Corrections

BIOPHYSICS. For the article "Toward high-resolution prediction and design of transmembrane helical protein structures," by P. Barth, J. Schonbrun, and D. Baker, which appeared in issue 40, October 2, 2007, of *Proc Natl Acad Sci USA* (104:15682–15687; first published September 28, 2007; 10.1073/pnas.0702515104), the authors note that "Renumbering the protein structure files to start at residue 1 in our calculations resulted in shifts in the residue numbering of the protein segments reported in Fig. 1 and Table 2 relative to those in the Protein Data Bank. In the Fig. 1 legend, the middle panels correspond to the helix of halorhodopsin kinked at Pro-117 rather than Pro-94, and the bottom panels correspond to bovine rhodopsin rather than halorhodopsin." These errors do not affect the conclusions of the article. The corrected table and its legend appear below.

Table 2. Native TMH docking tests

		Z_{lrms}	
Protein	Docked residues	Full	No weak/bif HB
Glycophorin A	All	3.26	1.02
Glycerol channel	44–60	2.56	1.89
	239–250	3.59	2.87
PsaL subunit of Photosystem I	47–57	2.22	1.82
Halorhodopsin	24–52	2.37	1.73
	227–255	1.71	1.66
Calcium ATPase	764–775	2.35	1.97
Cytochrome *c* oxidase	Subunit D: 76–89	2.87	2.63
Photosynthetic reaction center	Subunit L: 240–250	2.22	2.01
	Subunit M: 54–67	2.3	1.89
Mean ± SD		2.55 ± 0.55	1.95 ± 0.51

The energy gap between native, near-native (N), and nonnative (NN) docked complexes was assessed by using $Z_{lrms} = (\langle E\rangle_{NN} - \langle E\rangle_{N})/\sigma_E^{NN}$ (see *Materials and Methods*). The contribution of the membrane-specific hydrogen bonding term to the energy gap between native and nonnative docked complexes is analyzed: full membrane potential (Full), potential without membrane-specific side-chain–backbone bifurcated and side-chain–side-chain, backbone–side-chain weak hydrogen bonds (No weak/bif HB). Successful discrimination is defined as a Z score >1.

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EVOLUTION. For the article "Ancient bacteria show evidence of DNA repair," by Sarah Stewart Johnson, Martin B. Hebsgaard, Torben R. Christensen, Mikhail Mastepanov, Rasmus Nielsen, Kasper Munch, Tina Brand, M. Thomas P. Gilbert, Maria T. Zuber, Michael Bunce, Regin Rønn, David Gilichinsky, Duane Froese, and Eske Willerslev, which appeared in issue 36, September 4, 2007, of *Proc Natl Acad Sci USA* (104:14401–14405; first published August 29, 2007; 10.1073/pnas.0706787104), the authors note that, due to a printer's error, the GenBank accession numbers appeared incorrectly on page 14401 in the Data Deposition footnote and on page 14404, left column, last line in *Cloning and Sequencing*. The sequences are deposited in the GenBank database under accession numbers EU083531–EU083798. These errors do not affect the conclusions of the article.

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