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Supporting information for article:

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Figure S1 Alignment of the *M. fumariolicum* SolV DapA sequence with the DapA sequences from eight other bacterial species. The top line is the SolV sequence, the next four sequences are from DapA variants that are inhibited by lysine (allo+), and the last four sequences represent enzymes that are not inhibited by lysine (allo-), as reported by Da Costa *et al.* (2016). Position 56, which is occupied by His or Glu indicates allosteric inhibition is marked in green for allosterically inhibited enzymes, and in purple for enzymes that do not display inhibition by lysine. Furthermore, the catalytic lysine residue is marked in blue, the catalytic triad in red, and residues interacting with lysine in the allosteric pocket in yellow. These latter residues include Glu84 (marked with '#') which is partially conserved in allosterically inhibited enzymes, and is also present in SolV.