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CORRECTION

Correction: α-proton Chemical Shift Index and Amide Proton Chemical Shift Temperature Coefficient of Melittin in Methanol: Indicators for a Helix Structure and an Intra-Molecular Hydrogen Bond?

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In the original version of this article, one major error appears in the figure and two minor errors appear in the figure and the table.

Corrected figure: Fig. 4.
Corrected figure: Fig. 5.
Corrected table: Table 4.
These have been corrected by publishing this erratum.

The original article can be found online at https://doi.org/10.1007/s10930-022-10075-4.

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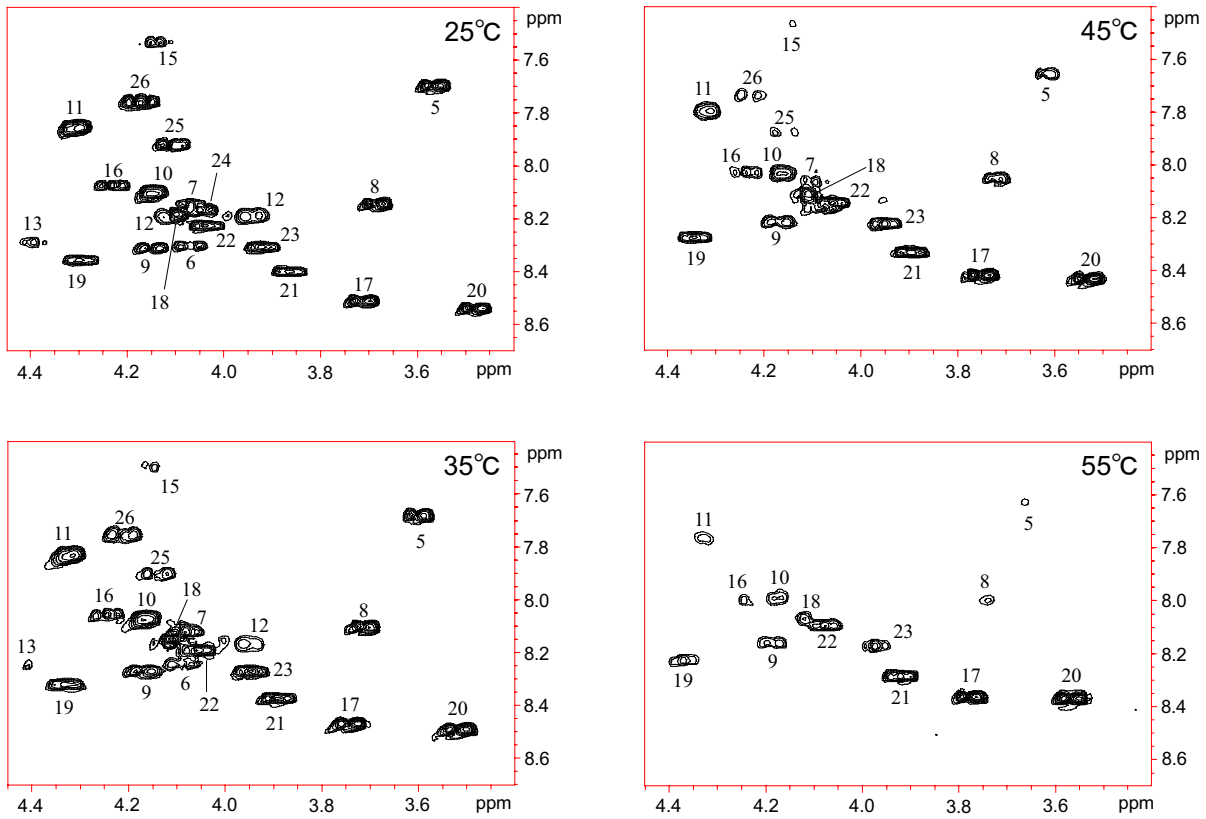

Fig. 4 The NH and αH region of the COSY spectra for melittin in CD_3OH at 25 °C, 35 °C, 45 °C and 55 °C. Intra-residue cross peaks between an NH and an αH are marked with the residue number of the corresponding amino acid

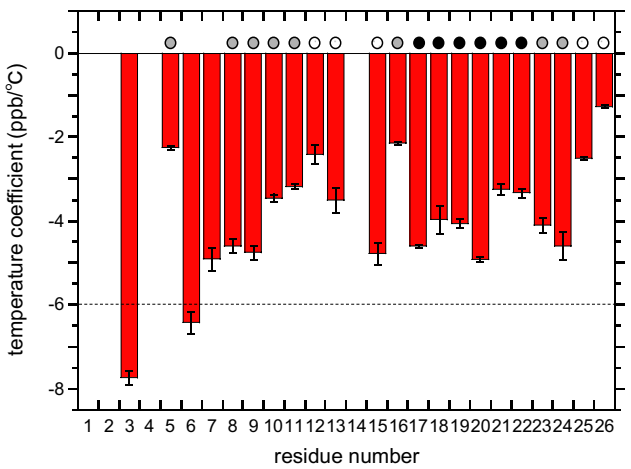

Fig. 5 The Δδ/ΔT's for melittin in CD_3OH versus the amino acid sequence. The broken line represents the Δδ/ΔT of − 6 ppb/°C. The error bars represent the combined standard uncertainty calculated from the standard error of the linear regression and the propagation of error. The Δδ/ΔT's for Gly1 and Ile2 are unclear because these NH resonance lines are not observed due to a fast exchange with solvent molecules, and that for Ala4 is unclear due to few experimental data points. The circles denote the relative stability of intra-molecular hydrogen bonds proposed in the published paper (open circle: low stability, gray circle: intermediate stability, closed circle: high stability) [13]

Table 4 NH chemical shift temperature coefficients (ppb/℃) for alamethicin-A6 and -U6 in methanol

residue	Δδ/ΔT	residue	Δδ/ΔT
Aib 1 A	unclear	Gly 11 A	− 3.96 (0.03)
Aib 1 U	unclear	Gly 11 U	− 4.66 (0.02)
Pro 2 A	–	Leu 12 A	− 3.23 (0.03)
Pro 2 U	–	Leu 12 U	− 3.11 (0.03)
Aib 3 A	unclear	Aib 13 A	− 4.62 (0.03)
Aib 3 U	unclear	Aib 13 U	− 4.83 (0.02)
Ala 4 A	+ 1.10 (0.03)	Pro 14 A	–
Ala 4 U	+ 1.13 (0.04)	Pro 14 U	–
Aib 5 A	unclear	Val 15 A	unclear
Aib 5 U	unclear	Val 15 U	− 0.37 (0.03)
Ala 6 A	− 3.53 (0.11)	Aib 16 A	unclear
Aib 6 U	− 3.67 (0.02)	Aib 16 U	unclear
Gln 7 A	− 2.30 (0.03)	Aib 17 A	unclear
Gln 7 U	− 0.50 (0.03)	Aib 17 U	unclear
Aib 8 A	− 4.87 (0.04)	Gln 18 A	unclear
Aib 8 U	− 3.60 (0.06)	Gln 18 U	unclear
Val 9 A	− 3.33 (0.11)	Gln 19 A	unclear
Val 9 U	− 2.45 (0.03)	Gln 19 U	unclear
Aib 10 A	− 4.55 (0.03)	Phol 20 A	− 2.60 (0.05)
Aib 10 U	− 3.98 (0.03)	Phol 20 U	unclear