ESRF

ESRF	**Experiment title:** StyR: styrene-catabolism regulator in *Pseudomonas fluorescens*	**Experiment number**: MX-267
Beamline: ID14-4	**Date of experiment**: from: 5/3/2004 to: 6/3/2004	**Date of report**: 30/06/2004
Shifts: 1	**Local contact(s)**:	*Received at ESRF:*

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Report:

Introduction

Two-component signal transduction system of response regulation are diffused among prokaryotes and even present in some lower eukaryotes (Stock *et al.* 2000). These systems determine the cellular response to various external solicitations, initiating the related genes expression machinery. Response regulators contains an highly conserved N-terminal regulatory domain, which receives the phosphorylation signal on an invariant Asp residue, and one or more C-terminal signal domains. In particular StyS/StyR constitute the two-component system that in *Pseudomonas fluoresciens* detects the presence of styrene (StyS is the sensor) and activates (StyR is the regulator) the specific genes which initiate the styrene's catabolic pathway. The activation mechanism is based on the autophosphorylation of the sensor kinase StyS that subsequently phosphorylate the regulator StyR determining its dimeric/active state, capable of DNA binding (Leoni et al., 2003). In order to study the dimerization/activation mechanisms we would like to solve StyR structure in

both the inactive (monomeric) and active (dimeric) states. The final goal will be the study of the crystallographic structure of the protein-oligonucleotide complex.

Dataset collected

MAD on StyR (monomeric/inactive form) soaked with $HgCl_2$
wavelenght energies: in=12.284 keV; pk=12.307 keV; rm=12.233 keV
res. 3.5 A

Results achieved

The crystal has high mosaicity and diffracts poorly. The datasets resulted unsuitable to allow the solution of the structure.