cAMP is an allosteric modulator of DNA-binding specificity in the cAMP receptor protein from Mycobacterium tuberculosis

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Signal transduction is an essential process that allows cells to cope and respond to changes in their environment (1). Many signaling pathways rely on small molecules to transduce external stimuli to one or more effector proteins inside the cell (2). cAMP is an ancient, ubiquitous small molecule that serves as a second messenger in many signal transduction pathways, including regulation of gene expression in response to changes in environmental conditions (3–5).

The cAMP receptor protein (CRP) is a homodimeric transcription factor targeted by cAMP (6–8). Each CRP subunit harbors a structured conserved N-terminal cAMP-binding domain that is covalently linked to a DNA-binding domain located in the C-terminal portion of the protein (9–14). Solution biophysical and structural studies have shown that cAMP binding to the CRP from Escherichia coli (CRP_Ecoli) stimulates a large conformational change in the DNA-binding domains (Fig. 1, A and B, top) (10, 13, 15–17). In contrast, structures of the CRP from Mycobacterium tuberculosis (CRP_MTB) in the apo-form and cAMP-bound form reveal smaller cAMP-induced conformational changes (Fig. 1, A and B, bottom) (11, 14). The CRP_Ecoli and CRP_MTb display structural differences in both the apo-state and cAMP-bound state, most notably in their DNA-binding domain orientations relative to the C-terminal domains (Fig. 1C). Additional differences are observed in the homodimer symmetry. In the CRP_Ecoli the two subunits in the apo-state are symmetric, but the cAMP-bound state shows asymmetry between the DNA-binding domains’ conformation (18) (Fig. 1D, top). Conversely, the subunits in the CRP_MTb in the apo-state are asymmetric at the dimer interface helix (c-helix) and the DNA-binding domains, but the cAMP-bound state is highly symmetric (Fig. 1D, bottom). Finally, the CRP_MTb harbors two additional α-helices, one at the N terminus and another at the C terminus, resulting in a slightly larger protein than the CRP_Ecoli (Fig. 1E).

The CRP_Ecoli and CRP_MTb show structural differences, and their functional response to cAMP binding also differs. In the CRP_Ecoli cAMP binding enhances the affinity of the protein to tightly interact with pseudopalindromic gene promoter sequences involved in carbohydrate metabolism (18–23). In the...
Figure 1. Structural comparison between the CRP_{Ecoli} and CRP_{MTB}. The CRP has a conserved structural organization with two identical subunits, each one harboring a cAMP-binding domain in the N terminus (pale cyan in the CRP_{Ecoli}; tan in the CRP_{MTB}) and a DNA-binding domain in the C terminus (dark teal in the CRP_{Ecoli}; dark brown in the CRP_{MTB}). A, structures of the CRP_{Ecoli} and CRP_{MTB} in the absence and presence of cAMP. B, alignment of apo-subunit (light teal and light brown) and cAMP-bound subunit for both the CRP_{Ecoli} (top) and CRP_{MTB} (bottom). C, alignment of the CRP_{Ecoli} and CRP_{MTB} homodimers. D, alignment of intraspecies monomers (left, apo-state; right, cAMP-bound state) for the CRP_{Ecoli} (top) and CRP_{MTB} (bottom). E, the CRP_{Ecoli} and CRP_{MTB} sequence alignment with mapped secondary structures (α-helices in blue; β-strands in light brown; asterisk indicates residue identity; colon indicates similar residues, and dot indicates weakly similar residues). Differences in the sequence between the CRP_{MTB} and CRP_{Ecoli} are located at positions E178 (red spheres) and L47 (light blue spheres). cAMP is shown as brown spheres. See Experimental procedures for description of alignment and Protein Data Bank codes. CRP, cAMP receptor protein; CRP_{Ecoli}, CRP from *Escherichia coli*; CRP_{MTB}, CRP from *Mycobacterium tuberculosis*. 

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Table 1

| Method | cAMP-binding affinity | Binding cooperativity |
|--------|-----------------------|----------------------|
| ITC    | $k_1$: 3.0 ± 0.9 | $k_2$: 1.2 ± 0.2 | $c$: 0.4 ± 0.2 |
| ANS    | $k_1$: 3.5 ± 0.2 | $k_2$: 2.2 ± 0.1 | $c$: 0.6 ± 0.1 |

DNA promoter sequences. We find that in the apo-state, the protein forms high-order CRPMTB–DNA oligomers. These oligomers are mediated by interactions between the CRPMTB and nonspecific DNA sequences, and by interactions between a CRPMTB–DNA complex and the free CRPMTB. Unexpectedly, the presence of cAMP decreases nonspecific interactions with DNA and reversibly dissociates high-order CRPMTB–DNA oligomers into stable, 1-to-1 stoichiometric complexes. We also investigated the double-mutant L47P/E178K, which is found in the CRP from the attenuated Mycobacterium bovis Bacille Calmette-Guérin strain (CRPBCG) (mutation sites shown in Fig. 1A, bottom) and only differs from the CRPMTB sequence in those two amino acid residues (28–30). While the CRPBCG displays negative cAMP-binding cooperativity like the CRPMTB, we find that cAMP does not prevent the formation of high-order CRPBCG–DNA oligomers. These functional differences are not observed in the single mutants L47P (CRPMTB–L47P) and E178K (CRPMTB–E178K), indicating nonlinear contributions and long-range interactions between the two mutation sites. In agreement with nonlinear mutant contributions, the thermodynamic stability and dimerization constant of the CRPBCG are also different from the single mutants.

In combination, these results provide an archetype of cAMP-mediated regulation that is significantly different from those described previously in other CRPs, such as the well-characterized E. coli homolog, and illustrate that structural homology does not imply allosteric homology. In other words, two structures could be very similar but respond very differently to the same allosteric effector.

Table 2

| Buffer  | $k_1$ | $k_2$ | $c$     |
|---------|-------|-------|---------|
| Cacodylate | 3.9 ± 0.9 | 1.8 ± 0.4 | 0.45 ± 0.13 |
| PBS     | 3.4 ± 0.5 | 1.2 ± 0.8 | 0.35 ± 0.13 |
| Heps    | 3.0 ± 0.9 | 1.2 ± 0.2 | 0.39 ± 0.11 |

C, cooperativity factor between cAMP-binding sites; CRPMTB, CRP from Mycobacterium tuberculosis; ITC, isothermal titration calorimetry; $k_1$, cAMP-binding affinity constant for the first cAMP-binding site; $k_2$, cAMP-binding affinity constant for the second cAMP-binding site; $c$, cAMP-binding affinity constant for the second cAMP-binding site.

CRPMTB, the affinity for DNA promoters with and without cAMP appears to be similar (12, 20, 24). The small cAMP-induced conformational change in the CRPMTB provides a structural explanation by which this protein does not change its affinity to DNA upon binding to the cyclic nucleotide (6, 12, 16, 25). It is therefore possible that the CRPMTB is not sensitive to cAMP, but previous studies have shown that cAMP interactions with the CRPMTB are important in the regulation of the gene whiB1 (12, 26). It is therefore possible that the allosteric regulation triggered by cAMP in the CRPMTB may not be directly associated to large changes in protein conformation that enhance the affinity for specific DNA promoter sequences, as seen in the CRP_Ecoli. To dissect the mechanisms by which cAMP allosterically regulates CRPMTB–DNA binding, in this study, we quantitatively characterize the linkage between cAMP and DNA interactions. We combine complementary solution biophysical approaches to measure cAMP-binding affinity and cooperativity, interactions with the DNA promoter SerC (6, 27) as a function of cAMP concentration, and protein solution structure, assembly, and thermodynamic stability.

The results from this study reveal that the CRPMTB binds cAMP with moderate negative cooperativity. In agreement with previous reports (12), the affinity of the CRPMTB for promoter sequences is similar in the presence and in the absence of cAMP, indicating that the cyclic nucleotide does not regulate transcription at the level of affinities to specific DNA promoter sequences. We find that in the apo-state, the protein forms high-order CRPMTB–DNA oligomers. These oligomers are mediated by interactions between the CRPMTB and nonspecific DNA sequences, and by interactions between a CRPMTB–DNA complex and the free CRPMTB. Unexpectedly, the presence of cAMP decreases nonspecific interactions with DNA and reversibly dissociates high-order CRPMTB–DNA oligomers into stable, 1-to-1 stoichiometric complexes. We also investigated the double-mutant L47P/E178K, which is found in the CRP from the attenuated Mycobacterium bovis Bacille Calmette-Guérin strain (CRPBCG) (mutation sites shown in Fig. 1A, bottom) and only differs from the CRPMTB sequence in those two amino acid residues (28–30). While the CRPBCG displays negative cAMP-binding cooperativity like the CRPMTB, we find that cAMP does not prevent the formation of high-order CRPBCG–DNA oligomers. These functional differences are not observed in the single mutants L47P (CRPMTB–L47P) and E178K (CRPMTB–E178K), indicating nonlinear contributions and long-range interactions between the two mutation sites. In agreement with nonlinear mutant contributions, the thermodynamic stability and dimerization constant of the CRPBCG are also different from the single mutants.

In combination, these results provide an archetype of cAMP-mediated regulation that is significantly different from those described previously in other CRPs, such as the well-characterized E. coli homolog, and illustrate that structural homology does not imply allosteric homology. In other words, two structures could be very similar but respond very differently to the same allosteric effector.

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$c$, cooperativity factor between cAMP-binding sites; CRPMTB, CRP from Mycobacterium tuberculosis; ITC, isothermal titration calorimetry; $k_1$, cAMP-binding affinity constant for the first cAMP-binding site; $k_2$, cAMP-binding affinity constant for the second cAMP-binding site.

The error corresponds to the SD from fitted parameters using a two-site binding model as described in Experimental procedures. The units of $k_1$ and $k_2$ are 10^{7} M^{-1} s and $c = k_2/k_1$. 

Figure 2. Characterization of cAMP binding to the CRPMTB. A, the upper panel corresponds to the calorimetry data of the titration of cAMP monitored by ITC in Hepes buffer. The lower panel shows the resulting cAMP-binding isotherm. The solid line represents the fit using a sequential two-site binding model with residuals (Equations 12 and 14 in Experimental procedures). B, buffer ionization enthalpy for each cAMP-binding event: from left to right: cacodylate, PBS, and Hepes buffer. The error bars correspond to the SD from three to four experimental repeats. We find that ΔH1 in each buffer is not statistically indistinguishable ($p = 0.23$), but ΔH2 shows statistical pairwise differences among all buffers ($p = 3 	imes 10^{-4}$). C, cAMP binding monitored by changes in ANS fluorescence. The solid line represents the fit using a two-site binding model (Equation 16 in Experimental procedures). CRPMTB, CRP from Mycobacterium tuberculosis; ITC, isothermal titration calorimetry; ΔH1, enthalpy change for the first cAMP-binding site; ΔH2, enthalpy change for the second cAMP-binding site; ANS, 8-anilino-1-naphthalenesulfonic acid.
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Figure 3. Effect of cAMP on the CRP<sub>MTB</sub> interactions with the SerC promoter. A, CRP<sub>MTB</sub>–DNA complex formation using 3 nM of the 32-bp SerC promoter with cAMP concentrations equal to 0, 0.1, 1 mM (light purple, light pink, and dark pink, respectively). The red arrow indicates the titration point at which the anisotropy in the absence of cAMP significantly increases from experiments in its presence. B, stoichiometric binding using 200 nM of DNA (32-bp SerC) for the apo-conformation (light purple) and doubly cAMP-bound (dark pink) conformations. The vertical dashed line shows the CRP<sub>MTB</sub>–DNA complex formed at a 1-to-1 molar ratio. C, cAMP binding to the preformed CRP<sub>MTB</sub>–DNA complex using 230 nM of protein and 3 nM of 32-bp SerC promoter fragment. Dark yellow and light purple squares correspond to the cAMP titration and buffer titration (i.e., control experiment), respectively. D, binding of the CRP<sub>MTB</sub> to a 32-bp scramble sequence (3 nM). Light purple and dark pink squares correspond to the apo-conformation and doubly cAMP-bound conformation, respectively. The solid line corresponds to a control experiment with the buffer added instead of the protein. E, the CRP<sub>MTB</sub>–DNA complex formation using a 20-bp-long SerC promoter (3 nM). Dark pink and light purple circles correspond to the cAMP titration curve for the apo-conformation and doubly cAMP-bound conformations, respectively. F, stoichiometric binding using 400 nM of DNA (20-bp-long SerC) for the apo-conformation (light purple) and doubly cAMP-bound (dark pink) conformations. The dashed line denotes the concentration of the CRP by which the formation of the CRP<sub>MTB</sub>–DNA complex is at a 1-to-1 molar ratio. Solid lines in panels A and E are the fit as described in Equation 18 in Experimental procedures. In all panels, error bars correspond to the SD of three to 5 experimental repeats. CRP<sub>MTB</sub>, CRP from Mycobacterium tuberculosis; CRP, cAMP receptor protein.

Results

CRP<sub>MTB</sub> exhibits negative cooperativity between the two cAMP-binding domains

We first used isothermal titration calorimetry (ITC) to quantitatively determine the cAMP-binding affinity constants, cooperativity, and their underlying thermodynamic driving forces (Fig. 2A, Table 1). To ensure full saturation of the CRP<sub>MTB</sub>, we conducted ITC experiments using up to a five-fold molar excess of cAMP to protein. By fitting the ITC data to various binding models, we found that a two-site sequential binding mechanism (19, 24) provided better fitting statistics than a set of independent binding sites (Fig. S1 and Table S1). The site-specific binding constants we obtained were \( k_1 = (3.0 \pm 0.9) \times 10^4 \text{ M}^{-1} \) and \( k_2 = (1.2 \pm 0.2) \times 10^5 \text{ M}^{-1} \) (all errors represent the SD of the fit). The ratio between the two binding constants, \( c = k_2/k_1 = 0.4 \pm 0.2 \), indicates negative cooperativity between the two cAMP-binding domains (Table 1). ITC experiments using various buffers (Hepes, PBS, and cacodylate, Fig. S2 and Table S1) were performed to dissect a potential contribution of proton ionization to the observed cAMP-binding enthalpies and to determine whether the release or uptake of protons is associated with the cAMP-binding reactions (31, 32). We find that both cAMP-binding events are endothermic (enthalpy change for the first cAMP-binding site = \( 4.7 \pm 0.3 \text{ kcal mol}^{-1} \) and enthalpy change for the second cAMP-binding site = \( 5.0 \pm 1.0 \text{ kcal mol}^{-1} \)) and therefore entropically driven (\( \Delta T\Delta S_1 = 10.8 \text{ kcal mol}^{-1} \) and \( \Delta T\Delta S_2 = 10.5 \text{ kcal mol}^{-1} \)). Moreover, we find that the first cAMP-binding event is independent of the buffer-ionization enthalpy, whereas the second one displayed a slope of \( 1.0 \pm 0.3 \), indicating proton uptake by the protein (Fig. 2B). The asymmetry in proton uptake during cAMP binding may be a consequence of the asymmetry seen in the apo-CRP<sub>MTB</sub> structure (Fig. 1D, bottom) or asymmetric states in partially liganded conformations (19, 22). Importantly, in all three buffers used in this study, a two-site sequential binding mechanism resulted in better fitting statistics (Table S2) and revealed negative cAMP-binding cooperativity (Table 2). In addition to ITC experiments, we monitored cAMP binding via changes in 8-anilino-1-naphthalenesulfonic acid (ANS) fluorescence (Fig. 2C) (19, 24, 33). The data were fitted to two binding polynomials, wherein a model allowing for cooperativity provided a statistically better fit than a model with independent binding sites (Fig. S3 and Table S2). Moreover, the binding constants obtained from the ANS-based assay are in agreement with the results using ITC and support the observed negative cooperativity between the two cAMP-binding sites: \( k_1 = (3.5 \pm 0.2) \times 10^4 \text{ M}^{-1} \) and \( k_2 = (2.2 \pm 0.1) \times 10^5 \text{ M}^{-1} \) and \( c = 0.6 \pm 0.1 \) (Table 1).

CRP<sub>MTB</sub>–DNA interactions as a function of cAMP concentration

Previous structural studies have shown that binding of cAMP induces small conformational changes to the DNA-binding domain of the CRP<sub>MTB</sub> allowing the protein to switch from an asymmetric structure to a symmetric, active

Table 3

| Promoter length | \( k_{DNA(apo)} \) | \( k_{DNA(cAMP)} \) | \( k_{DNA(cAMP-2)} \) |
|-----------------|------------------|------------------|------------------|
| 32-bp SerC promoter | \( 2.3 \pm 0.9 \) | \( 4.5 \pm 1.2 \) | \( 4.2 \pm 1.7 \) |
| 20-bp SerC promoter | \( 0.12 \pm 0.02 \) | — | \( 0.5 \pm 0.1 \) |

CRP<sub>MTB</sub>, CRP from Mycobacterium tuberculosis; \( k_{DNA(apo)} \), DNA-binding affinity constant in the apo conformation; \( k_{DNA(cAMP)} \), DNA-binding affinity constant in the doubly cAMP-bound state; \( k_{DNA(cAMP-2)} \), DNA-binding affinity constant in the singly cAMP-bound state. The error corresponds to the SD from fitted parameters as described in Experimental procedures. The units of \( k_{DNA(apo)} \), \( k_{DNA(cAMP)} \), and \( k_{DNA(cAMP-2)} \) are \( 10^8 \text{ M}^{-1} \).
conformation (11, 14) (Fig. 1D, bottom). However, the effect of this conformational transition on the affinity between the CRP\textsubscript{MTB} and DNA promoter sequences is not fully understood. Thus, we investigated the role that cAMP occupancy plays in the formation of the CRP\textsubscript{MTB}–DNA complex. The formation of the CRP\textsubscript{MTB}–DNA complex was monitored \textit{via} changes in fluorescence anisotropy, normalized to the first protein concentration point (19, 20). We used a 32-bp fluorescein-labeled SerC promoter, a well-characterized promoter targeted by the CRP\textsubscript{MTB} (6, 14, 27, 34). These experiments were conducted using 0, 0.1, and 1 mM of cAMP. At these concentrations, the protein is in the apo-state, in a mix of singly and doubly cAMP-bound states (based on the binding affinity constants determined in this study) and in the doubly cAMP-bound state, respectively (Fig. S4).

In all three cAMP concentrations, the anisotropy of the labeled promoter increased as a function of the protein concentration, indicating that the formation of the CRP\textsubscript{MTB}–DNA complex occurs even in the absence of cAMP (Fig. 3A), a result that is in agreement with Rickman \textit{et al}. (25) and Bai \textit{et al}. (6). The DNA binding constants for the apo-state and doubly cAMP-bound state are $k_{DNA(apo)} = (2.3 \pm 0.9) \times 10^8$ M$^{-1}$ and $k_{DNA(CAMP,2)} = (4.2 \pm 1.7) \times 10^8$ M$^{-1}$, respectively (Table 3). At intermediate concentrations of cAMP (0.1 mM), where populations of singly and doubly cAMP-bound states coexist, we obtained similar binding affinities as in conditions used where only the doubly cAMP-bound conformation is populated. Altogether, these results indicate that the allosteric linkage initiated by cAMP binding is not associated with enhancing the binding affinity for specific DNA promoter sequences.

**cAMP prevents the formation of high-order CRP\textsubscript{MTB}–DNA oligomers**

While the DNA-binding affinity constants were similar in all three concentrations of cAMP, we did observe important differences in the anisotropy signal toward the end of the titration (Fig. 3A, red arrow). In the absence of cAMP, the anisotropy signal gradually increased after the DNA-binding transition. In contrast, in the presence of cAMP (0.1 or 1 mM), the anisotropy signal remained nearly constant after the DNA-binding transition. This distinctive behavior suggests the formation of high-order CRP\textsubscript{MTB}–DNA oligomers in the apo-state that are prevented or reduced when the protein is bound to cAMP.

We confirmed these results by conducting stoichiometric DNA-binding assays using a concentration of the SerC promoter that is 10 to 20 times larger than the dissociation constant ($K_D$) (Table 3). These experiments revealed a linear increase in the anisotropy signal that plateaus at a 1-to-1 molar ratio of protein to DNA, demonstrating that one molecule of the CRP\textsubscript{MTB} binds to one molecule of DNA (Fig. 3B). In the absence of cAMP, we observe an overlap with the titration curve obtained with cAMP until a protein-to-DNA molar ratio of 1. However, after the 1-to-1 molar ratio is reached, the anisotropy signal in the apo-state continues to rise steadily, indicating again the formation of high-order CRP\textsubscript{MTB}–DNA oligomers.

In agreement with previous reports (12), our results show that cAMP does not have a large effect on DNA-binding affinities. However, titrations with a molar excess of protein to DNA, either with or without the cyclic nucleotide, suggest a noncanonical role for cAMP in allosteric signaling. Namely, that cAMP binding to the CRP\textsubscript{MTB} prevents the formation of high-order DNA–protein oligomers. We therefore sought to determine what intermolecular interactions are involved in the formation of these oligomers and how cAMP binding prevents their formation.

**cAMP reverses preformed CRP\textsubscript{MTB}–DNA oligomers**

Our previous experiments show that cAMP prevents the formation of high-order CRP\textsubscript{MTB}–DNA oligomers, yet to be determined is whether cAMP can reversibly dissociate such oligomers in a preformed state. To address this question, we preformed high-order CRP\textsubscript{MTB}–DNA oligomers and monitored changes in anisotropy as a function of the cAMP concentration (Fig. 3C). In these experiments, we used a concentration of CRP\textsubscript{MTB} = 230 nM and the 32-bp fluorescein-labeled SerC promoter = 3 nM. At these concentrations of protein and DNA, we obtained the highest normalized anisotropy value that is experimentally accessible in the absence of cAMP, around 1.25 (Fig. 3A).

Figure 3C shows that upon titration of cAMP, the anisotropy signal of preformed CRP\textsubscript{MTB}–DNA oligomers decreases systematically, whereas in the absence of cAMP, the anisotropy remained constant. Importantly, the change in normalized anisotropy (~0.09) upon cAMP binding is consistent with the difference in the normalized anisotropy signals seen between titration curves of the protein in the apo-state (~1.25) and cAMP-bound states (~1.15) (Fig. 3A). This quantitative agreement indicates that the decrease in anisotropy during the titration of cAMP corresponds to the reversible dissociation of high-order CRP\textsubscript{MTB}–DNA oligomers into a 1-to-1 complex. Furthermore, we fitted the changes in anisotropy as a function of cAMP to a single-site binding isotherm, which reflects the affinity of the preformed CRP\textsubscript{MTB}–DNA complex for cAMP. The apparent binding affinity constant was (6.3 ± 1.5) $\times 10^4$ M$^{-1}$, a value that is three times higher than the affinity of the first cAMP-binding site in the absence of DNA (Table 1). A two-site binding model did not improve the residuals of the fit (data not shown), suggesting that only one cAMP molecule per CRP dimer is sufficient to reversibly dissociate high-order CRP\textsubscript{MTB}–DNA oligomers. Given that apo-CRP\textsubscript{MTB} binds cAMP with modest negative cooperativity, it is possible that the anisotropy assay cannot detect small differences in affinity between one or two cAMP-binding events.

**CRP\textsubscript{MTB} binds nonspecifically to DNA in the absence of cAMP**

To begin uncovering the molecular interactions that stabilize high-order CRP\textsubscript{MTB}–DNA oligomers, we first studied nonspecific DNA interactions using a 32-bp fluorescein-labeled scramble sequence. Because the scramble sequence lacks the conserved SerC-binding site (6), any changes in anisotropy would reflect nonspecific binding of the CRP\textsubscript{MTB} to

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DNA. Figure 3D shows the titration curve of the CRP<sub>MTB</sub> to the 32-bp scramble DNA sequence in the absence and presence of 1 mM cAMP. The titration shows identical anisotropy in both conditions (i.e., apo-state and cAMP-bound state) up to a concentration of protein of ~80 nM. At higher protein concentrations, we observe an increase in anisotropy values only in the absence of cAMP, indicating that the protein in the apo-state is binding to DNA in a nonspecific manner. The control titration (solid black line, Fig. 3D), where only the buffer was added instead of the protein, shows negligible changes in anisotropy. These results suggest that the formation of high-order CRP<sub>MTB</sub>–DNA oligomers in the absence of cAMP can be driven by interactions with nonspecific DNA sequences.

**Formation of CRP<sub>MTB</sub>–DNA complexes with shorter promoter sequences**

Next, we explored the nature of nonspecific DNA binding. We reasoned that the increase in anisotropy fluorescence in the absence of cAMP could arise from (1) apo-proteins interacting nonspecifically to flanking sequences outside the DNA footprint region or (2) binding of free proteins to preformed CRP<sub>MTB</sub>–DNA complexes. To distinguish between these two scenarios, we used SerC promoter sequences of decreasing lengths, down to the DNA footprint of the CRP<sub>MTB</sub> based on the high-resolution structure, ~18 bp (11, 14).

First, we determined the shortest DNA fragment that stably binds to the CRP<sub>MTB</sub>. We performed EMSAs using six different lengths of the SerC promoter (18, 20, 22, 24, 26, and 32bps) (Fig. S5). Our data show that 20-bp is the minimum base pair length required for the CRP<sub>MTB</sub> to bind robustly to DNA. A 20-bp SerC promoter sequence would only have 1-bp of overhang on each side, thereby minimizing potential protein interactions to DNA flanking regions.

The DNA binding constant for the 20-bp SerC promoter was quantitatively determined by fluorescence anisotropy. Figure 3E shows the titration curve of the CRP<sub>MTB</sub> in the absence and presence of 1 mM cAMP. The DNA binding constants for the apo-state and cAMP-bound state were $k_{DNA(apo)} = (0.12 \pm 0.02) \times 10^8$ M$^{-1}$ and $k_{DNA(cAMP-2)} = (0.5 \pm 0.1) \times 10^8$ M$^{-1}$, respectively. These values are ~10-fold lower than the binding constant for the 32-bp-long SerC promoter (Table 3). Importantly, stoichiometric binding assays shown in Figure 3F demonstrate that even in the almost complete absence of DNA flanking regions, there is still formation of high-order CRP<sub>MTB</sub>–DNA oligomers when cAMP is absent. We interpret this result as the free CRP<sub>MTB</sub> binding to preformed CRP<sub>MTB</sub>–DNA complexes. Together with our previous results using the 32-bp scramble DNA sequence (Fig. 3D), our data indicate that these oligomers can be mediated by both nonspecific interactions between the protein and DNA and the binding of the free CRP<sub>MTB</sub> to a preformed CRP<sub>MTB</sub>–DNA complex.

**Effect of mutations L47P and E178K on cAMP-binding affinity and cooperativity**

The CRP<sub>BCG</sub> only differs in two amino acids at positions L47P and E178K relative to the CRP<sub>MTB</sub>, which are located in the cAMP-binding domain and the DNA-binding domain, respectively (Fig. 1A, bottom). These mutations, which are not present in other CRP orthologs found in *M. bovis, M. tuberculosis*, or *Mycobacterium leprae*, have been implicated as potential contributing factors to the attenuation of BCG strains (28, 30). However, it remains unclear how the CRP<sub>BCG</sub> differs from the CRP<sub>MTB</sub> in its interaction mechanisms with cAMP or what are the contributions of each individual mutation toward cAMP-binding affinities and cooperativity.

To answer these questions, we placed the individual mutations on the CRP<sub>MTB</sub> (termed CRP<sub>MTB</sub>–L47P and CRP<sub>MTB</sub>–E178K) or the two together (CRP<sub>BCG</sub>) and determined their...
cAMP-binding affinities and cooperativity by monitoring changes in ANS fluorescence. Our data show that the affinity constants for the first cAMP-binding site ($k_1$) are similar among the three CRP mutants, but the affinity for the second site ($k_2$) was significantly lower for the CRPBCG (Fig. 4A, Table 4). As a result, the cAMP-binding cooperativity ranges from neutral for CRPMTB–E178K and CRPMTB–L47P ($c = 1$) to negative for the CRPBCG ($c = 0.3$) (Fig. S6). These results suggest that the cAMP-binding mode of the CRPBCG is not attributed to a single mutation or a simple linear addition between the effects of the two individual mutations.

**Nonlinear effects of BCG mutations on CRP–DNA interactions**

Given the nonlinear contributions of the individual BCG mutations over cAMP binding, we investigated the role of each mutation on DNA interactions using the 32-bp fluorescein-labeled SerC promoter. In the absence of cAMP, we found that CRPMTB–L47P has a DNA-binding affinity similar to that of the CRPMTB–C. However, CRPMTB–E178K binds to the promoter sequence with a ~10-fold enhancement (Fig. 4B, Table 4). Because E178K is located at or is near the DNA-interaction surface (Fig. 1, bottom) and the mutation involves a change from a negatively to a positively charged amino acid side chain, it was not unexpected to observe a higher DNA-binding affinity than the CRPMTB or CRPMTB–L47P. The unexpected result was that the CRPBCG binds DNA with an affinity similar to that of the CRPMTB or CRPMTB–L47P, indicating that the enhancing DNA-binding affinity effect of E178K is largely reduced by the presence of L47P.

CRPMTB–L47P and the CRPBCG revealed an important difference in the formation of high-order CRP–DNA oligomers. In the absence of cAMP, both proteins did not form oligomers as pronouncedly as the CRPMTB and CRPMTB–E178K. For example, at a concentration of the CRPMTB of ~50 nM (with [DNA] = 3 nM) the presence of oligomers becomes very evident and pronounced for the CRPMTB and CRPMTB–E178K (red arrow in Figs. 3A and 4B, respectively). Neither CRPMTB–L47P nor the CRPBCG forms noticeable CRP–DNA oligomers (Fig. 4B). These results again highlight nonlinear contributions of each BCG mutation toward both DNA-binding affinities and reduction in the formation of high-order CRP–DNA complexes. By comparison, the functional phenotype of the CRPBCG is dominated by the contributions of the L47P mutation. Interestingly, the location of L47P is in the cAMP-binding domain, but its dominant effect over DNA interactions indicates long-range allosteric communication between cAMP- and DNA-binding domains.

**Figure 5. Biophysical characterization of CRPs.** A, tryptophan emission spectra of CRPs (5 mM) with an excitation wavelength of 295 nm. B, CD spectra of CRPs (5 mM). C, g(s) plots for CRPs showing concentration dependence for the CRPBCG. Solid gray lines in panels A–C represent the data for the CRPMTB (labeled MTB). Chemical denaturation monitored by changes in tryptophan fluorescence (D) and CD (E). For comparison, gray dashed lines correspond to the CRPMTB (labeled MTB). The solid lines are the fits using a two-state unfolding model for the individual mutants and a three-state unfolding model for the CRPBCG (Equations 6 and 11 in Experimental procedures, respectively). CRPMTB, CRP from *Mycobacterium tuberculosis*; CRP, cAMP receptor protein; CRPBCG, CAMP receptor protein from *Mycobacterium bovis* Bacille Calmette-Guérin strain; MTB, *Mycobacterium tuberculosis*.
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Table 5
Thermodynamic stability of the CRPMTB, CRPBCG, and single mutants

| CRP protein | ΔG° | m   | C1/2 |
|-------------|-----|-----|------|
| MTB         | 5.4 ± 0.8 | −3.4 ± 0.4 | 1.6 ± 0.4 |
| L47P        | 3.9 ± 0.9 | −2.5 ± 0.5 | 1.6 ± 0.7 |
| E178K       | 6.3 ± 0.9 | −3.8 ± 0.5 | 1.7 ± 0.5 |
| BCG         | ΔG°1 2.9 ± 0.5 | m1 4.2 ± 0.6 | 0.7 ± 0.2 |
|             | ΔG°2 3.4 ± 2.1 | m2 2.1 ± 1.1 | 1.6 ± 1.8 |
| Fluorescence| ΔG° | m   | C1/2 |
| MTB         | 2.6 ± 0.3 | −19 ± 0.2 | 1.5 ± 0.4 |
| L47P        | 2.6 ± 0.4 | −17 ± 0.2 | 1.4 ± 0.3 |
| E178K       | 1.8 ± 0.4 | −15 ± 0.1 | 1.2 ± 0.4 |
| BCG         | 2.0 ± 0.4 | −16 ± 0.2 | 1.3 ± 0.4 |

BCG, Bacille Calmette-Guérin; CRPBCG, cAMP receptor protein from Mycobacterium bovis Bacille Calmette-Guérin strain; CRPMTB, CRP from Mycobacterium tuberculosis; ΔG°, free energy change; MTB, Mycobacterium tuberculosis.

The error corresponds to the SD from fitted parameters using a two-state and three-state models as described in Experimental procedures. The units of ΔG°, m (m-value), and C1/2 (unfolding transition midpoint) are kcal mol⁻¹, kcal mol⁻¹ M⁻¹, and M⁻¹, respectively.

Effect of cAMP on CRPBCG–DNA interactions

We showed that the CRPMTB and CRPBCG have similar cAMP-binding affinity constants and display negative cooperativity (Tables 1 and 4). Here, we examined the linkage between cAMP and DNA binding for the CRPBCG. We monitored changes in anisotropy upon the formation of the CRPBCG–DNA complex (using the 32-bp fluorescein-labeled SerC promoter) at three cAMP concentrations: 0, 0.1, and 1 mM. At [cAMP] = 0.1 mM, 60% of the CRPBCG population corresponds to the singly bound conformation, whereas the other 40% corresponds to doubly bound conformation. At 1 mM of cAMP, 90% of the population corresponds to a doubly cAMP-bound state, thus almost reaching a saturated state (Fig. S7). The anisotropy data revealed indistinguishable DNA-binding constants in all cAMP concentrations: kDNA(apo) = (5.6 ± 3.0)×10⁻⁸ M⁻¹, DNA-binding affinity constant in the singly cAMP-bound state = (6.0 ± 5.3)×10⁻⁸ M⁻¹, and kDNA(CAMP-2) = (7.5 ± 3.4)×10⁻⁸ M⁻¹ (Fig. 4C, Table 4). This result is consistent with titrations with the CRPMTB that shows small cAMP effects over the interaction with the specific promoter-binding site. In contrast with the CRPMTB, the effect of cAMP binding in reducing high-order CRP-DNA oligomers was negligible for the CRPBCG. This was also observed in stoichiometric binding assays (Fig. 4D). We therefore explored the effect of cAMP on DNA interactions for each individual mutant (Fig. 4, E and F). We find that both the CRPMTB–L47P and CRPMTB–E178K form high-order CRP–DNA oligomers in the absence of cAMP, which are significantly reduced in the presence of intermediate (0.1 mM) or saturating (1 mM) amounts of cAMP (Fig. 4, E and F). Altogether, our DNA binding data are consistent with cAMP-binding studies that indicate asymmetric contributions of individual mutations to the CRPBCG homolog. In this case, their influence on DNA interactions (specific or nonspecific) does not follow a simple linear combination, an analogous observation to results obtained in cAMP-binding assays (Fig. 4A).

Solution structure and stability of the CRPBCG differs from single mutants and the CRPMTB

The functional differences observed between the CRPBCG and the single mutants CRPMTB–L47P and CRPMTB–E178K or the CRPMTB may arise from differences in their native solution structure, assembly state, or stability. The protein solution structure and assembly were evaluated by using three biophysical methods: intrinsic protein fluorescence, CD, and analytical ultracentrifugation (AUC). The intrinsic fluorescence emission spectra were similar for all four CRPs, indicating that the tertiary structures surrounding the tryptophan residues (with excitation wavelength at 295 nm) are largely unaffected by the mutations (Fig. 5A). Spectra obtained using an excitation wavelength of 280 nm that includes the contribution of one tyrosine residue per subunit show no differences between all four CRPs (data not shown). Similarly, the CD spectra for all CRPs overlapped, indicating that the global native fold and secondary structure content of the proteins are the same (Fig. 5B).

The degree to which CRP is a stable homodimer was assessed by AUC (i.e., sedimentation velocity [SV]). Experiments conducted at monomer concentrations ranging between 1 and 40 μM showed, with exception of the CRPBCG, a constant sedimentation coefficient corresponding to the molecular mass of the homodimer (52.2 kDa) and a dimerization Kd lower bound of 10 nM. This result indicates that the CRPMTB, CRPMTB–L47P, and CRPMTB–E178K were stable homodimers at concentrations of protein used throughout these studies (Fig. 5C). In contrast, the CRPBCG showed monomer–dimer association processes (Fig. 5C, cyan). Nonlinear square fitting of the SV data indicate that the double mutant has a significantly lower dimerization Kd of ~17.5 μM. This result suggests that the CRPBCG was in a monomeric state in the DNA-binding assays conducted with a protein concentration in the nanomolar range. However, stoichiometric DNA-binding data (Fig. 4D) show a plateau when the DNA and CRPBCG dimer concentrations reach a 1-to-1 ratio. This suggests that at equilibrium each CRPBCG dimer forms a stable 1-to-1 complex with DNA. The alternative scenario, in which the CRPBCG monomers were to form stable complexes with DNA, would reach a plateau in stoichiometric DNA-binding assays at molar ratios lower than 1. Thus, our results suggest that the CRPBCG readily dimerizes when it binds DNA, but the dissection and quantification of the linkage between CRPBCG dimerization and DNA interactions (with and without cAMP) remains unknown and is currently being investigated.

To determine mutational effects on protein stability, we monitored changes in tryptophan fluorescence (Fig. 5D) and CD (Fig. 5E) as a function of guanidine hydrochloride. Although all CRPs have indistinguishable tryptophan emission and CD spectra in their native state, the unfolding titrations...
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revealed important differences. Experiments monitoring changes in tryptophan fluorescence show that the CRP_{BCG} and CRP_{MTB}–E178K have lower unfolding free energies (free energy change [ΔG] ~ 2.0 kcal mol⁻¹) than the CRP_{MTB} and CRP_{MTB}–L47P (ΔG ~ 2.6 kcal mol⁻¹) (Table 5). It is possible that the lower stability is due to mutational perturbations of the tryptophan residue (W202) located in the DNA-binding domain, which is in close proximity to E178K. Experiments monitored with CD showed a different pattern: CRP_{MTB}–L47P has the lowest unfolding free energy (ΔG ~ 3.9 kcal mol⁻¹) and the smallest m-value (m) (~2.5 kcal mol⁻¹ M⁻¹) compared with the other proteins (Table 5). L47 is a fully buried residue (0% accessible surface area), and therefore, mutations in this position may contribute to a global destabilization of the protein. Interestingly, the unfolding curve of the CRP_{BCG} monitored by CD displayed two clear unfolding transitions (Fig. 5E). All the other CRPs displayed one unfolding transition, which was analyzed using a two-state unfolding model. These results again illustrate the nonlinear contributions and effects of the individual mutants to the CRP_{BCG}. Given that unfolding experiments were conducted using 5 μM of protein, which is three times lower than its dimerization constant, it is possible that the two transitions observed for the CRP_{BCG} represent unfolding transitions of monomers and dimers in the solution.

Discussion

Elucidating the role of cAMP signaling in M. tuberculosis is a biomedically important topic because cAMP plays an important role in virulence and host interactions (4). Despite the relevant role that the CRP_{MTB} plays in cellular processes, there is limited information regarding its mechanism of allosteric regulation of transcription by cAMP. This is in contrast to the well-studied CRP_{Ecoli} which shares high sequence and structural similarity with the CRP_{MTB}: ~ 53% sequence similarity and an r.m.s.d = 2.5 Å between all atoms in the cAMP-bound structures (9, 11, 35). In this study, we use several biophysical approaches to investigate the linkage between cAMP binding and DNA interactions in the CRP_{MTB}.

Physiological role of cAMP and the CRP_{MTB} in M. tuberculosis

To survive the host’s defense mechanisms, M. tuberculosis has developed a number of strategies that include the following: (1) interfering with phagosomal acidification and trafficking, (2) blocking autophagy and apoptosis-mediated killing, (3) perturbing calcium signaling, and (4) inhibiting inflammatory responses by modulating the host cytokine defenses and quenching the production of reactive oxygen and nitrogen species (5, 36). Some of these strategies can be accomplished by elevating levels of cAMP inside the host cell. Elevated levels of cAMP can suppress innate immune functions by modulating protein expression of inflammatory mediators, dampening the phagocytic response, and reducing intracellular killing of ingested pathogens (5). The best studied microbial strategy for elevating cAMP levels inside the host is by producing toxins that include adenyl cyclases themselves (M. tuberculosis has 17, compared with E. coli that has 1). One such adenyl cyclase is Rv0386, which is linked to the production and secretion of cAMP within macrophages and whose deletion decreases M. tuberculosis virulence and pathology in mice (37, 38). By using ¹⁴C-radiolabeled M. tuberculosis, Agarwal et al. showed that the increase in cAMP was mediated by the bacteria rather than by the host macrophages, and it was dependent on Rv0386 (37).

While the intracellular concentration of cAMP in E. coli has been well determined (1–40 μM) (39–41), reports on the concentration of the cyclic nucleotide in M. tuberculosis and M. bovis show variation between 0.5 and 7 pmol per 10⁸ bacteria, depending on the growth media (42). M. tuberculosis has an irregular shape, ranging between a length of 2 and 4 μm and a width of 0.2 and 0.5 μm (43). Using this information and assuming a rod-shape morphology (43), the concentration of cAMP has lower and upper boundaries of 6.3 μM to 1.1 mM. Our cAMP- and DNA-binding studies indicate that at the lowest cAMP concentrations, CRP_{MTB}–DNA oligomers formed via nonspecific interactions will be the dominant species, whereas at the highest concentration range, these oligomers will be lowly populated. Interestingly, the levels of cAMP inside M. tuberculosis from infected macrophages were reported to be 20 pmol per 10⁸ bacteria, which by a similar calculation as above result in an intracellular cAMP concentration range between 0.26 and 3.2 mM (42). At those concentrations, the reduction of CRP_{MTB}–DNA oligomers will be almost complete. Thus, the modulation of the cAMP concentration before and after macrophage infection will be accompanied by direct effects over the interactions between the CRP_{MTB} and DNA.

CAMP is an allosteric modulator of DNA-binding specificity

We provide evidence for a previously unrealized role of cAMP signaling, in which cAMP regulates the specificity of CRP_{MTB}–DNA interactions. This is in contrast to its structurally conserved CRP_{Ecoli} homolog, wherein cAMP controls the binding affinity to sequence-specific promoters (18–20, 44). This new role of cAMP in the CRP_{MTB} activation is supported by four experimental observations: first, fluorescence anisotropy experiments quantitatively show that the difference in CRP_{MTB}–DNA affinities in the presence and absence of cAMP are marginal, a result that is in agreement with previous studies (7). This indicates that the bound cyclic nucleotide does not regulate transcription at the level of affinity to specific DNA promoter sequences (Fig. 3A, Table 3). Second, the observed anisotropy at high protein concentrations (relative to the concentration of DNA) is significantly higher in the absence of cAMP than in its presence. This difference is related to the formation of high-order CRP_{MTB}–DNA oligomers that are prevented in the presence of cAMP or reversibly dissociated by adding cAMP after high-order CRP_{MTB}–DNA oligomers are formed (Fig. 3, C and D). Third, from stoichiometric DNA-binding assays (Fig. 3B), we conclude that high-order CRP_{MTB}–DNA oligomers only appear after 1-to-1 CRP_{MTB}–DNA complexes have formed.
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(i.e., one CRP dimer and one DNA promoter). This result indicates that the absence of cAMP increases the affinity for nonspecific interactions between a preformed CRP<sub>MTB</sub>–DNA complex and apo-CRP<sub>MTB</sub>, between two preformed CRP<sub>MTB</sub>–DNA complexes, or both. Future AUC experiments will address the size distribution of these oligomers to determine their stoichiometries and relative populations. Fourth, we provide experimental evidence showing that a single cAMP molecule per CRP<sub>MTB</sub> dimer prevents nonspecific DNA interactions and reverse the formation of high-order CRP<sub>MTB</sub>–DNA oligomeric complexes.

It is important to note that the aforementioned role of cAMP in regulating DNA-binding specificity occurs at concentrations of the CRP<sub>MTB</sub> higher than 0.1 μM (Fig. 3A and Fig. 4, B, C, and E). If we consider the intracellular concentration of the CRP<sub>MTB</sub> similar to that reported for the CRP<sub>Ecoli</sub> 2.5 μM (40), then CRP<sub>MTB</sub>–DNA oligomers will readily form when the concentration of cAMP is in the low micromolar range (<50 μM). From previous reports (42), we estimated the concentration of cAMP ranging between 6.3 μM and 1.1 mM. CRP<sub>MTB</sub>–DNA oligomers will be present at the lowest levels of cAMP, while dissociating at the highest level of cAMP from the range provided. These protein and cAMP concentration estimates therefore underscore the biological relevance of cAMP in regulating the CRP<sub>MTB</sub> specificity toward DNA sequences.

The ability of cAMP to modulate DNA-binding specificity is lost in M. bovis BCG

The CRP ortholog of the attenuated M. bovis BCG (CRP<sub>BCG</sub>), whose sequence only differs in two amino acids at positions L47P and E178K relative to the CRP<sub>MTB</sub>, exhibits significant differences in gene regulation (29). Furthermore, previous studies have shown that the CRP<sub>BCG</sub> has slightly higher DNA-binding affinities than the CRP<sub>MTB</sub> for the same promoter sequences (29). Studies dissecting the role of each mutation site in the CRP<sub>BCG</sub> showed that L47P, located at the cAMP-binding domain, had a greater effect in decreasing the ability of the protein to repress gene expression than E178K, located at the DNA-binding domain (30). Given these results, it has been proposed that the mutations observed in the CRP<sub>BCG</sub> play a significant role in the attenuation of M. bovis BCG (30). Here we investigated the mechanisms by which the CRP<sub>BCG</sub> differs from the CRP<sub>MTB</sub> in its interactions with cAMP and DNA.

We find that the CRP<sub>BCG</sub> binds the SerC promoter with a slightly higher affinity (~2-fold) than the CRP<sub>MTB</sub> (Table 4). However, the presence of cAMP for the CRP<sub>BCG</sub> has no effects on the prevention of formation of high-order CRP–DNA oligomers (Fig. 4C). This result indicates that the allosteric control exerted by cAMP is largely reduced by the mutations L47P and E178K found in the CRP<sub>BCG</sub>. Which of these mutations is responsible for this new behavior? When the two mutations were investigated individually, we found that CRP<sub>MTB</sub>–L47P and CRP<sub>MTB</sub>–E178K behave similarly to the CRP<sub>MTB</sub>, namely, that the presence of cAMP reduced the formation of high-order CRP–DNA oligomers (Fig. 4, E and F). Thus, our results suggest that the functional characteristics of the CRP<sub>BCG</sub> are not the consequence from a linear contribution of each individual mutant; rather, it is the result of cooperative interactions between the two mutation sites. For instance, the change in ANS emission due to cAMP binding is twice as large as compared with the single mutants. This is due to higher initial ANS–protein complex emission for the CRP<sub>BCG</sub> (data not shown), indicating that ANS has a different mode of interaction or that more ANS molecules bind to the CRP<sub>BCG</sub> or both. In agreement with this conclusion, the thermodynamic stability and dimerization K<sub>d</sub> of the CRP<sub>BCG</sub> are different from that of the CRP<sub>MTB</sub> or the single mutants, indicating long-range interactions between the two mutation sites that give rise to unique functional and biophysical characteristics.

Figure 6. Proposed cAMP allosteric signaling mechanism in the CRP<sub>MTB</sub>.
(I) the CRP<sub>MTB</sub> binds to both specific and nonspecific DNA sequences in the absence of cAMP or forms high-order CRP<sub>MTB</sub>–DNA complexes. (II) cAMP binds to preformed CRP<sub>MTB</sub>–DNA complexes. (III) Dissociation of CRP–cAMP from non specific DNA or high-order CRP–DNA complexes. (IV) Formation of CRP–cAMP<sub>2</sub> complexes

specific DNA binding site
nonspecific DNA binding site
Empty
Singly Bound
Doubly Bound

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Potential biological role for negative cAMP-binding cooperativity and DNA-binding specificity in transcription regulation mediated by the CRP<sub>MTB</sub>

What are the functional consequences of having negative cAMP-binding cooperativity and regulation of DNA-binding specificity in the CRP<sub>MTB</sub>? The observed negative cooperativity during cAMP-binding dictates that the probability of binding a second cAMP molecule to a singly cAMP-bound CRP<sub>MTB</sub> dimer is lower than the probability of binding an apo-CRP<sub>MTB</sub> dimer, resulting in a larger population of the singly cAMP-bound state. Given our results indicating that a single cAMP molecule bound to a CRP<sub>MTB</sub> dimer reverses high-order CRP<sub>MTB</sub>–DNA oligomeric complexes, we hypothesize that negative cAMP-binding cooperativity may maximize the pool of available cAMP to favor sequence-specific interactions between the CRP<sub>MTB</sub> and DNA. Thus, instead of requiring a doubly cAMP-bound CRP<sub>MTB</sub> to reduce nonspecific interactions or reverse high-order CRP<sub>MTB</sub>–DNA oligomeric complexes, our results indicate that one cAMP molecule is sufficient to achieve the same outcome.

The results from this study provide a previously unrecognized archetype of cAMP-mediated regulation of transcription that is different from previously described models for other CRPs. Figure 6 shows a model by which cAMP allosterically regulates CRP<sub>MTB</sub> interactions with DNA: (I) In the absence of cAMP, the CRP<sub>MTB</sub> binds to both specific (i.e., promoters) and nonspecific (i.e., intragenic) sequences of DNA or forms high-order CRP<sub>MTB</sub>–DNA complexes. (II) When cAMP levels increase inside the cell after macrophage infection, cAMP binds to a preformed CRP<sub>MTB</sub>–DNA complex. Because of the negative cooperativity of the CRP<sub>MTB</sub>, the first cAMP-binding event dominates over the second; thus, cAMP is preferably bound to a single subunit within homodimers. (III) While singly cAMP-bound proteins dissociate from nonspecific DNA sequences or dissociate high-order CRP<sub>MTB</sub>–DNA oligomers into 1-to-1 complexes, proteins that were interacting with specific DNA sequences remain bound to its promoter. (IV) Finally, as the cAMP concentration increases, the doubly cAMP-bound state is reached with mostly specific CRP<sub>MTB</sub>–DNA interactions taking place.

This model offers three scenarios by which the CRP<sub>MTB</sub> may regulate transcription and underscores its role as a global regulator. First, like removing roadblocks along the DNA structure (45, 46), cAMP will trigger the dissociation of the CRP<sub>MTB</sub> from nonspecific DNA sequences. Second, CRP<sub>MTB</sub>–cAMP will remain bound to specific promoter sequences, facilitating the recruitment of the transcription machinery such as other transcription factors or RNA polymerase. Third, and a less studied role attributed to the CRP<sub>MTB</sub>, is chromosome organization (26). The CRP<sub>MTB</sub> binds to >900 sites in the M. tuberculosis genome, 83% of which are intragenic regions (47). This type of binding resembles that of nucleoid-associated proteins and suggests that the CRP<sub>MTB</sub> might regulate the global architecture of the mycobacterial chromosome (48). The ability of the CRP<sub>MTB</sub> to bend DNA (6) could also alter the interaction mode of other factors that interact to DNA proximal to CRP sites. In the context of our results, the property of CRP<sub>MTB</sub>–DNA to form oligomeric complexes and then dissociate as a function of cAMP concentration might be a strategy for regulating gene expression via chromosomal organization. Altogether, the interplay between these three mechanisms results in the expression of genes involved in virulence, such as ESX-1 type VII secretion system (T7SS), espACD-Rv3613c-Rv3612c operon, Rv3616c-Rv3612c genes, espA operon, to name a few, all of which are associated to CRP<sub>MTB</sub> activity (26). The CRP<sub>MTB</sub> also activates expression of rpfA and whiB1 genes that encode proteins that are thought to be involved in reviving dormant bacteria (12, 25, 26, 49). Within this model, our results indicate that the variant CRP<sub>Bcg</sub> has difficulties dissociating from nonspecific DNA sequences or reverse the formation of high-order CRP–DNA oligomers, possibly obstructing transcription.

Similar structures, different allosteric activation mechanisms

It is intriguing that the CRP<sub>MTB</sub> and CRP<sub>Ecoli</sub> share high sequence and structural similarity (11, 35) but differ in their cAMP-mediated activation mechanisms. Although high-resolution structures indicate that these two homologs are cAMP-dependent transcription factors, it is more difficult to infer from the structures alone that these proteins would have very different cAMP-binding modes and cAMP-dependent DNA interactions. A close inspection of the two CRP structures reveals small differences that may be associated with their unique allosteric properties. For instance, the carboxy-terminal residues of the CRP dimerization helix in the apo-CRP<sub>Ecoli</sub> are not well structured, whereas in the CRP<sub>MTB</sub> they are (Fig. 1A). These residues are part of the hinge that connects the cAMP- and DNA-binding domains and have been shown to contribute to the allosteric communication in the CRP<sub>Ecoli</sub> (50–52). Moreover, cAMP-induced domain motions in the CRP<sub>MTB</sub> originate at the hinge that connects the cAMP-binding domain and the dimerization helix. Instead, in the CRP<sub>Ecoli</sub> domain, motions originate at the hinge that connects the DNA-binding domain and the dimerization helix (Fig. 1, B and D). The interplay between the sequence composition and the location of these domain motions may help further dissect the unique allosteric behavior in the CRP<sub>MTB</sub> and how cAMP reduces nonspecific DNA interactions.

Given that the structures of the CRP<sub>MTB</sub> in the apo-state and cAMP-bound state are similar, it is plausible that protein dynamics (16, 18, 21, 53–56) also play an important role in how cAMP allosterically reduces nonspecific DNA interaction. Our cAMP-binding studies show differences in ANS fluorescence between apo-state and cAMP-bound state (Fig. 4A), despite their similar structures (Fig. 1, A and B, bottom). This change in ANS fluorescence indicates dynamic transitions or protein fluctuations associated with cAMP binding that are not captured in static high-resolution structures. Future studies with high-resolution techniques such as hydrogen–deuterium exchange mass spectrometry (57, 58) will help elucidating the
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Figure 7. Comparison between the cAMP-induced allosteric effects in the CRP_{Ecoli} and CRP_{MTB}. The top panel shows the crystal structures of the CRP_{Ecoli} and CRP_{MTB} bound to cAMP (purple spheres). The lower panel shows the thermodynamic cycles that underlie the allosteric effect of cAMP in both proteins. For the CRP_{Ecoli} DNA-binding events are more favorable (i.e., have higher affinity) in the presence of cAMP. In contrast, CRP_{MTB}-DNA complexes are formed with similar affinity with and without cAMP. Nonspecific DNA interactions and high-order CRP_{MTB}-DNA oligomers are either reduced or prevented by cAMP, promoting the formation of a stable one-to-one CRP_{MTB}-DNA complex. CRP_{Ecoli} from Escherichia coli; CRP_{MTB}, CRP from Mycobacterium tuberculosis.

Concluding remarks

In this study, we begin to dissect the linkage between cAMP binding and DNA interactions in the CRP_{MTB}. Importantly, this study indicates that the linkage operates at a level of DNA regulation that is substantially different to that from the CRP_{Ecoli}. Figure 7 illustrates the functional differences between the CRP_{MTB} and CRP_{Ecoli} at the level of DNA interactions. Although cAMP enhances the affinity of the CRP_{Ecoli} for DNA promoter sequences and promote intersubunit communication (10, 13, 19, 23, 24, 59, 60), our results from this study show that DNA-binding affinity to the CRP_{MTB} is not sensitive to cAMP occupancy. Instead, cAMP plays a significant role on the specificity of DNA interactions and the reduction or prevention of high-order CRP-DNA oligomers. The exact functional consequences of such a mode of action will likely depend on the specific organization of regulatory elements for a particular gene (12) and the degree of energetic coupling between the four binding sites in CRP_{MTB}; i.e., binding at any site has the potential to alter the binding affinity of the other three sites.

Experimental procedures

R.M.S.D. analysis of structures of the CRP_{Ecoli} and CRP_{MTB}

Structural analyses were performed using PyMol Molecular Graphics System (Version 2.0 Schrödinger, LLC.). The Protein Data Bank used here were 2WC2 and 1G6N for CRP_{Ecoli} in the apo-state and cAMP-bound state, and 3D0S and 3I54 for CRP_{MTB} in the apo-state and cAMP-bound states. The cAMP-binding domain alignment (residues 21–104 in CRP_{Ecoli} and residues 28–110 in CRP_{MTB}) between interspecies subunits or between interspecies subunits served as an anchor for all the r.m.s.d. values reported in this study.

Cloning, expression, and purification of the CRP_{MTB}

The DNA sequence of WT CRP from M. tuberculosis (CRP_{MTB}) was used in the present study. CRP flanked by NdeI and BamHI restriction sites was synthesized by PCR with PfuUltra Polymerase (Agilent Technologies). The amplicon was digested with NdeI and BamHI according to manufactured directions (New England Biolabs). To generate the Histag fusion construct, the resultant digested fragment was inserted into a pET-3a expression vector (Addgene) previously digested with the same restriction enzymes. The resultant expression vector was named the CRP_{MTB}.

CRP_{MTB} mutants (E178K, L47P, and BCG [E178K/L47P double mutant]) were generated following the QuikChange II Site-Directed Mutagenesis protocol (Agilent Technologies). All proteins were purified from E. coli strain T7 Express pLysS competent cells (New England Biolabs). To generate the Histag fusion construct, the resultant digested fragment was inserted into a pET-3a expression vector (Addgene) previously digested with the same restriction enzymes. The resultant expression vector was named the CRP_{MTB}.

residue networks involved in cAMP-mediated allostery and communication.

It is well documented that the CRP_{Ecoli} exhibits positive cooperativity between the two cAMP-binding sites, wherein the first binding reaction is exothermic and the second is endothermic (18, 19, 24, 33). In contrast, by using two orthogonal techniques (ITC and fluorescence), we find that the CRP_{MTB} displays negative cAMP-binding cooperativity (Fig. 2, Table 1), where binding of the cyclic nucleotide is endothermic for both sites.

A previous study with ITC by Stapleton et al. (12) reported that the two cAMP-binding events in the CRP_{MTB} are independent from each other. Our cAMP-binding studies using ITC and ANS fluorescence and the underlying statistical analysis of the data (Table S2) do not agree with their results. A potential source for the difference is that we used a cAMP-to-CRP_{MTB} molar ratio of up to 5-fold for ITC experiments, whereas Stapleton et al. reached a maximum ratio of 2.5. Given the expected 2-to-1 binding stoichiometry between cAMP and the CRP_{MTB}, we used a higher molar ratio to ensure full saturation of the protein at the end of the titration. Alternatively, the buffer type and composition could be a source of differences between the two studies. We conducted ITC experiments at a constant pH using three buffers with different ionization enthalpies, including PBS, which was used by Stapleton et al. In all three experiments, we maintained a cAMP-to-CRP_{MTB} molar ratio up to 5-to-1 and obtained the same degree of negative cooperativity between the two cAMP-binding sites (Table 2, Figs. S1 and S2, and Tables S1 and S2).

Altogether, the three ITC experiments and fluorescence measurements used in this study are consistent with each other and strongly suggest that cAMP binds with negative cooperativity to the CRP_{MTB}.

Experimental procedures

R.M.S.D. analysis of structures of the CRP_{Ecoli} and CRP_{MTB}

Structural analyses were performed using PyMol Molecular Graphics System (Version 2.0 Schrödinger, LLC.). The Protein Data Bank used here were 2WC2 and 1G6N for CRP_{Ecoli} in the apo-state and cAMP-bound state, and 3D0S and 3I54 for CRP_{MTB} in the apo-state and cAMP-bound states. The cAMP-binding domain alignment (residues 21–104 in CRP_{Ecoli} and residues 28–110 in CRP_{MTB}) between interspecies subunits or between interspecies subunits served as an anchor for all the r.m.s.d. values reported in this study.

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ketone, 10-μM 3-isobutyl-1-methylxanthine, 1-mM PMSF). The bacterial suspension was homogenized with a glass homogenizer and lysed with an M-110P Microfluidizer at 10,000 psi (Microfluidics). The lysate was centrifuged at 15,000 rpm for 45 min at 4 °C in a JA 25.50 rotor (Beckman Coulter). The supernatant was mixed with the His60 Nickel Superflow Resin (Clontech) and allowed to bind overnight at 4 °C with constant shaking. The supernatant was supplemented with 30-mM imidazole to compete for nonspecific binding. The next day, the resin–supernatant mix was transferred to a prewashed column with the lysis buffer. The flow-through sample was collected, and the resin was washed twice with lysis buffer supplemented with 3-mM imidazole. 500-mM imidazole was added in the lysis buffer, the resin was incubated for 30 min, and the elutes were collected. Samples corresponding to the CRP MTB were pooled together, concentrated, and run through size-exclusion chromatography. All proteins in the apo-state were collected. Samples corresponding to the CRPMTB were stored at −80 °C in the storage buffer (50-mM Hepes, pH 7.6, 150-mM KCl, 1-mM EDTA, pH 7.2). Protein concentrations throughout this study were determined with the dimer extinction coefficient of 1 M 3-isobutyl-1-methylxanthine, 1-mM PMSF).

CD

Measurements were performed in an Aviv Model 202-01 spectrometer with 5-μM protein in a buffer containing 150-mM KCl, 50-mM Hepes, and 1-mM EDTA, pH 7.2. Protein concentrations throughout this study were determined with the dimer extinction coefficient at 280 nm: 25,480 cm⁻¹ M⁻¹.

Chemical denaturation with guanidine hydrochloride

Protein unfolding was monitored by changes in fluorescence (λex = 280 nm or 295 nm, and λem = 340 nm) and CD absorption at 222 nm. In both set of experiments, we used 5 μM of protein in a buffer containing 150-mM KCl, 50-mM Hepes, and 1-mM EDTA, pH 7.2. At least two independent titrations were performed for each protein and corrected for buffer contributions to the signal. Data were fitted according to the linear extrapolation method (61). For the WT CRP MTB and single mutants CRP MTB–E178K and CRP MTB–L47P, the data were fitted to a two-state unfolding model (61):

\[
S_T = S_N f_N + S_D f_D
\]

where \( S_T \) is the total observed signal, \( S_N \) and \( S_D \) correspond to the native and denatured state signals, respectively, and \( f_N \) and \( f_D \) are the fractions of native and denatured protein, respectively. \( f_N \) and \( f_D \) are related to the equilibrium constant between folded and unfolded states:

\[
f_N = \frac{1}{1 + K}
\]

\[
f_D = \frac{K}{1 + K}
\]

where:

\[
K = e^{-\Delta G^0/RT}
\]

And:

\[
\Delta G^0 = \Delta G^0_{H_2O} + m|d|
\]

Here, \( \Delta G^0_{H_2O} \) is the free energy of unfolding in the absence of a denaturant, \( m \) is the m-value or the slope of the linear dependence of \( \Delta G^0 \) on the denaturant concentration as described by the linear extrapolation method (61), and \( d \) is the denaturant concentration. Combining Equations 1–5 yields the data fitting equation:

\[
S_T = S_N f_N + S_D f_D + S_{De} \left( \frac{\Delta G^0_{H_2O} + m|d|}{1 + e^{\Delta G^0_{H_2O} + m|d|}} \right)
\]

The unfolding data for the CRP BCG displayed two transitions, and therefore, the total signal, \( S_T \), was fitted to a three-state unfolding model (62):

\[
S_T = S_N f_N + S_I f_I + S_D f_D
\]

where \( S \) and \( f \) are the signals and fractions of native (N), intermediate (I), and denatured (D) states, respectively. Expressing the fractions of species in terms of equilibrium constants yields:

\[
f_N = \frac{1}{1 + K_I + K_{ID}}
\]

\[
f_I = \frac{K_I}{1 + K_I + K_{ID}}
\]

\[
f_D = \frac{K_{ID}}{1 + K_I + K_{ID}}
\]

where \( K_I \) and \( K_{ID} \) are the equilibrium constants between the native and intermediate states and the intermediate and...
denatured states, respectively. $K_1$ and $K_D$ are expressed in terms of $\Delta G_{H,O}^c$ and $m$ as in Equation 5 for intermediate (subscript $I$) and denatured (subscript $D$) states, resulting in the following equation:

$$
S_T = \frac{S_N + S_D e^{-\left(\frac{\Delta G_{H,I}^c}{R T} + m q \phi \right)}}{1 + e^{-\left(\frac{\Delta G_{H,D}^c}{R T} + m q \phi \right)}} + S_D e^{-\left(\frac{\Delta G_{H,D}^c}{R T} + m q \phi \right)} - e^{-\left(\frac{\Delta G_{H,D}^c}{R T} + m q \phi \right)}
$$

(11)

To better compare the unfolding data of the four CRPs studied here, we plotted the fraction of folded protein. All fitting procedures of unfolding data were performed in Sigmaplot (Systat Software).

### Analytical ultracentrifugation

SV experiments were performed in a Beckman Optima XLA with absorbance optics in 12-mm cells at 280 nm, 50,000 rpm, and 19.7°C. The buffer density was measured in an Anton Paar DMA 5000. Extinction coefficients at 280 nm (12,740 M$^{-1}$ per monomer or 0.4855 ml/mg) and vbar (0.735639) are estimated from amino acid sequence in Sednterp (63). Three samples were run at approximately 0.2, 0.4, and 0.6 absorbance at 280 nm (equivalent to dimer CRP concentrations of 7.9, 15.8, and 23.7 μM) in 150-mM KCl, 50-

mM Heps, and 1-mM EDTA, pH 7.2. Data were analyzed with DCDT+ (64) to generate g(s) distributions and plotted versus s$^2$ (Fig. 5C). Superposition of the WT CRP$_{MTB}$ and single mutants CRP$_{MTB}$–E178K and CRP$_{MTB}$–L47P g(s) curves is consistent with no concentration dependence in the concentration regime tested. Data were then fit with SedAnal (version 7.14) (65) to determine global $S$ values and for the CRP$_{BCG}$ dimerization constants. The WT CRP$_{MTB}$ and single mutants CRP$_{MTB}$–E178K and CRP$_{MTB}$–L47P have an average $S_{20,w}$ of 3.587 s ± 0.082 or 2.3% consistent with an estimate using HullRad (66), 3.65 s. The SV data for the CRP$_{BCG}$ were fit to a monomer–dimer model constraining the dimer S2 value to the individual and average values for the dimeric constructs or float S1 values which constrain the ratio of S2/S1 to 1.5. The best value for the CRP$_{BCG}$ dimerization is 5.7·10$^5$ M$^{-1}$ or a $K_d$ of 17.5 μM (binding free energy -6.47 ± 0.73 kcal mol$^{-1}$).

### CAMP binding monitored by ITC

Experiments were performed in a Nano-ITC (TA instruments) using three different buffers (pH 7.2): Heps, PBS, and cacodylate. Each buffer was supplemented with 150-mM NaCl, 1-mM EDTA, and 0.2-mM TCEP. All solutions were filtered and degassed thoroughly prior use. The protein and CAMP concentrations were 16 to 20 μM and 1 mM, respectively. The CAMP solution was prepared in the buffer from the last step of protein dialysis to minimize artifacts due to differences in the buffer composition. The reaction cell contained 0.35 ml of the protein solution. The injection syringe was filled with CAMP, and the titration experiment consisted of 18 injections. The first injection was of 0.5 μl and was discarded from the analysis step. The other 17 injections were of 2 μl. A separate reference titration of the CAMP into each buffer was performed to determine the heat of dilution of the ligand which was then subtracted from the CAMP titration to the protein solution. Raw data were analyzed using the software NITPIC (67) and MicroCal Origin using two different models: independent and sequential CAMP-binding events. The incremental heat ($Q_i$) of the titration was fitted using Equation 12:

$$
\Delta Q_i = Q_i + \frac{d V_i}{V_0} \left( \frac{Q_i + Q_{i-1}}{2} \right) - Q_{i-1}
$$

(12)

where $V_i$ and $V_0$ are the initial and active volumes, respectively. For the independent binding model, the total heat ($Q$) is the following:

$$
Q = \frac{n[M]_t \Delta H V_0}{2} \left[ 1 + \frac{[x]_t}{n[M]_t} + \frac{1}{nK[M]_t} \right] - \sqrt{\left( 1 + \frac{[x]_t}{n[M]_t} + \frac{1}{nK[M]_t} \right)^2 - 4 \frac{[x]_t}{n[M]_t}}
$$

(13)

where $n$ is the number of binding sites, $[M]_t$ is the bulk protein concentration, $\Delta H$ is the ligand-binding enthalpy, $[x]_t$ is the total ligand concentration, and $K$ represents the binding constant.

The total heat for the sequential binding model is calculated via Equation 14.

$$
Q = [M]_t V_0 \left[ \frac{K_1 [x] + K_1 K_2 [x]^2}{1 + K_1 [x] + K_1 K_2 [x]^2} \right]
$$

(14)

where $[x]$ is

$$
[x] = \frac{[x]_t}{\sqrt{[M]_t}} \left( \frac{K_1 [x] + 2K_1 K_2 [x]^2}{1 + K_1 [x] + K_1 K_2 [x]^2} \right)
$$

(15)

Here, $K_1$ and $K_2$ correspond to the microscopic binding constants 2·$k_1$ and 1/2·$k_2$, respectively.

We performed one- and two-way ANOVA tests to determine differences between $\Delta H$ and the buffer used in ITC experiments. To compare pairwise differences between buffers, we used the post hoc Tukey test with a significance level of 0.05.
0.05. p-Values resulting from these tests are indicated in the legend of Figure 2. These tests were performed in Mathematica (Wolfram Research, Inc).

**EMSA**

Reaction mixtures contained 40 nM of six different lengths of the SerC promoter fragments (18, 20, 22, 24, 26, and 32 bps) and between 0.1- and 3.0-μM CRP<sub>MTB</sub> in 75-mM KCl, 50-mM Hepes, and 1-mM EDTA at pH 7.6. Sequences for the SerC promoter fragments were as follows: 32-bp (5'-GGCGGTAGTGGAAAGCTCAGTTGCAAGCC-3'), 26-bp (5'-CTAGTGGAAAGCTCAGTTGCAAGCC-3'), 24-bp (5'-GTTGGAAGGCTCAGTTGCAAGCC-3'), 22-bp (5'-TGTGGAAGGCTCAGTTGCAAGCC-3'), 20-bp (5'-AGTGTGGAAGGCTCAGTTGCAAGCC-3'), and 18-bp (5'-GATGTGGAAGGCTCAGTTGCAAGCC-3'). Underlined regions correspond to the CRP<sub>MTB</sub>-binding site in the SerC promoter fragment (29).

After 45 min of equilibration at room temperature, the reaction mixtures were loaded in an 8.5% polyacrylamide gel with 0.5x Tris-borate-EDTA buffer. Gels were run at 80 V for 70 min in 0.5x Tris-borate-EDTA buffer.

**CAMP binding monitored by ANS fluorescence**

CAMP binding to the CRP<sub>MTB</sub> was measured by the quenching of the fluorescent signal from the CRP–ANS complex (λ<sub>ex</sub> = 350 and λ<sub>em</sub> = 480 nm), using a PTI spectrometer (Horiba). Normalized intensity counts as a function of the cAMP concentration were fitted to a cooperative two-site binding model as described (19) and an independent two-site binding model. The cooperative model is shown in Equation 16.

\[
F_{480 \text{ nm}} = \frac{F_0 + 2F_1k_1[x] + F_2k_1k_2[x]^2}{1 + 2k_1[x] + k_1k_2[x]^2}
\]  

where \(F_{480 \text{ nm}}\) is the observed signal; \(F_0\), \(F_1\), and \(F_2\) represent the fluorescent signal of the apo, singly liganded, and doubly liganded states of the protein, respectively; \(k_1\) and \(k_2\) corresponds to the microscopic binding affinity constants of the first and second CAMP, respectively, and \(x\) is the concentration of ligand. In the independent binding model, \(k_2 = k_1\) which assumes that the ligand binding sites are identical (i.e., no cooperativity). The ANS-based fluorescence data is normalized to the initial fluorescence value in the absence of CAMP. DNA binding curves were fitted with Sigma Plot (Systat Software).

\[
A_{\text{obs}} = A_{\text{DNA}} + (A_{\text{P-DNA}} - A_{\text{DNA}}) \cdot \frac{K[D\text{NA}] + K[P] + 1 - \sqrt{(K[D\text{NA}] + K[P] + 1)^2 + 4K^2[D\text{NA}][P]}}{2K[D\text{NA}]}
\]  

**DNA binding monitored by fluorescence anisotropy**

Measurements were collected with a PTI spectrometer using a 32-bp SerC promoter (5'-GGCGGTAGTGGAAAGCTCAGTTGCAAGCC-3'), 20-bp SerC promoter (5'-AGTGTGGAAGGCTCAGTTGCAAGCC-3') and Scramble 32-bp DNA (5'-AGATCGGAACATGTCGAAACACCGGGTAA-3') covalently linked to a fluorescein-labeled DNA (IDT DNA). The excitation and emission wavelengths were 480 nm and 518 nm, respectively. The reaction mixture contained either 3 nM, 200 nM or 400 nM of fluorescein-labeled DNA and various concentrations of CAMP (0, 100 and 1000 μM). Fluorescence anisotropy measurements were collected with a PTI spectrometer (Horiba Scientific). Data was normalized to the first experimental anisotropy value, and analyzed as described previously by Heyduk and Lee (20) and Lanfranco et al. (19) with minor modifications. Briefly, we removed experimental data points displaying anisotropy values with 2 standard deviation higher than the plateau overserved after the first DNA-binding phase (indicated by the red arrow in Fig. 3A). The data were fitted according to Equation 18.

The f-ratio function to determine which CAMP binding model is statistically more robust in fitting the data from ITC and ANS experiments. First, we determine \(f_{\text{obs}}\), which is the f-ratio calculated from the fitted parameters of CAMP binding data:

\[
f_{\text{obs}} = \frac{\text{SSR}_1}{\nu_1} \left/ \frac{\text{SSR}_2}{\nu_2} \right.
\]  

where SSR is the sum of square of the residuals and \(\nu\) correspond to degrees of freedom. The subindexes 1 and 2 refer to model 1, which in this case is identical and independent binding sites with no cooperativity, and model 2, which corresponds to identical binding sites with cooperative interactions. The values for SSR, \(\nu\) and \(f_{\text{obs}}\) are listed in Table S2. In its application, \(f_{\text{obs}}\) is compared to the cumulative distribution of the f-ratio function using the corresponding degrees of freedom for models 1 and 2. This comparison provides a means to reject the hypothesis that model 1 is statistically equivalent to model 2 with a given confidence interval (68). Additionally, we calculated the probability that a value selected randomly from the f-ratio probability distribution exceeds \(f_{\text{obs}}\), i.e., the probability that model 1 provides a better fit than model 2. This is achieved by integrating the cumulative distribution of the f-ratio function from \(f_{\text{obs}}\) to infinity. The results are listed in Table S2. These tests were done in Mathematica (Wolfram Research, Inc).
Role of cAMP in MTB transcription regulation represents the association constant for the protein and DNA.

Data availability
Data not contained in this article are available upon request to Rodrigo Maillard (rodrigo.maillard@georgetown.edu, Georgetown University).

Supporting information—This article contains supporting information.

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Author contributions—F. G. designed, conducted and analyzed the research, and wrote the manuscript. S. D. and M. L. conducted and analyzed the research and wrote the manuscript. I. W., C. C., and J. C. conducted the research. R. A. M. designed and analyzed the research and wrote the manuscript.

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Abbreviations—The abbreviations used are: ANS, 8-anilino-1-naphthalenesulfonic acid; AUC, analytical ultracentrifugation; BCG, Bacille Calmette-Guérin; c, cooperativity factor between cAMP-binding sites; CRP, cAMP receptor protein; CRPBCG, cAMP receptor protein from Mycobacterium bovis Bacille Calmette-Guérin strain; CRPeColo, cAMP receptor protein from Escherichia coli; CRPMBTB, cAMP receptor protein from Mycobacterium tuberculosis; ΔG°, Gibbs free energy change; ITC, isothermal titration calorimetry; k1, cAMP-binding affinity constant for the first cAMP-binding site; k2, cAMP-binding affinity constant for the second cAMP-binding site; Kd, dissociation constant; kDNA, DNA-binding affinity constant; m, m-value; MTB, Mycobacterium tuberculosis; SV, sedimentation velocity.

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