errata

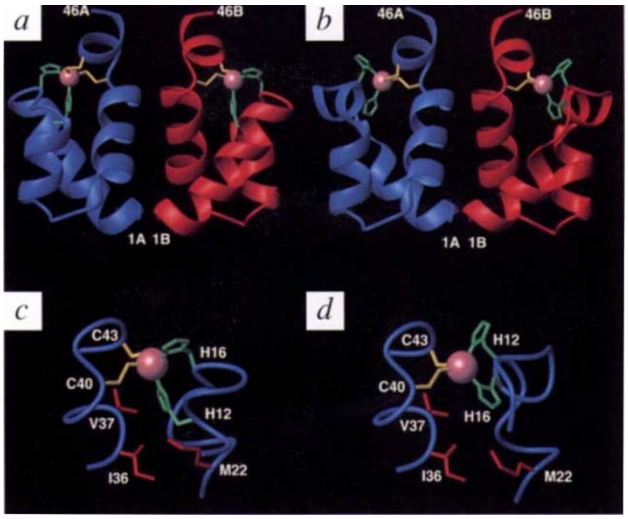

Fig. 6 Ribbon diagrams illustrating ***a***, the E and ***b***, the D forms of the IN^{1-55} dimer (residues 1–46). Detailed views of the region surrounding the zinc in ***c***, the E and ***d***, the D forms of IN^{1-55}. The backbone of one subunit is shown in blue and of the other subunit in red, the zinc atom is displayed as a pink colored ball, selected sidechains are shown in red, and the coordinating cysteines and histidine residues are shown in yellow and green respectively.

Bridging the gap

Joel L. Sussman, *Nature Struct. Biol.* 4, 517 (1997).

On pg. 517 of the July issue, in the first sentence of the second paragraph, "Natural Center for Biotechnology Information" should read: National Center for Biotechnology Information.

A low energy short hydrogen bond in very high resolution structures of protein receptor–phosphate complexes

Zhongmin Wang, Hartmut Luecke, Nanhua Yao, and Florante A. Quiocho, *Nature Struct. Biol.* 4, 519–522 (1997).

On pg. 519 of the July issue, a (sign was inadvertently left out of the first line of the report, which should read: Sir — Short (≤ 2.45 Å) or low barrier hydrogen bonds (LBHBs), which possess strengths of as much as 30 kcal mol^{-1} for model compounds in the gas phase[1], have recently attracted considerable attention and controversy for their possible major role in enzyme catalysis[1–5].

corrigenda

The following omissions were inadvertently made; below are the corrected items:

The solution structure of the first KH domain of FMR1, the protein responsible for the fragile X syndrome

Giovanna Musco, Abdelhakim Kharrat, Gunter Stier, Franca Fraternali, Toby J. Gibson, Michael Nilges and Annalisa Pastore, *Nature Struct. Biol.* 4, 712–716 (1997).

On pg. 716 of the September issue, the Brookhaven Protein Data Bank code for the reported structure should read: 1fmr.

Three-dimensional structure of the Ras-interacting domain of RalGDS

Lan Huang, Xiangwei Weng, Franz Hofer, G. Steven Martin and Sung-Hou Kim, *Nature Struct. Biol.* 4, 609–615 (1997).

The authors made an omission in their acknowledgements. They are also grateful to D. King of the Howard Hughes Medical Institute, University of California, Berkeley, for mass spectrometric work.

The ion core in RNA folding

Ignacio Tinoco, Jr. and Jeffrey S. Kieft, *Nature Struct. Biol.* 4, 509–512 (1997).

On pg. 510 in the July issue, Fig. 2*a* is incorrect. The version to the right is as it should have been.

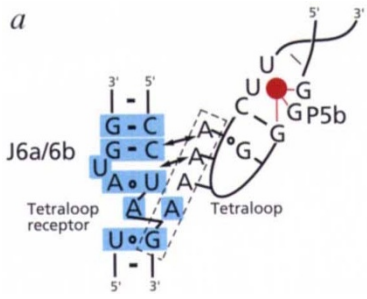

Fig. 2 ***a***, Schematic of the P5b GAAA tetraloop docking in the J6a/6b tetraloop receptor (light blue). An adenosine platform in the receptor allows continuous base stacking between the receptor and the tetraloop (dahsed box). Tertiary contacts, including an A–U–A base triple, further stabilize the interaction. A metal ion (red) is bound in the major groove of the P5b helix near two G•U base pairs. This figure is a slightly modified version of Fig. 4*b* of ref. 4.