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Perfect Robust Network Architecture of a Bacterial Circadian Clock

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The circadian core clock of cyanobacteria consists of only three proteins, KaiA, KaiB, and KaiC. The readout of the clock status is given by the phosphorylation level of KaiC hexamers that oszillates with 23h period even under *in vitro* conditions. We present a circadian clock model based on mass action kinetics that shows almost perfect agreement with the experimentally found phosphorylation dynamics. The model consists of two feedback loops, with the main oscillatory mechanism realised by a negative feedback via sequestration of the enhancer of KaiC autophosphorylation, that is KaiA. These feedbacks are the reason for the observed outstanding robustness of the KaiABC clock that keeps phase, frequency and amplitude even under concerted serveral fold changes of the Kai protein concentrations.

[1] Clodong S. et al, Molecular Systems Biology, (2007)