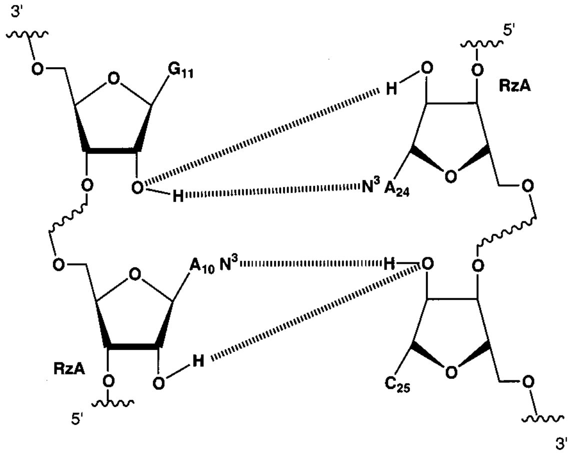
Corrections

Investigation of the Proposed Interdomain Ribose Zipper in Hairpin Ribozyme Cleavage Using 2′-Modified Nucleosides, by David J. Earnshaw, Michelle L. Hamm, Joseph A. Piccirilli, Alexander Karpeisky, Leo Beigelman, Bruce S. Ross, Muthiah Manoharan, and Michael J. Gait*, Volume 39, Number 21, May 30, 2000, pages 6410−6421.

Page 6411. Figure 2b, showing the hydrogen-bonding pattern in the ribose zipper predicted from molecular modeling and cross-linking studies of the hairpin ribozyme described by Earnshaw et al. [(1997) *J. Mol. Biol. 274*, 197−212], contains an error. The correct hydrogen-bonding pattern is shown in the revised Figure 2b below, where bifurcated hydrogen bonds project from the 2′-hydroxyl groups at G_{11} and C_{25} rather than incorrectly from A_{10} and A_{24}. There are three reasons for correcting this error. (1) Our data, for example, showing that 2′-fluoro substitution at C_{25} or G_{11} has a far greater effect than a similar substitution at either A_{10} or A_{24}, are now more consistent with the correct hydrogen-bonding pattern predicted by the ribose zipper, and the Discussion should be reconsidered in light of this. (2) The error has been carried through to the Discussion in a publication from another laboratory [Wilson, T. J., et al. (2001) *Biochemistry 40*, 2291−2302], where in Figure 9 the ribose zipper models of Earnshaw et al. (1997) and Ryder, S. P. and Strobel, S. A. [(1999) *J. Mol. Biol. 291*, 295−311] were thought to differ, when in fact they are identical between residues C_{25} and A_{10} and now fit perfectly with the data of Wilson et al. (3) The very recently determined crystal structure of the hairpin ribozyme [Rupert, P. B. and Ferré-d'Amaré, A. R. (2001) *Nature 410*, 780−786] confirms precisely the original hydrogen-bonding pattern of the ribose zipper predicted by Earnshaw et al. (1997).



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