

## Structure, rotation, and regulation of ATP synthase ( $F_0F_1$ )

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### 【Outline of survey】

ATP synthase ( $F_0F_1$ ) is one of most ubiquitous, abundant and unusual proteins on the earth. It synthesizes ATP by using a downhill proton flow across membrane. Protons drive the rotation of the central shaft which then sequentially alternate the conformations of the chemical catalytic sites of ATP synthesis. To know the details of this machine, we have to know its atomic structure. This challenge have been rejected for these ten years probably because of the rotational isomerization of the enzyme. Here, we have invented the methods to generate a homogeneous molecules in terms of the rotational positions of the shaft. Also, we plan to visualize the proton-driven rotation of ATP synthase. Another interesting aspect of this enzyme is regulation. Without fuel, this enzyme wastes ATP. We have found that one of subunit, epsilon, may prevent this ATP hydrolysis like a disk brake of the rotation. This regulation will be clarified more.

### 【Expected results】

For the first time, we can tell one of the most important process of life, energy production, in molecular term. This will provide a good reference for other biological process and man-made nano-machines.

### 【References by the principal researcher】

• Hiroshi Ueno, Toshiharu Suzuki, Kazuhiko Kinoshita, Jr., and Masasuke Yoshida  
ATP-driven stepwise rotation of  $F_0F_1$ -ATP synthase *Proc Natl Acad Sci USA*. 102:  
1333-1338 (2005)

【Term of project】 FY2006 - 2010

【Budget allocation】 7,200,000 yen

【Homepage address】 <http://www.res.titech.ac.jp/~seibutu/home.html>