



Research article

Globular bundles and entangled network of proteins (CorA) by a coarse-grained Monte Carlo simulation

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Supplementary material

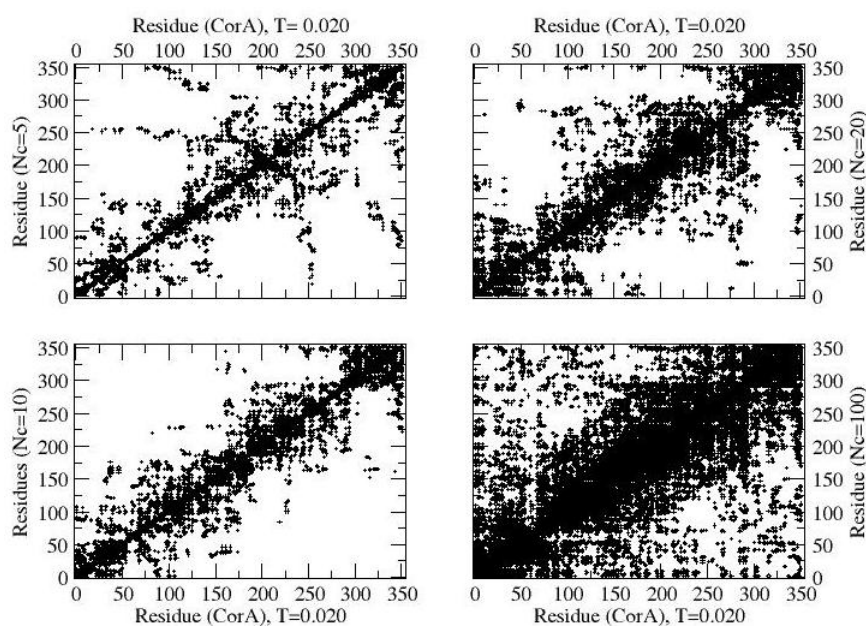


Figure S1. Contact map of residues around each of CorA ($^1\text{M} \ ^2\text{E} \dots \ ^{351}\text{L}$) residues in a simulation box with the number of protein chains $N_c = 5, 10, 20,$ and 100 at a low temperature ($T = 0.020$).

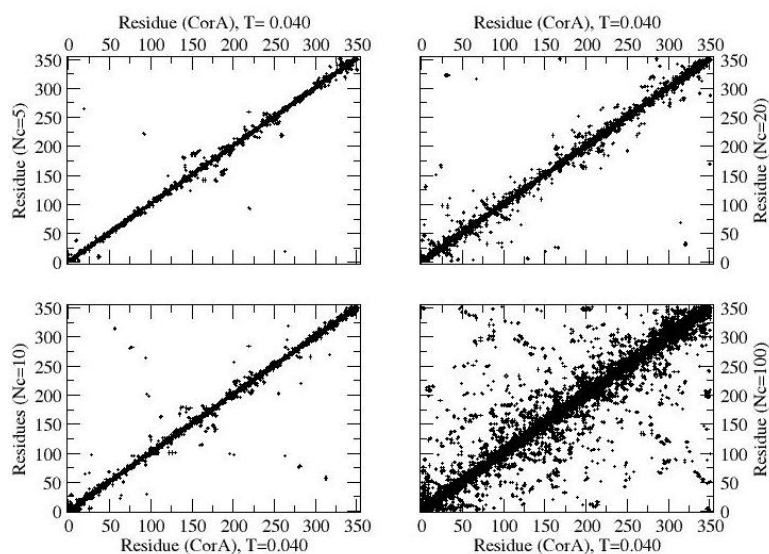


Figure S2. Contact map of residues around each of CorA ($^1\text{M} \ ^2\text{E} \dots \ ^{351}\text{L}$) residues in a simulation box with the number of protein chains $N_c = 5, 10, 20,$ and 100 at a high temperature ($T = 0.040$).

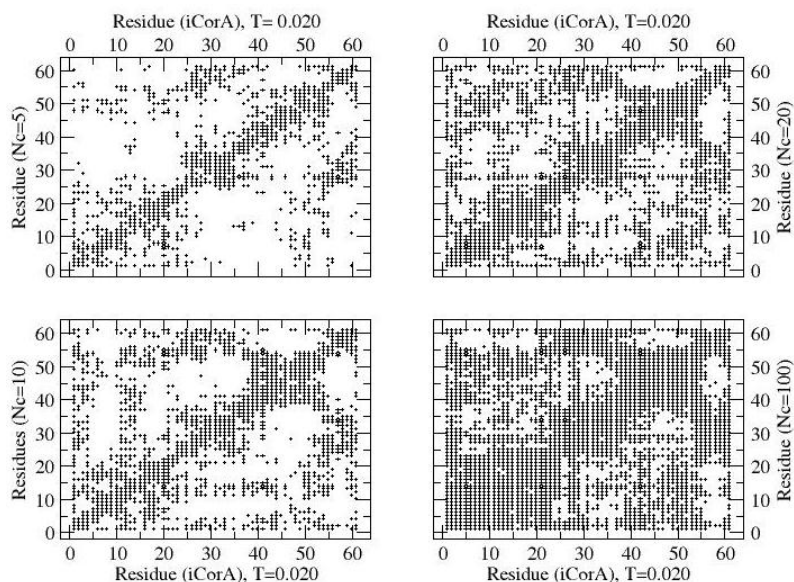


Figure S3. Contact map of residues around each of iCorA residues ($^1\text{M} \ ^2\text{V} \dots \ ^{61}\text{L}$, corresponding sequence in CorA $^{291}\text{M} \ ^{293}\text{V} \dots \ ^{351}\text{L}$) in a simulation box with the number of protein chains $N_c = 5, 10, 20,$ and 100 at a low temperature ($T = 0.020$).

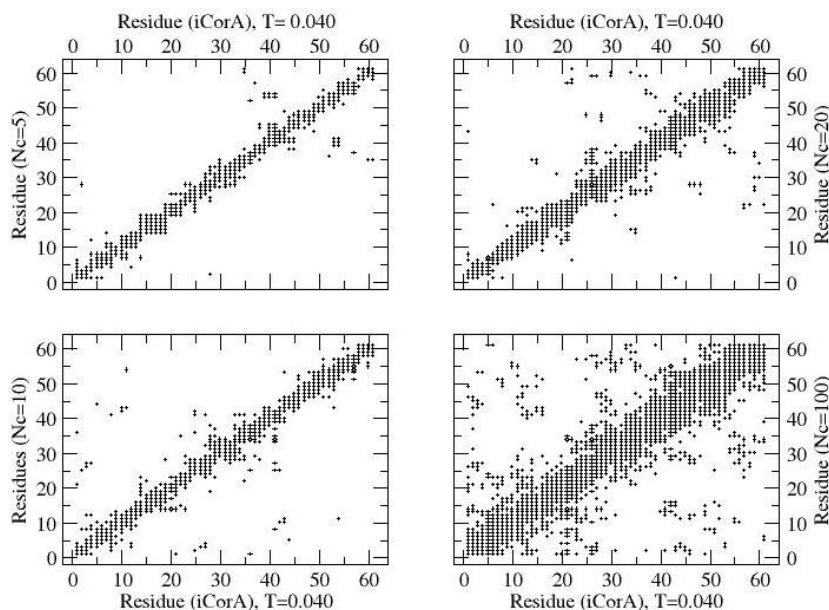


Figure S4. Contact map of residues around each of iCorA residues ($^1\text{M} \text{ } ^2\text{V} \dots \text{ } ^{61}\text{L}$, corresponding sequence in CorA $^{291}\text{M} \text{ } ^{293}\text{V} \dots \text{ } ^{351}\text{L}$) in a simulation box with the number of protein chains $N_c = 5, 10, 20,$ and 100 at a high temperature ($T = 0.040$).

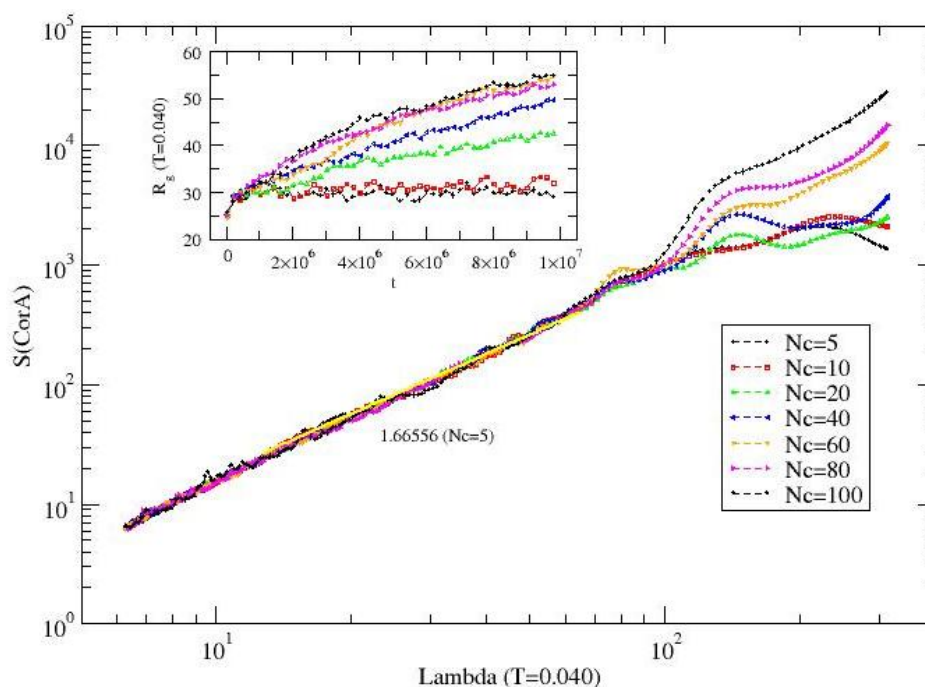


Figure S5. Structure factor $S(q)$ versus the wave length (Lambda λ) at temperature $T = 0.040$ with a wide range of the number N_c (5–100) of CorA proteins in simulation box. The inset shows the variation of the radius of gyration of proteins with the number N_c (5–100) of CorA proteins in simulation box.



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