Corrections

Structural Examination of Φ-Value Analysis in Protein Folding, by Hanqiao Feng, Ngoc-Diep Vu, Zheng Zhou, and Yawen Bai*, Volume 43, Number 45, November 16, 2004, pages 14325−14331.

In this paper, we reported a study that demonstrated a number of non-native side chain interactions in a partially folded intermediate of Rd-apocytochrome b_{562} even though mutation-dependent Φ-values measured for it were in the normal range, between 0 and 1. We suggested that future computer simulation studies of partially folded forms, pathway intermediates and transition states, should include such interactions. Dr. Valerie Daggett has pointed out that her molecular dynamics simulation protocol for calculating Φ-values (ref 7 in our paper) does allow non-native interactions and normal fractional Φ-values were already found to be related to non-native interactions.

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