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In Silico Analysis of Amyloidbeta Precursor Protein in Turkey

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Today, it is known that the breakdown products of amyloid beta precursor protein (APP) accumulate in certain brain areas and form plaques, which slowly and irreversibly damage memory and cognitive functions. This study was conducted with the aim of in silico analysis and understanding the structural relationships of APP in Turkey using bioinformatics tools. For this purpose, the intracellular location and physicochemical properties of APP were predicted using TargetP 1.1 and ProtParam tools, respectively. APP molecular function was predicted with InterProScan and post-translational modifications with the ScanProsite program. YASARA was used to analyze the secondary structure of the protein and, Protscale was used to assess its ability to cross or bind to the membrane. Based on the spatial prediction, the probability of protein transfer to mitochondria and the secretory pathway was 0.090, 0.093, and to other places 0.899, respectively. Physicochemical analysis of APP indicated that the isoelectric point (PI) of the beta-amyloid precursor protein is 4.68 and its instability index is 41.69, which shows the relative instability of this protein in the laboratory. In addition, the aliphatic index and the average total hydrophobicity index (GRAVY) were equal to 69.94 and -0.641, respectively, which indicates the relative hydrophilicity of this polypeptide. The results of the molecular function study of APP determined its role in heparin binding and serine-type endopeptidase inhibitory activity. APP undergoes various post-translational modifications that can affect its aggregation behavior and its relationship with Alzheimer's disease. Based on APP secondary structure analysis, it has an alpha-helix amino acid sequence, and based on Protscale analysis; it can cross the membrane to reach its target organelle through its epitopes. By understanding the cellular and molecular mechanisms of APP, we can diagnose and treat Alzheimer's disease more effectively.

Biography

Sogand Shayesteh is passionate about molecular and systems biology and eager to learn more. Her goal is to conduct an effective research in the field of the biggest neurodegenerative disease - Alzheimer's - by constantly training, targeting repetition, and utilizing a variety of bioinformatics tools. APP was analyzed in silico and its structural relationships in this article; according to research, it forms amyloid-beta, a substance that accumulates throughout the brain, leading to the formation of amyloid plaques or aging, which results in Alzheimer's disease. The number of Alzheimer's cases is predicted to increase to one every 30 seconds in 2050, so as the number of Alzheimer's cases rises, so will the need for diagnostic tests and effective stopping drugs, both of which require a better understanding of Alzheimer's disease's mechanisms. It is the cellular and molecular Alzheimer's disease in which bioinformatic analyzes come to the aid of researchers

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