Supplemental Materials

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Table S1: The ranking of residues according to correlation coefficients between "length of knot tails" and virtual torsional angle τ for knotting in coarse-grained "Go"-like model, unknotting in coarse-grained "Go"-like model and unknotting in all-atom model, respectively.



Figure S1: The average values of the radius of gyration at different temperatures in the coarsegrained "Go"-like model. The melting temperature T_m is labelled.



Figure S2: The correlation coefficients between the torsional angles and the "length of the knot tails" as a function of the time extension Δt .Panels (A), (B), (C) are for the cases of knotting in coarse-grained "Go"-like model, unknotting in coarse-grained "Go"-like model and unknotting in all-atom model, respectively. Each line in the figure represents the correlation coefficient at a residue in the protein.



Figure S3: The average correlation coefficients between the torsional angles and the "length of knot tails" as a function of the number of simulation replicas at different residues. The red dots are the average values and the blue error bars denote the standard deviations. The x- and y-axis represents the number of reolicas and the value of correlation coefficient, respectively. Each panel shows the correlation coefficients for a residue. The corresponding residue index for each panel (from 7 to 85) increases from left to right and top to bottom.



Figure S4: The average correlation coefficients of the virtual angles with "the length of knot tails" in the folding simulation with coarse-grained "Go"-like model. (A) The correlation coefficients between "length of knot tails" and κ . (B) The correlation coefficients between "length of knot tails" and τ . The key residues verified by experiment are labeled in the figure. The blue dots are the average values and the red error bars denote the standard deviations.



Figure S5: The evolution curve of the "length of knot tails" at the unfolding point of the AMD simulation with coarse-grained "Go"-like model. The snapshots corresponding to different "length of knot tails" (red points on the curve) are shown as insets.



Figure S6: The evolutions of the virtual bond angle κ (Panel A) and virtual torsional angle τ (Panel B) during the unfolding process in coarse-grained "Go"-like model.



Figure S7: The average correlation coefficients of the virtual angles with "the length of knot tails" in the unfolding simulation with coarse-grained "Go"-like model. (A) The correlation coefficients between "length of knot tails" and κ . (B) The correlation coefficients between "length of knot tails" and τ . The red dots are the average value and the blue error bars denote the standard deviations.



Figure S8: The evolution of RMSD in the unfolding simulation in all-atom model.



Figure S9: The evolution curve of the "length of knot tails" at the unfolding point of the AMD simulation with all-atom model. Some snapshots corresponding to different "length of knot tails" (red points on the curve) are shown as insets.



Figure S10: The evolution of virtual bond angle κ (panel A) and virtual torsional angle τ (panel B) during the unfolding process in all-atom model.



Figure S11: The average correlation coefficients of the virtual angles with "the length of knot tails" in the unfolding simulation with all-atom model. (A) The correlation coefficients between "length of knot tails" and κ . (B) The correlation coefficients between "length of knot tails" and τ . The blue dots are the average value and the red error bars denote the standard deviations.



Figure S12: Comparison on the rankings results of the residues between two different temperature settings in the AMD simulations.



Figure S13: Comparison on the rankings results of the residues between two different time settings in the AMD simulations.



Figure S14: Comparison on the rankings of each residue with correlation coefficients calculated from Eq. 2 and Eq. 4. Panels (A), (B), (C) are for the cases of knotting in coarse-grained "Go"-like model, unknotting in coarse-grained "Go"-like model and unknotting in all-atom model, respectively.



Figure S15: The ROC curve of key residue for knotting according to the predictions from Eq. 4.

Table S1: The ranking of residues according to correlation coefficients between "length of knot tails" and virtual torsional angle τ for knotting in coarse-grained "Go"-like model, unknotting in coarse-grained "Go"-like model and unknotting in all-atom model, respectively. The first column represents the index of residues, second to fourth columns represent the ranking for knotting in coarse-grained "Go"-like model, unknotting in coarse-grained "Go"-like model, nuknotting in coarse-grained "Go"-like model, unknotting in coarse-grained "Go"-like model, nuknotting in coarse-grained "Go"-like model, nuknotting in coarse-grained "Go"-like model and unknotting in all-atom model, respectively.

Res ID	Go-fold	Go-unfold	AA-unfold	Res ID	Go-fold	Go-unfold	A A_unfold
7	79	79	79	17 10 10	34	42	28
8	72	75	78	41	22	$\frac{42}{37}$	34
9	73	77	75	40		57 71	54 60
10	63	67	61	49 50	10 52	71 57	41
11	59	61	52	50	51	50	41
12	44	40	63	50	01 01	00 25	41
13	45	44	39	52 52	21 75	20 72	J8 46
14	71	68	56	50 54	15	10	40 54
15	13	8	20	54 55	10 57	13	54 65
16	76	76	53	00 56	57 69	52 70	40
17	12	2	28	50 57	00 66	70 62	40 72
18	9	1	42	57	00 20	02	() 45
19	52	38	74	08 50	30 20	11	40
20	61	56	59	59 C0	20	18	48
21	70	74	71	00 61	39 77	33 70	33 50
22	67	66	72	01 C0	(((8 20	50
23	29	17	43	62 C2	37	32	4
24	47	36	18	03 C4	24	19	0
25	17	16	31	04 CT	22	29	14 F
26	31	22	3	60 60	25	28	0 C
27	10	5	12	00 C7	18	24	8
28	19	14	19	07	20 25	20	21
29	2	4	17	08 C0	30 20	39	24
30	23	23	26	09 70	32 20	34 41	30 20
31	3	9	30	70 71	30 C 4	41 CT	32
32	4	12	51	(1 70	04 C0	00	07
33	8	21	57	(Z 72	60 07	58 20	70 40
34	49	47	55	73 74	21	30 55	49
35	65	64	66	(4 75	55 20	00 01	11
36	69	69	70	() 70	28	31 25	29 10
37	74	72	69	/0 77	38 16	30 20	10
38	56	60	62	/ / 70	10 C	20	10
39	54	53	68	(8 70	0 7	í C	22
40	62	63	64	(9	(1	0	15
41	50	54	25	80	1	3	11
42	43	45	36	81	11 ~	15	(
43	40	49	44	82	5 1 4	10	9
44	48	51	37	83	14	27	27
45	46	48	13	84 05	41	46	1
46	42	43	23	85	58	59	2