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#### **RSC Advances**

### ARTICLE

#### <Supplemental File>

Structural and conformational insights into the SOX2/OCT4-bound enhancer DNA: A computational perspective

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Running Title: SOX2/OCT4 induced DNA conformational alterations

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**Figure S1** | **Structural organization of SOX2/OCT4-DNA complex.** SOX2 and OCT4 proteins bind to their respective binding sites and interact directly over the DNA as well as through DNA mediated allostery. Proteins are indicated in ribbon style with SOX2 in red and OCT4 in green. The bases of DNA have been displayed in stick conformation, and the whole DNA is given in orange.



**Figure S2** | **Structural deviation from the initial structure. (A)** Root mean square deviation (RMSD) of the protein backbone from the protein-DNA complexes. (B) RMSD of DNA atoms from the protein-DNA complexes or from free DNA.



**Figure S3** | **Hydrogen bonds (H-bonds) between the protein and DNA.** H-bonds were counted based on the criteria as the donor-acceptor distance of 3.5 Å and the hydrogen-donor-acceptor bond angle of 30° or less.

# ARTICLE

Table S1. Hydrogen bonding kinetics. Hydrogen bond breaking and reformation kinetics as per

Luzar and Chandler's definition of kinetics of hydrogen bonds.

System	DG (kJ/mol)	Time forward (ps)
DNA <sup>SYN</sup>	25.523	3092.73
DNA <sup>CRY</sup>	23.421	1368.20
DNA <sup>SOX</sup>	23.585	1457.90
DNA <sup>OCT</sup>	17.457	135.29
DNA <sup>WT</sup>	23.544	1434.94
DNA <sup>MUT</sup>	17.788	153.80
DNA <sup>NS</sup>	21.067	548.93

#### ARTICLE

**Table S2: H-bond interaction between DNA and protein molecules in various complexes.** Those complexes having protein only have been included, whereas, DNA<sup>CRY</sup> and DNA<sup>SYN</sup> have not been considered due to the lack of proteins subunit. The numbering in the table up to 79 refers SOX2, 138-289 refers OCT4, and in DNA, first 24 base-pairs refer to chain A of DNA, and 25-48 refer to chain B of DNA.

Complex	H-bond interaction	Distance (Å)
DNA <sup>SOX</sup>	(ARG 43)NO(DA 44)	2.473
	(ARG 43)NO(DT 8)	2.492
	(ASN 46)C N(DG 7)	2.119
	(ASN 68)NO(DA 48)	2.385
	(ARG 113)NO(DC 43)	2.040
	(ARG 114)NN(DA 41)	2.718
	(LYS 115)NO(DA 42)	2.128
DNA <sup>OCT</sup>	(GLN 181)ON(DA 13)	2.043
	(GLN 283)ON(DA 18)	2.065
	(ASN 280)ON(DA 19)	1.976
	(THR 182)NO(DC 35)	1.909
	(ARG 157)NO(DG 12)	1.846
	(GLN 164)NO(DG 12)	2.251
	(LYS 195)NO(DT 32)	2.091
	(ASN 196)NO(DA 33)	2.384
	(ARG 275)NO(DC 27)	2.187
DNA <sup>WT</sup>	(LYS 4)NO(DA 45)	1.853
	(ARG 5)NO(DT 9)	2.279

	(ARG 15 NO(DA 46)	1.982
	(TRP 41)NO(DT 6)	2.438
	(TRP 41)NO(DG 7)	2.078
	(ARG 60)NO(DT 9)	1.990
	(ARG 75)NO(DA 42)	2.115
	(LYS 77) NO(DA 42)	1.779
	(ASN 280)ON(DA 19)	2.179
	(THR 182)ON(DC 35)	2.013
	(THR 235)NO(DA 18)	2.094
DNA <sup>MUT</sup>	(ARG 43)NO(DT 8)	2.049
	(ARG 43)NO(DT 9)	2.368
	(TRP 79)NO(DG 7)	2.106
	(LYS 117)NO(DA 44)	2.003
	(GLN 164)NO(DA 13)	2.074
	(ASN 196)NO(DA 33)	2.419
	(ARG 232)NO(DT 32)	2.412
	(THR 235)NO(DA 19)	2.283
	(ARG 282)NO(DC 27)	2.066
DNA <sup>NS</sup>	(ARG 5)NO(DT 8)	2.332
	(ASN 30)NO(DT 2)	2.091
	(ARG 75)NO(DA 41)	2.036
	(GLN 283)ON(DA 19)	2.264
	ARG 287)ON(DC 32)	2.025
	(GLN 181)NN(DA 13)	2.135
	(LYS 233)NO(DG 35)	2.038
	(ARG 275)NO(DC 23)	2.506
	(ARG 287)NO(DG 17)	2.431
	1	

# ARTICLE

#### Table S3. Relaxation time for the PO bond vector of DNA in different systems. P1 and P2

System/Time	Time				
	P1±SD	P2±SD			
DNA <sup>SYN</sup>	40710.9±4326.74	28925.6±7229.1			
DNA <sup>CRY</sup>	382990.4±4633.03	25759.8±6552.94			
DNA <sup>SOX</sup>	41635.4±5680.4	31334.2±9919.5			
DNA <sup>OCT</sup>	43357.3±4869.74	34431.2±8929.4			
DNA <sup>WT</sup>	44851.2±7209.96	38927.2±7513.98			
DNA <sup>MUT</sup>	35815.98±3657.7	21221.2±5456.1			
DNA <sup>NS</sup>	18800.74±4576.5	5830.5±2341.3			

are the first and second Legendre polynomials.

# ARTICLE

Table S4: Energetics of dsDNA. Coulomb and van der Waals interaction energies between the

DNA strands.

System	Coulomb (kJ/mol)	VdW (kJ/mol)
DNA <sup>SYN</sup>	1.963±0.131	-4.598±0.125
DNA <sup>CRY</sup>	6.862±1.684	-2.9273±0.182
<b>DNA<sup>SOX</sup></b>	1.87±0.125	-4.587±0.126
DNA <sup>OCT</sup>	2.03366±0.113	-4.542±0.11
DNA <sup>WT</sup>	1.942±0.115	-4.52±0.117
DNA <sup>MUT</sup>	1.877±0.14	-4.325±0.14
DNA <sup>NS</sup>	1.264±0.179	-4.143±0.154

## ARTICLE

**Table S5. Diffusive properties of DNA.** The diffusion coefficients were calculated on the basis of heavy atoms of DNA and phosphorus (P) atoms.

System	Heavy Atoms	Р		
	Diffusion Coefficient (cm <sup>2</sup> /s)	Diffusion Coefficient (cm <sup>2</sup> /s)		
DNA <sup>SYN</sup>	7.46E-05±4.14E-05	5.77E-05±7.65E-006		
DNA <sup>CRY</sup>	6.70E-05±4.13E-05	3.55E-05±0.00037		
<b>DNA<sup>SOX</sup></b>	5.34E-05±1.532E-05	20.0E-05±5.18E-005		
DNA <sup>OCT</sup>	2.22E-05±0.443E-05	2.03E-05±5.16E-005		
DNA <sup>WT</sup>	1.87E-05±0.23E-05	1.45E-05±3.81E-005		
DNA <sup>MUT</sup>	63.7E-05±0.001129	66.2E-05±0.0004666		
DNA <sup>NS</sup>	-512.01E-05±0.1263	2.05E-01±0.0155		

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Table S6: Correlation between different parameters of DNA structural properties.

System	<b>Roll/Twist</b>	Roll/Slide	Inclination	X-disp/	H-Rise/H-	DNA helical	X-disp/	X-disp/
			/H-Twist	Slide	Twist	bend/ Twist	P-Twist	Twist
DNA <sup>SYN</sup>	-0.417	0.1378	0.0022	0.0246	0.265	-0.0287	-0.015	0.0424
<b>DNA</b> <sup>CRY</sup>	-0.4922	0.1765	-0.485	0.485	0.244	-0.128	-0.288	0.6835
DNA <sup>SOX</sup>	-0.4404	0.3146	-0.282	0.433	0.2215	-0.120	-0.281	0.6475
DNAOCT	-0.2877	0.2953	-0.209	0.705	0.209	-0.139	-0.313	0.6969
DNAWT	0.002	0.5171	0.175	0.562	0.110	0.176	-0.0836	0.3361
<b>DNA</b> <sup>MUT</sup>	-0.2023	0.1066	-0.064	0.647	0.1339	0.358	-0.1808	0.5012
DNA <sup>NS</sup>	-0.1145	0.4130	0.086	0.422	-0.120	0.0282	-0.0306	0.1872
H-Twist: Helical Twist, X-displacement								