

Erratum to: Glycolytic regulation in aestivation of the sea cucumber *Apostichopus japonicus*: evidence from metabolite quantification and rate-limiting enzyme analyses

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In the original publication, under section heading “Results” two subsections text were incorrectly published. The correct versions are given below.

Identification of partial cDNA (complete CDS) of *Aj*-HK gene

The cDNA of hexokinase gene is 1703 bp, consisting of a 232-bp 5'-terminal untranslated region (UTR), a 130-bp

3'-UTR and a 1341-bp open reading frame (ORF) encoding 446 amino acid residues.

Identification of partial cDNA (complete CDS) of the *Aj*-PK gene

The cDNA of pyruvate kinase gene is 2280 bp, consisting of a 238-bp 5'-UTR, a 437-bp 3'-UTR and a 1605 bp ORF encoding 534 amino acid residues.

The online version of the original article can be found under doi: [10.1007/s00227-016-2936-5](https://doi.org/10.1007/s00227-016-2936-5).

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