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Figure s1. a) 2-D and, b) 3-D structures of AptBH.

 Table s1. Free energy content, guanine/cytosine percentage of selected aptamers, and corresponding docking score.

Aptamer	GC%	ΔG _{aptamer} (kcal/mol)	Docking Score
SMa#G11-6	66	-3.16	-313.86
SMa#G11-5	57	-0.20	-300.01
SMa#G11-20	60	-0.53	-332.89
SMa#G10-6	66	-1.47	-271.23
SMa#G10-11	60	-3.16	-423.04
ASM-1	56	-1.52	-292.26
ASM-2	59	-3.06	-297.61
ASM-3	54	-3.67	-301.65
ASM-4	59	-2.14	-323.57
ASM-5	56	-4.81	-322.15
ASM-6	56	-4.47	-280.24
ASM-7	56	-3.62	-325.28
FAM	47	-3.66	-287.02

Type of	Amino acid	Nucleotide	Distance (A ^o)
interaction	residue	residue	
Hydrophobic	Pro69	G36	3.02
Interactions			
	Phe148	G23	3.76
	Gln70	T35	3.99
Hydrogen bonds	Ser71	T12	3.07
	Thr74	T10	3.58
	Lys459	G31	3.88
	Gln507	G25	4.07
	Lys514	G31	3.85
	Lys515	G28	3.81
	Asn517	G7	3.96
	Arg530	C5	3.44
	Gly531	G27	2.99
	Lys533	G27	3.47
	Arg536	G25	3.51
Salt Bridges	Lys467	G25	2.55
	Glu512	G29	3.38
	Glu512	G30	4.47
π-Cation	Arg80	T39	5.01
interaction			

Table s2. Detail of interactions between AptBH aptamer and FBP of S. mutans



Figure s2. Gel retardation assay for DNA Ladder (L), AptBH aptamer (Ap), AgNPs (Ag) and AgNPs-AptBH (Ag-Ap)



Figure s3. Photographs of hemolysis of RBCs. DW (+) and PBS (-) are used as the positive and negative control, respectively.