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**STATISTICAL DISTRIBUTION OF
HYDROPHOBIC RESIDUES IN PROTEINS:
IMPLICATIONS FOR PROTEIN FOLDING.**

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The amino acid sequence of any protein reveals that hydrophobic residues appear to occur in clusters along the length of the chain. In this discussion we consider the statistical distribution of hydrophobic amino acid residues along the length of protein chains. For this purpose we use a binary hydrophobicity scale which assigns hydrophobic residues a value of unity and non-hydrophobes a value of zero.

The resulting binary sequences are tested for randomness using several standard tests. For the majority of the more than 5,000 sequences examined, the distribution of hydrophobic residues along the sequences cannot be distinguished from that expected for a random distribution. This suggests that (1) functional proteins may have originated from random sequences, (2) the folding of proteins into compact structures may be much more permissive than previously thought, and (3) the clusters of hydrophobic residues along chains which are revealed by hydrophobicity plots are a natural consequence of a random distribution and can be conveniently described by binomial statistics. Supported by grants from the NSF & NIH.