## Supporting Information

Solid-State NMR reveals a close structural relationship between amyloid β protofibrils and oligomers

*Holger A. Scheidt, Isabel Morgado, Daniel Huster**

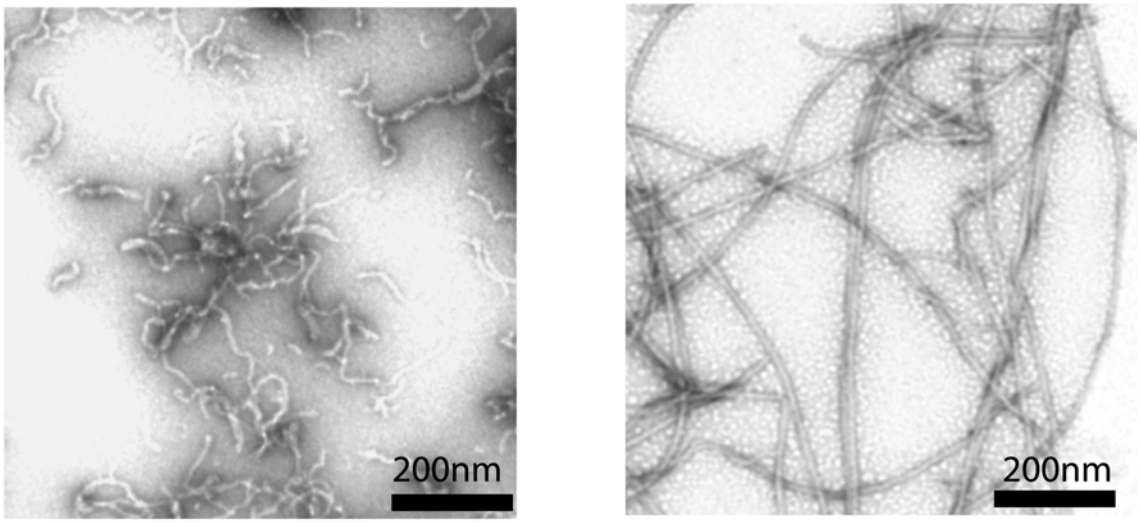


***Figure S1.*** Electron micrographs of Aβ(1-40) protofibrils stabilized by B10AP (left) and mature fibrils (right)

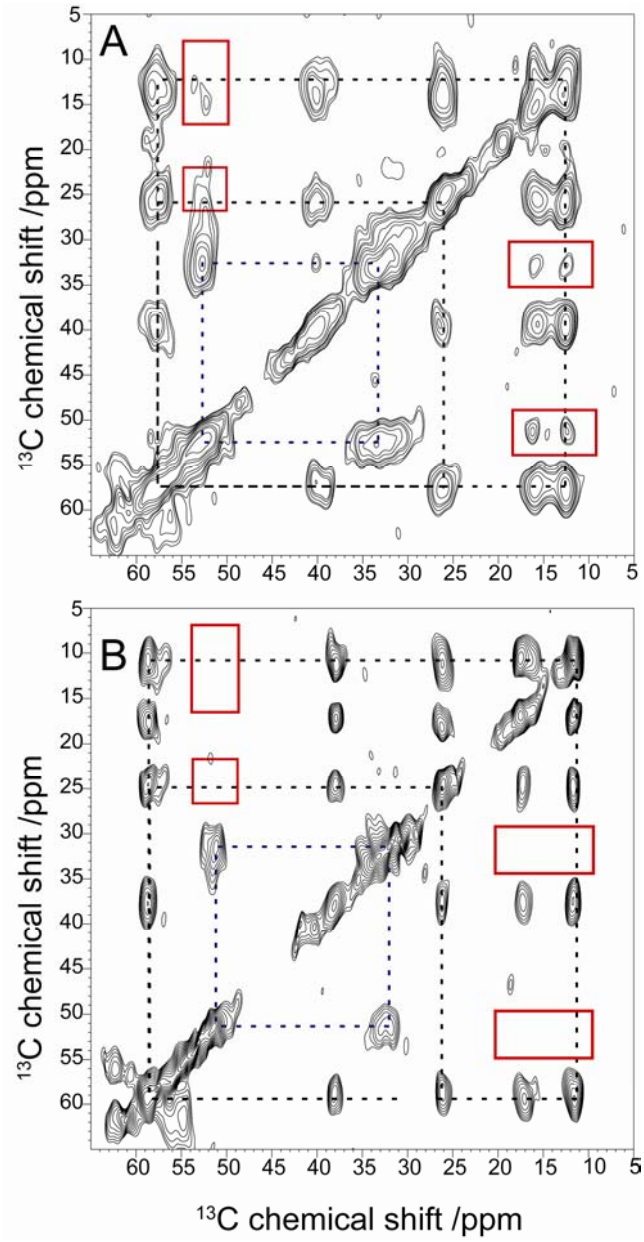


***Figure S2.*** Aliphatic region of the standard Fourier transform processed $^{13}C$-$^{13}C$ correlation spectra (by proton driven spin diffusion with a mixing time of 600 ms) for B10AP-stabilized Aβ protofibrils (A) and mature Aβ fibrils (B). The major correlations inside one and the same amino acid for Glu 22 (blue) and Ile 31 (black) are highlighted. Interresidual cross peaks between Glu 22 and Ile 31 in A and the lack of these cross peaks in B are marked with red boxes.

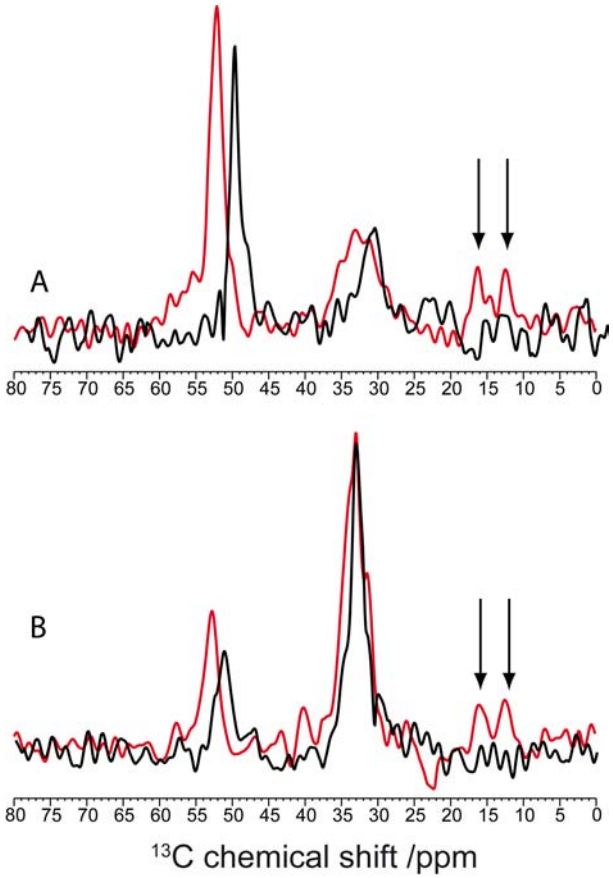


***Figure S3.*** Slices trough the (A) Cα and (B) Cβ peak of Glu 22 for B10AP-stabilized Aβ protofibrils (red) and mature Aβ fibrils (black) of the standard processed PDSD spectra. Interresidual cross peak between Glu 22 and Ile 31 are highlighted by the arrows.

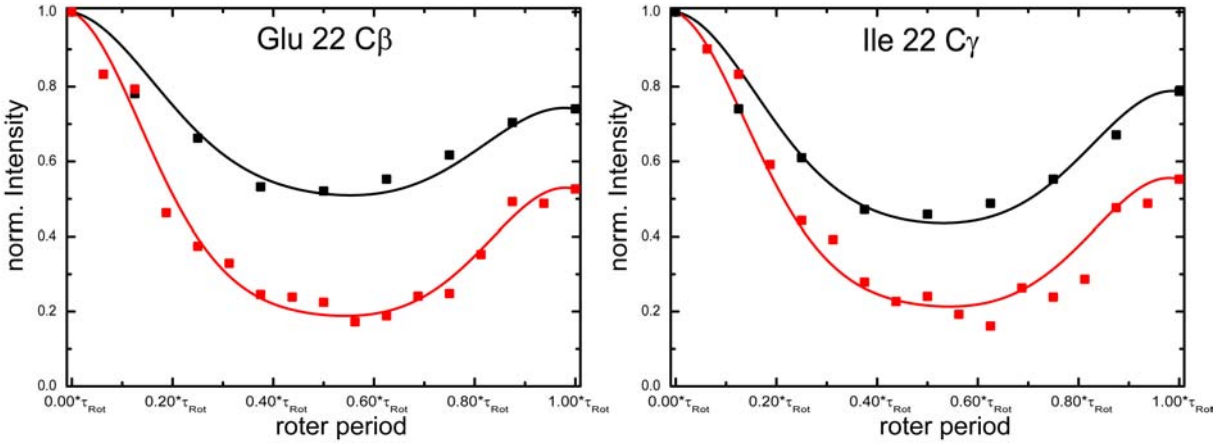


***Figure S4.*** Representative dipolar dephasing curves for the $^{13}C$ MAS NMR signals of Glu 22 Cβ and Ile 31 Cγ for protofibrils (red) and mature fibrils (black) as obtained in the DIPHSIFT experiments (data points). The corresponding numerical simulations for the determination of the dipolar couplings are given as straight lines.