ESRF	**Experiment title:** S-Adenosylmethionine-tRNA-ribosyl transferase/Isomerase	**Experiment number**: LS-1603
Beamline:	**Date of experiment**: from: 21-Feb-00 to: 22-Feb-00	**Date of report**: 07-Aug-00
Shifts: 3	**Local contact(s)**: Gordon Leonard	*Received at ESRF:*

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Report:

S-Adenosylmethionine-tRNA-ribosyl transferase/isomerase is involved in the biosynthesis of the hypermodified tRNA nucleoside queuosine. It transfers the ribosyl moiety of S-adenosylmethionine to the amino group of the premodified nucleoside 7-(aminomethyl)-7-deazaguanosine in the wobble position of the anticodon loop, and isomerizes the ribosyl moiety by introduction of an epoxy group. We have crystallized the QueA enzyme from *Bacillus subtilis*. At our in-house rotating anode X-ray generator the crystals diffract only to ca. 8 Å. During experiment LS1603 two complete MAD datasets of a selenomethionyl-QueA as well as three native datasets were collected at beamline ID 14-4 using a CCD detector. Diffraction of up to 2.9 Å was achieved. The space group was *P*422 with unit cell dimensions of ca. 101 Å × 101 Å × 151 Å. The MAD datasets, however, did not allow us the structure determination. Neither by means of the program SOLVE nor the program SnB nor SHELX heavy atom positions could be found which lead to a reasonable solution with the program SHARP. Problems with the refinement of the atomic scattering factors f´ and f´´

indicated a shift in the wavelength during data collection, which renders the repetition of the MAD experiment necessary.

Statistics of datasates collected during exp. LS-1603

Crystal	Wavelength [A]	Completeness [%]	R-factor [%]	Resolution [A]
Se-Deriv 1	0.9787	99.9	5.7	3.5
Se-Deriv 1	0.9791	99.8	5.8	3.6
Se-Deriv 1	0.9393	99.5	6.0	3.7
Se-Deriv 2	0.9788	99.7	5.7	3.4
Se-Deriv 2	0.9791	99.2	5.8	3.5
Se-Deriv 2	0.9393	98.5	6.2	3.6
Native 1	0.9393	98.8	5.9	3.3
Native 2	0.9393	85.6	6.4	2.85
Native 3	0.9393	99.3	5.7	3.2