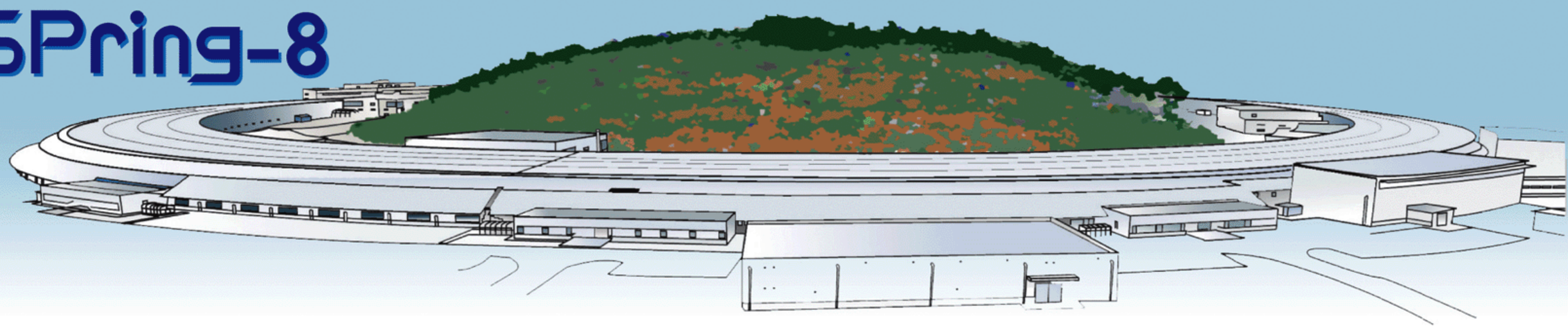
SPring-8



Rhythmic Structural Changes in Cyanobacterial Clock Protein

Professor Takao Kondo and Dr. Shuji Akiyama of the Graduate School of Science, Nagoya University, and their coworkers have clarified that a clock protein of cyanobacteria has a 24 h cycle involving rhythmic expansion and contraction similar to a heart beating. Cyanobacteria are the simplest known form of life with a circadian clock, which comprises three types of clock protein (KaiA, KaiB, and KaiC). Scientists of this research group previously demonstrated that when these clock proteins were mixed in the presence of ATP, the ATPase activity of KaiC and the phosphorylation state change with a period of 24 h. This indicates that the ATPase activity of KaiC is a significant factor in determining the period of circadian clocks. It was hoped to clarify how the molecular structure of KaiC changes with increasing or decreasing ATPase activity.

Scientists in this research group clarified that the shape of a KaiC molecule in solution rhythmically changes with a period of 24 h by means of fluorescence spectroscopy and using RIKEN Structural Biology I Beamline (BL45XU, small-angle X-ray scattering) at SPring-8. KaiC has a double-ring structure similar to a stack of two donuts: the radius of one ring repeatedly increases and decreases while closely associated with the controlled state of ATPase in the other ring. KaiA and KaiB sense these expansions and contractions and use them for the timing of their assembly with and disassembly from KaiC. KaiC converts the reference signals of ATPase into structural changes and couples the changes with the assembly with and disassembly from KaiA and KaiB, realizing dynamic and stable circadian ticking.

In this research, structural changes of KaiC were partly clarified, and a molecular technological basis clarifying the mechanism underlying the circadian ticking of KaiC through the self-control of its ATPase activity was established. It is hoped that the framework of research on molecular clocks using ATP, which is being clarified through the investigation of cyanobacteria, will provide clues leading to the clarification of circadian clocks in higher organisms including humans.

Reference: *The EMBO Journal* **30**, 68 – 78 (2011)

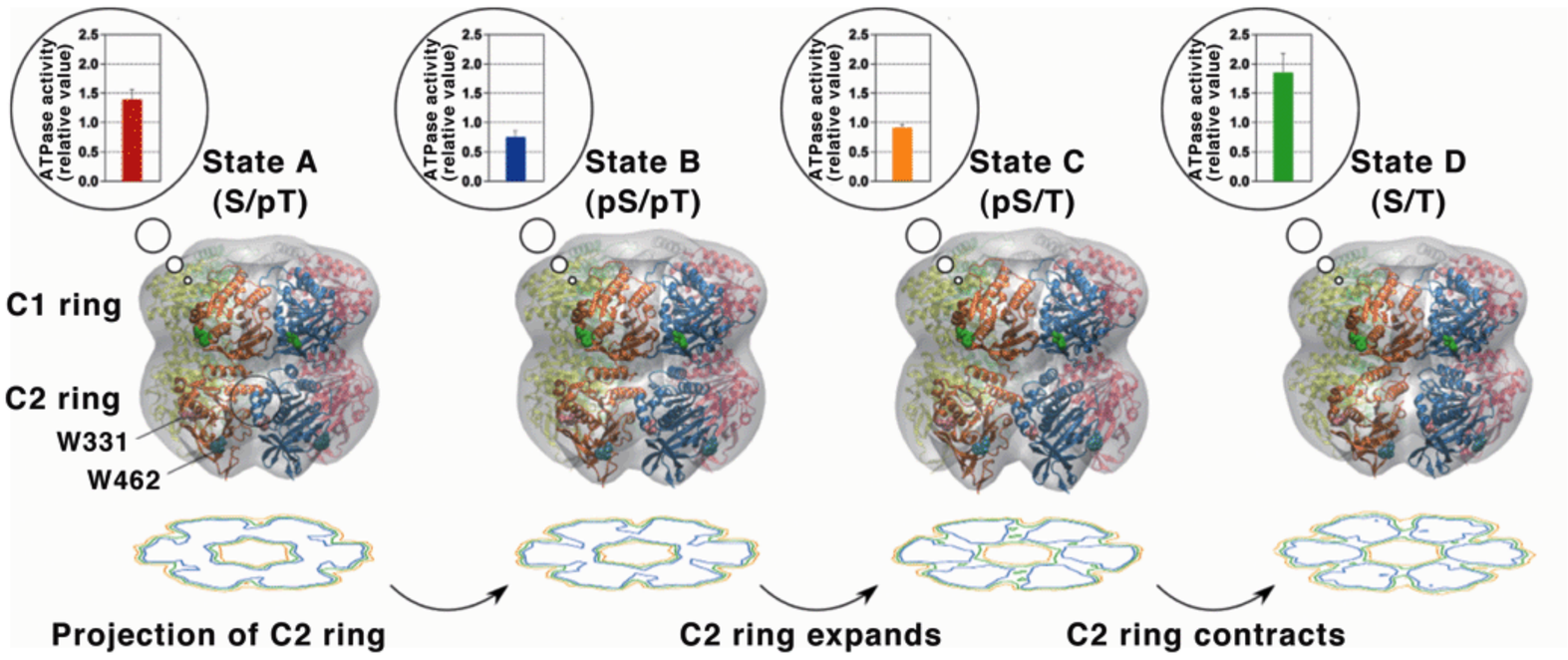


Fig. Expansion and contraction of C2 ring coupled with ATPase activity of KaiC
The gray region represents the shape of the KaiC molecule determined by small-angle X-ray scattering. The ribbon model is a high-resolution molecular model constructed by optimizing the known X-ray crystal structures so as to coincide with the small-angle X-ray scattering data. W331 and W462 represent the tryptophan residues in the C2 ring. Contour plots obtained by projecting the C2 ring alone are shown below each model. The radius of the C2 ring changes negligibly after the transition from state A to state B. After the transition from state B to State C, however, the radius of the C2 ring greatly increases, as indicated by the deepened trough of the counter plot. The expansion and contraction of the C2 ring are coupled with the increase and decrease in the ATPase activity of the C1 ring, respectively.