

Abstract Submitted
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New and simple post-translational circadian clock models MARK BYRNE, Spring Hill College — The first, and presently only known, protein-based circadian oscillator that functions outside cells (in a “test-tube”) was discovered by Takao Kondo’s lab in 2005 (Nakajima et al, Science 2005). There is evidence that other “post-translational” oscillators are operative in species other than the cyanobacterial species in which they were discovered (O’Neill and Reddy, Nature 2011; Edgar et al, Nature 2012). This raises the interesting experimental and theoretical question of the potential simplicity and ubiquity of protein-based clocks. I will describe some new and simple general designs (mathematical models) for protein-based post-translational circadian clocks. A protein with two modification sites can serve as a sustained limit cycle oscillator if two conditions are met. One condition is that there is a separation of timescales in the regulatory biochemical kinetics of the two sites (“fast” vs “slow” regulation). The second condition is that one of the four possible protein states sequesters the molecules (cofactors) regulating the dynamics of site occupancy.

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