Secondary Structure Bias in Generalized Born Solvent Models Roe, Okur, Wickstrom, Hornak and Simmerling



Figure S1. Local conformational propensities for each residue of Ala10 from unrestrained REMD simulations using various solvent models at 300.0 K. Residues 1 and 12 are the acetyl and amide N- and C-caps respectively. GB2 refers to GBOBC simulations with alternative α , β , and γ parameters (see Methods for details).



Figure S2. Average difference (over all structures used in analysis shown in Tables 4-6) of effective radii for the Alpha conformation calculated with either GBHCT, GBOBC, or GBNeck from perfect radii calculated with PE for several atom types (H=Amide Hydrogen, CA=Alpha Carbon, HA=Alpha Hydrogen, O=Carboxyl Oxygen, N=Amide Nitrogen, CB=Beta Carbon, C=Carboxyl Carbon) across all residues of Ala10. Residues 0 and 11 correspond to N-acetyl and C-amide capping groups respectively. Error bars are ± 1 standard deviation.



Figure S3. Average difference (over all structures used in analysis shown in Tables 4-6) of effective radii for the Hairpin conformation calculated with either GBHCT, GBOBC, or GBNeck from perfect radii calculated with PE for several atom types (H=Amide Hydrogen, CA=Alpha Carbon, HA=Alpha Hydrogen, O=Carboxyl Oxygen, N=Amide Nitrogen, CB=Beta Carbon, C=Carboxyl Carbon) across all residues of Ala10. Residues 0 and 11 correspond to N-acetyl and C-amide capping groups respectively. Error bars are ± 1 standard deviation.



Figure S4. Average difference (over all structures used in analysis shown in Tables 4-6) of effective radii for the Left conformation calculated with either GBHCT, GBOBC, or GBNeck from perfect radii calculated with PE for several atom types (H=Amide Hydrogen, CA=Alpha Carbon, HA=Alpha Hydrogen, O=Carboxyl Oxygen, N=Amide Nitrogen, CB=Beta Carbon, C=Carboxyl Carbon) across all residues of Ala10. Residues 0 and 11 correspond to N-acetyl and C-amide capping groups respectively. Error bars are ± 1 standard deviation.



Figure S5. Average difference (over all structures used in analysis shown in Tables 4-6) of effective radii for the PP2 conformation calculated with either GBHCT, GBOBC, or GBNeck from perfect radii calculated with PE for several atom types (H=Amide Hydrogen, CA=Alpha Carbon, HA=Alpha Hydrogen, O=Carboxyl Oxygen, N=Amide Nitrogen, CB=Beta Carbon, C=Carboxyl Carbon) across all residues of Ala10. Residues 0 and 11 correspond to N-acetyl and C-amide capping groups respectively. Error bars are \pm 1 standard deviation.



Figure S6. Average difference (over all structures used in analysis shown in Tables 4-6) of Self solvation energy for the Alpha conformation calculated with either GBHCT, GBOBC, or GBNeck from Self solvation energy calculated with PE for several atom types (H=Amide Hydrogen, CA=Alpha Carbon, HA=Alpha Hydrogen, O=Carboxyl Oxygen, N=Amide Nitrogen, CB=Beta Carbon, C=Carboxyl Carbon) across all residues of Ala10. Residues 0 and 11 correspond to N-acetyl and C-amide capping groups respectively. Error bars are ± 1 standard deviation.



Figure S7. Average difference (over all structures used in analysis shown in Tables 4-6) of Self solvation energy for the Hairpin conformation calculated with either GBHCT, GBOBC, or GBNeck from Self solvation energy calculated with PE for several atom types (H=Amide Hydrogen, CA=Alpha Carbon, HA=Alpha Hydrogen, O=Carboxyl Oxygen, N=Amide Nitrogen, CB=Beta Carbon, C=Carboxyl Carbon) across all residues of Ala10. Residues 0 and 11 correspond to N-acetyl and C-amide capping groups respectively. Error bars are ± 1 standard deviation.



Figure S8. Average difference (over all structures used in analysis shown in Tables 4-6) of Self solvation energy for the Left conformation calculated with either GBHCT, GBOBC, or GBNeck from Self solvation energy calculated with PE for several atom types (H=Amide Hydrogen, CA=Alpha Carbon, HA=Alpha Hydrogen, O=Carboxyl Oxygen, N=Amide Nitrogen, CB=Beta Carbon, C=Carboxyl Carbon) across all residues of Ala10. Residues 0 and 11 correspond to N-acetyl and C-amide capping groups respectively. Error bars are ± 1 standard deviation.



Figure S9. Average difference (over all structures used in analysis shown in Tables 4-6) of Self solvation energy for the PP2 conformation calculated with either GBHCT, GBOBC, or GBNeck from Self solvation energy calculated with PE for several atom types (H=Amide Hydrogen, CA=Alpha Carbon, HA=Alpha Hydrogen, O=Carboxyl Oxygen, N=Amide Nitrogen, CB=Beta Carbon, C=Carboxyl Carbon) across all residues of Ala10. Residues 0 and 11 correspond to N-acetyl and C-amide capping groups respectively. Error bars are ± 1 standard deviation.