

# Correction to Unfolding the Conformational Behavior of Peptide Dendrimers: Insights from Molecular Dynamics Simulations

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**P**age 5047. Table 3: The entries presented in Table 3 are incorrect due to a systematic exclusion of some data points

**Table 3. Average Radius of Gyration of the Dendrimers**

dendrimer	average $R_g$ (nm)
B1	1.439
B1H	1.445
B1HH	1.432
B1HHH	1.418
C1	1.060

in the average radius of gyration calculations. A corrected table is shown. The conclusions of the original article are in no way affected by this correction.