

(For JSPS Fellow)

Form B-5

Date (日付)

11/10/2016 (Date/Month/Year: 日/月/年)

Activity Report -Science Dialogue Program-
(サイエンス・ダイアログ事業 実施報告書)

- Fellow's name (講師氏名): Takahashi (ID No. P15386)

- Participating school (学校名): Junior High and Senior High School at Komaba, University of Tsukuba

- Date (実施日時): 24/09/2016 (Date/Month/Year: 日/月/年)

- Lecture title (講演題目): Journey to Crystallography,
From France to Japan

- Lecture summary (講演概要): Please summary your lecture 200-500 words.
Proteins are catalysing most of the chemical reactions in your body. There are a lot of proteins (250 000- 1 000 000) with various functions.

To understand the molecular mechanisms in human body, we need to understand how proteins work. Unfortunately, proteins are small and it is difficult to visualize their structure. There are several techniques to solve the structure of proteins; one of them is X-ray crystallography.

When **X-rays** encounter a crystal, X-ray **scattering** will be particularly strong at some specific angles. From this **X-ray diffraction** we can calculate the position of every atom in the protein.

Protein X-ray crystallography requires several steps:

- 1) Produce large quantity of one protein.
We use **genetically modified organisms** (often bacteria) to express high amount of one protein.
- 2) **Purification** of the protein
We use specific resins to collect our protein from the whole bacteria.
- 3) **Crystallisation** of the protein
We make a drop containing pure protein at high concentration. When the drop dries, protein concentration increases until it becomes precipitate (bad) or crystal (good).

4) **X-ray diffraction** by the protein crystal

We bring the crystal to SPring-8 facility in Hyogo-ken. SPring-8 is a large **synchrotron** radiation facility, in which we can shoot the crystal with X-ray (wavelength 0.1 nm).

Unfortunately, our trips to SPring-8 are not always successful, but sometimes, X-ray will be diffracted nicely. We can then calculate the position of every atom in the protein.

Other experiment will still be required to confirm the structure we observe really exist physiologically (in our body). And then, it is time to publish our finding and start another project!!

- Language used (使用言語): english

- Lecture format (講演形式):

◆Lecture time (講演時間) 80 min (分), Q&A time (質疑応答時間) 30 min (分)

◆Lecture style (ex.: used projector, conducted experiments)

(講演方法 (例: プロジェクター使用による講演、実験・実習の有無など))

powerpoint presentation with crystal preparation and observation using microscope_

◆Interpretation (ex.: assistance by accompanied person, provided Japanese explanation by yourself) (通訳 (例: 同行者によるサポート、講師本人による日本語説明))

None

◆Name and title of accompanied person (同行者 職・氏名)

◆Other note worthy information (その他特筆すべき事項):

- Impressions and opinions from accompanied person (同行者の方から、本事業に対する意見・感想等がありましたら、お願いいたします。):