Supporting Information for

Molecular Dynamics Simulation Analysis of Anti-MUC1 Aptamer and Mucin 1 Peptide Binding

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Snapshots of MUC1 peptide-aptamer simulations A) $MUC1_1$ B) $MUC1_2$ *(section III-B)*

Multiple simulations of the MUC1 peptide-aptamer combination are shown below. In each case there are association events with the arginine residue initiating the interaction with the 5'-3' open ends. Figure S1 shows the progression of the association events for the MUC1 peptide-aptamer simulation.

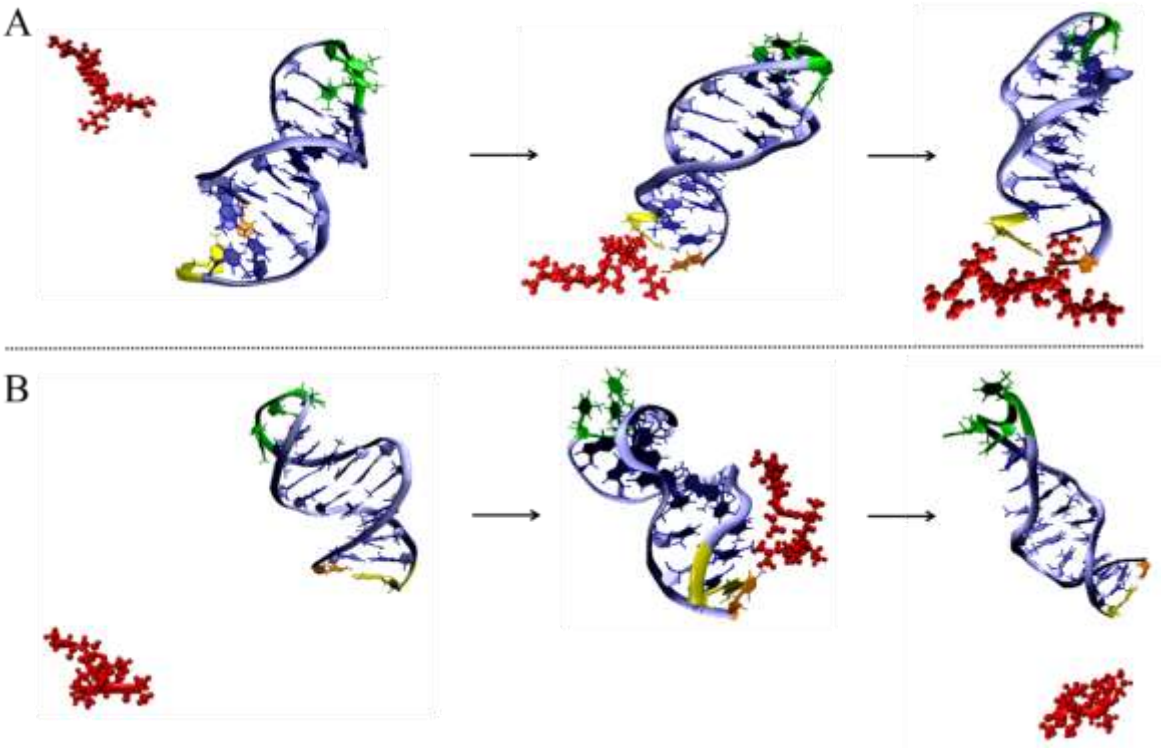

Figure S1: Snapshots of MUC1 peptide-aptamer simulations A) $MUC1_1$ B) $MUC1_2$

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Atoms used to Define the Binding region for All Simulations *(section III-C)*

Atoms specific to the binding region as they pertained to selected simulation are listed. In all cases peptide atoms specific to the binding region were from the arginine residue.

Table S1:Atoms used to define the binding region for all simulations

6ARG: H	1DC: O5'	13DT: P	12DT: P	23DG: P
6ARG: CA	1DC: H5T	13DT: O1P	12DT: O1P	23DG: O1P
6ARG: HA	1DC: C5'	13DT: O2P	12DT: O2P	23DG: O2P
6ARG: CB	1DC: H5'1	13DT: O5'	12DT: O5'	23DG: O5'
6ARG: HB1	1DC: H5'2	13DT: C5'	12DT: C5'	23DG: C5'
6ARG: HB2	1DC: C4'	13DT: H5'1	12DT: H5'1	23DG: H5'1
6ARG: CG	1DC: H4'	13DT: H5'2	12DT: H5'2	23DG: H5'2
6ARG: HG1	1DC: O4'	13DT: C4'	12DT: C4'	23DG: C4'
6ARG: HG2	1DC: C1'	13DT: H4'	12DT: H4'	23DG: H4'
6ARG: CD	1DC: H1'	13DT: O4'	12DT: O4'	23DG: O4'
6ARG: HD1	1DC: N1	13DT: C1'	12DT: C1'	23DG: C1'
6ARG: HD2	1DC: C6	13DT: H1'	12DT: H1'	23DG: H1'
6ARG: NE	1DC: H6	13DT: N1	12DT: N1	23DG: N9
6ARG: HE	1DC: C5	13DT: C6	12DT: C6	23DG: C8
6ARG: CZ	1DC: H5	13DT: H6	12DT: H6	23DG: H8
6ARG: NH1	1DC: C4	13DT: C5	12DT: C5	23DG: N7
6ARG: HH11	1DC: N4	13DT: C7	12DT: C7	23DG: C5
6ARG: HH12	1DC: H41	13DT: H71	12DT: H71	23DG: C6
6ARG: NH2	1DC: H42	13DT: H72	12DT: H72	23DG: O6
6ARG: HH21	1DC: N3	13DT: H73	12DT: H73	23DG: N1
6ARG: HH22	1DC: C2	13DT: C4	12DT: C4	23DG: H1
	1DC: O2	13DT: O4	12DT: O4	23DG: C2
	1DC: C3'	13DT: N3	12DT: N3	23DG: N2
	1DC: H3'	13DT: H3	12DT: H3	23DG: H21
	1DC: C2'	13DT: C2	12DT: C2	23DG: H22
	1DC: H2'1	13DT: O2	12DT: O2	23DG: N3
	1DC: H2'2	13DT: C3'	12DT: C3'	23DG: C4
	1DC: O3'	13DT: H3'	12DT: H3'	23DG: C3'
		13DT: C2'	12DT: C2'	23DG: H3'
		13DT: H2'1	12DT: H2'1	23DG: C2'
		13DT: H2'2	12DT: H2'2	23DG: H2'1
		13DT: O3'	12DT: O3'	23DG: H2'2
				23DG: O3'
				23DG: H3T

Initial Distance and RMSD Comparison for all Mucin 1 Peptide-Aptamer Complexes (*Section III-D*).

Initial configurations were chosen in such a way to place the aptamer and peptide at varying distances. The initial, equilibrated, and final center of mass (COM) distances are as shown in Table S2. The RMSD between the structures show that each of the MUC1-G complexes is similar. The RMSD of the MUC1 complexes vary (as seen in the visual results, Figure S1) as the final configurations show markedly different orientations.

Table S2: Initial Distance and RMSD Comparison for all Mucin 1 Peptide-Aptamer Complexes

Aptamer Peptide Complex	*Initial COM Distance (nm)*	*Equilibrated COM Distance (nm)*	*Final COM Distance (nm)*	*RMSD Between Original Complexes (nm)*
MUC1	*1.99*	*2.00*	*2.16*	-
$MUC1_1$	*2.25*	*5.31*	*3.25*	*1.13*
$MUC1_2$	*2.47*	*3.63*	*2.47*	*0.63*
MUC1-G	*2.67*	*5.62*	*1.63*	-
MUC1-G_1	*3.00*	*3.32*	*2.07*	*0.78*
MUC1-G_2	*2.83*	*3.61*	*1.97*	*0.72*
MUC1-G_3	*2.67*	*4.70*	*1.68*	*0.93*

<u>Radius of Gyration (R_g) of all MUC1-G Peptide-Aptamer Simulations</u> (*section III-D*)

The radius of gyration for all MUC1-G peptide-aptamer combinations obtained from simulations is shown in Figure S2. Though binding has occurred at different times, the R_g values reflect a convergence after binding in all MUC1-G peptide-aptamer simulations. In each case the R_g consistently converges to a value of 1.3nm upon binding.

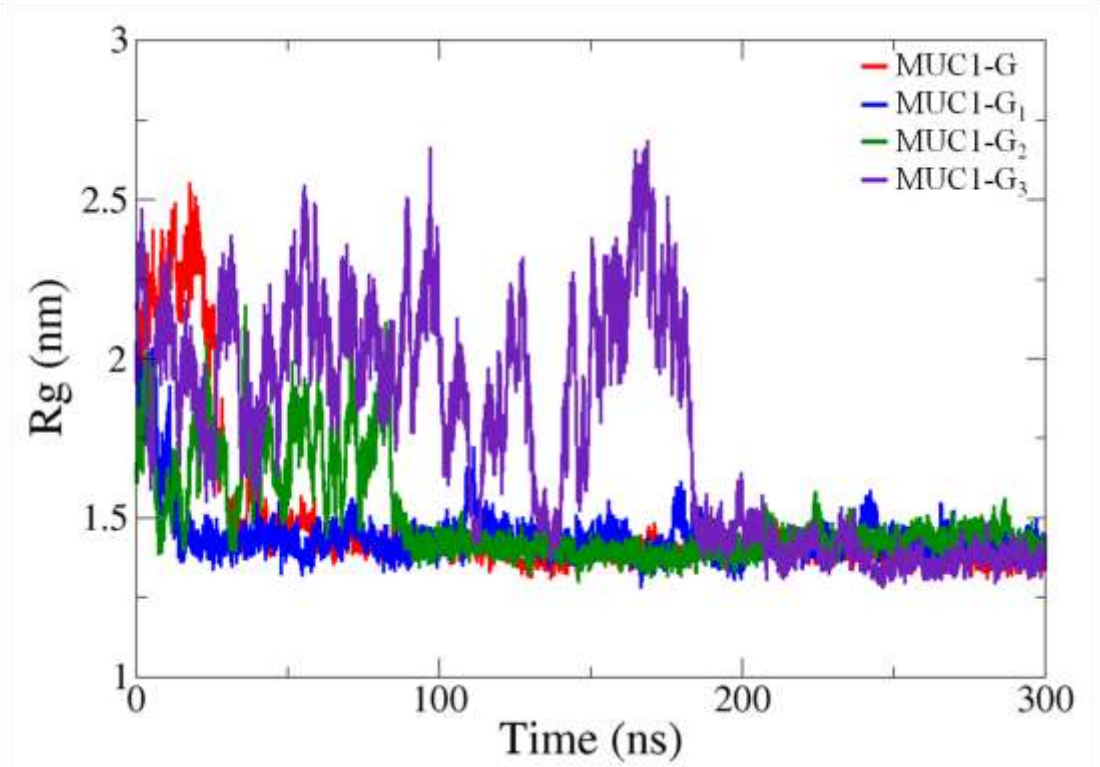

Figure S2: Radius of gyration for all MUC1-G peptide-aptamer combination simulations.

<u>Number of Hydrogen Bond Comparison in MUC1 and MUC1-G Complexes</u> (*Section III-E*)

Figure S3 compares the average number of hydrogen bonds for MUC1-G peptide-aptamer binding and MUC1 peptide and aptamer simulations. The MUC1 and MUC1-G peptide complexes follow a similar pattern until "binding moment". After the "binding moment" the number of hydrogen bonds decreases in the case of the MUC1 complex.

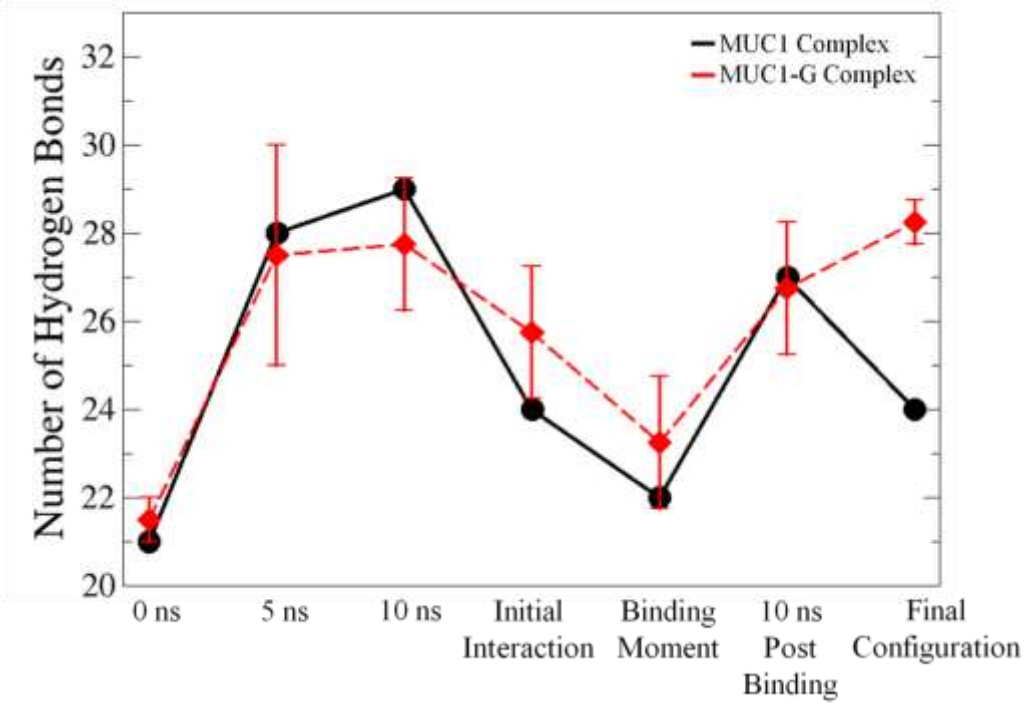

Figure S3: The number of hydrogen bonds within the aptamer structure at specific intervals is shown. Results for MUC1 peptide-aptamer complex are shown in black and the average results for MUC1-G peptide-aptamer complex are shown in red.

Description of All Prevalent Atoms Involved in Hydrogen Bonding for all MUC1-G complexes (*Discussion Section*)

An extended list of all prevalent atoms involved in the formation of hydrogen bonds between the MUC1-G peptide-aptamer complexes is shown below.

MUC1-G: Arginine-5 side chain NE with the Thymine-13 side chain O1P; Arginine-5 side chain NH2 with the Thymine-13 side chain O1P; Arginine-5 side chain NH1 with the Thymine-13 side chain O1P; Arginine-5 main chain N with the Thymine-12 side chain O1P; Arginine-5 main chain C with the Thymine-13 side chain O2; Arginine-5 side chain NH2 with the Glycine-14 side chain O1P

MUC1-G$_1$: Arginine-5 side chain NE with the Thymine-13 side chain O2P; Arginine-5 side chain NH2 with the Thymine-13 side chain O2P; Arginine-5 side chain NH1 with the Thymine-13 side chain O2P; Threonine-4 main chain N with the Thymine-12 side chain O2; Aspartic Acid-3 main chain N with the Thymine-12 side chain O2; Threonine-4 side chain OG1 with the Thymine-11 side chain O2

MUC1-G$_2$: Arginine-5 side chain NH1 with the Thymine-13 side chain OP2; Arginine-5 side chain NH1 with the Thymine-13 side chain P; Arginine-5 main chain N with the Thymine-13 side chain O4; Arginine-5 side chain NE with the Thymine-13 side chain OP2; Aspartic Acid-3 main chain N with the Thymine-12 side chain O2; Threonine-4 main chain N with the Thymine-12 side chain O2

MUC1-G$_3$: Thymine-13 side chain N3 with the Proline-6 main chain O; Arginine-5 side chain NH1 with the Thymine-13 side chain O2P; Arginine-5 side chain NH1 with the Thymine-13 side chain O2P; Arginine-5 side chain NH1 with the Thymine-13 side chain O5'; Alanine-1 side chain N with the Glycine-15 side chain N; Alanine-1 side chain N with the Thymine-8 side chain O