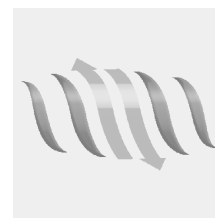


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HIGHLIGHT

Multidimensional HRMAS NMR: a platform for *in vivo* studies using intact bacterial cells

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On-bead screening of a library to detect host–guest complexation by an aniline reporter

Miwa Kubo, Ryosuke Nishimoto, Masanori Doi, Mitsuaki Kodama and Hideaki Hioki

Chem. Commun., 2006 (DOI: 10.1039/b604723h)

There are errors in the calculated concentrations of guest peptides **16a–16c**. The actual concentrations are ten times higher than those reported in the paper. The text should be revised as follows:

The final sentence of paragraph 4 should read: ‘The detection limit for **16a** was less than 130 $\mu\text{mol L}^{-1}$ (Fig. 4).’

The final sentence of the caption to Fig. 4 should read: ‘Guest concentration: (A) 13 mmol L^{-1} , (B) 1.3 mmol L^{-1} , (C) 130 $\mu\text{mol L}^{-1}$.’

In the caption to Fig. 6, the concentration of **16a** should be revised to 130 $\mu\text{mol L}^{-1}$.

In the caption to Fig. 7, second sentence, 13 $\mu\text{mol L}^{-1}$ should be revised to 130 $\mu\text{mol L}^{-1}$.

The final sentence in paragraph 6 should read: ‘These observations indicated that the present method can be applied to detect high-affinity binding of peptide complexation with host molecules (Fig. 7).’

In the electronic supplementary information, the concentration of **16a** has been revised to ‘130 $\mu\text{mol L}^{-1}$ in the phosphate buffer’.

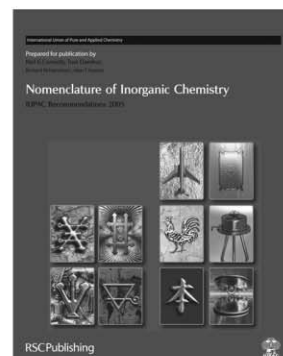
The Royal Society of Chemistry apologises for these errors and any consequent inconvenience to authors and readers.
Additions and corrections can be viewed online by accessing the original article to which they apply.

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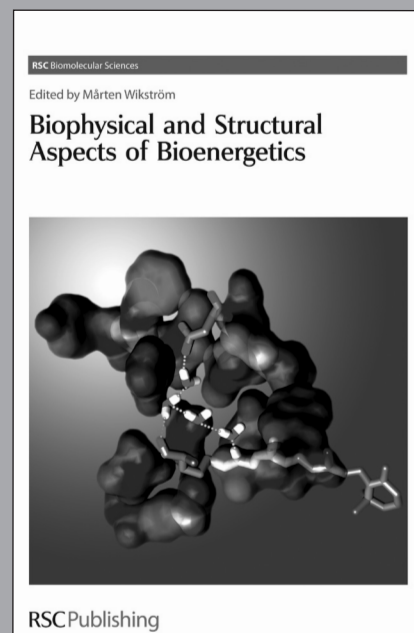
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