CORRIGENDUM

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Corrigendum: Mycocerosic acid synthase exemplifies the architecture of reducing polyketide synthases

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In this Letter, we studied the three-dimensional structure of a protein from *Mycobacterium smegmatis* assigned as mycocerosic acid synthase (MAS) in sequence databases as A0R1E8 in Uniprot (<http://www.uniprot.org/uniprot/A0R1E8>) and YP_888986.1 in NCBI (<https://www.ncbi.nlm.nih.gov/protein/118473069>). In conclusion, we provided a template structure of MAS-like polyketide synthases (PKSs) and a first example of reducing PKS architecture. However, we now note that Etienne *et al.*¹ provided a biochemical characterization of a deletion strain of the corresponding gene MSMEG_4727 (<https://www.ncbi.nlm.nih.gov/gene/4534621>), which indicated a physiological role of the protein in the production of 2,4-dimethyl-2-eicosenoic acid, a lipid component of lipooligosaccharides, rather than mycocerosic acids, via a reaction closely related to those of MAS. Until comprehensive characterization at the protein level is available, the protein we studied should therefore be referred to as a ‘mycocerosic-acid synthase like-PKS’ or ‘MAS-like PKS’; the database records will be updated accordingly. We thank the authors of ref. 1 for drawing our attention to this publication. The main scientific conclusions of our manuscript remain unchanged.

1. Etienne, G. *et al.* Identification of the polyketide synthase involved in the biosynthesis of the surface-exposed lipooligosaccharides in mycobacteria. *J. Bacteriol.* **191**, 2613–2621 (2009).