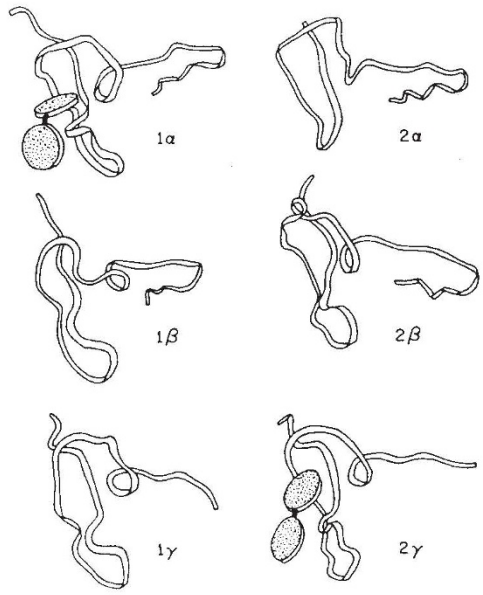

Fig. 3 Conformations of the individual subdomain units. The six subdomain units, presented as backbone ribbon drawings, have been positioned in the same orientation for comparative purposes.

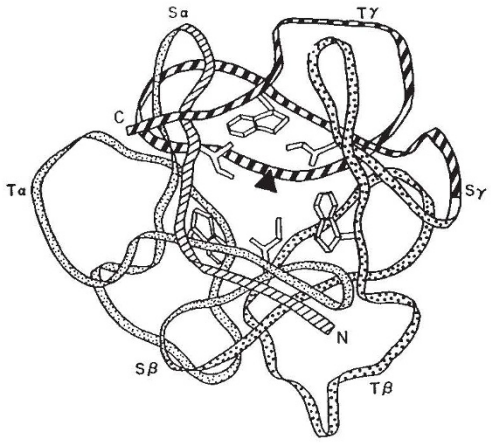

Fig. 4 The pseudo 3-fold arrangement of subdomain units in the amino-terminal domain of ricin B chain. The backbone of domain 1, plus the conservative Trp and Ile side chains are shown. Patterns to distinguish subdomains are as in Fig. 2. S, the start of each unit; T, the twist loop. The same folding pattern can be observed in domain 2 (not shown).

otic genomes, as suggested earlier[10], and with the typical ligand-binding modules suggested to form the building blocks for assembly of protein domains[11]. Interestingly, another plant lectin of known structure, wheat-germ agglutinin, is the product of repeated duplication and fusion of a different, similarly sized peptide[12]. Stringing together multiple copies of a small sugar-binding fold would appear to be a simple and effective method for lectin formation.

It is possible, however, that our primitive 40-residue peptide was itself a duplication product. Traut has suggested that the simplest peptide folding units should be monofunctional[11], but our progenitor peptide is clearly bifunctional, binding both galactose and itself. The α-subdomains contain the repeated motif of a cysteine followed several residues later by the sequence Gln–X–Trp. Both halves have a simple loop structure. A peptide strikingly similar in sequence to a half subdomain can be seen in the structure of *Escherichia coli* galactose-binding protein (GBP)[13] (Fig. 1*a*), although this peptide has no apparent structural similarity to ricin subdomains and is not thought to be part of the binding site of the *E. coli* enzyme. Nevertheless, the idea of a simple short loop structure, capable of binding a biologically important ligand and acting as one kind of primordial molecular building block, is appealing. It is hard to imagine a stable biological element much smaller or simpler than such a loop; in the B chain we see how such loops can be strung together, self-assemble and be perturbed to create a modern functional protein of some complexity.

This research was supported by a grant from the NIH and by a gift from the Cetus Corporation of Emeryville, California. We thank Vivian Benningfield and Terrie Kolvoord for their help with the manuscript and Fred Hoffman for assistance with the figures.

Received 29 October 1986; accepted 9 February 1987.

1. Olsnes, A. & Pihl, A. in *The Molecular Actions of Toxins and Viruses* (eds Cohen, P. & Van Heynigen, S.) 52–105 (Elsevier Biomedical, New York, 1982).
2. Nicolson, G. L. & Blaustein, J. *Biochim. biophys. Acta* **266**, 543–547 (1972).
3. Baenziger, J. U. & Fiete, D. *J. biol. Chem.* **254**, 9795–9799 (1979).
4. Nicolson, G. L., Lacorbiere, M. & Hunter, T. R. *Cancer Res.* **35**, 144–155 (1975).
5. Zentz, C., Frenoy, J. P. & Bourrillon, R. *Biochim. biophys. Acta* **536**, 18–26 (1978).
6. Houston, L. L. & Dooley, T. P. *J. biol. Chem.* **257**, 4147–4151 (1982).
7. Mise, T., Shimoda, T. & Funatsu, G. *Agric. Biol. Chem.* **50**, 151–155 (1986).
8. Hatakeyma, T., Yamasaki, N. & Funatsu, G. *J. Biochem.* **99**, 1049–1056 (1986).
9. Villafranca, J. E. & Robertus, J. D. *J. biol. Chem.* **256**, 554–556 (1981).
10. Robertus, J. D. & Ready, M. P. *J. biol. Chem.* **259**, 13953–13956 (1984).
11. Traut, T. W. *Mol. cell. Biochem.* **70**, 3–10 (1986).
12. Wright, H. T., Brooks, D. M. & Wright, C. S. *J. molec. Evol.* **21**, 133–138 (1985).
13. Mahoney, W. C., Hogg, R. W. & Hermodson, M. A. *J. biol. Chem.* **256**, 4350–4356 (1981).
14. Halling, K. C. *et al. Nucleic Acids Res.* **13**, 8019–8033 (1985).
15. Montfort, W. *et al. J. biol. Chem.* (in the press).

Corrigendum

Lead concentration changes in Antarctic ice during the Wisconsin/Holocene transition

Claude F. Boutron & Clair C. Patterson
Nature **323**, 222–225 (1986).

THERE are two misprints in the published version of this paper: Page 223, in line 26 of the section 'Character of the data', the age of the Wisconsin blue ice block is >10,000 years, not 10,000 years. Line 27 of the same section: lead concentration in this block is 1.75 pg Pb g^{-1}, not <1.75 pg Pb g^{-1}.

There is also some ambiguity in the way that depths are referred to. In most parts of the paper (including Table 1), depths are expressed as *real depths*, but in lines 9–11 of the 'Experimental techniques' section, depth limits for the four climatic stages taken from ref. 27 were expressed as metres of ice equivalent. Transforming these depths into *real depths* the depths of the limits of the four climatic stages become:

(1) Beginning of the Holocene stage: ~408 m (real depth) instead of ~380 m (ice equivalent depth given in Lorius *et al.*[27].

(2) Beginning of the Wisconsin/Holocene transition: ~548 m (real depth) instead of ~520 m (ice equivalent).

(3) Beginning of the Last Glacial Maximum: ~708 m (real depth) instead of ~680 m (ice equivalent). The corresponding paragraph then reads:

"The oxygen isotope profile of Lorius *et al.*[27] shows four main climatic stages: the Holocene stage from the surface down to ~408 m, the Wisconsin/Holocene transition from ~408 to 548 m, the Last Glacial Maximum from ~548 to 708 m, and the earlier Wisconsin stage from ~708 m to the bottom of the core".

Finally, the vertical bars at the top of Fig. 2, p. 224, which show the approximate limits of the four climatic stages are slightly erroneous: they should be slightly shifted toward the right: the Holocene/Transition limit should be at about 10,900 years BP instead of about 10,000 BP; the Transition/Wisconsin limit should be at about 15,800 yr BP instead of about 15,000 yr BP. □