



# Corrigendum: Chemical Diversity and Biochemical Transformation of Biogenic Organic Sulfur in the Ocean

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## A Corrigendum on

**Chemical Diversity and Biochemical Transformation of Biogenic Organic Sulfur in the Ocean** by Tang, K. (2020). *Front. Mar. Sci.* 7:68. doi: 10.3389/fmars.2020.00068

In the original article, there was an error “Two major sulfoglycolytic pathways, the sulfo-Embden–Meyerhof–Parnas pathway (originally found in *E. coli*) and the sulfo-Entner–Doudoroff pathway (originally found in *Pseudomonas putida* SQ1) (Roy et al., 2003; Denger et al., 2014), have been shown to degrade SQ in certain marine bacteria (Roy et al., 2003). These pathways are analogous to the classic glycolysis pathways (Figure 2) (Felux et al., 2015). The sulfo-Embden–Meyerhof–Parnas pathway and the sulfo-Entner–Doudoroff pathway yield the C3-organosulfonate products DHPS and sulfolactate (Figure 2), respectively (Roy et al., 2003; Denger et al., 2014).”

A correction has been made to “BIOCHEMICAL REACTION NETWORK FOR ORGANIC SULFUR,” “Sulfonate Metabolisms,” “Paragraph Number 1”:

“SQ has been shown to be degraded by certain aerobic as well as anaerobic bacteria (Roy et al., 2003; Denger et al., 2012, 2014; Felux et al., 2015; Burrichter et al., 2018) and two major sulfoglycolytic pathways, the sulfo-Embden–Meyerhof–Parnas pathway (originally found in *E. coli*) and the sulfo-Entner–Doudoroff pathway (originally found in *Pseudomonas putida* SQ1) have been described (Denger et al., 2014; Felux et al., 2015). These pathways are analogous to the classic glycolysis pathways (Figure 2) (Felux et al., 2015). Bacterial SQ degradation yields the C3-organosulfonate products DHPS and sulfolactate (Figure 2) (Roy et al., 2003; Denger et al., 2012, 2014; Felux et al., 2015; Burrichter et al., 2018).”

And the (Denger et al., 2012) citation has now been inserted in.

The authors state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

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