On the interaction between *D. gigas* SOR and rubredoxin

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Superoxide reductase (SOR) is a 29 kDa homodimeric metalloprotein present in the cytoplasm of *Desulfovibrio* (*D.*) *gigas* cells. This protein allows this anaerobic organism to survive under mild exposure to aerobic atmospheres, by converting the radical anion superoxide to hydrogen peroxide without formation of molecular dioxygen. The protein contains two distinct iron centers: center I consists of a tetra-coordinated Fe atom to cysteinyl residues' side chains, while center II, the catalytic center, is comprised of a Fe atom bound to four histidinyl residues' side chains in the equatorial plane, with a fifth ligand provided by a cysteinyl sulfur in the axial plane.[1]

Several attempts have been made to identify and characterize the electron-transfer (ET) partners of SOR [2]. Rubredoxin (Rd) is proposed to be one such partner. This small (6 kDa) monomeric metalloprotein is capable, among other things, of accepting electrons from NADPH:Rubredoxin Oxidoreductase and transferring them to the terminal oxidase of the oxygen detoxification pathway, Rubredoxin:Oxygen Oxidoreductase. Its metal center is very similar to center I of SOR.

ET has been demonstrated to occur between SOR and Rd *in vitro* [2]. In this work, we provide evidence for the formation of the ET complex via 2D NMR titration. This experiment showed that the complex is on fast exchange in the NMR time scale. We were also able to determine the Rd aminoacid residues affected by the formation of the complex. Furthermore, we estimate a value for the dissociation constant, K_d, consistent with the formation of a low-affinity, high-turnover complex.

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