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Supporting information for article:

**The first crystal structure of manganese superoxide dismutase
from the genus *Staphylococcus***

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S1. Crystallization of *S. equorum* MnSOD

Prismatic and polygonal shapes crystals of *S. equorum* MnSOD grown in the same conditions. The data used in the structure elucidation originated from the latter shape.

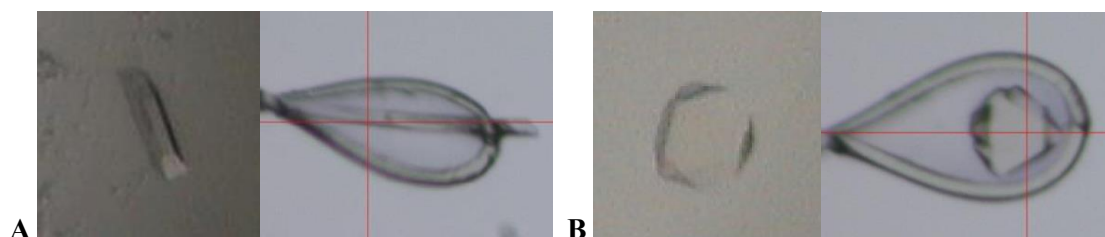


Figure S1 Prismatic (A) and polygonal (B) shapes crystals of *S. equorum* MnSOD under the microscope and positioned in front of the beam.

S2. Amino acid comparison and its solvent accessibility of *S. equorum* MnSOD to *B. subtilis* MnSOD

The sequence of *S. equorum* MnSOD contains more amino acids with charged side chains and the overall is more negatively charged.



Figure S2 Amino acid sequences homology of MnSOD from *S. equorum* (MnSODSeq) and *B. subtilis* (MnSODBsu). The color scheme is blue, red, green, and gray for positively charge, negatively charge, polar uncharge, and hydrophobic residues, respectively.

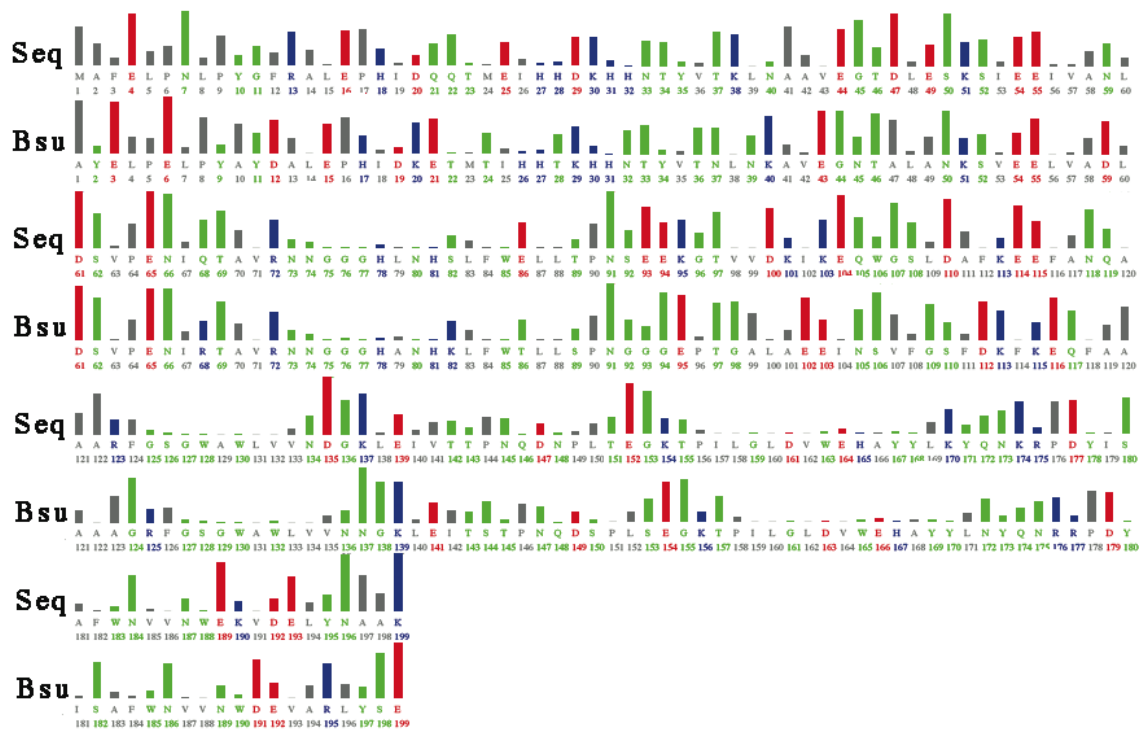


Figure S3 Solvent accessibility of amino acid in the sequences of *S. equorum* and *B. subtilis* MnSOD. The color scheme is blue, red, green, and gray for positively charge, negatively charge, polar uncharge, and hydrophobic residues, respectively. The higher coloured bar indicates higher solvent accessibility.