Corrections:

Robert B. Best, Nicolae-Viorel Buchete, and Gerhard Hummer. 2008. Are Current Molecular Dynamics Force Fields too Helical? *Biophys. J.* 95:L07–L09.

Due to an incorrect implementation of the force field Amber99SB in our simulations, and incorrect simulation parameters for the force field Amber03, the results reported for these two force fields were incorrect. In Table 1, the lines for Amber03 and Amber99SB need to be changed to:

		Unweighted					Reweighted								
		χ^2			Populations		DFT1			DFT2			Orig		
FORCE FIELD	Time (ns)	DFT1	DFT2	ORIG	% α	% β	χ^2	% α	% β	χ^2	% α	% β	χ^2	% α	% β
Amber03*	200	1.9	1.3	1.2	29.3	28.5	1.5	9.7	*40.5*	0.9	9.9	*27.8*	0.4	8.8	6.3
Amber99SB*	200	1.4	1.7	1.8	15.7	37.8	1.2	7.0	36.7	0.8	6.0	18.4	0.4	3.9	3.8

Details of the corrected simulation results are provided in Tables S5 and S6 in updated Supplementary Material, Data S1. Although these corrections do not affect the main conclusions of the paper, they substantially improve the agreement with experiment, particularly for the force field Amber99SB. With the corrections, Amber99SB is within the group of force fields with $\chi^2 \leq 2.25$ before reweighting. As a clarification, the SPC water model was used in the simulations utilizing the GROMOS and OPLS force fields.

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The title of the article published in the October 2008 issue of the Biophysical Journal, 95(7):3306–3321, should read: ''Interaction of Gramicidin S and its Aromatic Amino-Acid Analogs with Phospholipid Membranes'' instead of ''Interaction of Gramicidin S and its Aromatic Amino-Acid Analog with Phospholipid Membranes''.

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