Supplementary Figures

Mycobacterium tuberculosis utilizes a unique heterotetrameric structure for dehydrogenation of the cholesterol side chain

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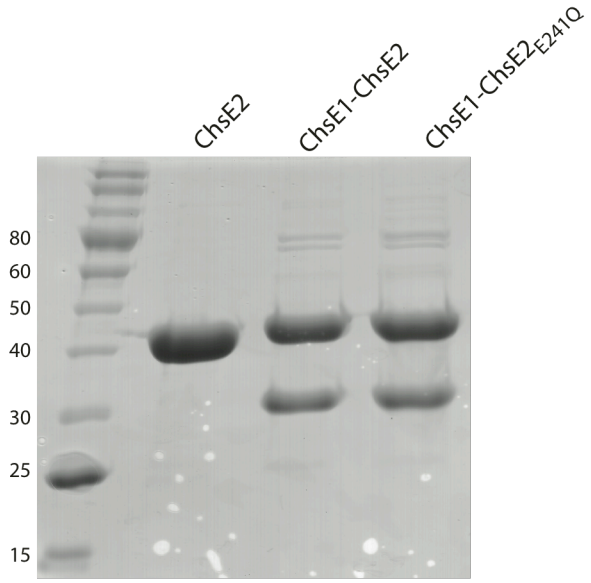

Figure S1. SDS-PAGE of purified proteins studied in this work. 10 μg of each protein sample was analyzed under denaturing conditions on a 15% SDS-PAGE. The gel was stained with coomassie blue.

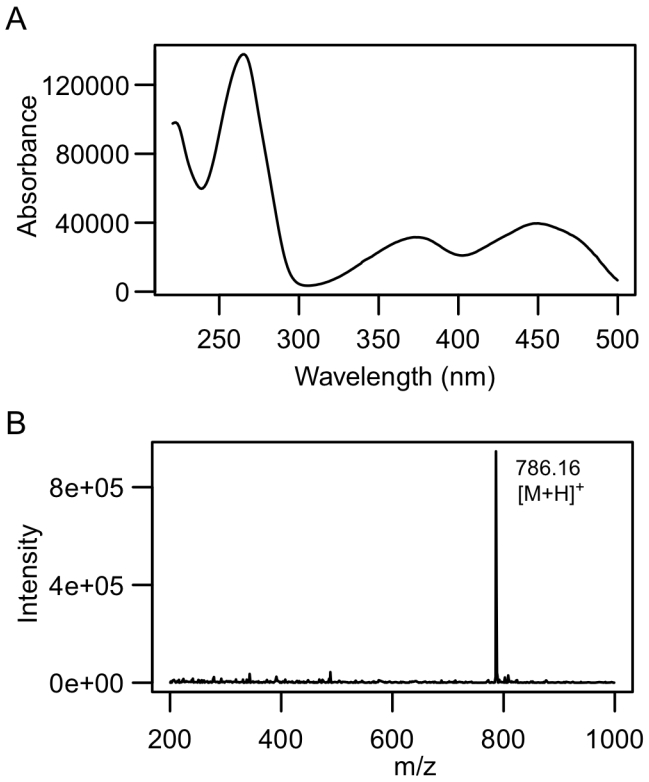

Figure S2. LC/UV/MS of isolated flavin from ChsE1-ChsE2. Isolated flavin from ChsE1-ChsE2 was analyzed by LC/UV/MS. The absorbance spectrum (**A**) and ESi+ MS (**B**) confirmed that ChsE1-ChsE2 was purified with noncovalently bound flavin adenine dinucleotide (FAD).

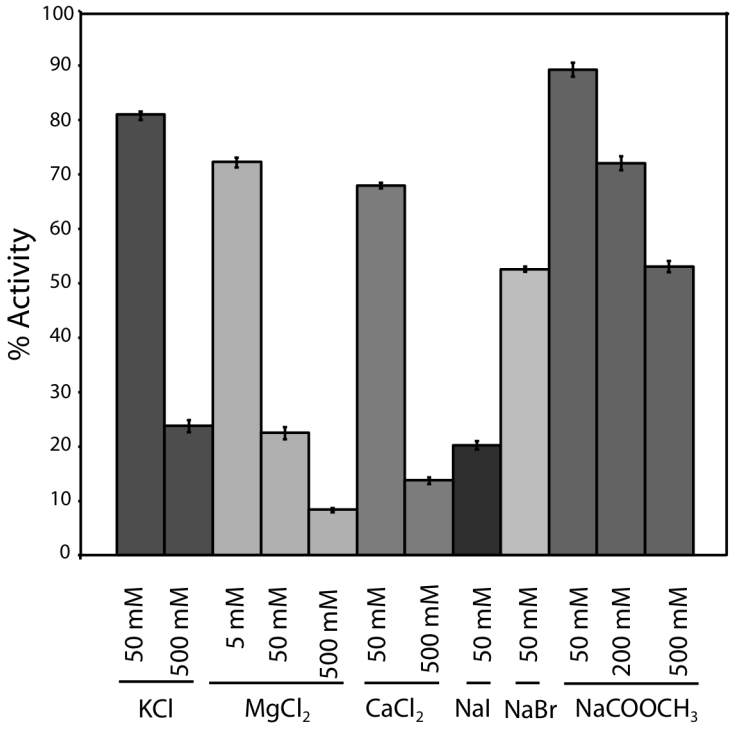

Figure S3. Salt dependence on dehydrogenase activity. ChsE1-ChsE2 was assayed in 100 mM TAPS buffer pH 8.5 with 50 μM of CoA thioester **1** and 250 μM ferricenium hexafluorophosphate. Initial rate data was determined from the reduction of ferricenium hexafluorophosphate at 300 nm. Each assay was conducted in triplicate and shown is the average % activity compared to without salt. The error represents the standard deviation of the measurement.