

The structure of *Acidithiobacillus ferrooxidans* *c*₄-cytochrome: a model for complex-induced electron transfer tuning. *Structure Fold Des.* (In press).

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The study of electron transfer between the copper protein rusticyanin (RCy) and the *c*₄-cytochrome CYC₄₁ of the acidophilic bacterium *Acidithiobacillus ferrooxidans* has evidenced a remarkable decrease of RCy 's redox potential upon complex formation. The structure of the CYC₄₁ obtained at 2.2 Å resolution highlighted a specific Glutamate residue (E121) involved in zinc binding as potentially playing a central role in this effect required for the electron transfer to occur. EPR and stopped flow experiments confirmed the strong inhibitory effect of divalent cations on CYC₄₁:RCy complex formation. A docking analysis of the CYC₄₁ and RCy structure allows us to propose a detailed model for the complex-induced tuning of electron transfer in agreement with our experimental data, which could be representative of other copper proteins involved in electron transfer.