| ESRF | **Experiment title:** Data collection on rhod crystals in complex with NO. | **Experiment number:** LS1517 |
|---|---|---|
| **Beamline:** ID14 1 | **Date of experiment:** from: 20/11/99 to: 21/11/99 | **Date of report:** 29.02.00 |
| **Shifts:** 1 | **Local contact(s):** H. Belrhali | *Received at ESRF:* |

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**Report:**

The structure of the enzyme from *A.vinelandii* has been solved at 1.8Å resolution. The active site loop displays striking similarity with the catalytic pocket of dual specific phosphatase Cdc25. The sulfurtransferase/phosphatase activity is under investigation by both biochemical and crystallographic techniques. Concerning the latter approach, soaking with several nucleophilic acceptors, such as cyanide, has shown that the extra sulfur atom covalently bound in the native enzyme to the catalytic Cys230, is assiciated to a structural rearrangement of the active site neighbourhood and partial loss of sulfurtransferase activity. Data collection carried out at middle/high resolution on sulfurtransferase / substrate (inhibitor) complexes is crucial to undestand the catalytic mechanism, also in correlation with the biochemical characterization carried our in parallel on the same substrates.

of complexes with substrates or inhibitors.