

The role of zinc finger linkers in zinc finger protein binding to DNA

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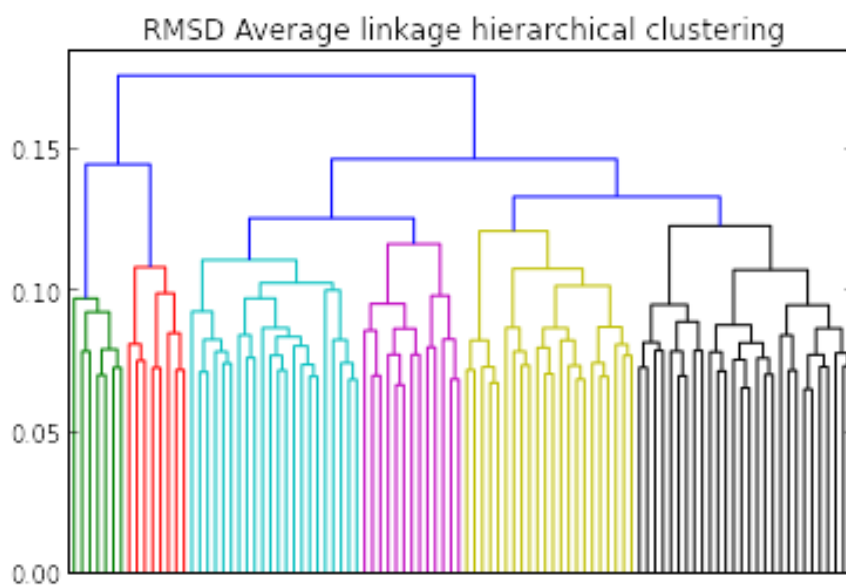


Figure 1S; shows a dendrogram (cluster trees) of the wild type ZFP-DNA complex employing RMSD. The Principal component analysis (PCA) technique transformed the trajectory frames into a set of orthogonal vectors (PCs) to help explain the variance in coordinate space. PCs represent certain modes of motion with the first PC shows the largest variance and the dominant motion in the system. This helped to gain insight into the dynamics of the system (the actual motion of the system) throughout the course of a simulation which is a combination of the individual

PCs. while motion along a single PC shows a transition, this does not necessarily indicate how the system undergoes that transition

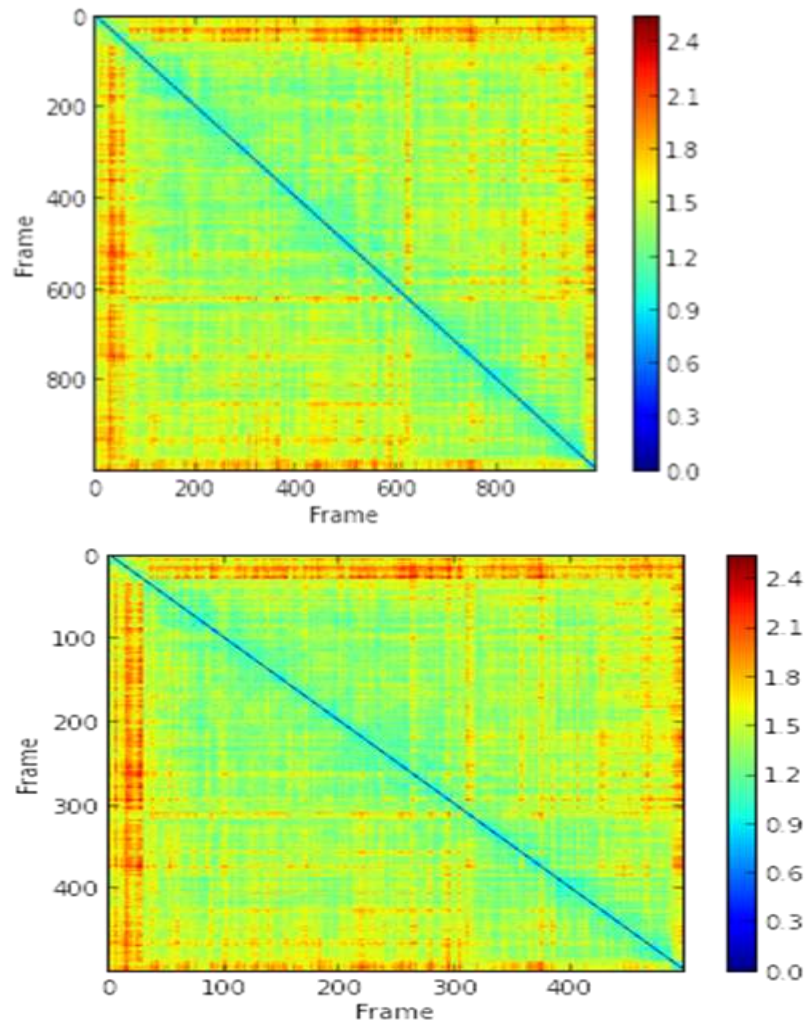


Figure2-S A cluster: plot of RMSD of mutant complex zinc finger protein(WT) DNA complex shows: A) RMSD pairwise computed for first 5000 snapshots and skip every 5 frames, B) RMSD pairwise computed for first 5000 snapshots and skip every 10 frames.

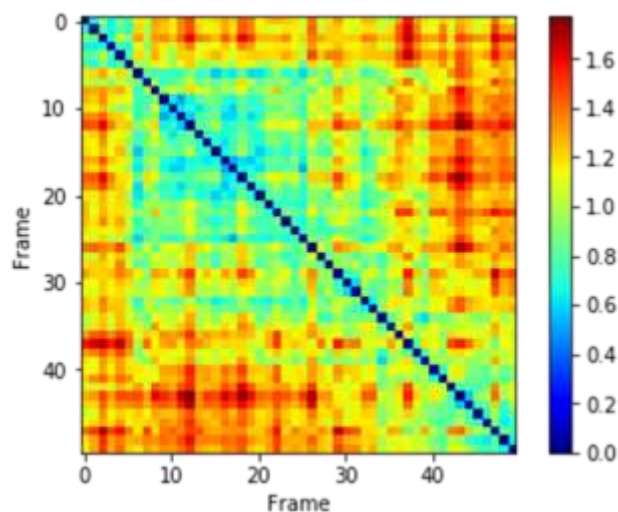


Figure 2S-B E58G-DNA RMSD
RMSD pairwise computed for first 500 snapshots and skip every 10 frames

Table 2S

Table 2_S: energy vlues for WT ZFP and mutants after 50, 100,150 ns simulation times

Prot ein	Simul ation time	ΔH_{MM} GBSA	err or	T Δ S	err or	ΔG_{MM} GBSA	err or	ΔH PBSA		TS	ΔG_{MM} PBSA		ΔH_{MM} GBSA- avrg
1AA Y	50ns	-84.6	4	- 74. 3 (5)	5	-10.3	3. 2	- 107 .23	6. 28	- 88. 36	-18.38	8. 5	-92.86
1AA Y	102 ns	-97.5	5	- 86. 7	4. 5	-10.8	2. 8	- 106 .74	6. 3	- 83. 9	-24.16	7	
1AA Y	150ns	-96.47	3. 3	- 85. 3	4	-11.27	3. 5	- 108 .06	5. 3	- 82. 66	-25.4	6	
T28 A	50 ns	-91.10	3. 70	- 83. 56	5. 70	-7.54		- 123 .00	5. 50	- 83. 56	-39.44		-93.70
100. 00	100.6n s	-95.40	4. 00			-8.60		- 124 .06			-40.50		

150.00	150 ns	-94.60	4.00			-8.30		-120.36			-36.80		
G29P	50 ns	-91.47	4.17	-82.80	5.40	-8.70	7.00	-125.70	5.40	-82.80	-42.90	7.40	-90.36
	100.6ns	-90.10	4.50			-7.30	4.00	-124.30			-41.50	7.00	
	150 ns	-89.50	4.40			-6.70	5.00	-125.90			-43.10	6.80	

Table 3-S: Comparison of Energies Between specific and nonspecific binding

protein	ΔH_{MMGB} SA avg		ΔH_M M-GBSAavg-DNA mutant	error	ΔH_{MMPB} SA avg			$\Delta \Delta H_{MMGB}$ SA	$\Delta \Delta H_{MMPB}$ SA
1AA Y	-92.86	4.00	-56.87	6.50	-107.34	5.60	1AA Y	0.00	0.00
T28A	-93.70	3.80	-56.57	5.50	-122.47	5.50	T28 A	-0.84	-15.13
G29P	-90.36	4.20	-55.44	5.60	-125.30	5.40	G29 P	2.50	-17.96
G29R	-93.37	3.80	-61.82	5.70	-128.90	5.90	G29 R	-0.51	-21.56
Q30E	-103.40	7.50	-62.02	6.10	-133.40	10.00	Q30 E	-10.54	-26.06
K31D	-81.43	5.90	-58.33	6.30	-103.30	6.00	K31 D	11.42	4.04
K31N	-94.67	4.80	-58.71	6.00	-130.40	6.00	K31 N	-1.81	-23.06
P32G	-101.78	4.50	-54.42	4.50	-123.60	10.00	P32 G	8.92	-16.26
T56A	-91.27	3.90	-49.57	5.30	-124.30	10.50	T56 A	1.59	-16.96
T56Y	-111.63	6.00	-58.06	4.90	-142.60	7.00	T56 Y	-18.78	-35.26
T56I	-94.44	3.90	-60.24	5.40	-137.22	8.00	T56I	-1.58	-29.88

G57 D	-94.83	4.2 0	- 63.19	6.0 0	-128.30	6.00	G57 D	-1.98	-20.96
K59 N	-92.40	4.7 0	- 59.18	5.0 0	-122.80	5.50	K59 N	0.46	-15.46
P60A	-101.39	6.0 0	- 64.34	5.5 0	-122.00	6.00	P60 A	-8.53	-14.66

Table 4S; **The role of zinc finger linkers in zinc finger protein binding to DNA**

	$\Delta G_{\text{MMGBSA-avrg}}$	error	$\Delta G_{\text{MMPBSA avrg}}$	error	$\Delta\Delta G_{\text{MMGBSA-avrg}}$	$\Delta\Delta G_{\text{MMPBSA-avrg}}$
1AAY	-10.79	3.5	-22.65	5.5	0	0
T28A	-8.15	3.9	-38.91	5.6	2.64	-16.27
G29P	-7.57	4.5	-42.50	5.4	3.22	-19.85
G29R	-12.37	4	-47.97	5.9	-1.58	-25.32
Q30E	-19.97	3.9	-49.84	6.5	-9.18	-27.19
K31D	-1.93	8.9	-23.77	7	8.86	-1.12
K31N	-13.27	4.5	-48.25	7.5	-2.48	-25.60
P32G	-21.74	5.5	-44.07	6.8	-10.95	-21.42
T56A	-7.86	4.6	-42.50	6.6	2.93	-19.85
T56Y	-24.87	6.5	-56.03	7.5	-14.08	-33.39
T56I	-16.27	4.5	-56.43	7.6	-5.48	-33.79
G57V	-33.17	6.8	-71.31	8	-22.38	-48.67
G57D	-18.33	4.5	-52.83	5.2	-7.54	-30.19
E58G	-11.87	4	-45.77	6.2	-1.08	-23.12
E58Q	-3.41	4.2	-45.48	6.3	7.38	-22.83
K59P	-25.83	4.3	-49	5.6	-15.04	-26.35
K59N	-11.49	4.5	-47	6.2	-0.70	-24.35
P60E	-21.17	6	-38.5	6.5	-10.38	-15.85
P60A	-16.27	5.6	-38.4	6.4	-5.48	-15.75