THE JOURNAL OF PHYSICAL CHEMISTRY B

Addition/Correction

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Correction to "On the Foldability of Tryptophan-Containing Tetra- and Pentapeptides: An Exhaustive Molecular Dynamics Study"

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J. Phys. Chem. B **2013**, *117* (18), 5522−5532. DOI: 10.1021/jp401239v

Supporting Information

The Ramachandran plots of the originally deposited Figure S8 of the Supporting Information file had inadvertently been inverted along their corresponding psi axes. The new version of the Supporting Information file corrects this problem.

■ ASSOCIATED CONTENT

Supporting Information

An example of an rmsd matrix, the evolution of interatomic distances and snapshot structures of a representative tetrapeptide, a graphical representation of the TF2 function, the rmsd matrices of 130 tetrapeptides (second pass in Table 1) calculated from 30 ns trajectories, the rmsd matrices of 36 tetrapeptides (third pass in Table 1) calculated from 100 ns trajectories, the inter-rmsd matrices for 16 pentapeptides and four different force fields (complementary to Figure 3), the rmsd matrices for eight pentapeptides (fourth pass in Table 1) and the AMBER99SB-ildn force field, and results from the simulations of the RWPD tetrapeptide using four temperatures and three force fields. This material is available free of charge via the Internet at http://pubs.acs.org.

Published: June 17, 2013