



Oxygen-isotope compositions of the GRIP⁴ and GISP2 (ref. 2) deep ice cores. The shallowest overturned folds, and the shallowest two regions of steep dips, are indicated for each core. The depths of major features in the cores differ slightly owing to well-understood differences in snow accumulation and layer thinning; significant mismatch not explainable in this way occurs deeper than about 2,700–2,750 m.

to the normal to the core axis, within a zone more than 1 m long of dips of 10° or more (compared with a borehole inclination of about 2°), occurs at about 2,757 m in the GRIP core, and steep dips also are observed near 2,847 m. In the GISP2 core, a 50-cm-long region with dips as steep as 20° was observed at 2,679 m, and a region several metres long with dips to more than 20° occurs around 2,809 m, with other regions of steep dips deeper (compared with a borehole inclination of about 5°). We cannot yet guarantee that these are the shallowest occurrences of disturbed features too large to be observed completely within a single core. Most of the ice around these features in both cores is less disturbed, although much disturbance is evident below the GRIP Eemian and below a similar level at GISP2. Significant mismatch between the palaeoclimatic records begins at about the same depth as the large deformational structures, but this correspondence is not exact and some deformation occurs without large mismatch.

(3) Both cores contain evidence of at least moderate simple-shear deformation (strains of the order of 10 or more), including z-shaped folds with overturned limbs smaller than the core diameter. Such z-shaped folds, millimetres high, appear as shallowly as 2,437 m at GISP2 and 2,483 m at GRIP with larger folds deeper, but those at GRIP do not appear as well-developed as those at GISP2 until the lower quarter of the Eemian (2,847 m and below, including the margins of event 2; refs 2,3). The shear sense is consistent within each core. In both cores, the c-axis fabrics are affected by folding and regions

of dips, indicating that deformation is ongoing or sufficiently recent (within about 3,000 years) that the fabric has not been reset by further deformation. GRIP today is near the ice divide, where flow patterns are not expected to produce stratigraphic discontinuities, whereas GISP2 is in a simple-shear, flank-flow regime where stratigraphic discontinuities are more likely. The simple-shear features observed at GRIP suggest recent or ongoing ice-divide migration^{5,6}.

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SIR — Lim *et al.*¹ and Feng *et al.*² showed that Src-homology-3 (SH3) domains can bind two classes of ligand that exist in opposite orientations on the protein-carbon backbone. These elegant studies represent an example of a protein-protein interaction in which the ligand sequence can exist in either N→C or C→N orientation. We have also demonstrated that antibody molecules can similarly recognize protein sequences presented in either orientation³.

These various findings should sound a general warning to the scientific community regarding the use of protein databases for similarity searches to detect related binding motifs. Clearly, such searches should be performed in both forward and reverse carbon-backbone orientations; otherwise, up to half of the functional homology regions could be overlooked.

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Chromosome correction

SIR — Reese *et al.* (*Nature* **371**, 523–527; 1994) published the isolation of two yeast TBP-associated proteins. One of them, named by the authors yTAFII90, corresponds to a gene that we have previously sequenced (L. M. *et al.* *Yeast* **10**, 819–831; 1994). In our paper, we mentioned the strong similarity of YBR1410 with the TAFII80 from *Drosophila* which was at that time the only known sequenced gene of this family. Reese *et al.* used our sequence present in the database, but they erroneously referred to chromosome III sequencing. Thus, we want to correct this point: YBR1410/yTAFII90 belongs to chromosome II (accession number S34023).

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