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ERRATUM

Erratum to: α-Amylase: An Ideal Representative of Thermostable Enzymes

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In the original publication, some citations and a reference were omitted. The corrections are as follows.

On page 2401, the last sentence of the Introduction should contain an additional reference [132], and read as follows:

"Bacterial and fungal α-amylases, and in particular the enzymes from the Bacillus species, are of special interest for large-scale biotechnological processes due to their remarkable thermostability and because efficient expression systems are available for these enzymes [132]."

On page 2407, the third-to-last sentence should contain a reference as follows: "According to Fitter and Heberle [133], as compared by faster H/D exchange..."

On page 2408, the first sentence of the third paragraph should contain a reference [132] as follows:

"Usually, the native and active protein structures are held together by a subtle balance of non-covalent factors or interactions such as hydrogen bonds, ion pairs, and hydrophobic and van der Waals interactions [132]."

The online version of the original article can be found at http://dx.doi.org/10.1007/s12010-009-8735-4.

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Also on p. 2408, in the third paragraph, the following sentences should be cited as follows:

"Small monomeric proteins (like α-amylase) commonly unfold via a two-state transition where the unfolding intermediates are not or barely detectable. Some proteins regain their native and active conformation upon cooling, and this is called thermodynamically reversible unfolding. However, larger multi-domain proteins generally exhibit a different behavior called irreversible unfolding [132]."

Also on p. 2408, paragraph 4 should contain two additional reference citations, and read as follows:

"According to Fitter [132], at least two approaches can help to overcome this problem: fluorescence correlation spectroscopy (FCS) and molecular chaperones. The former significantly reduces the aggregation of unfolded states and has already been employed successfully on studies on unfolded proteins [116], while the latter can suppress aggregation of non-native or unfolded proteins [117, 118]. The mild conditions of sol-gel encapsulation, provide a further technique to reduce aggregation of unfolded states [119]. But, these approaches have a number of limitations like limited temperature range and would be applicable only for some of the relevant aspects. However, studies with homologous α-amylase using these techniques have great potential in this field of application [132]."

In the reference list, the following entries should appear:
[132] Fitter, J. (2005). Cellular and Molecular Life Sciences, 62, 1925-1937.
[133] Fitter, J. & Heberle, J. (2000). Biophys J., 78, 1629.

The authors regret the errors.