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# Amyloid fibril aggregation by A- $\beta$ (16-22) and the shear-flow effects

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## Résumé

The aggregation of misfolded amyloid proteins into fibrils is a hallmark of several neurodegenerative diseases such as Alzheimer's, Parkinson's, and Huntington's. The structural characterization of self-assembled fibrils formed by  $\beta$ -amyloid and understanding the fibrilization mechanisms are of crucial interest for the prevention of their formation and for medical applications. It was demonstrated experimentally that the formation of fibrils is accelerated via agitation and under fluid shear-flow [1].

We studied the trimer of the seven-residue peptide called A $\beta$ (16-22), a useful model system for physical studies of amyloid fibril formation. We performed extensive replica exchange molecular dynamics (REMD) with a new version of the coarse-grained (CG) force field for proteins OPEP, including ion pairs interactions, which are treated effectively [2]. The most stable conformations extracted from the REMD simulations were used as the starting point for molecular dynamics simulations performed with an in-house developed code (MUPHY/OPEP)[3,4], which allows us to couple the CG model with hydrodynamic interaction and testing the effect of shear flow.

Clustering analysis shows the most probable aggregation states, for which we determined microscopic properties and monitor the stability as a function of temperature and shear flow. We also investigated a bigger system, 20-mer, and observed the starting of the formation of fibrils.

## References

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