

Crystal Structures of *Helicobacter Pylori* Antibacterial Targets

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Helicobacter pylori, a microaerophilic spiral-shaped Gram-negative bacterium, colonizes the human stomach and cause diseases such as gastritis, gastric ulcer, duodenal ulcer and gastric cancer. Approximately two-thirds of the world's population is infected with *H. pylori*. It has been a model system for the study of molecular virulence and pathogen-cell interaction at a molecular basis. Multiple factors are believed to participate in different outcomes of the infection: difference degree of virulence from bacterial polymorphisms, the host response itself, and environmental influences.

In this beamline study, several crystal data sets of HP1238-soaking proteins were collected using synchrotron radiation source. We collected one sets of complex data and the crystals diffract to the resolution of about 2.0 Å with mosaicity of 0.62 and the overall R_{merge} about 8.4 %.

In this beamtime, we also collected 3 sets of liganded N-acylamino acid racemase data. N-Acylamino acid racemase (NAAAR) catalyzes the racemization of N-acylamino acids and can be used in concert with an aminoacylase to produce enantiopure α -amino acids, a process that has potential industrial applications. The crystals diffract to the resolution of about 2.0 Å with the mosaicity of 0.33 and the overall R_{merge} below 10 %. Besides, we also collected Epimerase R57A mutant complex. The crystals diffract to the resolution of about 2.75 Å and overall R_{merge} below 10 %. And the Hydantoinase complex crystal, the crystal diffract to the resolution of about 2.75 Å and overall R_{merge} below 10 %.

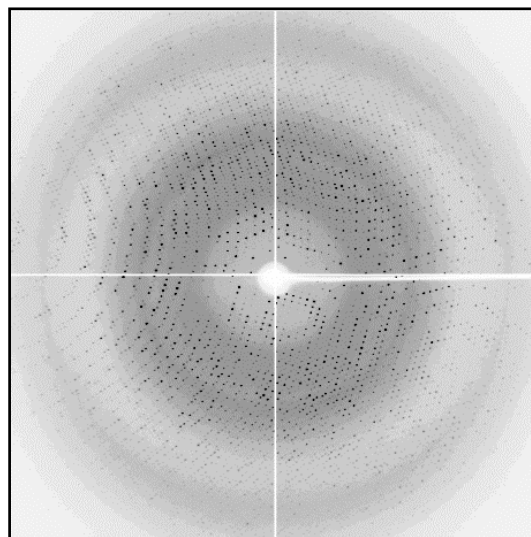


Figure1. Diffraction pattern of liganded NAAAR crystal with 1 degree collected.