MS11-1-4 Analysis of interfaces and packing of amyloid peptide structures
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Abstract
Amyloid fibrils are a type of protein aggregates that are associated with both diseases (Alzheimer's, Parkinson's and type 2 diabetes) and biological functions (folding and reservoir). Amyloids feature a common cross beta spine but they are very diverse in overall structure [1]. The dry interface has a particular interest; they are thought to be a main driving force behind the amyloid formation. These interfaces have been studied with smaller peptide sequence models that are still capable of self-assembly. In the last 15 years since the description of the 8 main amyloid classes [2], 180 peptide structures have been deposited in the PDB. In this review we summarize the characteristics of the known structures and analyze them for 3D classification. For assessing their interfaces we utilize novel metrics together with existing ones. Using these tools of structural characteristics of amyloid structures and their protein counterparts are compared.
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References
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