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Equilibrium Kinetic Network of the Villin Headpiece in Implicit Solvent

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ABSTRACT We applied the single-replica multiple-state transition-interface sampling method to elucidate the equilibrium kinetic network of the 35-residue-fragment (HP-35) villin headpiece in implicit water at room temperature. Starting from the native Protein Data Bank structure, nine (meta)stable states of the system were identified, from which the kinetic network was built by sampling pathways between these states. Application of transition path theory allowed analysis of the (un)folding mechanism. The resulting (un)folding rates agree well with experiments. This work demonstrates that high (un)folding barriers can now be studied.

INTRODUCTION

To elucidate and understand the detailed folding mechanism of proteins, it is desirable to have access to both experimental measurements and numerical simulation data. Up to now, only fast-folding proteins have fulfilled that criterion, since they fold sufficiently slowly for time-resolved experiments yet fast enough that their folding kinetics can be estimated by molecular dynamics simulations. One such fast-folding protein, the 35-residue subdomain of the villin headpiece (HP-35) (1,2) folds into a native state that is characterized by three α-helices packed together, thus forming a hydrophobic core (3,4) (see Fig. 1 for a visualization of the native structure). The experimental folding rate of the villin headpiece is on the order of a few microseconds (<0.5–5 μs⁻¹) (5–8). The experimental unfolding rate for wild-type HP-35 is much slower, specifically ~800 μs⁻¹, at 300 K (5). Thus, the stability of the native state with respect to the unfolded state is ~5–6 k_BT (where k_B is Boltzmann’s constant and T is temperature). Past experiments have revealed several important aspects of the villin headpiece folding/unfolding mechanism. Backbone mutagenesis (9) indicated that backbone hydrogen bonds mediate the helix formation from the transition state to the native state, and a folding nucleus found between helices II and III was predicted to accelerate folding. The finding that the transition state does not contain many native tertiary contacts and/or hydrogen-bonded helices, but may contain a hydrogen-bonded loop, is consistent with a relatively low folding free-energy barrier (10). Reiner et al. (11) used triplet-triplet energy transfer to monitor conformational fluctuations from equilibrium and found two conformational traps in the HP-35 unfolding process. They proposed that as it unfolds from the native structure, the protein encounters a relatively high barrier on the way to a major conformation where the C- and N-termini are proximate and then crosses a relatively low barrier on the way to a minor conformation where the two termini are farther apart.

The villin headpiece has been investigated extensively using molecular simulations (12–14) with both implicit (14–19) (including a study of a double mutant (19)) and explicit solvent (12,13,20–22). The first microsecond all-atom explicit-solvent molecular dynamics (MD) simulation of the villin headpiece took place in the late 1990s (20), and by only a few years later, the simulation length under the same condition had been extended 300-fold (12), by employing distributed computing. These long-time simulation trajectories clarified the folding mechanism to a large extent. A conformational search, after a quick (20-ns) molecular collapse, was proposed to be the rate-limiting step before the native state was finally reached (12). The folding rate was predicted to be ~5 μs. Freddolino and Schulten analyzed three folding trajectories from MD simulations (13). They found a folding time of 5.6–8.2 μs, during which the protein visited a long-lived intermediate state that has the native secondary structure, but with helix I flipped and rotated with respect to helix III. Folding to the native state was observed to proceed only after all three helices dissociate and reassociate with each other (13). A recent simulation of the Nle/Nle double mutant of the C-terminal fragment of the villin headpiece resulted in a folding rate of 2.8 μs at a melting temperature of 342 ± 5 K (23).

Similar to explicit-solvent simulations, implicit-solvent Monte Carlo simulations of the folding process by Yang et al. (14) showed early-stage collapse into a fairly compact structure, which remains compact until the native state is found, indicating the presence of well-formed secondary structure in the transition state. Later implicit-solvent simulations by Lei and Duan (17) proposed a well-defined two-stage folding process. Coming from the unfolded structure, the rate-limiting first stage leads to a folding intermediate...
where helices II and III form, which further facilitates the folding and docking of helix I in the second stage. Lei and Duan found on-pathway and off-pathway intermediates both with formed helices II and III. In contrast to the experiments by Reiner et al. (11), they found that the barrier separating the native state and the intermediate state is small, whereas that between the intermediate and the denatured states is large.

Most simulation approaches use either straightforward MD (23) or Markov-state modeling (24–26) to construct a (complex) transition network from a large but finite number of trajectories. However, when the trajectories spend most of their time in kinetic traps, these approaches can become inefficient. Parallel tempering or replica exchange, a popular simulation strategy to enhance sampling of protein conformational changes, efficiently generates a folding free-energy landscape but loses the direct connection to the kinetics. The path-sampling method (27,28) can alleviate these problems, since it samples unbiased rare trajectories between stable states and hence can sample transitions in which high barriers are encountered without losing any kinetic information.

In this study, we apply the recently developed single-replica multiple-state transition-interface sampling (SRMSTIS) (29,30) to HP-35 in implicit solvent. The aim of this work is to build up and analyze the equilibrium kinetic network for this protein and to show that we can overcome huge unfolding barriers (on the submillisecond timescale). For computational efficiency, we chose to work with a relatively small protein in implicit solvent. We note, however, that the method is fully applicable to explicit solvent (30). Starting with the native state, the SRMSTIS method builds up the equilibrium kinetic network by identifying metastable states and computing the kinetic-rate matrix between all these states. First, we performed a regular transition-interface sampling (TIS) of the native state to detect and define significant metastable states. Next, the SRMSTIS was applied to these states. During this sampling more metastable states were found, and these were added to the state set. A second SRMSTIS with nine states was applied to explore the kinetic network. Subsequent analysis using transition path theory (TPT) yielded new insight into the network, the unfolding mechanism, and the rate (31,32).

This article is organized as follows. In Materials and Methods, we introduce the molecular simulation and path-sampling conditions. In Results, we present the state identification along with the path sampling, followed by evaluation and analysis of the results. We end with concluding remarks.

MATERIALS AND METHODS

Molecular dynamics

All MD simulations were performed with the Gromacs-4.5.4 package (33–36). The experimental NMR structure (Protein Data Bank code 1YRF) (4) was used to initiate the simulation. We employed the CHARMM27 force field (37) with the multibody CMAP correction (38,39), which was parameterized to incorporate a-helix formation cooperativity in the force field (40) to deal with implicit-solvent systems. Protein configurations were visualized with VMD (41).

After putting the protein into a 6-nm cubic box, the energy was minimized by the steepest-descent method for 30 ps. In all simulations, the time step was 2 fs and the temperature was kept at 300 K by the v-rescale scheme (42). The nonbonded van der Waals cutoff radius was 1.4 nm, the LINCS algorithm constrained the bonds (43), and the Coulomb interaction cutoff was 4.8 nm. Frames were saved every 10 ps.

To represent solvation, we used the generalized Born surface area (GBSA) approach, which combines a GB electrostatic model with an approximation of the hydrophobic effect based on the solvent-accessible SA (44–49). Although the GBSA method can successfully identify native states of some short peptides with well-defined tertiary structure (50), in some studies, GBSA models predict different conformations compared with those from explicit solvent due to overly strong salt bridges and overpopulated a-helix (51).

Stable states were identified with the assistance of the k-centers cluster method (52,53).

Multiple-state transition interface sampling

The multiple-state TIS method samples the equilibrium kinetic network between predefined (meta)stable states and computes the corresponding rate
matrix. For each (meta)stable state \( I \), the method requires a definition of a series of \( m \) nonintersecting interfaces based on an order parameter \( \lambda_{kI} \), where each successive interface \( 1 \leq k \leq m \) delimits a volume in configuration space that encompasses the previous interface. The path ensemble belonging to each interface consists of all dynamical trajectories that start in the stable state and cross the interface, then return to the same state or end in any other state. The sampling of this interface-path ensemble is done via a Monte Carlo importance sampling by shooting off new trial trajectories from an existing pathway.

For this path sampling we use the one-way shooting algorithm (54). The stochastic one-way shooting move selects an initial point randomly from a previous accepted path and randomly decides whether to shoot forward or backward. For a forward move, an MD trajectory is initiated from the shooting point in the forward time direction until it reaches any stable-state definition. For a backward move, the momenta of all particles are reversed first, so that the integration effectively runs backward in time. The new trial path is constructed by joining the newly generated trajectory with the existing first half of the previous path (separated by the shooting point). This trial path can be accepted according to a metropolis Monte Carlo rule (for more details, see Du and Bolhuis (30)).

To identify the stable states, we used the root mean-square deviation (RMSD) of the backbone \( C_{\alpha} \) atoms with respect to a reference structure. As the heads and tails of polypeptides are usually flexible, we use only \( C_{\alpha} \) atoms from residue index 2–32. This order parameter, denoted \( r_{m\text{sd}_{2-32}} \), was used for both state and interface definitions. For instance, the native state S01 is defined by \( r_{m\text{sd}_{2-32}} < 0.13 \) nm, i.e., any structure with a distance of <0.13 nm to the reference structure S01 is considered to be in the native state. Using the same order parameter, \( \lambda \equiv r_{m\text{sd}_{2-32}} \), a series of 10 nonintersecting interfaces were defined around S01, with increasing radii. Starting from 0.17 nm, neighboring interfaces are separated by a fixed interval of 0.04 nm. The TIS set of interfaces is thus defined by \( \lambda = 0.17, 0.21, 0.25, 0.29, 0.33, 0.37, 0.41, 0.45, 0.49, \) and 0.53 nm.

In addition, we employ the minus interface shooting to ensure faster decorrelation in the first interface ensembles (29,55). Every time the first interface of a state is visited, instead of performing a shooting move, we simply continue the MD trajectory from one end point until it crosses the interface of a state is visited, instead of performing a shooting move, we do a qualified trial path for the first interface ensemble. The average duration of this sampling can start from any interface of any state, with a qualified initial path. Ideally, with state swapping and interface exchanging, one single replica could accomplish equal sampling of all path ensembles given enough time. However, for efficiency, we employ multiple independent replicas, or walkers. These walkers store their results in a shared file, which is used to update bias functions for state swapping and interface exchanging. These bias functions govern the state-swapping and interface-exchanging behavior in all walkers (30).

### Path-type analysis

The sampled path ensembles can be combined using a path-type analysis, as detailed in Du and Bolhuis (30). The rate-constant matrix is given by

\[
k_{ij} = \langle \phi_{ij} \rangle P_{i}(\lambda_{0j}|\lambda_{ij}),
\]

where \( \langle \phi_{ij} \rangle \) is the positive effective flux through the first interface \( \lambda_{ij} \), and \( P_{i}(\lambda_{0j}|\lambda_{ij}) \) is the crossing probability for reaching state \( J \) (defined by \( \lambda_{0j} \)) from state \( I \):

\[
P_{i}(\lambda_{0j}|\lambda_{ij}) = \frac{\sum_{k=1}^{m} n_{ij}(\lambda_{ij})}{\sum_{r=1}^{m} \sum_{k=1}^{m} n_{ij}(\lambda_{ij})}.
\]

Here, the reweighted path-type number, \( n_{ij}(\lambda_{ij}) \), is

\[
n_{ij}(\lambda_{ij}) = \sum_{i=1}^{m} \lambda_{ij}^{-1} \sum_{j=1}^{m} \lambda_{ij}^{-1}
\]

where \( n_{ij}(\lambda_{ij}) \) is the path-type number for interface ensemble \( i \), defined as the number of paths that start in state \( I \), end in state \( J \), and maximally reach interface \( \lambda_{ij} \). The weights \( \lambda_{ij} \) are obtained from a weighted histogram analysis of the crossing probabilities for state \( I \). See Du and Bolhuis (30) for more details.

### RESULTS

#### Finding the stable-state set

**Native-state TIS**

The NMR (Protein Data Bank) structure after equilibration with MD, labeled as S01, defines the native state N. Starting from this state, we performed regular TIS in implicit solvent at 300 K. A sampling of the path ensembles at all 10 interfaces comprised around 4000 shooting moves in total. Of these, 314 long trajectories, including accepted paths >10 ns and rejected paths >5 ns, were collected for the analysis. Together, these 314 paths add up to ~6.4 μs, and given the frame interval of 10 ps, they contain \( 6.4 \times 10^5 \) configurations. Using the k-center clustering method with \( r_{m\text{sd}_{2-32}} \) as the metric, all configurations were grouped into 2000 clusters with a near-equidistant radius of ~0.13 nm. Among these 2000 clusters, 55 clusters with >1000 members each comprise 79% of the total configurations. For each of these clusters, we extracted the
returns the minimum
Numbers in parentheses indicate the stable-state definition
the first three rows, with the microstate (cluster) structures.
In Table 1, the three stable-state definitions are listed in
trap structures were considered to be part of the T state.
were combined in the R state, whereas the two minor
see Fig. 1.

TABLE 1 Construction of all seven stable states by 26
structures

<table>
<thead>
<tr>
<th>State</th>
<th>Structures</th>
</tr>
</thead>
<tbody>
<tr>
<td>N</td>
<td>1 (0.13)</td>
</tr>
<tr>
<td>R</td>
<td>2 (0.13)</td>
</tr>
<tr>
<td></td>
<td>3 (0.13)</td>
</tr>
<tr>
<td></td>
<td>4 (0.13)</td>
</tr>
<tr>
<td></td>
<td>5 (0.13)</td>
</tr>
<tr>
<td></td>
<td>6 (0.13)</td>
</tr>
<tr>
<td></td>
<td>7 (0.13)</td>
</tr>
<tr>
<td>T</td>
<td>8 (0.13)</td>
</tr>
<tr>
<td></td>
<td>9 (0.13)</td>
</tr>
<tr>
<td></td>
<td>10 (0.13)</td>
</tr>
<tr>
<td></td>
<td>11 (0.13)</td>
</tr>
<tr>
<td></td>
<td>12 (0.13)</td>
</tr>
<tr>
<td></td>
<td>13 (0.13)</td>
</tr>
<tr>
<td>A</td>
<td>14 (0.10)</td>
</tr>
<tr>
<td></td>
<td>15 (0.10)</td>
</tr>
<tr>
<td></td>
<td>16 (0.10)</td>
</tr>
<tr>
<td></td>
<td>17 (0.10)</td>
</tr>
<tr>
<td></td>
<td>18 (0.10)</td>
</tr>
<tr>
<td></td>
<td>19 (0.10)</td>
</tr>
<tr>
<td></td>
<td>20 (0.10)</td>
</tr>
<tr>
<td>B</td>
<td>21 (0.10)</td>
</tr>
<tr>
<td></td>
<td>22 (0.10)</td>
</tr>
<tr>
<td></td>
<td>23 (0.10)</td>
</tr>
<tr>
<td></td>
<td>24 (0.10)</td>
</tr>
<tr>
<td>C</td>
<td>25 (0.10)</td>
</tr>
<tr>
<td>D</td>
<td>26 (0.10)</td>
</tr>
</tbody>
</table>

The RMSD cutoff for each structure is given in parentheses.
ensembles from $\lambda_1$ to $\lambda_{10}$ of all states, see Fig. 8 in the Appendix).

Based on a total of ~ 64,000 trial shooting moves, we extract the flux and transition count matrices. Using path-type reweighting (see Du and Bolhuis (30)) we compute the crossing probability matrix, the rate matrix, and the transition time-length matrix (see Table 4). To check the reliability of the reweighting, we compare the crossing probability at each interface of a state as computed from path-type reweighting analysis with the results from ensemble-based crossing probability analysis. Deviations of crossing probabilities from the two analysis methods are small for all interfaces of the seven sampled states (see Table 7 in the Appendix).

During sampling, the denatured state M was sampled by many paths. Exemplary structures of state M are shown in Fig. 4. However, state U was not visited by any path. To gain more information about the unfolded state and build up the connection from U to any other states, we performed

<table>
<thead>
<tr>
<th>State</th>
<th>Shootings</th>
<th>Exchanges</th>
<th>Swaps</th>
</tr>
</thead>
<tbody>
<tr>
<td>N</td>
<td>9309</td>
<td>84,567</td>
<td>118</td>
</tr>
<tr>
<td>R</td>
<td>10,011</td>
<td>89,190</td>
<td>238</td>
</tr>
<tr>
<td>T</td>
<td>10,016</td>
<td>87,757</td>
<td>178</td>
</tr>
<tr>
<td>A</td>
<td>8118</td>
<td>72,340</td>
<td>53</td>
</tr>
<tr>
<td>B</td>
<td>7575</td>
<td>67,244</td>
<td>145</td>
</tr>
<tr>
<td>C</td>
<td>9562</td>
<td>86,521</td>
<td>55</td>
</tr>
<tr>
<td>D</td>
<td>9278</td>
<td>84,736</td>
<td>220</td>
</tr>
</tbody>
</table>

FIGURE 2  The last three biasing functions (in the order red, green, and blue, where blue is the last bias condition) for all sampled states, N, R, T, A, B, C and D, compared with the final crossing probability of the respective state (black dotted line). The near overlap of the curves implies convergence. To see this figure in color, go online.

FIGURE 3  Replica index as a function of the number of exchange moves for all 40 walkers. On the x axis, the walkers are separated by vertical lines. On the y axis, each successive set of 10 replicas corresponds to a different state, with each replica in the set corresponding to $\lambda_1-\lambda_{10}$. States are in the order (lowest to highest) N, PN, SN, Mg, meta, and Pd.

FIGURE 4  Three exemplary denatured structures in state M. The stable helix III is formed in all structures, but helices I and II are mostly deformed. The protein backbone runs blue to red from N-terminus to C-terminus. To see this figure in color, go online.
additional straightforward MD trajectories, which will be discussed in the next section.

**MD trajectories start from fully unfolded structures**

Eight 1-μs-long MD trajectories were started from randomly selected unfolded structures to extract more information from the unfolded region U and make a connection to the sampled network of states. As the experimental and theoretical folding time is ~5 μs, these MD trajectories should be able to sample the early stage of folding. Indeed, two out of the eight MD trajectories form helix III, whereas the remaining trajectories do not form helix III during the entire 1-μs trajectory. Two exemplary trapped structures in the unfolded region are shown in Fig. 5. Lysine residues form an obstacle to folding, especially in the formation of helix III. Helix III forms only slowly, but once formed it is stable and hard to deform. In contrast, helices I and II showed much more flexible and fast dynamics; they form and deform, merge into one helix or break up into two helices, and flip with respect to each other.

**Flux at the first interface of sampled states**

For the seven sampled states, the flux through the first interface, \( \lambda_1 \), was extracted directly from the inverse of the average length of the paths in the minus shooting move (55,56). For states M and U, the flux follows directly from straightforward MD simulation by keeping track of their mean first passage time (MFPT). We list the fluxes for all nine states in Table 3.

**Analysis of the network**

**The transition probability and the rate matrices**

SRMSTIS enables construction of the transition network among states N, R, T, A, B, C, D, M, and the MD trajectories initiated from the unfolded region yield transitions between M and U. By combining these two results, we construct the complete kinetic network for all nine states, as detailed in Du and Bolhuis (30). The transition matrix, the rate matrix \( \mathbf{K} \), and the transition time matrix are shown in Table 4. In addition, we estimated the relative statistical error in the rates by assuming a normal distribution of the path-type numbers at the first interface. This statistical error estimate is mostly <10% and never higher than 50% for rarely sampled transitions.

These matrices indicate that, kinetically, A and B are close to N and R, whereas C and D are close to T. The M state acts as a bridge between all states and the unfolded state U. The reciprocal eigenvalues of the rate matrix yield the most important timescales in the kinetic network. These timescales in descending order are \( \tau = \{ \infty, 982.265, 378.568, 15.8943, 13.6639, 8.81709, 2.28238, 2.00341 \} \) ns. The slowest timescale (apart from infinity, which is the equilibrium solution) corresponds to the overall folding process, and other timescales are fast processes related to transition between the metastable states. This slowest timescale corresponds to the single-exponential kinetics observed in time-resolved experiments. However, we also see a 378 ns timescale that has not been observed in experiments up to now, indicating the presence of at least one intermediate state.

**Population of states**

Applying \( \mathbf{p}(t) = \mathbf{p}(0) \exp(\mathbf{K} t) \) for \( t \to \infty \) for the rate matrix \( \mathbf{K} \) yielded the stationary distribution for the nine states (see Table 5). Besides the native state, N, the only other significantly populated state is R, which accounts for ~30% of the overall population. In this state, all three helices are intact, but their relative positions are rearranged. Structurally, state R (defined by structures 2–13 (Fig. 1)) is very similar to the intermediate state identified by Lei and Duan (17). Those authors found that this state is an off-pathway intermediate that is not connected to N. However, in our calculations, the R state is kinetically very close to N, and carries a significant amount of unfolding flux (see section Transition-path theory analysis). The other, much less populated, states, T, A, B, C, and D (Fig. 1) have helix I flipped relative to helices II and III. This structural feature is very similar to the on-pathway intermediate state found in Lei and Duan (17).

**FIGURE 5** Two randomly selected metastable structures in the unfolded regime, visited by MD trajectories coming from the completely unfolded states. The protein backbone runs blue to red from N-terminus to C-terminus. Lysine is shown in gray. To see this figure in color, go online.
and to the folding intermediate proposed in Freddolino and Schulten (13), where the flipped helix I prevents the formation of the hydrophobic interactions present in the native state.

The relaxation of the population is shown in Fig. 6. From an initially completely folded state, there is a quick relaxation toward the R state within 50 ns. Relaxation to the other states is much slower, on the order of 1 μs (Fig. 7, lower).

**Transition-path theory analysis**

Using flux analysis (32) based on TPT (31,57), we computed the committor values for states R, T, A, B, C, and D from the overall transition from N to U (see Table 5). Based on the effective net flux matrix for the N → U transition (Table 6), the unfolding mechanisms can be summarized as a plot shown in Fig. 7. Note that direct flux transitions between (N, R, T, A, B, C, D) and U are rare. Although the rates for (N, R, T, A, B, C, D) → U are all zero in the rate matrix K, they appear in the transition matrix, via the matrix exponent of K. Because of symmetry, the net fluxes for the folding transition U → N are identical to the unfolding fluxes, but then, of course, reversed. Note also that the corresponding committor values are defined as $q_{\text{fold}} = 1 - q_{\text{unfold}}$.

State M transfers 84% net flux between the two sets, confirming its key role in the (un)folding process. Using TPT, we also computed the overall folding and unfolding mean FPTs (MFPTs) as 1.3 and 748 μs, respectively. We stress that to compute the rate of such a slow unfolding process using straightforward MD simulations would have taken orders of magnitude more computer time.

---

**TABLE 4 Transition probability, rate constant, transition time matrix, and relative error**

<table>
<thead>
<tr>
<th>N</th>
<th>R</th>
<th>T</th>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
<th>M</th>
<th>U</th>
</tr>
</thead>
<tbody>
<tr>
<td>N</td>
<td>9.96 × 10⁻¹</td>
<td>3.95 × 10⁻¹</td>
<td>8.96 × 10⁻⁶</td>
<td>1.19 × 10⁻⁴</td>
<td>1.22 × 10⁻⁴</td>
<td>1.04 × 10⁻⁶</td>
<td>1.84 × 10⁻⁶</td>
<td>2.72 × 10⁻⁷</td>
</tr>
<tr>
<td>R</td>
<td>1.85 × 10⁻²</td>
<td>9.81 × 10⁻¹</td>
<td>1.09 × 10⁻⁵</td>
<td>2.58 × 10⁻⁴</td>
<td>9.25 × 10⁻⁵</td>
<td>4.90 × 10⁻⁷</td>
<td>2.28 × 10⁻⁵</td>
<td>1.49 × 10⁻⁶</td>
</tr>
<tr>
<td>T</td>
<td>4.94 × 10⁻⁴</td>
<td>1.28 × 10⁻¹</td>
<td>9.93 × 10⁻¹</td>
<td>4.77 × 10⁻⁶</td>
<td>9.05 × 10⁻¹</td>
<td>9.66 × 10⁻⁵</td>
<td>1.27 × 10⁻³</td>
<td>4.67 × 10⁻³</td>
</tr>
<tr>
<td>A</td>
<td>6.44 × 10⁻²</td>
<td>2.98 × 10⁻²</td>
<td>4.67 × 10⁻⁵</td>
<td>9.05 × 10⁻¹</td>
<td>9.66 × 10⁻⁵</td>
<td>5.86 × 10⁻⁵</td>
<td>4.51 × 10⁻⁴</td>
<td></td>
</tr>
<tr>
<td>B</td>
<td>1.05 × 10⁻¹</td>
<td>1.69 × 10⁻²</td>
<td>1.53 × 10⁻⁴</td>
<td>8.78 × 10⁻¹</td>
<td>2.62 × 10⁻⁵</td>
<td>3.27 × 10⁻⁴</td>
<td></td>
<td></td>
</tr>
<tr>
<td>C</td>
<td>8.83 × 10⁻⁵</td>
<td>8.87 × 10⁻⁵</td>
<td>1.95 × 10⁻²</td>
<td>9.78 × 10⁻¹</td>
<td>1.16 × 10⁻³</td>
<td>1.01 × 10⁻³</td>
<td></td>
<td></td>
</tr>
<tr>
<td>D</td>
<td>6.08 × 10⁻⁴</td>
<td>1.61 × 10⁻⁵</td>
<td>2.80 × 10⁻²</td>
<td>3.59 × 10⁻⁵</td>
<td>1.01 × 10⁻⁵</td>
<td>4.54 × 10⁻⁴</td>
<td>9.68 × 10⁻⁴</td>
<td>1.27 × 10⁻³</td>
</tr>
<tr>
<td>M</td>
<td>2.56 × 10⁻³</td>
<td>2.99 × 10⁻³</td>
<td>2.89 × 10⁻²</td>
<td>7.87 × 10⁻³</td>
<td>3.60 × 10⁻³</td>
<td>1.12 × 10⁻²</td>
<td>3.61 × 10⁻²</td>
<td>9.03 × 10⁻³</td>
</tr>
</tbody>
</table>

Values were determined by path-type-reweighting analysis.
DISCUSSION

Using SRMSTIS, we computed the entire unfolding kinetics network of the villin headpiece. This resulted in identification of nine metastable states, and a $9 \times 9$ rate matrix. The experimental folding and unfolding times are 0.5–5 μs, and 800 μs, respectively, whereas our calculations yielded times of 1.3 and 748 μs, respectively, in very good agreement with experiment. Flux analysis shows that the unfolding goes via intermediates R or T (and to a much lesser extent A, B, C, and D), and a mandatory intermediate M. There are two prominent unfolding routes, $N \rightarrow T \rightarrow M \rightarrow U$ and $N \rightarrow R \rightarrow D \rightarrow M \rightarrow U$, observed from the flux plot (Fig. 7). The intermediate states have formed

TABLE 5  Equilibrium populations and committors

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<tr>
<th>State</th>
<th>Population</th>
<th>Committor</th>
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<tbody>
<tr>
<td>N</td>
<td>0.6719</td>
<td>0</td>
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<tr>
<td>R</td>
<td>0.2882</td>
<td>0.000036</td>
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<tr>
<td>T</td>
<td>0.0235</td>
<td>0.015</td>
</tr>
<tr>
<td>A</td>
<td>0.0089</td>
<td>0.00026</td>
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<tr>
<td>B</td>
<td>0.0011</td>
<td>0.00014</td>
</tr>
<tr>
<td>C</td>
<td>0.0016</td>
<td>0.016</td>
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<tr>
<td>D</td>
<td>0.0035</td>
<td>0.015</td>
</tr>
<tr>
<td>M</td>
<td>0.0001</td>
<td>0.049</td>
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<tr>
<td>U</td>
<td>0.0013</td>
<td>1</td>
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Corresponding to each state, the second column gives the population obtained from the rate matrix and the third column lists the committors for the $N \rightarrow U$ transition following from transition path theory analysis.

![Figure 6](upper) (Upper) Plot of the population relaxation, $P(t) = p(0) \exp(\mathbf{K}t)$, as a function of time $t$ for all nine states in the villin headpiece system. At time $t = 0$, only the native state is populated. (Lower) Enlarged population versus time plot of the bottom region of the top figure, where the population relaxation of the less populated seven states can be seen. Lines in decreasing order of final population represent states T, A, D, U, B, and M, respectively. To see this figure in color, go online.

![Figure 7](upper) Villin headpiece flux for both unfolding (upper) and folding (lower). Numbers on the left indicate the committor probabilities of the corresponding levels. Thickness of the arrows indicates the $N \rightarrow U$-related flux density. This figure only considers fluxes $> 10^{-8}$ ns$^{-1}$. To see this figure in color, go online.

![Figure 6](lower) TABLE 6  Flux matrix of nine states for transition from $N$ to $U$ ($in 10^{-8}$ ns$^{-1}$)

<table>
<thead>
<tr>
<th></th>
<th>N</th>
<th>R</th>
<th>T</th>
<th>A</th>
<th>B</th>
<th>C</th>
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<td>48.53</td>
<td>11.09</td>
<td>4.95</td>
<td>0.76</td>
<td>10.72</td>
<td>5.54</td>
<td>0.89</td>
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<tr>
<td>R</td>
<td>13.94</td>
<td>4.40</td>
<td>0.62</td>
<td>0.69</td>
<td>25.37</td>
<td>5.04</td>
<td>0.87</td>
<td></td>
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<tr>
<td>T</td>
<td>12.13</td>
<td>9.86</td>
<td>33.22</td>
<td>8.12</td>
<td>0.74</td>
<td>0.11</td>
<td>0.86</td>
<td>11.69</td>
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<td>A</td>
<td>0.12</td>
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<td>4.31</td>
<td>0.84</td>
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<tr>
<td>B</td>
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<td></td>
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<tr>
<td>C</td>
<td>108.14</td>
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helix II and helix III, which compared well with the previously detected on-pathway (states T, A, B, C, D) and off-pathway (state R) intermediates by implicit-solvent simulations (17). Moreover, we found a very fast N → R transition, a slower N → T transition, and extremely slow transitions R → U and T → U, in agreement with the conclusions of Lei and Duan (17) that the transition from native state to intermediates is easy, whereas that from the intermediates to the unfolded state is hard.

Both our SRMSTIS and straightforward MD simulations have proved that helix III is much more stable than helix I and helix II. In our SRMSTIS with seven structure-based states, the sampled paths witnessed the formation and deformation of helices I and II, but helix III was nearly always intact. In a similar way, MD simulations initiated from the unfolded state, as reported in the Results section, indicated that helix III was hard to form/deform, whereas helixes I and II were more flexible and exhibited (de)formation, helical merging, and bending more frequently. We thus defined the structures with intact helix III and denatured helix I and II as the intermediate state M, allowing it to connect the structure-based states to the fully unfolded region (with helix III deformed) as a transition.

Explicit-solvent simulations by Freddolino and Schulten (13) corroborate this finding. In all three MD folding trajectories, helix III was formed within the first 2 μs and remained stable ever after. The following 4–6 μs showed rearrangement of the relative positions of the three helices, and in one trajectory this was accompanied by formation and deformation of helices I and II before the native structure was reached. The different properties of helix III (stable) compared with the other two helices also has theoretical support, since helix III, as the longest helix in the villin headpiece, is composed of 10 residues, among which four are Lysine residues. Once formed, helix III is stabilized by those long residues due to the space constraints and/or electrostatic interactions.

Our unfolding flux calculation has highlighted the key role state M plays in (un)folding process (see Fig. 7). It acts as the mandatory intermediate state between the native and unfolded states. The importance of state M correlates with the properties of the three helices: helices I and II are flexible and experience multiple (de)formations, whereas helix III is the bottleneck of the (un)folding process.

CONCLUSIONS

To summarize, we have performed an extensive sampling of the kinetic network of the villin headpiece using SRMSTIS. Although the initialization phase is currently rather ad hoc and would benefit from automation, this work shows that this method can be used to sample complex folding networks, which would cost orders of magnitude longer simulation time with straightforward MD.

APPENDIX

In this appendix, we present additional information on the sampling. Fig. 8 shows the path-length distribution of all ensembles. Table 7 contains a comparison between the ensemble-based computation of the crossing probabilities and the path-reweighting analysis.

ACKNOWLEDGMENTS

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REFERENCES

TABLE 7 Comparison of crossing probabilities from ensemble-based analysis and path-reweighting analysis for all states

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<tr>
<th>State</th>
<th>Exchanges</th>
<th>Path type</th>
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<th>Exchanges</th>
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Interface values of the state are shown in the first column. The second column shows the trial interface exchange moves. Columns 3 and 4 list crossing probabilities $P(\lambda_i|\lambda_l)$ at corresponding interfaces of the state from path-type-rewighting analysis and ensemble-based crossing probability analysis, respectively.

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