

		CRP cluster											
		β4			hinge			α6					
<i>E. coli</i>	P0ACJ8	CAP	D <sup>54</sup> s <sup>a,H</sup> <sup>b</sup>	S <sup>63</sup> F <sup>b</sup>	R <sup>83</sup> G <sup>a</sup>	R <sup>124</sup> N <sup>c</sup>	T <sup>128</sup> L,C,I <sup>b</sup>	S <sup>129</sup> T <sup>b</sup>	D <sup>139</sup> N,K <sup>b</sup>	G <sup>142</sup> S,Q,K,D <sup>b</sup>	R <sup>143</sup> C <sup>b</sup>	A <sup>145</sup> T,S,Q,Y,L,F,V,C <sup>b</sup>	L <sup>149</sup> K <sup>a</sup> ,R <sup>b</sup>
<i>P. aeruginosa</i>	P55222	<i>Vfr</i>	D	S	R	D	T	S	D	G	R	A	L
<i>M. tuberculosis</i>	P9WMH3	<i>Crp</i>	D	S	R	R	T	S	D	G	R	A	L
<i>Y. pestis</i>	Q79RU4	<i>Crp</i>	D	S	R	N	T	S	D	G	R	A	L
<i>V. cholerae</i>	D7HFP5		D	S	R	R	T	S	D	G	R	A	L
<i>K. pneumoniae</i>	Q9F435		D	S	R	R	T	S	D	G	R	A	L
<i>S. meliloti</i>	Q92SD2	<i>Clr</i>	T	R	R	A	T	T	D	A	R	A	L
<i>R. centenum</i>	B6IXV7	<i>CgrA</i>	S	N	R	R	T	S	N	R	R	A	L
<i>M. magnetotacticum</i>	Q2W4U7		S	G	R	D	A	D	S	S	R	A	L
<i>P. aeruginosa</i>	Q916L5		S	I	R	K	A	F	P	Q	R	A	L

**FIG S5** Differences for sequence motifs in the cNMP binding site and the hinge/α5 and α6 regions. Several mutations in these regions as indicated below the *E. coli* CAP sequence render CAP cGMP-sensitive (a: Yoon *et al.*, Bacteriol 190, 4532–4540 (2008); b: Passner *et al.*, J Mol Biol. 304, 847-59 (2000); c: Yoon *et al.*, J Biol Chem 282, 3632–3639 (2007)). Almost all of these residues are conserved in the main Crp cluster, whereas the proteins from cluster G like Clr show higher diversity.