Supporting Information

Molecular Simulation Guided Aptasensor Design of Robust and Sensitive Lateral Flow Strip for Cadmium Ion Detection

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Table of contents

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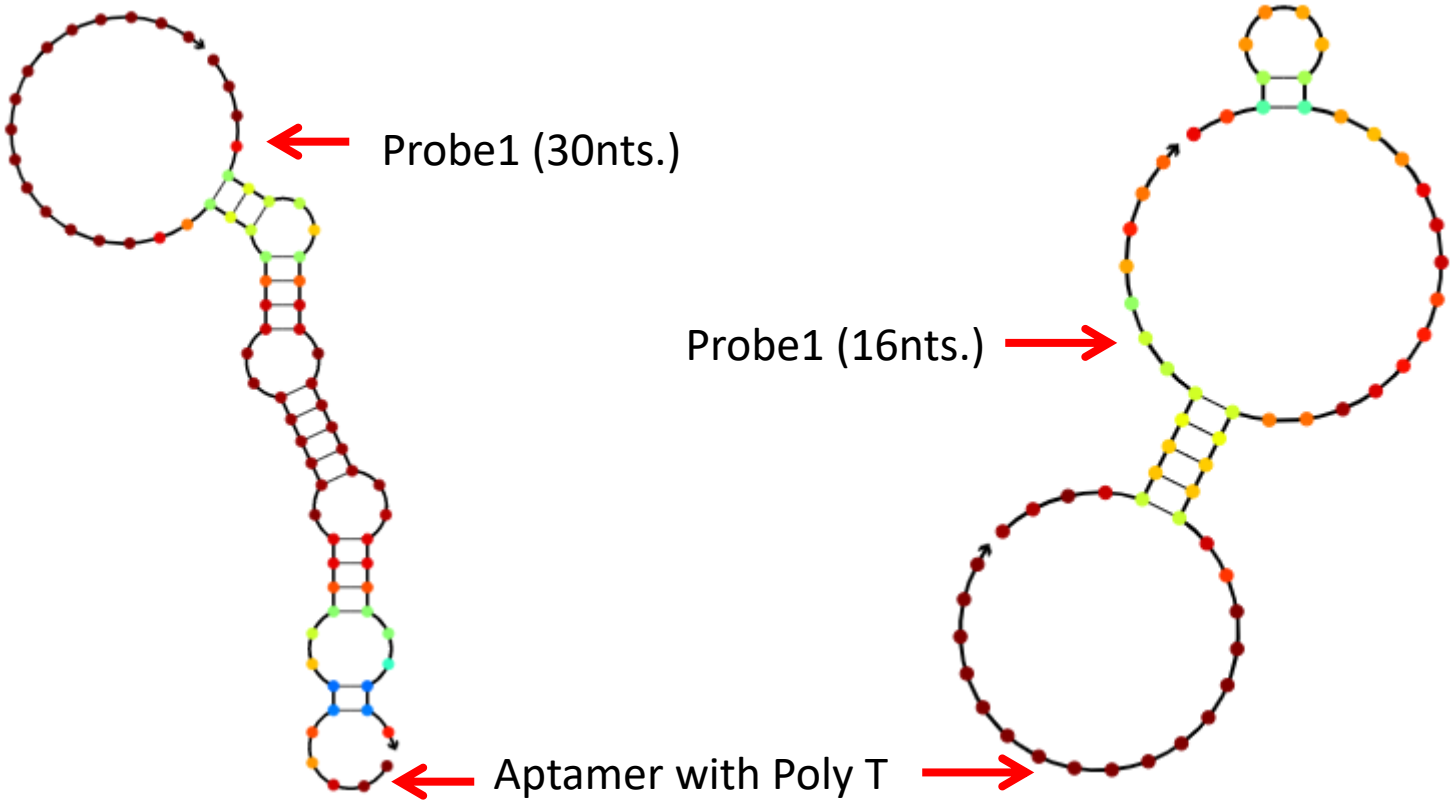


Figure S1: Secondary structure based hybridization prediction of aptamer with probe 1 (lengths 30nts and 16nts). An apparent change in secondary structure influenced by reduced numbers of nucleotides leads to change in ΔG.

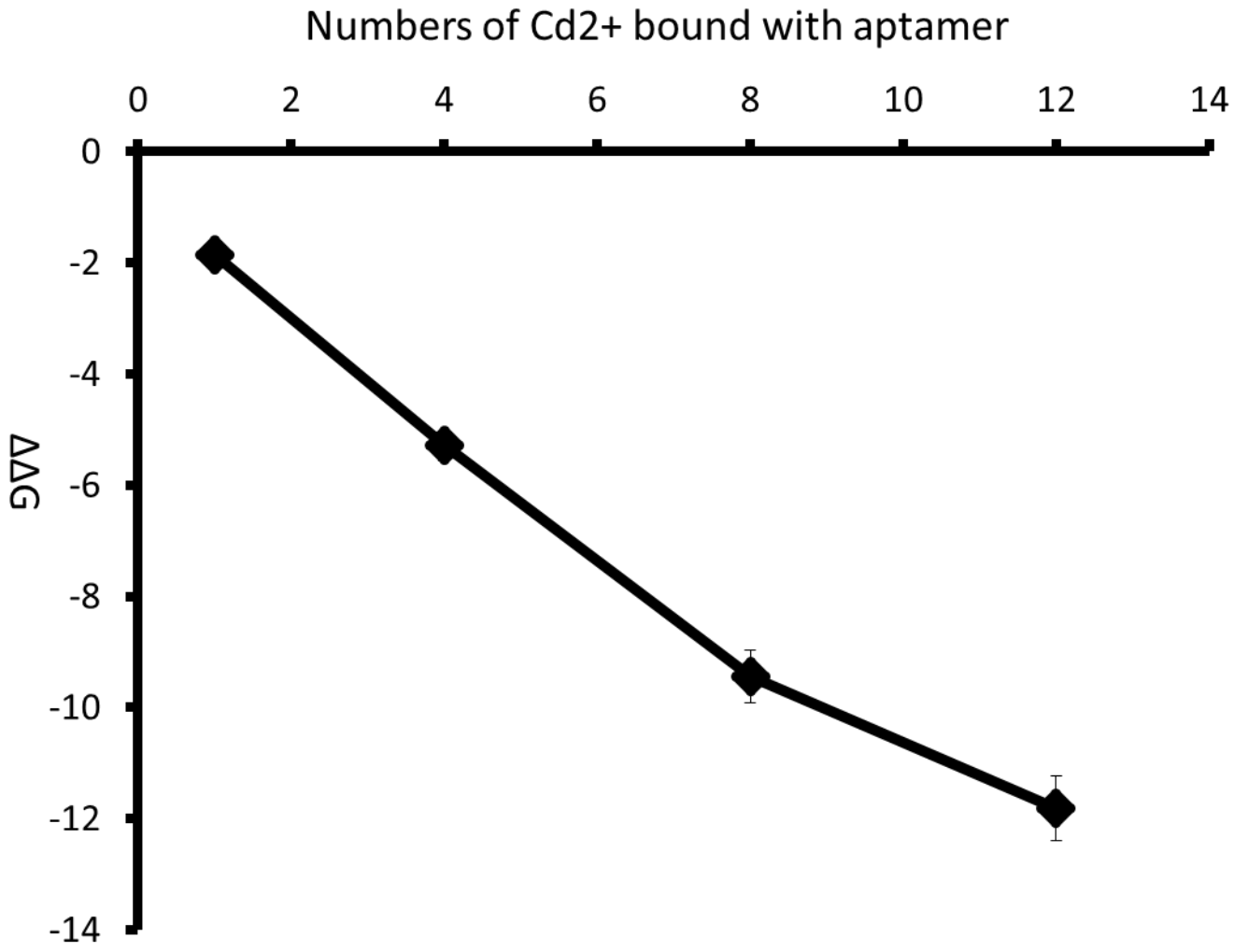


Figure S2: Change in binding affinity of aptamer with probe1 in presence of different concentrations of Cd2+. ΔΔG is the change in ΔG when aptamer hybridized with probe1 in abscence of Cd2+ as compared to aptamer/Cd2+ (1,4,8, and 12) complexes bind with prob1.

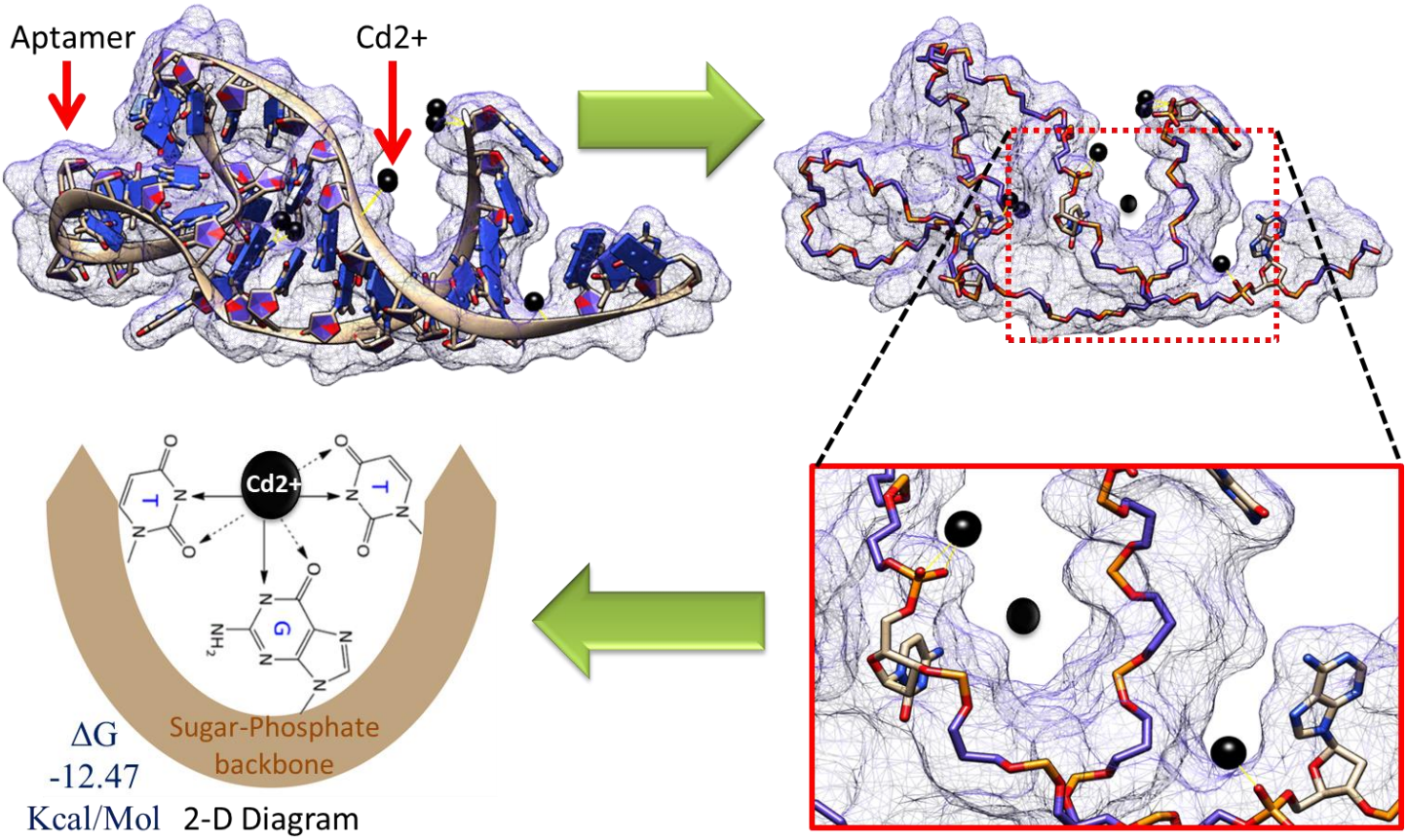


Figure S3: *In silico* analysis of Cd^{2+} binding with aptamer. Binding of single Cd^{2+} is characterized at the end in form of 2D diagram, which shows tendency of Cd^{2+} toward G and T.

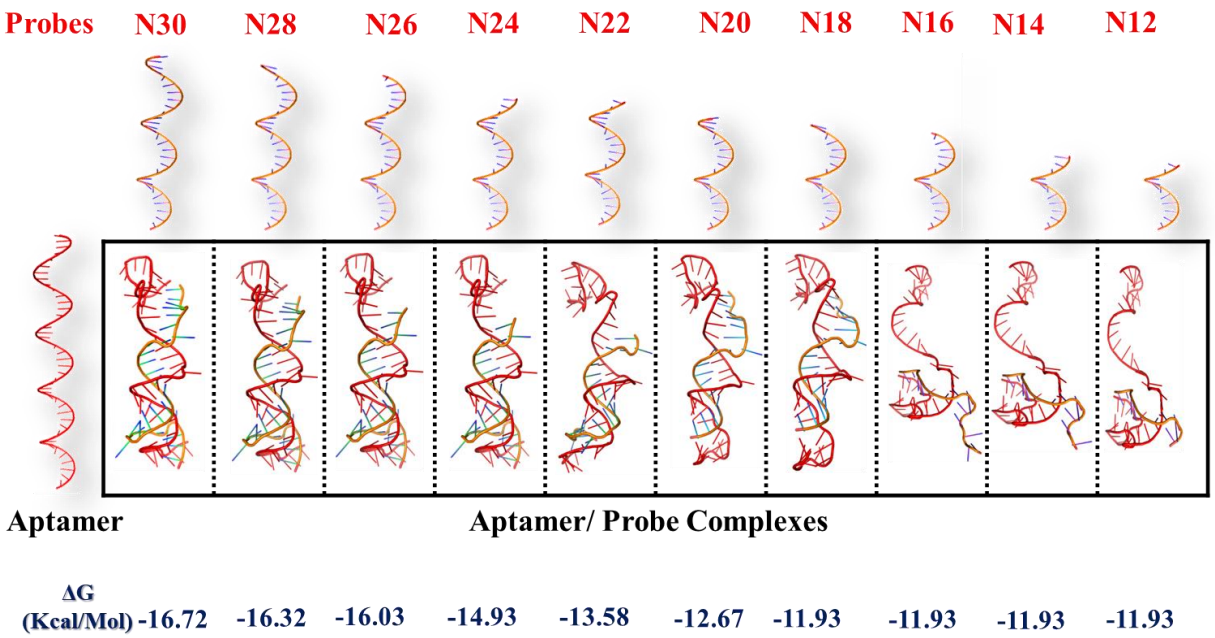
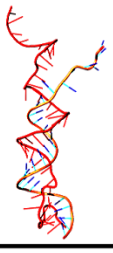
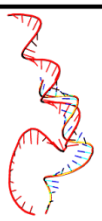
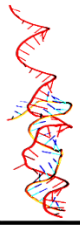
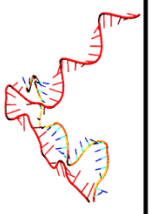
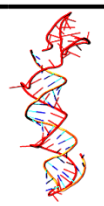


Figure S 4: Simulations oriented optimization of probe length based upon hybridization Yield and ΔG. The simulated presentations of aptamer hybridization with different lengths of probes, showing the conformational changes directly impacted by length which influenced the Δ G that leads to the hybridization yield.

Complex (Apt. and probe)								
Mutation	Wild Type	1-2	3-4	5-6	7-8	9-10	11-12	13-14
ΔG° (kcal/mol)	-16.72	-16.27	-16.20	-14.80	-15.80	-15.90	-14.88	-15.35
HY# (%)	100	95.50	97.80	73.30	91.90	92.60	75.60	83.00
Complex (Apt. and probe)								
Mutation	15-16	17-18	19-20	21-22	23-24	25-26	27-28	29-30
ΔG° (kcal/mol)	-11.44	-13.64	-13.47	-13.83	-12.59	-16.01	-16.18	-16.27
HY# (%)	26.10	61.20	59.10	68.60	47.00	80.90	90.00	95.60

HY# is hybridization yield.

Figure S5: Molecular simulations based sequence optimization of selected probe 30 nt. The 15 mutated sequences were generated by two consecutive mutations in each sequence starting from 1-2 position till end 29-30. Mutations were made such in a way that a purine is substituted with purine (A→G/G→A) and pyrimidine with pyrimidine (T→C/C→T). The molecular simulation complexes are shown along with binding free energies and hybridization yields.

TableS1: Table of mutated sequences of probe 30 nt for molecular simulations based sequence optimization.

No.	Sequence	Mutation
1.	CCTGACAACACCATAATAAAAACCAACACG	Wild type
2.	**TT**TGACAACACCATAATAAAAACCAACACG	1-2
3.	CC**CA**ACAACACCATAATAAAAACCAACACG	3-4
4.	CCTG**GT**AACACCATAATAAAAACCAACACG	5-6
5.	CCTGAC**GG**CACCATAATAAAAACCAACACG	7-8
6.	CCTGACAA**TG**CCATAATAAAAACCAACACG	9-10
7.	CCTGACAACA**TT**ATAATAAAAACCAACACG	11-12
8.	CCTGACAACACC**GC**AATAAAAACCAACACG	13-14
9.	CCTGACAACACCAT**GG**TAAAAACCAACACG	15-16
10.	CCTGACAACACCATAA**CG**AAAACCAACACG	17-18
11.	CCTGACAACACCATAATA**GG**AACCAACACG	19-20
12.	CCTGACAACACCATAATAAA**GG**CCAACACG	21-22
13.	CCTGACAACACCATAATAAAAA**TT**AACACG	23-24
14.	CCTGACAACACCATAATAAAAACC**GG**CACG	25-26
15.	CCTGACAACACCATAATAAAAACCAA**TG**CG	27-28
16.	CCTGACAACACCATAATAAAAACCAACA**TA**	29-30