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addenda and errata

Structure of human apolactoferrin at 2.0 Å resolution. Refinement and analysis of ligand-induced conformational change. Addendum

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The coordinates and structure factors have now been deposited with the Protein Data Bank for the high-resolution structure described in the paper by Jameson, Anderson, Norris, Thomas & Baker [*Acta Cryst.* (1998). D**54**, 1319–1335]. The PDB reference code for this structure is 1cb6.

Initiating a crystallographic study of UDP-galactopyranose mutase from *Escherichia coli*. Erratum

Stephen A. McMahon,[a] Gordon A. Leonard,[b] Louise V. Buchanan,[a] Marie-France Giraud[a] and James H. Naismith[a]*

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In the paper by McMahon, Leonard, Buchanan, Giraud & Naismith [*Acta Cryst.* (1999). D**55**, 399–402] an author's error has resulted in the fifth sentence of the Abstract being incorrect. The sentence should read 'They are monoclinic, space group $P2_1$, with unit-cell dimensions $a = 71.12$, $b = 58.42$, $c = 96.38$ Å, $\beta = 96.38^\circ$. 92% (native) and 94% (selenomethionine) complete data sets have been recorded to 2.9 Å ($R_{\rm merge} = 5.0\%$) and 3.0 Å ($R_{\rm merge} = 6.9\%$), respectively.'

Remarks about protein structure precision. Erratum

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The following are corrections to the paper by Cruickshank [*Acta Cryst.* (1999). D**55**, 583–601]. On p. 589 §4.2 line 13, $Z_i^{\#}$ should read Z_i; also in line 13, Z_i should read $Z_i^{\#}$. In line 18, $Z_i^{\#}$,$\sigma(r)$ should read $Z_i^{\#}\sigma(r)$. In the caption for Fig. 7, $\sigma_{\rm diff}(2)$ should be $\sigma_{\rm diff}(l)$. Equation (30) should read as follows,

$$\sigma(r, B_{\rm avg}) = 3^{1/2}(N_i/p)^{1/2}C^{-1/3}Rd_{\rm min} \qquad (30)$$

and equation (49) should read as follows,

$$\sigma_i^2 = \left[\left(\sum_3 w\Delta^2\right)/(n_{\rm obs} - n_{\rm params})\right](a^{-1})_{ii} \qquad (49).$$

On the first line of p. 599, (47) should read (49).