Article:
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Figure Captions

Figure 1 – Schematic representation of amylose and amylopectin starch in our model, with each chains consisting of 1890 saccharide monomers. For hydrophobically modified starch, 63 of the monomers are made hydrophobic, thus giving SD = 3.3 %.

Figure 2 – Volume fraction of starch at different distances away from a hydrophobic interface, for unmodified amylopectin (solid line) and unmodified amylose (dashed line). The concentration of the starch in the bulk solution was 10^{-3} v/v in both cases.

Figure 3 – Biopolymer mediated colloidal interactions between two approaching emulsion droplets of size 1 μm, in unmodified starch solutions of Figure 2. The graphs in the inset show the energy potentials in more detail at separation distances close to the point of overlap of the depleted zones. The van der Waals interactions have not been included in these calculations.

Figure 4 – Adsorption isotherms, showing the number of adsorbed chains per unit monomer area, for hydrophobically modified amylopectin (solid line) and hydrophobically modified amylose (dashed line) in starch bulk concentration range 10^{-8} to 10^{-3}. The molecular weight and the degree of hydrophobic modification was the same for both sets of biopolymers.

Figure 5 – The variation of starch concentration across the adsorbed films of amylopectin and amylose, plotted as a function of distance away from an isolated hydrophobic interface. The films are at equilibrium with starch solutions of 10^{-5} v/v. The size of both macromolecules is 1890 monomers, and their degree of hydrophobic modification SD = 3.3%. The inset graphs show the same data, but at larger distances away from the surface.

Figure 6 – The architecture of amylopectin and its degree of branching as used in our calculations. The highlighted part is the only section of the molecule for which it is necessary to perform the calculations, as all the other monomers that comprise the rest of the amylopectin have an equivalent counterpart in the marked section.

Figure 7 – Average distance from the interface for each of the 151 monomers in the highlighted part of the hydrophobically modified amylopectin (solid line), as indicated in Figure 6. The same results are also included for two different sections of amylose, each also consisting of 151 monomers (dashed lines). In Figure (a) these are chosen from the end of the chain while in figure (b) they are from the middle part of the modified amylose. One of the branch points of amylopectin is highlighted by an arrow in Figure (a).

Figure 8 – Calculated interaction potentials between two droplets of size 1 μm, arising from the overlap of hydrophobically modified starch layers adsorbed on their surface. The direct van der Waals component has also been included in the resulting potentials. The mediated

interactions are calculated for starch solutions of bulk concentration 10^{-5} v/v, for amylopectin (solid line) and amylose (dashed line).

Figure 9 – Variation of the induced energy potential, given in units of k_BT, as a function of droplet-droplet separation distance, in 10^{-5} v/v solutions of three differently sized amylopectin; 3810 monomers (short dashed line), 1890 monomers (solid line) and 946 monomers (dashed-dotted line). The number of hydrophobic attachments is 63, for all the three cases.

Figure 10 – The same as Figure 8, but now for adsorbed interfacial layers consisting of a mixture of both the hydrophobically modified amylose and modified amylopectin. The total bulk volume fraction of starch in the solution is 10^{-5}, with 20% consisting of amylose and 80% amylopectin.

Figure 1.

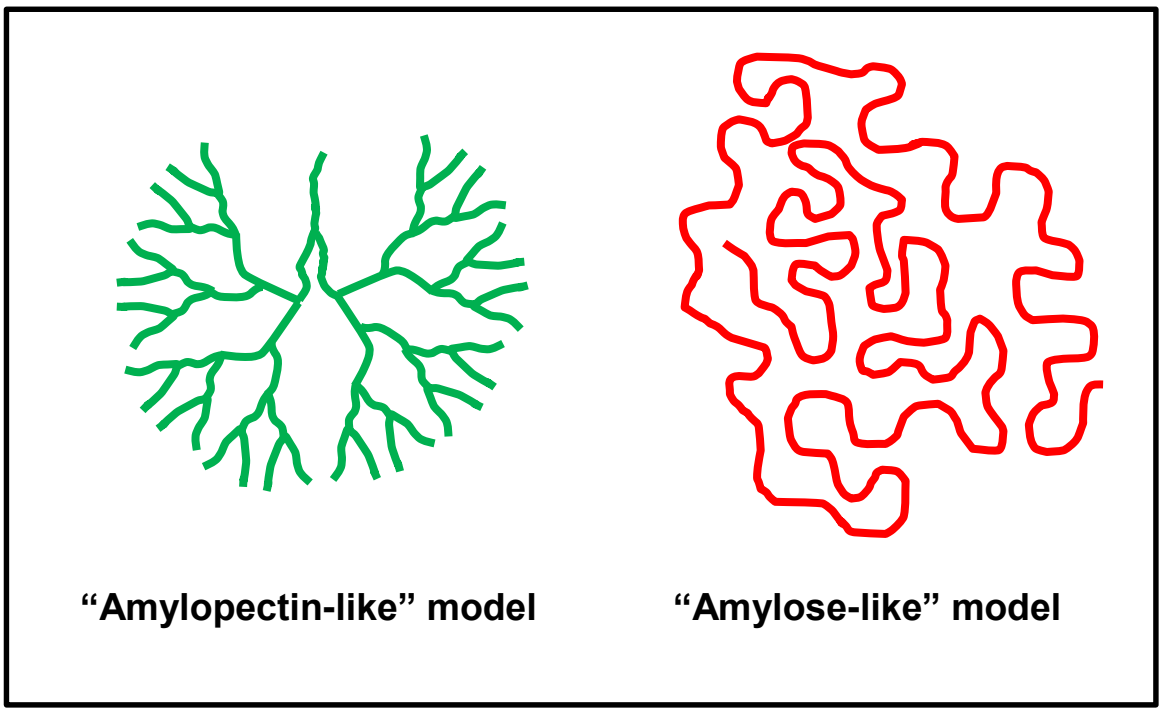


Figure 2.

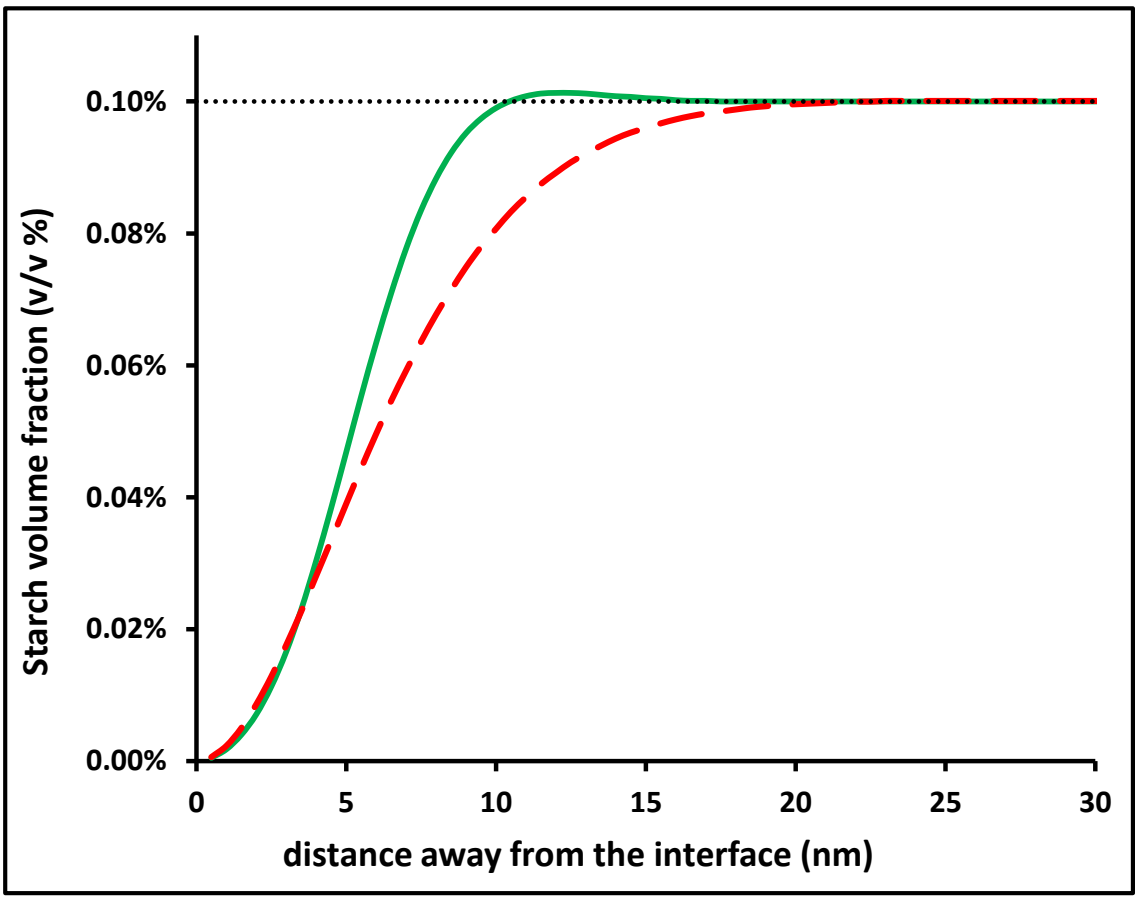

0.10%
0.08%
0.06%
0.04%
0.02%
0.00%
Starch volume fraction (v/v %)
0
5
10
15
20
25
30
distance away from the interface (nm)

Figure 3.

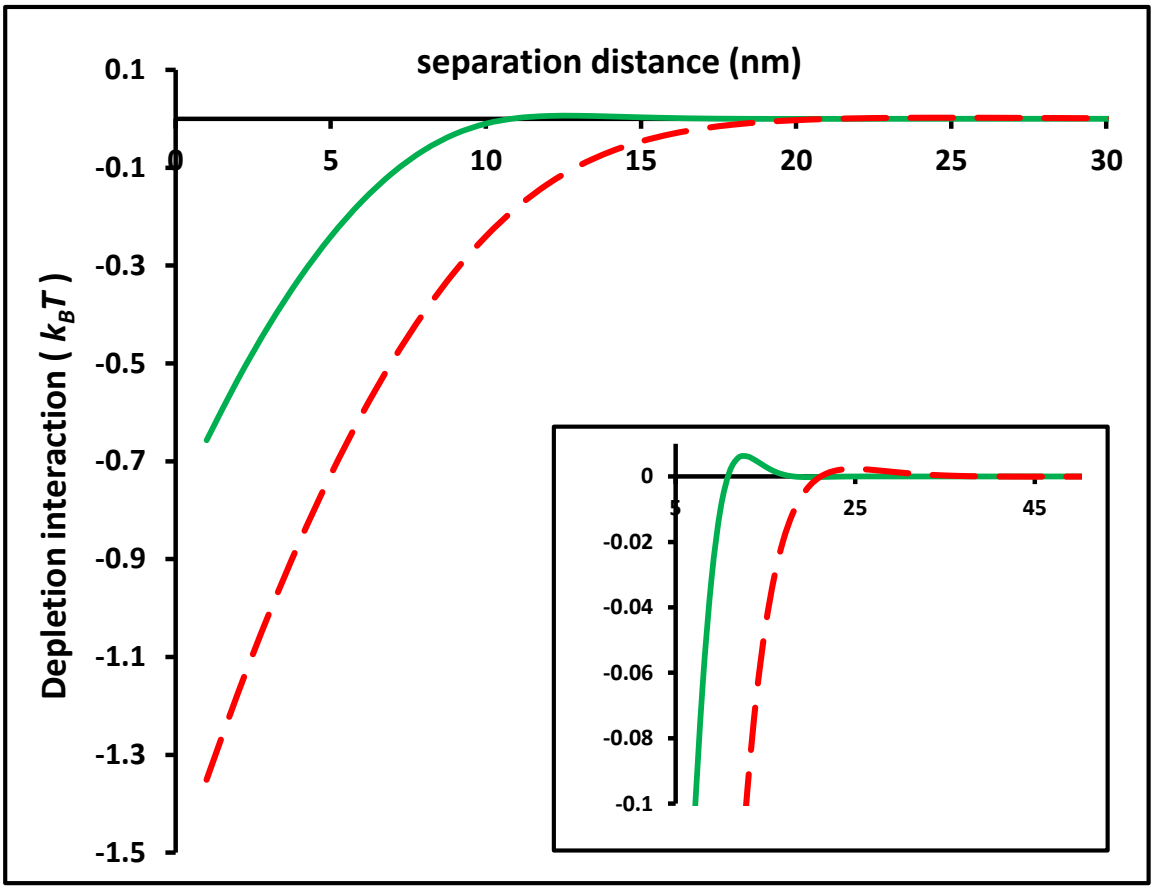

separation distance (nm)
Depletion interaction (k_BT)
0.1
-0.1
-0.3
-0.5
-0.7
-0.9
-1.1
-1.3
-1.5
0
5
10
15
20
25
30
0
-0.02
-0.04
-0.06
-0.08
-0.1
5
25
45

Figure 4.

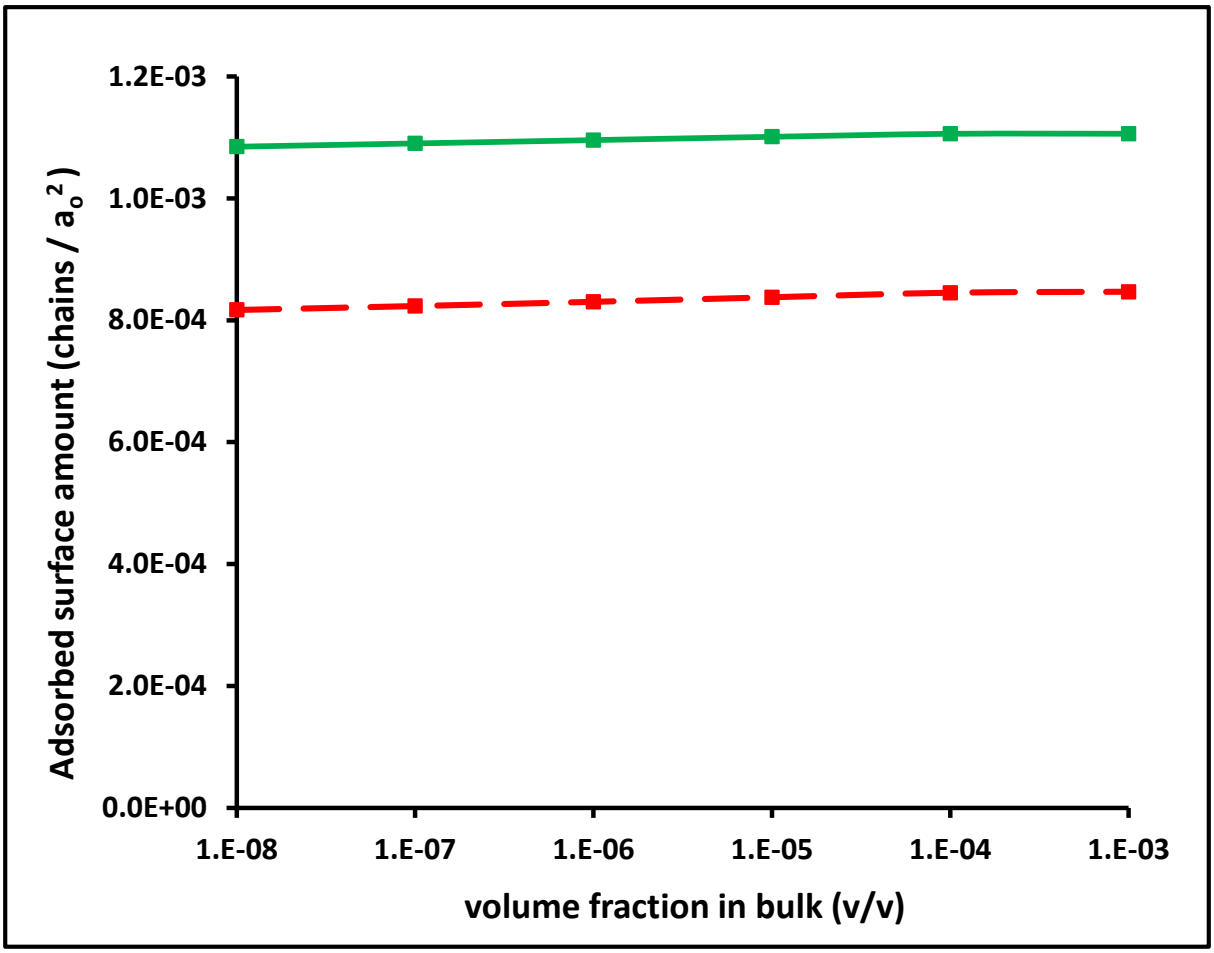

1.2E-03
1.0E-03
8.0E-04
6.0E-04
4.0E-04
2.0E-04
0.0E+00
Adsorbed surface amount (chains / a_o^2)
1.E-08
1.E-07
1.E-06
1.E-05
1.E-04
1.E-03
volume fraction in bulk (v/v)

Figure 5.

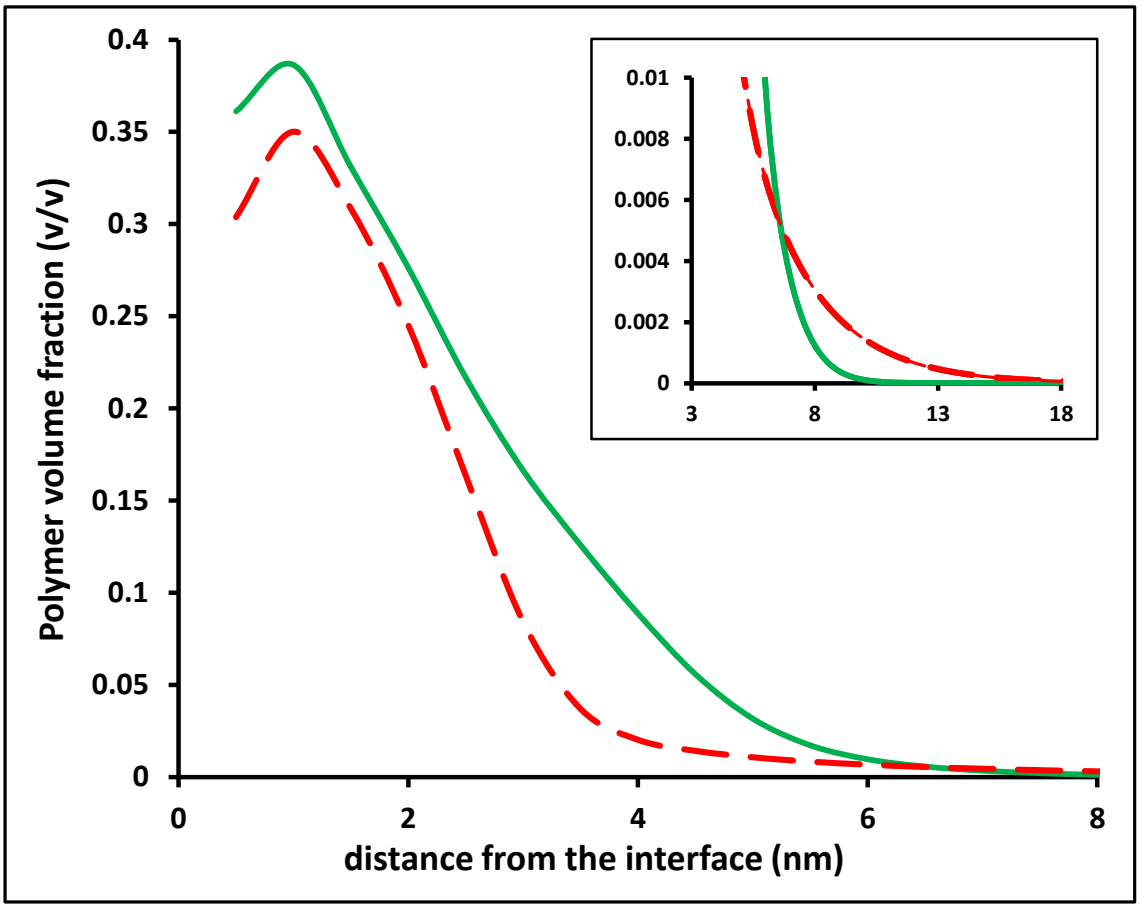

Polymer volume fraction (v/v)
0.4
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
0
2
4
6
8
distance from the interface (nm)
0.01
0.008
0.006
0.004
0.002
0
3
8
13
18

Figure 6.

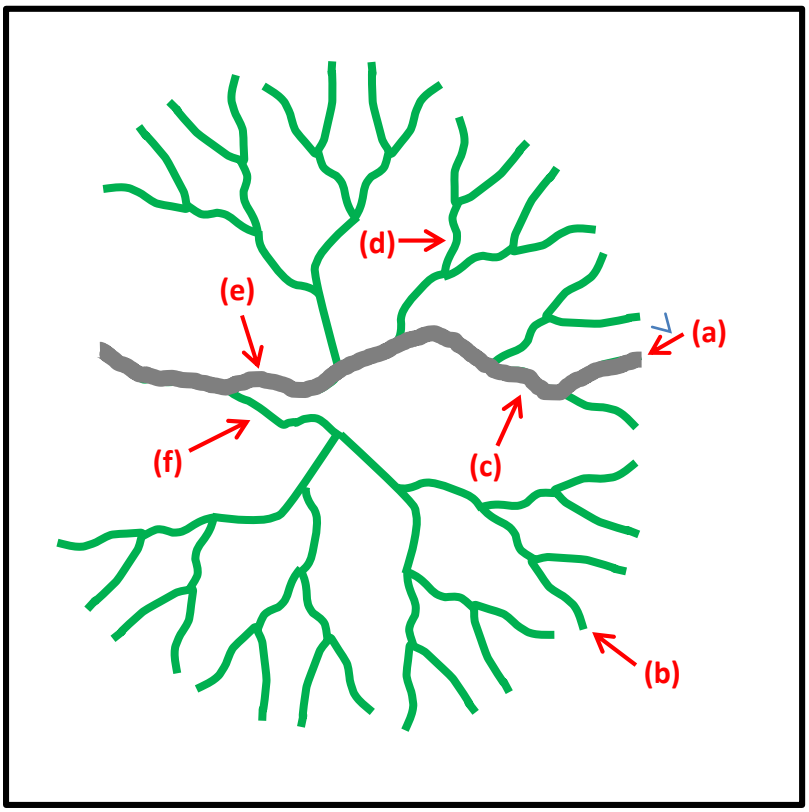


Figure 7a.

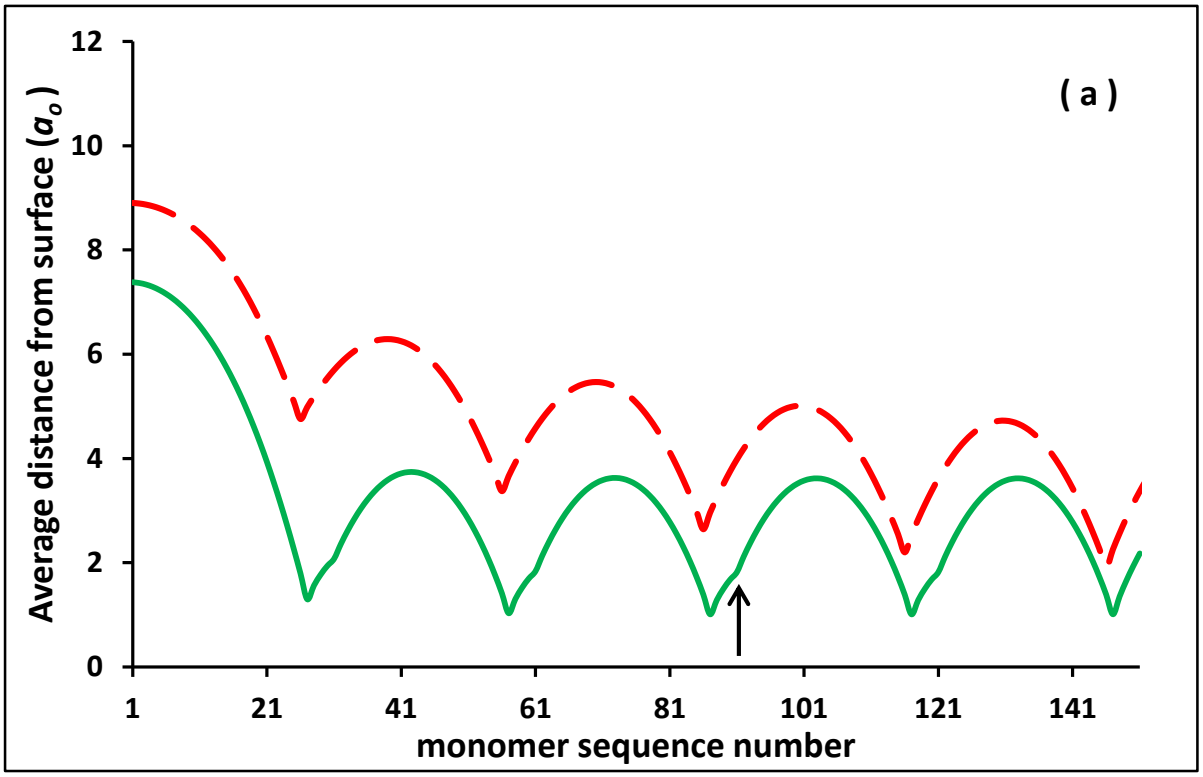

(a)
Average distance from surface (α_o)
0
2
4
6
8
10
12
1
21
41
61
81
101
121
141
monomer sequence number

Figure 7b.

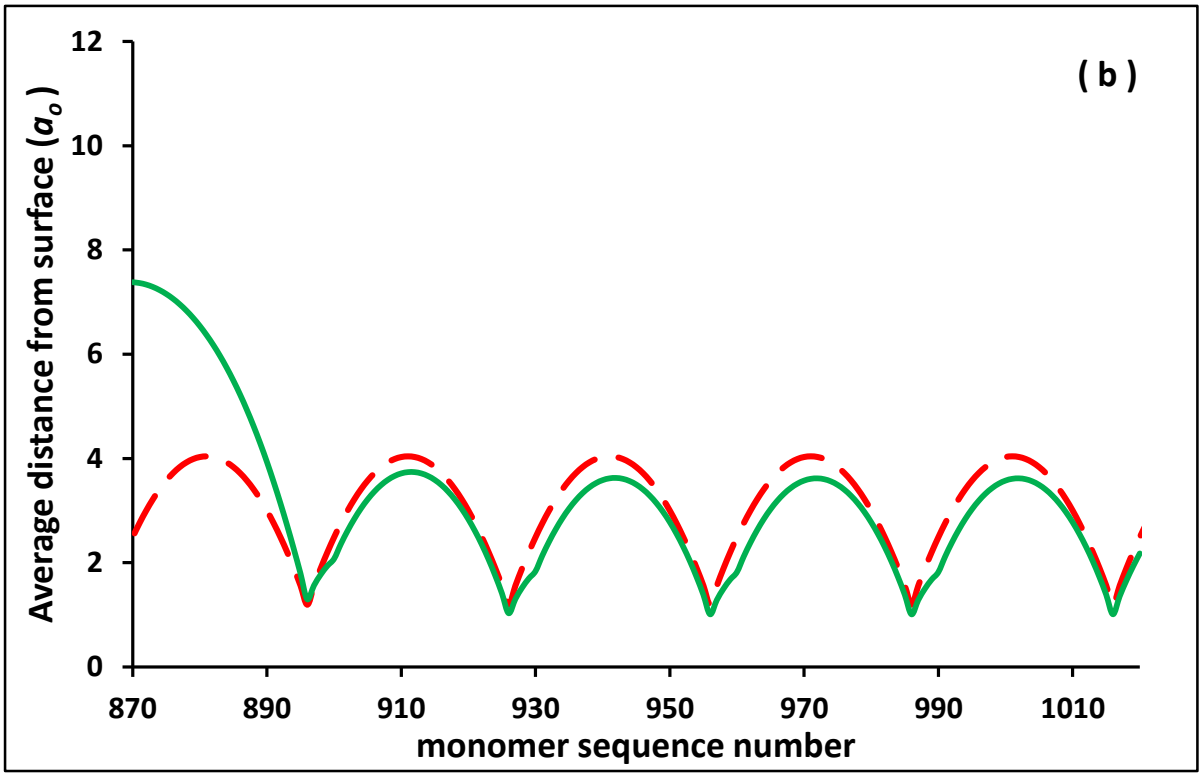

(b)
Average distance from surface (a_o)
12
10
8
6
4
2
0
870
890
910
930
950
970
990
1010
monomer sequence number

Figure 8.

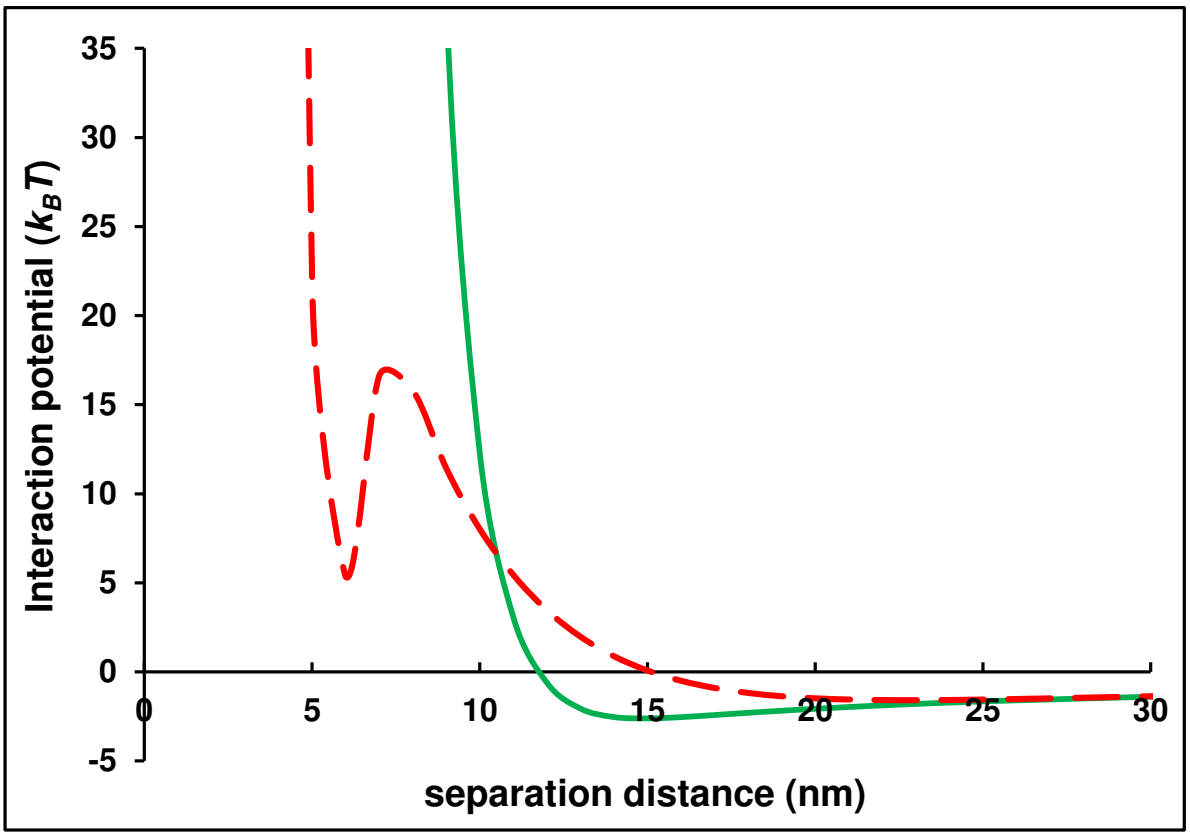

35
30
25
20
15
10
5
0
-5
0
5
10
15
20
25
30
Interaction potential (k_BT)
separation distance (nm)

Figure 9

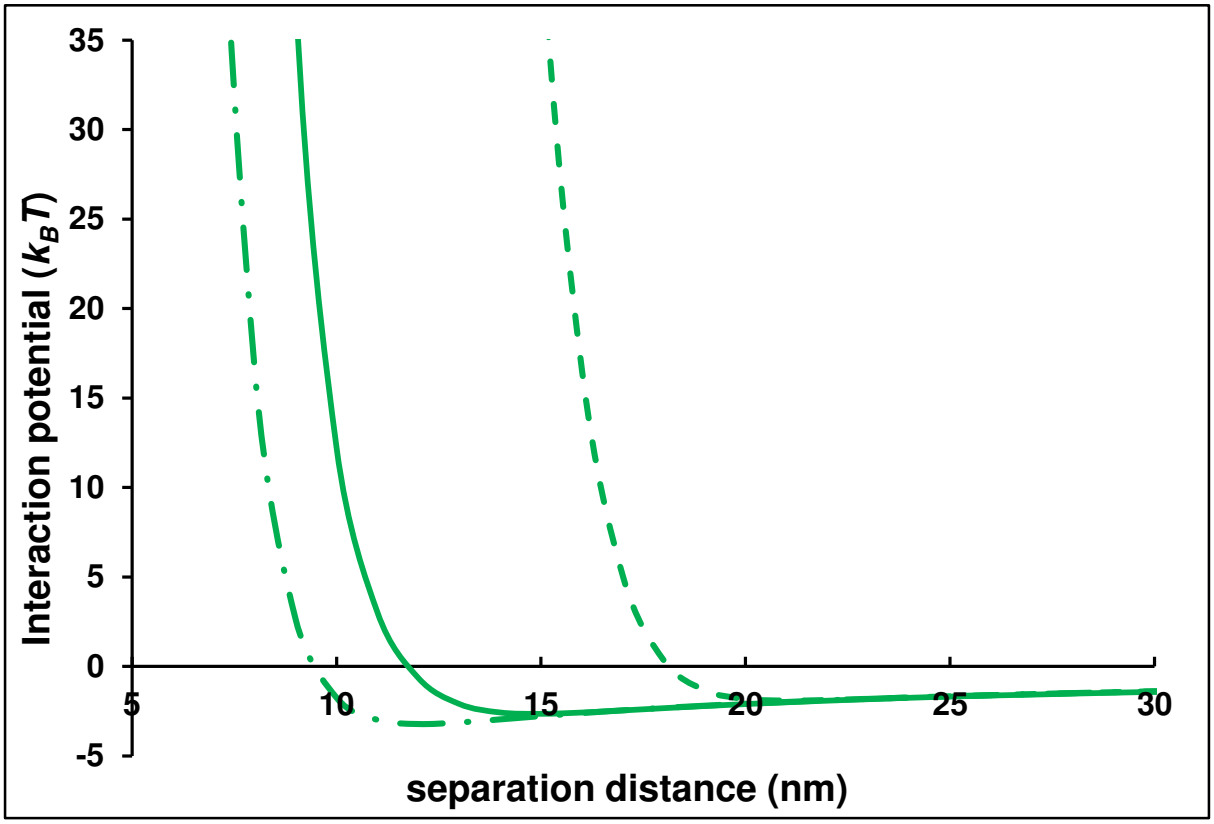
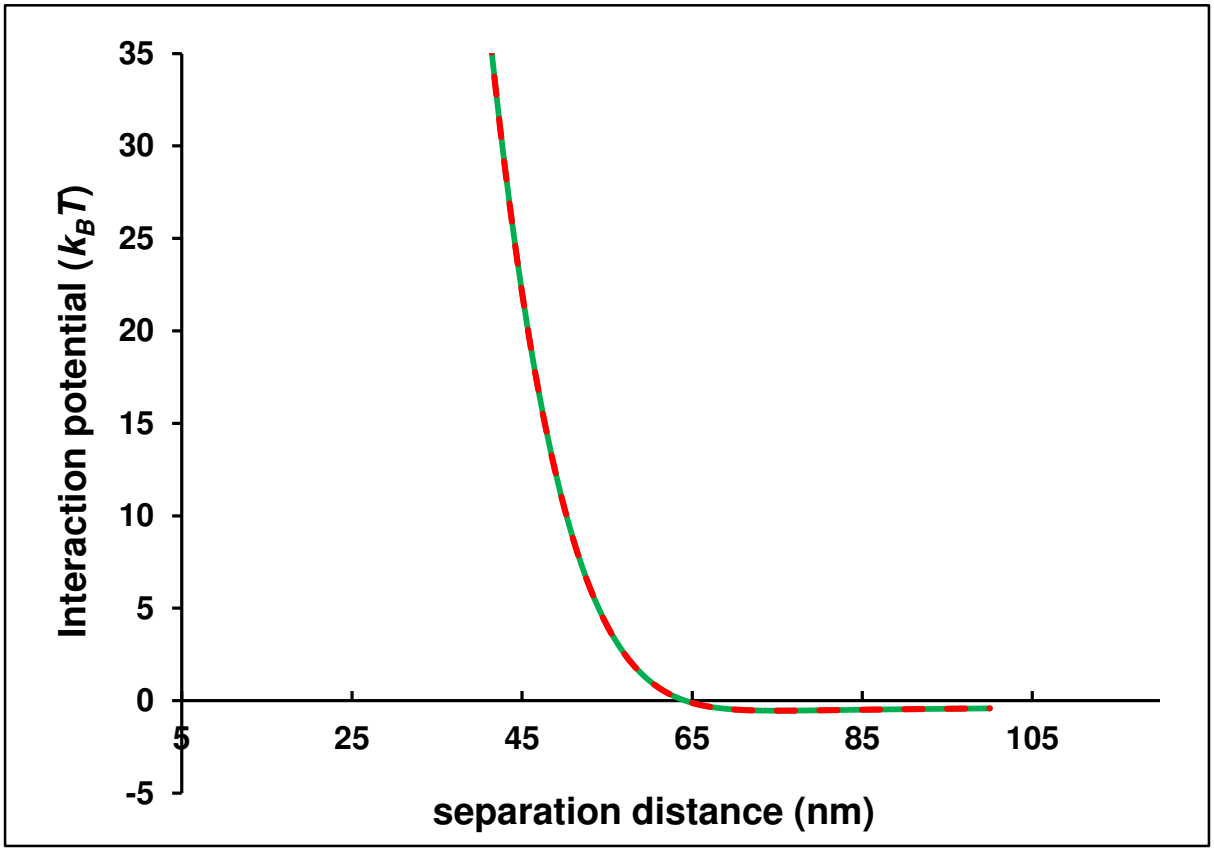

35
30
25
20
15
10
5
0
-5
Interaction potential (k_BT)
5
10
15
20
25
30
separation distance (nm)

Figure 10


35
30
25
20
15
10
5
0
-5
Interaction potential (k_BT)
5
25
45
65
85
105
separation distance (nm)