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addenda and errata

Structures of SAICAR synthetase (PurC) from *Streptococcus pneumoniae* with ADP, Mg^{2+}, AIR and Asp. Corrigendum

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The caption for Figure 3 of the article by Wolf *et al.* [(2014), *Acta Cryst.* D**70**, 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.

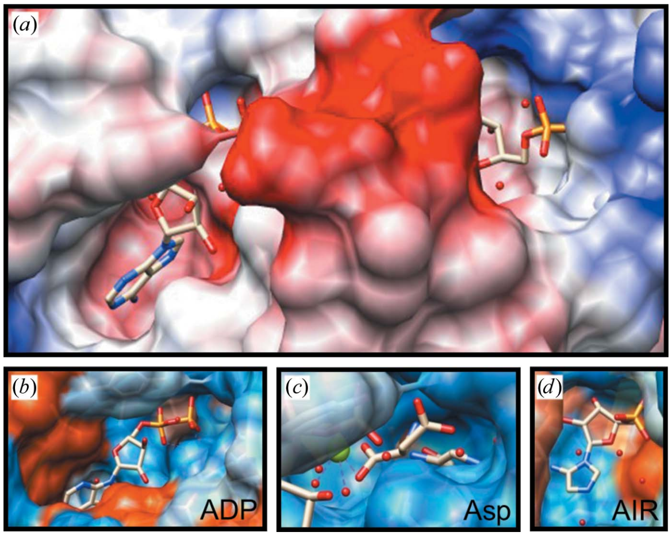

Figure 3
Electrostatic and hydrophobic representations of the active-site tunnel of structure 1, chain *A*, with negatively charged residues in red and positively charged residues in blue in (*a*), and blue for the most polar residues to orange red for the most hydrophobic residues, and white in between (*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*).

References

Wolf, N. M., Abad-Zapatero, C., Johnson, M. E. & Fung, L. W.-M. (2014). *Acta Cryst.* D**70**, 841–850.

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