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addenda and errata

Purification, crystallization and preliminary X-ray analysis of an acetylxylan esterase from *Bacillus pumilus*. Erratum

Stefano Benini,[a]* Giuliano Degrassi,[a] Ivet Krastanova,[b] Doriano Lamba[a,c] and Vittorio Venturi[a]

[a]International Centre for Genetic Engineering and Biotechnology, Area Science Park, Padriciano 99, I-34012 Trieste, Italy, [b]International School for Advanced Studies, Via Beirut 2/4, I-34014 Trieste, Italy, and [c]Istituto di Strutturistica Chimica 'G. Giacomello', Consiglio Nazionale delle Ricerche, Sez. di Trieste, Area Science Park, Basovizza, S.S 14 Km 163.5, I-34012 Trieste, Italy. Correspondence e-mail: benini@ysbl.york.ac.uk

This erratum is to apologise for having reported the crystallization and X-ray characterization of *Bacillus pumilus* acetylxylan esterase (AXE) while the protein crystallized was instead an inorganic pyrophosphatase, a contaminant of the expression in *E. coli*. The protein was purified by hydrophobic interaction, ionic exchange and gel filtration, but still contained traces of contaminant proteins. Crystals were obtained in the *R*32 space group perfectly compatible with the homohexameric structure of AXE. The cell parameters were compatible with a reasonable crystal packing as in the model cephalosporin C deacetylase from *Bacillus subtilis* kindly provided before publication by Dr Jim Brannigan *et al*. (PDB code 1ods crystallized in *R*3 and 1odt crystallized in *R*32). Since every attempt to solve the structure by molecular replacement using 1odt as a model failed, a search of the PDB using the cell parameters of the data collected revealed a match with *Escherichia coli* inorganic pyrophosphatase (1ipw). A molecular-replacement solution confirmed that the protein crystallized was indeed *E. coli* inorganic pyrophosphatase present as a contaminant in the protein preparation used for crystallization. This experience should be kept in mind because proteins used for crystallization should be as pure as possible not only to favour the process itself but also to avoid the crystallization of contaminants.

References

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