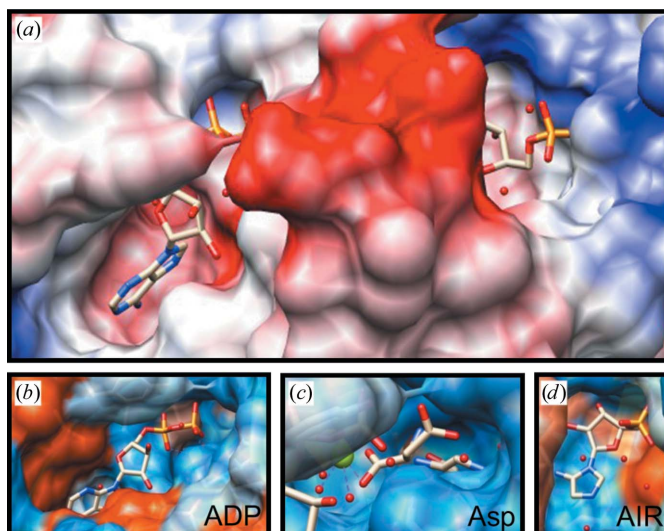


addenda and errata

Structures of SAICAR synthetase (PurC) from *Streptococcus pneumoniae* with ADP, Mg²⁺, AIR and Asp. CorrigendumNina M. Wolf,^a Celerino Abad-Zapatero,^b Michael E. Johnson^b and Leslie W.-M. Fung^{a*}^aDepartment of Chemistry, University of Illinois at Chicago, Chicago, IL 60607, USA, and ^bCenter for Pharmaceutical Biotechnology, University of Illinois at Chicago, Chicago, IL 60607, USA

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The caption for Figure 3 of the article by Wolf *et al.* [(2014), *Acta Cryst.* D70, 841–850] is corrected.In the article by Wolf *et al.* (2014) the caption to Figure 3 was incorrect. The correct caption and the figure are given here.**References**Wolf, N. M., Abad-Zapatero, C., Johnson, M. E. & Fung, L. W.-M. (2014). *Acta Cryst.* D70, 841–850.**Figure 3**

Electrostatic and hydrophobic representations of the active-site tunnel of structure 1, chain A, with negatively charged residues in red and positively charged residues in blue in (a), and blue for the most polar residues to orange red for the most hydrophobic residues, and white in between (b, c and d). Generally, the active-site tunnel is polar (b, c, d). The solvent-exposed portion of loop 3 is seen as folding over at the center and composed of negatively charged residues (a). The adenine ring of ADP is at the left side of the tunnel (b) and the phosphate of AIR is at the right side of the tunnel (d). The Asp pocket, enclosed by loop 3 at the top, is polar (c).