

Corrections

COMMENTARY. For the article “Meshing the gears of the cyanobacterial circadian clock,” by Susan S. Golden, which appeared in issue 38, September 21, 2004, of *Proc. Natl. Acad. Sci. USA* (101,

13697–13698; first published September 14, 2004; 10.1073/pnas.0405623101), Fig. 1 was printed incorrectly due to a printer’s error. The corrected figure and its legend appear below.

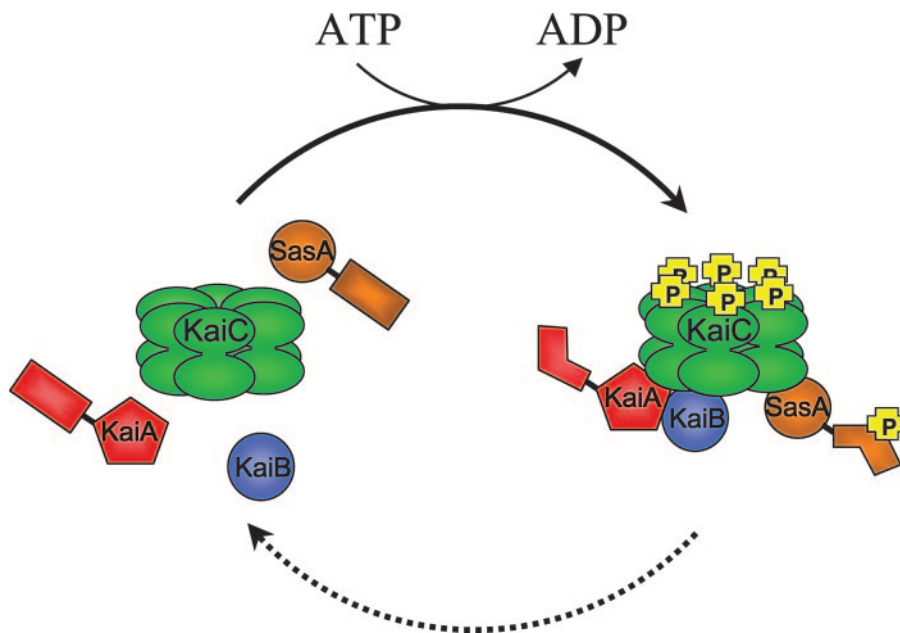


Fig. 1. Phosphorylation of the KaiC hexamer is required for association with the other proteins of the periodosome. Late at night, when KaiC phosphorylation is maximal in the cyanobacterium, KaiA, KaiB, and KaiC, as well as the clock-associated kinase SasA, are recovered together in a high-molecular-weight complex: the periodosome. In wild-type cells, assembly and disassembly of the periodosome occur once per cycle, as does a wave of phosphorylation of KaiC. When key residues of KaiC have been mutated to preclude phosphorylation, the periodosome proteins do not associate, and the circadian rhythms of gene expression are abolished, even though KaiC still forms a hexamer. The figure depicts autophosphorylation of the KaiC hexamer (forward arrow, with ATP hydrolysis) as a prerequisite for association with the other proteins. Only one phosphoryl group is depicted per monomer, although two or more may be present on each subunit. Dissolution of the complex (dashed arrow) may accompany dephosphorylation, but the molecular details of these events have not yet been defined. Drawing by S. R. Canales.

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APPLIED BIOLOGICAL SCIENCES. For the article “*In planta* engineering of viral RNA replicons: Efficient assembly by recombination of DNA modules delivered by *Agrobacterium*,” by Sylvestre Marillonnet, Anatoli Giritch, Mario Gils, Romy Kandzia, Victor Klimyuk, and Yuri Gleba, which appeared in issue 18, May 4, 2004, of *Proc. Natl. Acad. Sci. USA* (**101**, 6852–6857; first published April 21, 2004; 10.1073/pnas.0400149101), the authors note that the communicating editor, Meinhard H. Zenk, is a member of the Supervisory Board for Icon Genetics. Icon Genetics is a provider of new plant engineering technologies that address expression control and safety of transgene management in plants.

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MEDICAL SCIENCES. For the article “Comparative *PRKARIA* genotype–phenotype analyses in humans with Carney complex and *prkar1a* haploinsufficient mice,” by Mark Veugelers, David Wilkes, Kimberly Burton, Deborah A. McDermott, Yan Song, Marsha M. Goldstein, Krista La Perle, Carl J. Vaughan, Art O’Hagan, Kenneth R. Bennett, Beat J. Meyer, Eric Legius, Mervi Karttunen, Reijo Norio, Helena Kaariainen, Michael Lavyne, Jean-Philippe Neau, Gert Richter, Kaan Kirali, Alan Farnsworth, Karen Stapleton, Peter Morelli, Yoshinori Takashi, John-Steven Bamforth, Franz Eitelberger, Irene Noszian, Waldimiro Manfroi, James Powers, Yoshihiko Mochizuki, Tsuneo Imai, Gary T. C. Ko, Deborah A. Driscoll, Elizabeth Goldmuntz, Jay M. Edelberg, Amanda Collins, Diana Eccles, Alan D. Irvine, G. Stanley McKnight, and Craig T. Basson, which appeared in issue 39, September 28, 2004, of *Proc. Natl. Acad. Sci. USA* (**101**, 14222–14227; first published September 15, 2004; 10.1073/pnas.0405535101), the authors note that the abbreviation rMSSD has been incorrectly defined on page 14225 as “root mean square of successful differences” and should have read “root mean square of successive differences.”

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