

Ta and Honjo reply:

Although we have not done any structural studies, we agree that elucidation of the structure of AID is essential for understanding the function of AID. Zaim and Kierzek suggest yeast CD as a template for AID structure prediction by using 3DJury, a newly developed software package. However, it is difficult at present to evaluate the

accuracy of this prediction. It would be of interest to compare the domains of the AID structure proposed by Zaim and Kierzek to those proposed by Wedekind *et al.*¹, which seem to be different despite the use of yeast CD as the basis of calculation by both groups. Moreover, it remains useful to compare the structures of AID and APOBEC-1 because they are evolutionarily closest.

Van-Thanh Ta & Tasuku Honjo

*Department of Medical Chemistry and Molecular Biology, Graduate School of Medicine, Kyoto University, Yoshida, Sakyo-ku, Kyoto, 606-8501, Japan.
e-mail: honjo@mfour.med.kyoto-u.ac.jp*

1. Wedekind, J.E., Dance, G.S., Sowden, M.P. & Smith, H.C. *Trends Genet.* **19**, 207–216 (2003).