Supporting Information for:

Quality of Force Fields and Sampling Methods in Simulating pepX Peptides: A Case Study for Intrinsically Disordered Proteins

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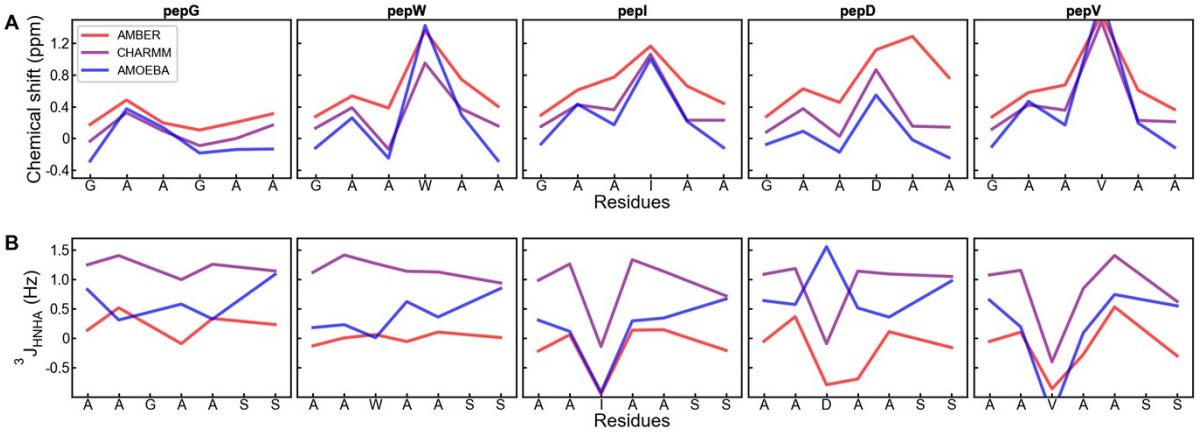

Figure S1. Residue-level differences of Cα chemical shifts (A) and $^3J_{HNHA}$ couplings (B) between simulated and experimentally measured values. The first to fifth columns represent the structural measures of pepG, pepW, pepI, pepD, and pepV, respectively.

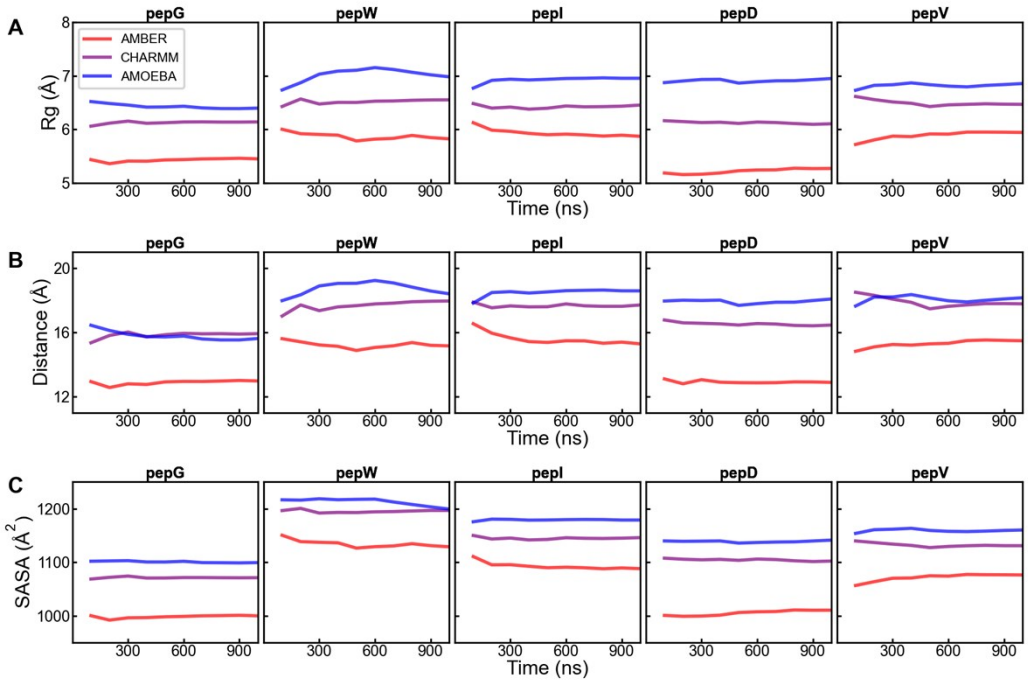

Figure S2. Reweighted running average for *R*g (A), end-to-end distance (B), and SASA (C) during the IaMD simulations. The running averages were calculated and reweighted with an interval of 100 ns.

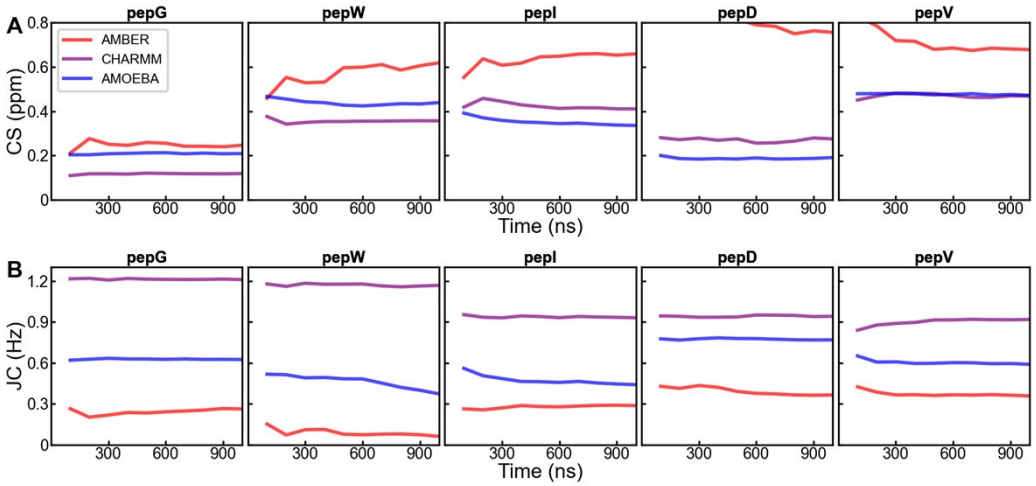

Figure S3. Reweighted running AUE for Cα chemical shifts (A) and $^3J_{HNHA}$ couplings (B) during the IaMD simulations. The running AUEs were calculated and reweighted with an interval of 100 ns.

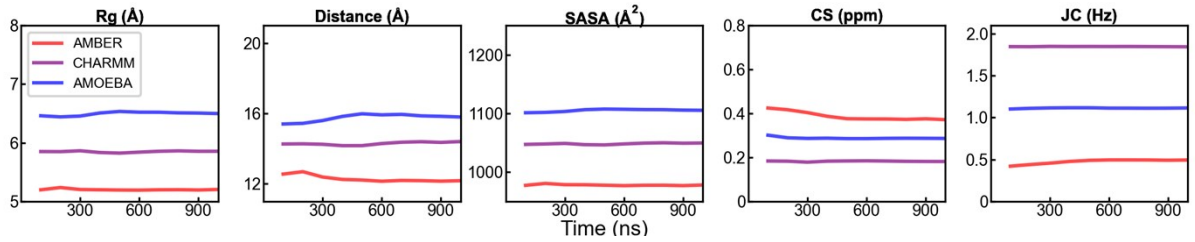

Figure S4. From left to right, the reweighted running average for *R*g, end-to-end distance, SASA, reweighted running AUE for Cα chemical shifts, and $^3J_{HNHA}$ couplings during the aMD simulations of peptide pepG. The running averages or AUEs were calculated and reweighted with an interval of 100 ns.

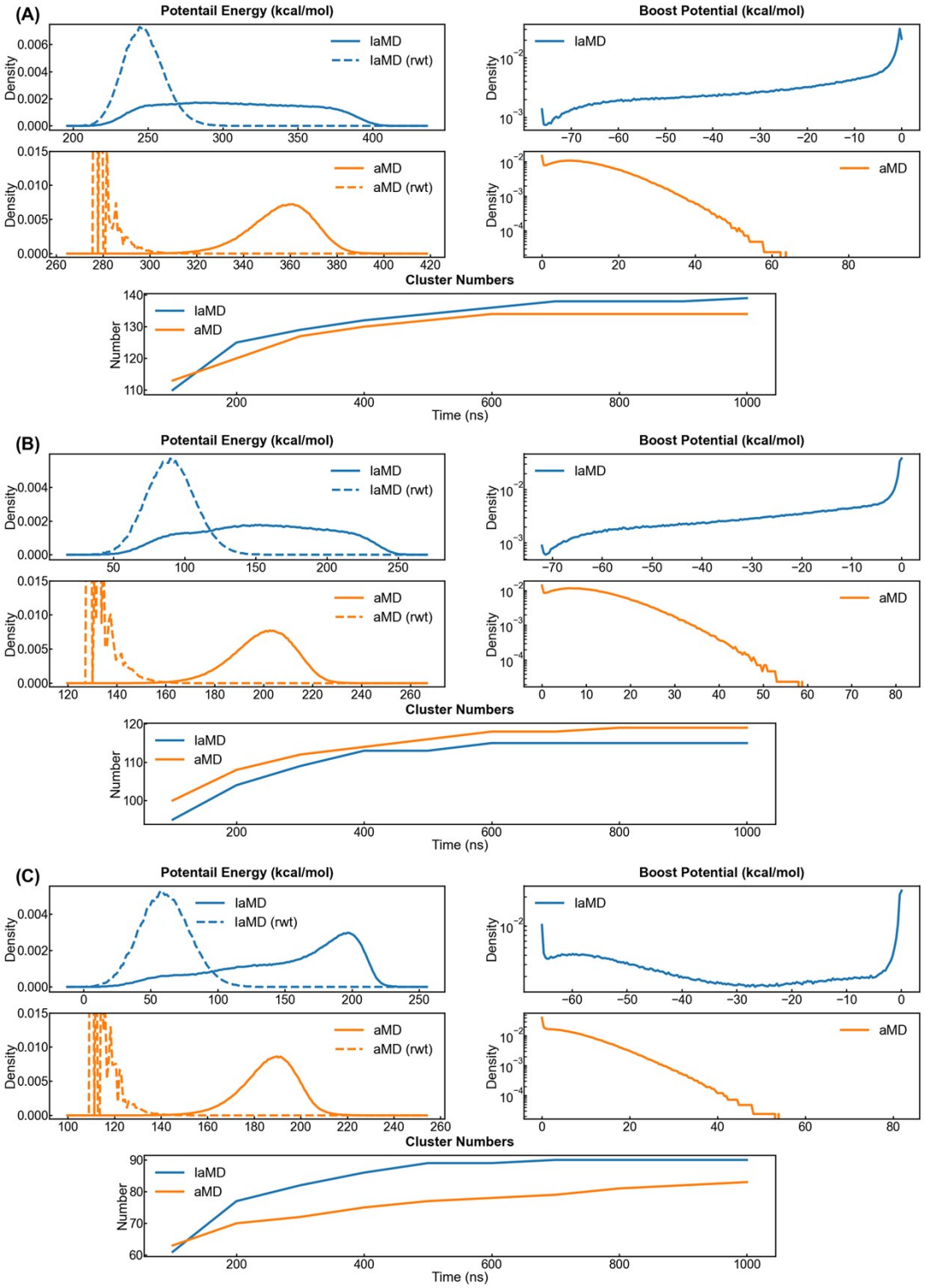

Figure S5. Distributions of torsional potential energies and boost potentials, and numbers of conformation clusters explored as a function of time for AMBER (A), CHARMM (B), and AMOEBA (C) simulations of pepG. For the distribution of torsional potential energies, the original and reweighted energies are shown in solid and dashed lines.

Table S1. Comparison of ensemble-averaged structural measures for AMBER99SB and AMBER14SB IaMD simulations.

peptide	force field	Rg (Å)	distance (Å)	SASA (Å²)	no. of H-bonds			secondary structure (%)			
					P−P	P−W	P−W/P−P	helix	β-sheet	turn	coil
pepG	99SB	5.45	12.98	999.92	1.75	28.18	16.12	5.04	1.82	13.96	79.18
	14SB	5.30	12.73	981.19	2.04	27.31	13.38	9.43	1.66	15.21	73.71
pepW	99SB	5.82	15.16	1128.89	1.75	28.71	16.38	9.78	0.38	12.50	77.35
	14SB	5.31	14.56	1079.06	2.68	26.59	9.94	28.27	0.14	10.92	60.67
pepI	99SB	5.87	15.29	1088.02	1.59	28.53	18.00	8.02	0.42	10.92	80.64
	14SB	5.41	14.78	1033.72	2.49	26.55	10.66	24.21	0.19	11.08	64.52
pepD	99SB	5.27	12.89	1010.50	2.84	31.78	11.20	16.49	0.52	14.60	68.38
	14SB	5.02	13.64	974.95	3.50	29.85	8.54	36.54	0.16	12.8	50.51
pepV	99SB	5.94	15.48	1076.27	1.52	28.72	18.94	6.49	0.36	10.57	82.58
	14SB	5.59	14.96	1037.20	2.15	27.17	12.64	17.1	0.35	10.71	71.84