



ESRF	Experiment title: Protein crystallographic studies of flagellar HAP2 and F41 fragment of flagellin.	Experiment number: LS952
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Names and affiliations of applicants (*indicates experimentalists):

Namba K.

International Institute for Advanced Research, Matsushita Electric Industrial Co., Ltd.
3-4 Hikari-dai, Seika, Kyoto 619-02, Japan

Imada K*, Samatey F.*, Nagashima S.*

ERATO JST, 3-4 Hikari-dai, Seika, Kyoto 619-02, Japan

Report:

During our beam time, we carried out X-ray diffraction experiments for crystals of two proteins, 1) flagellin fragment F41 and 2) flagellar HAP2. We collected seven data sets and two of them were useful for structure analysis.

1) The F41 fragment was **crystallized** by the hanging drop vapor diffusion method. Although the crystal can diffract up to **3.0Å** resolution, the exposure time required for data collection on a conventional X-ray source was too long (more than 4 hours for one frame). The space group of the crystal is P21 with the cell constant **a=51.9Å b=37.0Å c=120Å β=91.6°**. Four complete data sets were collected at ID14 3. The data was processed to **2.4Å** resolution with a completeness of 94% and an Rmerge of 5%. One crystal diffracted well up to **1.7Å** resolution, but we could not process the diffraction data due to crystal defects. Heavy atom derivative search is underway.

2) HAP2 was crystallized in two crystal forms (C2 $a=225\text{\AA}$ $b=157\text{\AA}$ $c=212\text{\AA}$ $\beta=102^\circ$ and hexagonal $a=125\text{\AA}$ $c=271\text{\AA}$) by the hanging drop vapor diffusion method. Both crystals can diffract around 3.5\AA on a conventional x-ray source, but several hours of the exposure time is needed for recording one frame. Diffraction data sets were collected at ID14.3. The hexagonal crystal diffracted to higher than 3.0\AA resolution, but it had a serious disorder in one direction. Two data sets were collected for the C2 crystal to 3.5\AA resolution, but they could not be processed because of high **mosaicity**. To overcome the problem, improvement of the freezing condition is now in progress.