

CORRECTION

[View Article Online](#)
[View Journal](#) | [View Issue](#)Cite this: *Chem. Sci.*, 2025, 16, 23408**Correction: Structural insights into a bacterial terpene cyclase fused with haloacid dehalogenase-like phosphatase**Keisuke Fujiyama, ^a Hiroshi Takagi, ^a Nhu Ngoc Quynh Vo, ^a Naoko Morita, ^a Toshihiko Nogawa ^b and Shunji Takahashi ^{*a}

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rsc.li/chemical-scienceCorrection for 'Structural insights into a bacterial terpene cyclase fused with haloacid dehalogenase-like phosphatase' by Keisuke Fujiyama *et al.*, *Chem. Sci.*, 2025, 16, 15310–15319, <https://doi.org/10.1039/d5sc04719f>.

Upon publication of the original article, the authors were made aware that the preprint by Osika *et al.* (ref. 57 in our original manuscript) had been published,¹ and is closely related to our study on drimenol synthase from *Aquimarina spongiae* (AsDMS). We hereby correct the sentence on page 15311, left column, line 20, as follows: In this study, we report the co-crystallographic analyses of AsDMS, an enzyme that converts substrate 1 into product 2, and the biochemical characterization of site-specific variants. During the preparation of this manuscript, Osika *et al.*¹ disclosed the structure of AsDMS in complex with a non-physiological ligand. In this report, we obtained co-crystal structures of the AsDMS-1 and AsDMS-3 complexes. The obtained co-crystal structures of AsDMS represent the first experimentally determined physiological substrate-bound structures of a HAD-TC β enzyme, revealing distinct substrate-binding pockets for the HAD and TC β domains.

The co-crystal structures reported in this study involve the physiological substrate, whereas the physiological substrate-free structure of AsDMS was independently reported contemporaneously by Osika *et al.*,¹ highlighting the complementary nature of these studies. Based on ¹⁸O-labelling, MESG assays, and the substrate-free crystal structure, Osika *et al.*¹ proposed a mechanism that releases Pi in a stepwise manner. In the present study, we elucidate the catalytic mechanism (Fig. 6) through co-crystal structures with the physiological substrates and comprehensive site-directed mutagenesis analyses, providing firm experimental evidence for the catalytic process.

The Royal Society of Chemistry apologises for these errors and any consequent inconvenience to authors and readers.

References

- 1 K. R. Osika, M. N. Gaynes and D. W. Christianson, *Proc. Natl. Acad. Sci. U. S. A.*, 2025, 122(26), e2506584122.

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