Structural Investigation of a SAM-dependent Methyltransferase Ecm18 Responsible for an Unprecedented Enzymatic Conversion of a Disulfide into a Thioacetal Bond

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The Ecm18 protein crystals we prepared did not diffract well enough to warrant data set collection. However, we were able to collect useful data for another protein; DQ2/DQ8. This crystal diffracted to 3.1 Ang resolution at beamline 13B1. We were able to solve the structure while at the beamline using molecular replacement method.

Diffraction statistics are:

- No. of independent reflections: 19,972
- Resolution range: 30 – 3.1 Å
- Completeness: 92.2%
- I/Sigma: 16

Current refinement statistics are:

- No. of reflections used: 18,943
- Resolution range: 30 – 3.1 Å
- R-free: 0.296
- R-work: 0.230

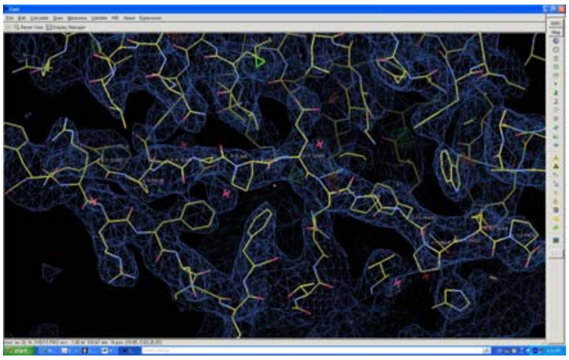

Fig. 1: 3.1 Å molecular replacement structure of HLA-DQ2/DQ8 protein.

For next year, we will improve the quality of both Ecm18 and DQ2/DQ8 crystals in order to obtain higher resolution diffraction data.