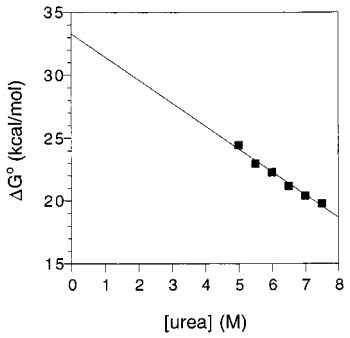
Corrections

A Buried Polar Interaction Imparts Structural Uniqueness in a Designed Heterodimeric Coiled Coil, by Kevin J. Lumb and Peter S. Kim*, Volume 34, Number 27, July 11, 1995, pages 8642−8648.

Page 8645. The inset to Figure 3 and the reported $\Delta G°$ for ACID-pLL/BASE-pLL are incorrect. The correct $\Delta G°$ (25 °C, pH 7.0) for the ACID-pLL/BASE-pLL heterotetramer is −33.3 kcal/mol (corrected figure below), resulting in a predicted hydrogen exchange protection factor of 10^4. Thus, the slowest amide proton exchange rates of the ACID-pLL/BASE-pLL heterotetramer are 2 orders of magnitude faster than expected for a global unfolding mechanism. The hydrogen exchange data still indicate that ACID-pLL/BASE-pLL has a fluctuating structure. The conclusions of the paper are unaffected by the correction. We thank Dr. Toshiki Tanaka for bringing this error to our attention.



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Crystal Structure of the *Escherichia coli* Peptide Deformylase, by Michael K. Chan,* Weimin Gong, P. T. Ravi Rajagopalan, Bing Hao, Chris M. Tsai, and Dehua Pei, Volume 36, Number 45, November 11, 1997, pages 13904−13909.

Page 13904. Weimin Gong's affiliation should be listed as Department of Biochemistry, School of Medicine, Emory University, Atlanta, GA 30322, and he was supported by NIH Grant GM49245, awarded to Dr. Xiaodong Cheng of the same Department. The model building and refinement of the *E. coli* peptide deformylase were done by Weimin Gong while he was a postdoctoral research fellow in Dr. Xiaodong Cheng's laboratory.

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Dissection of the Sequence Specificity of the Holliday Junction Endonuclease CCE1, by Mark J. Schofield, David M. J. Lilley, and Malcolm F. White*, Volume 37, Number 21, May 26, 1998, pages 7733−7740.

Page 7736. In column 2, the equation should read $\Delta\Delta G^{\circ\ddagger} = -RT \ln(k_1/k_2)$.

Page 7738. In Table 3, the values for $\Delta\Delta G°_{bind}$ should read −0.66, −0.81, −0.52, −1.4, −0.34, and −0.34.

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Protein Farnesyltransferase: Structure and Implications for Substrate Binding, by Pete Dunten,* Ursula Kammlott, Robert Crowther, David Weber, Rober Palermo, and Jens Birktoft, Volume 37, Number 22, June 2, 1998, pages 7907−7912.

Page 7907. The following footnote should be appended to the title: The coordinates have been deposited in the Brookhaven Protein Data Bank (code 1FPP).

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