2)—favourable in both β_P and β_A, favourable in β_A but not in β_P, and unfavourable in both β_A and β_P. (2) β_P 'abhors' polar and charged groups and favours hydrophobic side chains more strongly than β_A: only the purely hydrophobic residues Val, Ile, Leu, Met, Phe are significantly preferred (>1.2) in β_P, whereas in β_A also Thr, Cys, Tyr and Trp, all containing polar atoms, show values above 1.2. (3) Val and Ile are particularly favoured in β_P, with the second largest secondary structure enhancement values reported so far—2.6. Only the value for Pro at the second position in reverse turns[16] is larger—3.4. In β_A the preferences for Tyr and Trp (1.7) are exceptionally large. Note that both have a large non-polar ring in combination with a polar group. (4) The differences between β_A and β_P are particularly large for Gln, Thr, His and Trp (favourable in β_A and unfavourable in β_P); Gln is less favoured in β_P by about a factor of 4.

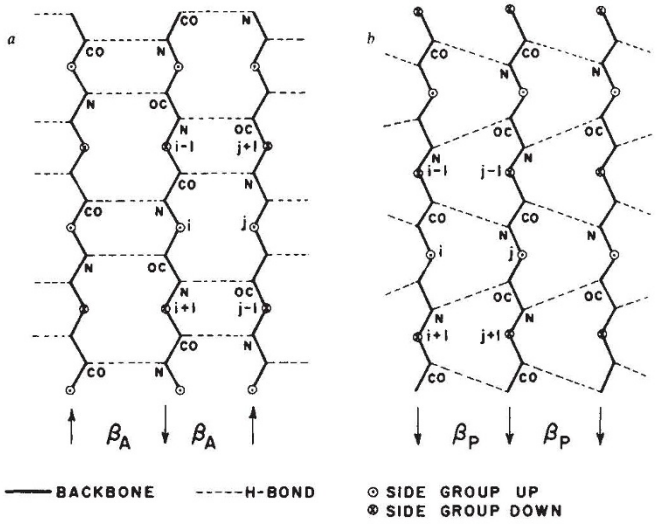

Fig. 1 A schematic drawing of antiparallel (*a*) and parallel (*b*) β-strands. The arrows indicate the N-terminal to C-terminal direction of the polypeptide backbone. Although the (ϕ, ψ) backbone angles are similar for β_A and β_P, the arrangement of the strands and the hydrogen-bonding patterns are fundamentally different. This difference is also reflected in different amino acid preferences.

The results presented here are potentially useful in two ways. On the one hand, they help to pose more specific questions, by focusing attention on those residues which have a special structural role. In this, residues which are both abundant and preferred are the most interesting. For example, one may ask: can Val and Ile serve as nucleation points for β_P-strands by restricting the backbone conformation with their side chains? Do they pack particularly well in the environment of the crossover connection between β_P-strands? Do they interact preferably with each other in forming clusters on the surface of β-sheets? The aim in investigating this type of question is to understand the physical basis of the statistical preferences.

On the other hand, the conformational preferences can be incorporated into structure prediction schemes, allowing distinct predictions for antiparallel and parallel β-stands. However, when this is done the limitations inherent in all statistical approaches to protein structure must be kept in mind: proteins are biologically evolved molecules with a particular structure tailored to a particular function. Only average properties of protein structures can be understood by statistical methods, but not the highly individual character of each protein.

Thus, the main conclusions regarding protein architecture are: (1) antiparallel and parallel β-strands are as distinct in their amino acid preferences as are α-helices and β-strands; (2) parallel β-strands impose much more severe constraints on their amino acid content than antiparallel β-strands or α-helices; (3) Val and Ile have an outstanding role in parallel strands. In a related paper[10], we analyse interstrand pair recognition of amino acid residues and its role in the tertiary structure assembly of strands into sheets.

As more protein structure data become available, further distinctions of secondary structure elements according to the type of tertiary contacts should be made. For example, one can distinguish different hydrogen-bonding positions in β-sheets, solvent-exposed and interior faces of sheets or helices, segments in tertiary contact with sheets compared with those in contact with helices. Such distinctions are likely to lead to more clearcut statistical preferences, and also serve as a starting point for predicting tertiary structure.

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Errata

The letter 'Local destabilisation of a DNA double helix by a T–T wobble pair', *Nature* **281,** 235, was printed with errors in the author line. This line should read:

A. G. Cornelis Haasnoot, Jeroen H. J. den Hartog, Jan F. M. de Rooij, Jacques H. van Boom & Cornelis Altona.

In the paper 'Isolation, cloning and sequence analysis of the cDNA for the α-subunit of the human chorionic gonadotropin', *Nature* **281,** 351, figures 1 and 2 should be transposed. The legends remain as published.

In the paper 'Unmasking of fetal determinants on adult bone marrow cells', *Nature* **281,** 484, the second author should be spelt B. M. Shéinberg.

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