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Corrections

Views of Helical Peptides: A Proposal for the Position of 3_{10} -Helix along the Thermodynamic Folding Pathway, by Glenn L. Millhauser, Volume 34, Number 12, March 28, 1995, pages 3873–3877.

Page 3874. The abscissa of Figure 1, labeled as the total fraction of helix, represents the fraction of peptide chains that contain at least one hydrogen bond. However, in the last paragraph of the first column on page 3874, the abscissa was referred to as the fractional helicity. This use of fractional helicity is incorrect since this phrase is usually reversed, in Zimm–Bragg theory, to indicate the number of helical hydrogen bonds formed divided by the maximum number of hydrogen bonds possible in the fully helical state (N_h). Recalculation of components represented in Figure 1 against the proper definition of fractional helicity indicates that the population of peptides containing short helical domains reaches a maximum at a fractional helicity of 0.20. At 0.50 fractional helicity, short domains comprise approximately 12% of the peptide chains containing helix (but only 3% of the hydrogen bonds). While the result of this illustrative calculation is rendered somewhat less emphatic, the conclusions from the calculation and the rest of the paper remain unchanged and support the proposal of 3_{10} -helix as a thermodynamic folding intermediate. Prof. A. Holtzer is gratefully acknowledged for identifying this issue and for many helpful suggestions.

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