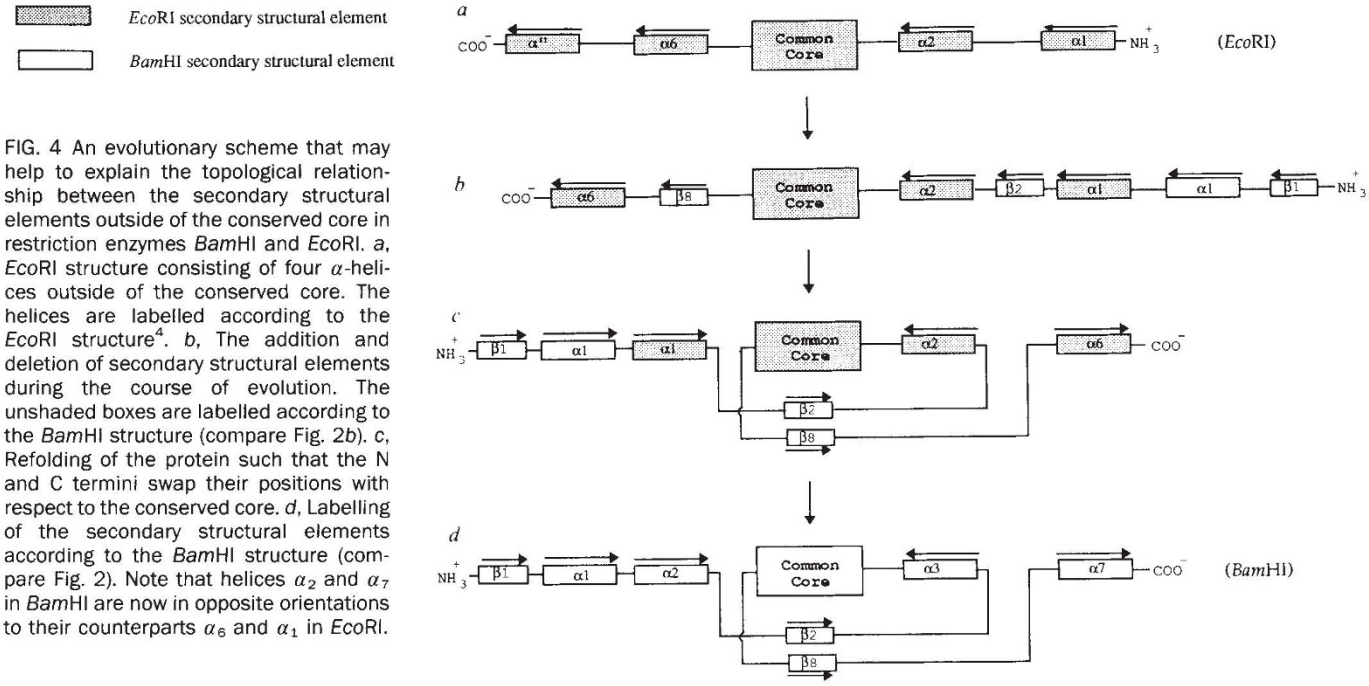

FIG. 4 An evolutionary scheme that may help to explain the topological relationship between the secondary structural elements outside of the conserved core in restriction enzymes *Bam*HI and *Eco*RI. *a*, *Eco*RI structure consisting of four α-helices outside of the conserved core. The helices are labelled according to the *Eco*RI structure[4]. *b*, The addition and deletion of secondary structural elements during the course of evolution. The unshaded boxes are labelled according to the *Bam*HI structure (compare Fig. 2*b*). *c*, Refolding of the protein such that the N and C termini swap their positions with respect to the conserved core. *d*, Labelling of the secondary structural elements according to the *Bam*HI structure (compare Fig. 2). Note that helices α_2 and α_7 in *Bam*HI are now in opposite orientations to their counterparts α_6 and α_1 in *Eco*RI.

unsuccessful attempts to alter the specificity of *Eco*RI (ref. 1) may be indications of the substantially different strategies by which the two enzymes dock to their DNA sites.

In *Bam*HI and *Eco*RI dimers, the active sites are separated by ~17–19 Å along the DNA axis, whereas in *Eco*RV the distance is only ~2 Å. These distances are consistent with the cleavage properties of these enzymes. *Bam*HI and *Eco*RI cleave their DNA recognition sequences at positions that are staggered by four base pairs (bp), producing 5′ overhanging ends, whereas *Eco*RV cleaves its DNA site with a 0-bp stagger, producing blunt ends. The conformation of the common core motif in *Bam*HI and *Eco*RI is ideally suited for the positioning of the two active sites at a relative separation of ~4 bp, spanning the major groove of DNA. In considering other restriction enzymes that might share structural similarity with *Bam*HI and *Eco*RI, it is most likely to be those that also cleave their DNA sites with a (5′) 4-bp stagger[15]. Nature of the cleavage pattern, rather than the actual DNA sequence recognized, may be the most important constraint on the overall conformation of restriction enzymes. □

Received 9 December 1993; accepted 14 February 1994.

1. Heitman, J. in *Genetic Engineering* (ed. Setlow, J. K.) 57–107 (Plenum, New York, 1993).
2. Roberts, R. J. & Halford, S. E. in *Nucleases* (eds Linn, S. M., Lloyd, R. S. & Roberts, R.) (Cold Spring Harbor, New York, 1993).
3. Kim, Y., Grable, J. C., Choi, P. J., Greene, P. & Rosenberg, J. M. *Science* **249,** 1307–1309 (1990).
4. Rosenberg, J. M. *Curr. Opin. struct. Biol.* **1,** 104–113 (1991).
5. Winkler, F. K. *et al. EMBO J.* **12,** 1781–1795 (1993).
6. Hendrickson, W. A. *Trans. Am. cryst. Assoc.* **21,** 11–22 (1985).
7. Otwinowski, Z. in *Isomorphous Replacement and Anomalous Scattering* (eds Wolf, W., Evans, P. R. & Leslie, A. G. W.) (SERC, Daresbury Laboratory, Warrington, UK, 1991).
8. Connolly, B. A., Eckstein, F. & Pingoud, A. *J. biol. Chem.* **259,** 10760–10763 (1984).
9. Grasby, J. A. & Connolly, B. A. *Biochemistry* **31,** 7855–7861 (1992).
10. Xu, S.-Y. & Schildkraut, I. *J. biol. Chem.* **266,** 4425–4429 (1991).
11. Selent, U. *et al. Biochemistry* **31,** 4808–4815 (1992).
12. Jeltsch, A., Alves, J., Maass, J. & Pingoud, A. *FEBS Lett.* **304,** 4–8 (1992).
13. Jeltsch, A., Jurgen, A., Wolfes, H., Maass, G. & Pingoud, A. *Proc. natn. Acad. Sci. U.S.A.* **90,** 8499–8503 (1993).
14. Creighton, R. E. *Protein: Structures and Molecular Properties* (Freeman, New York, 1993).
15. Anderson, J. E. *Curr. Opin. struct. Biol.* **3,** 24–30 (1993).
16. Kabsch, W. & Sander, C. *Biopolymers* **22,** 2577–2637 (1983).
17. Dorner, L. F. & Schildkraut, I. *Nucleic Acids Res.* **22,** 1068–1074 (1994).
18. Kraulis, P. J. *J. Appl. Crystallogr.* **24,** 946–950 (1991).

ACKNOWLEDGEMENTS. We thank W. Hendrickson for advice and encouragement; S. Ealick, C. Escalante, J. Hirsch, E. Jacobson, T. Irving, A. Nakagawa, C. Ogata, N. Sakabe and D. Wah for helping with data collection at CHESS and Photon Factory; and R. Roberts and A. M. Pyle for discussion. Supported by an NIH grant to A.K.A., and in part by a Fogarty International fellowship to M.N.

CORRECTION

Formation of haematopoietic microenvironment and haematopoietic stem cells from single human bone marrow stem cells

Shiang Huang & Leon W. M. M. Terstappen

Nature **360,** 745–749 (1992)

We retract the conclusion of this letter that a single cell can give rise to both a haematopoietic microenvironment and haematopoietic stem cells. Flaws in the material covered in the second paragraph of page 748 to the second paragraph on page 749 in particular lead us to misinterpret some of the critical results. Our subsequent attempts to confirm our key claim have been inconclusive. Cells depicted from the colonies attached to the complex bone marrow structures in Fig. 3*a* can give rise to cell colonies and round dispersed cells with a 'haematopoietic appearance', as shown in Fig. 4*a* and *c*, but immunohistochemical staining indicates that there is a large diversity of mesenchymal-derived cell types. □

ERRATUM

A convective model for the zonal jets in the atmospheres of Jupiter and Saturn

Scott A. Condie & Peter B. Rhines

Nature **367,** 711–713 (1994)

In this letter a line of text was accidentally transposed: the first line of text in the left-hand column on page 713 ("columnar convection[18–20]. However, realistic estimates of . . . ") should have appeared as the first line of text in the right-hand column on page 712. □