

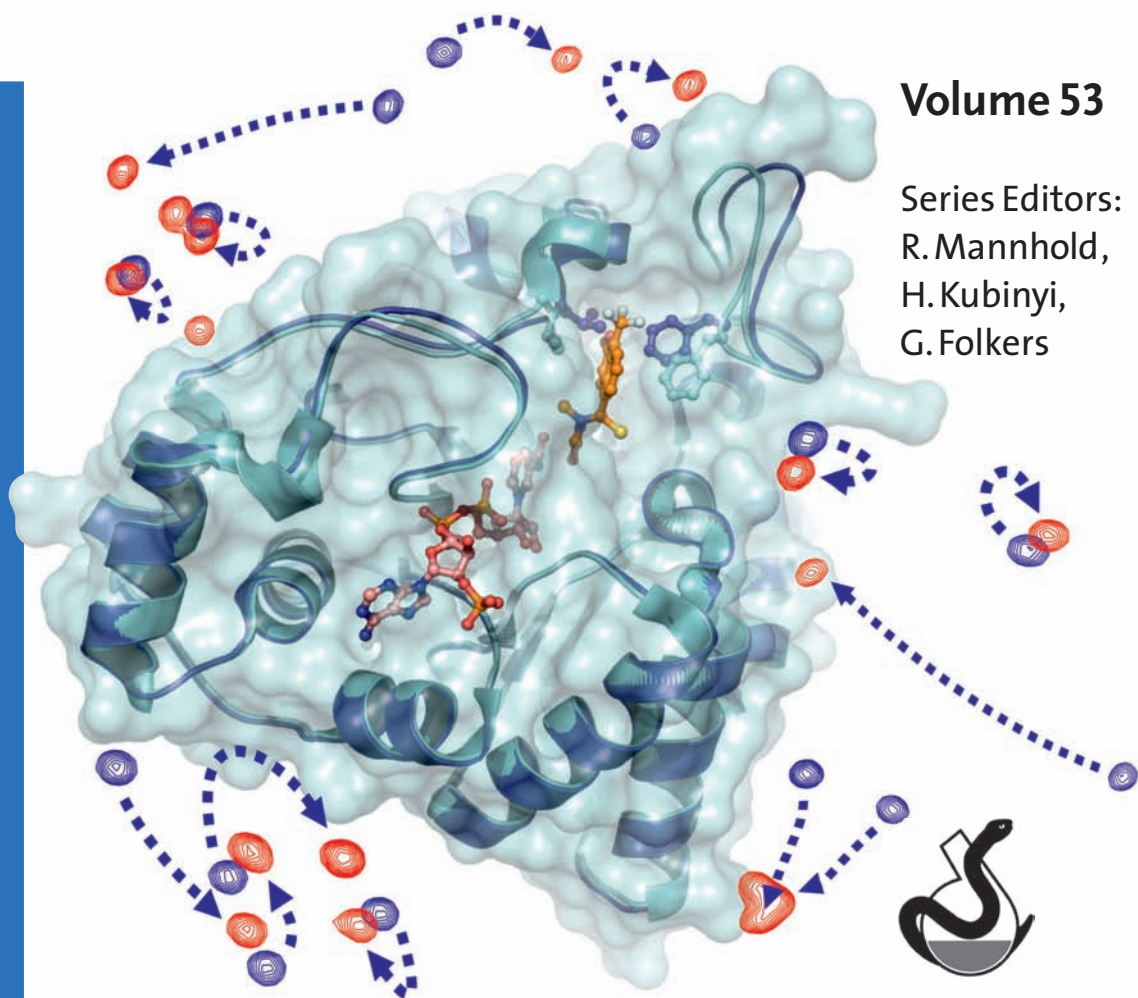
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# Protein-Ligand Interactions

**Volume 53**

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## **Protein-Ligand Interactions**



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#### Cover Description

Aldose reductase bound to NADP (PDB code: 1ads; dark blue) as well as bound to NADP and the inhibitor tolrestat (PDB code: 2fzd; light blue). The protein shows pronounced movements of Phe122 and Leu300 to accomodate hydrophobic parts of the inhibitor. Such movements can be detected by perturbations of NMR chemical shifts, as schematically shown around the protein.

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## Preface

*“Um ein Bild zu gebrauchen, will ich sagen, dass Enzym und Glucosid wie Schloss und Schlüssel zueinander passen müssen, um eine chemische Wirkung aufeinander ausüben zu können”* [To use a picture, I would like to say that enzyme and glucoside have to fit like a lock and a key, in order to exert a chemical action on each other] wrote Emil Fischer in 1894, to illustrate his concept on protein-ligand interactions. Well, our picture of the protein-ligand interaction has developed further. Instead of a rigid fit, the concepts of induced fit and, later, flexible fit were formulated. Indeed, we have to understand the interaction like a handshake, where the one partner adapts to the other, in a mutual fit. Of course, this accommodation should not waste too much conformational energy, otherwise the affinity of the ligand would be significantly reduced. Correspondingly experience shows that compounds where the bioactive conformation is fixed or at least stabilized are most often high-affinity ligands. On the other hand, ligands that cannot achieve such a conformation will have no affinity at all. However, these geometric requirements are only part of the story. In addition, there must be complementary properties - *similia similibus*. Lipophilic groups should find their counterpart, charges or partial charges should have opposite signs, and hydrogen bond donor and acceptor groups should find together. The better this complementarity, the higher will be the affinity, provided that there are no steric clashes. Now, whereas this is a correct description of the requirements of a protein-ligand interaction, it is a very simple one.

Holger Gohlke assembled a team of leading experts in this field to describe not only the thermodynamics of binding but also the underlying biophysical approaches. The major part of the book is devoted to the discussion of factors that are responsible for the intermolecular interactions. Finally some challenges in molecular recognition are discussed. In a logical and didactic way, this volume is organized in four sections. The three introductory chapters review statistical thermodynamics of binding and molecular recognition models, practical rules for the thermodynamic optimization of drug candidates, and the puzzling concept of enthalpy-entropy compensation, as deduced from measurements of temperature dependence. A section on the impact of biophysical experiments focuses, in particular, on interaction kinetic data generated by surface plasmon resonance biosensors as well as NMR methods for the determination of protein-ligand interactions. The central and most comprehensive section is dedicated to aspects of modeling

protein-ligand interactions including polarizable force fields, quantum mechanics in structure-based ligand design, the role of water in hydrophobic association, implicit solvation models and electrostatics in molecular recognition, conformational aspects, free energy calculations in drug lead optimization, as well as scoring functions for protein-ligand interactions. The final section on challenges for protein-ligand interaction modelling considers druggability prediction, protein plasticity, and protein-protein interactions.

The series editors are grateful to Holger Gohlke for his enthusiasm to organize this volume and to work with such a selection of excellent authors. We believe that this book adds a fascinating new facet to our book series on “Methods and Principles in Medicinal Chemistry”. Last, but not least we thank the publisher Wiley-VCH, in particular Frank Weinreich and Heike Nöthe, for their valuable contributions to this project and the entire series.

February 2012  
Düsseldorf  
Weisenheim am Sand  
Zürich

*Raimund Mannhold*  
*Hugo Kubinyi*  
*Gerd Folkers*

## A Personal Foreword

Ever since I started my scientific work I have been fascinated by the questions what makes two molecules bind to each other and how can one make use of this knowledge to modulate biological processes: After all, “*corpora non agunt nisi fixata*”, as Paul Ehrlich put it almost 100 years ago. Ehrlich’s statement that “bodies do not act if they are not bound” is strikingly exemplified by about 130,000 binary interactions in the human protein-protein “interactome” [1]. Along the same lines and more oriented towards the topic of this book, the famous wall chart “Biochemical Pathways” introduced by Gerhard Michal [2] is a vivid picture in the eyes of a life science scientist, with its comprehensive view on metabolic pathways and cellular and molecular processes, particularly involving interactions between proteins and endogenous small-molecules.

For a xenobiotic ligand to exert an influence on an organism, it must bind to a biological target, too. While this statement seems unspectacular nowadays, it still has far-reaching consequences because it provides a valuable handle to explain and predict *biological activity*, both beneficial and detrimental, in terms of *affinity*, a well-defined thermodynamic property, of a ligand towards a (or multiple) targets. In fact, the fields of medicinal chemistry and drug design have made use of different variations of this theme over time depending on which type of information about binding was available in each case.

From an *inductive point of view*, already since the very early days of modern chemistry [3] structures of ligands and, hence, their binding properties, have been correlated to activities. Further milestones on this route were the establishment of quantitative structure-activity relationships and the comparison of ligands based on concepts of similarity or dissimilarity of shape and chemical properties. From a *deductive point of view*, the above theme summons medicinal chemists to look at biological activity from the perspective of processes and contributions that lead to binding, with structural information of the binding partners being of invaluable help. As such, the event of (reversible) binding is a consequence of association and dissociation processes and involves enthalpic and entropic components. If and how these separate processes and components can be modulated by modification of a ligand’s structure for the sake of overall optimized binding properties is a “hot topic” at present in drug research. Furthermore, the deductive point of view allows one to

apply a divide-and-conquer strategy when it comes to understanding and predicting binding from a theoretical perspective. As a first approximation, binding can be attributed to direct interactions between the binding partners mediated by an aqueous environment, to which contributions due to changes in the conformation and configuration of the binding partners add. While this approximation is valuable in that it allows optimizing the description of each of these terms separately, it also provokes the question to what extent does it hold or, phrased differently, when do cooperativity or compensation effects prevail over additivity?

The majority of topics for this book were selected following this deductive point of view, with an emphasis on rigorous approaches because I believe that these will be more successful in the long term than ad hoc ones. The selection also focused on topics that, at that time, had most quickened interests, had seen considerable progress, or had still been major stumbling blocks in the description and prediction of binding. Unsurprisingly, while much has been achieved in all of the covered areas as undoubtedly laid out in each of the chapters, not in all cases have methods or approaches lived up to one's expectations so far. I am grateful to the authors for pointing this out clearly – such insights will drive further developments that aim at improving our understanding of protein-ligand interactions. Finally, I also tried to balance topics related to biophysical experiments against theoretical and computational approaches, because I have learnt from my own work how well both sides can complement and enhance each other, and what joy this gives.

Last but not least, I express my gratitude to all contributors for providing insightful accounts on the topic of protein-ligand interactions, to the series editors Raimund Mannhold, Hugo Kubinyi, and Gerd Folkers for giving me the opportunity to address this topic, to my current working group for providing fruitful comments about the chapters, and to Frank Weinreich and Heike Nöthe from the publisher Wiley-VCH for their continuous support, great help, and even greater patience.

Düsseldorf, Germany

Holger Gohlke

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## **Part I**

### **Binding Thermodynamics**





## 1

## Statistical Thermodynamics of Binding and Molecular Recognition Models

*Kim A. Sharp*

## 1.1

### Introductory Remarks

Equilibrium binding or association of two molecules to form a bimolecular complex,  $A + B \rightleftharpoons AB$ , is a thermodynamic event. This chapter will cover some of the fundamental thermodynamics and statistical mechanics aspects of this event. The aim is to introduce general principles and broad theoretical approaches to the calculation of binding constants, while later chapters will provide examples. Only the noncovalent, bimolecular association under ambient pressure conditions will be considered. However, extension to higher order association involves no additional principles, and extension to high pressure by inclusion of the appropriate pressure–volume work term is straightforward. In terms of the binding reaction above, the association and dissociation constants are defined as  $K = [AB]/[A][B]$  and  $K_D = [A][B]/[AB]$  respectively, where  $[]$  indicates concentration. Either  $K$  or  $K_D$  is the primary experimental observable measured in binding reactions.  $K_D$  is sometimes obtained indirectly by inhibition of binding of a different ligand as a  $K_i$ . From a thermodynamic perspective, the information content from  $K$ ,  $K_D$ , and  $K_i$  is the same.

## 1.2

### The Binding Constant and Free Energy

To connect the experimental observable  $K$  to thermodynamics, one often finds in the literature the relationship

$$\Delta G_{\text{bind}} = -kT \ln K, \quad (1.1)$$

where  $k$  is the Boltzmann constant,  $T$  is the absolute temperature, and  $\Delta G_{\text{bind}}$  is the “absolute” or “standard” binding free energy. Several comments are given to avoid misuse of this expression. First, one cannot properly take the logarithm of a quantity with units such as  $K$ , so Eq. (1.1) is implicitly

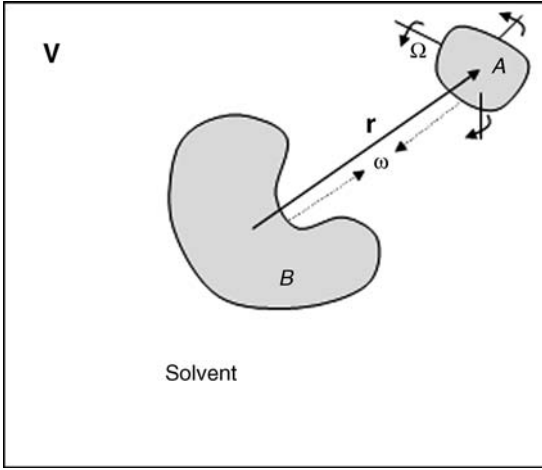
$$\Delta G_{\text{bind}} = -kT \ln \frac{K}{V_{\text{ref}}}, \quad (1.2)$$

where  $V_{\text{ref}}$  is the reference volume in units consistent with the units of concentration in  $K$ , that is, 1 l/mol or about  $1660 \text{ \AA}^3$ /molecule for molarity units. The choice of  $V_{\text{ref}}$  is often referred to as the “standard state” problem. Equivalently, one says that  $\Delta G_{\text{bind}}$  is the free energy change when reactants A and B and the product AB are all at the reference concentration. Second, although the units of concentration used in  $K$  are almost always moles/liter, this is entirely a *convention*, so the actual numerical value for  $\Delta G_{\text{bind}}$  obtained from Eq. (1.2) is arbitrary. Put another way, any method for calculating the free energy of binding must explicitly account for a particular choice of  $V_{\text{ref}}$  before it can meaningfully be compared with experimental values of  $\Delta G_{\text{bind}}$  obtained using Eq. (1.2). Furthermore, ligand efficiency-type measures, such as  $\Delta G_{\text{bind}}/n$  where  $n$  is the number of heavy atoms in a ligand or the molecular weight of a ligand [1], can change radically with (arbitrary) choice of concentration units. Of course, differences in  $\Delta G_{\text{bind}}$  can be sensibly compared provided the same reference state concentration is used. Finally, in Eq. (1.2), the free energy actually depends on the ratio of activities of reactants and products, not on concentrations. For neutral ligands and molecules of low charge density at less than micromolar concentrations, the activity and concentration are nearly equal and little error is introduced. However, this is not true for high charge density molecules such as nucleic acids and many of the ligands and proteins that bind to nucleic acids. Here, the activity coefficient can be substantially different from unity even at infinitely low concentration. Indeed, much of the salt dependence of ligand–DNA binding can be treated as an activity coefficient effect [2–4]. The issue of standard state concentrations, the formal relationship between the binding constant and the free energy, and the effect of activity coefficients are all treatable by a consistent statistical mechanical treatment of binding, as described in Section 1.3.

### 1.3

#### A Statistical Mechanical Treatment of Binding

Derivation of a general expression for the binding constant follows closely the approach of Luo and Sharp [5], although somewhat different treatments using chemical potentials, which provide the same final result, are given elsewhere [6–8]. It is a statistical mechanical principle that any equilibrium observable can be obtained as an ensemble, or Boltzmann weighted average, of the appropriate quantity. Here, the binding constant  $K = [AB]/[A][B]$  is the required observable. Consider a single molecule each of A and B in some volume  $V$  (Figure 1.1) and for convenience define a coordinate system centered on B (the target) in a fixed orientation. Over time, the ligand (A) will explore different positions and orientations (poses) relative to B, where  $\mathbf{r}$  and  $\Omega$  represent the three position and three orientation coordinates of A with respect to B. Now A and B interact with each other with an energy that depends not only on their relative position ( $\mathbf{r}, \Omega$ ) but in general also on the conformations of A, B, and the surrounding solvent. If  $n_a, n_b, n_s$  are the number of atoms in A, B, and solvent, then the energy is a function of  $3n_a + 3n_b + 3n_s - 6$  coordinates. In principle, one could keep all these degrees of freedom explicit. From a



**Figure 1.1** Schematic illustration of two molecules A and B interacting through solvent with a potential of mean force  $\omega$  as a function of their relative position  $\mathbf{r}$  and orientation  $\Omega$ .

practical standpoint, this would be a complicated and expensive function to evaluate. However, one may integrate over the solvent coordinates and the  $(3n_a - 6) + (3n_b - 6)$  internal coordinates so that the interaction between A and B for a given  $(\mathbf{r}, \Omega)$  is described by an interaction potential of mean force (pmf)  $\omega(\mathbf{r}, \Omega)$ . If one defines the pmf between A and B at infinite separation in their equilibrium conformations to be 0, then  $\omega(\mathbf{r}, \Omega)$  is the thermodynamic work of bringing A and B from far apart to some mutual pose  $(\mathbf{r}, \Omega)$ , accounting for both solvent effects and internal degrees of freedom of A and B. A will sample each pose  $(\mathbf{r}, \Omega)$  with a probability given by the Boltzmann factor of the pmf:

$$p(\mathbf{r}, \Omega) \propto e^{-\beta\omega(\mathbf{r}, \Omega)}, \quad (1.3)$$

where  $\beta = 1/kT$ . Indeed, one may consider the pmf to be defined by this equation. The binding constant will then be given by the fraction of time A is in the bound state,  $f_{ab}$ , relative to that in the free state,  $f_f$ :

$$K = \frac{[AB]}{[A][B]} = \frac{f_{ab}/V}{(f_f/V)(f_f/V)} \xrightarrow{V \rightarrow \infty} f_{ab}V, \quad (1.4)$$

where in the dilute limit  $f_f \rightarrow 1$ . It is convenient to introduce a function  $H(\mathbf{r}, \Omega)$  that takes a value of 1 for poses where A is bound and a value of 0 when it is free. Then, the fraction of the time A is bound is given by the ensemble average of  $H$ :

$$f_{ab} = \int d\mathbf{r} d\Omega H(\mathbf{r}, \Omega) e^{-\beta\omega(\mathbf{r}, \Omega)} / \int d\mathbf{r} d\Omega e^{-\beta\omega(\mathbf{r}, \Omega)}. \quad (1.5)$$

The integrals are taken over all orientations and over the entire volume of the solution, so the denominator gives  $8\pi^2V$ . Substituting into Eq. (1.4), the final expression for the association constant is

$$K = \frac{1}{8\pi^2} \int d\mathbf{r} d\Omega H(\mathbf{r}, \Omega) e^{-\beta\omega(\mathbf{r}, \Omega)}. \quad (1.6)$$

One may then convert this to an “absolute” binding free energy using Eq. (1.2):

$$\Delta G_{\text{bind}} = kT \ln(8\pi^2 V_{\text{ref}}) - kT \ln \int d\mathbf{r} d\Omega H(\mathbf{r}, \Omega) e^{-\beta\omega(\mathbf{r}, \Omega)}. \quad (1.7)$$

- Equation 1.6 is a general and exact expression for the association constant. The integral depends explicitly on just six variables describing the pose of A with respect to B. The other degrees of freedom are included implicitly, but exactly through the thermodynamic quantity  $\omega(\mathbf{r}, \Omega)$ , the potential of mean force.
- The different treatment of coordinates for translation/orientation versus the others is a formal one: Any subset of coordinates may in principle be kept explicit, with the appropriate pmf being used for the rest. For example, one may keep the internal coordinates of A and B explicit, making the solvent coordinates implicit. The choice here is designed to highlight the translation/rotation contribution to binding that has been widely discussed, with some disagreement, in the literature [5, 6, 9–13]. It also reflects the practical fact that in many docking and screening applications, a particular pose is generated explicitly, that is,  $(\mathbf{r}, \Omega)$  is specified, and then the pose is “scored” in some way. The pmf also provides a natural way to introduce approximations necessary for any practical calculation of  $K$  in biological systems, for example, in the treatment of solvent.
- The integral has the correct units of volume, with the length scale for the translation coordinates being determined by the units of concentration used in  $K$ . The first term in Eq. (1.7) is the contribution of the rotation/translation (R/T) entropy in the unbound state, which depends on the reference concentration. The integral term in Eq. (1.6) is the Boltzmann phase volume of the bound state.
- Through  $H(\mathbf{r}, \Omega)$ , there is explicit consideration of what constitutes the bound complex, in terms of the relative position and orientation of A with respect to B. For example, if B has more than one binding site for A, this would be taken into account in the specification of where  $H = 1$ .
- Either Cartesian coordinates or the bond length, bond angle, and dihedral angle coordinates may be used. The trend now is toward the latter, as they lend themselves more naturally to the analysis of different internal motions of the molecules and their contribution to binding.

The meaning of Eq. (1.6) is illustrated by two simple examples.

### 1.3.1

#### Binding in a Square Well Potential

Let the pmf be approximated by a simple, three-dimensional square well potential of depth  $\varepsilon$  and width  $b$  in each of the  $x$ ,  $y$ ,  $z$  directions and the bound complex be the region in the well only. From Eq. (1.6), the association constant is

$$K = b^3 e^{\beta \varepsilon} \quad (1.8)$$

and Eq. (1.2) yields

$$\Delta G_{\text{bind}} = -\varepsilon + kT \ln(V_{\text{ref}}/b^3). \quad (1.9)$$

The first term, the well depth, makes a direct, linear contribution to the binding free energy. The second term is positive and comes from the restriction of the ligand to the square well. It is the translation entropy penalty for binding, and it depends on the ratio of the volumes available to the ligand in the free state at say 1 M (the entire volume  $V_{\text{ref}}$ ) versus that in the bound state. In this simple example, there is no rotational entropy penalty because in the bound state the ligand can rotate freely in  $8\pi^2$  of orientation phase volume, just as in the free state. However, restriction in rotation in the bound state will add another positive term to  $\Delta G_{\text{bind}}$ , the rotation entropy penalty, with a similar form:  $kT \ln(8\pi^2/V_{\Omega})$ , where  $V_{\Omega} < 8\pi^2$  is the orientation phase volume in the bound state. We can see even from this simple example that for any meaningful degree of binding, the translational and rotational phase volumes available to a ligand in the bound state must be less than  $V_{\text{ref}}$  and  $8\pi^2$ , respectively, so there is *always* a R/T entropy penalty to be overcome for binding to occur. The question is how much is it in specific cases. A related point is that even though the depth of the well may be known, for example, from some calculation (in the parlance of the field, from a single point energy determination), this cannot be directly compared with  $\Delta G_{\text{bind}}$  because the second term is not included. The numerical value of the binding free energy depends on the reference concentration, which is nowhere in the single point calculation. One way or another, the residual R/T entropy of A in the bound state must be accounted for.

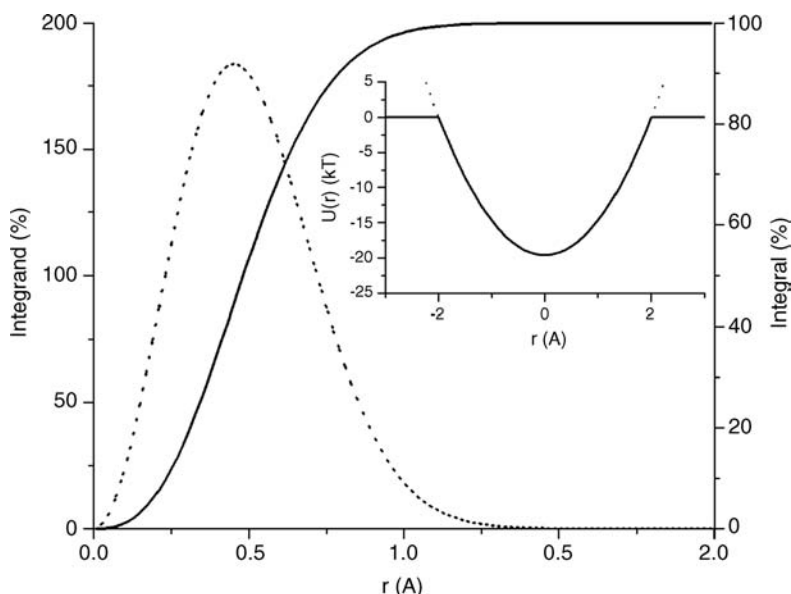
### 1.3.2

#### Binding in a Harmonic Potential

If one is starting from a known complex structure derived from, for example, X-ray, NMR, or molecular mechanics minimization, one is presumably close to the minimum energy (pmf) configuration. The pmf in this region may be close to harmonic or at least expandable in a Taylor expansion, which to second order is harmonic. It is, therefore, instructive to consider binding in a harmonic potential, although this is a simplified model of the real situation. Let the potential well be a three-dimensional harmonic potential of the form

$$\omega(r) = \varepsilon \left( \left( \frac{r}{b} \right)^2 - 1 \right) (r < b), \quad \omega(r) = 0 (r \geq b), \quad (1.10)$$

where  $\varepsilon$  is the depth of the well at the minimum,  $r$  is the radial distance from the minimum, and  $b$  defines the width so that for  $r \geq b$ ,  $\omega = 0$  (Figure 1.2). Again, the bound complex is defined to be the region in the well only. Substituting Eq. (1.10) into Eq. (1.6) and integrating, the association constant for this truncated harmonic potential is



**Figure 1.2** Contributions to the binding-phase integral. *Dotted line*: Value of the integrand of Eq. (1.6) at  $r$ . *Solid line*: Value of the resulting integral from 0 to  $r$ . Both are expressed as a percentage of the total association constant.

Contributions were calculated for a truncated three-dimensional harmonic well potential, half-width  $2 \text{ \AA}$ , and depth  $19.6 kT$  (inset) that has  $K_d = 10 \mu\text{M}$ .

$$K = b^3 e^{\beta\epsilon} \left( 4\pi \sum_{n=0}^{\infty} \frac{-1^n (\beta\epsilon)^n}{(2n+3)n!} \right) \approx b^3 e^{\beta\epsilon} \left( \frac{\pi}{\beta\epsilon} \right)^{3/2}. \quad (1.11)$$

The approximate equality comes from using an untruncated harmonic potential (i.e., the potential goes to infinity as the complex is dissociated), which for this case gives a binding free energy of

$$\Delta G_{\text{bind}} = -\epsilon + kT \ln(V_{\text{ref}}/b^3) - 3/2 kT \ln(\pi/\beta\epsilon). \quad (1.12)$$

Comparing the square well and harmonic potential models, one sees that the “depth” and “volume” factors,  $e^{\beta\epsilon}$  and  $b^3$ , contribute in the same way to the binding constant, the difference being a “well shape” factor. We see from the form of the expression for the association constant that the lower the pmf, the more the contribution to the integral by that region, so most of the contribution to binding should come from the near minimum energy configuration. This is illustrated in Figure 1.2, using a well half-width of  $2 \text{ \AA}$  and a depth of  $19.6 kT$ . These parameters are chosen to give a moderate affinity of  $10 \mu\text{M}$  – typical of the compounds studied by virtual screening and docking calculations in early lead identification – with a reasonable degree of motion in the binding pocket. It can be seen that almost all the contribution to the binding constant comes significantly before reaching the well boundary. Thus, the problem of giving the exact definition of the complex in