

Corrections

BIOCHEMISTRY. For the article “Kernel energy method: Application to insulin,” by Lulu Huang, Lou Massa, and Jerome Karle, which appeared in issue 36, September 6, 2005, of *Proc. Natl. Acad. Sci. USA* (**102**, 12690–12693; first published August 24, 2005; 10.1073/pnas.0506378102), the authors note an error in a funding acknowledgment: “L.M. thanks the National Institutes of Health for National Institute of General Medical Sciences Grant MBRS SCORE5 S06GM606654 and National Center For Research Resources Grant RR-0307 and the National Science Foundation for Centers of Research Excellence in Science and Technology grant support” should read: “L.M. thanks the National Institutes of Health for National Institute of General Medical Sciences Grant MBRS SCORE5 S06GM606654 and the National Science Foundation for Centers of Research Excellence in Science and Technology grant support. This investigation was supported by Research Centers in Minority Institutions’ Award RR-03037 from the National Center for Research Resources, National Institutes of Health.”

www.pnas.org/cgi/doi/10.1073/pnas.0507559102

BIOPHYSICS. For the article “Random-coil behavior and the dimensions of chemically unfolded proteins,” by Jonathan E. Kohn, Ian S. Millett, Jaby Jacob, Bojan Zagrovic, Thomas M. Dillon, Nikolina Cingel, Robin S. Dothager, Soenke Seifert, P. Thiyagarajan, Tobin R. Sosnick, M. Zahid Hasan, Vijay S. Pande, Ingo Ruczinski, Sebastian Doniach, and Kevin W. Plaxco, which appeared in issue 34, August 24, 2004, of *Proc. Natl. Acad. Sci. USA* (**101**, 12491–12496; first published August 16, 2004; 10.1073/pnas.0403643101), the authors note the following: “Due to a mathematical error in our analysis, we incorrectly reported the prefactor (R_0) for the Flory scaling relationship observed between the experimental R_G of chemically denatured proteins and their sequence length:

$$R_G = R_0 N^{\nu}.$$

The correct, best-fit value for the prefactor R_0 is $1.927^{+0.271}_{-0.238}$ Å (bounds represent 95% confidence intervals). We apologize for any inconvenience this error may have caused. This error does not affect the conclusions of the article.”

www.pnas.org/cgi/doi/10.1073/pnas.0507472102

EVOLUTION. For the article “The application of statistical physics to evolutionary biology,” by Guy Sella and Aaron E. Hirsh, which appeared in issue 27, July 5, 2005, of *Proc. Natl. Acad. Sci. USA* (**102**, 9541–9546; first published June 24, 2005; 10.1073/pnas.0501865102), the authors note the following: “The stationary distribution of fixed genotypes (Eq. 9) was previously derived (1, 2) in the context of the evolution of transcription factor binding sites, by using detailed balance of the substitution dynamics (Eq. 3). The formula appears slightly different between refs. 1 and 2 and ref. 3, because of slight differences in assumptions; in refs. 1 and 2, continuous time is assumed, whereas in ref. 3, discrete time is assumed. Furthermore, in refs. 1 and 2, fitness is parameterized in terms of molecular distance from an optimum sequence. These authors also discuss a linear combination of fitness and a quantity they call ‘mutational entropy’; when the system is at equilibrium, this combination is very similar to our free fitness.”

1. Berg, J. & Laessig, M. (2003) *Biophysics (Moscow)* **48**, Suppl. 1, S36–S44.
2. Berg, J., Willmann, S. & Laessig, M. (2004) *BMC Evol. Biol.* **4**, 42.
3. Sella, G. & Hirsh, A. E. (2005) *Proc. Natl. Acad. Sci. USA* **102**, 9541–9546.

www.pnas.org/cgi/doi/10.1073/pnas.0507361102

GENETICS. For the article “Loss and gain of chromosome 5 controls growth of *Candida albicans* on sorbose due to dispersed redundant negative regulators,” by M. Anaul Kabir, Ausaf Ahmad, Jay R. Greenberg, Ying-Kai Wang, and Elena Rustchenko, which appeared in issue 34, August 23, 2005, of *Proc. Natl. Acad. Sci. USA* (**102**, 12147–12152; first published August 11, 2005; 10.1073/pnas.0505625102), on page 12152, the first sentence of the last paragraph in the left column, “If each region encompasses at least one *CSU* gene, *CSU51–CSU55*, then three more genes in regions B, C, and 139 are expected” should read: “If each region encompasses at least one *CSU* gene, *CSU51–CSU55*, then four more genes in regions B, 135, C, and 139 are expected.” The conclusions of the article remain unchanged.

www.pnas.org/cgi/doi/10.1073/pnas.0507247102