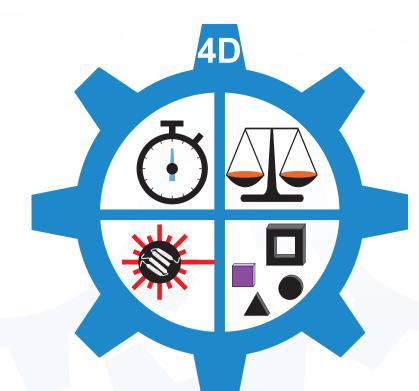
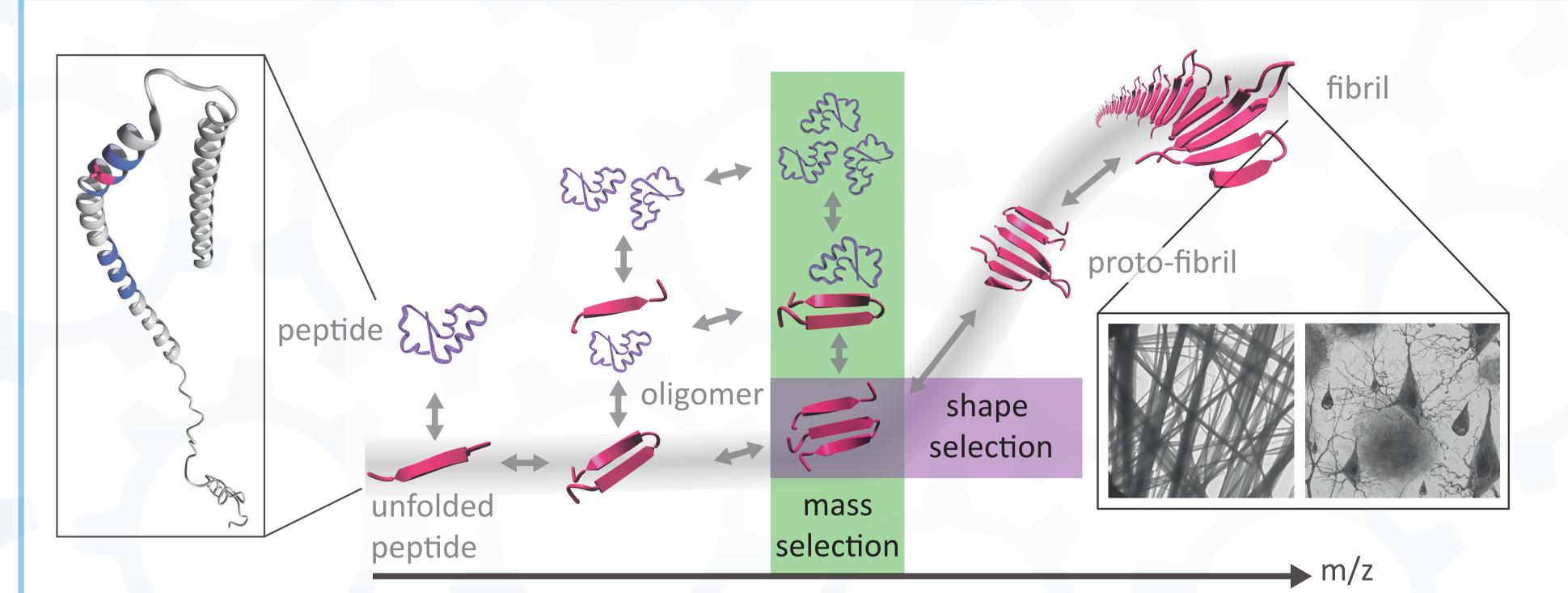
Hyphenation of Ion Mobility Mass Spectrometry and Action Spectroscopy to Probe Structure and Kinetics of Peptide Aggregation

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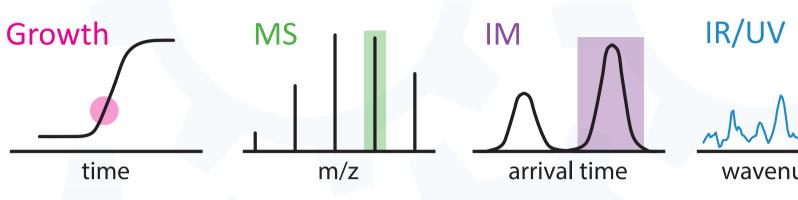
2. MS Vision, Spectrometry Vision B.V., Almere, The Netherlands

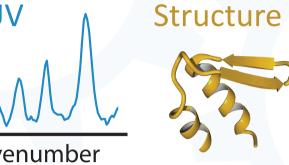




Introduction

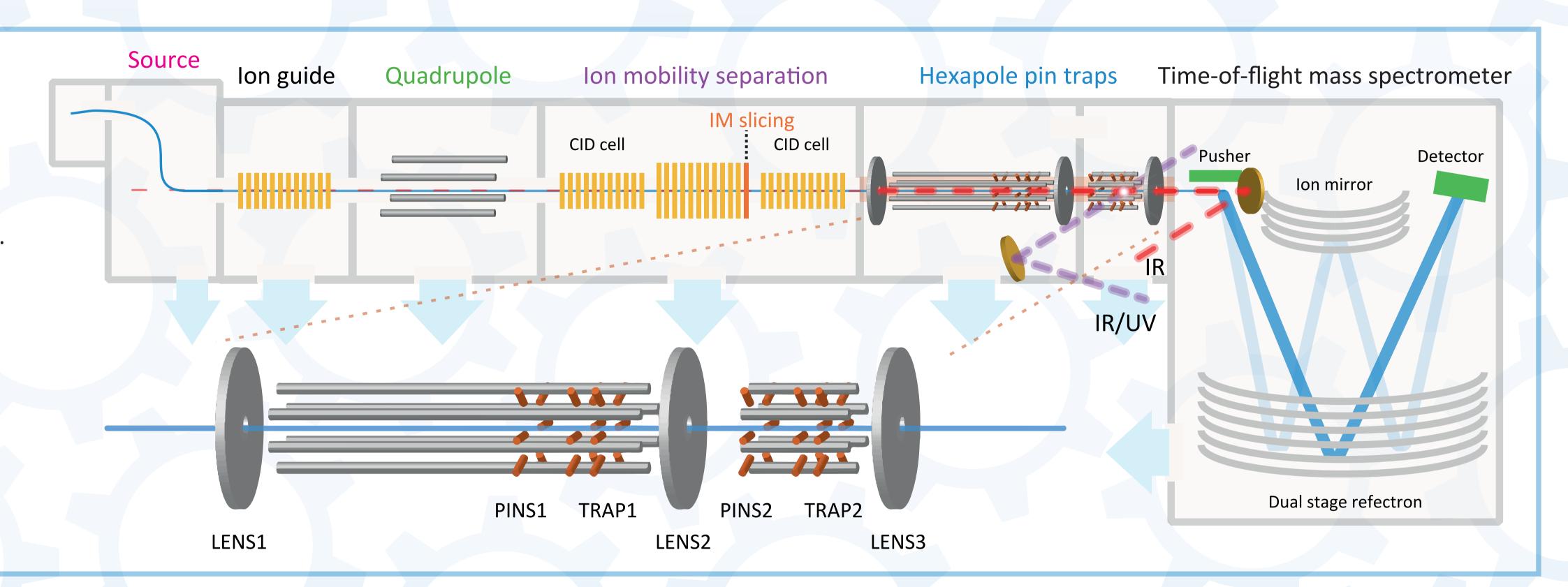
- Aggregation of peptides associated with neurodegenerative diseases such as Parkinson's and Alzheimer's Disease results in complex mixtures.
- Information about specific oligomers, thought to be the toxic species, is lacking as a result of the inability to isolate and study them.
- An ion mobility-mass spectrometer (IM-MS) was modified to allow both mass- and shape selection of the ions, after which they can get stored in an ion trap and irradiated by UV or IR light (Photo-Synapt).



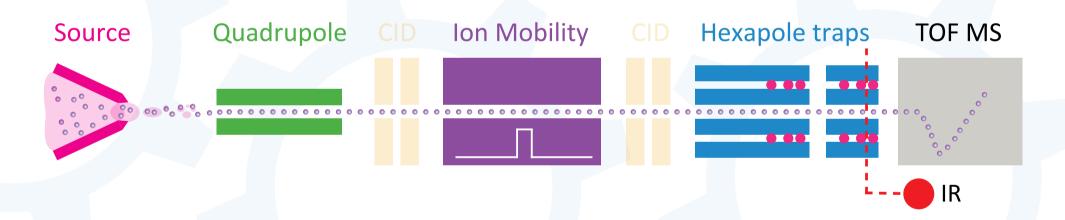


The Photo-Synapt

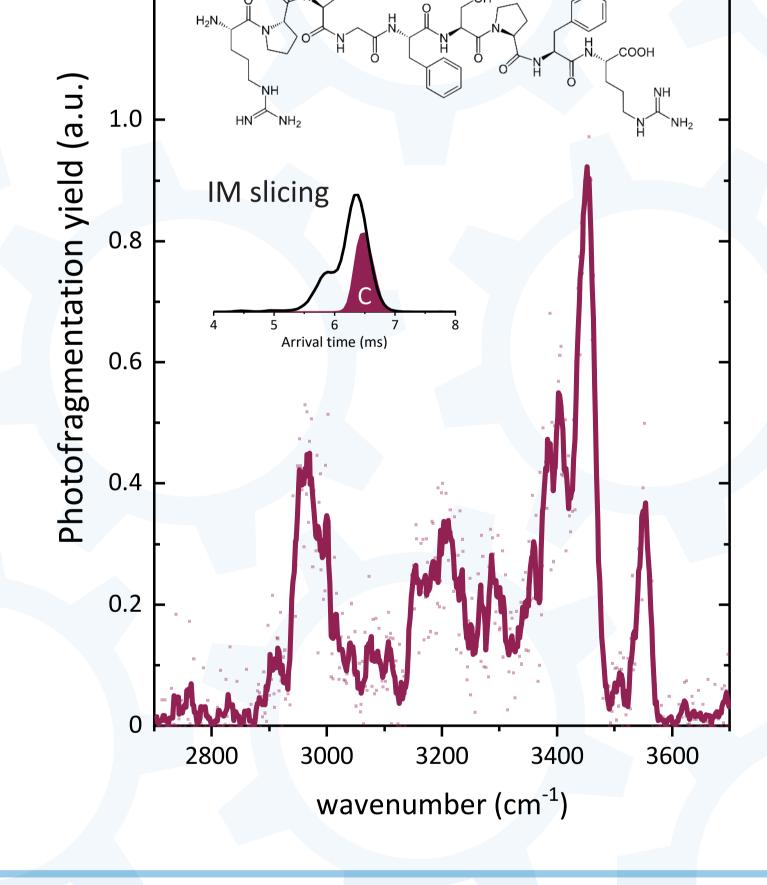
- A commercial IM-MS instrument (Waters Synapt G2) was modified by adding optical access for lasers, additional gas inlets to control the pressure in the trap, and two hexapoles pin traps.
- This design allows for m/z-selecting an ion (quadrupole), slicing out a specific shape or isobaric charge state (ion mobility slicing), trap it in the new ion pin traps, interrogate it with either UV or IR laser light (in TRAP2) and detect the resulting fragment masses in the mass spectrometer.
- Characterization and benchmarking experiments are currently on their way.



IM sliced IRMPD of bradykinin



- The triply charged monomer of **bradykinin** (m/z 354, 5 μ M in H₂O:MeOH, 0.1% formic acid) is a well-studied nonapeptide and can adopt **3 conformations**.
- We slice out a single conformer of this molecule using ion mobility slicing and trap it and irradiate for 2.5s in the hexapole ion traps to induce IR photofragmentation.
- The IR laser: M Squared FireFly (100 mW, 150 kHz, 2.7-4.1 μm).
- The fragmentation (via Internal Vibrational Redistribution) is monitored as a function of the wavelength.
- Fragmentation yield is calculated by $\frac{\sum Fragments}{\sum Fragments + Precursor}$

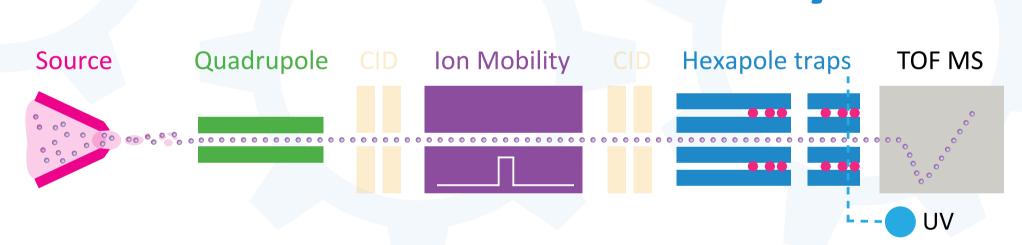


Tryptophan IR yield @ 3551 cm⁻¹ Tryptophan IR - 2.5 seconds irradiation ■ 1.1e-6 mbar 0.8 yield (a 90 90 Photofragmentation y 4.0e-6 mbar Photof ■ 8.0e-6 mbar ■ 1.1e-6 mbar ■ 4.0e-6 mbar ■ 8.0e-6 mbar 1000 2000 3000 4000 5000 3450 3500 Irradiation time (ms) wavenumber (cm⁻¹)

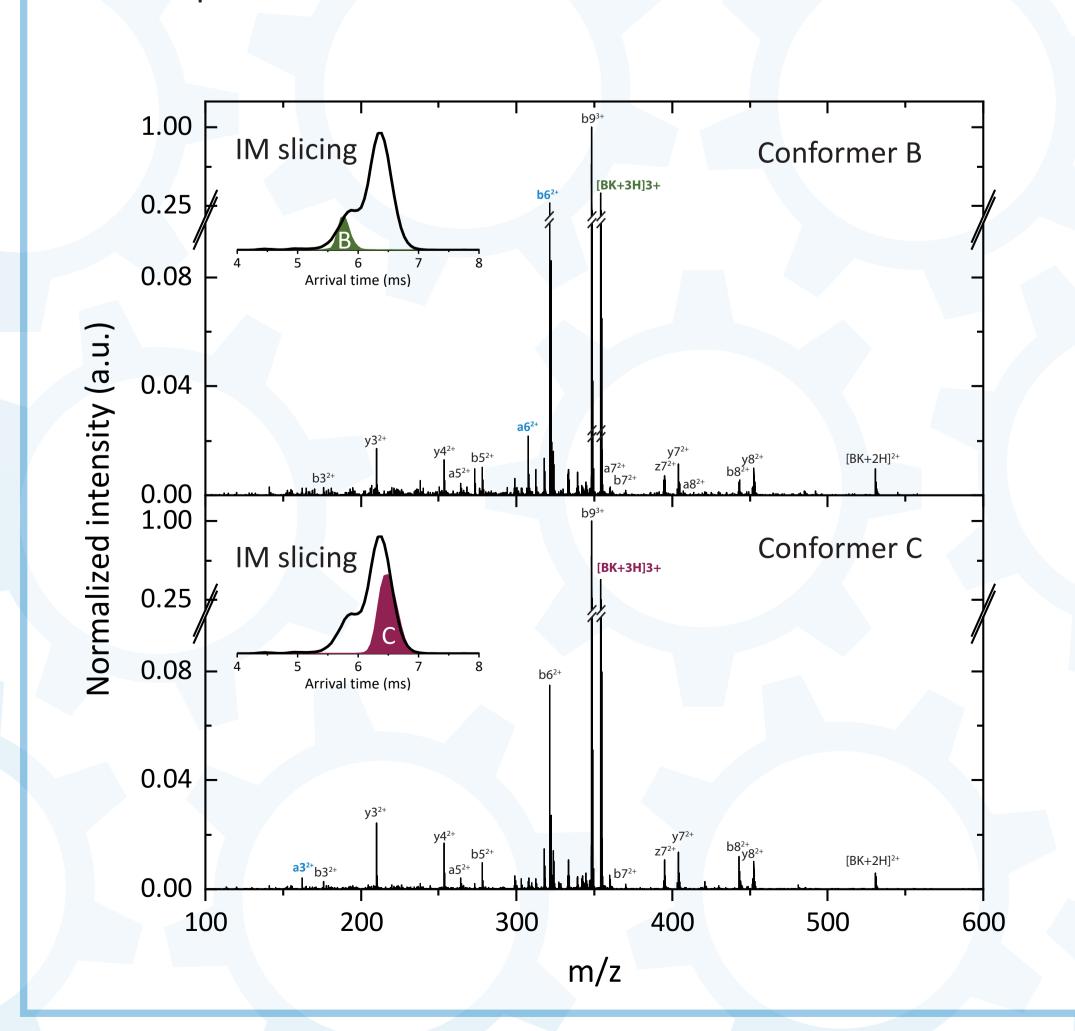
IRMPD vs pressure

- The singly charged monomer of **tryptophan**, m/z 205, (5 μ M in H₂O:MeOH) is used to characterize IRMPD on this instrument.
- The cooling by the nitrogen to efficiently trap the ions and the heating by the IR to fragment them are competing processes.
- Lower pressures lead to considerably higher fragmentation yields for the same irradiation time.
- The next step is to move to larger or more complex systems such as peptide aggregates.

IM sliced UVPD bradykinin



- The same procedure is followed as with IRMPD (see left box): so quadrupole mass selection, ion mobility slicing and trapping and irradiating for 250 ms of triply charged bradykinin in the hexapole traps at 3.1e-5 mbar.
- We irradiate the ions with a 213 nm UV laser (CryLas eMOPA 213 (1000 Hz, 20 mW) for 150 ms.
- Both direct dissociation and internal vibrational redistribution pathways by UVPD are resulting in fragmentation, which leads to a higher sequence coverage than other fragmentation techniques such as CID.











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