

## Corrections

**BIOPHYSICS.** For the article “Determination of the binding sites of the proton transfer inhibitors Cd<sup>2+</sup> and Zn<sup>2+</sup> in bacterial reaction centers” by H. L. Axelrod, E. C. Abresch, M. L. Paddock, M. Y. Okamura, and G. Feher, which appeared in number 4, February 15, 2000, of *Proc. Natl. Acad. Sci. USA* (97, 1542–1547), the authors note the following correction. Under the Data

collection heading of Table 1, the second subheading should read, “Total unique observations (highest resolution shell).” A corrected table is reprinted below.

Correction published online before print: *Proc. Natl. Acad. Sci. USA*, 10.1073/pnas.080080297. Text and publication date are at [www.pnas.org/cgi/doi/10.1073/pnas.080080297](http://www.pnas.org/cgi/doi/10.1073/pnas.080080297)

**Table 1. X-ray data collection and refinement statistics**

|                                                             | Cd <sup>2+</sup> -DQ <sub>A</sub> Q <sub>B</sub><br>state (dark) | Cd <sup>2+</sup> -D <sup>+</sup> Q <sub>A</sub> Q <sub>B</sub> <sup>-</sup><br>state (light) | Zn <sup>2+</sup> -DQ <sub>A</sub> Q <sub>B</sub><br>state (dark) |
|-------------------------------------------------------------|------------------------------------------------------------------|----------------------------------------------------------------------------------------------|------------------------------------------------------------------|
| <b>Data collection</b>                                      |                                                                  |                                                                                              |                                                                  |
| Maximum resolution, Å                                       | 2.49                                                             | 2.49                                                                                         | 2.49                                                             |
| Total unique observations (highest resolution shell)        | 94,449 (13,013)                                                  | 92,263 (12,363)                                                                              | 94,967 (12,576)                                                  |
| Redundancy*                                                 | 3.9                                                              | 3.9                                                                                          | 3.9                                                              |
| Mean $I/\sigma(I)$ <sup>†</sup> (highest resolution shell)  | 8.8 (3.6)                                                        | 7.0 (2.3)                                                                                    | 7.0 (2.3)                                                        |
| $R_{\text{sym}}$ <sup>‡</sup> (highest resolution shell), % | 6.5 (21.0)                                                       | 8.9 (33.4)                                                                                   | 8.1 (32.8)                                                       |
| Completeness <sup>§</sup> (last shell), %                   | 99.1 (94.9)                                                      | 95.5 (88.4)                                                                                  | 96.7 (89.0)                                                      |
| <b>Refinement</b>                                           |                                                                  |                                                                                              |                                                                  |
| Resolution range, Å                                         | 50–2.50                                                          | 50–2.50                                                                                      | 50–2.50                                                          |
| Reflections                                                 | 93,504                                                           | 92,156                                                                                       | 94,672                                                           |
| $R$ factor, <sup>¶</sup> %                                  | 22.7                                                             | 22.6                                                                                         | 23.8                                                             |
| $R_{\text{free}}$ , <sup>  </sup> %                         | 25.7                                                             | 25.2                                                                                         | 26.5                                                             |
| Deviation from ideal bond lengths, Å                        | 0.012                                                            | 0.013                                                                                        | 0.014                                                            |
| Deviation from ideal bond angles, °                         | 1.7                                                              | 1.6                                                                                          | 1.7                                                              |

\*Ratio of the total number of reflections measured to the total number of unique reflections.

<sup>†</sup> $I/\sigma(I)$  is the ratio of the average of the diffraction intensities to the average background intensity.

<sup>‡</sup> $R_{\text{sym}} = \sum_{hkl} \sum_j |I_{hkl} - \langle I_{hkl} \rangle| / \sum_{hkl} \sum_j I_{hkl}$ , where  $\langle I_{hkl} \rangle$  is the average intensity for a set of  $j$  symmetry-related reflections and  $I_{hkl}$  is the value of the intensity for a single reflection within a set of symmetry-related reflections.

<sup>§</sup>Completeness is the ratio of the number of reflections measured to the total number of possible reflections.

<sup>¶</sup> $R$  factor =  $(\sum_{hkl} |F_o| - |F_c|) / \sum_{hkl} |F_o|$  where  $|F_o|$  is the observed structure factor amplitude and  $|F_c|$  is the calculated structure factor amplitude.

<sup>||</sup> $R_{\text{free}} = (\sum_{hkl, T} |F_o| - |F_c|) / \sum_{hkl, T} |F_o|$ , where a test set, T (5% of the data), is omitted from the refinement.

**GENETICS.** For the article “Conserved characteristics of heterochromatin-forming DNA at the 15q11-q13 imprinting center” by John M. Greally, Todd A. Gray, James M. Gabriel, Li qun Song, Sharon Zemel, and Robert D. Nicholls, which appeared in number 25, December 7, 1999, of *Proc. Natl. Acad. Sci. USA* (96, 14430–14435), the authors note the following correction. The institutional affiliation of Todd A. Gray, James M. Gabriel, and Robert D. Nicholls is the Department of Genetics, Case Western Reserve University School of Medicine and Center for Human Genetics, University Hospitals of Cleveland, Cleveland, OH 44106. The institutional affiliation of Li qun Song and Sharon Zemel is the Department of Pediatrics, Yale University School of Medicine, 333 Cedar Street, New Haven, CT 06520.

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**GENETICS.** For the article “Quantifying single gene copy number by measuring fluorescent probe lengths on combed genomic DNA” by John Herrick, Xavier Michalet, Chiara Conti, Catherine Schurra, and Aaron Bensimon, which appeared in number 1, January 4, 2000, of *Proc. Natl. Acad. Sci. USA* (97, 222–227), the authors note the following: We wish to thank J. M. Delabar and, particularly, C. Lopes for the gift of the cosmid clones (isolated from the Imperial Cancer Research Fund chromosome 21 library), which are localized in the CBR-ERG region as described in ref. 1 below.

1. Dahmane, N., Ghezala, G. A., Gosset, P., Chamoun, Z., Dufresne-Zacharia, M. C., Lopes, C., Rabatel, N., Gassanova-Maugenre, S., Chettouh, Z., Abramowski, V., et al. (1998) *Genomics* 48, 12–23.