



Hydrogen bonds are a primary driving force for *de novo* protein folding. Corrigendum

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The paper by Lee *et al.* [(2017). *Acta Cryst. D* **73**, 955–969] is withdrawn.

We wish to withdraw the paper by Lee *et al.* (2017) on the crystal structure of a protein believed to have been AID (activation-induced cytidine deaminase). It has subsequently been shown that the crystal studied was of *E. coli* RNA-binding protein Hfq, a contaminant in the protein preparation. The associated PDB entry, 5w09, has also been made obsolete. Our conclusions regarding the critical role of proline residues in protein folding, successful folding of proteins at high pH, and hydrogen bonds as a driving force in *de novo* protein folding are not affected, and further details will be published elsewhere.

References

Lee, S., Wang, C., Liu, H., Xiong, J., Jiji, R., Hong, X., Yan, X., Chen, Z., Hammel, M., Wang, Y., Dai, S., Wang, J., Jiang, C. & Zhang, G. (2017). *Acta Cryst. D* **73**, 955–969.

