corrigenda

The X-ray structure of an anti-tumour antibody in complex with antigen

Philip D. Jeffrey, Jürgen Bajorath, Chieh Ying Y Chang, Dale Yelton, Ingegerd Hellström, Karl Erik Hellström and Steven Sheriff
Nature Structural Biology **2**, no. 6, 466–471 (1995).

On pg. 71 beneath the heading 'Structural analysis', the Protein Data Bank accession numbers should read: 1CLY and 1CLZ.

Amino-acid substitutions in a surface turn modulate protein stability

Paul F. Predki, Vishal Agrawal, Axel T. Brünger and Lynne Regan
Nature Structural Biology **3**, no. 1, 54–58 (1996).

In Table 3, the free-*R* factor should be 0.272.

Insights into protein adaptation to a saturated salt environment from the crystal structure of a halophilic 2Fe-2S ferredoxin

Felix Frolow, Michal Harel, Joel L Sussman, Moshe Mevarech and Menachen Shoham
Nature Structural Biology **3**, no. 5, 452–458 (1996).

In Table 2, row 2, entry HmMDH, the values for accessible surface area and net charge density should appear as they do below:

Table 2 The most negatively charged water-soluble proteins in the Protein Data Bank

	Accessible surface area ($Å^2$)	Net charge density $\times 10^3$ ($Å^{-2}$)
HmMDH[1]	13431	–2.4

erratum

Detection of rare partially folded molecules in equilibrium with the native conformation of RNase H

Aaron K. Chamberlain, Tracy M. Handel and Susan Marqusee
Nature Structural Biology, **3**, no. 9, 782–787 (1996).

Figure 1*b* was inadvertently misprinted. The version to the right is as it should have appeared in the September issue of *Nature Structural Biology*.

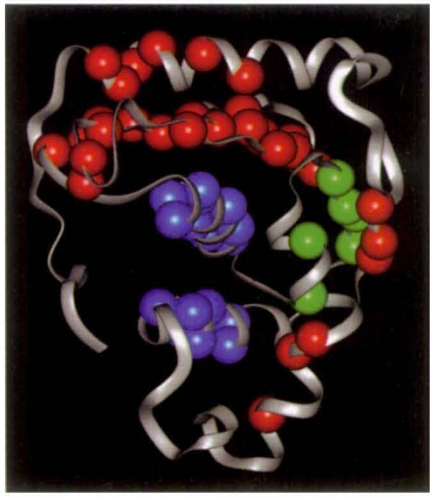

Fig. 1 RNase H* separates into three regions based on the stability of protons to hydrogen exchange. *b*, The three regions with differing stabilities shown on a ribbon diagram of the RNase H crystal structure[8] (INSIGHTII, Biosym Technologies). The regions consist of: helices A and D (blue), helix B and strand 4 (green), and the remaining protons in helices C, E and strands 1, 2, 3, and 5 (red).