Poster Presentation

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"How missense mutations contribute towards the stability and morphology of a-synuclein protofibril: A computational study"

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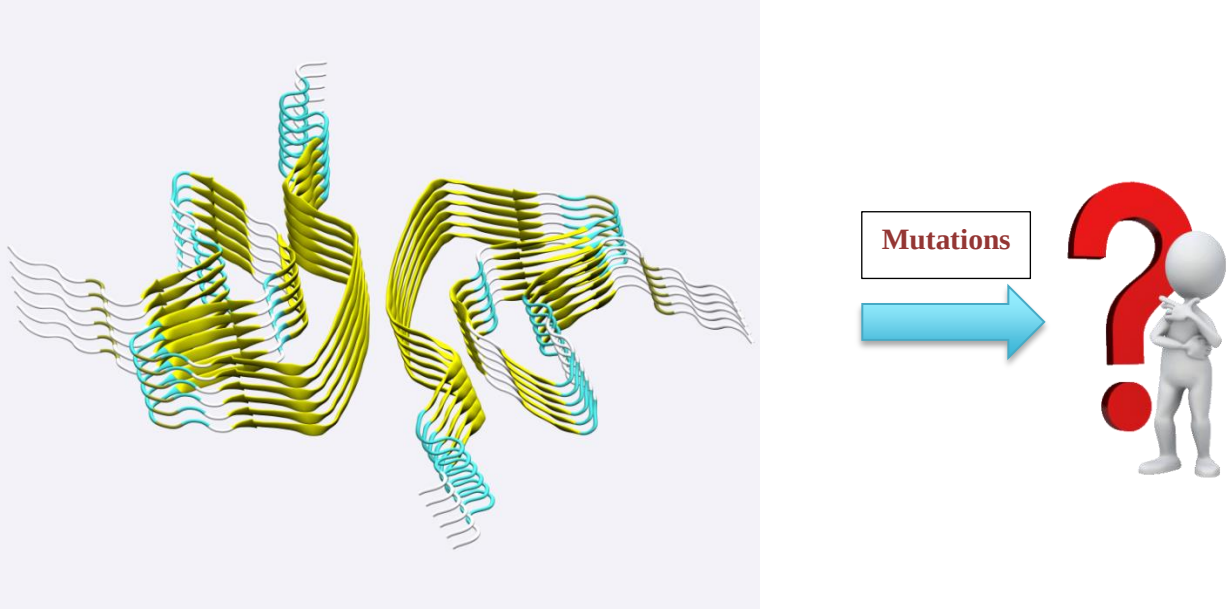
Abstract:

Parkinson's disease, a neurodegenerative disorder, is characterized by progressive deterioration of motor functions due to forfeiture of dopamine-releasing neurons. The neurons affected by Parkinson's disease lose their functionality that results in cognition impairment and forgetfulness, commonly called as dementia. The amyloid aggregation of α-synuclein is central to the etiology of Parkinson's disease. In a recent reported structure[1], researchers have strived to elucidate the structural organization and stability of α-synuclein fibrils at a near atomic resolution (3.07Å). Remarkably, six familial mutations (i.e., A30P, E46K, H50Q, G51D, A53E, and A53T) in α-synuclein are known to be associated with Parkinson's disease and other synucleinopathies. In the present work, we focus on understanding the effects of these missense mutations on the stability and the morphology of α-synuclein fibril using atomistic molecular dynamic simulations and enhanced sampling technique.

Figure:



References and Notes:

[1](1) Li, Y.; Zhao, C.; Luo, F.; Liu, Z.; Gui, X.; Luo, Z.; Zhang, X.; Li, D.; Liu, C.; Li, X. Amyloid Fibril Structure of α-Synuclein Determined by Cryo-Electron Microscopy. *Cell Res.* **2018**, *28* (9), 897–903.