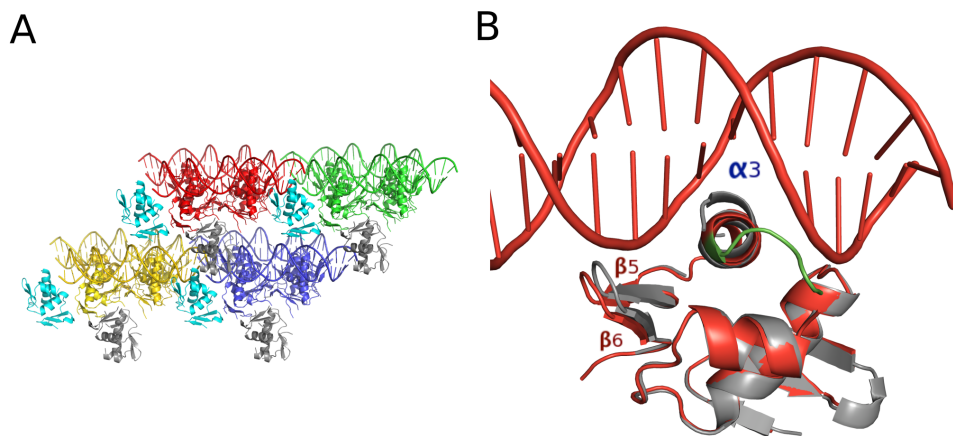
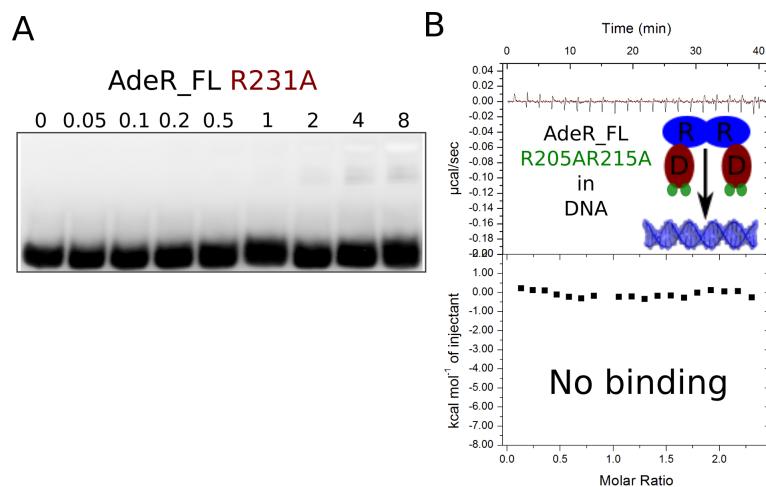


Supplementary Figure S1. A Crystal packing of the AdeR in complex with intercistronic region DNA fragments. 4 asymmetry units were generated and colored related to the DNA molecules in red, green, blue and yellow respectively. In one asymmetry unit, there are 6 AdeR_DBD monomers with 4 of them binding to two DNA molecules, the 5th AdeR_DBD monomer (cyan) were trapped between two DNA molecules. The 6th monomer (grey) has barely interaction with the DNA. B. Alignment of the DNA bound and DNA unbound AdeR_DBD indicated that conformation change of $\beta 5$ & $\beta 6$ hairpin to adapted into the DNA minor groove and more residues were traced of the flexible loop (green) linked with $\alpha 3$ resulted from DNA binding.



Supplementary Figure S2. A. EMSA experiments cross-validated the isothermal titration calorimetry that the R231A abolished the interaction between AdeR and intercistronic region DNA. B. Isothermal titration calorimetry revealed the R205A/R215A double mutation could diminish the AdeR binding to the intercistronic region DNA.



Supplementary Table S1. Primers used in the cloning PCR and site directed mutagenesis

Primer name	Sequence (5' to 3')
Cloning PCR	
AdeRFL-F	5' CATGCCATGGGCCATCATCATCATCACCTTTGATCATTCTTTTTCTTTTG 3'
AdeRFL-R	5' GGAATTCTTATTTAGGCATCATCTTTTAC 3'
AdeRRD-R	5' GGAATTCTTATGCTTTGTTTGCAAAGTGA 3'
AdeRDBD- F	5' CATGCCATGGGCCATCATCATCATCACACTAATAAAAAATAAAGTCTATAAAAAATATT 3'
Site Directed Mutagenesis	
D108A-F	5' CGCATAGGTGCAGATGCGTTTGTGGTGAAGCCTTTTAACCCAAATG 3'
D108A-R	5' GGCTTCACCACAAACGCATCTGCACCTATGCGTAATGCCATAAC 3'
F109A-F	5' CATAGGTGCAGATGACGCGGTGGTGAAGCCTTTTAACCCAAATG 3'
F109A-R	5' GTTAAAAGGCTTCACCACGCGTCATCTGCACCTATGCGTAATGCC 3'
R122A-F	5' CAAATGAAGTCATCGCTGCGGTTCCAGGCAGTCTTAAGACGTAATC 3'
R122A-R	5' CTTAAGACTGCCTGAACCGCAGCGATGACTTCATTTGGGTTAAAAG 3'
R205A-F	5' GATAGCGATGCACTAGAGGCGACCGTAGATAGCCATGTAAGTAAGC 3'
R205A-R	5' CATGGCTATCTACGGTCGCCTCTAGTGCATCGCTATCATTATGC 3'
R215A-F	5' CATGTAAGTAAGCTGGCGAAAAAACTAGAAGAACAAGGCATATTTTC 3'
R215A-R	5' GTTCTTCTAGTTTTTTCGCCAGCTTACTTACATGGCTATCTACGG 3'
R231A-F	5' CAAATGTTAATTAATGTGGCGGGCGTGGGATATAGGCTAGATAATC 3'
R231A-R	5' GCCTATATCCCACGCCCGCCACATTAATTAACATTTGAAATATG 3'

Supplementary Table S2. SAXS data collection and analysis statistics.

AdeR Samples	DBD	RD	FL	DBD DNA	FL DNA
Data Collection Parameters					
Beamline	BL19U2, SSRF, Shanghai				
Beam size	0.33mm×0.55mm				
Detector	Pilatus 1M				
q range (\AA^{-1})	0.04-4.5				
Temperature	293K				
Concentration	1-6 mg/ml	1-7 mg/ml	1-5 mg/ml	15-120 μM	20-160 μM
Structural Parameters					
$I(0)$ (\AA^{-1})	72.31	98.74	248.60	595.70	321.80
R_g (\AA)	17.43	22.04	30.04	24.25	33.30
D_{max} (\AA)	49	66	87	77	102
Porod estimate V_p (\AA^3)	22630	46558	85989	43782	99041
Molecular Weight Determination					
Molecular mass (kDa)	13.915 Monomer	32.724 Dimer	58.551 Dimer	43.308 2M: DNA	74.030 D: DNA
SAXS MoW2 (kDa)	14.559	37.737	66.959	34.602	73.274
Superdex75 SEC (kDa)	14.727	25.813	50.464	42.195	60.906