

Table S2, Related to Figures 3 and 4. Summary of X-ray data collection from SERCAT 22-ID beamline and refinement statistics (*)

mZFP568	ZF1-11 (ZF11 was not observed)	ZF1-10	ZF2-11
DNA (mIgf2-P0) (5'-3')	TGCCCTTTTTTACCTGTGCCACGCCACA	GCCCTTTTTTACCTGTGCCACGCCAC	TGCCCTTTTTTACCTGTGCCACGCCACA
(3'-5')	ACGGGAAAAATGGACACGGTGCGGGTGT	CGGGAAAAATGGACACGGTGCGGGTG	ACGGGAAAAATGGACACGGTGCGGGTGT
PDB	5V3M	5V3J	5WJQ
Space group	C222 ₁	P1	P2 ₁ 2 ₁ 2
Cell dimensions a, b, c (Å)	34.9, 92.7, 353.6	55.8, 65.7, 73.0	180.7, 35.2, 81.9
α, β, γ (°)	90, 90, 90	100.5, 104.2, 97.2	90, 90, 90
Resolution (Å)	32.2-2.09 (2.16-2.09)	34.5-2.06 (2.13-2.06)	39.9-2.79 (2.89-2.79)
^a R _{merge}	0.067 (0.479)	0.076 (0.764)	0.132 (0.596)
^b I/ σ I	26 (2.6)	12.9 (1.9)	17.6 (4.5)
CC _{1/2} / CC	(0.910 / 0.976)	(0.941 / 0.985)	(0.933 / 0.983)
Completeness (%)	81.7 (32.9)	97.9 (96.6)	99.9 (100)
Redundancy	13.9 (6.8)	4.4 (4.3)	13.7 (13.5)
Observed reflections	408,866	254,225	188,742
Unique reflections	29,385 (1,160)	58,341 (5,723)	13,731 (1,328)
Bijvoet pairs (I⁺ and I)	14,406	-	-
Mean FOM (Zn-SAD)	0.414	-	-
Refinement			
Resolution (Å)	2.09	2.06	2.79
No. reflections	29,248	58,177	13,562
^c R _{work} / ^d R _{free}	0.213 / 0.253	0.192 / 0.237	0.192 / 0.263
No. Atoms			
Protein	2,079	4,228	2,137
DNA	1,142	2,123	1,142
Zn	10	20	10
Water	139	358	31
B Factors (Å²)			
Protein	74.2	61.2	69.1
DNA	73.5	58.1	56.4
Zn	82.2	59.5	76.0
Water	47	46.3	44.1
R.m.s. deviations			
Bond lengths (Å)	0.025	0.008	0.008
Bond angles (°)	1.1	1.05	1.0
All atom clash score	11.9	6.7	11.1
Ramachandran plot (%)			
favored	94.9	98	92.8
allowed	5.1	2	7.2
C β deviation	0	0	0

* Values in parenthesis correspond to highest resolution shell; ^a R_{merge} = $\sum |I - \langle I \rangle| / \sum I$, where I is the observed intensity and $\langle I \rangle$ is the averaged intensity from multiple observations; ^b $\langle I / \sigma I \rangle$ = averaged ratio of the intensity (I) to the error of the intensity (σI); ^c R_{work} = $\sum |F_{obs} - F_{cal}| / \sum |F_{obs}|$, where F_{obs} and F_{cal} are the observed and calculated structure factors, respectively; ^d R_{free} was calculated using a randomly chosen subset (5%) of the reflections not used in refinement; Wavelength=1.0 Å

Table S3, Related to Figure 5. DNA Minor and major groove widths

 Program 3DNA v2.0

 Minor and major groove widths: direct P-P distances and refined P-P
 distances which take into account the directions of the sugar-
 phosphate backbones

Ref: M. A. El Hassan and C. R. Calladine (1998). Two Distinct Modes of
 Protein-induced Bending in DNA. J. Mol. Biol., v282, pp331-343.

 File name: 5V3M.pdb (ZF1-11 in complex with 28-bp DNA)

	Minor Groove		Major Groove	
	P-P	Refined	P-P	Refined
1 TG/CA	---	---	---	---
2 GT/AC	---	---	---	---
3 TG/CA	12.8	---	18.5	---
4 GG/CC	13.5	13.5	17.5	17.4
5 GG/CC	13.4	13.2	16.7	16.7
6 GC/GC	13.5	13.3	15.3	15.0
7 CG/CG	13.6	13.5	16.1	15.1
8 GT/AC	12.2	12.1	19.6	19.1
9 TG/CA	11.3	11.1	19.4	19.2
10 GG/CC	12.4	12.2	16.4	16.1
11 GC/GC	14.3	13.9	16.3	15.4
12 CA/TG	14.7	14.3	19.5	18.8
13 AC/GT	13.7	13.6	21.3	21.1
14 CA/TG	13.4	13.2	21.5	21.5
15 AG/CT	13.5	13.3	19.4	19.3
16 GG/CC	12.2	12.1	16.2	15.9
17 GT/AC	10.2	10.1	17.6	17.6
18 TA/TA	9.3	9.3	17.8	17.8
19 AA/TT	8.9	8.9	16.7	16.7
20 AA/TT	9.2	9.2	19.0	19.0
21 AA/TT	9.2	9.2	18.4	18.4
22 AA/TT	8.7	8.7	17.4	17.4
23 AG/CT	9.1	9.1	20.4	20.4
24 GG/CC	10.7	10.7	16.3	16.2
25 GG/CC	12.8	---	13.7	---
26 GC/GC	---	---	---	---
27 CA/TG	---	---	---	---

Table S3 - Continues

 File name: 5WJQ.PDB (ZF2-11 in complex with 28-bp DNA)

	Minor Groove		Major Groove	
	P-P	Refined	P-P	Refined
1 TG/CA	---	---	---	---
2 GT/AC	---	---	---	---
3 TG/CA	13.7	---	18.8	---
4 GG/CC	13.6	13.5	18.6	18.1
5 GG/CC	13.4	13.2	16.5	16.3
6 GC/GC	13.3	13.1	14.7	14.5
7 CG/CG	13.4	13.2	15.7	15.1
8 GT/AC	12.9	12.8	18.7	18.4
9 TG/CA	12.6	12.4	19.6	19.2
10 GG/CC	13.4	13.1	16.7	16.2
11 GC/GC	14.6	14.1	16.6	15.6
12 CA/TG	14.5	14.1	19.2	18.5
13 AC/GT	13.4	13.2	21.4	21.3
14 CA/TG	13.1	12.9	22.0	22.0
15 AG/CT	13.3	13.2	19.7	19.6
16 GG/CC	12.7	12.7	16.2	15.9
17 GT/AC	10.9	10.9	17.8	17.8
18 TA/TA	9.6	9.6	17.8	17.8
19 AA/TT	9.3	9.2	18.6	18.6
20 AA/TT	9.1	9.1	19.0	19.0
21 AA/TT	8.8	8.8	18.8	18.8
22 AA/TT	8.9	8.8	19.7	19.7
23 AG/CT	10.6	10.5	22.1	21.6
24 GG/CC	12.9	12.8	18.4	17.5
25 GG/CC	13.9	---	17.6	---
26 GC/GC	---	---	---	---
27 CA/TG	---	---	---	---

Table S3 - Continues

 File name: 5V3J.pdb (ZF1-10 in complex with 26-bp DNA)
 Note: 2 protein-DNA complexes per crystallographic asymmetric unit

	Minor Groove		Major Groove	
	P-P	Refined	P-P	Refined
3 GG/CC	12.4	---	17.2	---
4 GG/CC	13.2	13.1	16.2	16.1
5 GC/GC	14.0	13.8	16.4	16.1
6 CG/CG	13.4	13.3	15.3	14.4
7 GT/AC	11.6	11.6	17.7	17.3
8 TG/CA	10.6	10.5	17.1	17.0
9 GG/CC	12.2	12.0	15.9	15.7
10 GC/GC	14.6	14.4	16.0	14.8
11 CA/TG	15.5	15.2	18.4	17.6
12 AC/GT	14.5	14.1	21.1	21.0
13 CA/TG	13.9	13.5	21.6	21.6
14 AG/CT	14.8	14.6	19.5	19.4
15 GG/CC	14.1	14.0	15.8	15.5
16 GT/AC	11.0	11.0	17.5	17.5
17 TA/TA	9.3	9.3	18.2	18.2
18 AA/TT	9.0	8.9	17.1	17.1
19 AA/TT	9.3	9.3	19.5	19.4
20 AA/TT	9.0	9.0	19.3	19.3
21 AA/TT	8.9	8.9	19.4	19.3
22 AG/CT	9.9	9.9	21.8	21.7
23 GG/CC	12.1	---	17.8	---
3 GG/CC	13.3	---	16.6	---
4 GG/CC	13.4	13.3	17.7	17.5
5 GC/GC	14.2	14.1	17.0	16.7
6 CG/CG	14.0	13.9	15.4	14.3
7 GT/AC	11.9	11.8	17.5	17.0
8 TG/CA	10.7	10.5	17.2	17.1
9 GG/CC	12.2	12.1	15.8	15.6
10 GC/GC	14.7	14.5	16.0	14.9
11 CA/TG	15.6	15.2	18.3	17.5
12 AC/GT	14.3	13.9	21.1	21.1
13 CA/TG	13.4	13.1	21.9	21.9
14 AG/CT	14.3	14.1	19.6	19.5
15 GG/CC	13.6	13.5	16.0	15.7
16 GT/AC	10.6	10.6	17.7	17.7
17 TA/TA	9.1	9.1	18.3	18.2
18 AA/TT	8.9	8.9	17.3	17.3
19 AA/TT	9.3	9.3	19.8	19.7
20 AA/TT	9.1	9.1	19.5	19.4
21 AA/TT	9.0	8.9	19.3	19.2
22 AG/CT	10.2	10.1	21.5	21.4
23 GG/CC	12.1	---	17.9	---

Table S4. Igf2 promoter sequences including binding motif and cloning sites

Mouse_Igf2_P0_promoter sequence

GCTAGCCCGGGCTCGAGCCCTAATTTGCATAAGCCACGCCCTTTTTTACCTGTGCCACGCCCA CAGACATTCCAGGGTGT CAGGTGACT
GCCAGGTGTCAATCCAGTGAAGCCCCACCCACTCTCCACCCCTGCACATAGTCCCTACCCCTAGCTAACAGGAAGTGCTTCTAGCTTA
ATTCAAACCTGCATAGACGCCTTCCTGTCTGT CAGGCAGGGGCCAAAGCCCCACCCTCTAATGCCCCATAACCCTAGTGTGGGAAAGCG
CCATAGCCAGCTGCCCCATAAGTCTTTGCAGTACTTTACTGGCATATCATTTCCTCAAATTTGGAGGGGGCTGGAAGTGGGCGTGGAGGG
GACGAGGTGAGGGATAAAAGCGTGGTGTCAATTCGAGCAGGTGCCTTACTCAGTGGAAAGCTTGGCATTCCGGTA

Chimp_Igf2_P0_promoter sequence

GCTAGCCCGGGCTCGAGCCCCCCCATTTTTACCAGTGCCACGTCCACCAACATTCCGGGGTGTCAAGTAACTGCCAAGTGTCACTCTAA
GTAAAGCTACACCCACTCCCCACCACCTCCACATAGCCCCACCTCCTAGCTGGCAGGGAGCTTCTGGCTTATGCCACGCCACAGGC
GCCTTTCTGCCAGGT CAGGGGTGGGCCAAACCTCCACCCCTAATGTACCATGCCCTGGTGTCTGGAAAGTGCCTGAGCCAGCTGCCCA
GCGGCCTCAGCACTACCAAGTTGGCACAAAGCTCCCCAAATTCGGAGGGGGCTCAGGGAAACGAGTGGAGGGGATGAGGAGGTGAGGGGT
AAACCCATCATTTCAGTTGGCATTGAGCAGGTGCCATGCTCAGCAAGCTTGGCATTCCGGTA

Human_Igf2_P0_promoter sequence

GCTAGCCCGGGCTCGAGCCCCCCGCATTTTTACCAGTGCCACGTCCACCAACATTCCAGGGTGTCAAGTAACTGCCAAGTGTCACTCTA
AGTAAAGCTACACCCACTCCCCACCACCTCCACATAGCCCCACCTCCTAGCTGGCAGGGAGCTTCTGGCTTATGCCACGCCACAGG
CGCCTTTCTGCCAGGT CAGGGGTGGGCCAAACCTCCACCCGCTAATGTACCATGCCCTGGTGTCTGGAAAGTGCCTGAGCCAGCTGCCCC
AGCGGCCTCAGCACTACCAAGTTGGCACAAAGCTCCCCAAATTCGGAGGGGGCTCAGGGAAACGAGTGGAGGGGATGAGGAGGTGAGGGG
TAAACCCATCATTTCAGTTGGCATTGAGCAGGTGCCATGCTCAGCGGAAGCTTGGCATTCCGGTA

RheMac_Igf2_P0_promoter sequence

GCTAGCCCGGGCTCGAGTATTCCTCCACATTTTTACCAGTGCCACGCCCAACCAACATTCCAGGGTGTCAAGTAACTGCCAAGTGTCACT
CTAAGTAGAGCTACACCCACTCCCCACTACCTCCACATAGCCCCACCTCCTGGCAGGCAGGGGGCTTCTGGCTTATACCCACGCCAC
AGGCGCCTTTCTGCCAGGT CAGAGGTGGGCCAAACCTCCATCCCCTAATGCACCATGCCCTGGTGTCTGGAAAGTGCCTGAGCCAGCTGC
CCCAGCGCCTCAGCACTACCAAGTTGGCACAAAGCTCCCCAAATTTGGAGGGGGCTCAGGGAAAGGAGTGGAGGGGAAGAGGAGGTGAG
GGGTGAACCCATCATTTCAGTTGGCATTGAGCAGGTGCCATGCTCAAGCTTGGCATTCCGGTA