Corrections

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Biochemistry. In the article "Synergistic binding of the *Vibrio fischeri* LuxR transcriptional activator domain and RNA polymerase to the *lux* promoter region" by Ann M. Stevens, Katherine M. Dolan, and E. P. Greenberg, which appeared in number 26, December 20, 1994, of *Proc. Natl. Acad. Sci. USA*

(**91**, 12619–12623), Fig. 4 was printed incorrectly. Specifically, the lower parts of lanes 3 and 10 in *A* were partially obscured, and the entire figure appeared too light, so that some bands were not clearly visible. The corrected figure and its legend are shown here.
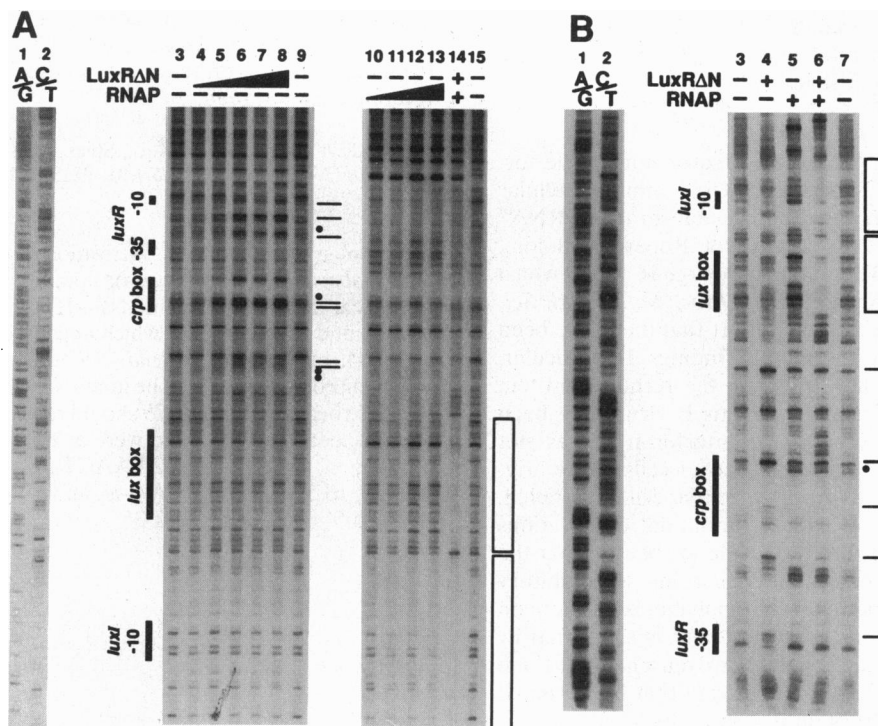

Fig. 4. DNase I protection analysis of LuxRΔN binding and RNAP binding to wild-type *lux* regulatory DNA from pAMS103. (*A*) *luxR* coding DNA strand. Lanes: 1 and 2, A/G and C/T sequencing ladders; 3, 9, and 15, no protein added; 4–8, LuxRΔN at 1.7, 3.5, 6.9, 10, and 14 μM; 10–13, RNAP holoenzyme at 11.5, 23, 46, and 92 nM; 14, LuxRΔN (10 μM) and RNAP (23 nM) together. (*B*) *luxI* coding strand. Lanes: 1 and 2, A/G and C/T sequencing ladders; 3 and 7, no protein added; 4, LuxRΔN (10 μM); 5, RNAP holoenzyme (23 nM); 6, LuxRΔN (10 μM) and RNAP (23 nM) together. The locations of the *luxI* −10 region, *lux* box, *crp* box, and *luxR* −10 and −35 regions are indicated by the solid lines. Hypersensitivity in the presence of LuxRΔN is indicated by the lines, and protection by LuxRΔN is indicated by the dots (not all hypersensitive or protected bands are indicated). The regions protected by LuxRΔN and RNAP together are indicated by the open boxes.

Medical Sciences. In the article "Infectious amyloid precursor gene sequences in primates used for experimental transmission of human spongiform encephalopathy" by L. Cervenáková, P. Brown, L. G. Goldfarb, J. Nagle, K. Pettrone, R. Rubenstein, M. Dubnick, C. J. Gibbs, Jr., and D. C. Gajdusek, which

appeared in number 25, December 6, 1994, of *Proc. Natl. Acad. Sci. USA* (**91**, 12159–12162), the authors request that the following correction be noted. The last entry in the middle column of Table 1 (page 12162) should have been 95.3%, rather than 96.3%. The corrected table reads as follows.

Table 1. Comparison of infectious amyloid precursor nucleotide and predicted amino acid homology to transmission rates of human spongiform encephalopathy in experimental primates

Species	Nucleotide homology, %	Amino acid homology, %	Transmission rate (positive/total animals)
Gorilla (ape)	99.6	99.2	Not inoculated
Chimpanzee (ape)	99.3	99.2	97 (28/29)
Rhesus (Old World) monkey	95.8	96.8	73 (19/26)
Spider (New World) monkey	95.3	96.1	97 (30/31)
Squirrel (New World) monkey	94.3	95.3	93 (196/211)