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Toward the Structural Characterization of the Cyanobacterial KaiABC Circadian Clock. *Rekha Pattanayek, ++Carl H. Johnson, *Martin Egli. *Dept. of Biochemistry, Nashville, TN 37232, ++Dept. of Biological Sciences, Vanderbilt Univ., Nashville, TN 37235.

The properties of circadian clocks, or self-sustained biochemical oscillators, include temperature compensation, a time constant of approximately 24h, and high precision. Analysis continues on the structures, functions, and interactions of the molecular components of circadian clocks in the simplest cells known to exhibit circadian phenomena, prokaryotic cyanobacteria, whose basic clock is composed of three essential clock genes, *kaiA*, *kaiB*, and *kaiC*. We recently determined the crystal structure of the central cog of the KaiABC clock, the KaiC homo-hexamer, in complex with ATP γ S at 2.8 Å resolution (Pattanayek, R. et al., 2004, *Mol. Cell* 15, 375-388). KaiC is an auto-kinase and auto-phosphatase and three potential phosphorylation sites at T432, S431, and T426 have been identified within 10 Å from ATP γ S binding sites (Xu, Y. et al., 2004, *PNAS* 101, 13933-13938). Single or combination mutation of these residues to Ala affects KaiC phosphorylation levels and abolishes circadian rhythmicity. Since KaiC phosphorylation oscillates over the daily cycle, its regulation (by KaiA and KaiB) is essential for clock function. The status of structural work on Kai proteins and their complexes will be discussed.

