Intrinsic disorder as a generalizable strategy for the rational design of highly responsive, allosterically cooperative receptors

Anna J. Simon\textsuperscript{a}, Alexis Vallée-Bélisle\textsuperscript{b}, Francesco Ricci\textsuperscript{c}, and Kevin W. Plaxco\textsuperscript{a,d,e,1}

\textsuperscript{a}Biomolecular Science and Engineering Program, \textsuperscript{b}Department of Chemistry and Biochemistry, and \textsuperscript{c}Center for Bioengineering, University of California, Santa Barbara, CA 93106; \textsuperscript{d}Laboratory of Biosensors and Nanomachines, Département de Chimie, Université de Montréal, Montreal, QC, Canada H3T 1J4; and \textsuperscript{e}Dipartimento di Scienze e Tecnologie Chimiche, University of Rome, Tor Vergata, Via della Ricerca Scientifica, 00133 Rome, Italy

Control over the sensitivity with which biomolecular receptors respond to small changes in the concentration of their target ligand is critical for the proper function of many cellular processes. Such control could likewise be of utility in artificial biotechnologies, such as biosensors, genetic logic gates, and “smart” materials, in which highly responsive behavior is of value. In nature, the control of molecular responsiveness is often achieved using “Hill-type” cooperativity, a mechanism in which sequential binding events on a multivalent receptor are coupled such that the first enhances the affinity of the next, producing a steep, higher-order dependence on target concentration. Here, we use an intrinsic-disorder–based mechanism that can be implemented without requiring detailed structural knowledge to rationally introduce this potentially useful property into several normally noncooperative biomolecules. To do so, we fabricate a tandem repeat of the receptor that is destabilized (unfolded) via the introduction of a long, unstructured loop. The first binding event requires the energetically unfavorable closing of this loop, reducing its affinity relative to that of the second binding event, which, in contrast occurs at a preformed site. Using this approach, we have rationally introduced cooperativity into three unrelated DNA aptamers, achieving in the best of these a Hill coefficient experimentally indistinguishable from the theoretically expected maximum. The extent of cooperativity and thus the steepness of the binding transition are, moreover, well modeled as simple functions of the energetic cost of binding-induced folding, speaking to the quantitative nature of this design strategy.

utrasensitivity | intrinsically disordered proteins | biosensors | synthetic biology | ribozymes

The ability to control the shape and midpoint of binding curves is critical to nature’s ability to optimize many cellular processes (1). One of the most widely used mechanisms by which nature so tunes the behavior of her receptors is allostery, in which the binding of one ligand alters the affinity with which subsequent ligands bind. Allostery comes in two “flavors.” Heterotropic allostery, in which the two ligands differ, provides a means of shifting the midpoint of a binding curve to higher or lower target concentrations without changing the curve’s intrinsically hyperbolic shape and thus without altering its sensitivity to small changes in the relative concentration of its molecular target (Fig. 1, Left). An example is the binding of bisphosphoglycerate to mammalian hemoglobin, which decreases the protein’s affinity for oxygen, thus pushing its binding curve to higher concentrations and enhancing oxygen transport efficiency, while leaving the intrinsic shape of its binding curve unaltered. Homotropic allostery, in contrast, occurs when the ligands are the same; that is, when the binding of one copy of a ligand changes the affinity with which subsequent copies of the same molecule bind. This mechanism, commonly referred to as “cooperativity,” changes not only the placement but also the shape of the binding curve, producing either a more responsive, higher-order dependence on ligand concentration (positive cooperativity) (Fig. 1, Right) or a less responsive, lower-order dependence (negative cooperativity). Like heterotropic allostery, cooperativity is also seen in the function of hemoglobin; the protein uses this mechanism to bind four oxygen molecules in a positively cooperative, approximately “all-or-nothing” fashion, steepening its binding curve and enhancing its ability to deliver oxygen over the rather modest concentration gradient present between the lungs and the peripheral tissues.

The ubiquity with which nature exploits homotropic and heterotropic allostery has motivated efforts to rationally engineer these mechanisms into biomolecular receptors normally lacking them, both to test our understanding of the principles underlying these effects and to harness them to improve the utility of artificial biotechnologies. The rational introduction of heterotropic allostery into otherwise nonallosteric receptors, for example, has seen significant prior exploration (e.g., refs. 2–8), with both mechanical coupling (e.g., refs. 2 and 5–8) and mutually exclusive folding (e.g., refs. 3 and 4) approaches all having been used to successfully introduce this useful mechanism into a range of protein- and nucleic acid-based receptors. The design of allosterically cooperative receptors, in contrast, has seen far less success. That is, although a handful of examples of rationally designed cooperativity have been reported to date (9–12), no general approach has previously been reported by which such behavior can be rationally introduced into any arbitrarily complex biomolecule. This failure has limited the extent to which cooperativity, which could provide a powerful means of improving the ability of artificial biotechnologies to respond to value in many biotechnologies. In nature, this control is often achieved using “Hill-type” allosteric cooperativity, an elegant mechanism that has, unfortunately, hitherto proven difficult to achieve via generalizable design strategies. In response, we demonstrate here a quantitative and apparently versatile means of rationally introducing this useful mechanism into a range of normally noncooperative receptors. We achieve in the best of our examples cooperativity, and thus sensitivity, experimentally indistinguishable from the theoretically expected maximum.


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1To whom correspondence should be addressed. Email: kwp@chem.ucsb.edu.

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PNAS毁灭性作为-一个可推广的策略的理性设计的高反应性，共价位点相互作用的受体

Anna J. Simon\textsuperscript{a}, Alexis Vallée-Bélisle\textsuperscript{b}, Francesco Ricci\textsuperscript{c}, and Kevin W. Plaxco\textsuperscript{a,d,e,1}

\textsuperscript{a}Biomolecular Science and Engineering Program, \textsuperscript{b}Department of Chemistry and Biochemistry, and \textsuperscript{c}Center for Bioengineering, University of California, Santa Barbara, CA 93106; \textsuperscript{d}Laboratory of Biosensors and Nanomachines, Département de Chimie, Université de Montréal, Montreal, QC, Canada H3T 1J4; and \textsuperscript{e}Dipartimento di Scienze e Tecnologie Chimiche, University of Rome, Tor Vergata, Via della Ricerca Scientifica, 00133 Rome, Italy

控制对敏感性的影响，其中共价分子受体对小变化的浓度的其目标配体受到的控制是非常关键的，因为多个细胞过程。这种控制同样可能在艺术 biomechanical technologies，如生物传感器，遗传逻辑门，和“智能”材料，其中高响应性行为是重要的。在自然界中，分子响应性控制通常是通过“山型”协同作用实现的，一种机制，其中在目标浓度上的后续配体的绑定事件是耦联的。为了做到这一点，我们制造了两个不同的DNA aptamers，实现了其中最好的一个Hill系数实验上难以区分。协同作用程度和因此的协同作用曲线的陡度是可用的作为简单函数的该绑定诱导折叠的能量成本，讲到这种设计策略的定性性质。

超敏感性 | 本质上无序蛋白 | 生物传感器 | 合成生物学 | 里佐泽

大自然控制形状和中期的绑定曲线能力是其自然能力优化许多细胞过程的关键（1）。其中的其中一个最广泛使用机制是通过在其自然中，一个配体的绑定是另外一种的“风味”。异源型的雄性，其中的两种配体不同，提供一种在绑定曲线上的两种变化，可以是更高的或更低的靶向浓度，而不会改变曲线的固有的双曲线形状，而且不改变其敏感性对小变化在相对浓度的其分子目标（图1，左）。一个例子是糖二糖磷酸肌酸对哺乳动物的血红蛋白，它降低了蛋白质的氧气 affinity，因此推动其绑定曲线到更高的浓度和增强氧气运输效率，同时保持其绑定曲线的固有的双曲线形状。同源型的雄性，相反，是当相同的配体的绑定改变了其与后续拷贝的分子的绑定形状时发生的。这种机制，通常被称为“协同作用”，变化的不只放置位置，而且是绑定曲线的形状，产生一个更响应的，更高的绑定浓度的依赖性（正协同作用）（图1，右）或者一个较低的响应的，较低的绑定浓度的依赖性（负协同作用）。血红蛋白也是如此，使用了这种机制，以四个氧分子在一种正协同作用，近似“所有或无”的方式，加深其绑定曲线和增强其能力来交付氧气相对于肺部和周围组织的相对微小浓度梯度之间。这种协同作用的性能有限，这种性能，可能提供一个强大的手段，改善人工生物技术对响应的控制。
small changes in molecular concentration (9, 13), can be applied in applications, such as biosensing (14, 15), “smart” drug delivery materials (16, 17), and molecular (18) and genetic (19) logic gates, in which such enhanced responsiveness would be of value.

Two reasons account for why, despite its underlying simplicity and elegance, achieving the rational design of positive cooperativity has proven far from straightforward. First, to achieve the effect requires the creation of systems in which a higher affinity site is occupied only after a lower affinity site (which would normally be filled only at higher ligand concentrations) that binds the same ligand is already filled. This contrasts sharply with heterotropic allostery, in which the two binding sites typically exhibit little if any cross-reactivity. Second, all of the binding sites of a cooperative receptor recognize copies of the same ligand, rendering it more difficult to alter the affinity of one independently of that of the others. This is again in contrast to heterotropic allostery, in which each binding site is chemically distinct, allowing each to be independently optimized. Given these difficulties, and given the relative infancy of biomolecular design efforts (20–22), the ability to perform the structure-based design of cooperativity appears beyond current capabilities except for the simplest, most well-understood receptors (9–12).

Here, however, we use an approach to the rational engineering of allosterically cooperative receptors that does not require detailed, structure-based design. Indeed, our approach is so simple that it can be performed, as demonstrated here, even in the absence of detailed knowledge of the parent receptor’s structure.

Our design approach is inspired by intrinsically disordered proteins, proteins that are normally unfolded and only fold upon binding their target ligand. Specifically, both theoretical (23) and experimental (24, 25) studies have demonstrated that the global conformation change these proteins undergo upon an initial ligand binding event provides a convenient means of preorganizing a second, distal ligand binding site. This improves the affinity of the second binding event (because binding need no longer pay the unfavorable cost associated with folding), leading to positive allosteric behavior. Ferreon et al. (24), for example, have shown that the intrinsically disordered oncoprotein adenovirus early region 1A (E1A) folds upon binding either of its two (different) target ligands (CREB binding protein or retinoblastoma protein), thus increasing the affinity with which the second ligand binds and rendering the system heterotropically allosteric. In addition, Furukawa et al. (25) have shown that the partially intrinsically disordered protein STIM 1 exhibits strongly homotropic allosteric binding to calcium. Here, we use this same mechanism to rationally introduce cooperativity into a number of normally noncooperative aptamers (DNA-based receptors often adopting complex tertiary folds), thus producing steeper, more responsive binding curves than those seen for the unmodified parent molecule.

**Results**

Positive cooperativity arises when the first binding event on a multisite receptor improves the binding affinity of additional copies of the same ligand. Thus, once one copy of the ligand is bound the probability of the second binding event becomes high, generating effectively “all-or-none” behavior. The resulting binding curve (26) is given by the Hill equation:

\[
\text{Receptor site occupancy } Y = \frac{[\text{target}]^{n_H}}{[\text{target}]^{n_H} + (K_{1/2})^{n_H}}
\]

in which \(K_{1/2}\) is the ligand concentration at which one-half of the receptor sites are bound, and \(n_H\), the Hill coefficient, describes (E1A) folds upon binding either of its two (different) target ligands (CREB binding protein or retinoblastoma protein), thus increasing the affinity with which the second ligand binds and rendering the system heterotropically allosteric. In addition, Furukawa et al. (25) have shown that the partially intrinsically disordered protein STIM 1 exhibits strongly homotropic allosteric binding to calcium. Here, we use this same mechanism to rationally introduce cooperativity into a number of normally noncooperative aptamers (DNA-based receptors often adopting complex tertiary folds), thus producing steeper, more responsive binding curves than those seen for the unmodified parent molecule.

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the order of the dependence on ligand concentration (Fig. 1, Bottom Right). For a noncooperative receptor, in which each copy of the ligand binds independently of all others, \( n_H = 1 \).

For an ideally cooperative receptor, in which all of the binding sites on any one receptor molecule are simultaneously either fully occupied or fully unoccupied, the Hill equation equals the number of binding sites. The Hill coefficient is, in turn, related to the useful dynamic range of a receptor (a convenient measure of responsiveness that is typically defined as the ratio between the target concentration at which occupancy is 90% to that at which it is 10%; \( C_{90\%} \) and \( C_{10\%} \), respectively) by the following (27):

\[
\text{Dynamic range} = \frac{C_{90\%}}{C_{10\%}} = 81^{1/n_{H}}. \tag{2}
\]

From this, we see that the useful dynamic range of a noncooperative receptor (\( n_H = 1 \)) is quite broad; such a receptor requires an 81-fold change in target concentration to transition from 10% occupancy to 90% occupancy, rendering it relatively insensitive to small changes in this input. The dynamic range falls to just ninefold, however, for an ideally cooperative, two-site receptor (\( n_H = 2 \)), rendering such a receptor many times more sensitive to small changes in target concentration.

In naturally occurring receptors, the energetic difference between the first and subsequent binding events required to generate allosteric cooperativity usually arises due to mechanical coupling between the relevant binding sites. That is, structural changes that occur upon the first binding event are transduced throughout the receptor in a manner that improves affinity at other, distal, sites. In hemoglobin, for example, this occurs when the protein undergoes a global conformational switch from a low-affinity state that dominates when no ligand is bound, to a higher affinity conformation upon the binding of the first oxygen molecule. Here, we hypothesize that the requisite global conformational switch can also be driven by a mechanism analogous to the binding-induced folding seen for intrinsically disordered proteins. That is, via a binding-induced switch from a largely or entirely disordered state lacking preconfigured binding sites to a well-defined folded conformation exposing multiple, well-structured binding sites (Fig. 2, Top). In this scenario, the affinity of a binding site is reduced when its neighboring site is empty because the receptor is unfolded, and thus binding must pay the cost associated with folding it. Equivalently, the affinity of a binding site is enhanced when its neighboring site is already occupied. The relative (microscopic; see refs. 27 and 28) dissociation constants of the two binding scenarios (neighboring site open, \( K_{D1} \), and neighboring site occupied, \( K_{D2} \)) are then related to \( K_S \), the equilibrium constant for forming the folded conformation in the absence of the target ligand, by the following (12):

\[
\frac{K_{D2}}{K_{D1}} = \frac{K_S}{1 + K_S}. \tag{3}
\]

The Hill coefficient, in turn, is related to this ratio by the following (12, 27):

\[
n_H = \frac{2}{1 + \left(\frac{K_{D2}}{K_{D1}}\right)} = \frac{2}{1 + \sqrt{1 + K_S}}. \tag{4}
\]

From this, we see that a folding equilibrium constant of just 0.1, which corresponds to a folded state that is unstable in the absence of the target ligand by just 6 kJ/mol (at room temperature), is sufficient to achieve \( n_H = 1.5 \). This, in turn, narrows the receptor’s dynamic range by more than a factor of 4 (Eq. 2), significantly enhancing sensitivity to small changes in the concentration of the target ligand (Fig. 2, Bottom).

To physically realize such folding-based cooperativity, we have reengineered several normally noncooperative receptors into constructs comprised of a tandem repeat of one half of the receptor connected to a tandem repeat of the second half of the same receptor via an unstructured linker (Fig. 2, Top). In the absence of target, the unfavorable entropic cost of closing this linker, i.e., of ordering this disordered region, destabilizes the folded, binding-competent conformation, producing a largely unfolded state lacking structured binding sites. The binding of the first copy of the target ligand brings the two halves of the construct into association, forming both binding sites. The second binding event thus need not pay the unfavorable free energy cost associated with folding, improving its affinity and, in turn, producing a cooperative response.

For the preliminary exploration of our design approach, we used as our recognition sites a simple, mercury(II)-binding thymine–thymine mismatch (29). Specifically, we inserted two thymine–thymine mismatches into an otherwise complementary DNA stem, the two strands of which are linked via an unstructured poly-AC loop, and the two termini of which are modified with a fluorophore–quencher pair that reports on folding (Fig. 3, Left).

**Fig. 3.** Our first testbed system is a cooperative mercury(II)-binding receptor (Left), which consists of a short, double-stranded stem containing two mercury(II)-binding thymine–thymine mismatches linked via a variable length, unstructured, poly-AC sequence. (Middle) The cooperativity and binding affinity of these constructs scales monotonically with the loop length, ranging from a Hill coefficient of 1.51 ± 0.03 (dynamic range, 18-fold) for the construct with a 50-base loop to a Hill coefficient of 1.05 ± 0.05 (dynamic range, 66-fold) for the construct with a 6-base loop, with the latter being quite close to the behavior observed for single-site binding (Fig. S1). (Right) Speaking to the quantitative nature of this design, the observed Hill coefficients and dynamic ranges fit Eqs. 7 and 2 with \( R^2 \) values of 0.920 and 0.956, respectively, using only a single fitted parameter (\( K_{closed} \), the best-fit value of which is within experimental uncertainty of independent estimates (see Results). Of note, all of these constructs equilibrate within the 30- to 60-s mixing dead time of our experiments (Fig. S2).
Using a loop length of 50 bases, this construct is reasonably cooperative, achieving a Hill coefficient of 1.51 ± 0.03 and a useful dynamic range of just 18 (±1)-fold (Fig. 3, Middle). This represents a substantial increase in responsiveness relative to that of the equivalent, 50-base linker receptor in which one of the two thymine-thymine mismatch sites has been replaced with a nonbinding cytosine-cytosine mismatch; as expected, this single-site construct exhibits a Hill coefficient within experimental uncertainty of unity and a dynamic range within uncertainty of 81-fold (Fig. S1).

The degree of cooperativity depends on the equilibrium constant for switching the receptor from its low-affinity state to its high-affinity state (Eq. 4). In our design, this equilibrium constant is the product of the equilibrium constant for forming the intact binding sites in the absence of the linker, \( K_{\text{close}} \), and the unfavorable equilibrium constant associated with closing the linker, \( K_{\text{link}} \):

\[
K_s = K_{\text{link}} K_{\text{close}}.
\]  

[5]

Consistent with this, the cooperativity of our two-site mercury receptor falls monotonically as we shorten its loop (thus decreasing \( K_{\text{link}} \)) from 50 bases (\( n_{\text{link}} = 1.51 ± 0.03 \)) to 6 bases (\( n_{\text{link}} = 1.05 ± 0.05 \)) (Fig. 3, Middle). To put these observations on a still more quantitative footing, we note that, for linkers longer than the ~3-4 base persistence length of single-stranded DNA (30), \( K_{\text{link}} \) is dominated by the entropic cost of loop closure and thus should go as follows:

\[
K_{\text{link}} = L^{-1.75},
\]  

[6]

where \( L \) is linker length (31). Combining Eqs. 4–6, we can thus relate the degree of cooperativity of our constructs to the length of their unstructured loops as follows:

\[
n_H = \frac{2}{1 + \sqrt{K_{\text{close}} L^{-1.75} + 1}}.
\]  

[7]

Despite using only a single floating parameter, \( K_{\text{close}} \), this equation fits the observed Hill coefficients of our family of cooperative mercury receptors quite well (\( R^2 = 0.92 \)), speaking to the validity of our design model (Fig. 3, Right). Moreover, the fitted value of \( K_{\text{close}} \), 59 ± 30, corresponds to a free energy of −10.6 (±1.4) kJ/mol for the formation of the two-mismatch-containing stem. This, in turn, agrees to within experimental uncertainty with the −12.2 (±1.6) kJ/mol predicted by adding the −4.6 kJ/mol stability of the stem as predicted by the “DINAMelt Mfold” secondary structure prediction algorithm (32, 33) to the −7.6 (±1.6) kJ/mol prior literature estimates of the stabilization produced by the fluorophore–quencher pair we have used (34, 35).

Encouraged by these successful test case design efforts, we next adapted our simple strategy to engineer cooperativity into two structurally more complex receptors. For the first, we employed a sequence based on the doxorubicin-binding aptamer of Wochner et al. (36), which binds this important cancer chemotherapy agent with a dissociation constant of ~200 nM. Of note, the 3D structure of this aptamer is unknown, rendering this a significantly more challenging test of our design approach. To introduce cooperativity into the doxorubicin-binding aptamer, we first used DINAMelt Mfold as a guide to predict its likely secondary structure (Fig. 4, Top). Then we “cut” the parent aptamer sequence at a position within the single putative loop identified by Mfold and linked tandem repeats of the two resulting half-aptamers via unstructured polythymine sequences of either 30 or 50 bases. As expected, the construct using a 50-base linker is quite cooperative, exhibiting a Hill coefficient of 1.98 ± 0.04 and a dynamic range of just 9.2 (±0.4)-fold (Fig. 4, Bottom), values within experimental uncertainty of ideal behavior for a fully cooperative, two-site receptor. The construct using the shorter, 30-base linker is, as likewise expected, slightly less cooperative, achieving a Hill coefficient of 1.88 ± 0.03 and a useful dynamic range of 18.4-fold and 9.2-fold. The Hill coefficient of the parent aptamer, in contrast, is within experimental uncertainty of unity.

The quantitative model for folding-based cooperativity outlined above (Eq. 7) for our mercury receptors likewise describes the behavior of our doxorubicin-binding constructs. Specifically, Mfold (32, 33) predicts that the parent aptamer forms a stem loop structure with folding free energy that is unstable by 0.75 kJ/mol (per monomeric aptamer) in the absence of doxorubicin. When added to the favorable association energy of the fluorophore–quencher pair (34, 35), this yields a closing free energy of −6.1 kJ/mol and a \( K_{\text{close}} \) of 11.2 for the tandem repeat. Inserting the latter value into Eq. 7 predicts Hill coefficients of 1.71 and 1.80 for our 30-thymine and 50-thymine constructs, respectively, estimates that are reasonably close to the experimental values.
As a final test of the generality of our approach, we applied it to the cocaine-binding aptamer of Stojanovic et al. (37), the conformation of which is likewise not known in detail. Using a previously identified cut site (38), we engineered a cooperative receptor in which tandem repeats of the two halves of the aptamer are linked via an unstructured, 50-base polythymine sequence (Fig. 5, Top). The resultant construct exhibits a Hill coefficient of 1.65 ± 0.12 and dynamic range of binding of 14 (±) -fold (Fig. 5, Bottom). As with the cooperative mercury(II)- and doxorubicin-binding aptamers, the behavior of the cooperative cocaine-binding aptamer likewise appears consistent with Eq. 7. Complicating this analysis, however, is the fact that the aptamer is thought to contain a large number of non-Watson-Crick base pairs (38), and thus DINAMelt Mfold likely fails to accurately model its folding free energy. To overcome this, we instead used the experimentally determined folding free energy of the parent aptamer (39) to determine $K_{\text{close}}$. Specifically, the folding free energy of the fluorophore-and-quencher-modified parent aptamer is -7.5 kJ/mol. Given the known stabilizing effects of the fluorophore–quencher pair (34, 35), we thus estimate that the folding free energy of the dye-free parent aptamer is +0.1 kJ/mol. The folding free energy of a dimer of aptamers, one of which is dye-labeled, should thus be -7.4 kJ/mol, which in turn corresponds to a $K_{\text{close}}$ of 19. Inserting this value into Eq. 7 predicts a Hill coefficient of 1.75, which is again within experimental uncertainty of the observed value.

Here, we have demonstrated the utility of using binding-induced folding as an effective, quantitative, and potentially versatile means of engineering allosteric cooperativity into normally noncooperative biomolecular receptors. Specifically, we have used this approach to generate cooperative receptors starting from three distinct, unrelated aptamers that bind three distinct and unrelated molecular targets. The most cooperative of these redesigned receptors exhibits a Hill coefficient within experimental uncertainty of the theoretically expected maximum, thus converting the 81-fold dynamic range associated with single-site binding to a ninefold dynamic range and rendering the resultant receptor far more sensitive than its parent to small changes in the concentration of its target ligand. Finally, the approach is quantitative, with the degree of cooperativity attained for each of eight different receptors (again, binding three quite different molecular targets) closely matching the values expected given the switching equilibrium constant, $K_S$, of each of the modified aptamers (Fig. 6).

The ability to rationally engineer biomolecular receptors such that they overcome the “tyranny of the Langmuir isotherm” (40) and respond robustly to relatively small changes in the concentration of their target ligand has proven an important goal in molecular engineering and synthetic biology (14–19). Unfortunately, however, although nature frequently uses the simple, elegant mechanism of allosteric cooperativity to overcome this limitation, the generalizable ability to recapitulate this behavior in normally noncooperative biomolecular receptors has hitherto remained elusive, with successful examples of artificially engineered, allosteric cooperativity having been restricted to a small number of more-or-less nongeneralizable examples (9–12). In part, this is because our ability to rationally design biomolecules that switch reversibly between two well-defined conformations likewise remains limited (22). In response, we have demonstrated here a means of engineering cooperativity that circumvents this challenge by using the (easily achievable) unfolded state as one of the two required conformations. Given

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**Fig. 5.** As a final test of the generality of our approach, we applied it to the cocaine-binding aptamer of Stojanovic et al. (37). (Top) This aptamer is thought to form a three-way junction. (Bottom) The modified aptamer achieves substantial cooperativity, exhibiting a Hill coefficient of 1.65 ± 0.12. The parent aptamer, in contrast, exhibits a Hill coefficient within experimental uncertainty of unity.

**Fig. 6.** We have achieved the rational, quantitative introduction of cooperativity into a range of aptamer-based receptors. As shown here, for example, Eq. 4 (solid line), which defines the expected relationship between $K_S$, the equilibrium constant for receptor “folding,” and $n_H$, the Hill coefficient, describes the behavior of all eight of the receptors reported in this paper with reasonable accuracy despite its lacking any fitted parameters. The biomolecules shown include receptors designed to cooperatively bind mercury ions (Hg), doxorubicin (Dox), and cocaine (Coc), and featuring, as denoted in the figure, unstructured loops of between 6 and 50 bases.
the case with which single domain proteins can similarly be reengineered to undergo binding-induced folding (see, e.g., refs. 41 and 42), and the recent report of a naturally occurring protein that employs intrinsic disorder to generate cooperative binding (25), we suspect that intrinsic disorder may also prove a useful means of rationally optimizing the responsiveness of protein-based receptors.

Materials and Methods

Detailed methods are available in SI Materials and Methods. Briefly, DNA probes modified with a carboxyfluorescein (FAM) and a black-hole-quencher-1 (BHQ-1) were used as purchased (BioSearch Tech and IBA). We obtained all fluorescence measurements with excitation at 485 (±5) nm and acquisition at 515 (±10) nm. We used GraphPad Prism plotting software to fit titration curves to the Hill equation. Confidence intervals represent 95% confidence based on SEs derived from the fitting software.

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