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Abstract

Identifying amyloidogenic regions in protein sequences is useful in understanding the underlying cause of several human diseases and finding potential therapeutic targets. Given the laborious nature of experimental validation of segments most prone to form fibrils, it was essential that computational approaches be developed that could produce reliable, affordable and testable in silico predictions. In this paper, we present and assess some of the recently developed computational tools for predicting amyloid fibril forming motifs that remain as one of the key means used to decipher the role of such regions in disease diagnosis, prognosis and

drug discovery.

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Index Terms

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Key words

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