Corrections

BIOPHYSICS AND COMPUTATIONAL BIOLOGY

Correction for “Structural insights into the histone H1-nucleosome complex,” by Bing-Rui Zhou, Hanqiao Feng, Hidenori Kato, Liang Dai, Yuedong Yang, Yaoqi Zhou, and Yawen Bai, which appeared in issue 48, November 26, 2013, of *Proc Natl Acad Sci USA* (110:19390–19395; first published November 11, 2013; 10.1073/pnas.1314905110).

The authors note that, due to a printer’s error, references 41–50 appeared incorrectly. The corrected references follow.

41. Schalch T, Duda S, Sargent DF, Richmond TJ (2005) X-ray structure of a tetranucleosome and its implications for the chromatin fibre. *Nature* 436(7047):138–141.
42. Clore GM, Tang C, Iwahara J (2007) Elucidating transient macromolecular interactions using paramagnetic relaxation enhancement. *Curr Opin Struct Biol* 17(5):603–616.
43. Dominguez C, Boelens R, Bonvin AM (2003) HADDOCK: a protein-protein docking approach based on biochemical or biophysical information. *J Am Chem Soc* 125(7):1731–1737.
44. Thakar A, et al. (2009) H2A.Z and H3.3 histone variants affect nucleosome structure: biochemical and biophysical studies. *Biochemistry* 48(46):10852–10857.
45. Vogler C, et al. (2010) Histone H2A C-terminus regulates chromatin dynamics, remodeling, and histone H1 binding. *PLoS Genet* 6(12):e1001234.
46. Wong H, Victor JM, Mozziconacci J (2007) An all-atom model of the chromatin fiber containing linker histones reveals a versatile structure tuned by the nucleosomal repeat length. *PLoS ONE* 2(9):e877.
47. Lee KM, Hayes JJ (1998) Linker DNA and H1-dependent reorganization of histone-DNA interactions within the nucleosome. *Biochemistry* 37(24):8622–8628.
48. Boulikas T, Wiseman JM, Garrard WT (1980) Points of contact between histone H1 and the histone octamer. *Proc Natl Acad Sci USA* 77(1):127–131.
49. Travers AA, Muyldermans SV (1996) A DNA sequence for positioning chromatosomes. *J Mol Biol* 257(3):486–491.
50. Goytisolo FA, et al. (1996) Identification of two DNA-binding sites on the globular domain of histone H5. *EMBO J* 15(13):3421–3429.

www.pnas.org/cgi/doi/10.1073/pnas.1323266111

DEVELOPMENTAL BIOLOGY

Correction for “Organ-specific function of adhesion G protein-coupled receptor GPR126 is domain-dependent,” by Chinmoy Patra, Machteld J. van Amerongen, Subhajit Ghosh, Filomena Ricciardi, Amna Sajjad, Tatyana Novoyatleva, Amit Mogha, Kelly R. Monk, Christian Mühlfeld, and Felix B. Engel, which appeared in issue 42, October 15, 2013, of *Proc Natl Acad Sci USA* (110:16898–16903; first published September 30, 2013; 10.1073/pnas.1304837110).

The authors note that on page 16902, right column, third full paragraph, lines 24–25 “5’-CGGGTTGGACTCAAGACGATAG-3’” should instead appear as “5’-ACAGAATATGAATACCTGATACTCC-3’.”

www.pnas.org/cgi/doi/10.1073/pnas.1323830111

PHYSICS

Correction for “Stable three-dimensional metallic carbon with interlocking hexagons,” by Shunhong Zhang, Qian Wang, Xiaoshuang Chen, and Puru Jena, which appeared in issue 47, November 19, 2013, of *Proc Natl Acad Sci USA* (110:18809–18813; first published November 4, 2013; 10.1073/pnas.1311028110).

The authors note: “Our paper unfortunately missed reference to an earlier suggestion of the T6 structure (43). This work entitled ‘A hypothetical dense 3,4-connected carbon net and related B_2C and CN_2 nets built from 1,4-cyclohexadienoid units’ by M. J. Bucknum and R. Hoffmann was published in *J Am Chem Soc* 116:11456–11464 (1994), where the electronic structure of a hypothetical 3,4-connected tetragonal allotrope of carbon is discussed. The results in this article are consistent with what we find. The same group had also suggested a metallic carbon structure (44) that was published in *J Am Chem Soc* 105:4831–4832 (1983), which we also missed to cite. We thank Prof. Hoffmann for bringing these papers to our attention.”

The complete references appear below.

43. Bucknum MJ, Hoffmann R (1994) A hypothetical dense 3,4-connected carbon net and related B_2C and CN_2 nets built from 1,4-cyclohexadienoid units. *J Am Chem Soc* 116(25):11456–11464.
44. Hoffmann R, Hughbanks T, Kertesz M, Bird PH (1983) Hypothetical metallic allotrope of carbon. *J Am Chem Soc* 105(14):4831–4832.

www.pnas.org/cgi/doi/10.1073/pnas.1323385111

CELL BIOLOGY

Correction for “Visualization of repetitive DNA sequences in human chromosomes with transcription activator-like effectors,” by Hanhui Ma, Pablo Reyes-Gutierrez, and Thoru Pederson, which appeared in issue 52, December 24, 2013, of *Proc Natl Acad Sci USA* (110:21048–21053; first published December 9, 2013; 10.1073/pnas.1319097110).

The authors note that, due to a printer’s error, references 25–29 appeared incorrectly. The corrected references are:

25. Miyanari Y, Ziegler-Birling C, Torres-Padilla ME (2013) Live visualization of chromatin dynamics with fluorescent TALEs. *Nat Struct Mol Biol* 20(11):1321–1324.
26. Sanjana NE, et al. (2012) A transcription activator-like effector toolbox for genome engineering. *Nat Protoc* 7(1):171–192.
27. Ma H, et al. (2012) A highly efficient multifunctional tandem affinity purification approach applicable to diverse organisms. *Mol Cell Proteomics* 11(8):501–511.
28. Uetake Y, et al. (2007) Cell cycle progression and de novo centriole assembly after centrosomal removal in untransformed human cells. *J Cell Biol* 176(2):173–182.
29. Jacobson MR, Pederson T (1997) *RNA traffic and localization reported by fluorescence cytochemistry. Analysis of mRNA Formation and Function*, ed Richter JD (Academic, New York), pp 341–359.

www.pnas.org/cgi/doi/10.1073/pnas.1323494111