

Far Infrared spectroscopy of gas phase peptides: Signatures from experiments and DFT-MD simulations.

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Purpose: Find the structure of peptides in the gas phase combining experiments and DFT-MD.

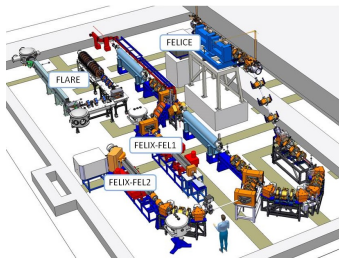


Theoretical signatures



Experimental signatures

- Far IR range: $< 800 \text{ cm}^{-1}$
- Setup: IR-UV ion dip. Mass and conformer selection
- Neutral species
- Molecular Beam conditions
- Chromophore: Phenylalanine

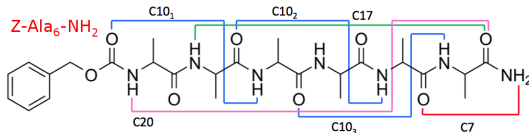
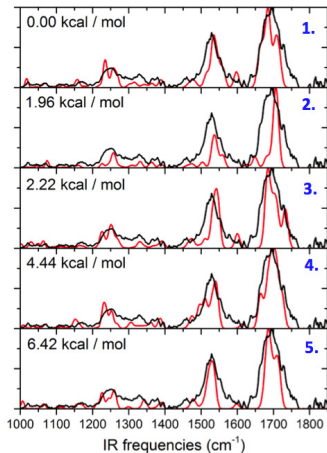


Free Electron Laser (FEL)

Felix Facility

The Netherlands

Mid - IR vibrational spectroscopy: possible non-selectivity of the IR spectrum.



3000-4000 + 1000-2000 cm^{-1} ranges

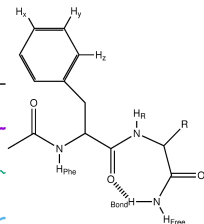
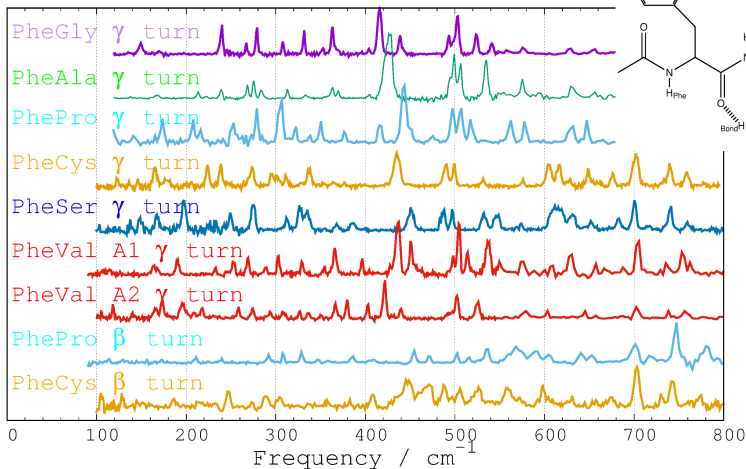
- Vibrational modes not very selective
- Multiplication of conformers
- Spectral congestion

Far - IR range : < 400 cm^{-1}
has been able to assign one conformation
for Z-Ala₆-NH₂.

Series of the Dipeptides Ac-Phe-Xxx-NH₂. Xxx: Gly, Ala, Pro, Cys, Ser, Val.

Structures well defined: PCCP (2005) **8** 1033-1048 / PCCP (2014) **16** 10770-10778 / PCCP (2015) **17** 2169-2178

Gly: R=H **Ala:** R=CH₃ **Pro:** R=CH₂-CH₂-CH₂-N
Cys: R=CH₂-SH **Ser:** R=CH₂-OH **Val:** R=CH-(CH₃)₂



DFT-MD: Density Functional Theory - Molecular Dynamics

Classical propagation of the atomic nuclei: $\sum \vec{F}_{\text{ext}} = m\vec{a}$

Energies, forces and dipole moments are calculated using the DFT formalism: BLYP-D3 functional

Calculation of an anharmonic vibrational spectrum: $I(\omega) \propto \int_{-\infty}^{\infty} \langle \delta \vec{M}(t) \cdot \delta \vec{M}(0) \rangle e^{i\omega t} dt$

Length of trajectories: $t=20\text{ps}$, $\delta t: 0.4\text{fs}$. Several trajectories are needed for good statistics and to correctly reproduce the relative intensity of the absorption peaks.

No adjustments of the IR spectra (no scaling factors)

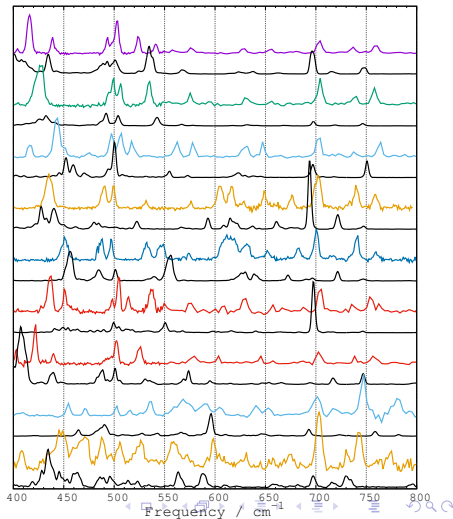
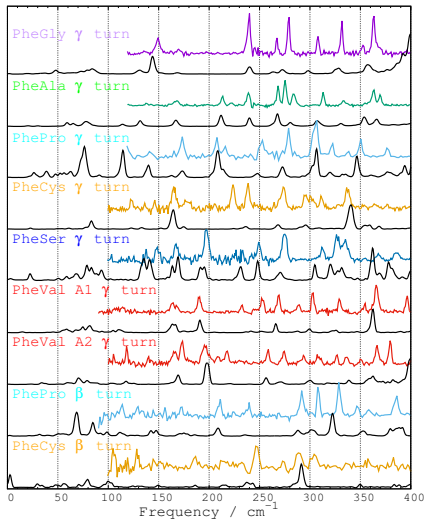
This method allows us to reproduce

- Anharmonicities of the PES and of the dipole moments
- Modes coupling
- Temperature of the experimental setup
- Conformational dynamics

DFT-MD spectra provide good (even excellent) agreement with exps.

(PCCP (2015) 17 25905-25914 / Angew Chem Int (2014) 53 3663-3666) / All comparisons, To be submitted (2016)

Positions difference Exp/DFT-MD: 20 cm^{-1} Max (6 cm^{-1} average).



How to analyse vibrational modes with molecular dynamics?

Two theoretical tools: ICDOS and PCA.

ICDOS: local motions

Fourier transform of the autocorrelation function of an intra coordinate.

$$I(\omega) = \int_{-\infty}^{\infty} \langle \delta \vec{IC}(t) \cdot \delta \vec{IC}(0) \rangle e^{i\omega t} dt$$

PCA: delocalized coupled motions

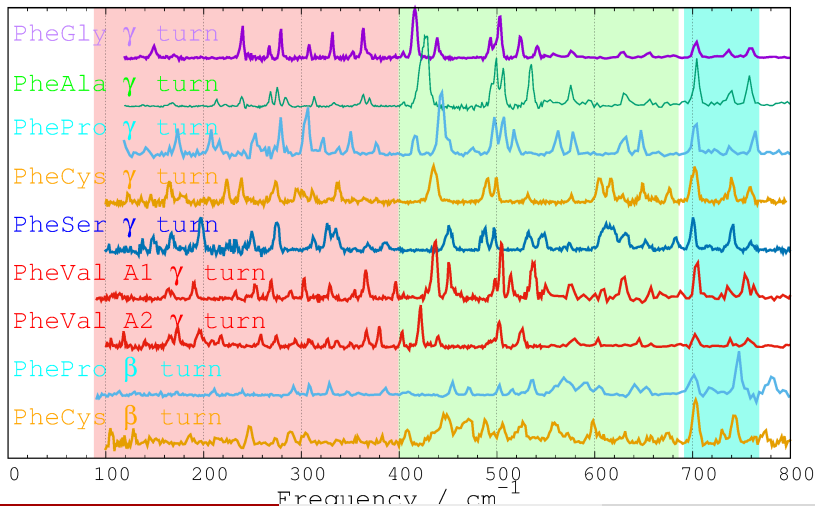
Covariance of the intracoordinates.

Diagonalization of the covariance matrix.

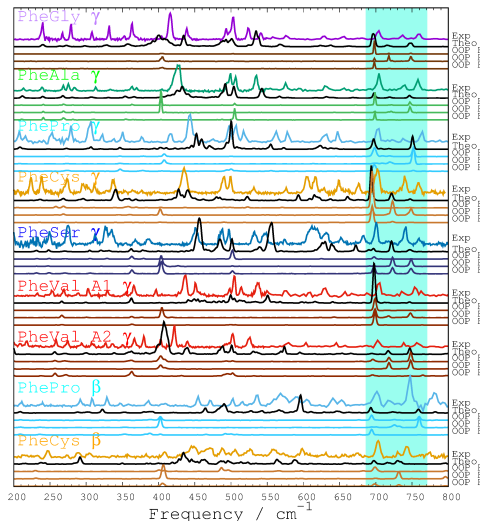
Which vibrational modes dominate the far-IR absorption spectra for peptides ?

400-800 cm^{-1} : Wagging motions of Hydrogen atoms

0-400 cm^{-1} : Delocalized motions

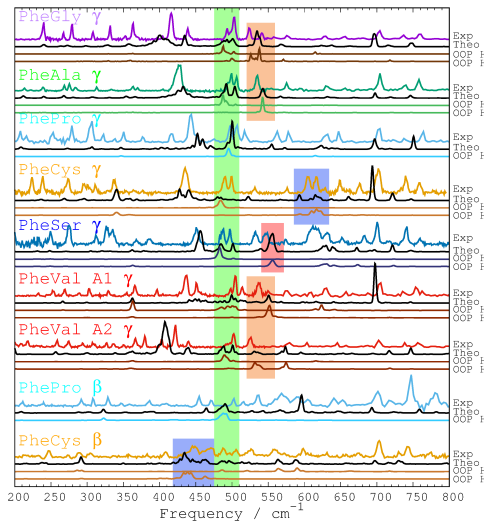


:Deformation of the ring: Out of plane motions of the H that belong to the phenylalanine ring.



This mode is not conformer selective.

Wagging of backbone N-H groups.

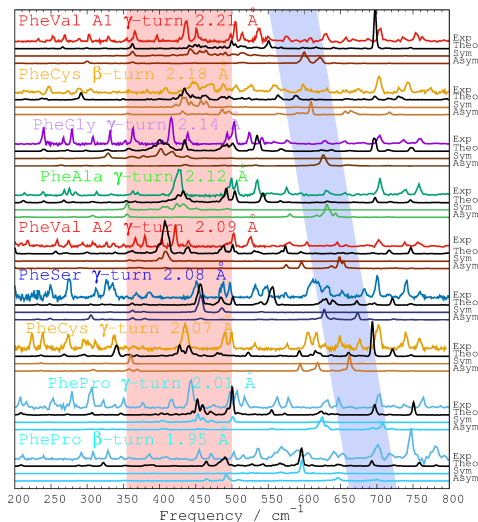


Highly diagnostic for its environment
 This chemical function is responsible for the folding of bigger peptides.

Wagging of the NH_2 terminal group.

Symmetric

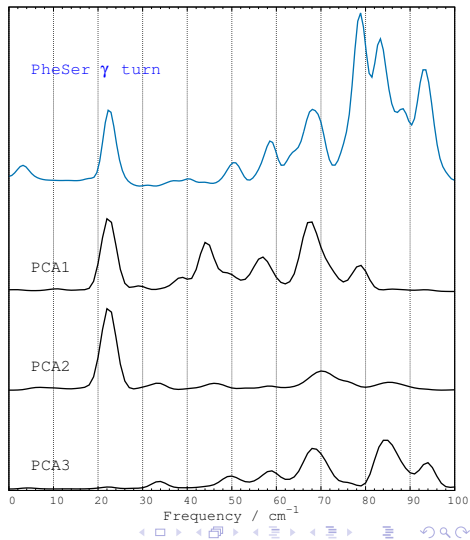
Asymmetric



Strong correlation between the frequency of the asymmetric wagging and the length of the hydrogen bond.

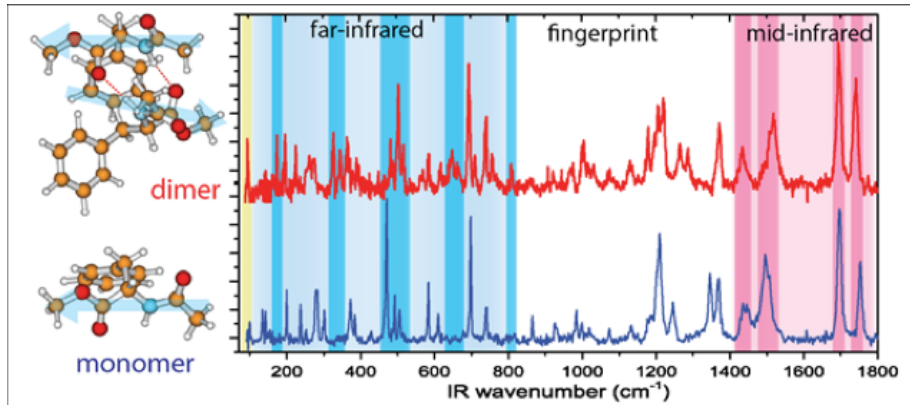
0-400 cm^{-1} : Delocalized motions

Principle Components Analysis "PCA" provide much better results than ICDOS.



β -sheets are common structures of proteins.

These structures are involved in certain diseases like Alzheimer.

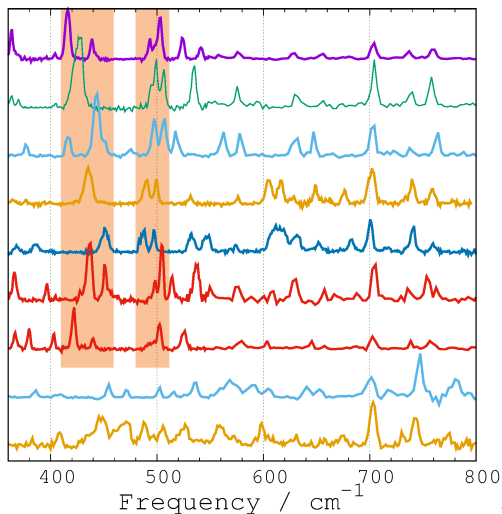


Simulations are done !

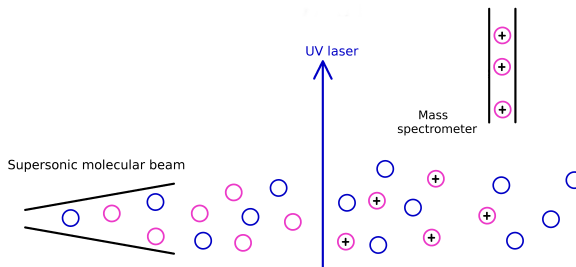
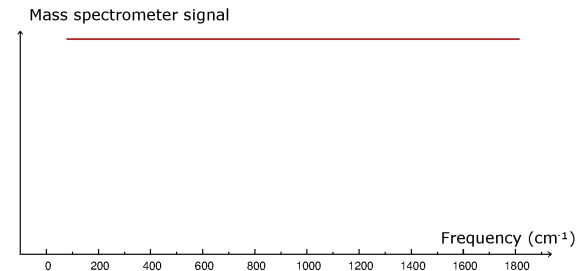
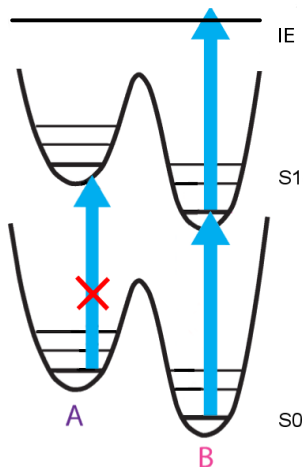
Series of the Dipeptides PheXxx. Xxx: Gly, Ala, Pro, Cys, Ser, Val. Structures

already well defined: PCCP (2005) **8** 1033-1048 / PCCP (2014) **16** 10770-10778 / PCCP (2015) **17** 2169-2178

C7



Spectroscopy IR-UV ion-dip - Conformer separation -Anouk Rijs's setup



Spectroscopy IR-UV ion-dip - Conformer separation -Anouk Rijs's setup

