

Addition/Correction

Unexpectedly Strong Energy Stabilization Inside the Hydrophobic Core of Small Protein Rubredoxin Mediated by Aromatic Residues: Correlated Ab Initio Quantum Chemical Calculations [*J. Amer. Chem. Soc.* 2005, 127, 2615–2617].

Jiri Vondrasek, Lada Bendova, Vojtech Klusak, and Pavel Hobza

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Unexpectedly Strong Energy Stabilization Inside the Hydrophobic Core of Small Protein Rubredoxin Mediated by Aromatic Residues: Correlated Ab Initio Quantum Chemical Calculations [*J. Amer. Chem. Soc.* **2005**, *127*, 2615–2617]. Jiri Vondrasek, Lada Bendova, Vojtech Klusak, and Pavel Hobza*

Page 2615. The first paragraph of our article should read: “Protein folding involves two critical elements,” stability and specificity. The native structure of a typical protein is more stable by only 5–15 kcal/mol over the unfolded state.¹ “Hence, small differences in energy between” multitudes “of possible noncovalent interactions are summed up to provide the properly folded structure”. To gain “control of protein secondary and tertiary structure requires an understanding of how these” noncovalent interactions “provide both stabilization and specificity”. (The quoted text is taken from paper of Waters et al.)²

We apologize to authors of Waters et al.² that, because of an oversight in preparing our manuscript, although the wording in this paragraph was very similar to their wording, we did not place the material within quotation marks. Although we did cite their paper for the ideas expressed in this paragraph, we should have indicated that the wording was very similar as well.

(1) Branden, C.; Tooze, J. *Introduction to Protein Structure*, 2nd ed.; Garland Publishing: New York, 1999.

(2) Tatko, C. C.; Waters, M. L. *J. Am. Chem. Soc.* **2004**, *126*, 2028.

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