

# CORRIGENDUM

In the communication by **V. Thuillier, M. Famulok, and co-workers** (*Angew. Chem. Int. Ed.* **2000**, 39, 4369–4373), a correction is necessary in Figure 3: The authors noticed that clone D16-05 contains an additional C residue in position 42 between G41 and G43 (5'-end of the sequence region shown in orange). This mutation slightly alters the computer-generated secondary structure of the point mutant D16-05 to the folding shown in Figure 3 b. The RNA decoys incubated with D16-05 (Figure 3 a, lanes 7, 8, 10, and 11) did not contain C42 because they were transcribed from a template DNA that was obtained by means of PCR with a 5' primer that lacks C42. The authors therefore repeated the analysis represented in Figure 3 with the correct primers. The analysis revealed that constructs 10 and 11 in Figure 3 a can effectively restore the cleavage activity. As a consequence, the previous statement that helix I (red) plays an important structural role in doxycycline binding is still valid but it now appears that the effect of helix I can be exerted in a sequence-independent manner. All other conclusions of this communication remain unaffected..

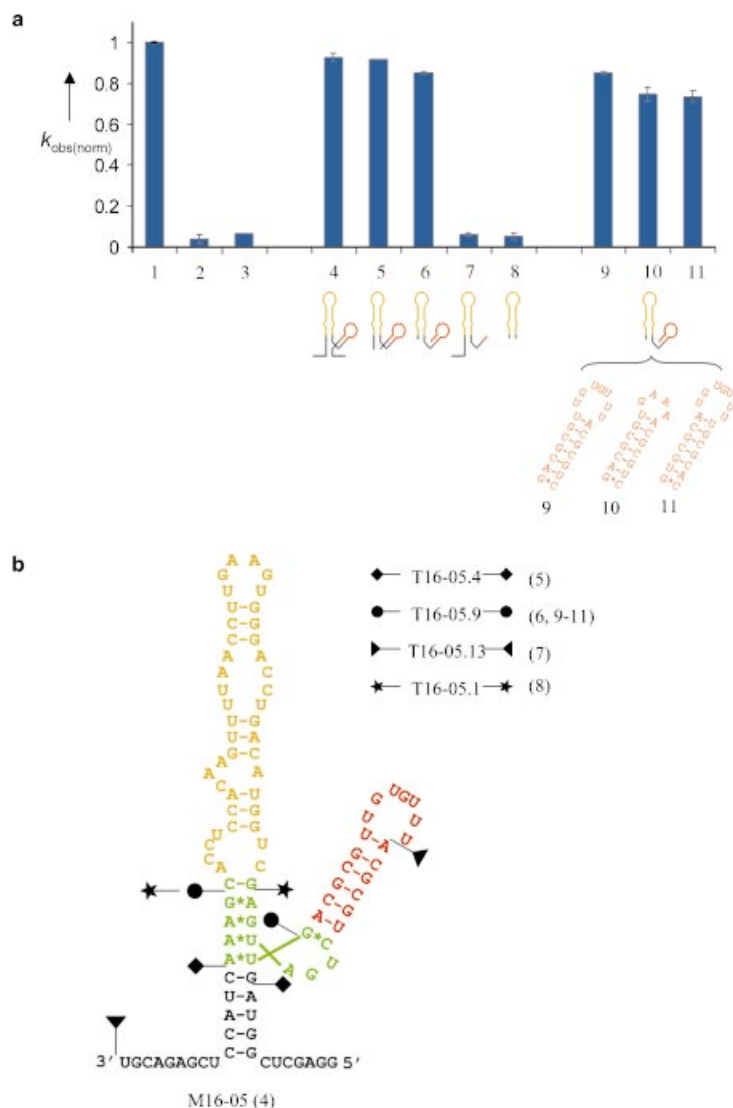


Figure 3. Determination of the minimal sequence of clone D16-05. a) Relative activity  $k_{\text{obs(norm)}}$  of the cleavage reaction under various conditions (always in the presence of 1  $\mu\text{M}$  tRNA as an unspecific competitor). 1: Cleavage activity of D16-05 (1 nM). 2: Same in the presence of 200 nM **1**. 3: Same as in 2 in the presence of 2.0  $\mu\text{M}$  unselected pool as an unspecific competitor. 4–8: Same as in 2 in the presence of 2.0  $\mu\text{M}$  cleavage inactive point mutant M16-05 (4), construct T16-05.4 (5), construct T16-05.9 (6), construct T16-05.13 (7), construct T16-05.1 (8). 9–11: Same as in 2 in the presence of 2.0  $\mu\text{M}$  T16-05.9 with the depicted variations in helix I. b) Computer-generated secondary structure of the point mutant D16-05. The various marker symbols flank the sequences of the truncated versions tested. To enable T7-transcription two guanosine residues, which are not shown here, were inserted into the 5'-position of the truncated constructs. Orange: The original randomized region; red: constant region from the HHR (helix I); green: catalytic core. The guanosine residue shaded in black shows the point-mutation C-G. The numbers in parentheses refer to the numbering in (a).

In the communication by **D. Zhao and co-workers** in Issue 11, 2001, pp. 2166–2168, two relevant references were not cited, for which the authors apologize: a) A. K. Cheetham, G. Férey, T. Loiseau, *Angew. Chem.* **1999**, 111, 3466–3492; *Angew. Chem. Int. Ed.* **1999**, 38, 3268–3292; b) N. Guillou, Q. Gao, M. Nogues, R. E. Morris, M. Hervieu, G. Férey, A. K. Cheetham, *C.R. Acad. Sci. Ser. IIc* **1999**, 2, 387–392.

Table 1 in the communication by **J. T. Groves, S. Shaik, and co-workers** in Issue 15, 2001, pp. 2874–2878 contains an incorrect sign. The first energy datum in entry 2 should be +0.07 kcal mol<sup>-1</sup> and not –0.07.