# Corrections

BIOPHYSICS. For the article "Detecting remotely related proteins by their interactions and sequence similarity," by Jordi Espadaler, Ramón Aragüés, Narayanan Eswar, Marc A. Marti-Renom, Enrique Querol, Francesc X. Avilés, Andrej Sali, and Baldomero Oliva, which appeared in issue 20, May 17, 2005, of *Proc. Natl. Acad. Sci. USA* (**102,** 7151–7156; first published May 9, 2005; 10.1073/pnas.0500831102), the authors note that Fig. 2*b* also inadvertently appeared as Fig. 2*c*. The corrected figure and its legend appear below.
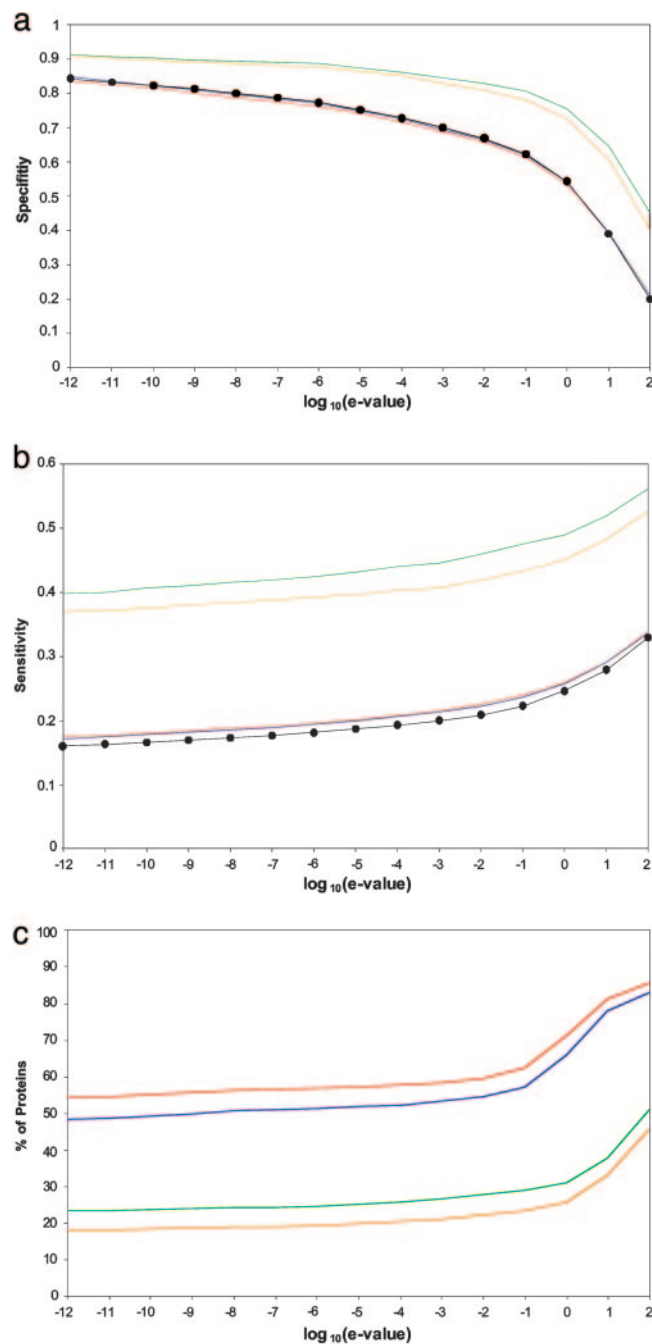
Fig. 2. Specificity, sensitivity, and applicability of fold assignment based on a combination of sequence similarity and protein interactions. The specificity (*a*), sensitivity (*b*), and applicability (*c*) are plotted as a function of the threshold on the PSI-BLAST *e* value for groups G_2 (orange), $G_{1,2}$ (green), $G_{2,4}$ (blue), $G_{1,2,3,4}$ (red), and G_0 (black with filled circles).

MICROBIOLOGY. For the article "The genome sequence of *Bifidobacterium longum* reflects its adaptation to the human gastrointestinal tract," by Mark A. Schell, Maria Karmirantzou, Berend Snel, David Vilanova, Bernard Berger, Gabriella Pessi, Marie-Camille Zwahlen, Frank Desiere, Peer Bork, Michele Delley, R. David Pridmore, and Fabrizio Arigoni, which appeared in issue 22, October 29, 2002, of *Proc. Natl. Acad. Sci. USA* (**99**, 14422–14427; first published October 15, 2002; 10.1073/pnas.212527599), the authors note that, in the course of analyzing repeated elements within the genome of *B. longum* NCC2705, the original genome sequence provided by GATC-Biotech (Constance, Germany) was misassembled because of misplacement of several repeated regions. The genome assembly was corrected and verified by PCR analysis and by Southern blot hybridization, and it was resubmitted to the GenBank database (accession no. AE014295). Region I from the original Fig. 1 is now split into Regions I and IV in the revised figure. The corrected figure and its legend appear below. In addition, on page 14423, the opening sentence of the first paragraph in the second column, which reads "Total GC-skew analysis (9, 16) did not identify any clear origin of replication (OriC), but cumulative GC-skew at the third codon position using ORILOC (17) showed reversal in 6 regions (Fig. 1*B*)," should be replaced by the following: "Cumulative GC-skew analysis at the third codon position using ORILOC (17) showed reversal in two regions (Fig. 1*B*) and identified the origin of replication (OriC) within the region containing *parB*, *parA*, *gid*, *rnpA*, *rpmH*, *dnaA*, *dnaN*, *recF*, *gyrB*, and *gyrA*, with several putative DnaA binding motifs in exact synteny with the confirmed OriC region of *Mycobacterium tuberculosis* (18)." These corrections do not affect the conclusions of the article. We thank Caroline Barretto and Deborah Moine for help in reassembly of the genome sequence and C. A. Roten for helpful discussions.
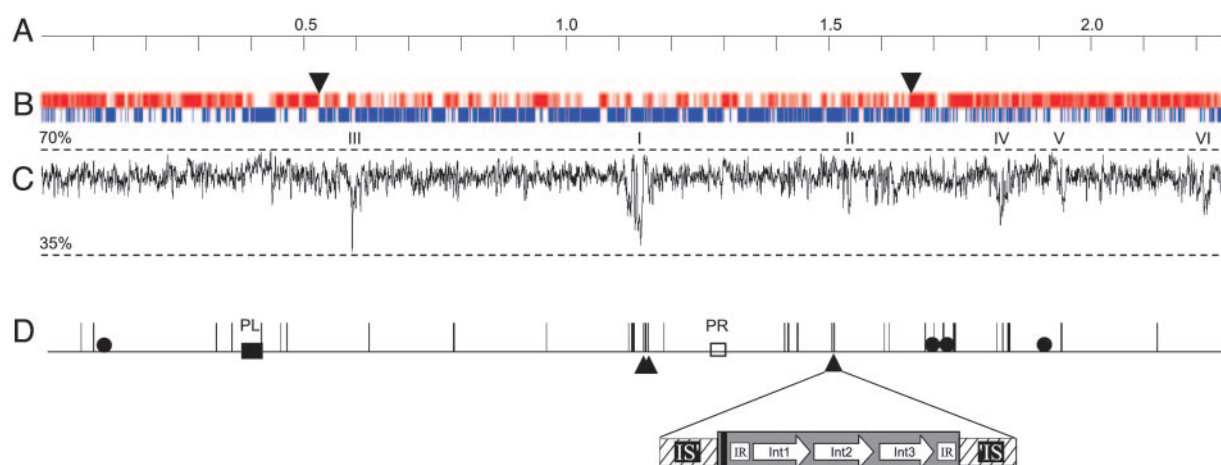
Fig. 1. Linear map of the *B. longum* chromosome. (*A*) Scale in Mb. (*B*) Coding regions by strand. Upper and lower lines represent plus and minus strand ORFs, respectively. Arrows indicate transition points in cumulative GC skew from ORILOC. (*C*) G+C content with scale (window = 1,000). Roman numerals mark regions where G+C is 2.5 SD units below average. (*D*) Intact (two IS*3*-type, five IS*21*-type, three IS*30*-type, five IS*256*-type, and one IS*607*-type) as well as partial IS elements are represented by vertical lines; boxes mark possible prophage remnant (PR) and integrated plasmid (PL). Filled circles represent rRNA operons. Positions of the three nearly identical copies of the potentially new type of mobile genetic element in *B. longum* are indicated by triangles, and an expanded view of one of them is shown. The three different integrases (Int) are represented by arrows; the interrupted IS*3*-type element containing them is hatched. Black bar, 20-bp palindrome; IR, 97-bp perfect inverted repeat.

MICROBIOLOGY. For the article "Cellulose utilization by *Clostridium thermocellum*: Bioenergetics and hydrolysis product assimilation," by Yi-Heng Percival Zhang and Lee R. Lynd, which appeared in issue 20, May 17, 2005, of *Proc. Natl. Acad. Sci. USA* (**102,** 7321–7325; first published May 9, 2005; 10.1073/pnas.0408734102), the authors note that in line 9 of the abstract, $(n - 1)/n$ should be $(n - 2)/n$. According to the analysis presented in the paper, G_{ATP}^{P-T} should be equal to $(n - 2)/n$, as indicated by Eq. **3** and the accompanying text in the main body of the paper. This correction does not alter the conclusions of the article.