

On the determination of the activation energies for the thermal relaxation of photoisomers by state-of-the-art mass spectrometry methods



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Context

Photoswitching molecules allow reversible control of their structure and properties using light. Their effective design, however, requires precise tuning of key parameters, particularly the half-life time of the metastable photoisomer.[4] Conventional solution-based methods to measure back-isomerization kinetics are limited by time and temperature constraints. To address this, we explore gas-phase strategies using tandem ion mobility spectrometry and collisional activation, offering a faster and more efficient way to study thermal back-isomerization kinetics of photoswitching systems.

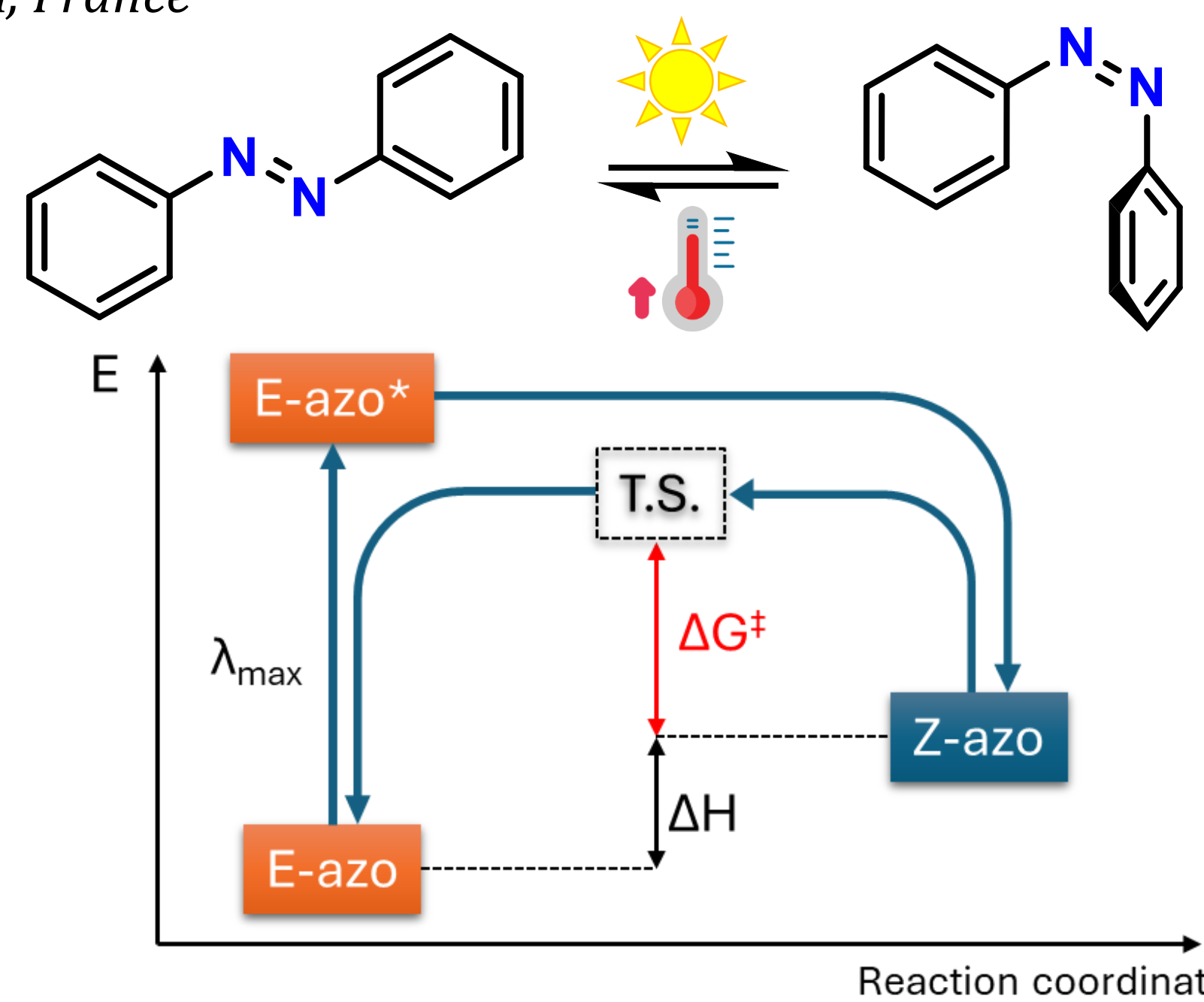


Figure 2. Schematic representation of azobenzene photoswitching and thermal back-isomerization processes.[5]

Photoswitches studied

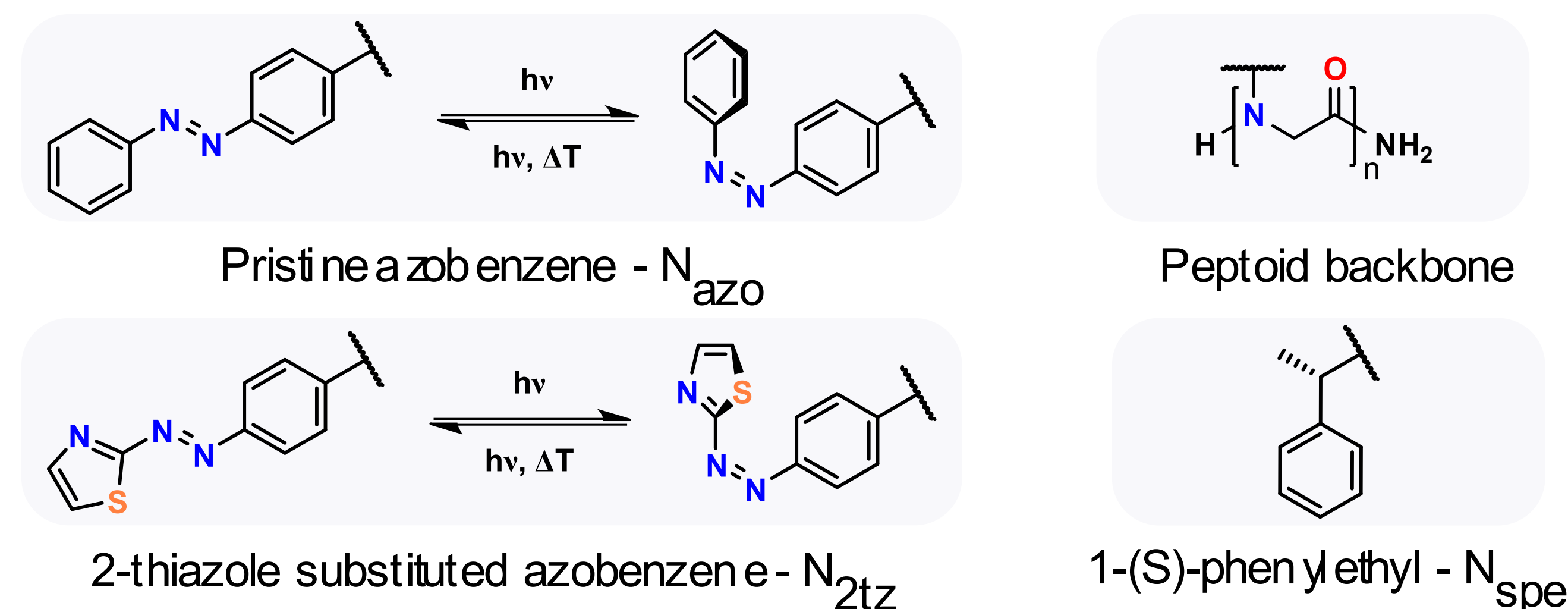


Figure 3. General structure of the systems studied, which consist of selected side chains grafted onto a backbone (top right) in a sequence-defined peptoid. Sequences are given from the N- to C-terminus.[6]

What does happen when the N=N bond rotates?

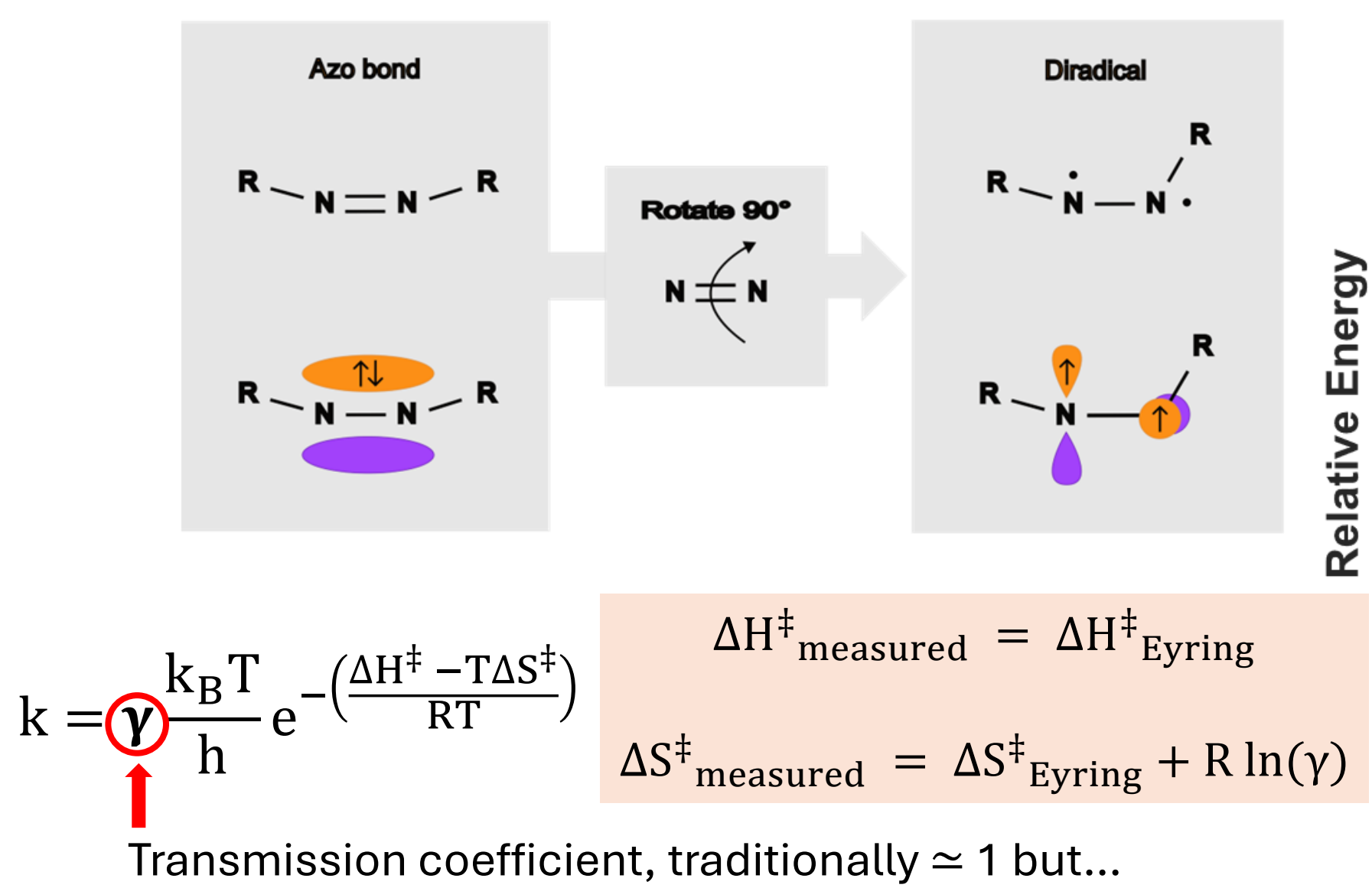


Figure 4. Schematic representation of the intersystem crossing process involved in the AZO bond rotation.[7]

Kinetics in the gas phase – thermal activation

- 1) Z-photoisomers selection in IMS1
- 2) Trapped ions relaxation at a controlled temperature for a variable time = **kinetic monitoring** (different T)
- 3) Photoisomers population sampling by IMS2

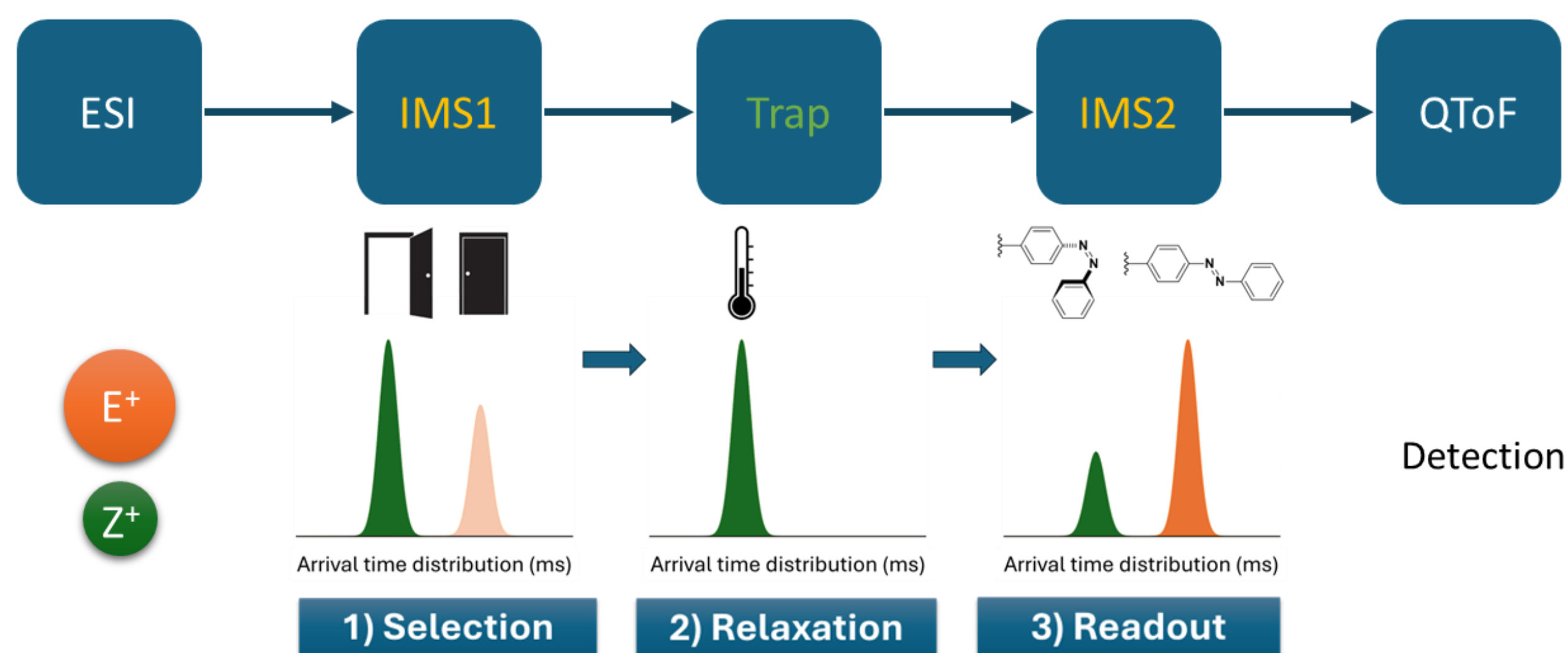


Figure 5. Principle of the tandem-IMS experiments.[8]

Kinetics in the gas phase – collisional activation

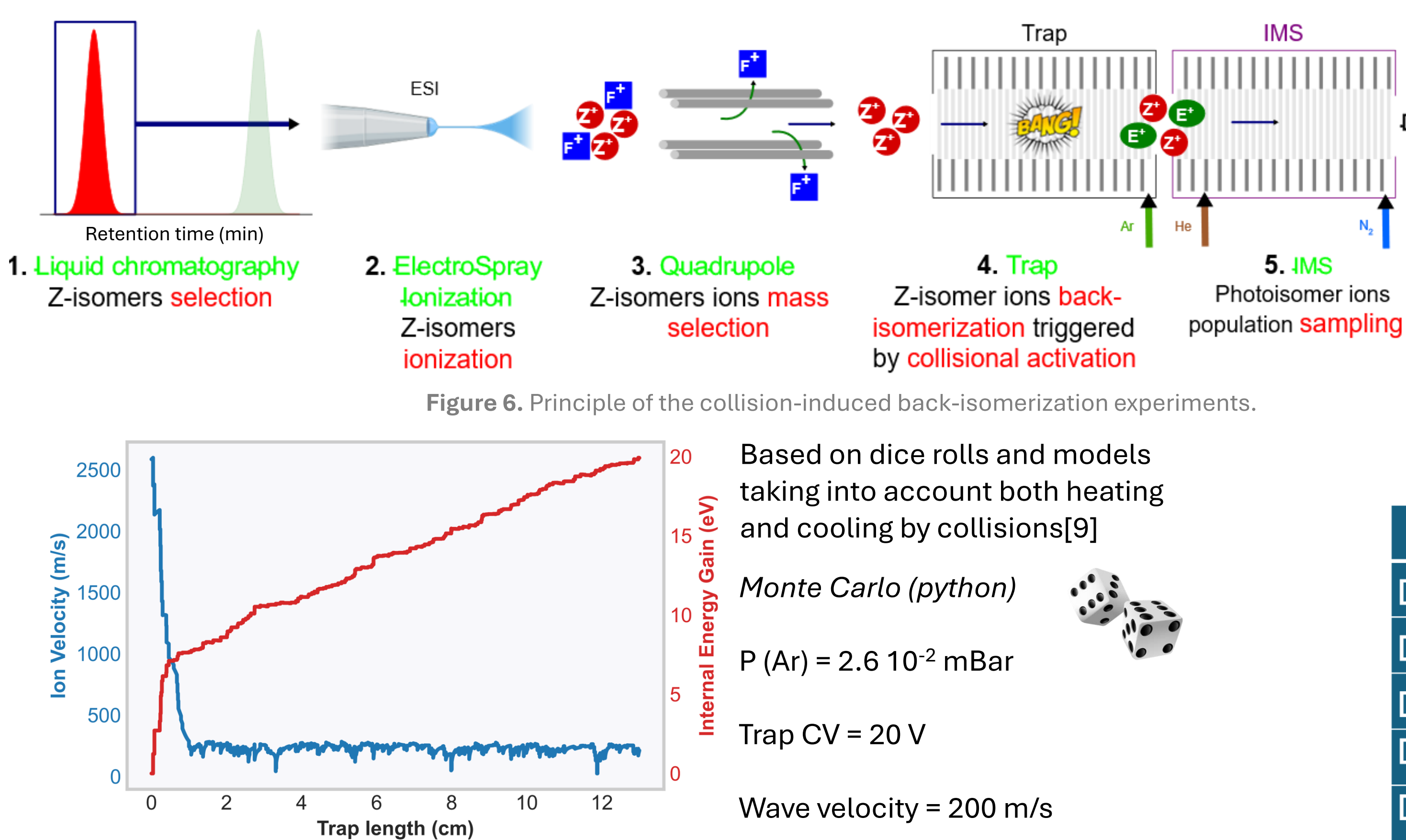


Figure 6. Principle of the collision-induced back-isomerization experiments.

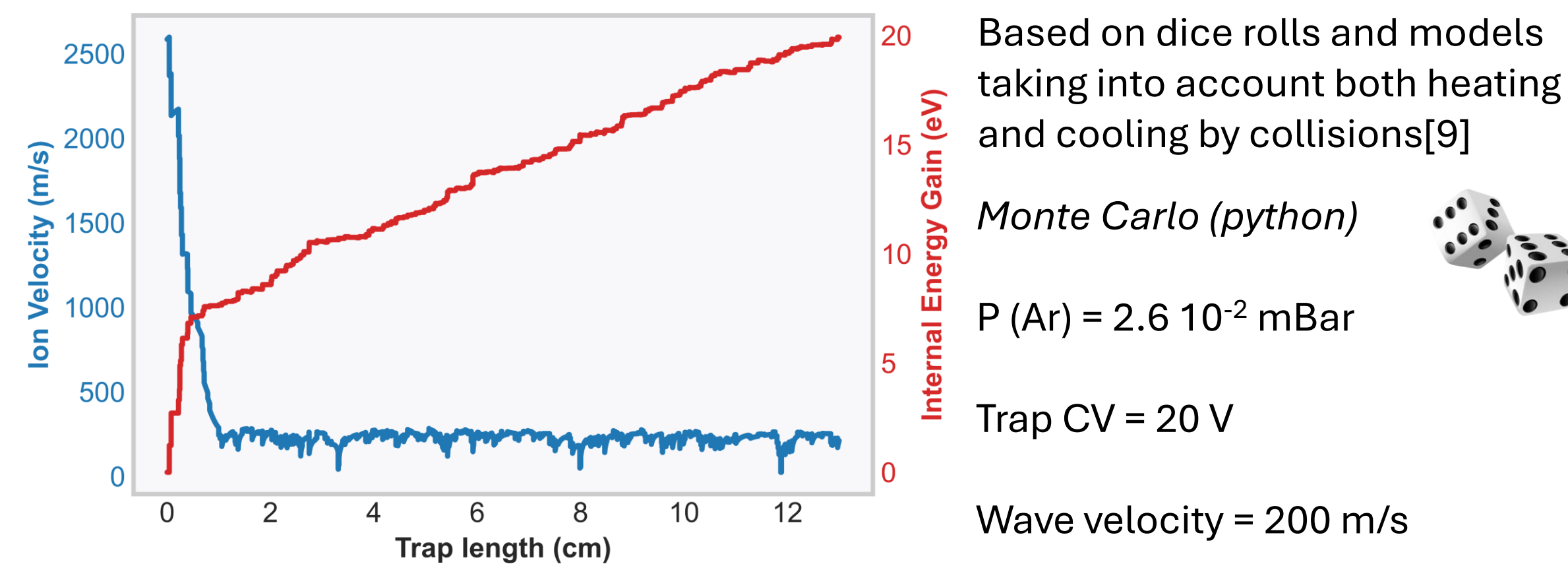


Figure 8. Monte Carlo simulations showing the evolution of the velocity and internal energy of an ion within the trap.

Conclusions and perspectives

- Gas-phase measurements reveal clear structure-dependent differences in activation entropies, reflecting distinct back-isomerization pathways.
- Tandem IMS enables extraction of activation parameters by monitoring gas-phase thermal back-isomerization.
- Collision-induced isomerization provides a fast, calibration-based method to obtain kinetic constants and compare photoswitching systems.
- Expanding the photoswitch library and refining calibration will establish a robust framework for rapid gas-phase kinetic measurements.

The entropy puzzle

➔ The intersystem crossing process is confirmed by differences observed in the relaxation kinetics in solution with and without NH₄I [8]

Peptoid sequence	Ion	ΔH [‡] Gas phase kJ mol ⁻¹	ΔS [‡] Gas phase J mol ⁻¹ K ⁻¹	ΔG [‡] (293K) Gas phase kJ mol ⁻¹	Mechanism pathway identified
N _{spe} N _{spe} N _{azo}	[M+H] ⁺	101.6 ± 1.8	-25.4 ± 0.5	109.0 ± 1.9	Rotation
	[M+Na] ⁺	98.1 ± 0.9	-32.9 ± 0.3	107.9 ± 1.0	Rotation
N _{spe} N _{spe} N _{2tz}	[M+H] ⁺	93.1 ± 0.5	9.85 ± 0.05	90.2 ± 0.5	Inversion
N _{spe} N _{2tz} N _{spe} N _{spe}	[M+H] ⁺	91.7 ± 2.2	-41.6 ± 1.1	103.8 ± 2.5	Rotation

Table 1. Activation parameters for thermal gas-phase back-isomerization measured by tandem IMS experiments and the corresponding relaxation mechanism.[8]

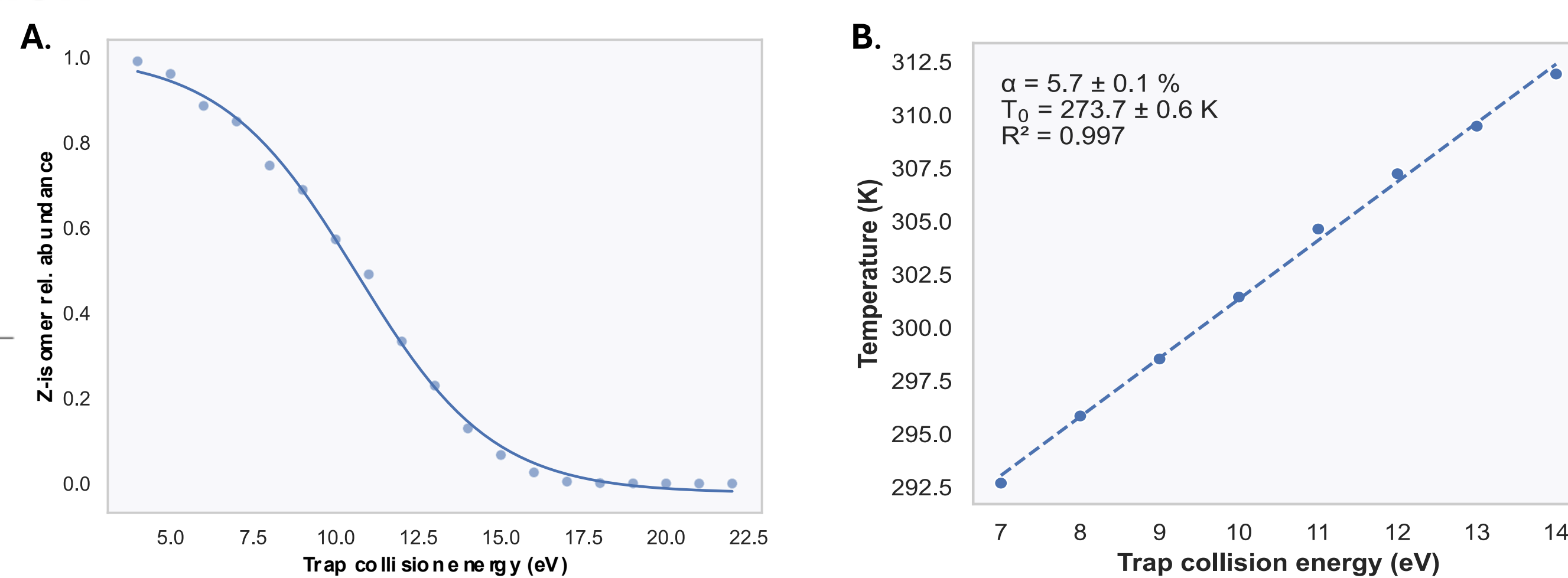


Figure 7. A) Relative abundance of Z photoisomers measured as a function of Trap CE and fitted using a sigmoidal function (solid line). B) Effective temperature calculated from relative abundances for each Trap CE value and fitted using a linear function (dashed line).

Peptoid system	α (%)	T ₀ (K)
[N _{spe} N _{spe} N _{azo} + H] ⁺	7.6 ± 0.4	325.8 ± 0.9
[N _{spe} N _{spe} N _{2tz} + H] ⁺	5.7 ± 0.1	273.7 ± 0.6
[N _{spe} N _{2tz} N _{spe} N _{spe} + H] ⁺	8.5 ± 0.3	304.2 ± 1.9
[N _{spe} N _{spe} N _{azo} + Na] ⁺	9.0 ± 0.3	316.8 ± 1.5
[N _{spe} N _{2tz} N _{spe} + Na] ⁺	8.2 ± 0.2	323.1 ± 1.2

Table 2. Temperature calibration parameters measured for reference systems.

Acknowledgments

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