## Folding kinetics and unfolded state dynamics of the GB1 hairpin from molecular simulation Supporting information

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## Calculation of the rate matrix K

As described in the main text the rate matrix  $\mathbf{K}$  is calculated using the approximate expression

$$k_{ji} \approx \begin{cases} t_{ji}(\Delta t)/\Delta t & \text{for } i \neq j \\ -\sum_{j \neq i} k_{ji} & \text{for } i = j \end{cases}$$
(1)

In this expression we use the transition probability matrix  $\mathbf{T}(\Delta t)$  for a given "lag time"  $\Delta t$ , which is obtained using the maximum likelihood estimator<sup>1</sup>

$$t_{ji}(\Delta t) = n_{ji}(\Delta t) / \sum_{j} n_{ji}(\Delta t).$$
<sup>(2)</sup>

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Figure 1: Comparison of relaxation times from the transition matrix and the approximated rate matrix. We show a comparison of relaxation times for different lag times  $\Delta t$  used to count transitions. The dashed gray line is the y = x.

Here  $n_{ji}(\Delta t)$  are the elements of the transition count matrix  $\mathbf{N}(\Delta t)$ , determined from the simulation trajectories as the number of transitions from microstate *i* to microstate *j* after a specified lag  $\Delta t$ . This approximation in Eq. (1) becomes exact in the limit  $\Delta t \rightarrow 0$ . In S.I. Figure 1, we compare the relaxation times for the transition matrix and those of the rate matrix. We see that the relaxation times from both methods agree quantitatively up to time-scales approximately equal to the lag time used for counting transitions.

## Lumping of microstates into macrostates

In Table 1 we list the most populated states found in each of the macrostates of the 9-macrostate model (see Figure 7 A-B, bottom, in the main text).

| Macrostate | $P_{eq}$ | Representative microstates |
|------------|----------|----------------------------|
|            |          | EEEEEAAALEEAEE             |
| 1          | 7.52e-03 | AEEEEAAALEEAEE             |
|            |          | EEEEEAAALEEAEA             |
|            |          | EAEAAEAALEEEEE             |
| 2          | 3.02e-03 | EAEAAEAALEAEEE             |
|            |          | EEEAAEAALEEEEE             |
|            |          | EEEAAAAAAALAEE             |
| 3          | 4.85e-03 | EEEAAAAAAALAEA             |
|            |          | AEEAAAAAAALAEE             |
| 4          | 3.90e-04 | EAAAEAAEEELEEE             |
|            |          | EAAAEAAEEELEEA             |
|            |          | EAAAAAAAAAAEE              |
| 5          | 2.63e-01 | EAAAAAAAEEEEE              |
|            |          | EAAAAAAAAEEEE              |
|            |          | EEEEAEAAAEEEEE             |
| 6          | 5.57e-02 | EEEEAEAAEEEEEE             |
|            |          | EAAAAEAAAEEEEE             |
|            |          | EEEEEAAALEEEEE             |
| 7          | 3.90e-01 | EEEEEAAALEEEEA             |
|            |          | AEEEEAAALEEEEE             |
|            |          | EEEAAAAAAAAAEE             |
| 8          | 1.44e-01 | EEEAAAAAAEEEEE             |
|            |          | EEEAAAAAAEEEE              |
|            |          | EAAAEAAAAAAAEE             |
| 9          | 1.32e-01 | EAAAEAAAAAAEEE             |
|            |          | EEEEEAAEAEEEEE             |

Table 1: Equilibrium populations and epresentative sets of torsional states lumped into the different clusters for the 9-macrostate model.

## References

 Prinz, J.-H.; Wu, H.; Sarich, M.; Keller, B.; Senne, M.; Held, M.; Chodera, J. D.; Schutte, C.; Noe, F. J. Chem. Phys. 2011, 134, 174105.