemical engineering, and environmental science.

We had three goals in mind as we wrote this book. First, we tried to make extensive connections with experiments and familiar contexts, to show the practical importance of this subject. We have included many applications in biology and polymer science, in addition to applications in more traditional areas of chemistry and physics. Second, we tried to make this book accessible to students with a variety of backgrounds. So, for example, we have included material on probabilities, approximations, partial derivatives, vector calculus, and on the historical basis of thermodynamics. Third, we strove to find a vantage point from which the concepts are revealed in their simplest and most comprehensible forms. For this reason, we follow the axiomatic approach to thermodynamics developed by HB Callen, rather than the more traditional inductive approach; and the Maximum Entropy approach of Jaynes, Skilling and Livesay, in preference to the Gibbs ensemble method. We have drawn from many excellent texts, particularly those by Callen, Hill, Atkins, Chandler, Kubo, Kittel and Kroemer, Carrington, Adkins, Weiss, Doi, Flory, and Berry, Rice and Ross.

Our focus here is on molecular driving forces, which overlaps with—but is not identical to—the subject of thermodynamics. While the power of thermodynamics is its generality, the power of statistical thermodynamics is the insights it gives into microscopic interactions through the enterprise of model-making. A central theme of this book is that making models, even very simple ones, is a route to insight and to understanding how molecules work. A good theory, no matter how complex its mathematics, is usually rooted in some very simple physical idea.

Models are mental toys to guide our thinking. The most important ingredients in a good model are predictive power and insight into the causes of the predicted behavior. The more rigorous a model, the less room for ambiguity. But models don't need to be complicated to be useful. Many of the key insights in statistical mechanics have come from simplifications that may seem unrealistic at first glance: particles represented as perfect spheres with atomic detail left out, neglecting the presence of other particles, using crystal-like lattices of particles in liquids and polymers, and modelling polymer chains as random flights, etc. To borrow a quote, statistical thermodynamics has a history of what might be called the *unreasonable effectiveness of unrealistic simplifications*. Perhaps the classic example is the two-dimensional Ising model of magnets as two

types of arrows, up spins or down spins, on square lattices. Lars Onsager's famous solution to this highly simplified model was a major contribution to the modern revolution in our understanding of phase transitions and critical phenomena.

We begin with entropy. Chapter 1 gives the underpinnings in terms of probabilities and combinatorics. Simple models are used in chapters 2 and 3 to show how entropy is a driving force. This motivates more detailed treatments throughout the text illustrating the Second Law of thermodynamics and the concept of equilibrium. Chapters 1, 4, and 5 lay out the mathematical foundations—probability, approximations, multivariate calculus—that are needed for the following chapters.

These threads culminate in chapter 6, which defines the entropy and gives the Boltzmann distribution law, the lynch-pin of statistical thermodynamics. The key expressions, $S = k \ln W$ and $S = -k \sum p_i \ln p_i$, are often regarded in physical chemistry texts as given, but here we provide optional material in which we derive these expressions from a principle of fair apportionment, based on treatments by Jaynes, Skilling, Livesay, and others.

The principles of thermodynamics are described in chapters 7–9. The statistical mechanics of simple systems follows in chapters 10 and 11. While temperature and heat capacity are often regarded as needing no explanation (perhaps because they are so readily measured), our chapter 12 uses simple models to shed light on the physical basis of those properties. Chapter 13 applies the principles of statistical thermodynamics to chemical equilibria.

Chapters 14–16 develop simple models of liquids and solutions. We use lattice models here, rather than ideal solution theories, because such models give more microscopic insight into real molecules and into the solvation processes that are central to computational chemistry, biology, and materials science. For example, theories of mixtures often begin from the premise that Raoult's and Henry's laws are experimental facts. Our approach, instead, is to show why molecules are driven to obey these laws. An equally important reason for introducing lattice models here is as background. Lattice models are standard tools for treating complex systems: phase transitions and critical phenomena in chapters 25 and 26, and polymer conformations in chapters 30–33.

We explore the dynamic processes of diffusion, transport, and physical and chemical kinetics in chapters 18 and 19 through the random-flight model, the Langevin model, Onsager relations, time correlation functions and transition-state theory.

We treat electrostatics in chapters 20–23. Our treatment is more extensive than in other physical chemistry texts because of the importance, in our view, of electrostatics in understanding the structures of proteins, nucleic acids, micelles and membranes; for predicting protein- and nucleic acid-ligand interactions and the behaviors of ion channels; as well as for the classical areas of electrochemistry and colloid science. We develop the Nernst and Poisson–Boltzmann equations and the Born model, modern workhorses of quantitative biology. Chapter 24 describes intermolecular forces.

We describe simple models of complex systems, including polymers, colloids, surfaces, and catalysts. Chapters 25 and 26 focus on cooperativity: phase equilibria, solubilities, critical phenomena, and conformational transi-

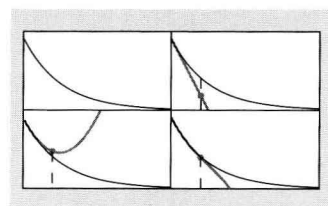
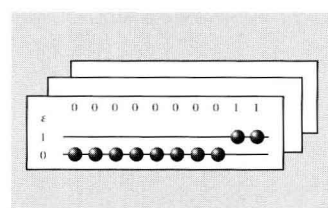
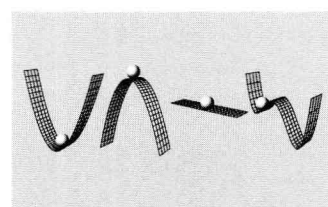
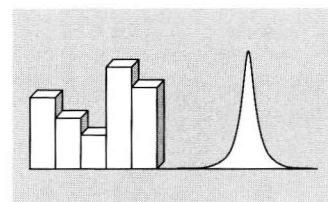
tions, described through mean-field theories, the Ising model, helix-coil model, and Landau theory. Chapters 27 and 28 describe binding polynomials, essential to modern pharmaceutical science. Chapters 29 and 30 describe water, the hydrophobic effect, and ion solvation. And chapters 31--33 focus on the conformations of polymers and biomolecules that give rise to the elasticity of rubber, the viscoelasticities of solutions, the immiscibilities of polymers, reptational motion, and the folding of proteins and RNA molecules.

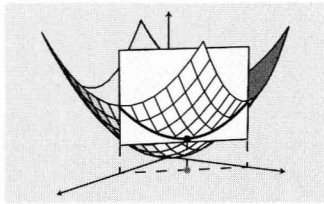
Acknowledgements

We owe a great debt to Brad Anderson, Victor Bloomfield, Robert Cantor, Hue Sun Chan, John Chodera, Margaret Daugherty, John von Drie, Roland Dunbrack, Burak Erman, Tony Haymet, Peter Kollman, ID Kuntz, Michael Laskowski, Alenka Luzar, Andy McCammon, Chris Miller, Terry Oas and Eric Toone and their students, Rob Phillips, Miranda Robertson, Kim Sharp, Krista Shipley, Noel Southall, Vojko Vlachy, Peter von Hippel, Hong Qian, Ben Widom, and Bruno Zimm for very helpful comments on this text. We owe special thanks to Jan WH Schreurs, Eugene Stanley, and John Schellman for careful reading and detailed criticism of large parts of various drafts of it. We are grateful to Richard Shafer and Ron Siegel, who in co-teaching this course have contributed considerable improvements, and to the UCSF graduate students of this course over the past several years, who have helped form this material and correct mistakes. We thank Claudia Johnson who created the original course notes manuscript—with the good spirits and patience of a saint. We are deeply grateful to the talented people who worked so hard on book production: Danny Heap and Patricia Monohon who keyboarded, coded, extended and converted the manuscript into this book format; to Jolanda Schreurs who worked tirelessly on the graphics; and to Emma Hunt, Matthew Day and Denise Schanck, who patiently and professionally saw us through to bound books. The preparation of this text was partially funded by a grant from the Polymer Education Committee of the Divisions of Polymer Chemistry and Polymeric Materials of the American Chemical Society.

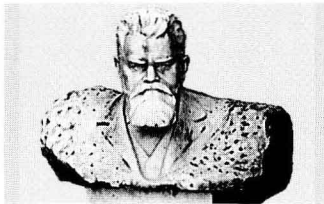
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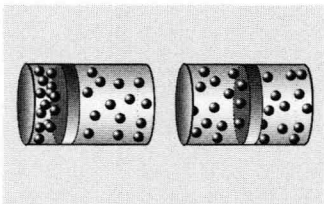




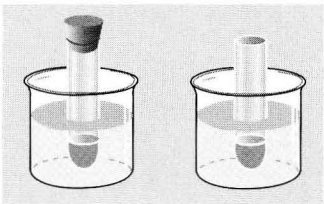
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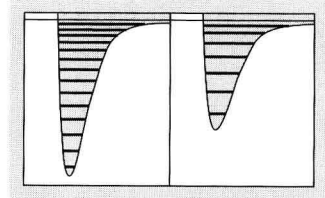
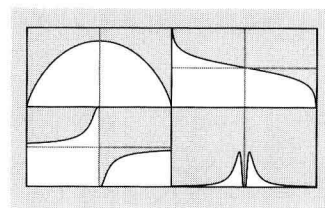
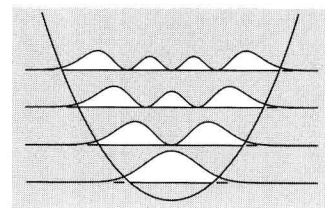
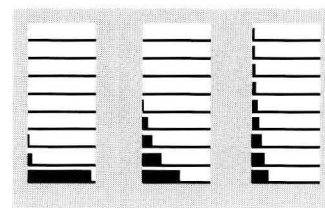
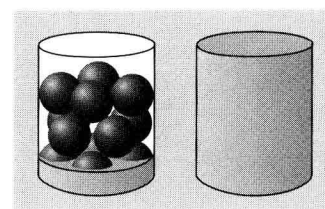


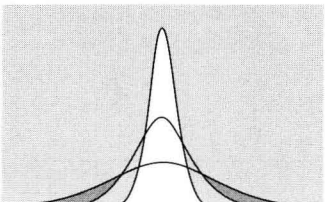
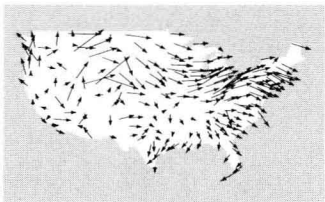
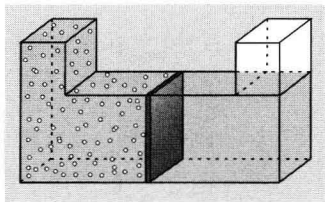
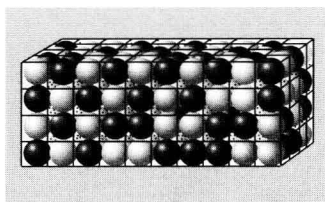
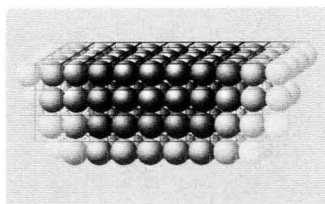
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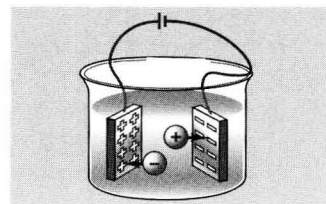
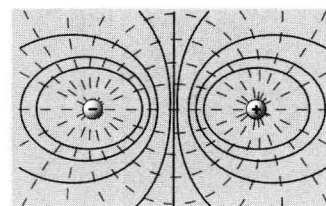
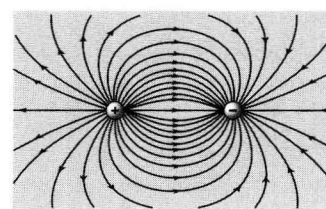
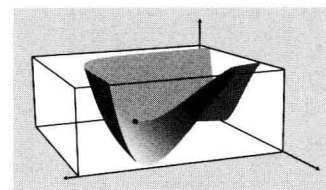
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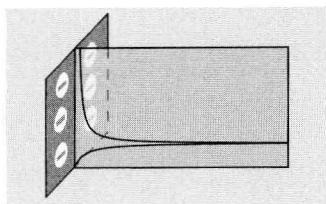




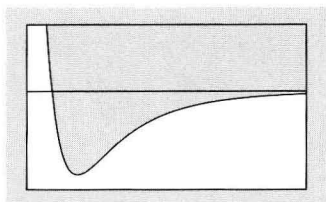
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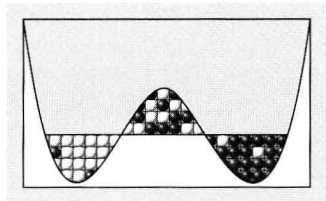




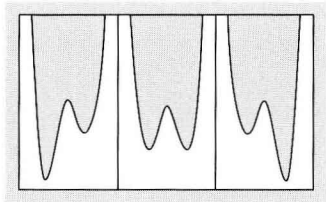
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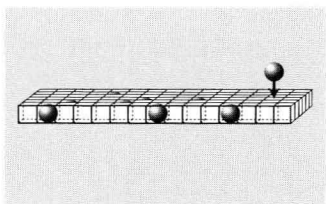
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