

Supplementary Information

Establishing the Link between Fibril Formation and Raman Optical Activity

Spectra of Insulin

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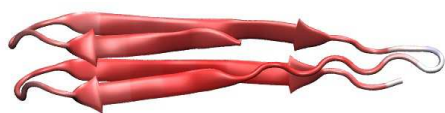
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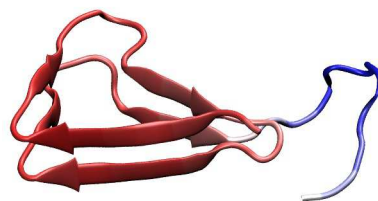
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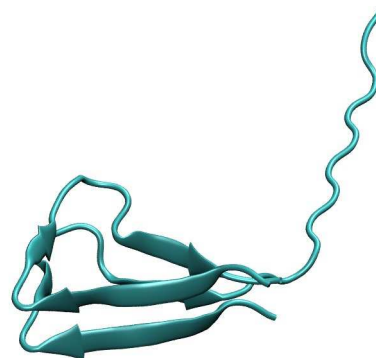
1VH4



1DAB



β -roll



β -helix

Figure S1. The mimicked parts of the 1VH4 and 1DAB proteins (top) and the two initial insulin geometries (bottom).

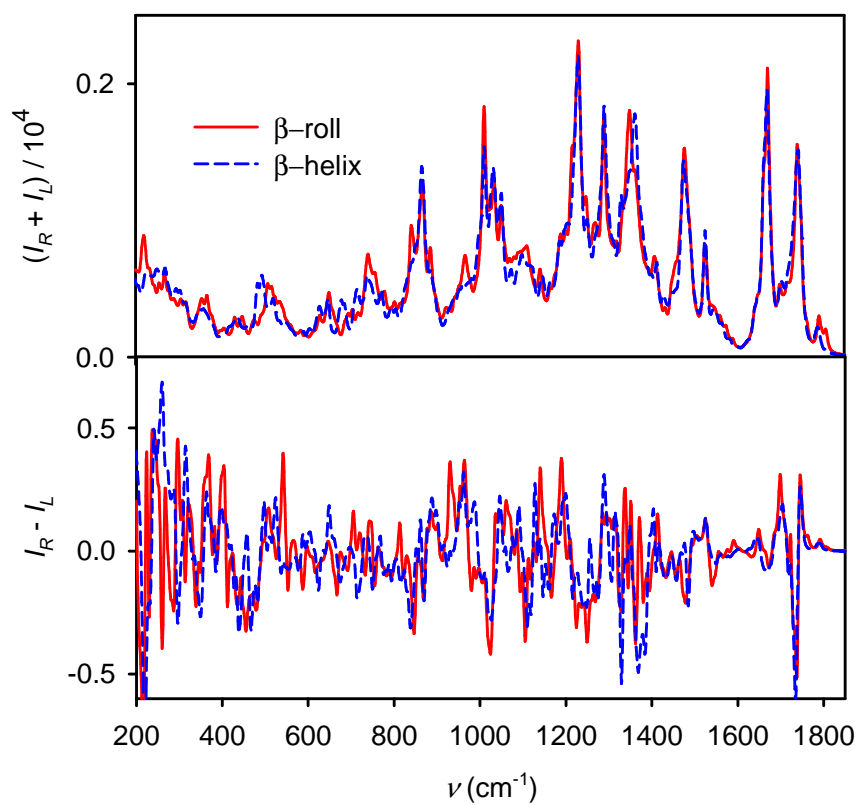


Figure S2. Raman and ROA spectra simulated for the β -roll and β -helix amyloid conformations of insulin.

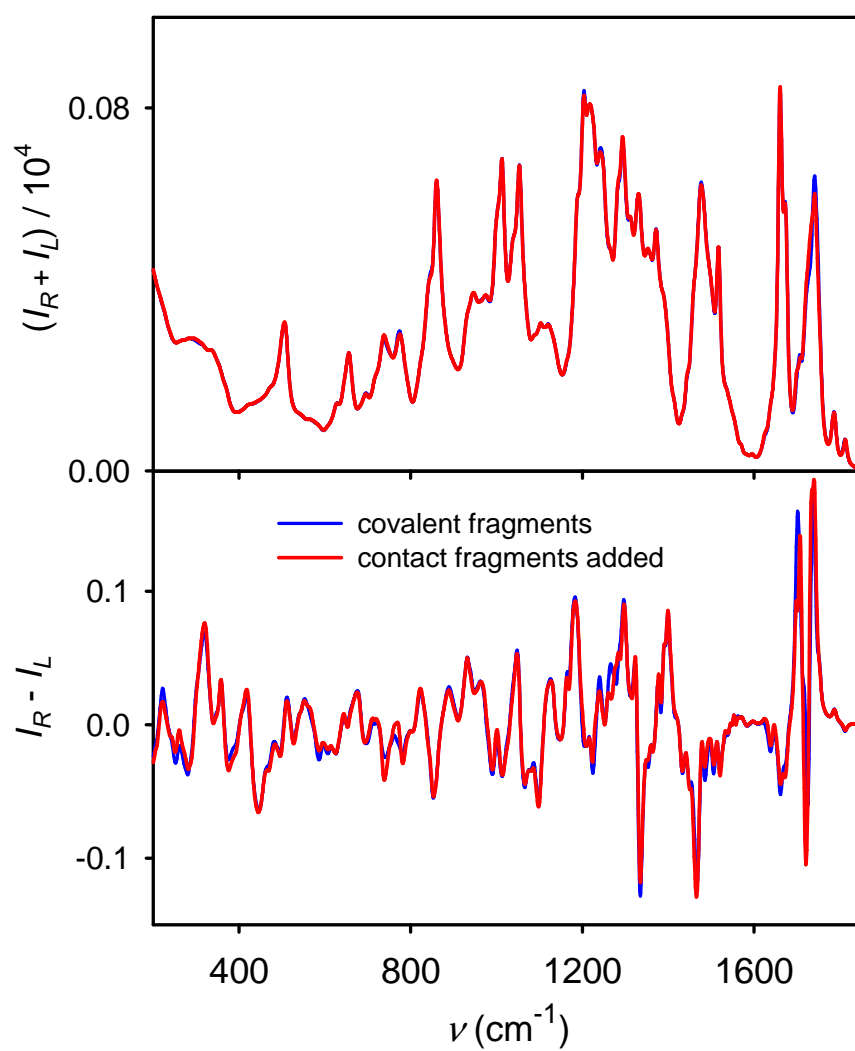


Figure S3. Insulin Raman and ROA spectra (average of 865 MD snapshots) simulated with and without fragments comprising non-covalent interactions between peptide chains.

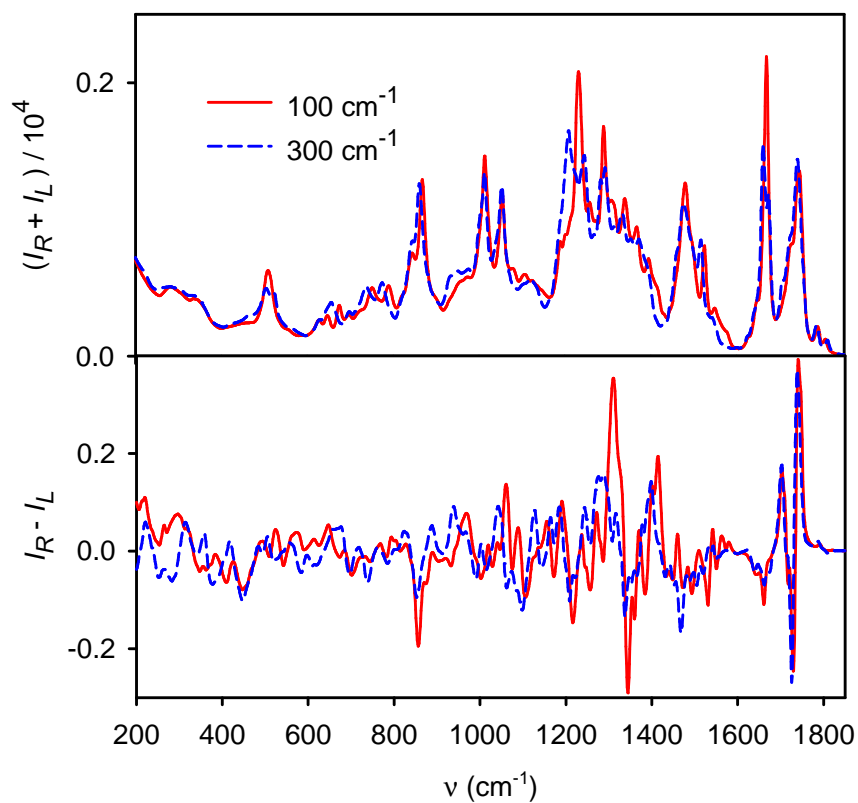


Figure S4. Raman and ROA spectra of the β -roll insulin fibril structure simulated as an average of 865 MD snapshots from fragments optimized with the lower (100 cm^{-1} , red) and higher (300 cm^{-1} , blue) normal mode frequency limit.

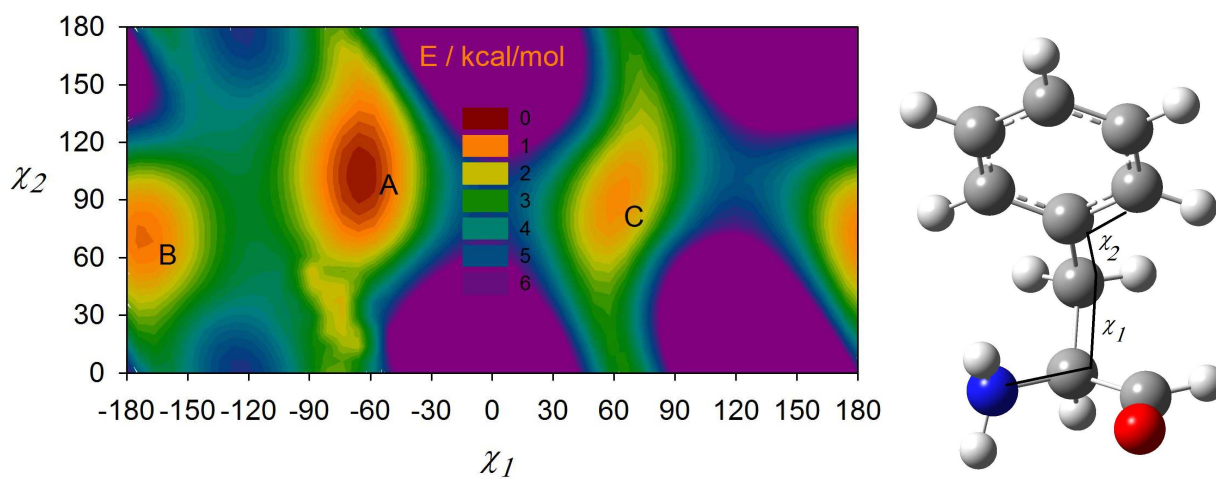


Figure S5. Calculated (B3LYP/6-311++G**/PCM) potential energy surface of the model $\text{NH}_2\text{-Phe-COH}$ residue.

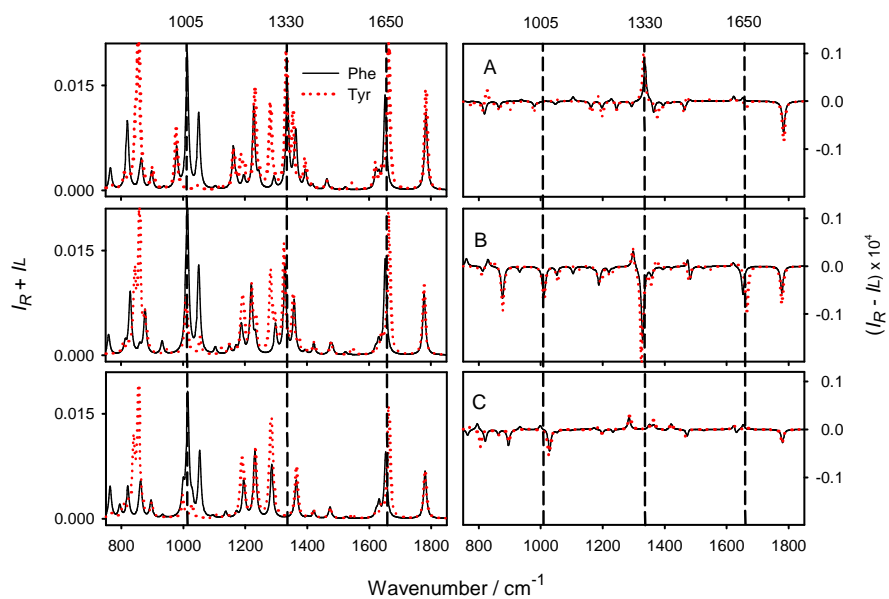


Figure S6. Calculated Raman and ROA spectra of the NH₂-Phe-COH and NH₂-Tyr-COH model molecules; the three A-C conformers are marked as in **Figure S4**.

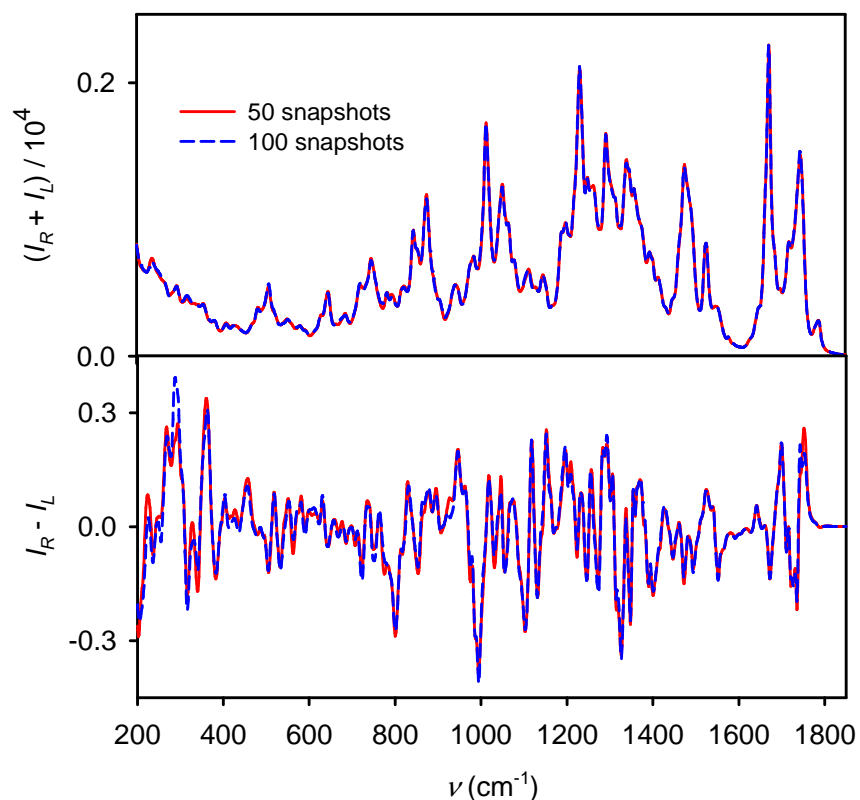


Figure S7. Raman and ROA spectra of a twisted insulin fibril (cf. **Figure 4**, $\tau = -6^\circ$) obtained as averages of 50 and 100 snapshots.

Table S1. Populations (p , in %) and χ_1 and χ_2 angles of the three Phe and Tyr side chain conformers (**Figure S4**) in native and fibrous insulin obtained by molecular dynamics.

Conformer	$\chi_1 / ^\circ$	$\chi_2 / ^\circ$	p , native	p , fibril
A	-63	102	49	24
B	-173	72	31	68
C	57	92	20	8