Erratum to: The Phylogenomic Roots of Modern Biochemistry: Origins of Proteins, Cofactors and Protein Biosynthesis

Gustavo Caetano-Anollés · Kyung Mo Kim ·
Derek Caetano-Anollés

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Root mean square deviation (RMSD) values in Fig. 6d are published incorrectly as 2.63. The correct values are 2.83 and 3.41 for the GlyRS and CDC-like structures, respectively.

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G. Caetano-Anollés (✉) · D. Caetano-Anollés
Evolutionary Bioinformatics Laboratory, Department of Crop
Sciences, University of Illinois, Urbana, IL 61801, USA
e-mail: gca@illinois.edu

K. M. Kim
Korean Bioinformation Center (KOBIC), Korea Research
Institute of Bioscience and Biotechnology (KRIBB),
111 Gwahangno, Yuseong-gu, Daejeon 305-806, Korea

Fig. 6 Structural origins of fold structure. **a** Structural alignment of the in vitro evolved 18–19 “artificial nucleotide binding protein” (ANBP) selected to bind ATP with high specificity and affinity (1UW1; structure colored in *green*) to a structural derivative selected to improve folding stability (2P09; *blue*). Increases in protein stability do not change the original fold structure. A total of five secondary structure elements and 67 amino acid residues (all in the structure) were aligned with an RMSD of 0.48 Å. **b** GANGSTA+ structural comparison of the 2P09 structural ANBP derivative to protein folds in the ASTRAL40 compendium. The diagram correlates the number of aligned residues with individual RMSD for structure alignments. All results with more than 20 aligned residues are displayed and the *dashed line* delimits structures with more than 70% of residues being aligned. Alignments described in **c** are labeled. **c** The evolutionary age of structural alignments with more than 70% amino acid residues matching the 2P09 structure. **d** Structural models of the oldest and best (GlyRS with d.104.1.1 FF) and the oldest (CDC-like, c.37.1.20) structural alignments of 2P09 (*blue*) to target structures (*green*)