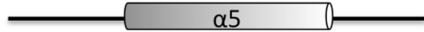
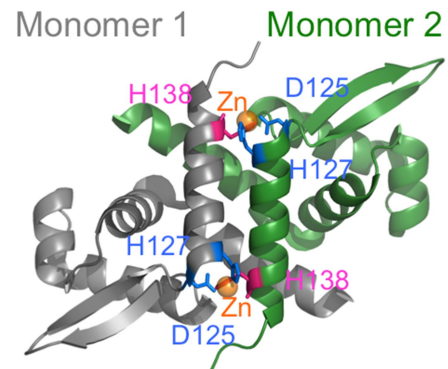


S2 Fig

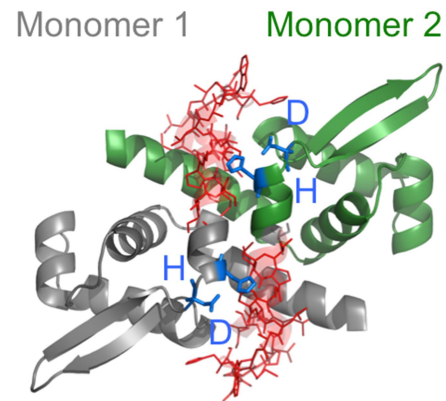
A

			
CrzA	<i>S. aureus</i>	77 MIYSLDDI H VATMLKQAI H ANHPKESGL*	106
SmtB	<i>S. elongatus</i>	98 VYYQLQD H HIVALYQNALD H LQECR*	122
RV2358	<i>M. tuberculosis</i>	111 VLYRLAD H HLAHIVLDAVA H AGEDAI*	135
ML0825	<i>M. leprae</i>	119 MLYRLAD Y HLTHIVVDAVA H AGVDAL*	144
ML0825m	<i>M. leprae mut.</i>	120 MLYRLAD Y HLTHI SSSMPSPTLAWMHCDPRQLRCSRGTARLRGTTR*	168

B



C



S2 Fig. Structure and polymorphisms in SmtB. Panel A shows the sequence alignment of SmtB homologs. The locations of the $\alpha 5$ metal-binding sites are highlighted in blue and pink. In red is the mutated sequence of SmtB. Panel B shows the structure of the CzrA dimer from *Staphylococcus aureus*. Zn, in orange, binds at the interface between

the two monomers. Panel C shows a model of the effect of the mutation in ML0825 on the dimer, which compromises the binding of Zn ions. The mutated part is represented in red lines. The protein was modeled using the homology modeling webserver SWISS-MODEL⁷ and the structure of the transcriptional repressor CzrA from *Staphylococcus aureus* (PDB code 1R1V) as template.

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