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Supporting information for: Modeling of Reversible Single Chain Polymer Self-Assembly: From the Polymer towards the Protein Limit

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For each chain length L we performed all-atom Metropolis Monte Carlo with several 10^9 steps at constant temperatures in the range from 220 K to 340 K using SIMONA[S1] with GAFF force field parameters.[S2] Calculations of the gyration radius and the shape measures are applied only to the polystyrene chain excluding α and ω end groups. The shape of the α–ω complex does not change significantly between the closed configurations because of the

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strong hydrogen bonding. The hydrodynamic radius of the polymer was computed using the HYDROPRO computer program.[S3]

S1 CA–HW recognition pair

The polymer has two hydrogen bonding recognition units based on six-point cyanuric acid (CA)–Hamilton wedge (HW) interaction. We compute an optimized configuration of the recognition CA–HW pair using a semiempirical quantum chemistry PM7 method.[S4] The optimized geometry configuration is shown in Fig. S1. The computed difference in the total energy between the bound configuration in Fig. S1 and an unbound configuration is equal to $\Delta E = 0.6$ eV $= 13.8$ kcal/mol.

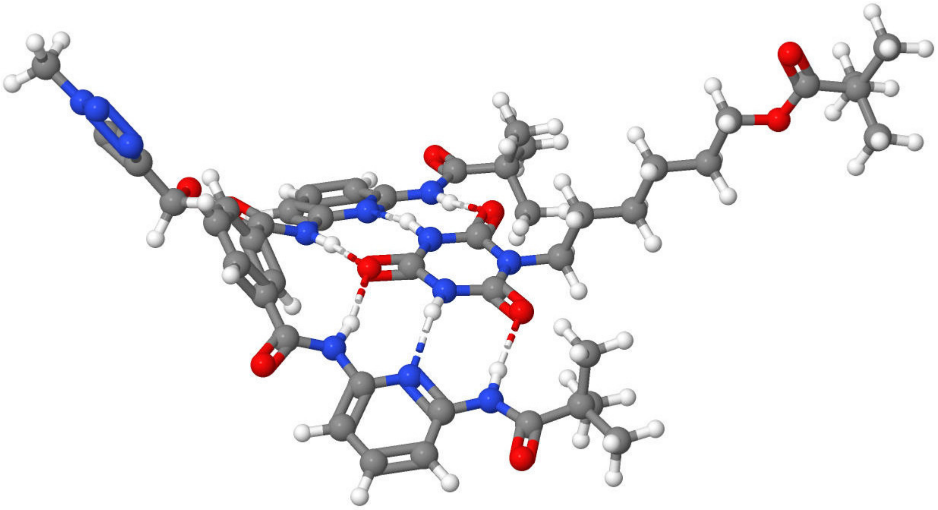

Figure S1: Six-point CA–HW geometry. The dashed lines show hydrogen bonds.

S2 Molecular mechanics

To sample the conformations of the whole polymer, we use a molecular mechanics approach and generate GAFF[S2] force field parameters using the `acpype` tool[S5] with the partial charges computed according to the AM1-BCC[S6,S7] method. To take implicitly into account the effect of van der Waals (vdW) interaction with a solvent and the resulting cancellation of dispersion forces, we scale the vdW contribution in the force field by factor 0.1. This approach and the scaling factor are motivated by the recent experimental measurement[S8] of the vdW dispersion forces between alkyl chains in different solvents. The experimental data show that the vdW interaction energies in solutions are an order of magnitude smaller than the estimated energies between alkyl chains in vacuum.

The electrostatic interaction is calibrated by the binding energy of the CA–HW recognition pair. From the quantum mechanical (QM) calculation in Sec. S1 we know the energy difference between the bound and unbound CA and HW molecules. Using the force field parameters introduced above, for the dielectric constant $\varepsilon = 1$ we have obtained the energy difference $\Delta E = 31.2$ kcal/mol which is larger than $\Delta E = 13.8$ kcal/mol predicted by QM. In order to match the QM energy difference in the force field calculations, the value of the dielectric constant has to be equal to $\varepsilon = 2.6$. This value of the dielectric constant was used for the simulations of the whole polymer chain.

The Monte Carlo simulations are carried out using the SIMONA software package.[S1]

S3 Free energy and transition temperature

From a Monte Carlo trajectory at a given temperature T we can compute a probability density function $p(E)$ as function of the potential energy E. Fig. S2 shows the probability density at different temperatures for the polymers of different lengths. The free energy F as a function of the potential energy can be obtained from $p(E)$ by

$$F(E) = -RT \ln p(E), \tag{1}$$

where R is the gas constant. The probability density and the free energy at two temperatures for the polymer with $L = 50$ are shown in Fig. S3.

The maxima of the probability density and the corresponding minima of the free energy represent the closed and open configurations of the polymer. The whole profile $p(E)$ can be

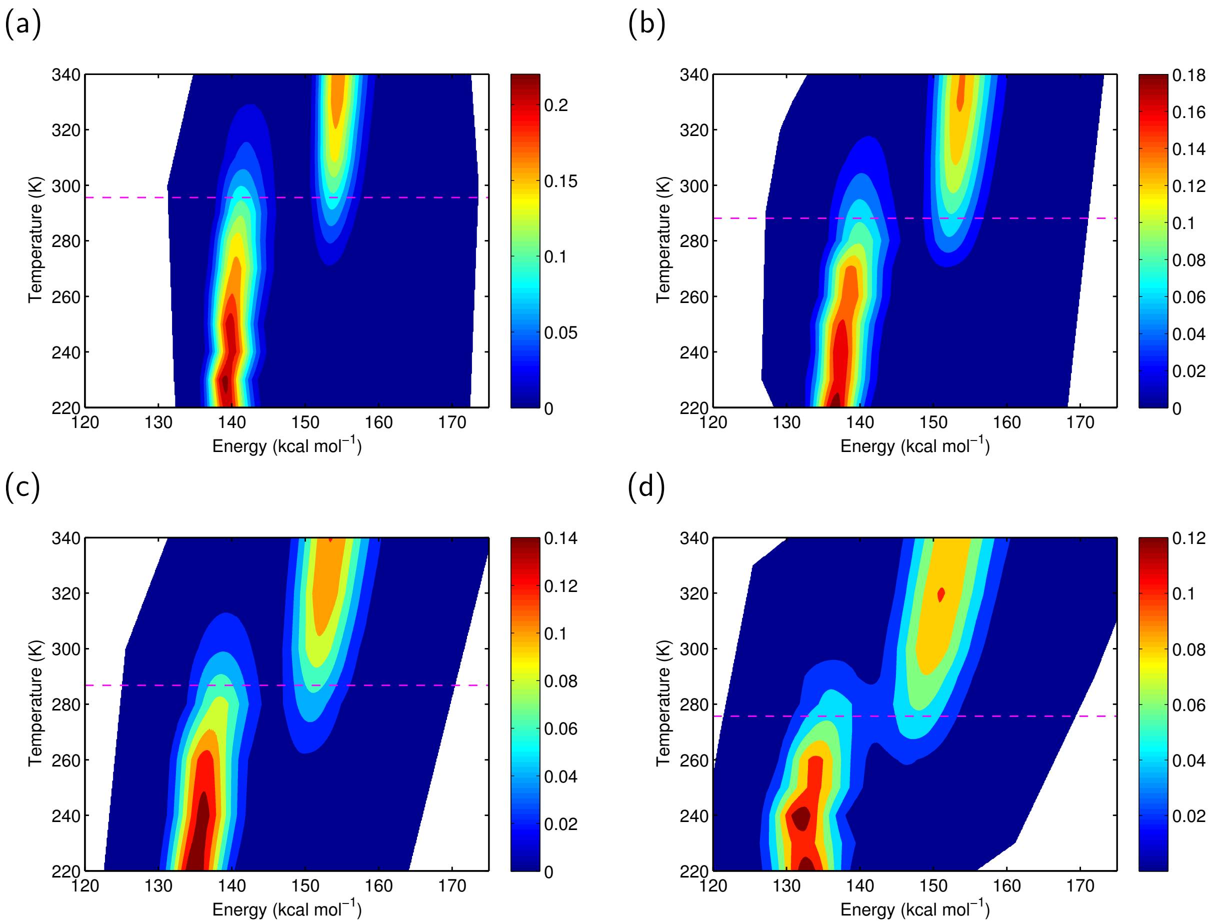

Figure S2: Energy probability density for polymers with (a) $L = 10$, (b) $L = 20$, (c) $L = 30$ and (d) $L = 50$. The dashed line corresponds to the transition temperature.

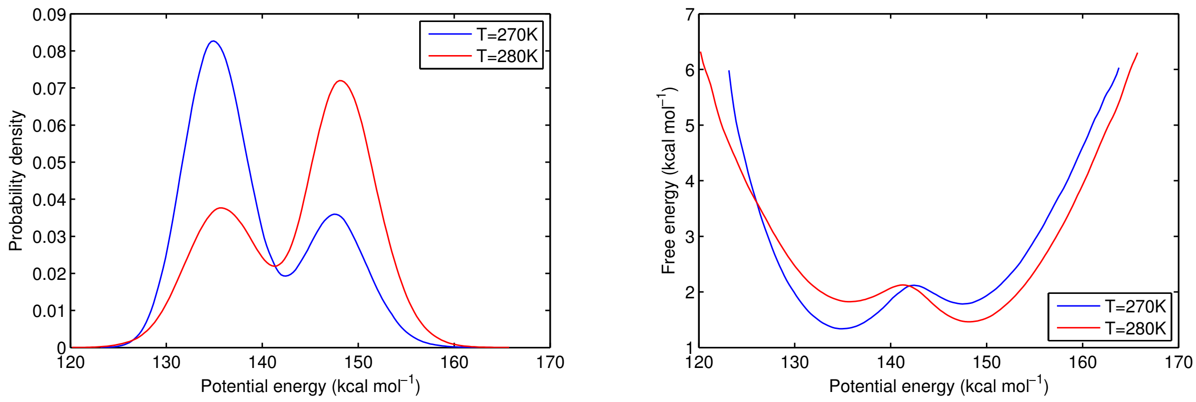

Figure S3: Probability density and free energy for the polymer with $L = 50$.

divided into the two states A (closed) and B (open) by means of the transition point at the energy E_0 as indicated in Fig. S4. Then the probabilities to find the system in state A or B

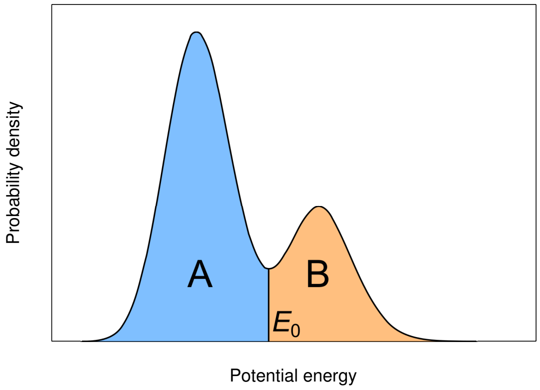

Figure S4: Definition of the two states A and B by the transition point at E_0.

are given by

$$P_A = \int_{-\infty}^{E_0} p(E)dE, \quad P_B = \int_{E_0}^{+\infty} p(E)dE \tag{2}$$

with the average potential energies of the two states obtained as

$$H_A = \int_{-\infty}^{E_0} p(E)EdE, \quad H_B = \int_{E_0}^{+\infty} p(E)EdE \tag{3}$$

and the free energies of the states

$$F_A = -RT \ln P_A, \quad F_B = -RT \ln P_B. \tag{4}$$

From the quantities defined in Eqs. (3) and (4) we can compute difference in the free energy ΔF, in the potential energy ΔH and in the entropy ΔS:

$$\Delta F = F_B - F_A = -RT \ln \frac{P_B}{P_A}, \tag{5a}$$

$$\Delta H = H_B - H_A, \tag{5b}$$

$$\Delta S = S_B - S_A = \frac{\Delta H - \Delta F}{T}. \tag{5c}$$

For the temperatures below the transition temperature T_m, the closed configuration is thermodynamically favorable one because of lower value of the free energy. For the temperatures $T > T_m$, the open configuration becomes more favorable than the closed. We obtain the value of T_m defined by the condition $\Delta F(T_m) = 0$ and the values of $\Delta H(T_m)$ and $\Delta S(T_m)$ by linear interpolation between the data for two temperatures $T_1 < T_m$ and $T_2 > T_m$.

A comparison with scaling theory of polymers can be made on basis of simple two-state model. Let us define the closed conformation as the state with end-to-end distance $R_{ee} = a$ for a chain with monomer size a. All other conformations correspond to the open state. Then the probability P_A to find the chain in the closed conformation scales with the chain size $L \gg 1$ as $P_A \sim L^{-\alpha}$, where $\alpha = 3/2$ for the ideal chain and $\alpha \approx 1.97$ for the "real" chain (with excluded-volume effects) in good solvent.[S9] Correspondingly, the probability of the open conformation is $P_B = 1 - P_A = 1 - O(L^{-\alpha})$. Using the two-state model we can estimate the entropy difference between the closed and open states as

$$\frac{\Delta\widetilde{S}}{R} = \ln\frac{P_B}{P_A} \sim \alpha \ln L. \tag{6}$$

Fig. S5 shows three fits of the scaling law in Eq. (6) to the simulation data. The first fit to the all simulation points leads to the scaling exponent $\alpha = 1.55$ close to the value $\alpha = 3/2$ for the ideal chain, but with a large scattering. Taking into account the transition in the reduced fluctuation of the gyration radius (Fig. 3 in the main text), two sets of the simulation data (small and large chain lengths) are fitted separately with $\alpha = 2.41$ and $\alpha = 1.88$. The two fits show much better agreement with the simulation data that the single overall fit.

In Ref.[S10] transition of hard-sphere chain from open to closed conformation have been studied numerically and the scaling exponent $\alpha = 2$ was found from simulation data.

S4 Shape measures of polymer chain

Consideration only of the eigenvalues of the gyration tensor limits the image of a polymer chain to an ellipsoidal shape. Several additional shape measures have been introduced to

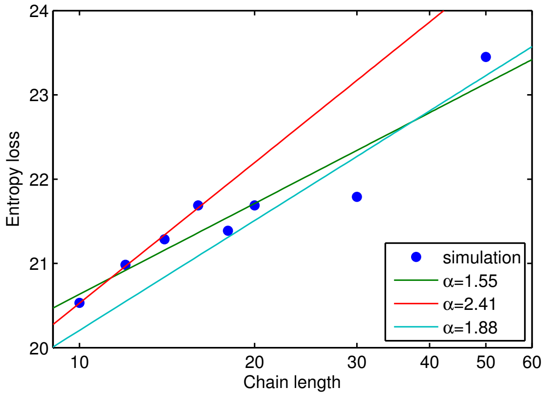

Figure S5: Scaling of the entropy loss ΔS with the chain length L.

Table S1: Transition temperature, changes in enthalpy and entropy, mean radius of gyration of the closed ensemble and the width of its distribution.

L	T_m	ΔH	ΔS	R_g	σ
10	299.0	12.21	0.0408	0.662	0.0317
12	294.5	12.27	0.0417	0.729	0.0364
14	292.9	12.38	0.0423	0.795	0.0423
16	292.7	12.61	0.0431	0.855	0.0500
18	292.8	12.44	0.0425	0.917	0.0582
20	292.0	12.58	0.0431	0.982	0.0666
30	290.5	12.58	0.0433	1.251	0.0856
50	276.9	12.91	0.0466	1.736	0.1175

characterize the shape of polymer chains in terms of anisotropy, asphericity and acylindricity.[S11]

Let us assume that the eigenvalues of the gyration tensor are defined as $R_1 \geqslant R_2 \geqslant R_3$ and the radius of gyration R is

$$R^2 = R_1^2 + R_2^2 + R_3^2. \tag{7}$$

Following the definitions in Ref.[S11] we introduce the asphericity b,

$$bR^2 = R_1^2 - \frac{R_2^2 + R_3^2}{2}, \tag{8}$$

the acylindricity c,

$$cR^2 = R_2^2 - R_3^2, \tag{9}$$

and the relative shape anisotropy κ,

$$\kappa^2 = \frac{b^2 + \frac{3}{4}c^2}{R^4}. \tag{10}$$

The relative shape anisotropy κ is varying between 0 and 1. The limit $\kappa = 0$ corresponds to a case when all points are distributed spherically symmetric and the limit $\kappa = 1$ corresponds to the points lying on a line.

Many closed conformations for the polymer with chain length $L = 50$ feature a disk-like shaped polystyrene chain (refer to Fig. S7 a, d, f). Hairpin configurations are also present with low acylindricity and high asphericity as noted in Fig. S7 c.

An alternative way to characterize the structure is to define a distance between the parts of the CA–HW recognition pair. As the measure, we use average value of two interatomic distances as indicated in Fig. S9. The CA–HW distance and the chain radius of gyration along the MC trajectory for $L = 50$ are shown in Fig. S10.

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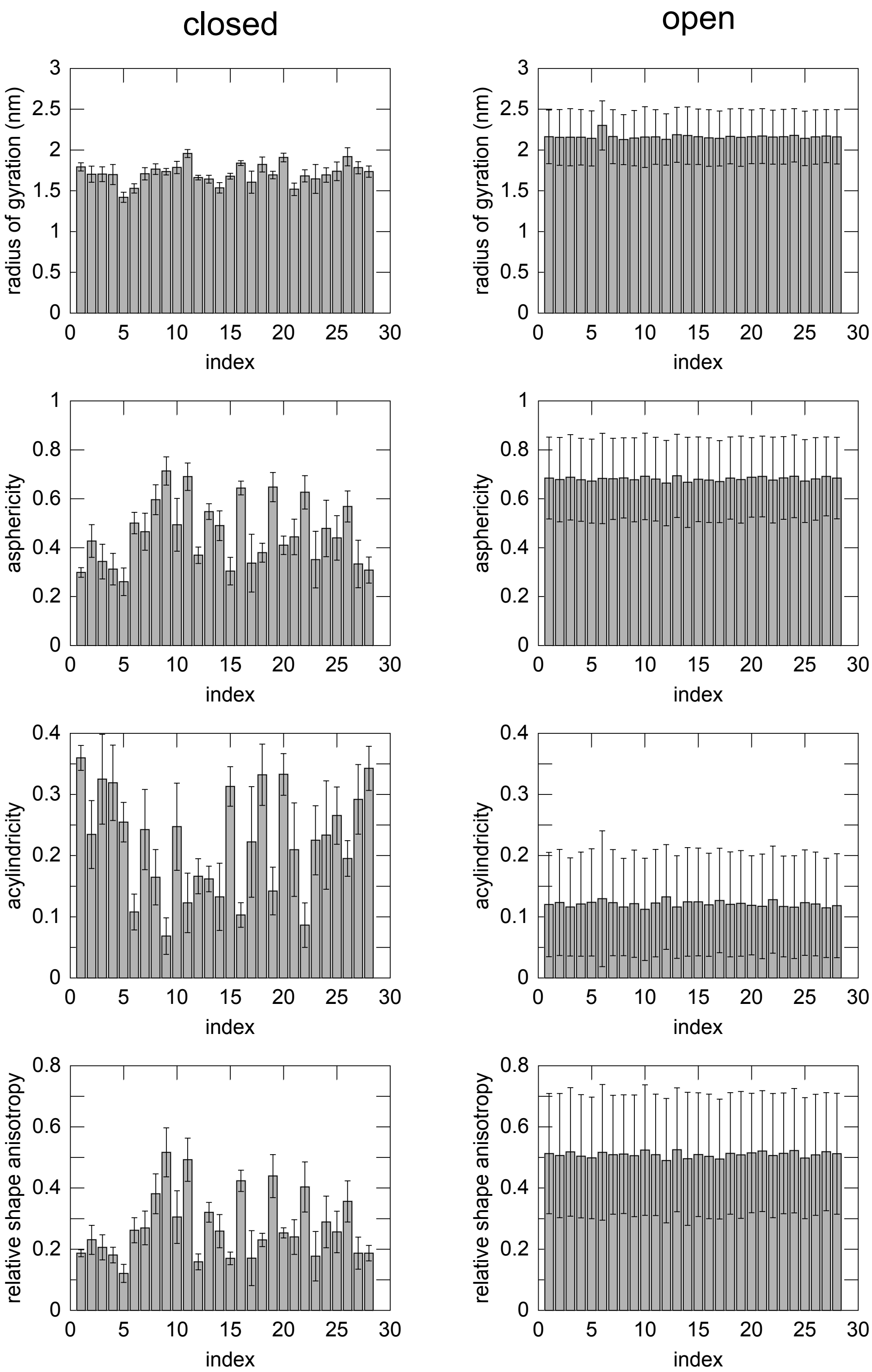

Figure S6: Radius of gyration, asphericity, acylindricity and relative shape anisotropy of closed (left) and open (right) chain conformations with $L = 50$ for the MC trajectory at $T = 270$ K. The number along x-axis indicates the index of the distinct closed or open configuration along the trajectory.

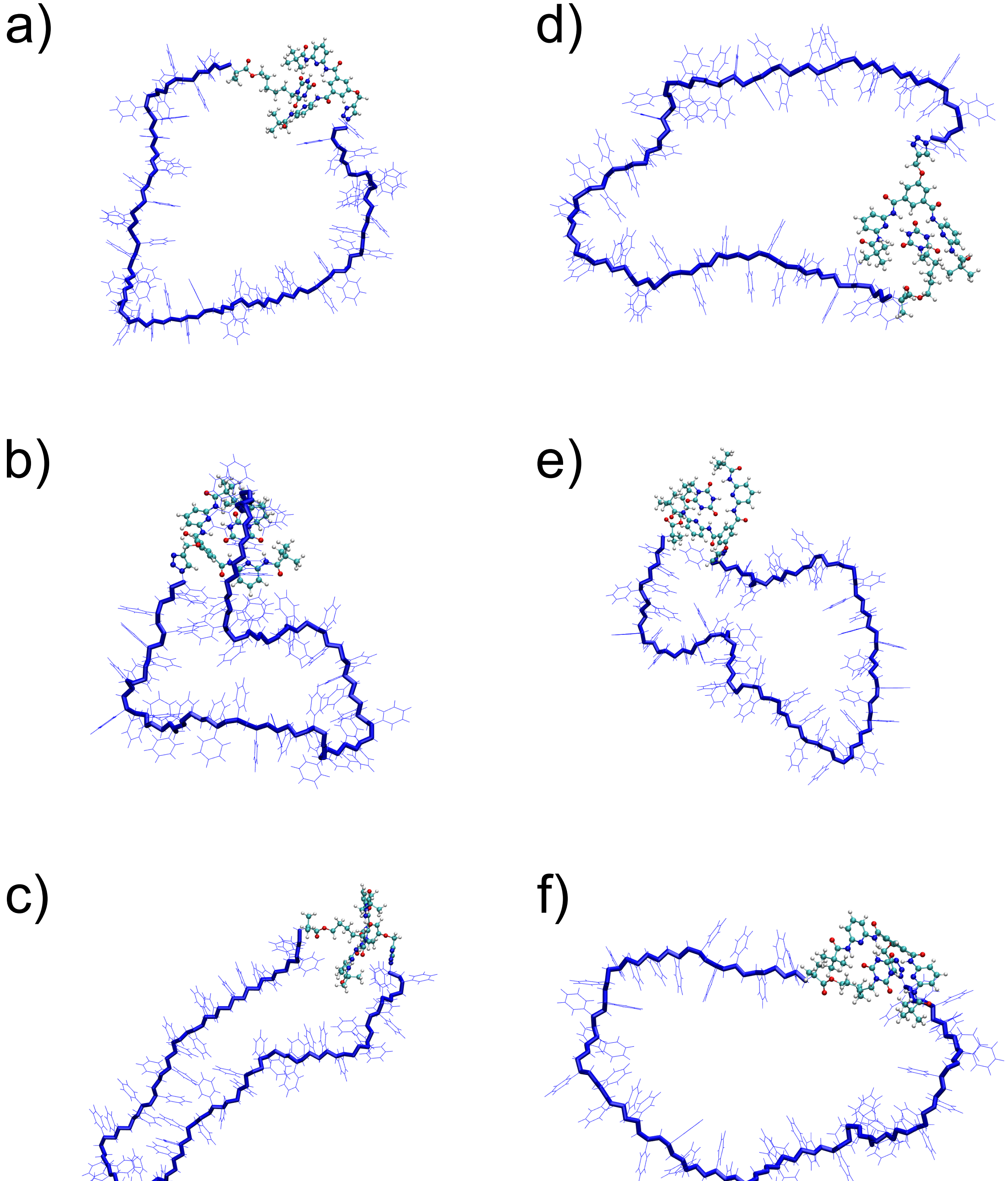

Figure S7: Representative closed conformations for the polymer with chain length $L = 50$.

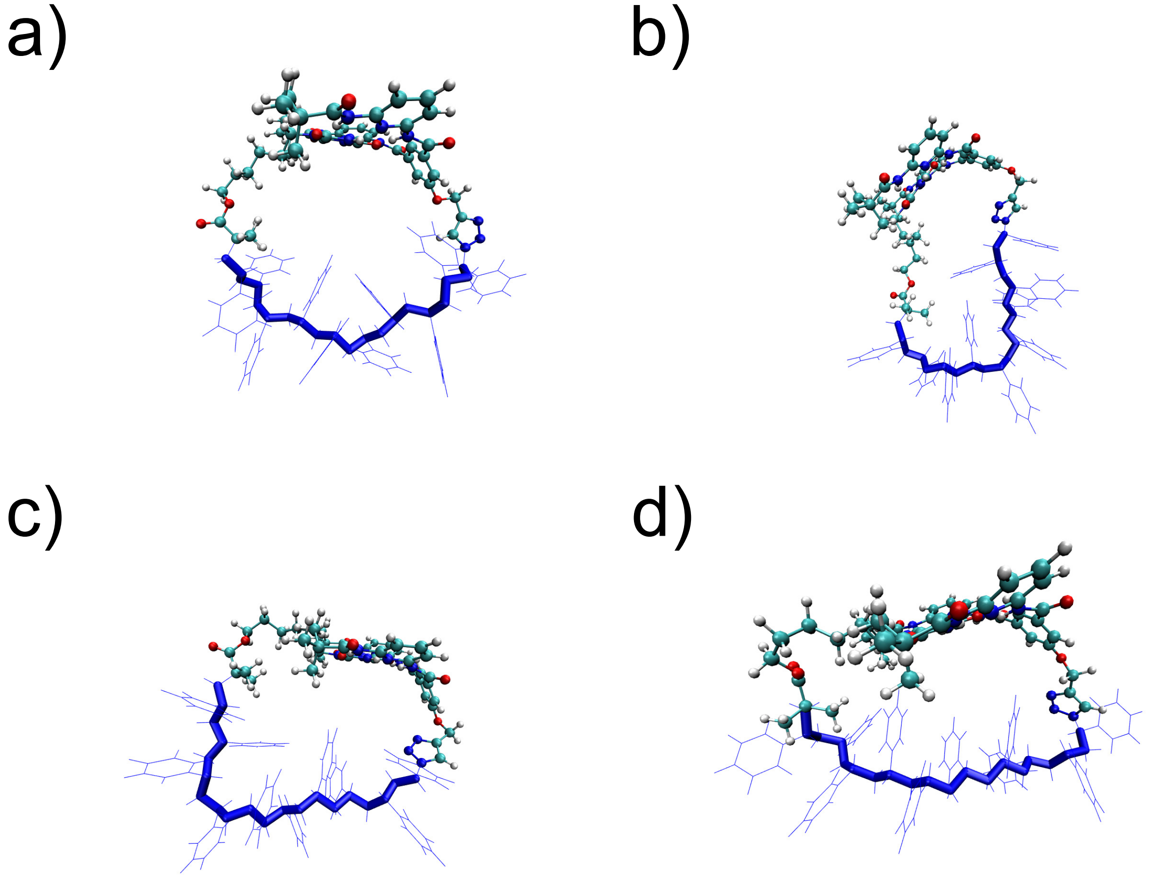

Figure S8: Representative closed conformations for the polymer with chain length $L = 10$.

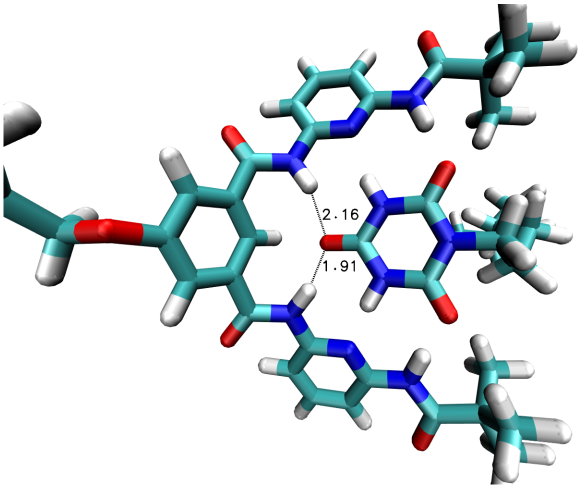

Figure S9: Definition of the distance between the CA and HW.

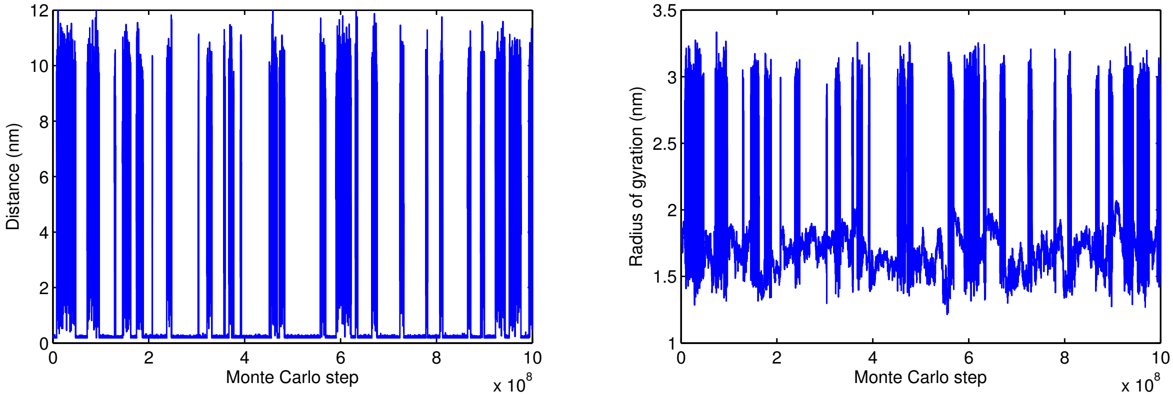

Figure S10: CA–HW distance and chain radius of gyration along the MC trajectory at $T = 270$ K and $L = 50$.