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Supporting information for article:

Crystal structure of acetoacetyl-CoA reductase from *Rickettsia felis*

**Justas V. Rodarte, Jan Abendroth, Thomas E. Edwards, Donald D. Lorimer,
Bart L. Staker, Sunny Zhang, Peter J. Myler and Krystle J. McLaughlin**



R. felis
B. pseudomallei
B. anthracis
S. aureus

Supplementary Figure S1. Structural Alignment of acetoacetyl-CoA reductases from *Rickettsia felis* (PDB entry 4kms) and *Burkholderia pseudomallei* (PDB entry 3ezl), and FabGs from *Staphylococcus aureus* (PDB entry 3osu) and *Bacillus anthracis* (PDB entry 2uvd). Tetramers were generated using crystallographic symmetry and aligned in PyMOL.