

Supplementary figure S3

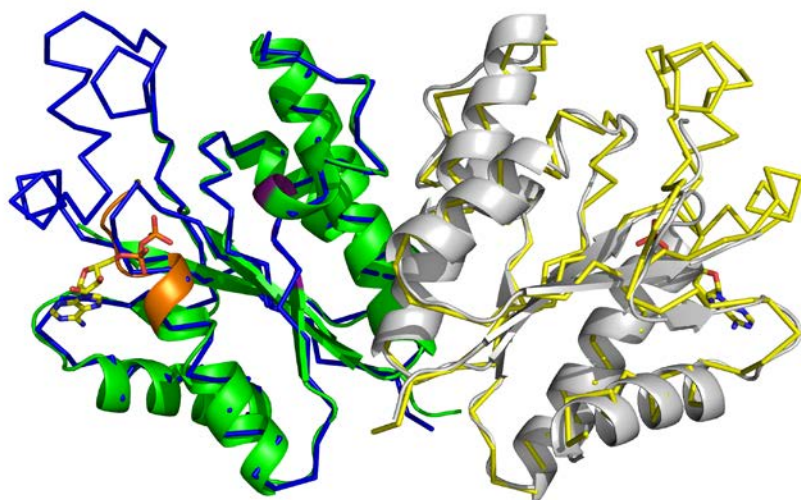
Evidence of redox regulation by a single cysteine residue in the kinase domain of the sulfate-activating complex in *Mycobacterium tuberculosis*

Ömer Poyraz^{a,§}, Katharina Brunner^a, Bernhard Lohkamp^a, Hanna Axelsson^b, Lars G.J. Hammarström^b, Robert Schnell^a and Gunter Schneider^{a*}

Department of Medical Biochemistry and Biophysics, Karolinska Institutet, S-171 77 Stockholm, Sweden

Chemical Biology Consortium Sweden, Science for Life Laboratory Stockholm, Department of Medical Biochemistry and Biophysics, Karolinska Institutet, Solna, Sweden.

[§]Present address: Department of Clinical Neuroscience, Therapeutic Immune Design Unit, Karolinska Institutet, Stockholm, Sweden



S3 Figure. Superposition of the structure of the Cys556Ser mutant and the ADP-bound wild-type CysC. The crystal structure of the Cys556Ser mutant is shown as a cartoon in green (chain A) and grey (chain B). The ligand binding motifs such as the P-loop (orange) and the conserved LDGD motif (purple) are highlighted in chain A. The backbone of the ADP complex of wild-type CysC is shown as ribbon in blue (chain A) and yellow (chain B) and the ADP molecule is shown as stick model.