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Article

Optimizing the Specificity Window of Biomolecular Receptors Using Structure-Switching and Allostery

Stéphanie Bissonnette, Erica Del Grosso, Anna J. Simon, Kevin W. Plaxco, Francesco Ricci,* and Alexis Vallée-Bélisle*

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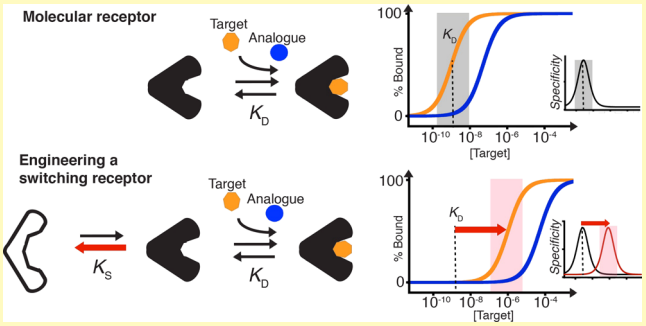
ABSTRACT: To ensure maximum specificity (i.e., minimize cross-reactivity with structurally similar analogues of the desired target), most bioassays invoke "stringency", the careful tuning of the conditions employed (e.g., pH, ionic strength, or temperature). Willingness to control assay conditions will fall, however, as quantitative, single-step biosensors begin to replace multistep analytical processes. This is especially true for sensors deployed in vivo, where the tuning of such parameters is not just inconvenient but impossible. In response, we describe here the rational adaptation of two strategies employed by nature to tune the affinity of biomolecular receptors so as to optimize the placement of their specificity "windows" without the need to alter measurement conditions: structure-switching and allosteric control. We quantitatively validate these approaches using two distinct, DNA-based receptors: a simple, linear-chain DNA suitable for detecting a complementary DNA strand and a structurally complex DNA aptamer used for the detection of a small-molecule drug. Using these models, we show that, without altering assay conditions, structure-switching and allostery can tune the concentration range over which a receptor achieves optimal specificity over orders of magnitude, thus optimally matching the specificity window with the range of target concentrations expected to be seen in a given application.



KEYWORDS: *structure-switching biosensors, molecular beacons, rational design, riboswitches, intrinsically unfolded proteins*

Optimizing the specificity of biomolecular receptors, i.e., minimizing cross-reactivity with close structural analogues of the targeted molecule, represents an important challenge in the field of bioengineering.[1−7] A key element of specificity is, obviously, the design of a precise lock-and-key complementarity between the receptor and its targets.[8−14] A receptor's specificity can thus be optimized by increasing the difference in binding energy between the properly matched (PM) target and any mismatched (MM) molecular analogues via alterations in its binding interface. A second element of specificity, however, is that it is optimal over only a limited range of target concentrations, its specificity window (Figure 1A, gray rectangle). That is, at concentrations well below a receptor's dissociation constant (K_D), neither the properly matched target nor mismatched molecular analogues bind avidly enough to generate any significant output; where there is no binding, specificity is "moot". Similarly, even mismatched structural analogues binding less avidly than the properly matched target will, at sufficiently high concentrations, achieve near 100% occupancy, pushing the discriminatory power of the receptor toward zero. Optimal specificity thus depends on both a receptor's lock-and-key complementarity and also on its affinity relative to the range of target/analogue concentrations over which it will be working.

Optimal discriminatory power has historically been achieved in bioassays via careful control over the temperature, pH, or ionic strength employed so as to achieve good "stringency". As biology-based detection moves away from complex, multistep, bench-top assays (such as polymerase chain reaction (PCR) and Southern blots) and toward direct, single-step devices (such as the home glucose monitor), willingness to employ these cumbersome methods will fall. This is particularly true when sensors are deployed in vivo, where the tuning of assay conditions is not so much inconvenient as it is impossible. How, then, can we tune the affinity of the receptors used in biotechnologies so as to optimize their specificity window without resorting to tuning the experimental conditions? Alterations of the binding interface are one solution, but given

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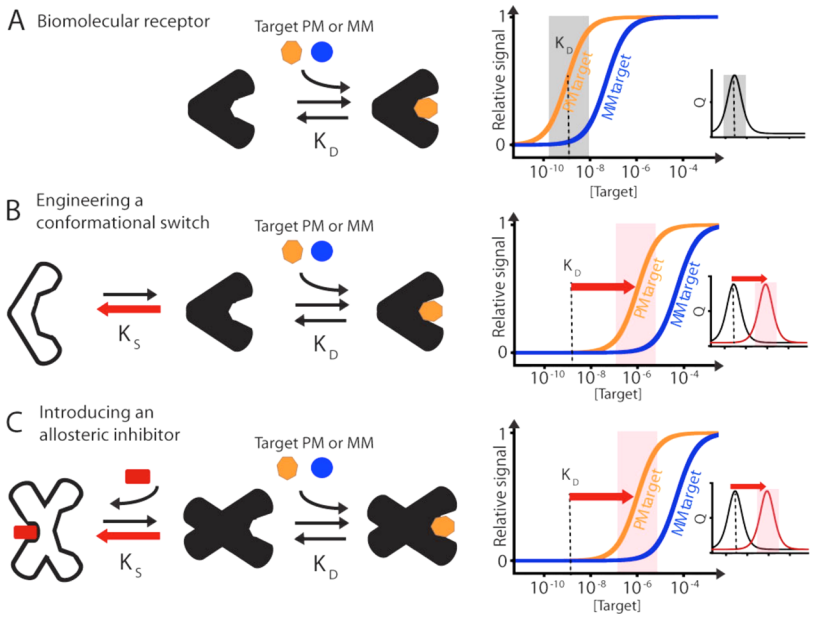

Figure 1. (A) Biomolecular receptors achieve high specificity over only a limited range of target concentrations (the "specificity window", gray rectangle). Here, we define this specificity window using the discrimination factor, Q, which is the ratio of the output signal seen for the properly matched (PM) target to that produced by a structurally analogous mismatched (MM) target at the same concentration.[21] In this work, we have explored two strategies to tune the specificity window so as to achieve maximal specificity over a given range of target concentrations. The first is by engineering a structure-switching system (conformational switch) (B) and the second by introducing allosteric inhibition (C).

the current state of biomolecular design, this remains challenging.[27] For more facile approaches, we look here to evolution, which has also developed methods to tune the specificity windows of biomolecular receptors. One such strategy is to introduce a "conformational switch" that reduces affinity in a "tunable" way by coupling recognition to an unfavorable conformational change (Figure 1B). This mechanism is seen, for example, in the case of intrinsically unfolded proteins, which couple target binding to an unfavorable folding free energy,[15] simultaneously altering the receptor's affinity for both its properly matched target and any mismatched analogues and thus providing a route toward tuning the specificity window. A second strategy used by nature to tune the affinity of a receptor "on-the-fly" is to employ allosteric regulators that, upon binding, likewise alter affinity and thus the placement of the specificity window (Figure 1C).[16,17] Here, we employ the programmability of synthetic DNA to demonstrate the adaptation of these mechanisms to some of the receptors commonly employed in artificial biotechnologies.

RESULTS

To quantify specificity for our comparisons, we employ the following definition. The output signal, S, produced by a receptor is given by

$$S = \chi(S_F + \Delta S) + (1 - \chi)S_F = S_F + \chi\Delta S \quad (1)$$

where χ is the fraction of receptor bound to the target, S_F is the signal from the unbound (free) receptor and thus represents the background signal, and ΔS is the signal change observed upon target binding. Using this, we define a discrimination factor, Q, such that it reports on the relative signal that would be expected from the properly matched (PM) target versus that that would be seen from a mismatched (MM) analogue of the target at the same concentration. From eq 1, we have thus

$$Q = \frac{S_F + \chi_{PM}\Delta S}{S_F + \chi_{MM}\Delta S} \quad (2)$$

adding to this the dependence of receptor occupancy on target concentration, we have

$$Q = \frac{S_F + \Delta S\left(\frac{[\text{target}]}{[\text{target}] + K_D^{PM}}\right)}{S_F + \Delta S\left(\frac{[\text{target}]}{[\text{target}] + K_D^{MM}}\right)} \quad (3)$$

where K_D^{PM} and K_D^{MM} are the receptor's affinities for the proper target and the mismatched analogue, respectively. For the sake of the work here, we arbitrarily define "good specificity" (and the associated specificity window) as concentrations for which $Q > 5$ (i.e., the signal arising from the perfectly matched target is 5 times greater than that arising from the mismatched analogue at the same concentration) (Figure S1). With this definition of specificity in hand, we next set out to explore the use of structure-switching and allostery as means of tuning the placement of the specificity window such that maximum Q is, optimally, achieved in the midpoint of the expected target concentration.

To explore the use of structure-switching (Figure 1B), we first employed a linear, 13-base DNA as a receptor for its complementary sequence (black) (Figure 2A). In our constructs, this 13-base recognition element is flanked on both sides by five additional noncomplementary nucleotides (red) that, in the studies described below, we later used to introduce structure-switching (Figure 2B). Receptor occupancy is then reported by the fluorophore−quencher pair attached at the sequences' two termini; upon target binding, the receptor extends from a random coil configuration, separating its termini and enhancing emission. As with any receptor, the linear DNA binds to both its target and to close structural analogues, albeit its affinity for the latter is poorer.

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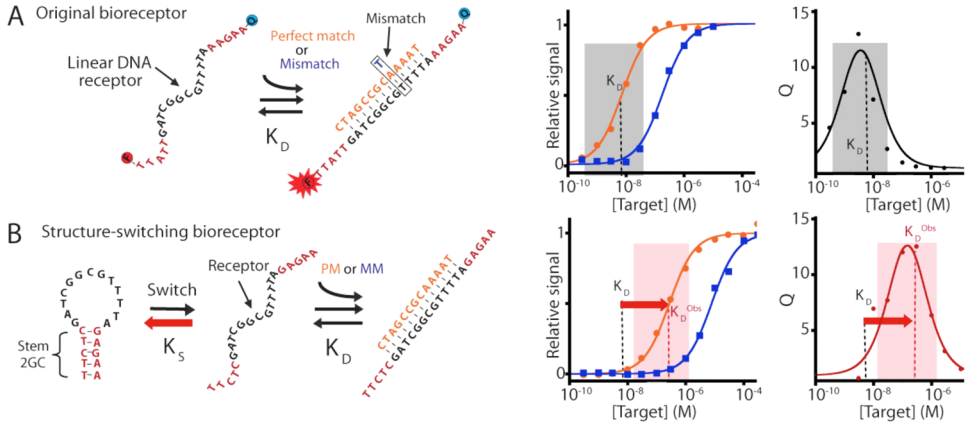

Figure 2. Coupling recognition to an unfavorable conformational change (a "switch") provides a convenient means of tuning the specificity window of many receptors. (A) To demonstrate this, we have used a DNA receptor (labeled with a fluorophore and a quencher) containing a 13-base target recognition element (black) and five additional bases at either end (red). If the two end sequences lack complementarity, there is no switch, and the receptor recognizes its perfectly matched (PM) complement with high affinity (K_D^{PM} = 7 ± 1 nM). It also recognizes, however, a sequence containing a single mismatch, albeit with lower affinity (K_D^{MM} = 180 ± 20 nM). The concentration window over which we can observe good specificity (here defined as the concentration range at which we achieve a discrimination factor, *Q*, greater than 5; see gray box) is fixed and located close to K_D^{PM}. (B) By altering the tail sequences such that they self-hybridize, causing the receptor to form a stem-loop structure, we introduce a structure-switching mechanism that provides a means of tuning its specificity window (see red box). Experimental values represent the average of three independent measurements. To simplify data comparison, we have presented relative fluorescence (see the Material and Methods), which corrects for variations in the background fluorescence caused by the differing conformations of the original receptor and its structure-switching variant.

For example, the receptor's dissociation, K_D^{PM}, is 7 ± 1 nM when it is challenged with a perfectly matched (fully complementary) target (Figure 2A, orange). When challenged with a single-base mismatch (blue), in contrast, the receptor's affinity is 26 times poorer (K_D^{MM} = 180 ± 20 nM). Together, these values define a specificity window (again defined here as the range of concentrations for which *Q* > 5) that spans ∼2 orders of magnitude centered around 4 nM (Figure 2A, right).

Tuning the Placement of the Specificity Window Using a Structure-Switching Mechanism. To tune the location of the specificity window of our linear DNA receptor, we redesigned it so that it undergoes binding-induced structure-switching (Figure 2B).[18] That is, we modified the 5 bases on each of its termini to render them complementary (Figure 2B), causing the receptor to form a stem-loop structure that must be broken in order for the target to bind. This couples binding to an unfavorable free energy that we can alter to tune affinity and thus the specificity window. Under these circumstances, the receptor's observed affinity, K_D^{obs}, for both its perfectly matched target and any mismatched analogues is related to the equilibrium constant of the structural switch, K_S, and its affinity in the absence of switching, K_D, by the relationship[18a]

$$K_D^{obs} = K_D\left(\frac{1 + K_s}{K_s}\right) \quad (4)$$

Following this, a modified receptor containing a fully complementary stem composed of 2GC and 3AT base pairs ("2GC") binds with ∼40-fold poorer affinity than that of the "nonswitching" parent receptor (K_D^{PM} = 270 ± 30 versus 7 ± 1 nM; Figure 2B). Moreover, because the change in target affinity is due to alteration of the stem sequence, which is distal to the binding site, the affinity of the mismatched analogue target is likewise shifted ∼40-fold (K_D^{MM} = 7 ± 1 μM versus 180 ± 30 nM; Figure 2B), thus shifting the specificity window of the receptor to 40-fold higher concentrations without altering its 2-orders-of-magnitude width (Figure 2B).

We can rationally and quantitatively control the range of concentration at which optimal specificity is achieved by varying the switching equilibrium constant, K_s. For the stem-loop receptor, we do this by varying the stability of the stem via the replacement of A−T base pairs with G−C base pairs, each of which stabilizes the stem by ∼4 kJ/mol (determined via urea melts; see ref 18a for experimental details), shifting both affinity and the specificity window another 4.3-fold (at room temperature) to higher concentrations.[22] Using this approach, we have thus created a set of structure-switching receptors displaying specificity windows that shift over 4 orders of magnitude (Figures 3 and S2).

Tuning the Placement of the Specificity Window Using Allosteric Inhibition. Allosteric control provides a second strategy by which we can rationally tune the specificity windows (Figures 1C and4A). In this, the binding of an effector at a site distal from the target binding site alters K_S and thus, in turn, target affinity and the placement of the specificity window.[19,20] As a test bed to explore such control, we employed a DNA aptamer binding the antimalarial drug, quinine (Figure 4A).[24−26] As an allosteric inhibitor, we employed an oligonucleotide complementary to 14 bases in the aptamer's sequence. Hybridization of this to the aptamer creates a switch (between the double-stranded state and the native fold) that again alters affinity (Figure 4A). Using this inhibitor, we have tuned the specificity window of the aptamer over many orders of magnitude (Figure 4B). In the absence of the inhibitor, for example, the aptamer's affinity for quinine (i.e., $K_D^{quinine}$ = 0.84 ± 0.07 μM) is 19-fold higher than its affinity for the structural analogue cinchonine (i.e., $K_D^{cintochine}$ = 16 ± 0.8 μM), with the discrimination factor *Q* peaking at 0.8 μM (Figure 4B, top). Upon addition of the inhibitor (at 10 μM), the two dissociation constants shift to 63 ± 6 and 790 ± 90 μM, respectively (Figure 4B, bottom), and optimal

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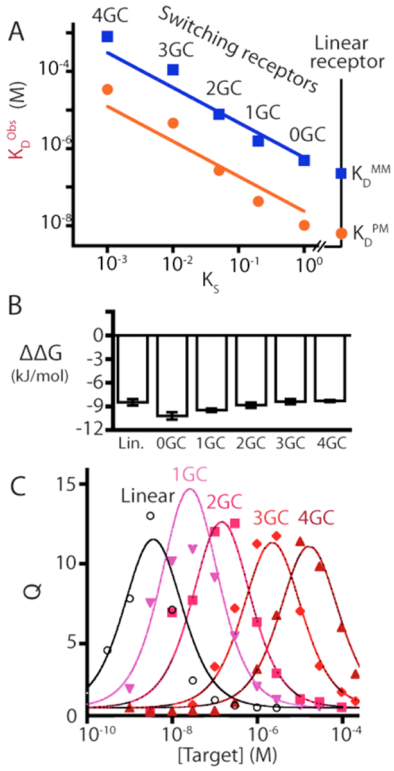

Figure 3. (A) Placement of the specificity window can be tuned by altering the equilibrium constant, K_S, of the receptor's conformational switch.[23] In the case of our model DNA receptor, this can be achieved by increasing the G−C content of the stem (i.e., stabilizing the nonbinding conformation). (B) Introducing the switching mechanism does not perturb the overall specificity of the receptor ($\Delta\Delta G_{PM-MM}$) nor its discrimination factor (Q); it only changes the range of concentration over which the receptor achieves its maximum specificity (C).

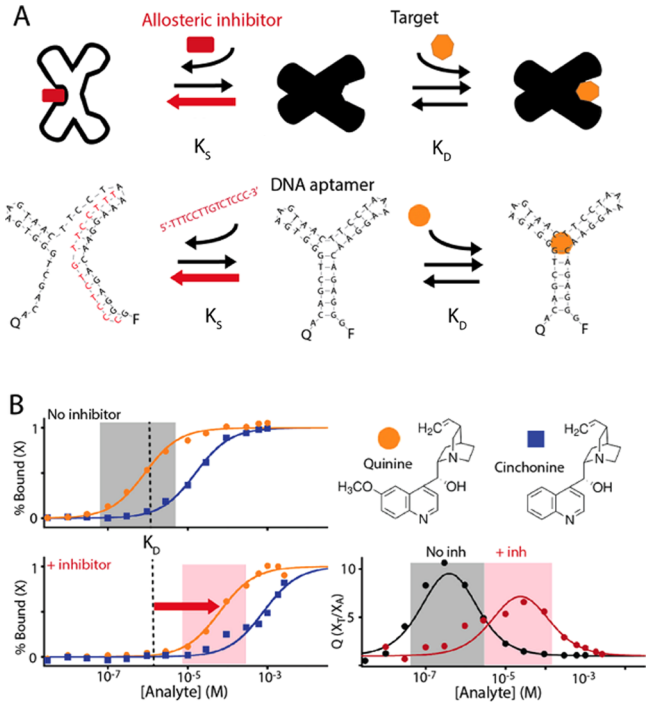

Figure 4. Allosteric regulation provides a second approach to tuning the placement of the specificity window. (A) To demonstrate this, we employed a quinine-binding aptamer[24] labeled at its two termini with an optically reporting fluorophore−quencher pair. The aptamer folds upon binding to its molecular target,[24] causing emission to fall. (B) We can reduce the aptamer's affinity and thus shift its specificity window to higher target concentrations using a complementary DNA strand that, upon hybridization to the aptamer, stabilizes a nonbinding, double-stranded conformation.[20] The introduction of this inhibitor changes the range of concentration at which the receptor binds to its perfectly matched target (quinine) and a mismatched analogue (cinchonine), thus shifting its specificity window to 75-fold higher target concentrations. Also, in this case, to simplify data comparison, we have presented relative fluorescence (see the Material and Methods), which corrects for variations in the background fluorescence caused by the allosteric inhibitor (see Figure S3).

discrimination is reached at a 75-fold higher target concentration.

CONCLUSIONS

Here, we have shown that the placement of the specificity window can be optimized by coupling recognition to an unfavorable conformational switch or to allosteric control, with either approach allowing the precise, rational placement of the specificity window. Moreover, these approaches involve modifications and interactions that are distal from the binding site, thus rendering them easier to introduce than would be the redesigns of the receptor's binding interface itself.[27]

The findings described here are likely generalizable to other receptors. This is particularly true, obviously, for nucleic acids, as the equilibrium constants of nucleic acids switch, or the binding energy of a DNA or RNA inhibitor can be rationally varied by altering the strength of their base pairing. Indeed, nucleic acid folding and hybridization prediction programs, such as mfold, produce relatively accurate estimates of the thermodynamics of specific RNA or DNA conformations,[22] thus providing precision guidance for such rational design efforts. This said, similar approaches can also be employed to tune the specificity of protein-based switches. A single, key residue, for example, controls the switching thermodynamics of the bacterial periplasmic binding protein superfamily.[28] In a similar context, the ability to introduce conformational switching into otherwise nonswitching proteins has been demonstrated for many proteins in applications ranging from biosensing to smart materials and therapeutics.[29] Finally, we have shown that binding-induced protein folding, which is perhaps a switching mechanism often employed by proteins,[15,30] is readily tuned via substitutions distant from the binding interface that stabilize or destabilize the native state.[31] We expect that the strategies we present in this work will be useful to both optimize the specificity of biosensors[32] as well as to optimize the specificity of engineered receptors to be implemented in synthetic bioorganisms.[33]

In addition to providing a rational framework for optimizing the placement of the specificity windows of structure-switching biosensors, the thermodynamic principles presented here may also improve our understanding of the mechanisms behind the evolution of receptor specificity. A good example is provided by the intrinsically disordered proteins, proteins that only fold upon binding to their specific target.[15,30] This switching mechanism, which has been employed in several protein-based biosensors,[31] has been proposed as an efficient strategy by which nature reduces the affinity of biomolecules without simultaneously reducing their specificity.[15,30,34] As our knowledge of the thermodynamics of natural biomolecular switches

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progresses, it will be interesting to uncover if they have evolved switching mechanism or allosteric regulation mechanism to achieve optimal specificity in vivo.

MATERIAL AND METHODS

High-performance liquid chromatography (HPLC)-purified DNA sequences modified with a 6-carboxyfluorescein (FAM) and black hole quencher (BHQ-1), the quinine-binding aptamer, the 13-nucleotide target (both perfect match and mismatch), and the 15-base inhibitor were all purchased from Sigma-Genosys (all stem-loop constructs possess an additional A, after the FAM, and G nucleotides, before the BHQ-1). The sequences of these DNA strands are as follows. Linear receptor (nonswitching): 5′-(FAM)-A-*TTATT*-GATCGGCGTTTTA-*AAGAA*-G-(BHQ)-3′; 0GC (stem-loop): 5′-(FAM)-A-*TTATT*-GATCGGCGTTTTA-*AATAA*-G-(BHQ)-3′; 1GC (stem-loop): 5′-(FAM)-A-*CTATT*-GATCGGCGTTTTA-*AATAG*-G-(BHQ)-3′; 2GC (stem-loop): 5′-(FAM)-A-*CTCTT*-GATCGGCGTTTTA-*AAGAG*-G-(BHQ)-3′; 3GC (stem-loop): 5′-(FAM)-A-*CTCTC*-GATCGGCGTTTTA-*GAGAG*-G-(BHQ)-3′; 4GC (stem-loop): 5′-(FAM)-A-*CTCGC*-GATCGGCGTTTTA-*GCGAG*-G-(BHQ)-3′; 13-base target: 5′-TAAAACGCCGATC-3′; Quinine-binding aptamer: 5′(FAM)-GGG AGA CAA GGA AAA TCC TTC AAT GAA GTG GGT CGA CA(BHQ)-3′; Inhibitor: 5′-TTT CCT TGT CTC CC-3′.

The length of the DNA target (13 bases) and of the inhibitor (14 bases) were selected to optimize the utilization of the available concentration range for the experiment (between 1 nM and 1000 μM). For example, the 13-base target provided the smallest K_D that we could measure (around 5 nM) without structure-switching. Mismatch and structure-switching will only reduce affinity.[18a] The length of the inhibitor was selected using a similar argument and based on our previous knowledge of its effect.[20]

All reagents (including phosphate monobasic, sodium chloride, quinine, and cinchonine) were obtained from Sigma-Aldrich (St. Louis, Missouri) and used without further purification.

All experiments were conducted at pH 7 in 50 mM sodium phosphate buffer and 150 mM NaCl at 45 °C, except for the experiments with the quinine aptamers (Figure 4), which were conducted at 37 °C. All fluorescence measurements were obtained using a Cary Eclipse Fluorimeter with excitation at 480 (±5) nm and acquisition between 514 and 520 nm using either 5 nm (unfolding curves) or 20 nm (binding curves) bandwidths.

Binding curves were obtained by sequentially increasing the target concentration via the addition of small volumes of solutions with increasing concentrations of the target with the receptor concentration held constant (at 3 nM for the linear DNA and stem-loop receptors and 100 nM for the quinine-binding aptamer). The observed K_D was obtained using the following equation

$$F([T]) = F(0) + \left(\frac{[T](F_B - F(0))}{[T] + K_D^{obs}} \right) \quad (5)$$

where $F([T])$ is the fluorescence signal obtained at a certain target concentration, F_B is the maximum fluorescence signal, and $F(0)$ is the background signal in the absence of the target. Since $F(0)$ and F_B vary between the different receptors employed, we simplified data comparison by normalizing the binding curves from 0 to 1 (relative signal). For the linear DNA receptor and the structure-switching bioreceptor (Figure 2), we did this using the equation

$$\text{relative signal} = \left(\frac{F([T]) - F(0)}{F_B - F(0)} \right) \quad (6)$$

Because of the signal-off nature of the allosteric-regulated DNA aptamer (Figure 4), we did this using the equation

$$\text{relative signal} = 1 - \left(\frac{F([T]) - F(0)}{F_B - F(0)} \right) \quad (7)$$

The stability of the stem-loop (i.e., which defines K_S) was measured using urea unfolding curves (see ref 18 for experimental details).

The simulations presented in Figures 3C and 4B (solid lines) were generated using the observed K_D values of each receptor for its target and the selected analogue.

ASSOCIATED CONTENT

Supporting Information

The Supporting Information is available free of charge at https://pubs.acs.org/doi/10.1021/acssensors.0c00237.

Discrimination efficiency parameter (Q) definition (Figure S1); Modulation of affinity by tuning K_s (Figure S2); Raw binding curves of the quinine-binding aptamer (Figure S3) (PDF)

AUTHOR INFORMATION

Corresponding Authors

Francesco Ricci − *Dipartimento di Scienze e Tecnologie Chimiche, University of Rome, 00133 Rome, Italy; Consorzio Interuniversitario Biostrutture e Biosistemi "INBB", Rome 00136, Italy;* orcid.org/0000-0003-4941-8646; Email: Francesco.ricci@uniroma2.it

Alexis Vallée-Bélisle − *Laboratory of Biosensors & Nanomachines, Département de Chimie, Département de Biochimie et Médecine Moléculaire, Université de Montréal, Montréal, Québec H3C 3J7, Canada;* orcid.org/0000-0002-5009-7715; Email: a.vallee-belisle@umontreal.ca

Authors

Stéphanie Bissonnette − *Laboratory of Biosensors & Nanomachines, Département de Chimie, Département de Biochimie et Médecine Moléculaire, Université de Montréal, Montréal, Québec H3C 3J7, Canada*

Erica Del Grosso − *Dipartimento di Scienze e Tecnologie Chimiche, University of Rome, 00133 Rome, Italy; Consorzio Interuniversitario Biostrutture e Biosistemi "INBB", Rome 00136, Italy*

Anna J. Simon − *Department of Chemistry and Biochemistry and Interdepartmental Program in Biomolecular Science and Engineering, University of California, Santa Barbara, California 93106, United States*

Kevin W. Plaxco − *Department of Chemistry and Biochemistry and Interdepartmental Program in Biomolecular Science and Engineering, University of California, Santa Barbara, California 93106, United States;* orcid.org/0000-0003-4772-8771

Complete contact information is available at: https://pubs.acs.org/10.1021/acssensors.0c00237

Notes

The authors declare no competing financial interest.

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