

Structures of d(GCGAAGC) and d(GCGAAAGC) (tetragonal form): a switching of partners of the sheared G·A pairs to form a functional G·A×A·G crossing. Erratum

Tomoko Sunami,^a Jiro Kondo,^a Ichiro Hirao,^b Kimitsuna Watanabe,^c Kin-ichiro Miura^d and Akio Takénaka^{a*}

^aGraduate School of Bioscience and Biotechnology, Tokyo Institute of Technology, Yokohama 226-8501, Japan, ^bRIKEN GSC, Wako-shi, Saitama 351-0198, Japan,

^cGraduate School of Engineering, University of Tokyo, Tokyo 113-8656, Japan, and

^dFaculty of Science, Gakushuin University, Tokyo 171-8588, Japan. Correspondence e-mail: atakenak@bio.titech.ac.jp

In the paper by Sunami *et al.* (2004), an asterisk was inadvertently missed out from the last sentence of §3.6 on p. 428. The corrected sentence should read as follows: In the base-stacked column, the ribose rings of the A_{3,5} residues adopt a C3'-endo pucker to make

space for accepting an A₄* base of the counter-strand between the A_{3,5} and A₄ residues.

Table 4 of this paper also contained an error and a corrected version of the table is given below.

Table 4
Sugar puckers of the 7hmt duplex.

Residue	Chain A	Chain B	Chain C	Chain D	Chain E	Chain F
G ₁	C3'-exo	C3'-exo	C3'-exo	C3'-exo	C3'-exo	C3'-exo
C ₂	C1'-exo	C1'-exo	C1'-exo	C2'-endo	C1'-exo	C2'-endo
G ₃	C3'-exo	C2'-endo	C2'-endo	C2'-endo	C2'-endo	C2'-endo
A ₄	C4'-exo	C3'-endo	C3'-endo	C3'-endo	C3'-endo	C3'-endo
A ₅	C2'-endo	C2'-endo	C2'-endo	C2'-endo	C2'-endo	C2'-endo
G ₆	C1'-exo	C1'-exo	C1'-exo	C4'-exo	O4'-endo	C1'-exo
C ₇	C4'-exo	C4'-exo	C4'-exo	C4'-exo	C4'-exo	C4'-exo
A-form	C3'-endo					
B-form	C2'-endo					

References

Sunami, T., Kondo, J., Hirao, I., Watanabe, K., Miura, K. & Takénaka, A. (2004). *Acta Cryst.* **D60**, 422–431.