## Erratum



## Maltose fermentation to acetate, $CO_2$ and $H_2$ in the anaerobic hyperthermophilic archaeon *Pyrococcus furiosus*: evidence for the operation of a novel sugar fermentation pathway

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Figure 8 contains a number of unforturate errors. In step 8, ADP and ATP were printed in the wrong positions. In step 10, the arrow pointed in the wrong direction.

The correct version of Fig. 8 is printed besides, together with the legend.

Fig. 8. Proposed pathway of maltose fermentation to acetate,  $CO_2$  and  $H_2$  in *Pyrococcus furiosus*. Number in circles refer to enzymes involved. 1:  $\alpha$ -glucosidase (Costantino et al. 1990); 2: glucose: ferredoxin oxidoreductase; 3: gluconate dehydratase (this enzyme activity has not yet been demonstrated); 4: KDG aldolase; 5: glyceraldehyde: ferredoxin oxidoreductase; 6: glycerate kinase (2-phosphoglycerate forming); 7: enolase; 8: pyruvate kinase; 9: pyruvate: ferredoxin oxidoreductase; 10: ADP-dependent acetyl-CoA synthetase; 11: hydrogenase. The ferredoxin dependence of enzymes 2, 5, and 11 has been demonstrated by Mukund and Adams (1991) and Bryant and Adams (1989). The enzymes 9, 10, and 11 were also involved in pyruvate fermentation to acetate,  $CO_2$  and  $H_2$  (Schäfer and Schönheit 1991). CoA, coenzyme A;  $Fd_{ox}$ , oxidized ferredoxin;  $Fd_{red}$ , reduced ferredoxin