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STRUCTURAL ROLE OF EXON-CODED FRAGMENT OF POLYPEPTIDE CHAINS IN SELECTED ENZYMES*

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ABSTRACT

The paper [1] discusses the structural role of fragments encoded by individual exons in proteins. Selected enzymes (hydrolases, transferases, ligases) reveal the presence of at least one exon fragment whose contribution to the protein's hydrophobic core is in line with theoretical expectations. This phenomenon is confirmed by quantitative analysis of the hydrophobicity density distribution in protein molecules. Results are compared with a $3D$ Gaussian function, treated as an "idealized" distribution of hydrophobicity density, with the highest values observed near the center of the molecule and near-zero values on its surface. At least one accordant exon fragment has been identified in each of the proteins subjected to analysis. On the basis of these results the authors propose that accordant exons are responsible for tertiary structural stabilization of proteins by ensuring the generation of a stable hydrophobic core.

REFERENCES

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