ESRF	**Experiment title:** Structure-function relationships in metalloproteins	**Experiment number**: mx-231
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Shifts: 3	**Local contact(s)**: Gordon Leonard	*Received at ESRF:*

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Report:

The di-haem protein cytochrome *c*4 from *Pseudomonas stutzerii* is used as a model system for cooperative behaviour between metal centres. It consists of two domains, the n- and the c-terminal domain, which are connected by pseudo two-fold symmetry (see Fig. *A*). Previous work on the oxidized and reduced form of the protein make us conclude that the main differences of these are in the dynamics and in the water content (pdb-entries 1m70 and 1m6z). Data collected on ID14-4 to 2.7Å resolution on a mutant protein, Y39F, show that the change in the hydrogen bonding network between the haem groups severely alters the structure of the c-terminal domain. Data to 2.5Å resolution were collected on ID23-1 on a truncated n-terminal form of cytochrome c_4. The structure shows a homo-dimer, where two n-terminal domains fold up like the n- and c-terminal domains in the native cytochrome c_4 (see Fig. *B*). The hydrogen bond network at the interface between the domains is conserved. To provide us with more detailed information we are working on improving the crystal qualities of both the Y39F and of the n-terminal domain protein.

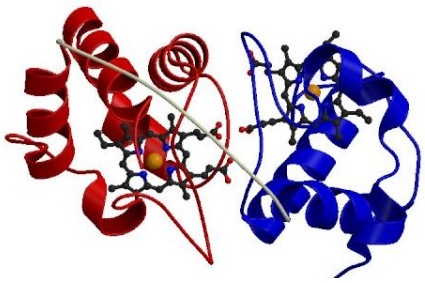

Fig. A: native cytochrome c_4

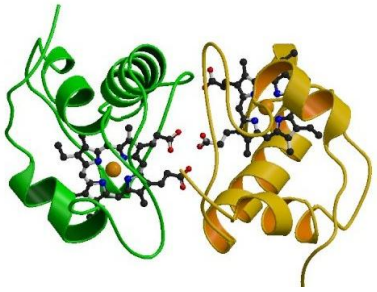

Fig. B: nterminal dimer of cytochrome c_4