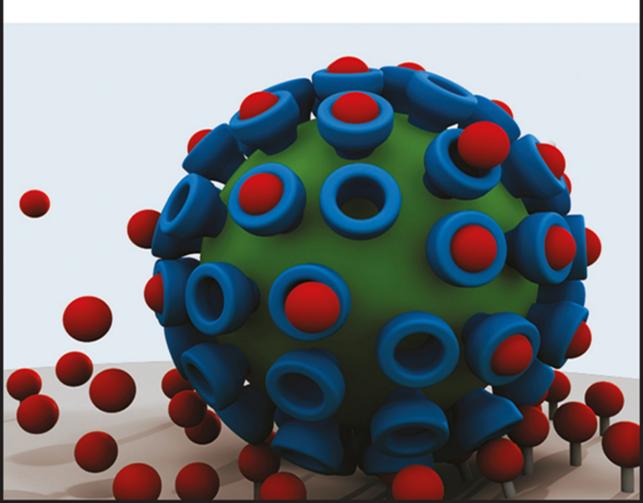


Edited by Jurriaan Huskens, Leonard J. Prins, Rainer Haag, Bart Jan Ravoo

Multivalency

Concepts, Research & Applications





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Foreword

Scientific challenges come and go; only a few of them remain for a long time. Multivalency is one of those research topics that has been prominent for many years, as this intriguing phenomenon is of profound importance in many biological processes as well as very difficult to understand and mimic. Personally, I became intrigued by the challenge of multivalency when our group entered the field of dendrimers in 1990. The controlled number of end groups – 4, 8, 16, 32, and 64 amines of the polypropylene imines – opened many opportunities for us to explore the controlled use of multiple interactions. However, our ideas were more simple than our experiments in making full use of the potential of multivalency; many of them remained in the realm of dreaming. The broad potential of multivalency as well as its complex mode of action was beautifully illustrated by George Whitesides and coworkers [1] in the seminal *Angewandte Chemie* review paper in 1998. Their review initiated a world-wide search for synthetic mimics of these highly effective natural systems, a search that turned out to be long lasting.

Nature uses both similar interactions (homovalency) and different interactions (heterovalency) to control selectivity and specificity, even leading to ultra-sensitivity. Beautiful examples are found in substrate—cell interactions and immunology. Ever since this elegant mechanism and its importance in biological systems has been recognized, chemists have been intrigued to fully understand the enhancement factors obtained in binding multiple weak interactions through multivalency. Artificial systems are designed, synthesized, and studied, while a number of applications are proposed. Multivalent medication can have lower toxicity while simultaneously having higher medical efficacy.

Although the knowledge on the modus operandi of these systems has increased significantly in time and the systems synthesized have become more active, the full potential of the proposed applications remains. Hence, a number of challenging questions need to be answered before the potential of this intriguing concept can be explored. How to design the ideal structure to arrive at the theoretical maximum avidity and how to obtain scaling with valency are just a few of these intriguing questions. Theoretical and experimental studies of multivalent systems have revealed several design parameters that are critical in obtaining effective multivalent constructs. Next to the binding affinity, linker flexibility plays an important role, as rigid linkers require extremely precise ligand positioning to obtain high binding affinities and selectivity, while flexible linkers offer more freedom in molecular design at the cost of lower affinity and selectivity. Furthermore, additional competing equilibria can be used to enhance binding

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selectivity or to steer an assembly towards a preferred state. However, the complexity of all these effects and their interference makes the field one of the most challenging areas in the molecular sciences.

Therefore, it is great to see that four outstanding scientists have edited a book on the intriguing topic of multivalent interactions. It is a book full of excellent chapters written by the most active experts in the field, covering all aspects of multivalent interactions with special emphasis on theory, synthesis, surfaces, chemical biology, and supramolecular chemistry. I am convinced that this book will be a great asset for all active in this intriguing field of science.

Eindhoven, May 2017

E.W. Meijer

Reference

1 Mammen, M., Choi, S.-K., Whitesides, G. M. Polyvalent interactions in biological systems: Implications for design and use of multivalent ligands and inhibitors. *Angew. Chem. Int. Ed.* **1998**, *37*, 2754–2794.

Preface

Multivalent interactions play a role in molecular and biomolecular systems in which molecules interact by multiple noncovalent bonds. Studying and describing these interactions in a quantitative manner constitute therefore an important way to obtain insight into the functional behavior of the biological and chemical systems in which they are involved. Over the past decades, the research of multivalent interactions has greatly expanded. This growth fits in the overall trends observed in the natural sciences which encompass the merging and overlapping of disciplines, like the biology and chemistry involved here. It also aligns with the emphasis on the study of complex systems, and the development of systems biology and systems chemistry, for example. Therefore, we have observed the need for a book that brings together fundamental aspects of multivalent interactions and relevant current examples of biological as well as chemical multivalent systems.

The disciplines of chemistry and biology are strongly represented in this area of science because they exert a mutual influence on both the understanding of fundamental aspects of multivalency as well as the development of practical research tools and applications. In biology, multivalent interactions play an eminent role in the immune system, but at the same time also describe the interactions between a virus and the host cell which the virus tries to infect. Tools from chemistry and nanotechnology are being developed that assist in studying such complex biological systems, for example, by synthesizing model cell membranes in which the interactions can be studied in a more controllable fashion. Likewise, probe techniques allow quantification of interactions at the single molecule level in individual cells. Conversely, the increase in understanding of the biomolecular interactions in living systems sparks the generation of new types of drugs and inhibitors that can make smart use of the multivalent character to improve both selectivity and activity.

A quantitative understanding of multivalent interactions is essential to promote progress in the field that deals with multivalent systems. Both experimental techniques as well as modeling can be used to stimulate this depth of understanding. Therefore, we decided that chapters with a strong educational character should be an essential part of this book. We present a section (Part I) of four chapters that serve to guide new researchers as well as more experienced researchers in their efforts to contribute to this lively area. These chapters provide a background in thermodynamics, data modeling and the description of multivalent equilibrium systems, numerical modeling of multivalent systems and superselectivity, and an introduction to multivalent biological systems. These chapters build on, and for some aspects briefly review, knowledge that most readers

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with a background in chemistry or biology will have encountered in their regular academic education, but from there quickly integrate this knowledge into the description of multivalent systems.

Another explicit aim of the book is to expose the active nature of the research on multivalent systems. This is achieved in the two other sections of the book (Parts II and III), dealing with chemical and biological examples of multivalency, respectively. In the chemistry oriented chapters, timely topics such as the host–guest interactions of cyclodextrins and cucurbiturils are covered, as well as soft matter systems, such as vesicles, polymers, and nanoparticles. Not only equilibrium thermodynamics is shown, but also systems in which multivalent interactions control catalysis. In the more biological section, several biological interactions are put forward, such as protein–protein and lectin–glycan interactions. The strong connection between chemistry and biology in this area is emphasized by the examples that describe cell targeting by molecules and nanoparticles, as well as receptor inhibition by multivalent inhibitors.

We hope that this book will serve a need, for new and experienced researchers alike, both for those requiring a deeper understanding as well as those that try to get an overview of existing activities in the field. We thank all contributing authors for their efforts in summarizing and describing their research and that of others, as their joint work makes this book so much more than the individual chapters alone. We also express our gratitude to the Wiley staff for smoothing the pathway for the book that lies before you.

September 2017

Jurriaan Huskens, Leonard J. Prins, Rainer Haag, and Bart Jan Ravoo Part I

General Introduction to Multivalent Interactions

1

Additivity of Energy Contributions in Multivalent Complexes

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1.1 Introduction

Additivity of individual binding contributions is the very basis of multivalency. In classical coordination chemistry such simultaneous actions are described as the chelate effect. They offer almost unlimited ways to enhance the affinity [1,2,3,4,5,6], and therefore within certain limitations also the selectivity [7] of synthetic and natural complexes. Although additivity is often implied in experimental and theoretical approaches it is subject to many limitations which will be also discussed in the present chapter.

1.2 Additivity of Single Interactions – Examples

If only one kind of interaction is present in a complex one can expect a simple linear correlation between the number n of the individual interaction free energies $\Delta\Delta G_i$ and the total ΔG_t (Equation 1.1), as illustrated in Figure 1.1 for salt bridges [8]. Even though the organic ion pair complexes are based on cations and anions of very different size and polarizability one observes essentially additive salt bridges; the slope of the correlation indicates an average of $\Delta\Delta G = (5\pm1)$ kJ/mol per salt bridge. The value of (5 ± 1) kJ/mol is observed in usual buffer solution, but varies as expected from the Debye–Hückel equation with the ionic strength of the solution [9]. Scheme 1.1 shows a corresponding value of $K \approx 10\,\mathrm{M}^{-1}$ per salt bridge for typical complexes where the affinity depends as expected on the degree of protonation [7].

$$\Delta G_{\rm t} = n \cdot \Delta \Delta G_{\rm i} \tag{1.1}$$

The additivity depicted in Figure 1.1 and Scheme 1.1 for salt bridges is in line with the Bjerrum equation, which describes ion pair association as a function of the ion charges z_A and z_B ; Figure 1.2 shows for over 200 ion pairs a linear dependence of log K vs. $z_A z_B$ [3]. For inorganic salts one finds similar $\Delta\Delta G$ values of 5–6kJ/mol per salt bridge and a similar dependence on charges [10]. At zero ionic strength the stability decreases in the

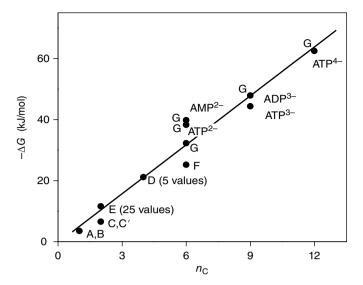
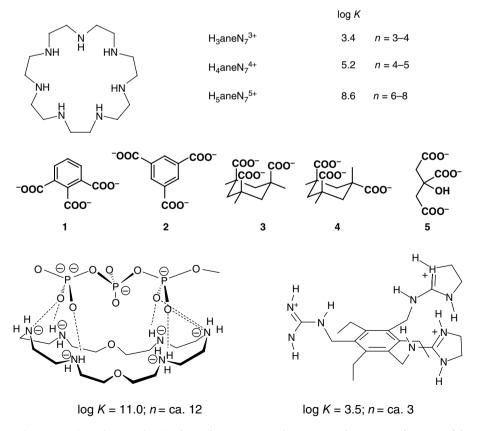


Figure 1.1 Additive ion pair contributions in a variety of complexes with a number n_C of salt bridges. From slope: average (5 ± 1) kJ/mol per salt bridge. A,B and C,C' – complexes of a tetraphenolate cyclophane (4-) with Me₄N⁺ and an azoniacyclophane (4+) with mono- and dianionic naphthalene derivatives; D – anionic (sulfonate or carboxylate) with cationic (ammonio) triphenylmethane derivatives; E – organic dianions with organic dications; F – cationic azamacrocycle (6+ charges) with aliphatic dicarboxylates; G – cationic azacrowns with adenosine mono-, di- and triphosphates. *Source*: Ref. [8]. Reproduced with permission of John Wiley and Sons.



Scheme 1.1 Complexation $\log K$ values of anions **1–5** with a macrocyclic amine as function of the degree of protonation of the amine; and ion pairing with some representative complexes; $\log K$ values in water; n is the estimated number of salt bridges.

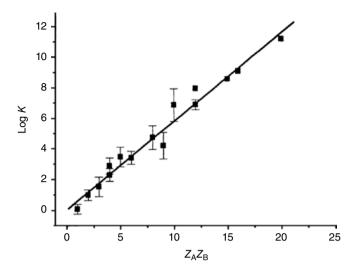


Figure 1.2 Ion pair association constants at zero ionic strength as a function of charge product, calculated for 203 ion pairs. Source: Ref. [8]. Reproduced with permission of John Wiley and Sons.

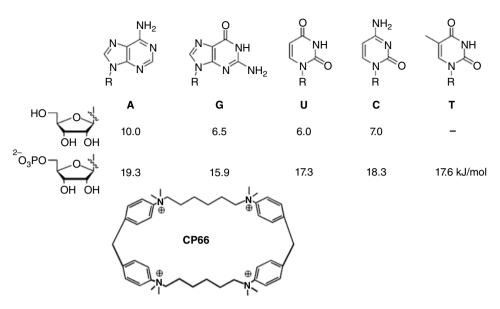
order $Ca^{2+} > Mg^{2+} > > Li^+ > Na^+ > K^+$ and can be described by Equation 1.2 [11]. Additivity is observed although ion pairing in water is determined entirely by entropic contributions[11], unless other contributions dominate [12].

$$\log K = 0.5z + A/z$$
 (where A = -0.24 for Li⁺, -0.30 for Na⁺, -0.43 for K⁺) (1.2)

If there is more than one kind of interaction, Equation 1.3 applies. Often however, only one of the contributions is the same, like salt bridges in complexes of nucleotides with a positively charged host (Scheme 1.2) [13]. Additivity is then observed by the constant stability difference of $2 \times \Delta \Delta G \approx 10 \text{ kJ/mol}$ between complexes with charged nucleotides and neutral nucleosides. The 10kJ/mol reflects the presence of two salt bridges between the phosphate dianion and the host ammonium center, which agrees with structural analyses by NMR spectroscopy.

$$\Delta G_{t} = n \cdot \Delta \Delta G_{A} + m \cdot \Delta \Delta G_{B} \tag{1.3}$$

The complexes shown in Scheme 1.2 exhibit constant single $\Delta\Delta G_A$ values only for the salt bridges, whereas the second contribution $\Delta \Delta G_{\mathrm{B}}$ varies as a function of the different nucleobases. Figure 1.3 illustrates a case where both $\Delta\Delta G_A$ and $\Delta\Delta G_B$ remain constant, the latter reflecting cation- π interactions. In principle one could use Equation 1.3 to derive both $\Delta\Delta G_A$ and $\Delta\Delta G_B$, but more reliable values are obtained if for one interaction a $\Delta\Delta G$ value is used which is known from independent analyses, such as $\Delta \Delta G_A = 5 \text{ kJ/mol}$ for each salt bridge (see above). Then one observes a rather linear correlation with the number of phenyl units which shows a contribution of $\Delta \Delta G_{\rm B} \approx 1.5 \,\text{kJ/mol}$ for the single $^{+}\text{N} - \pi$ interaction [14].



Scheme 1.2 Complexation free energies ΔG of nucleotides and nucleosides with the cyclophane CP66.

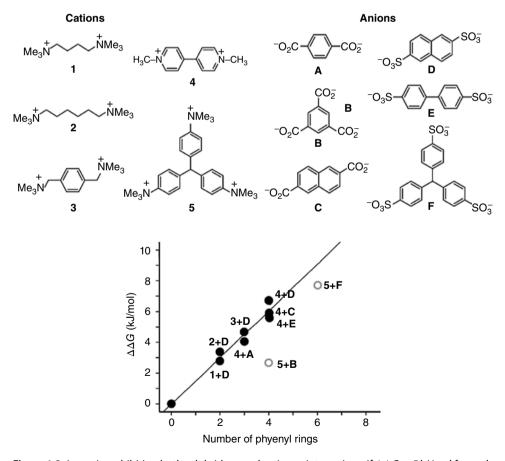


Figure 1.3 Ion pairs exhibiting both salt bridges and cation– π interactions; if $\Delta\Delta G_A = 5$ kJ/mol for each salt bridge are subtracted from ΔG_t of each complex. Outliers (open circles) are due to conformational mismatch. *Source*: Ref. [14]. Reproduced with permission of American Chemical Society.

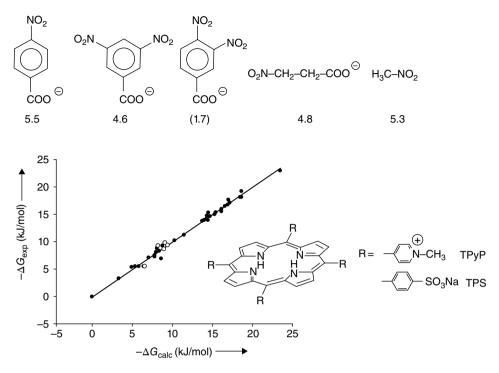


Figure 1.4 Additive $\Delta \Delta G_X$ increments in complexes of porphyrins bearing cationic or anionic substituents R in meso position (TPyP or TPS) in water, after deduction of 5 kJ/mol for ion pair contribution where applicable. $\Delta \Delta G_X$ increments in TPyP complexes for nitro substituents as an example (deviation for ortho-dinitro due to steric hindrance); correlation between measured complexation energies $\Delta G_{\rm exp}$ and $\Delta G_{\rm calc}$ calculated on the basis of experimentally determined averaged single contributions $\Delta G_{\rm S}$. Filled circles, complexes with TPyP; open circles, complexes with TPS. Source: Ref. [15]. Reproduced with permission of John Wiley and Sons.

The effect of nitro substituents on dispersive interactions is another example of additive energy contributions (Figure 1.4) [15,16]. Additivity with respect to substituent effects is observed in Hammett-type linear free energy relationship correlations; Figure 1.5 shows an example for hydrogen bonds with C—H bonds as donor and with hexamethylphosphoramide as acceptor [17].

1.3 Limitations of Additivity

1.3.1 Free Energy Values ΔG Instead of Enthalpic and Entropic Values ΔH , $T\Delta S$

The examples shown above as well as most others in the literature rely on free energy values ΔG , although consideration of the corresponding ΔH and $T\Delta S$ parameters could shed more light on the underlying binding mechanisms. As pointed out earlier by Jencks, the empirical use of ΔG "avoids the difficult or insoluble problem of interpreting observed ΔH and $T\Delta S$ values for aqueous solution" [18]. Furthermore, according to Jencks, there

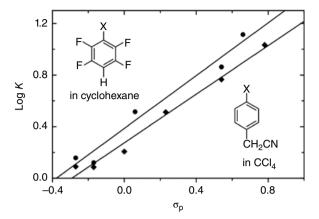


Figure 1.5 Hammett-type correlation of equilibria of hydrogen bonds with hexamethylphosphoramide as acceptor and para-substituted tetrafluorobenzenes or phenylacetonitriles as donor; log *K* versus Hammett substituent constants. *Source*: Ref. [17]. Reproduced with permission of John Wiley and Sons.

is often an additional "connection Gibbs energy, ΔG_S " (Equation 1.4) which he ascribed largely to changes in translational and rotational entropy. These connection ΔG_S can be either negative or positive and will be discussed as major liming factors for additivity below in the context of cooperativity and allostery.

$$\Delta G_{\rm t} = \Delta G_{\rm A} + \Delta G_{\rm B} + \Delta G_{\rm S} \tag{1.4}$$

The success of using free energy values instead of enthalpic and entropic values is in an essential part due to entropy—enthalpy compensation which has empirically been found to hold with many complexations, although it is theoretically not well-founded [19,20,21]. Another factor is that in typical supramolecular complexes the loss of translatory freedom is already paid by a single association step. The loss of rotational freedom upon complex formation has been experimentally [9] found to be smaller than theoretically expected (see below).

Entropy contributions pose particular problems, not only for the precise experimental determination, which in the past often relied on the temperature dependence of equilibrium constants (the *Van 'tHoff* method) instead of on more reliable calorimetry techniques. Also their theoretical interpretation is hampered by several factors, for instance because ΔS values depend on the choice of the standard concentration, in contrast to ΔH [8]. Configurational entropy, which refers also to solute motions has been addressed in several papers [22,23,24]. Data for the loss of translatory degrees of freedom in complex formation range from $T\Delta S=3$ to 9kJ/mol, and depend also on the reaction medium [25]. In multivalent associations this $T\Delta S$ penalty plays, as mentioned above, a minor role as it is paid already by a single interaction. For the loss of rotatory degrees of freedom in complex formation values from $T\Delta S=1.5$ to 6kJ/mol were proposed [26], which also should depend on the nature of the bond involved in the rotation [27]. Measurements of complexes involving an increasing number n of single bonds between two binding units furnished values of only $\Delta \Delta G=0.5$ to 1.3kJ/mol per single bond (e.g. from the slope in Figure 1.6) [9,28]. Similar small numbers have been found in

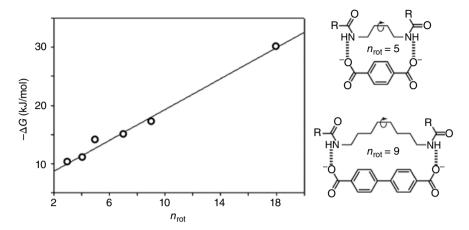
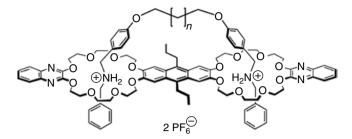


Figure 1.6 Free energies of complex formation between α , ω -diamides and α , ω -dicarboxylates in CHCl₃ as a function of the number of rotatable single bonds (n_{rot}) between the terminal amide and carboxylate functions. *Source*: Ref. [28]. Reproduced with permission of VCH/Wiley.

complexes involving peptide- ß-sheets [29], with calcium-EDTA complexes [30], and for example in the coordination of nickel or copper with either *trans*-1,2-diaminocyclohexane or the more flexible ethylene diamine [31]. In line with these rather small numbers it has been found that preorganization of a linker in host molecules has no or a small effect on supramolecular effective molarities [32,33].

1.3.2 Mismatch as Limitation of Additivity

The most obvious limitation for additivity of non-covalent interactions and therefore also for the lock-and-key principle is the necessary geometric fit between host and guest [34]. Insufficient fit between receptor and ligand is a major factor, in particular for a conformationally more rigid polyvalent entity [1]. The steric requirements for an optimal binding between host and guest depend on the nature of the non-covalent bonds. In particular, electrostatic interactions fall off with only with r^{-1} between binding sites whereas dispersive interactions fall off with r^{-6} . In addition, the latter interactions have no or only a small directional dependence, whereas for example the strength of hydrogen or halogen bonds depends on the orientation of donor and acceptor. Exceptions are molecular containers [35] in which the binding of substrates is in most cases controlled by the size of the portals. However, here as in other supramolecular complexes another important restriction is the presence of solvent molecules in a ligand-containing cavity, so that the guest molecule can only use a limited number of interactions which are possible, again depending on the binding mechanism. Thermal motions as well as vibrational and translatory freedom of movement of host and guest are also responsible for the limited fitting; moreover, the surfaces of interacting molecules are characterized by corners and dimples. Recent studies with cryptophanes composed of two bowl-shaped cyclotriveratrylene units showed large solvent molecules such as tetrachloroethane inside the cavity [36]. It has been found earlier [37] that for example some cryptophanes bind, say, chloroform better than methane, although methane fits geometrically as well in the cavity. An occupancy factor or packing coefficient (PC) of 0.886 was calculated for



Scheme 1.3 Complex with crown-ammonium pseudorotaxanes [39], with a very large affinity difference between spacer length of either n=0 or n=1.

the chloroform complex, similar to that in a closely packed crystal. For methane the occupancy factor amounts to a PC of only 0.35. These values are in the range with later systematic evaluations with many container- and capsule-type hosts [38], which were leading to generally observed $55 \pm 9\%$ occupancy of the space available.

Even small geometric changes can have a dramatic impact on the stability of supramolecular complexes, such as in recently described associations with crown-ammonium pseudorotaxanes [39] (Scheme 1.3). Here insertion of just one methylene group in the spacer leads to a drop from $K = 25\,000\,\mathrm{M}^{-1}$ for the optimal spacer (n = 0) to $K = 1100\,\mathrm{M}^{-1}$ with the longer spacer (n = 1), due to differences in both ΔH ($-4.8\,\mathrm{kJ/mol}$) and $T\Delta S$ ($2.9\,\mathrm{kJ/mol}$).

Frequently one interaction in a supramolecular complex is significantly larger than another one, which then can lead to an induced misfit. Figure 1.7 illustrates schematically the consequences for cyclodextrin complexes as an example [40]. Only in ideal situations like in Case I (Figure 1.7a) one can expect additivity (as for example with the nucleotide complexes in Scheme 1.2). In Case II (Figure 1.7b) the force between D and A is so strong that the second interaction is severely diminished, with an ensuing loss of additivity. Such situations have been seen for example with complexes of nucleotides and cyclodextrins, which bear a different number n of aminoalkyl substituents at the rim [41,42].

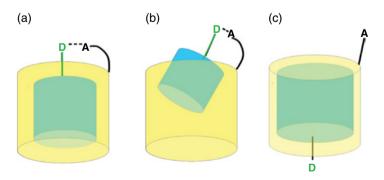


Figure 1.7 Schematic consequences of mismatch: (a) similar interaction in- and outside and sufficient matching (e.g. Case I); (b) stronger interaction outside (Case II); (c) stronger interaction inside cavity (e.g. Case III). *Source*: Ref. [40]. Reproduced with permission of Royal Society of Chemistry. See color section.