Supplementary Materials

Table S1. The 17 sequences analyzed in this research. In the table, Column 1 shows the label of each sequence. Column 2 shows the sequence, with Arg (R) residues in blue, and Ile (I) residues in orange. Column 3 shows the net charge per residue (*NCPR*). Column 4 shows the mean hydrophobicity (*H*). Column 5 shows the sequence hydropathy decoration (*SHD*). Column 6 shows the sequence charge decoration (*SCD*). Column 7 shows the λ. Column 8 shows the scaling exponent (ν).

No	Sequence	*NCPR*	*H*	*SHD*	*SCD*	λ	ν
1	RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	1.0	0	0.00000	94.06174	0.00000	1.00000
2	RRRRRRRRRRIRRRIRIRRIRRIRIRRRIRIRRIRRIRRRRRRRRRRRR	0.8	0.2	1.45379	62.19584	0.19460	0.99
3	RRRRRIRIRRIRRRIRIRRIRRIRIRRRIRIRRIRRIRRIRRIRIRRRRR	0.7	0.3	2.12193	47.23371	0.29190	0.96077
4	RRIRRIRIRRIRRRIRIRRIRRIRIRRRIRIRRIRRIRRIRRIRIRRIRR	0.66	0.34	2.35304	41.26164	0.33082	0.90680
5	RRRRIIIRRIIIRIRIIRIRIRIRIRIRIIRIRIRIRIRIRIRIIIRRRR	0.5	0.5	3.51335	24.39638	0.48650	0.73292
6	RIRRIIIRRIIIRIRIIRIRIRIRIRIRIIRIRIRIRIRIRIRIIIRRII	0.44	0.56	3.81297	18.01707	0.54488	0.67304
7	RRRRIIIIRRIIIRIRIIIIRIIRIIIIRIRIIIRIRIIIIRRRR	0.4	0.6	4.23002	15.99013	0.58380	0.64040
8	IIRIIRIRIIRIIIRIRIIRIRIIIRIRIIRIIRIIRIRIIRII	0.34	0.66	4.45642	10.55528	0.64218	0.59060
9	RRRIIIRIIIIRRIIIIIRIRIIIIIRIIIIIRIIIIIRIIIRIRR	0.3	0.7	4.90794	9.04070	0.68110	0.56030
10	IIIIIIIRIIIRIRIRIIIIIRIRIIIIIRIIIRIIIRIIIIIIIRIIII	0.2	0.8	5.39020	3.27975	0.77840	0.49726
11	RIIIIIRIIIIIIRIIIRIIIIIIRIIIIIIIIRIIIIIIRIIIIIIR	0.16	0.84	5.78468	2.44858	0.81732	0.47443
12	RIIIIIRIIIIIIRIIIIIIIIIIRIIIIIIIIIRIIIIIIRIIIIIIR	0.14	0.86	5.93060	1.91330	0.83678	0.46429
13	IIIIIIRIIIIIIRIIIIIIIIIIRIIIIIIIIIRIIIIIIRIIIIIIR	0.12	0.88	6.01776	1.30953	0.85624	0.45614
14	IRIIIIRIIRRIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	0.1	0.9	6.15177	0.41218	0.87570	0.44383
15	RIIIIIIIIIIIRIIIIIIIIIIIIIIIIIIRIIIIIIIIIIIIR	0.08	0.92	6.34729	0.61784	0.89516	0.43708
16	IIIIIIIIIIIIRIIIIIIIIIIIIIIIIIIRIIIIIIIIIIIIR	0.06	0.94	6.43445	0.28911	0.91462	0.43096
17	RIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIR	0.04	0.96	6.63512	0.14000	0.93408	0.42137
18	IIIIIIIIIIIIIIIIIIIIRIIIIIIIIIIIIIIIIIIIIII	0.02	0.98	6.66171	0.00000	0.95354	0.41921
19	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	0	1.0	6.80945	0.00000	0.97300	0.41296

Table S2. The 3 sequences with different distributions of charged and hydrophobic residues at *H*=0.9 analyzed in this research, other description parameters are the same as Table S1

No	Sequence	*NCPR*	*H*	*SHD*	*SCD*	λ	ν
S1	IIIIIIIIRIIIIIIIIRIIIIIIIIRIIIIIIIIRIIIIIIIIR	0.1	0.9	6.15032	0.86689	0.87570	0.44726
S2	RRRRRIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	0.1	0.9	6.25281	0.27413	0.87570	0.43853
S3	IIIIIIIIIIIIIIIIIIIIRRRRRIIIIIIIIIIIIIIIIIII	0.1	0.9	6.07107	0.27413	0.87570	0.44622

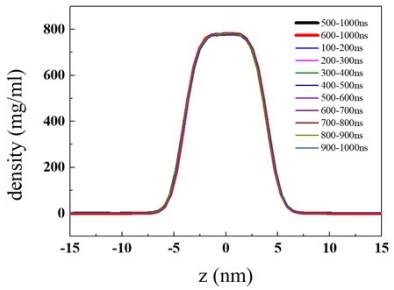

Figure SI 1. Convergence test：Here, the distribution curve of the density of high-density phase along the z-axis is given for the random polypeptide with H=0.96 and the temperature of T=400K.

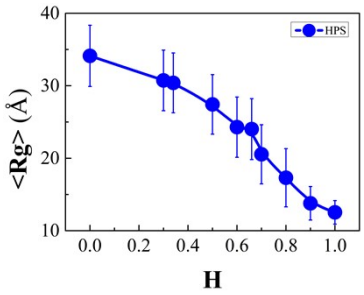

Figure SI 2. The total gyration radius Rg vs. the mean hydrophobicity for HPS model, the error bar represents the conformational fluctuation of the same trajectory after equilibrium.

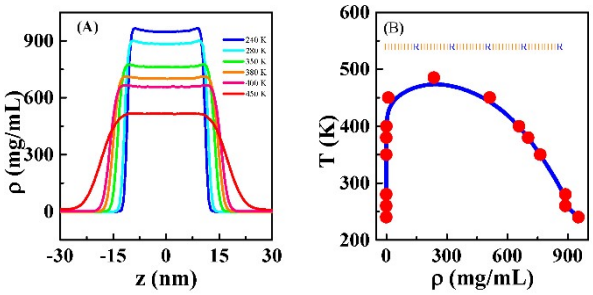

Figure SI 3. Phase separation of disordered random polypeptides S1 system: (A) density distribution curve along the z-axis at different temperatures; (B) Phase diagram of S1 obtained from the density profile (temperature, and density curve);

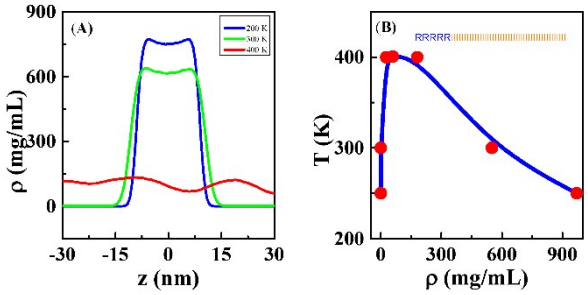

Figure SI 4. Phase separation of disordered random polypeptides S2 system: (A) density distribution

curve along the z-axis at different temperatures; (B) Phase diagram of S2 obtained from the density profile (temperature, and density curve).

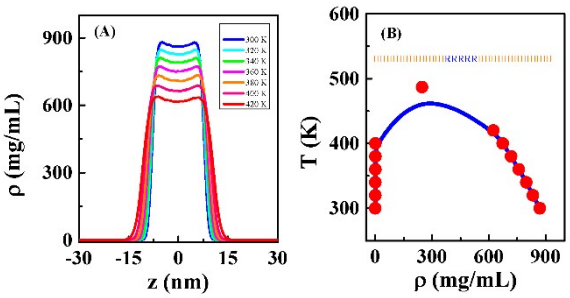

Figure SI 5. Phase separation of disordered random polypeptides S3 system: (A) density distribution curve along the z-axis at different temperatures; (B) Phase diagram of S3 obtained from the density profile (temperature, and density curve).

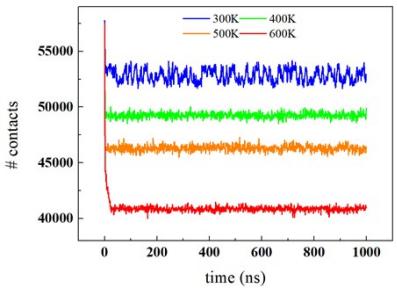

Figure SI 6. Evolution of the total contacts with simulation time at different temperatures for 200 chains I_{50} peptides.

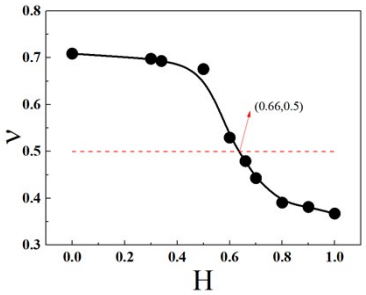

Figure SI 7. At 298 K, scaling exponent ν fitting from all-atom REMC simulation

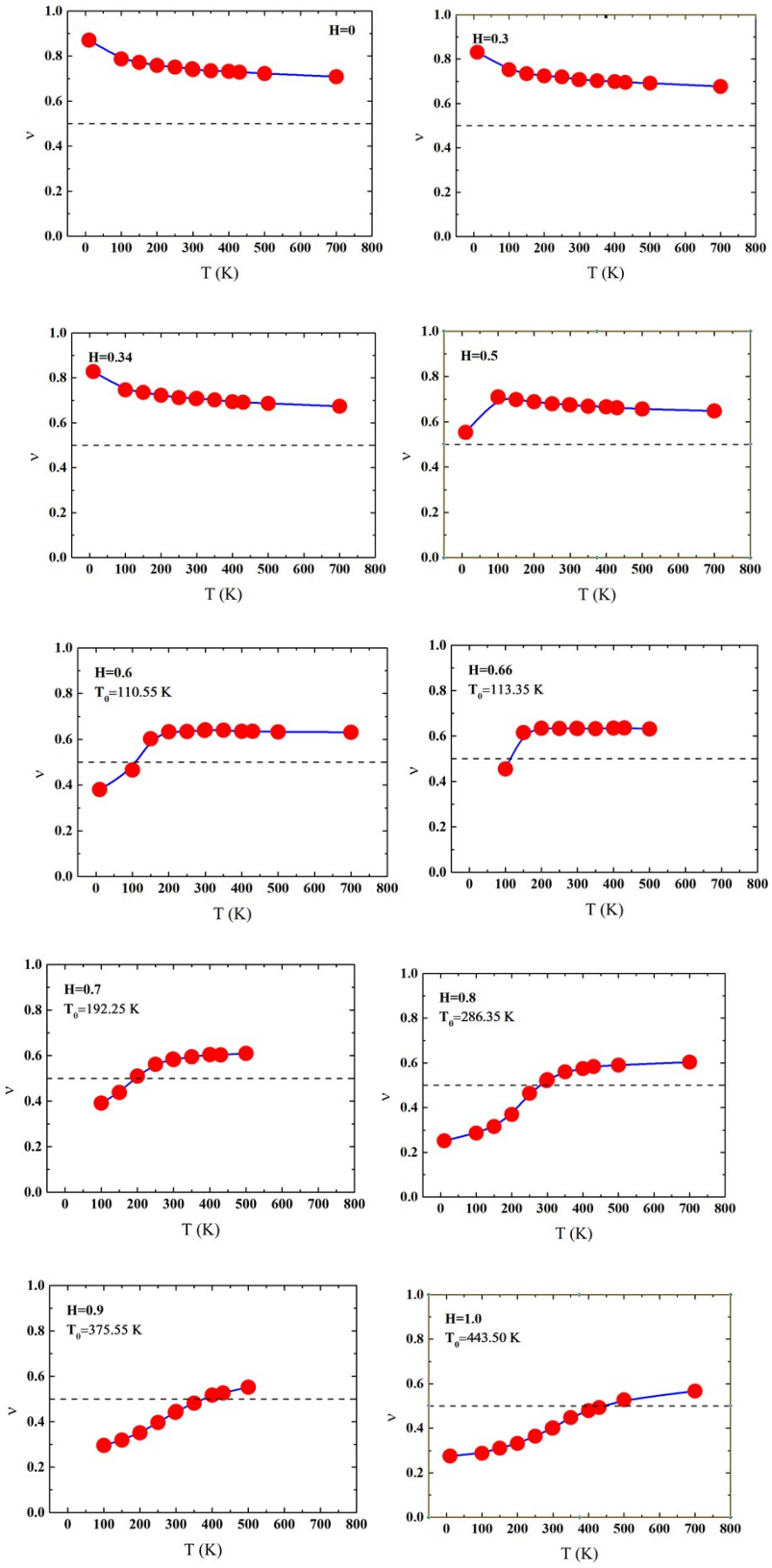

Figure SI 8. The relationship between the scaling exponent ν and temperature T obtained by the simulation of random peptide coarsening is given, where T_θ indicates the transition temperature from compact to extend of the system.