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Corrigendum: Molecular characterization of a family 5 glycoside hydrolase suggests an induced-fit enzymatic mechanism

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In this Article, the legend of Figure 5 is incorrect:

(a) BICel5B in the crystallographic and closed configuration; (b) *Bacillus halodurans* Cel5B (BhCel5B) (PDB id: 4V2X) (c) *Piromyces rhizinflata* GH5 endoglucanase (PDB id: 3AYR); (d) *Clostridium cellulolyticum* GH5 endoglucanase (PDB id: 1EDG); (e) *Clostridium cellulovorans* GH5 endoglucanase (PDB id: 3NDY); (f) *Bacteroides ovatus* GH5 xyloglucanase (PDB id: 3ZMR); (g) *Paenibacillus pabuli* GH5 xyloglucanase (PDB id: 2JEP); (h) *Prevotella bryantii* GH5 endoglucanase (PDB id: 3VDH); (i) *Ruminiclostridium thermocellum* multifunctional GH5 cellulase, xylanase and mannanase (PDB id: 4IM4); (j) *Bacteroidetes bacterium* AC2a endocellulase (PDB id: 4YHE).

should read:

The main difference between BICel5B and BhCel5B is that the latter exhibits a deeper cleft due to the presence of residue W181 in the loop between F177 and R185. We conjecture that this difference in the binding site architecture relates to the importance that the CBM46 plays in the BICel5B enzymatic mechanism.

In addition, the legend of Figure 6 is incorrect:

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