 Cite this: *Phys. Chem. Chem. Phys.*, 2017, **19**, 18102

DOI: 10.1039/c7cp90146a

rsc.li/pccp

Correction: A critical comparison of coarse-grained structure-based approaches and atomic models of protein folding

 Jie Hu, ^a Tao Chen, ^b Moye Wang, ^a Hue Sun Chan ^{*cd} and Zhuqing Zhang ^{*ac}

 Correction for 'A critical comparison of coarse-grained structure-based approaches and atomic models of protein folding' by Jie Hu et al., *Phys. Chem. Chem. Phys.*, 2017, **19**, 13629–13639.

It has come to our attention that there is a typographical error in the legend of Fig. 2: “The black solid curve and the shaded band represent $R_g = R_0 \times N^\nu$ with $R_0 = 1.330$ and $\nu = 0.598 \pm 0.028$ obtained from fitting experimental data on an extensive set of proteins (ref. 38)” should read “The black solid curve and the shaded band represent $R_g = R_0 \times N^\nu$ with $R_0 = 0.1927$ and $\nu = 0.598 \pm 0.028$ obtained from fitting experimental data on an extensive set of proteins (ref. 38)”. The value $R_0 = 0.1927$ nm was what we actually used to produce Fig. 2. This value follows the Correction to ref. 38 published in *Proc. Natl. Acad. Sci. U. S. A.*, 2005, **102**, 14475, which states that “the prefactor R_0 is $1.927 \text{ \AA}$ ”. This typographical error has no effect on the results presented in our paper.

The Royal Society of Chemistry apologises for these errors and any consequent inconvenience to authors and readers.

^a College of Life Sciences, University of Chinese Academy of Sciences, Beijing, 100049, China. E-mail: zhuqingzhang@ucas.ac.cn

^b College of Chemistry and Materials Science, Northwest University, Xi'an, 710127, China

^c Department of Biochemistry, University of Toronto, Toronto, Ontario, M5S 1A8, Canada. E-mail: chan@arrhenius.med.toronto.edu

^d Department of Molecular Genetics, University of Toronto, Toronto, Ontario, M5S 1A8, Canada