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Supporting information for article:

**Structural analysis of cofactor binding for a prolyl 4-hydroxylase
from the pathogenic bacterium *Bacillus anthracis***

Nicholas J. Schnicker and Mishtu Dey

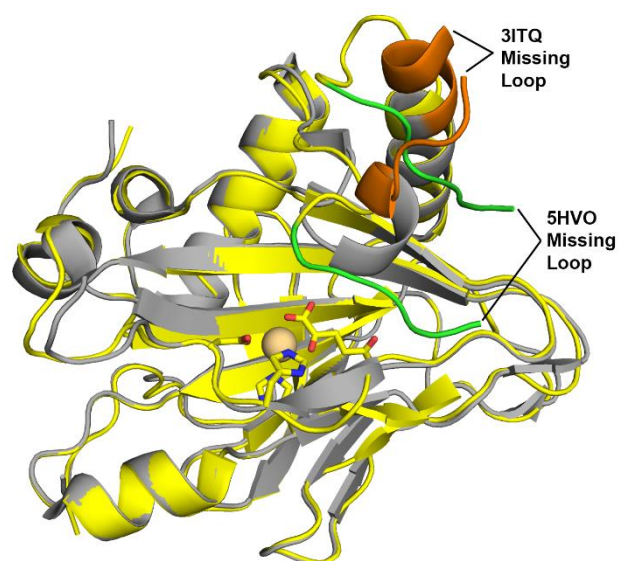


Figure S1 Overall structural comparison of α KG-Cd-BaP4H (yellow, 5HV0) and apo-BaP4H (grey, 3ITQ) showing the differences in the disordered loop region. The region leading up to the missing loop (residues 73-75) for α KG-Cd-BaP4H is shown in green and the region around the missing loop (residues 66-73) for apo-BaP4H is in orange.