Kinetics and thermodynamics insights in conformational relaxation from trap and release tandem-IMS measurements

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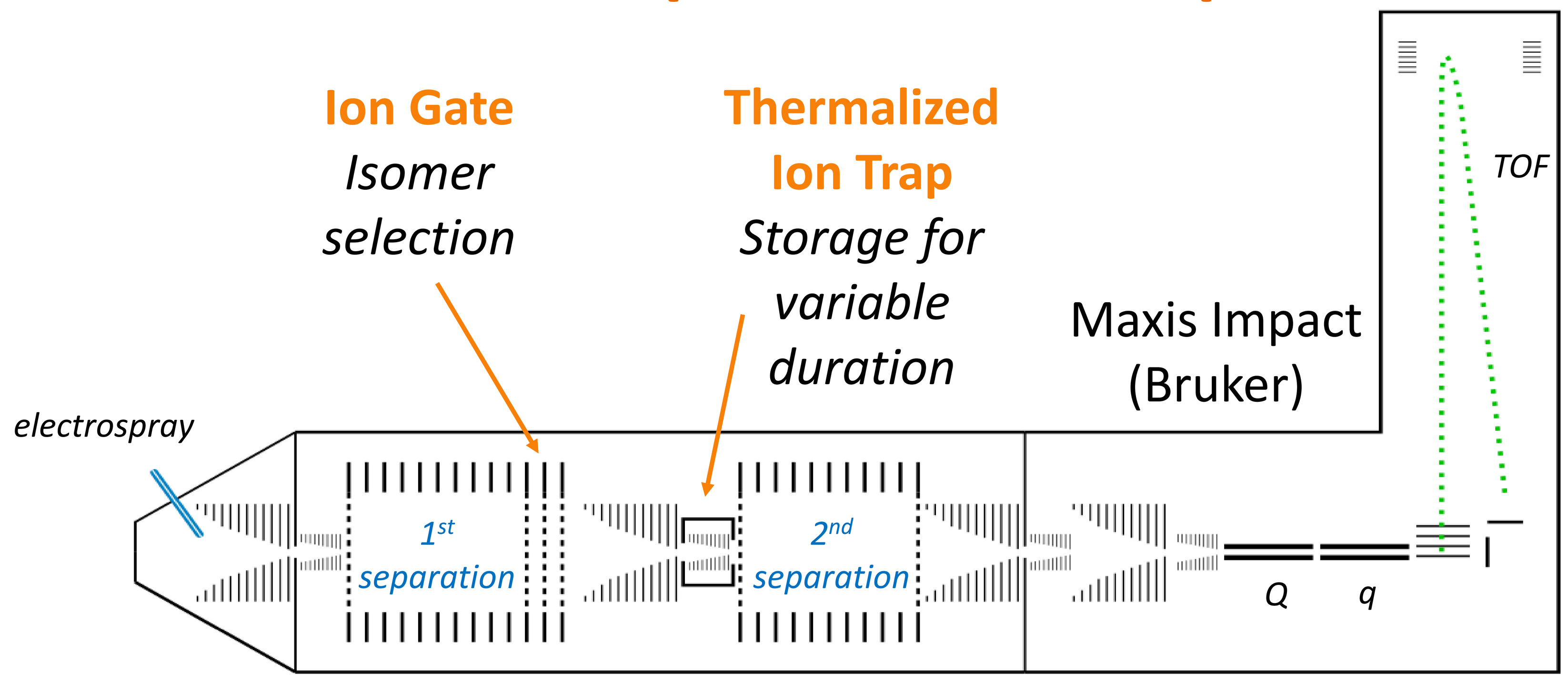
Context: A classical route to the characterization of reaction kinetics and to the characterization of transition states consists in temperature dependent kinetics measurements. The evolution of reaction rates as a function of temperature can then be exploited to derive the relative enthalpy and entropy of the transition state. This procedure was largely exploited in the gas phase, especially to investigate ion fragmentation kinetics in thermalized ion traps. We recently demonstrated that this procedure can also be applied to characterize isomerization processes, based on tandem-IMS measurements, yielding detailed insight in the conformational landscape of the investigated system.[1]

(1) Le Fèvre, A.; Dugourd, P.; Chirot, F. Anal. Chem. 2021, 93 (9), 4183–4190.

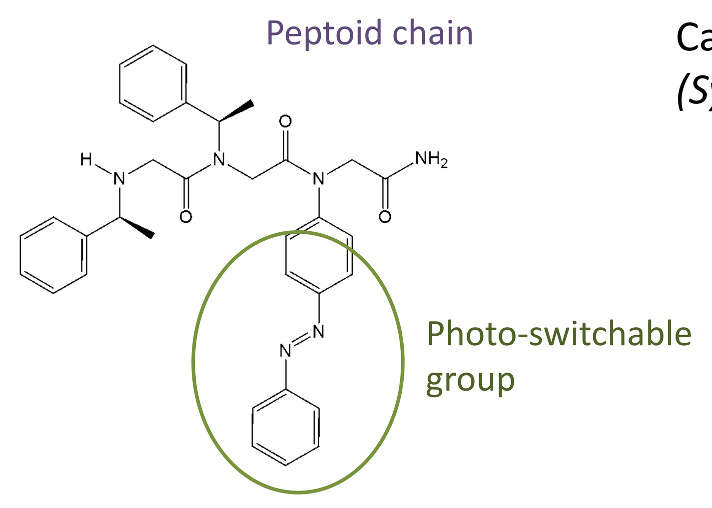
Experimental setup[1,2]



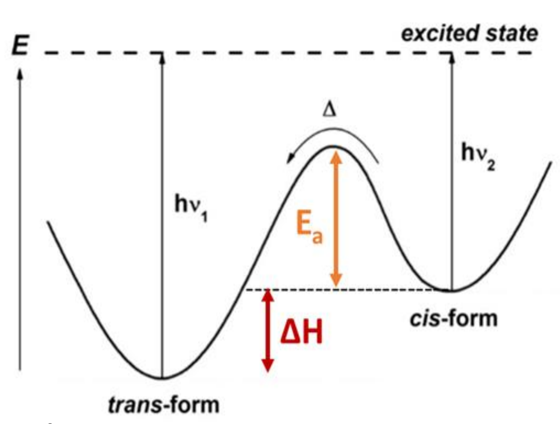
(2) Simon, A.-L.; Chirot, F.; Choi, C. Met al. Rev. Sci. Instrum. 2015, 86 (9), 094101

- Ions can be selected based on their drift time after a first drift tube
- Selected ions can be stored in a thermalized ion funnel before a second IMS analysis

Thermal relaxation of a photoswitch



Candidate for solar-energy storage
(Synthesis B. Tassignon, Univ. Mons)

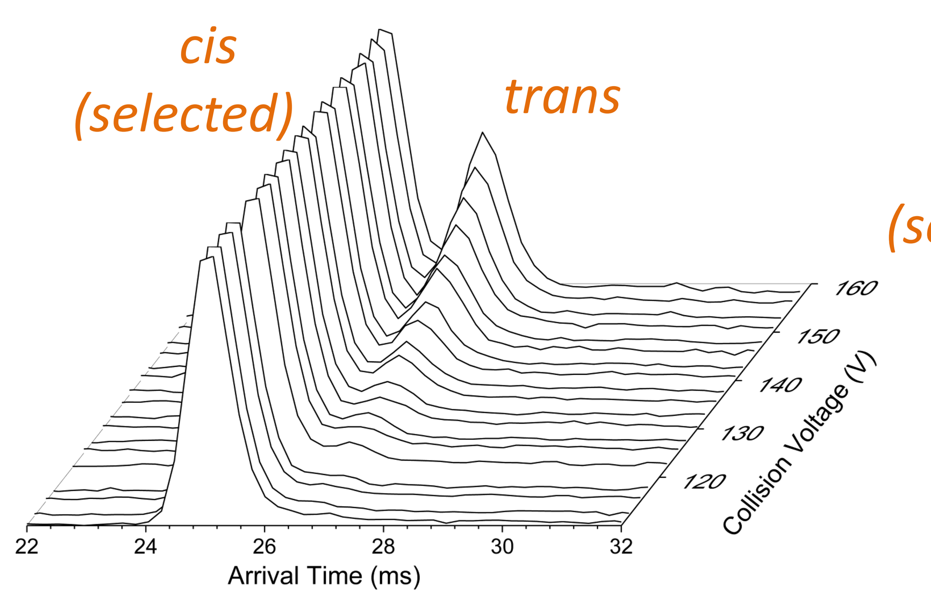


Half-life of the *cis* state at 25°C in solution: ~ 3 days
(=difficult to characterize)

Sample preparation

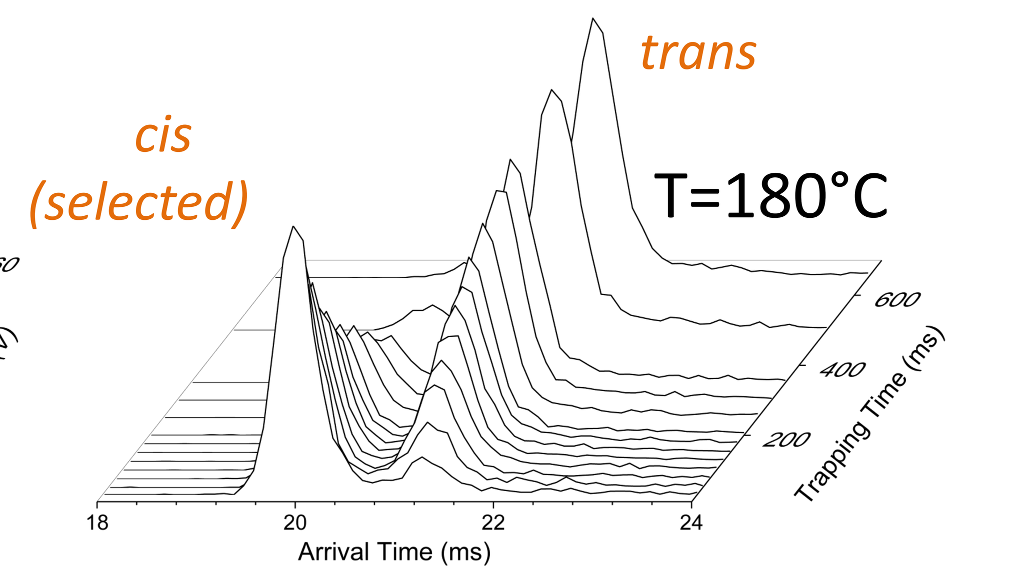
Solution in acetonitrile 10 µmol.L^{-1}. Irradiation for 20 min at 365 nm, 2,7 mW.cm^{-2}.
Direct ESI injection in positive mode.
Main observed species: singly protonated ion at m/z 577.3.

Collisional activation



- High fields are needed to observe significant isomerization

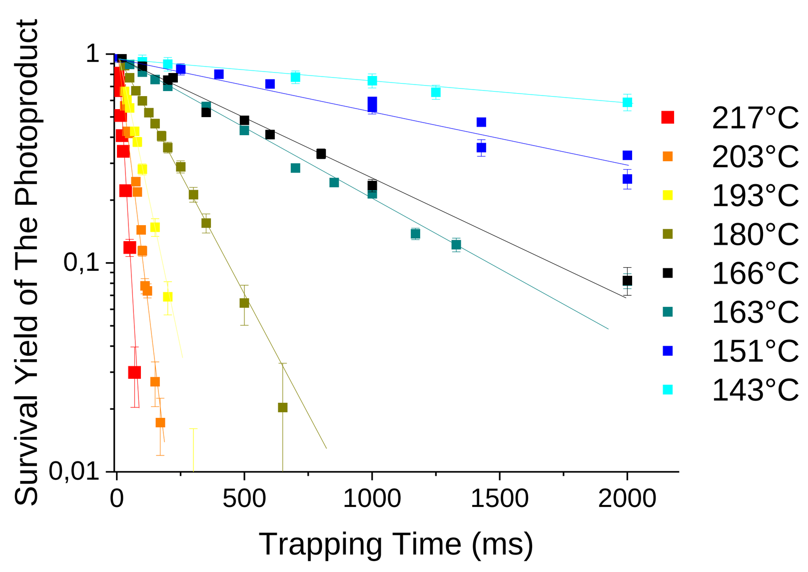
Trap and release measurements

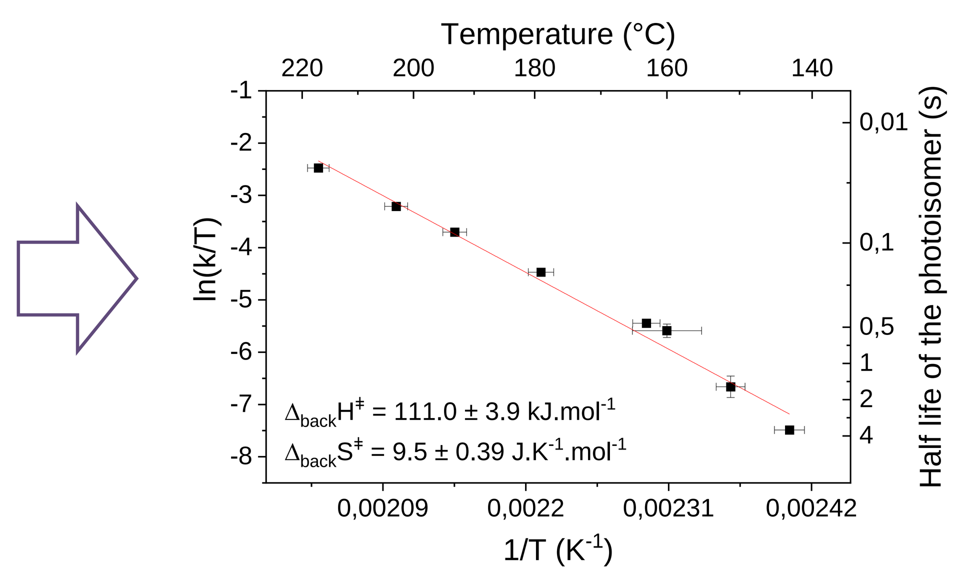


- Complete relaxation to *trans* observed at sufficiently long trapping times

Drift conditions: T = 297 K, p =4,0 Torr He, V = 450 V, L = 80 cm, ATDs for m/z 285 (z=+2).
Collision activation: Voltage applied between 2 grid electrodes spaced by 2.2 mm in the drift region.

Temperature-dependant kinetics and Eyring's plot





- Direct characterization of the back isomerization barrier
- In agreement with values published for similar systems

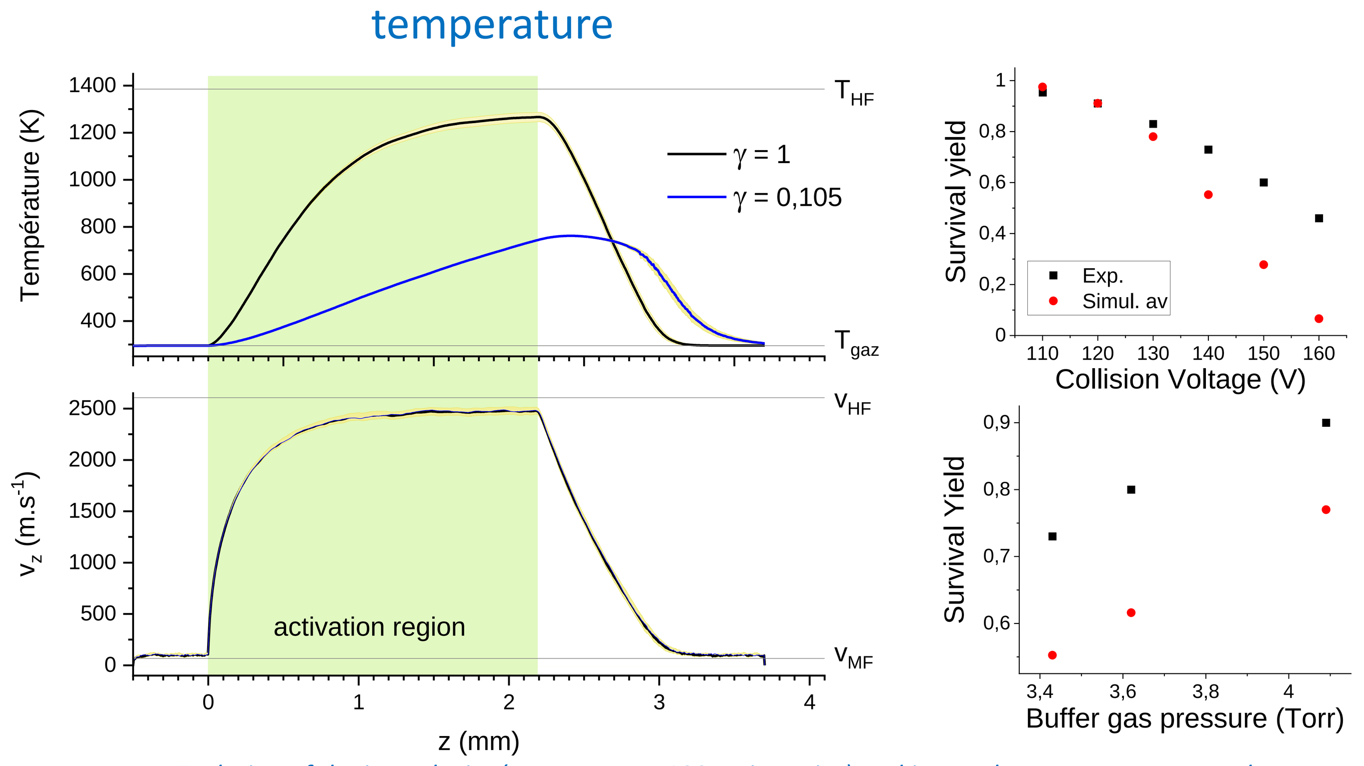
Collisional energy transfer

Model

- Ion propagation with stochastic collisions
  (adaptative time step, adaptative collision probability, random collision velocity, cross section assumed constant)
- Energy transfer Model: transient complex with partial temperature accomodation
  - If a collision occurs the internal energy of the transient complex E* = internal energy of the ion + the collision energy => vibrational temperature T*
  - The projectile is then re-emitted with a random velocity based on a Maxwell-Boltzmann distribution at temperature T*.
  - The internal energy of the ion is then decreased from the released kinetic energy.
  - To achieve partial accommodation, the kinetic energy of the re-emitted particle is scaled by a factor γ.
- Results are compared to velocities and effective temperatures computed from expansions of the ion transport equations in a gas at High (HF) or moderate (MF) electric fields.[3]
- Isomerization rates are calculated at each step using Eyring equation with the experimental values for $\Delta_{back}H^{‡}$and $\Delta_{back}S^{‡}$

Results

- Estimation of the thermalization/ heating kinetics
- 2-Temperature theory[3] overestimates the ion temperature



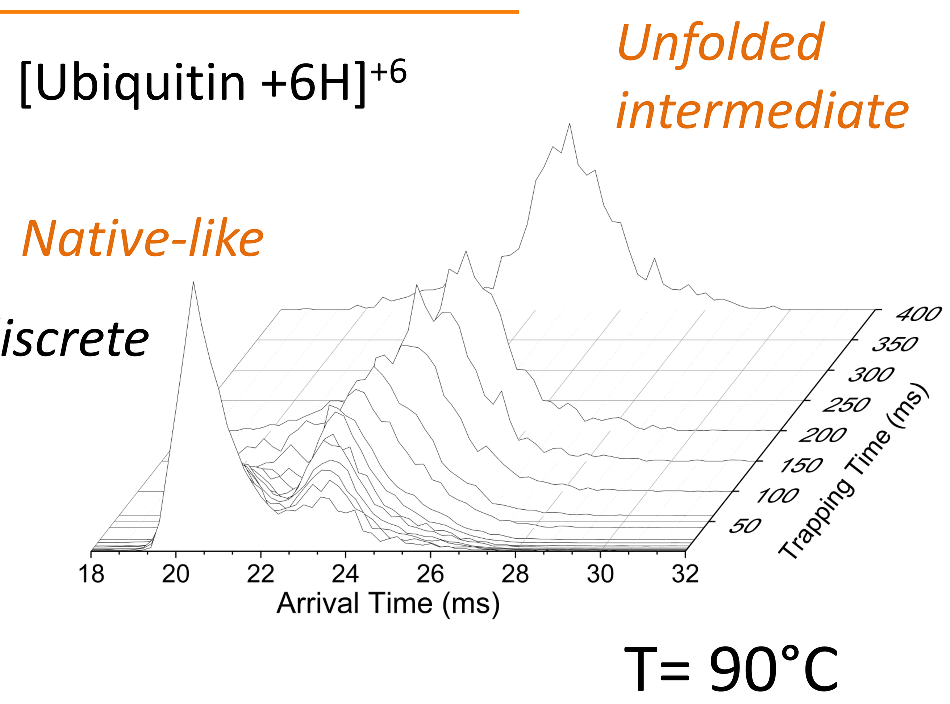
Evolution of the ion velocity (average over 100 trajectories) and internal temperature across the activation region. « Normal » relatively low fields are applied before and after activation. Black lines correspond to simulation with full internal energy accommodation, and blue lines to an accommodation factor of 0,105, which provides reasonable survival yield values.

(3) L. A. Viehland and E. A. Mason, Ann. Phys., 1975, 91, 499– 533

Preliminary data:

Protein denaturation

- More complicated
  Not discrete states, but pseudo-discrete
- Possible interconversion
  Equilibrium distributions



Perspectives

- More complex systems
  Proteins → unfolding kinetics
  non-covalent complexes → dissociation barriers
- Refine the inelastic model based on experimental data
  (less simulations needed)

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