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Supporting information for article:

Crystal structure of an  $N^{\omega}$ -hydroxy-L-arginine hydrolase found

in the D-cycloserine biosynthetic pathway

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**Figure S1** Sequence alignment between DcsB and human arginase I. Structurally equivalent residues are shown in uppercase, while non-equivalent residues are in lowercase. Identical residues are indicated by the colored background (light blue). Secondary structures of DcsB are shown above the sequence. The ligands for the manganese ions in DcsB or human arginase I are indicated by asterisks, while the *C*-terminal S-shape motif in human arginase I, which is important for the trimer formation, is underlined. Structure-based sequence alignment between DcsB and human arginase I was conducted by the DALI program (Holm, 2019).



**Figure S2** Gel filtration analysis of DcsB. A portion of the purified DcsB (340  $\mu$ M) was injected into Superdex 200 Increase 10/300 GL filtration column (GE Healthcare) equilibrated with 10 mM HEPES-NaOH buffer (pH 8.0) containing 200 mM NaCl, 1 mM DTT, and 100  $\mu$ M MnCl<sub>2</sub> at 4°C at a flow rate of 0.5 mL min<sup>-1</sup>. Retention time of DcsB (16.6 mL) indicates that the molecular weight of DcsB is 29 kDa, which is similar to the calculated one deduced from the amino acid sequence (30 kDa).

## Reference

Holm, L. (2019) Bioinformatics 35, 5326–5327.