

# The effect of surface adsorption on tertiary structure formation in helical polymers

Matthew J. Williams<sup>1,2,a)</sup> and Michael Bachmann<sup>2,b)</sup>

<sup>1</sup>Institute of Engineering, Murray State University, Murray, Kentucky 42071, USA <sup>2</sup>Soft Matter Systems Research Group, Center for Simulational Physics, The University of Georgia, Athens, Georgia 30602, USA

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The formation of tertiary structures made up of helical polymer segments is influenced by the introduction of an attractive substrate onto which the polymer can adsorb. We perform replica-exchange Monte Carlo simulations to study the formation of helical structures in the vicinity of an attractive generic substrate by means of a coarse-grained hybrid model and compare the structural phase space for both adsorbed and free helical polymers. We introduce suitable structural order parameters to understand the features of distinct structural phases. Hyperphase diagrams, parameterized by the torsional energy scale and temperature, enable the investigation of structural properties of entire classes of helical polymers. *Published by AIP Publishing*. [http://dx.doi.org/10.1063/1.4991564]

# I. INTRODUCTION

Effective-potential homopolymer models<sup>1</sup> are useful tools for understanding macromolecular physical systems. By using a coarse-grained approach which facilitates the formation of helical structures, we recently investigated the formation of tertiary helix bundles and found that bending restraints stabilize these tertiary conformations.<sup>2</sup> The exploration of free-energy landscapes and transition channels in generalized ensembles<sup>3,4</sup> helped in identifying helix-bundle formation pathways.

Generic properties of polymer structure formation processes are typically governed by cooperative effects of interacting parts of the system. It is, therefore, possible to reduce the complexity by introducing collective, relevant degrees of freedom and effective interactions between monomers. Simulations of polymers modeled with effective potentials have been performed to understand the structural behavior of individual flexible<sup>5–8</sup> and semiflexible polymers<sup>9–11</sup> as well as the aggregation of polymers.<sup>12–14</sup>

Extensive previous work has also been dedicated to the effect of an adsorbent on the formation of stable structural phases of macromolecules<sup>15</sup> by means of computer simulations of simplified models.<sup>16–33</sup> It has been shown experimentally that helical structures can be stabilized by adsorption onto silica nanoparticles, and it has been theorized that this effect is a contributing factor to the evolution of early life.<sup>34</sup>

Helical segments, typical for biopolymers, are considered to be generic geometries of linear polymers.<sup>35–38</sup> Microscopically, secondary structures such as single helices or sheets are stabilized by hydrogen bonds. The most common process for the formation of structures with helical order is the helix-coil transition between disordered random-coil and helical conformations. These transitions are found to exhibit features of phase transitions.<sup>39–42</sup>

Noncovalent interactions, e.g., attractive van der Waals forces, can support the assembly of helix bundles. For polymers of sufficient length, tertiary structures composed of several helix bundles are observed.<sup>43–51</sup> Our recent work<sup>2,52,53</sup> expands on previous work studying the stability of these bundles.<sup>54–56</sup> We found that helical order is induced by the inclusion of a torsion potential and tertiary structures consisting of bundled helices are stabilized with the addition of a bending restraint.

In this paper, we continue our investigation of helical structure stability with the inclusion of an attractive substrate onto which the polymer can adsorb. The presence of a substrate has been shown to influence conformation geometry, transition dynamics, and stability of structural phases.<sup>20,21,30,57</sup> The impact of adsorption on helix-coil transitions has been explored experimentally.<sup>58</sup> Adsorption of helical polymers has also been studied for very large systems using an exactly solvable model.<sup>59</sup>

In this study, we use Monte Carlo simulation to examine the effect of a generic attractive substrate on the tertiary helix-bundle formation of polymers with bending restraint. We analyze structural stability as well as structure types for an array of model parameters and use the results to construct and compare hyperphase diagrams in the space of torsion strength and temperature for free polymers and in the presence of an attractive substrate.

The paper is organized as follows. In Sec. II, we describe the model used in this study and the simulation methodology. The structural properties of adsorbed polymer conformations under the influence of torsion barriers and the thermodynamic hyperphase diagram are discussed in Sec. III. The paper is concluded by the summary in Sec. IV.

a) E-mail: mwilliams72@murraystate.edu

b)E-mail: bachmann@smsyslab.org. URL: http://www.smsyslab.org.

#### **II. MODEL AND SAMPLING ALGORITHM**

#### A. Model

We model the hybrid system of helical polymers and an adsorbent using a standard model for elastic flexible polymers with the addition of torsion, bending, and adsorption potentials. The total energy of a polymer conformation  $\mathbf{X} = {\mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_N}$ , where  $\mathbf{x}_i$  is the position of the *i*th monomer and *N* is the number of monomers, can be written as

$$E(\mathbf{X}) = \sum_{i=1}^{N-1} E_{\text{FENE}}(r_{i\,i+1}) + \sum_{i=1}^{N-2} \sum_{j=i+2}^{N} E_{\text{LJ}}(r_{ij}) + \sum_{k=1}^{N-2} E_{\text{bend}}(\theta_k) + \sum_{l=1}^{N-3} E_{\text{tor}}(\tau_l) + \sum_{i=1}^{N} E_{\text{ads}}(z_i).$$
(1)

The finitely extensible nonlinear elastic (FENE) potential acts between each pair of bonded monomers and is given by 60-62

$$E_{\text{FENE}}(r) = -\frac{1}{2}KR^2 \log\{1 - [(r - r_0)/R]^2\}.$$
 (2)

We use the typical parameter values  $r_0 = 1$ , R = 3/7, and K = 98/5.<sup>2</sup> Any bond which is stretched beyond the limit of the FENE potential, having a bond length of less than  $r_0 - R$  or greater than  $r_0 + R$ , is considered to have infinite energy and is specifically disallowed. The FENE potential effectively makes the polymer act as a single chain of monomers which cannot be split.

The Lennard-Jones (LJ) potential,

$$E_{\rm LJ}(r) = 4\epsilon [(\sigma/r)^{12} - (\sigma/r)^6] - U_{\rm shift},$$
 (3)

describes the interaction between all pairs of non-bonded monomers separated by a distance *r* less than  $r_{\text{cutoff}}$ . For the LJ potential, we use  $\epsilon = 1$ ,  $\sigma = 2^{-1/6}$ ,  $r_{\text{cutoff}} = 2.5\sigma$ , and  $U_{\text{shift}} = 4\epsilon [(\sigma/r_{\text{cutoff}})^{12} - (\sigma/r_{\text{cutoff}})^6]$ . Because Lennard-Jones contacts provide an energetic benefit for the polymer, the potential is supportive of the formation of collapsed dense structures which maximize the number of monomer-monomer contacts.

The torsion potential is given by

$$E_{\rm tor}(\tau) = S_{\tau} \left[ 1 - \cos{(\tau - \tau_0)} \right]$$
(4)

for all dihedral angles.<sup>63</sup> The reference angle  $\tau_0 = 0.873$  is chosen to allow for helical segments with approximately 4 monomers per turn.

The torsion potential alone forms highly unstable structures, exhibiting some helical segments but no long-range helical order in polymers of significant length. The instability of the helical order can be remedied by the inclusion of a bending potential. The bending potential reads as

$$E_{\text{bend}}(\theta) = S_{\theta} \left[ 1 - \cos\left(\theta - \theta_0\right) \right], \tag{5}$$

and the reference bending angle  $\theta_0 = 1.4$  induces the formation of  $\alpha$ -helix-like secondary structures.<sup>2</sup> Using a strong bending energy scale of  $S_{\theta} = 200$  allows for the local helical order and the global ordering associated with helix bundles. By varying  $S_{\tau}$ , we can control the number of helical segments present in helix bundles. Larger values of  $S_{\theta}$  produce bundles with fewer but more stable helices. For example, at torsion strength  $S_{\tau}$ = 6, we see the formation of 3- and 4-helix bundles with different types of helical segment alignments at low temperatures. A substrate which acts as an adsorbent for the polymer is included in our model as well, using a potential depending on each monomer's distance z from the surface (located at z = 0). The adsorption energy is obtained by integration of the LJ potential over the entire half-space of the substrate ( $z \in [-\infty, 0]$ ),<sup>30,64</sup> which yields

$$E_{\rm ads}(z) = S_A \left[ \frac{2}{15} \left( \frac{\sigma}{z} \right)^9 - \left( \frac{\sigma}{z} \right)^3 \right]. \tag{6}$$

In this paper, we study the adsorption behavior of the polymer for adsorption strengths  $S_A \in [0, 2]$ . The polymer is not tethered to the substrate and can move freely in the available space. Therefore, a steric, impenetrable boundary is imposed at a distance of  $z_{max} = 200$  from the surface to prevent the polymer from escaping. We primarily investigate the structural behavior of polymers with N = 40 monomers but have performed simulations of other system sizes to verify the qualitative adsorption properties.

### **B.** Sampling

In our study, we performed replica-exchange Monte Carlo (parallel tempering) simulations at 32 temperatures in the interval  $T \in [0.03, 2.00]$ . Initially, a random polymer conformation is generated in each temperature thread and conformational updates of the individual replica are accepted according to the Metropolis criterion,<sup>65</sup>

$$P_i^{\text{metro}} = \min(1, e^{-\beta_i \Delta E}), \tag{7}$$

where  $\beta_i = 1/k_B T_i$  is the inverse thermal energy at temperature  $T_i$  of the *i*th thread and  $\Delta E$  is the change of the energies due to the update.

A significant factor in the efficiency of the simulation is the choice of the update type. In our simulations, we used a combination of different Monte Carlo moves. The simplest and most common update is local monomer displacement. An individual monomer is chosen at random and moved to a new random location within a box of size  $r_d$  surrounding the monomer's original position. Optimization of the box size can lead to gains in simulation efficiency.<sup>66</sup> At low temperatures, where dense conformations are dominant and autocorrelation times are supposedly large,  $r_d$  should be much smaller than at high temperatures, where the structural phase is governed by random-coil structures.

We choose  $r_d$  such that the acceptance rate is approximately 0.5. This is done during an initialization period before data collection begins. After every 100 updates, the displacement size is changed to  $r'_d = r_d + p(\chi_{accept} - 0.5)$ , where p is a factor determining the size of each iterative adjustment of  $r_d$  and  $\chi_{accept}$  is the current measured acceptance rate of displacement updates. It turned out that p = 0.04 was a good choice.

Since in our adsorption study the polymer is not grafted to the substrate, it can spend large periods of simulation time without being in contact with the substrate, in particular, in the entropy-dominated desorbed phases. For this reason, we also implemented a translational update of the entire polymer relative to the adsorption surface, which changes only the adsorption energy and leaves the intrinsic monomer-monomer interactions unchanged. While this update is not important at low temperatures for which the polymer is adsorbed most of the time, it can greatly improve the efficiency of the simulation near the adsorption transition.

As our model also contains torsion and bending restraints, we find it helpful to also include a torsion update which only changes one torsion angle, leaving all other torsion and bending angles unaffected. This can be done by choosing a single bond at random and letting it act as a rotation axis around which all monomers on one side of that bond are rotated by a random angle.

Replica exchange between neighboring temperature threads significantly helps overcome transition barriers.<sup>67–70</sup> The 32 temperature threads run in parallel and an attempt to exchange polymer conformations is performed periodically. Each thread alternates between exchange attempts with its higher and lower temperature neighbors. An exchange attempt between threads with temperatures  $T_i$  and  $T_j$  and respective energies  $E_i$  and  $E_j$  of the current polymer conformations at these temperatures is accepted or rejected according to the acceptance probability

$$P_{ii}^{\text{PT}} = \min(1, e^{-(\beta_i - \beta_j)(E_j - E_i)}).$$
(8)

We find that the exchange rates are most consistent when each temperature is chosen according to  $T_i = 1.15 T_{i-1}$ . Using this spacing, it is important to include enough threads so that in the highest-temperature thread the polymer is in the random-coil phase.

# **III. RESULTS AND DISCUSSION**

#### A. Properties of adsorbed structures

For simulations of the hybrid model with the torsion strength  $S_{\tau} = 6$ , we considered an array of values for adsorption strengths in the interval  $S_A \in [0, 2]$ . Examples of the structures generated in this series of simulations are shown in Fig. 1. Considering the top row ( $S_A = 0$ ), polymer structures at low temperatures are dominated by three-helix bundles and exhibit variability in terms of alignment and helix segment length. As the adsorption strength is increased, we see that the polymer adsorbs onto the surface of the substrate at low temperatures and tends to form two-helix instead of three-helix bundles. We also qualitatively find that the adsorbed structures exhibit far less variability over a wider range of temperatures, which can be interpreted as an enhanced structural stability of the polymer in the vicinity of the attractive substrate.

To aid in classifying helix-bundle structures, we introduce a pair of structural order parameters  $(q_1 \text{ and } q_2)$  which make a distinction between local helical order and tertiary order in a polymer structure.<sup>2</sup> The parameter  $q_1$  is defined as the average total Lennard-Jones potential between pairs of monomers within 6 or fewer bonds,

$$q_1(\mathbf{X}) = \frac{1}{N} \sum_{i=1}^{N-2} \sum_{j=i+2}^{N} \Theta_{6,j-i} E_{\text{LJ}}(r_{ij}).$$
(9)

Conversely,  $q_2$  is the average Lennard-Jones energy of pairs of monomers more than 6 bonds distant from each other,

$$q_2(\mathbf{X}) = \frac{1}{N} \sum_{i=1}^{N-2} \sum_{j=i+2}^{N} \Theta_{j-i,7} E_{\text{LJ}}(r_{ij}).$$
(10)

Here we have introduced the symbol

$$\Theta_{kl} = \begin{cases} 1, \, k \ge l, \\ 0, \, \text{otherwise.} \end{cases}$$
(11)

Let us consider two examples to show the usefulness of this parameter pair. In a single long helix, all monomers have Lennard-Jones contact with other monomers within 6 bonds along the chain but no contact with monomers outside of this local neighborhood;  $q_1$  is minimal and  $q_2$  is maximal. In contrast, for a two-helix bundle, local LJ interaction at the joint between the two helix segments is sacrificed for the formation of contacts between monomers belonging to the different segments. These monomers are more than 6 bonds distant along the chain. Therefore, compared to the single-helix case,  $q_2$ decreases at the expense of  $q_1$ . Similarly, higher-order helix bundles can also be distinguished by means of these parameters. In order parameter space, qualitatively similar structures form distinct clusters.

It can be useful to calculate canonical averages for structural quantities to investigate their changes as temperature and model parameters are varied. The parameter  $\langle q_2 \rangle / \langle q_1 \rangle$  is the



FIG. 1. Representative polymer conformations formed under varied conditions. Each row shows structures for a single value of  $S_A$  along an array of temperatures between T = 0.03 and 1.62. The adsorption strength increases from top to bottom from  $S_A = 0$  to 2, and the torsion strength is fixed at  $S_{\tau} = 6$ .

ratio of the global to local Lennard-Jones energy, and it allows us to distinguish between various helical structure types. For three-helix bundles observed at low temperatures in the case of  $S_A = 0$ ,  $\langle q_2 \rangle / \langle q_1 \rangle \approx 0.64$ . In the case of the two-helix bundles which dominate at low temperatures when  $S_A \ge 0.75$ , we find that  $\langle q_2 \rangle / \langle q_1 \rangle \approx 0.33$ .

Figure 2(a) shows  $\langle q_2 \rangle / \langle q_1 \rangle$  as a function of *T* for each value of  $S_A$  which we have simulated. Towards low temperatures, the curves for different values of  $S_A$  split between twoand three-helix bundle branches. The thermal fluctuation of the center of mass distance from the substrate  $(d\langle h_{\rm cm} \rangle/dT)$  is depicted in Fig. 2(b). The adsorption transition can be identified by the peak in each curve as it corresponds to the temperature at which there is a balance between adsorbed and desorbed structures. There is agreement between the desorption temperature noted in panel (b) and the convergence to the free case ( $S_A = 0$ ) for the curves in panel (a). We can also see that the desorption temperature increases with increasing adsorption strength as is expected. More interestingly, in the range from  $S_A \in [0.75, 2]$ , the low-temperature are small.



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The thermal fluctuation of the average number of monomer-monomer contacts,  $d\langle N_c \rangle/dT$ , is shown in Fig. 2(c) as a function of *T*. The gas-liquid transition and the liquid-solid transition are both marked by a rapid rate of change in the number of monomer-monomer contacts and can be located in this plot by finding inverted peaks and shoulders. We can see that as the adsorption strength increases, the temperature range over which the liquid phase occurs narrows.

We can better understand the relationship between the ensembles formed at each value of  $S_A$  by considering the structures created in each of these simulations in  $q_1$ - $q_2$  space, as depicted in Fig. 3. The low-energy structures (found at the lowest simulation temperature) must, in general, have more negative  $q_1$  and  $q_2$  values and therefore lie towards the lower left in this presentation.

For purely steric or weakly attractive substrates, i.e.,  $S_A = 0$  and 0.5, low-temperature structures form several unique clusters in this space. Each of these clusters represents an individual structure type. The inset in Fig. 3 shows only the low-energy clusters corresponding to  $S_A = 0$  along with example structures for each discernible cluster. While the lower right-hand cluster is made up of three-helix bundles in which all helices are parallel and of approximately the same length, the cluster in the upper left contains structures in which two long helical segments are wrapped around each other and a short helical segment connects their ends.

The presence of multiple low-temperature clusters for both  $S_A = 0$  and 0.5 is due to local free-energy minima in phase space near the ground state. Ensembles exhibiting this behavior are inherently metastable due to the varied structure type accessible at low temperatures. Additionally, they are highly sensitive to changes to their environment, as seen by the drastic change in structure type with the introduction of even a weak adsorption surface.

By increasing  $S_A$  beyond a threshold value, dominant three-helix conformations are replaced by two-helix structures. The system sacrifices nonlocal monomer-monomer contacts ( $q_2$  increases) in favor of reducing the torsion potential and primarily, a larger number of contacts with the adsorption surface. The two are correlated with each other and lead



FIG. 2. (a) The ratio of global and local LJ energies,  $\langle q_2 \rangle / \langle q_1 \rangle$ , as a function of temperature for an array of different values for adsorption strength  $S_A$ and fixed torsion strength  $S_{\tau} = 6$ . (b) Temperature variation of the center of mass distance of polymers at several different adsorption strengths. Note that the peak locations correspond to the temperature at which the polymer desorbs from the surface. (c) Temperature variation of the average number of monomer-monomer contacts vs temperature,  $d\langle N_c \rangle / dT$ .  $\langle N_c \rangle$  decreases most rapidly during structural transitions between solid, liquid, and gas phases exhibiting inverted peaks or shoulders in the plot of  $d\langle N_c \rangle / dT$ .

FIG. 3. A plot of  $q_1$  vs  $q_2$  for a collection of example structures created across all temperatures simulated for torsion strength  $S_{\tau} = 6$ . The color of each point corresponds to the torsion energy scale at which the structure it represents was formed. Conformations in a cluster belong to the same structural class. Lowtemperature structures for  $S_A = 0$  are shown independently in the lower right inset along with example structures for each cluster. Colors agree with the legend shown in Fig. 2.





FIG. 4. Putative ground states of the polymer, if no attractive substrate is present ( $S_A = 0$ ), compared with adsorbed conformations ( $S_A = 2$ ) for an array of torsion strengths  $S_{\tau}$ . This collection of structures highlights the dependence of helical structures on the adsorption and torsion energy scales.

to an increase in local monomer-monomer contacts as well (associated with a decrease of  $q_1$ ).

The inherent instability and high sensitivity shown in the ensembles with  $S_A = 0$  and 0.5 are greatly reduced by the inclusion of the adsorption surface as demonstrated by the consistent and single-peaked clusters corresponding to two-helix bundles formed,  $S_A \in (0.75, 2.00)$ . At these higher values of adsorption strength, the low-temperature conformations are predictable, consistent, and highly resilient to changes in their environment.

# B. Torsion strength dependence of polymer structures with and without adsorbent

In the above discussion of adsorption properties for the particular case of a helical polymer with torsion strength  $S_{\tau} = 6$ , we already noted a dramatic qualitative change in the structural behavior if the polymer is exposed to an attractive adsorbent. We will now explore in more detail how much the adsorption properties depend on  $S_{\tau}$ . For this purpose, simulations of the helical polymer model with adsorption were performed for a wide array of values  $S_{\tau} \in [0, 30]$ . With regard to the adsorption strength, it is sufficient to limit our discussion to the comparison of the model with  $(S_A = 2)$  and without  $(S_A = 0)$  an adsorbent.

In Fig. 4, examples of structures formed at low temperatures for scenarios with and without adsorption are depicted. We see that for the free case (top row), amorphous solids, four-helix bundles, three-helix bundles, two-helix bundles, and single helices are formed. If an attractive adsorbent is present (bottom row), the types of structures formed are limited. Above  $T \approx 2$ , we consistently observe predominant folding into two-helix bundles.

This is analyzed quantitatively in Fig. 5, where the two cases are compared at different temperatures. At the lowest

temperature T = 0.035, the polymer clearly tends to form threeand four-helix bundles in the region  $1 \le S_{\tau} < 8$  if no adsorbent is present, whereas it prefers to fold into two-helix structures otherwise. The  $S_{\tau}$  range in which the two-helix bundle dominates is significantly larger than that for the system without an adsorbent. Similarly, the single-helix phase dominates over a larger region of phase space in the adsorbed case. The binding to the substrate entropically suppresses the two-helix conformations more than single-helix structures unless different helix segments are perfectly aligned on the substrate.

As the temperature is increased, structural variability increases. At T = 0.45, we already observe a more gradual transition in  $S_{\tau}$  space for the free-polymer case, but if the polymer is adsorbed, the phase structure remains very stable. For T = 0.7, there is almost no stratification between single-, double-, three-, and four-helix phases in the free case anymore. In contrast, the double-helix phase remains far more discernible in case the polymer is adsorbed at a substrate. An attractive adsorbent apparently stabilizes double-helix polymer conformations.

To further draw distinction between the free and adsorbed cases, we investigate more closely the density of structural types in  $q_1$ - $q_2$  space. Each panel in Fig. 6 represents all of the structures generated in a single parallel tempering simulation. The structures collected in the simulation at all temperatures are projected onto the two-dimensional  $q_1$ - $q_2$  space which is divided into bins. For a given  $S_{\tau}$  value, any bin which is visited during the simulation is in black. The gray background represents the bins visited across the entire range of  $S_{\tau}$  values for which simulations were performed. It serves as reference and shows the clear separation of entropically suppressed regions from populated areas. Both the black (for a single  $S_{\tau}$  value) and gray regions (for the array of all  $S_{\tau}$  values simulated) represent generalized statistical ensembles since data from



FIG. 5. The panel shows the dependence of structural parameter  $\langle q_2 \rangle / \langle q_1 \rangle$  on the torsion strength  $S_{\tau}$  for systems with and without an adsorbent at three different temperatures. For T = 0.035, the two systems depart from each other strongly in their behavior in the range  $1 < S_{\tau} < 8$ . The free polymer forms three- and fourhelix bundles, whereas the adsorbed polymer folds into two-helix conformations. Similar behavior is observed for T = 0.45 and T = 0.7 but exhibits progressively less dramatic transitions as temperature is increased.



FIG. 6. Population of states in  $q_1-q_2$  order parameter space. For each panel, the gray dots represent structures found at all values of  $S_{\tau}$  and T, for which simulations were performed and for the two scenarios of the free polymer (no substrate) [left column, (a)-(e)] and in the presence of an attractive substrate with  $S_A = 2$  [right column, (f)-(j)]. Black dots form the subset of states at the given single  $S_{\tau}$  value in each panel at all simulated temperatures. Red dots correspond to dominant conformations at lowest temperatures (T < 0.075).

all simulation temperatures are accounted for. Red dots are associated with lowest-energy structures found at temperatures T < 0.075.

The result is that, in this representation, the value of  $q_2$  increases for low-energy structures as  $S_{\tau}$  is increased. By establishing local helical order along the chain, energetic contacts between nonbonded monomers are sacrificed. There are distinct branches which can be associated with different structure-formation scenarios. Note that, in principle, there are no limitations for any  $q_1$ - $q_2$  pair of values. The blank regions in the figure mean that structures in these areas are statistically highly suppressed and were not found in the simulations.

To get a first idea, let us discuss the well-studied case of the free, semiflexible polymer ( $S_A = 0, S_{\tau} = 0$ ) [Fig. 6(a)]. The black dots represent the generalized ensemble of conformations sampled in our simulations in  $q_1$ - $q_2$  space. Structures dominant at lowest temperatures gather at smallest  $q_2$  values, i.e., structures are compact but not helical. The structural analysis reveals that the lowest-energy states do not have a preferred order, and we classify them as amorphous solids. Values of  $q_1$  of the sampled structures do not vary much at all temperatures, i.e., at increased temperatures larger  $q_2$  values simply correspond to less compact structures ("liquid") and fully extended, random-coil conformations towards  $q_2 \rightarrow 0$ . If the torsion strength  $S_{\tau}$  is increased in the free case  $S_A = 0$ , the  $q_1$  parameter becomes more relevant and allows for the discrimination of different types of helix bundles. In the examples shown, we find that at  $S_{\tau} = 2$  [Fig. 6(b)], ground states are predominantly four-helix bundles, and at  $S_{\tau} = 4$ , we find primarily three-helix bundles in the solid phase [Fig. 6(c)], at  $S_{\tau} = 8$ , we find double-helical conformations [Fig. 6(d)], and at  $S_{\tau} = 30$ , we find a stable single helix [Fig. 6(e)]. The free case has been discussed in detail elsewhere recently.<sup>2,52,53</sup>

By comparing the gray areas of the free case with those when adsorption can occur [Figs. 6(f)-6(j)], we find that the distribution of structures exhibits noticeable differences. The branch that leads into the sector of amorphous low-energy structures shows more details, which is due to different dominant metastable non-helical conformations (wetting and layering effects) of the adsorbed polymer, which we do not further pursue here. What is more interesting in our context is the almost complete disappearance of the four-helix phase. Furthermore, three-helix bundles turn out to be more like an irrelevant artifact of the all-dominant two-helix conformations. We can conclude that the two-helix phase almost completely preempts the more complex structural phases if the polymer adsorbs at an attractive substrate with sufficiently high adsorption strength. If the torsion barrier is strong enough, singlehelix conformations become the dominant structure type and the conformational behavior of the adsorbed polymer is similar to that of the free one.

Figure 6 provides an in-depth insight into details of the different structural behaviors of a semiflexible polymer in the presence of an attractive adsorbent. However, we would now like to go a step further and investigate the thermodynamic phase behavior more systematically by constructing the structural phase diagrams for classes of polymers in both scenarios.

By studying the locations of structures generated within the  $q_1$ - $q_2$  space and by making use of the transition signals in order parameters and fluctuating quantities like those shown in Fig. 2, we can analyze the ensemble of structures in multiple simulations at different constant  $S_{\tau}$  values and determine the character of the structural transitions and their locations in temperature space. Considering the branch along which the majority of structures in Fig. 6 occurs can help distinguish between single helices, two-helix bundles, three-helix bundles, four-helix bundles, and amorphous solids. For polymers of length N = 40, which we study here, the branches formed by three- and four-helix bundles are overlapping and difficult to distinguish in all but the lowesttemperature cases. This means that these structures are not very stable. The area of the plots where the regions converge represents the liquid phase of globular conformations with no helical order. Upon further temperature increase, structural compactness is lost and  $q_1$  and  $q_2$  converge to zero. This region in the  $q_1$ - $q_2$  diagrams is therefore dominated by random coils.

By systematically changing the torsion strength  $S_{\tau}$  in our simulations, we can analyze the transition behavior more quantitatively and identify the regions in  $S_{\tau}$ -T parameter space in which certain polymer structures dominate. For both scenarios,  $S_A = 0$  and  $S_A = 2$ , the results are shown in Fig. 7. Colors represent different structural phases, and by comparing the color patterns, we immediately note that the areas covered by the most compact phases such as A (amorphous), 4h, and 3h (four- and three-helix bundles, respectively) shrink if adsorption competes with internal structure formation processes. Given the rather short polymer length with 40 monomers, it is not surprising that the higher-order helix bundles are destabilized by the perturbation caused by the attractive adsorption force exerted upon the compact structures. Two-helix structures (2h) become dominant at lower torsion strengths, but at higher  $S_{\tau}$  values, single helices (1h) intrude into former 2h terrain. Overall, the ordered phases are shifted to smaller  $S_{\tau}$ values. The disordered phases dominated by liquid-like (L) and random-coil conformations are less affected.



FIG. 7. Hyperphase diagrams in  $S_{\tau}$ -T space. Colors represent the dominate structural phases present at each  $S_{\tau}$ -T combination for both free ( $S_A = 0$ ) and adsorbed cases ( $S_A = 2$ ): yellow—single helix (1h), green—two-helix (2h), blue—three-helix (3h), magenta—four-helix (4h), cyan—amorphous solid (A), orange—liquid (L), red—random coil (C).

#### **IV. SUMMARY**

By employing replica-exchange Monte Carlo (parallel tempering) across a wide range of temperatures, we have simulated a model for semiflexible, helical polymers. We extend previous studies of the structural behavior of the free chain by introducing an adsorbent to which the polymer can bind by means of attractive van der Waals forces. In this paper, we systematically analyze the competition of adsorption effects upon polymeric structure formation in the folding process and the structural phases under thermodynamic conditions for entire classes of helical and nonhelical semiflexible polymers (by varying the torsion strength). These simulation results enable the construction of the structural hyperphase diagram in the combined parameter space of torsion strength and temperature under the influence of an attractive adsorbent.

In comparison with the free polymer case, we find that adsorption has a significant impact on the dominant types of polymer structures. Compact conformations such as amorphous solids (no torsion) or helix bundles with three or more helices (moderate torsion strengths), which are found dominant and stable in regions of the phase diagram for the polymer without facing an adsorbent, are strongly suppressed by adsorption effects. Under the influence of attractive substrate interaction, the "flatter" double-helix structures with parallel alignment of the helices and single-helix conformations cover almost entirely the parameter space that is dominated by folded and adsorbed structures.

As the phase diagram shows, the single- and two-helix structures are more stable in the presence of an adsorbent; the transition temperature towards disordered phases increases. Effectively, this can be interpreted in a way that an attractive substrate supports the formation of simple helical structures. The stabilization of functional protein structures by its environment may have been an influential step at an early stage of the evolution of primitive life forms.<sup>34</sup> To pursue further, how environmental factors have helped stabilizing helical and other secondary structures common to functional biomolecules is an exciting topic for future research. Furthermore, hyperphase diagrams, which parametrize the phase space with respect to model and thermodynamic control parameters, are supportive of hybrid materials' design as studies of coarse-grained models provide a general insight into the types of possible structural phases of polymers.

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