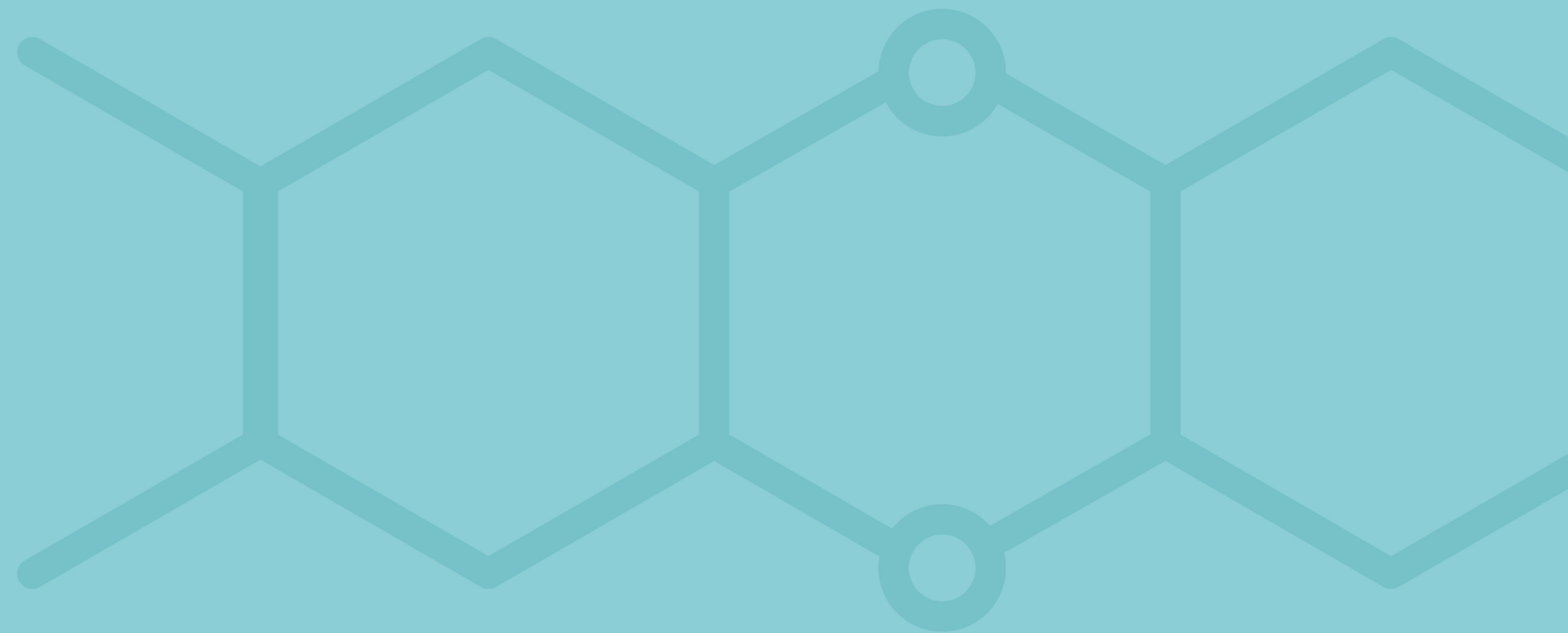


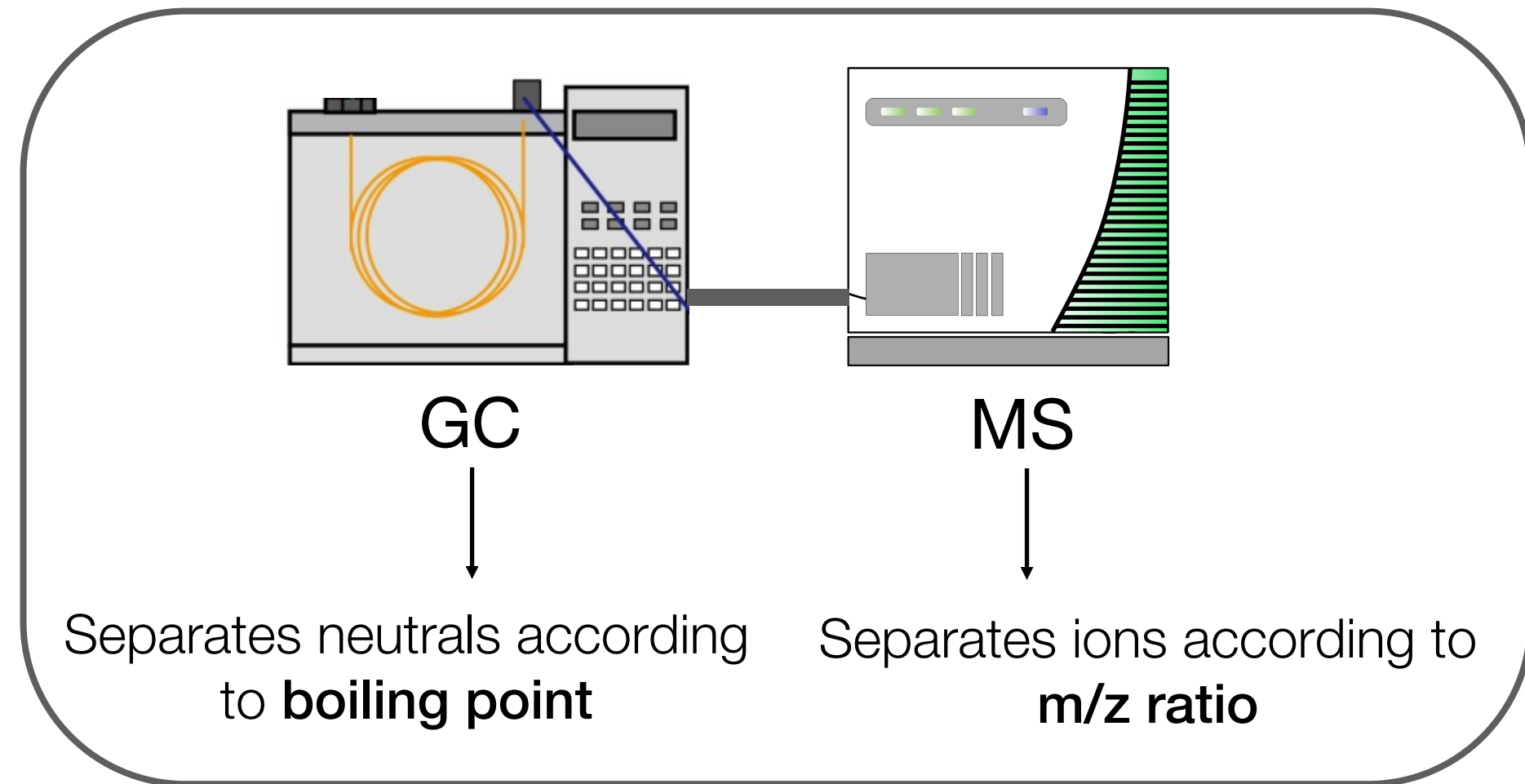
Sliding windows in ion mobility (SWIM): a new approach to increase the separation power in trapped ion mobility-mass spectrometry hyphenated with chromatography



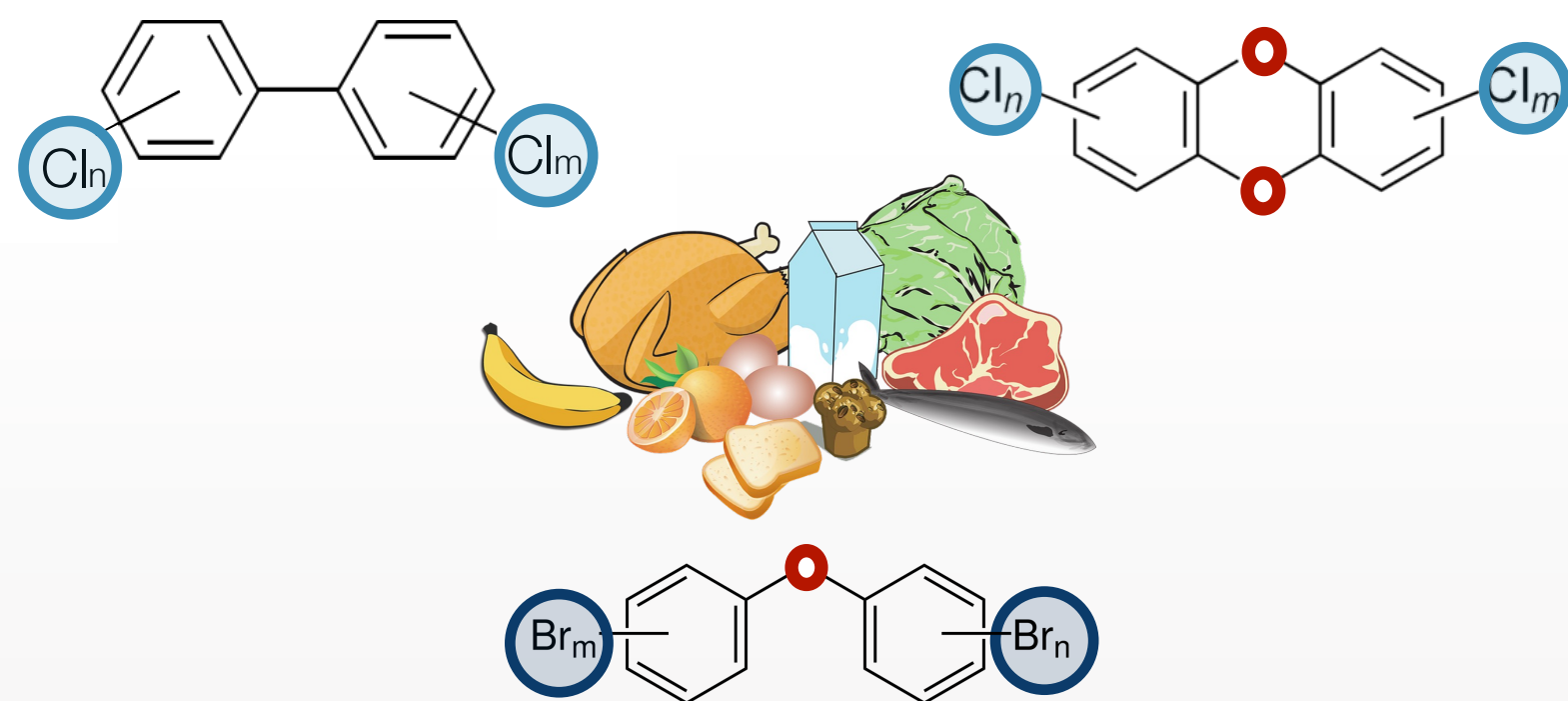
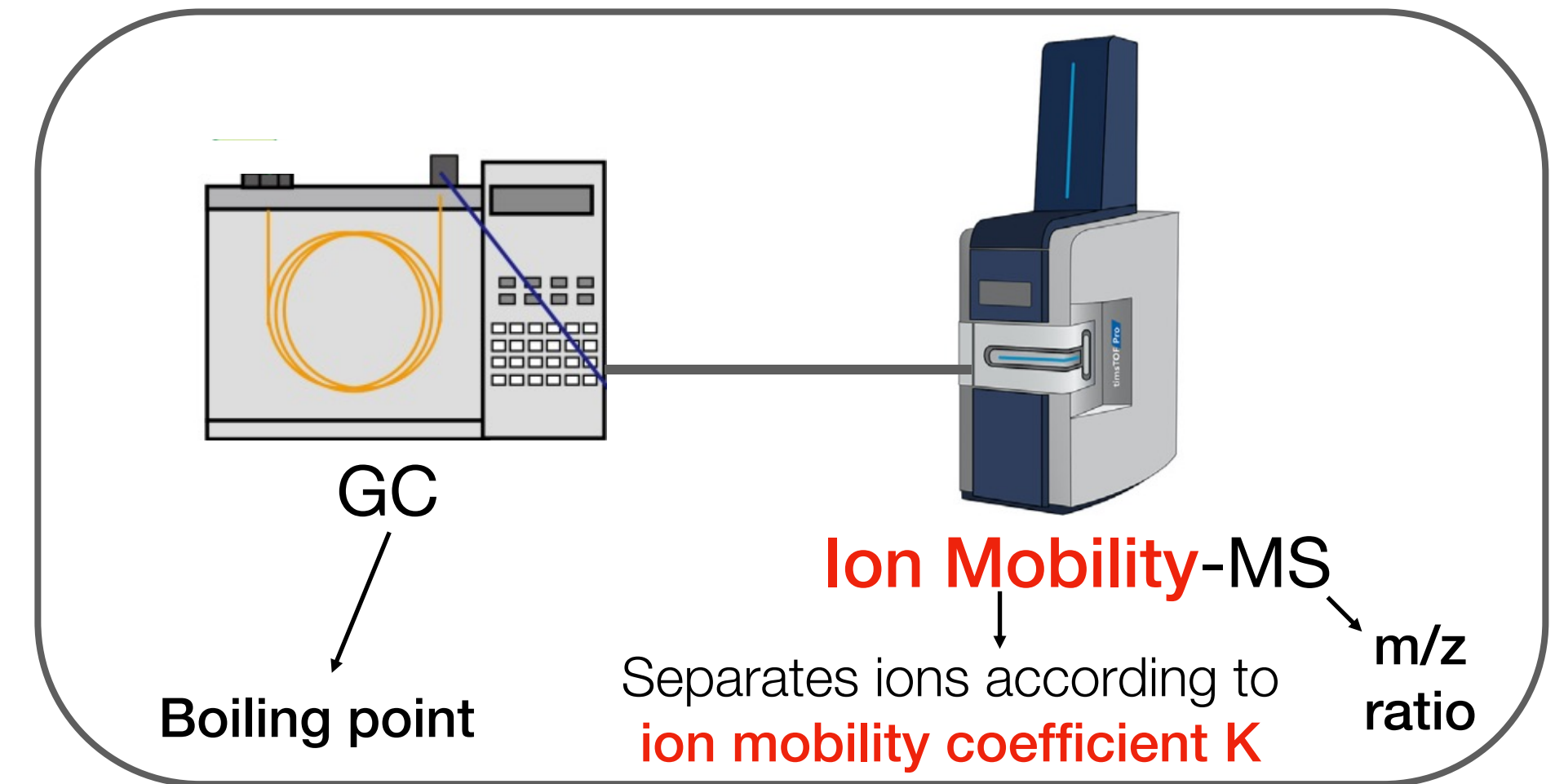
Introduction

POPs analysis in food

Traditional approach



Our approach



Ion mobility

- Origin: end of the 19th century
- First commercial IM-MS instruments: mid-2000s
- Exponential growth in the last decade

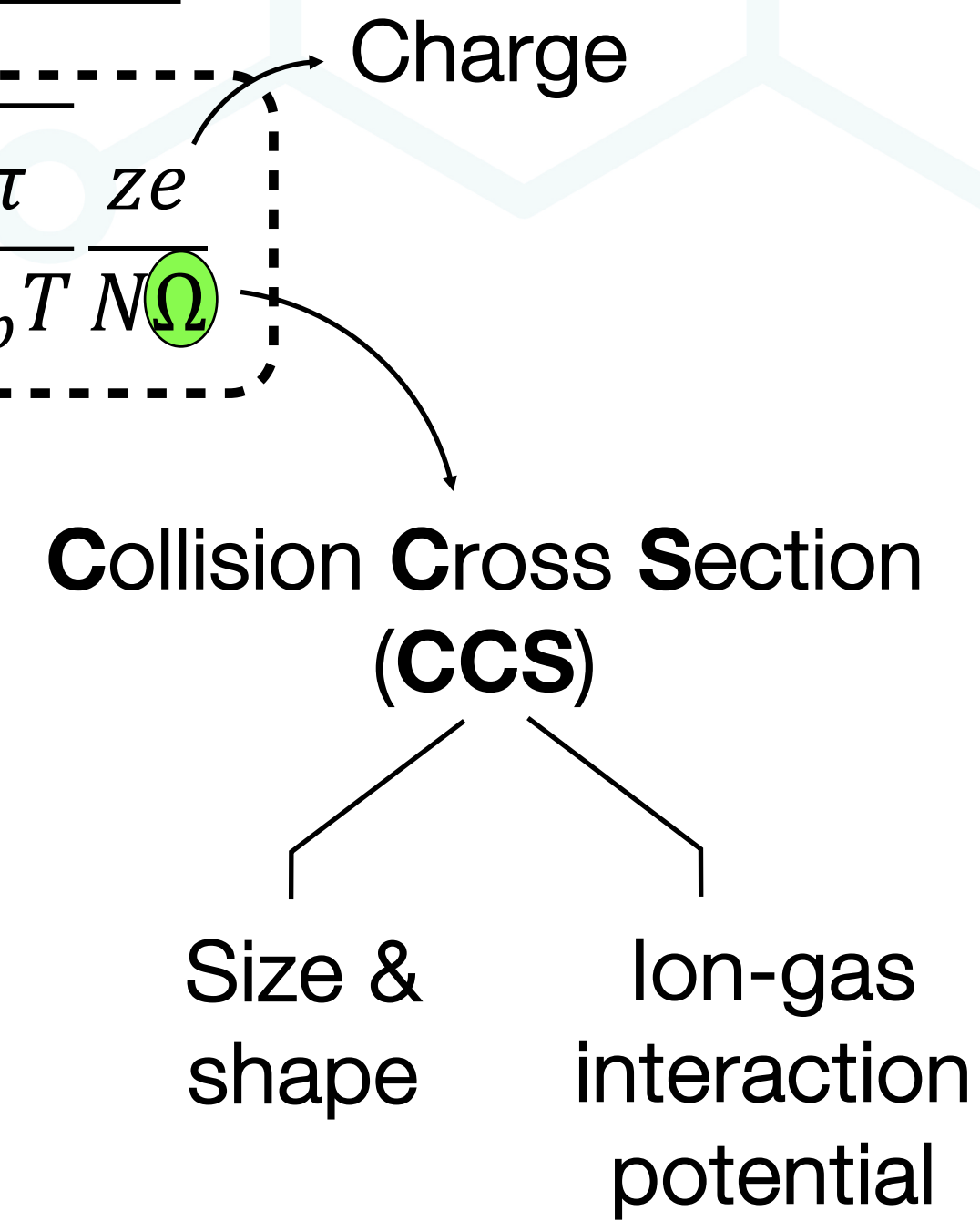
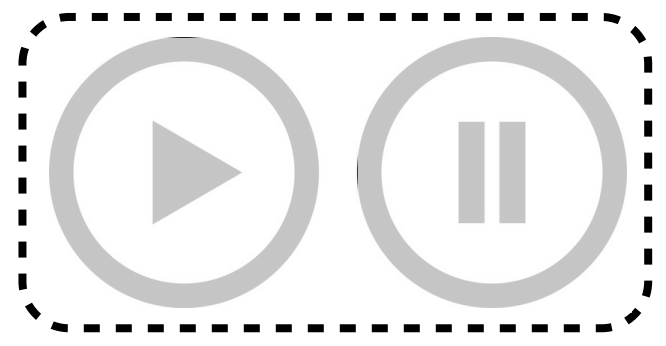
Drift speed

$$v_d = KE$$

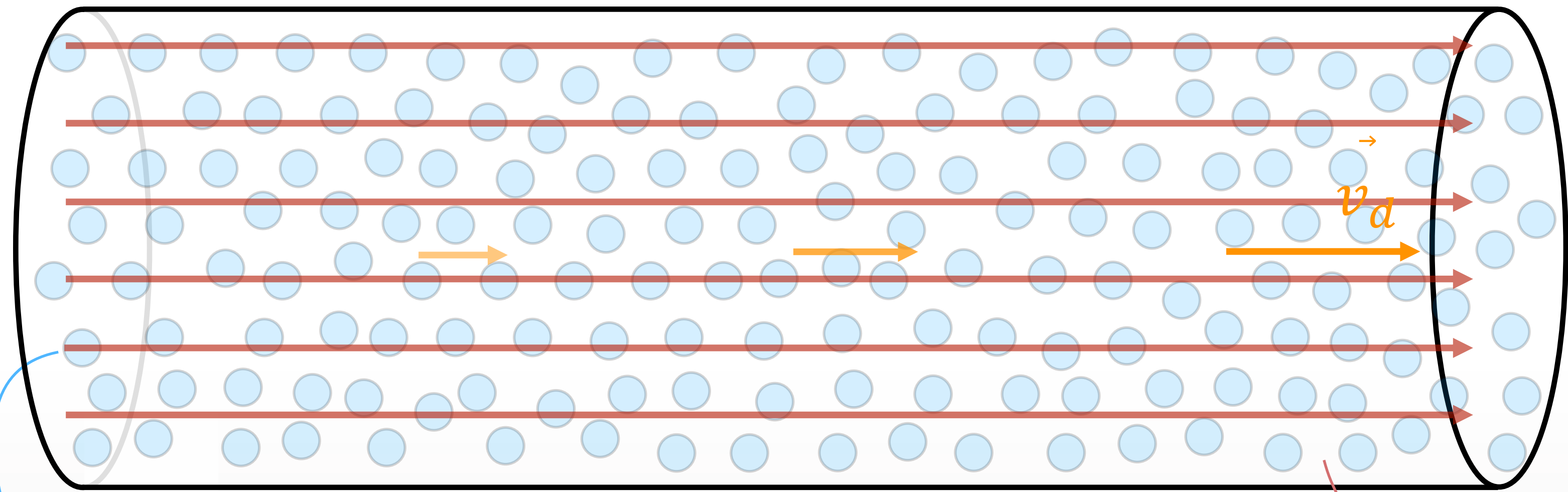
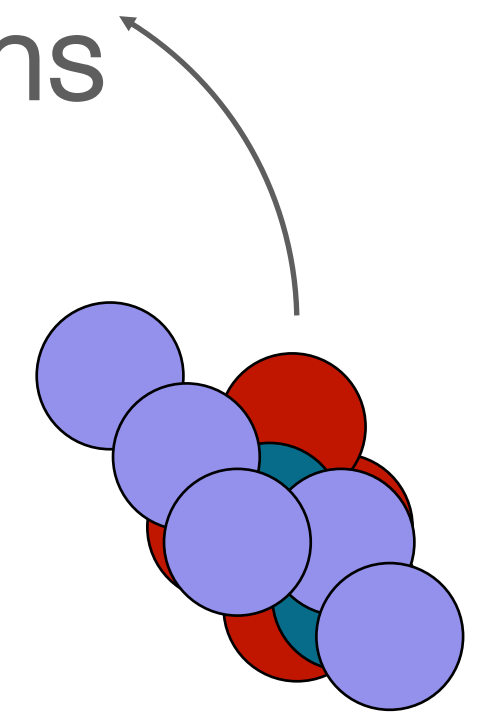
Ion mobility coefficient

Fundamental low-field mobility equation

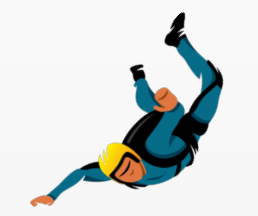
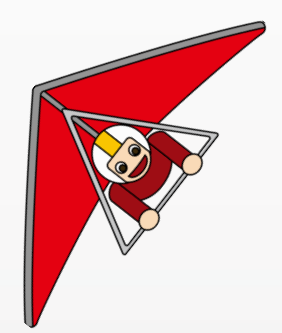
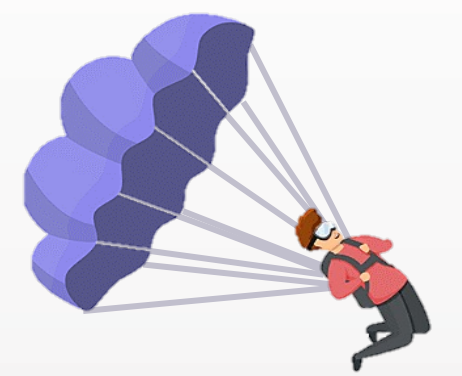
$$K = \frac{3}{16} \sqrt{\frac{2\pi}{\mu k_b T}} \frac{ze}{N\Omega}$$



Mixture of ions

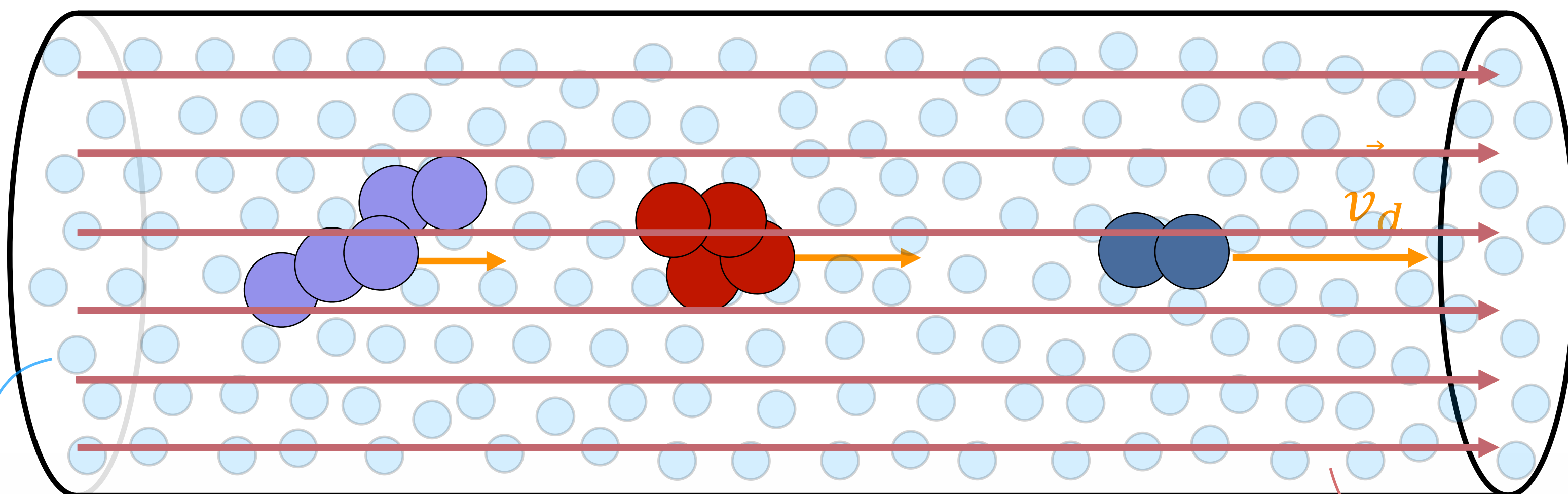


Drift gas (N₂)



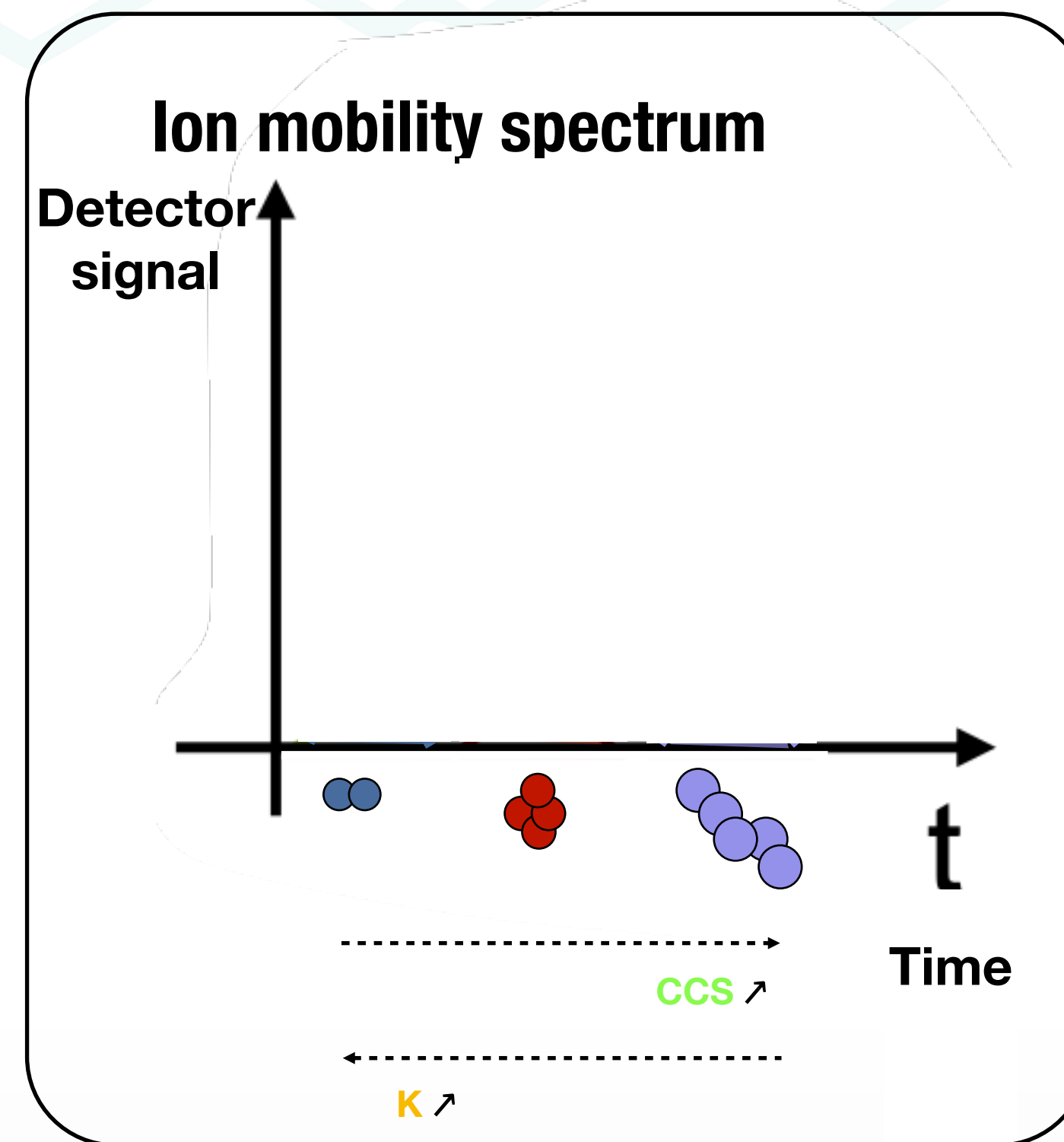
Electric field E

Ion mobility



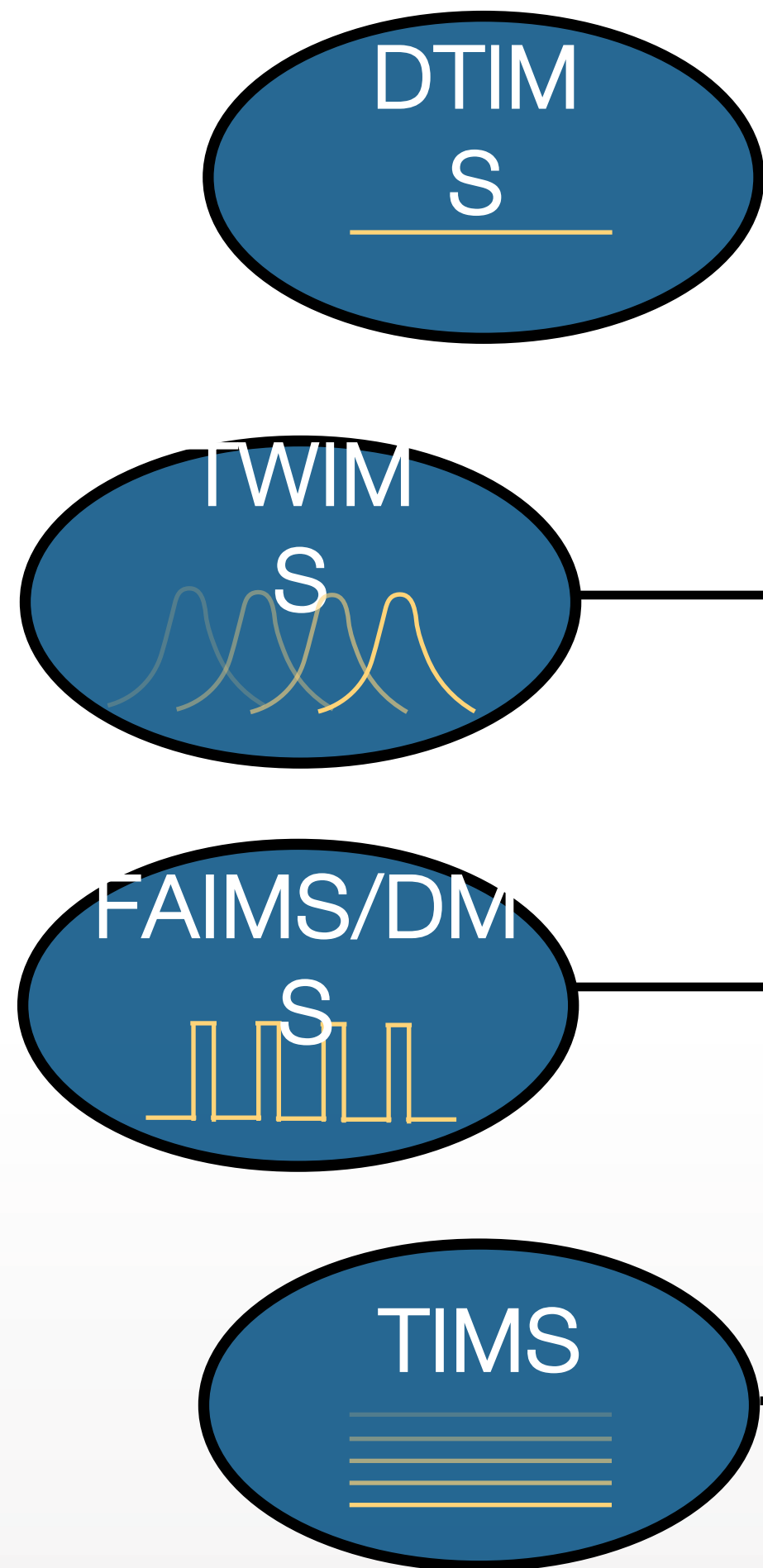
Drift gas
(N₂)

Electric field
→
E

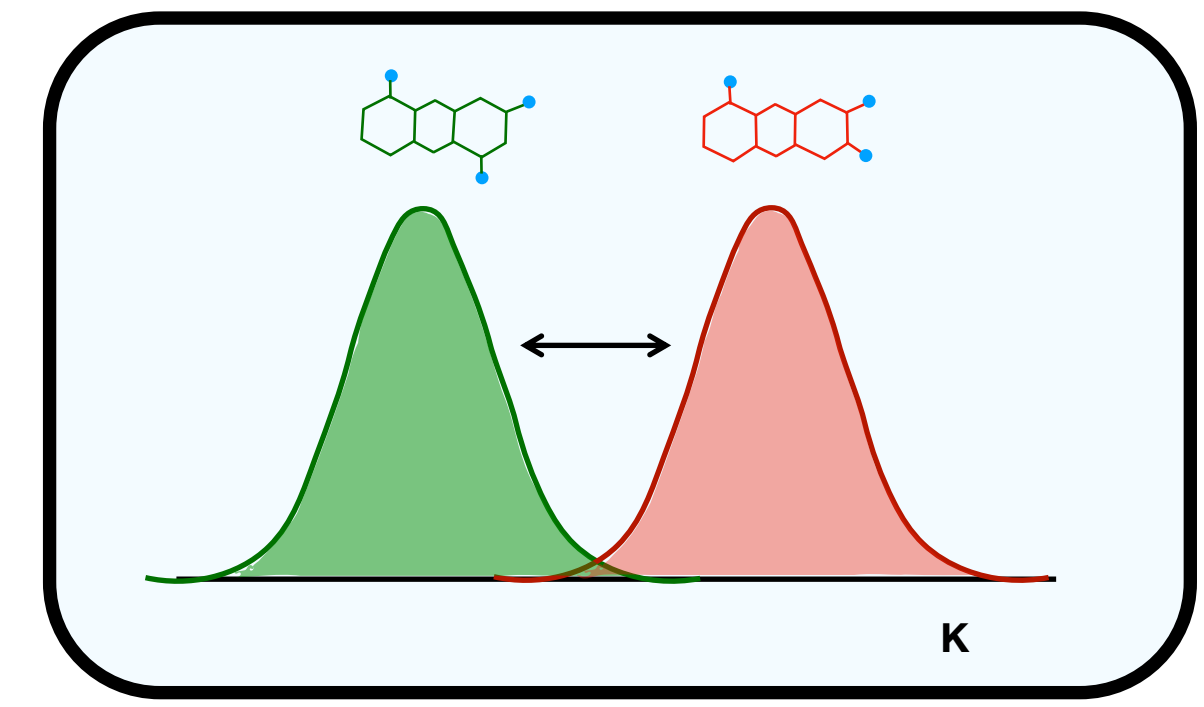
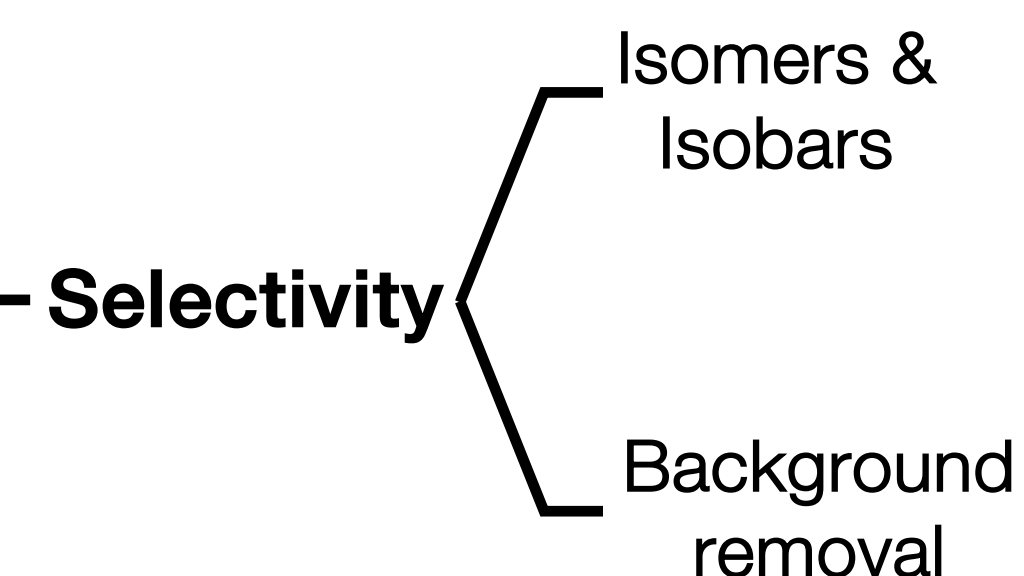


Ion mobility

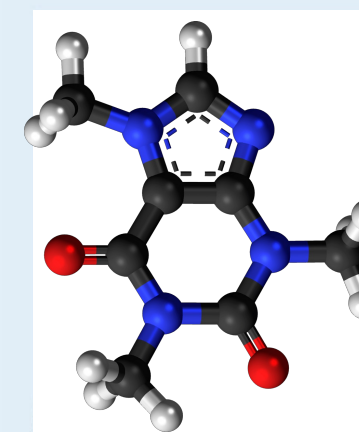
Technologies



Advantages



ID CARD




Name: 1,3,7-Trimethyl-3,7-dihydro-1H-purine-2,6-dione

Formula: C₈H₁₀N₄O₂

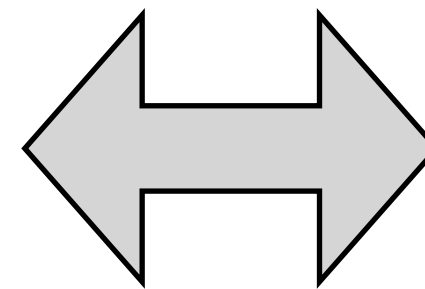
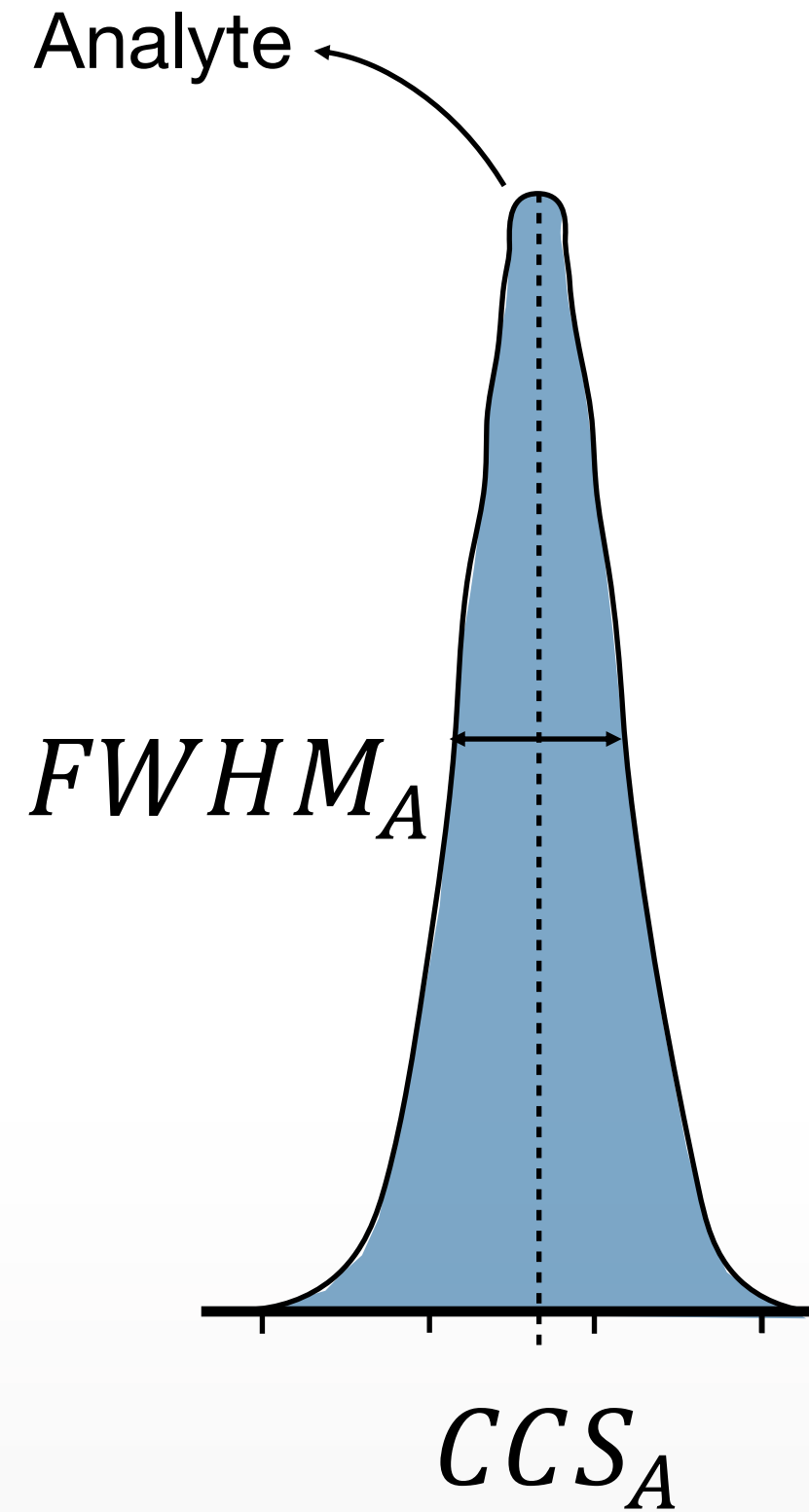
Mass: 194.191 Da

CCS: 145.40 Å²



Resolving power

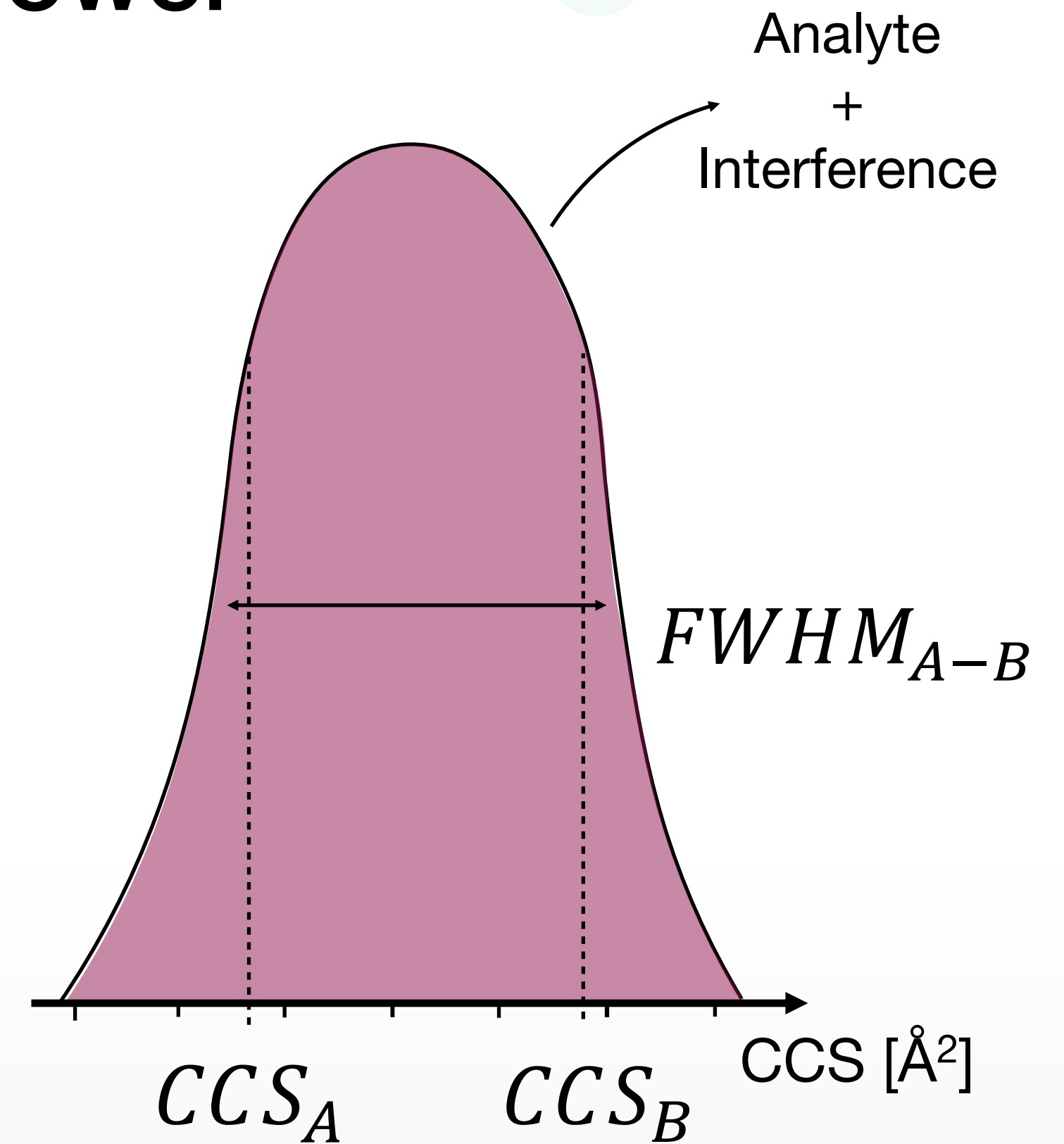
High resolving power



Resolving power

$$R_p = \frac{CCS_X}{FWHM_X}$$

Low resolving power



Rp in TIMS



Analysis time

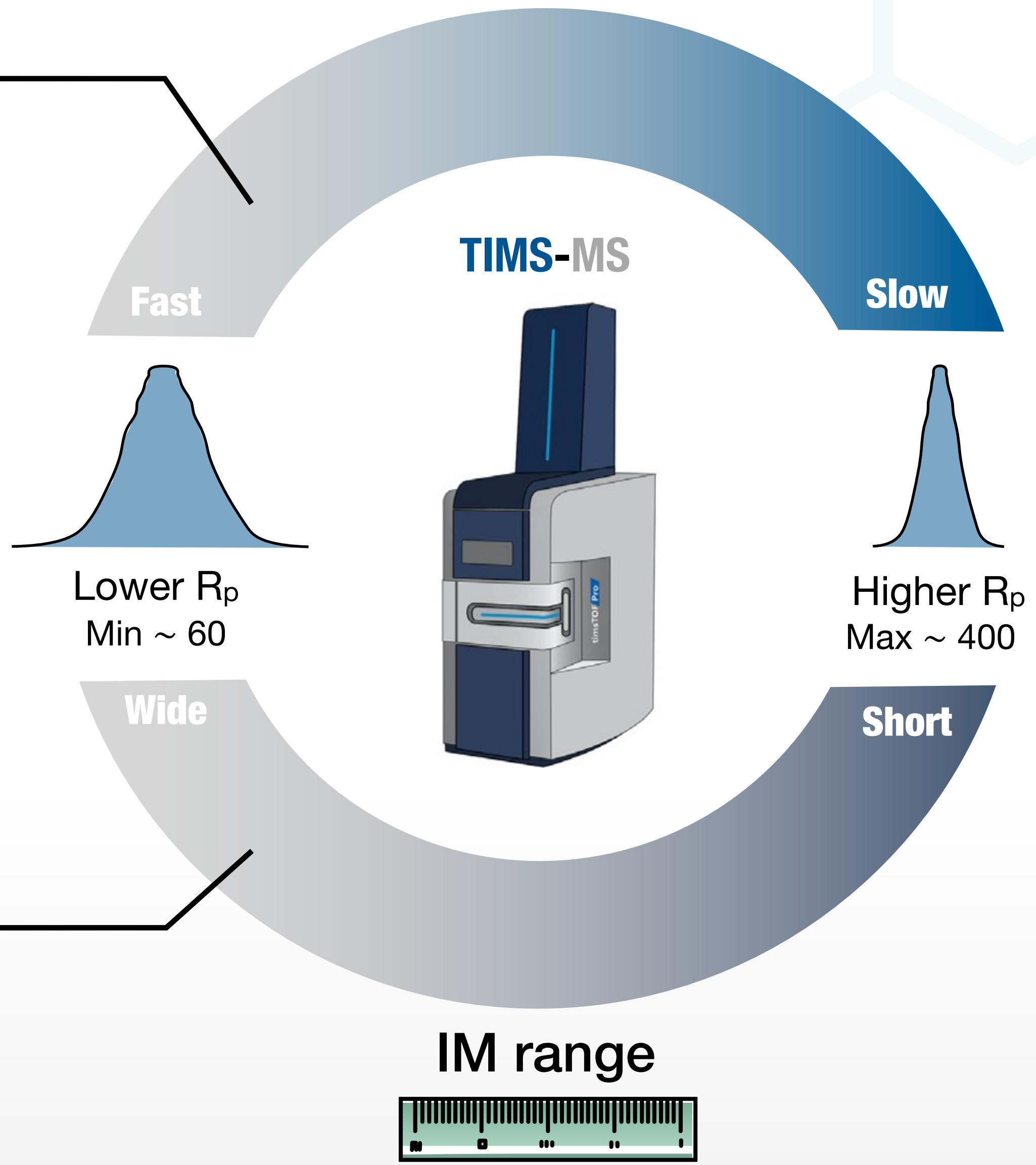
GC coupling

⇒ Fast IM separations

Limited R_p

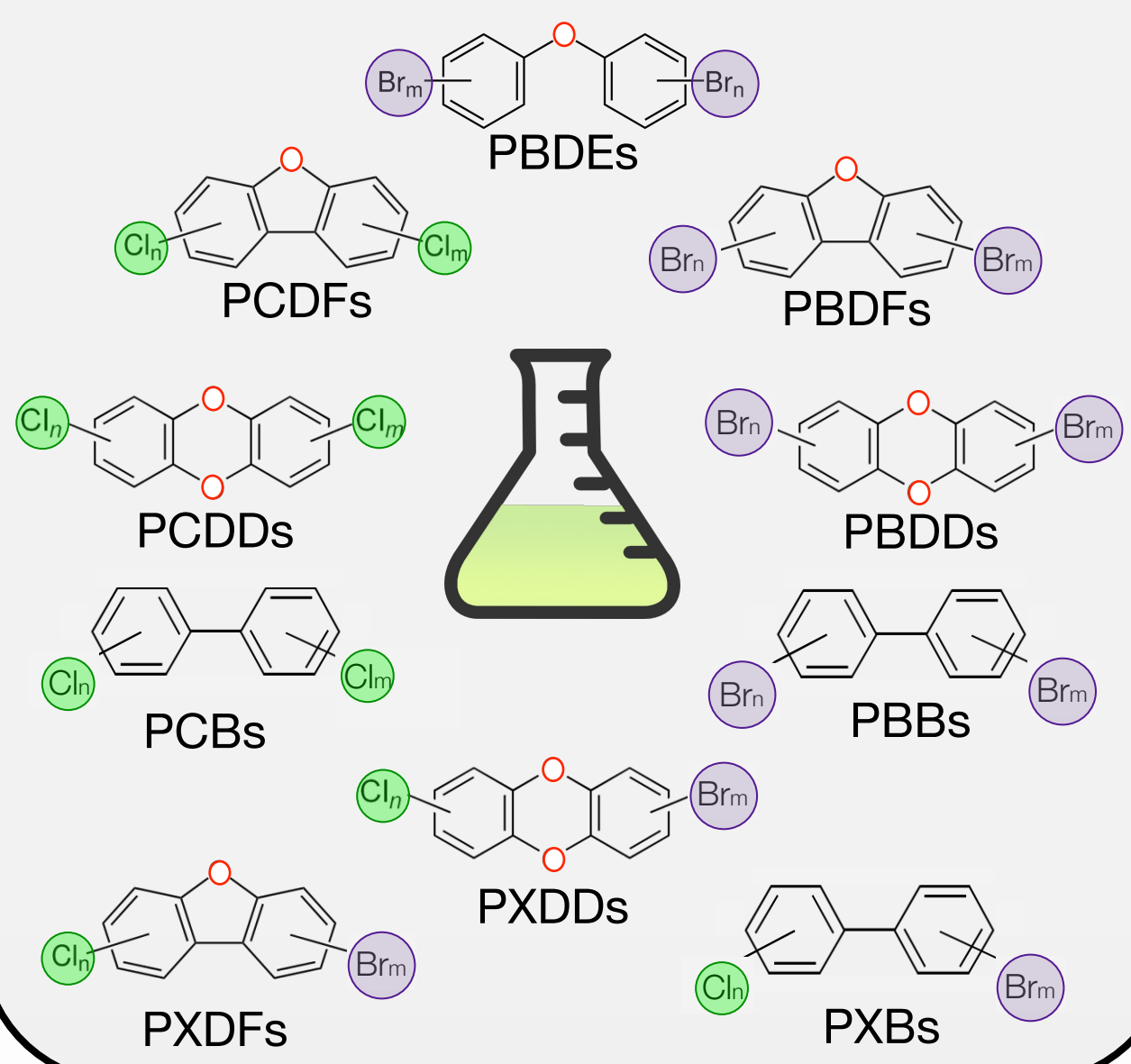
Diversity of POPs

⇒ Wide IM range

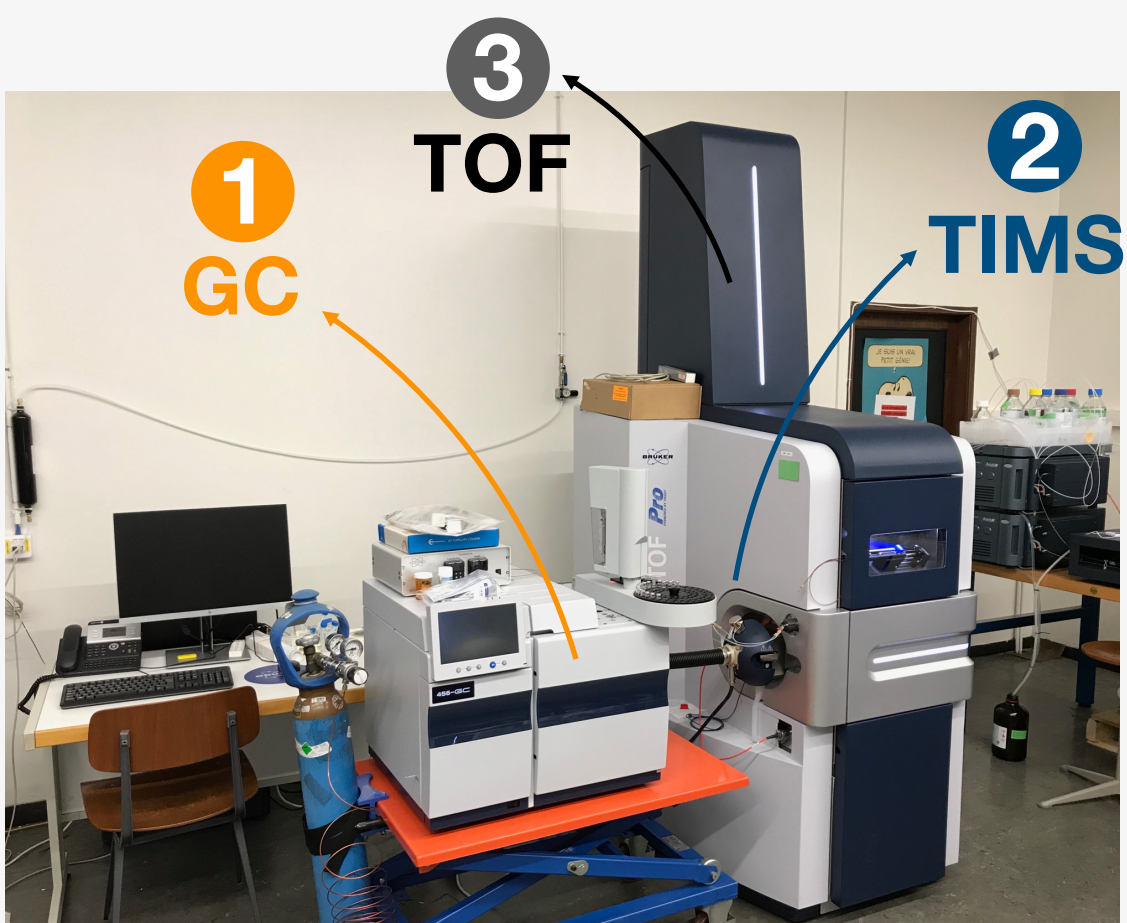



R_p in TIMS

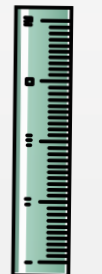
Mixture of 174 POP standards



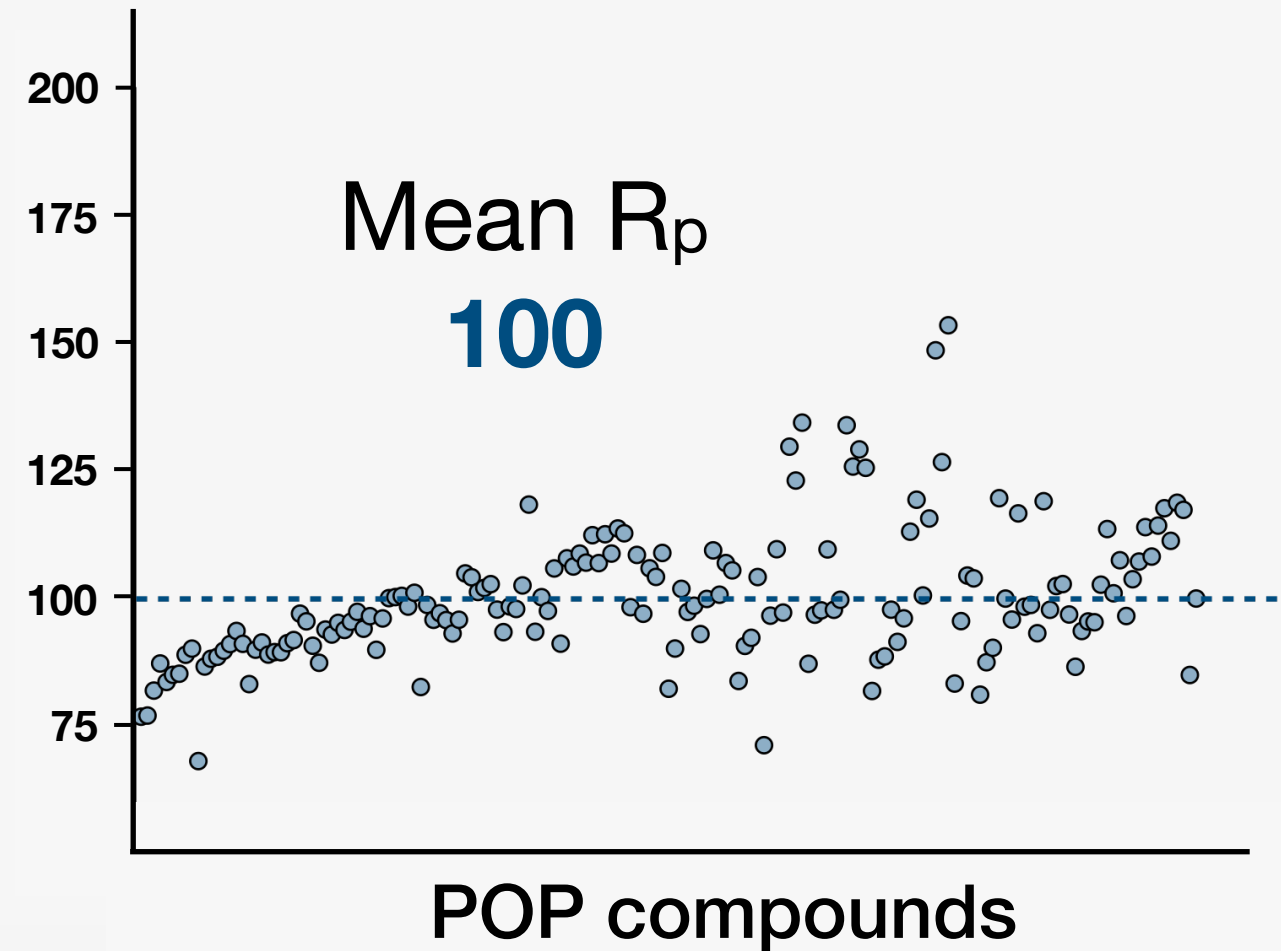
GC-TIMS-MS analysis



 **Analysis time:**
350 ms

 **IM range:**
1.00 - 1.67 K₀

Resolving power

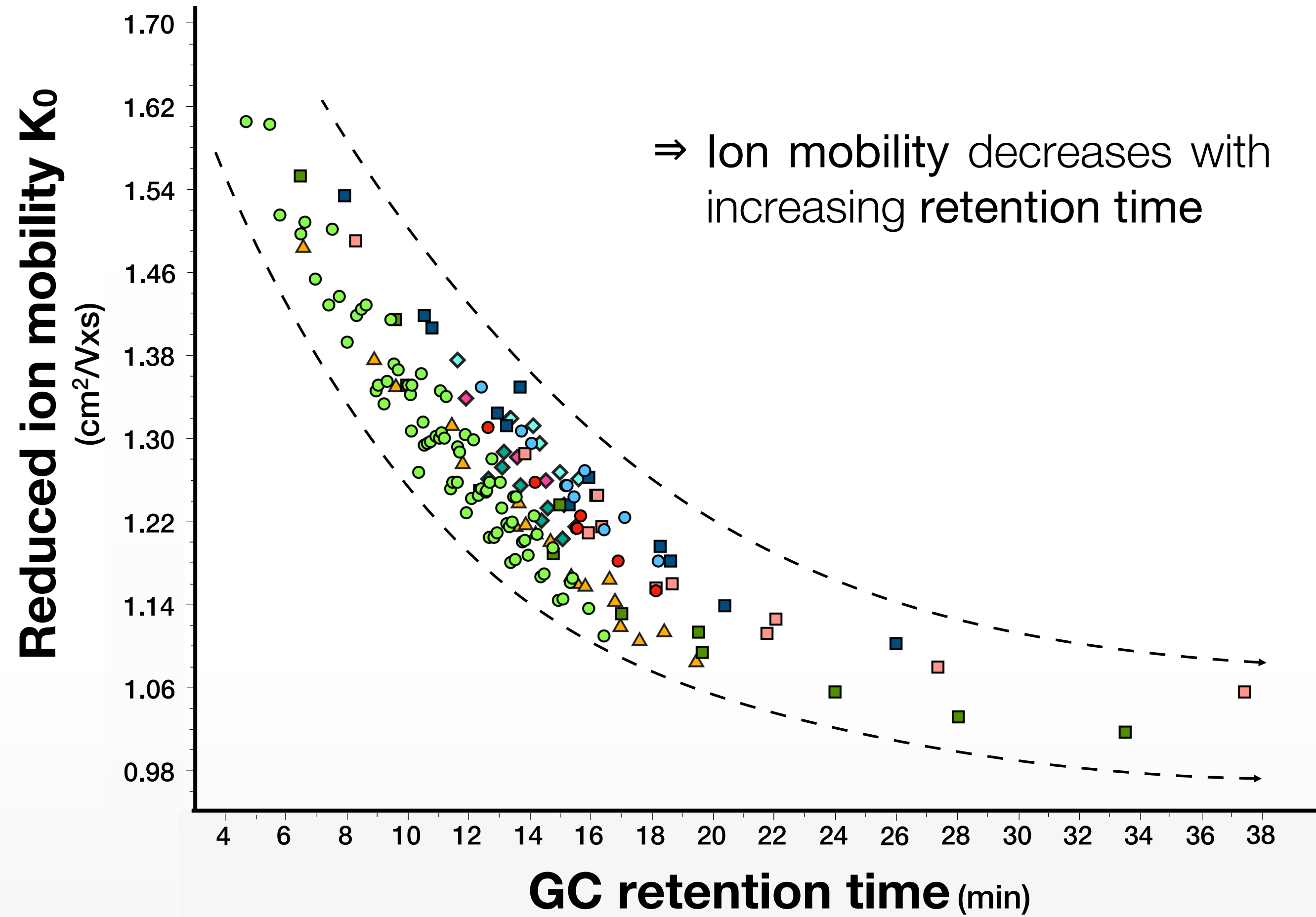
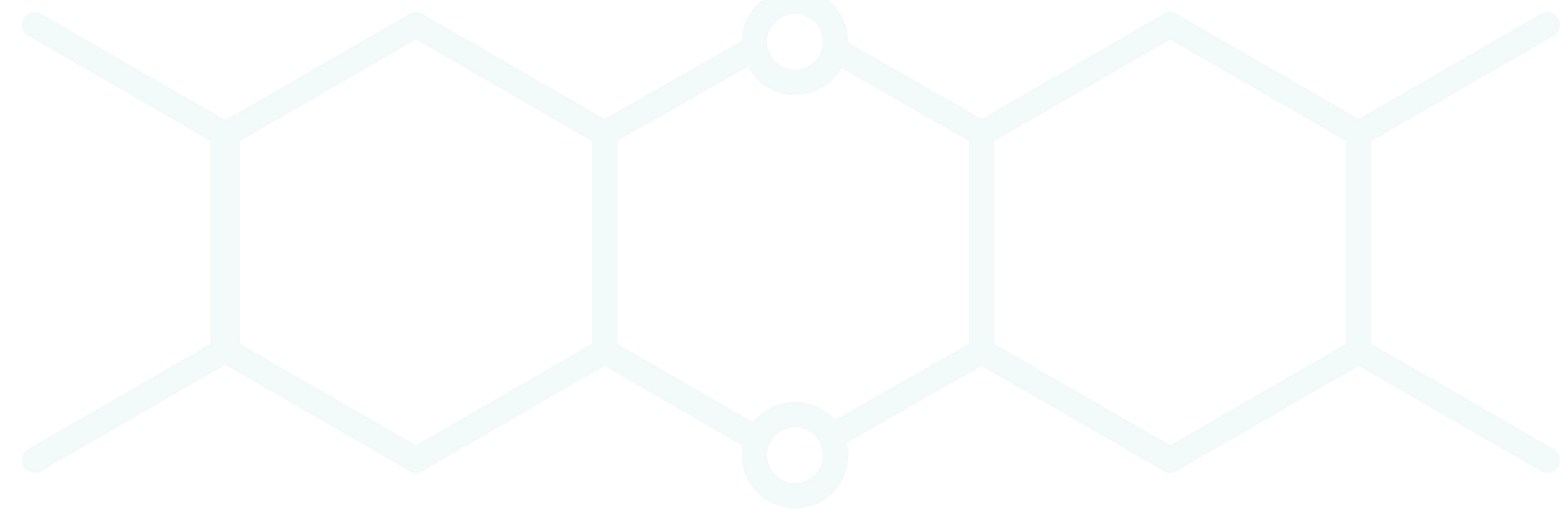


Can we still improve the resolving power?!

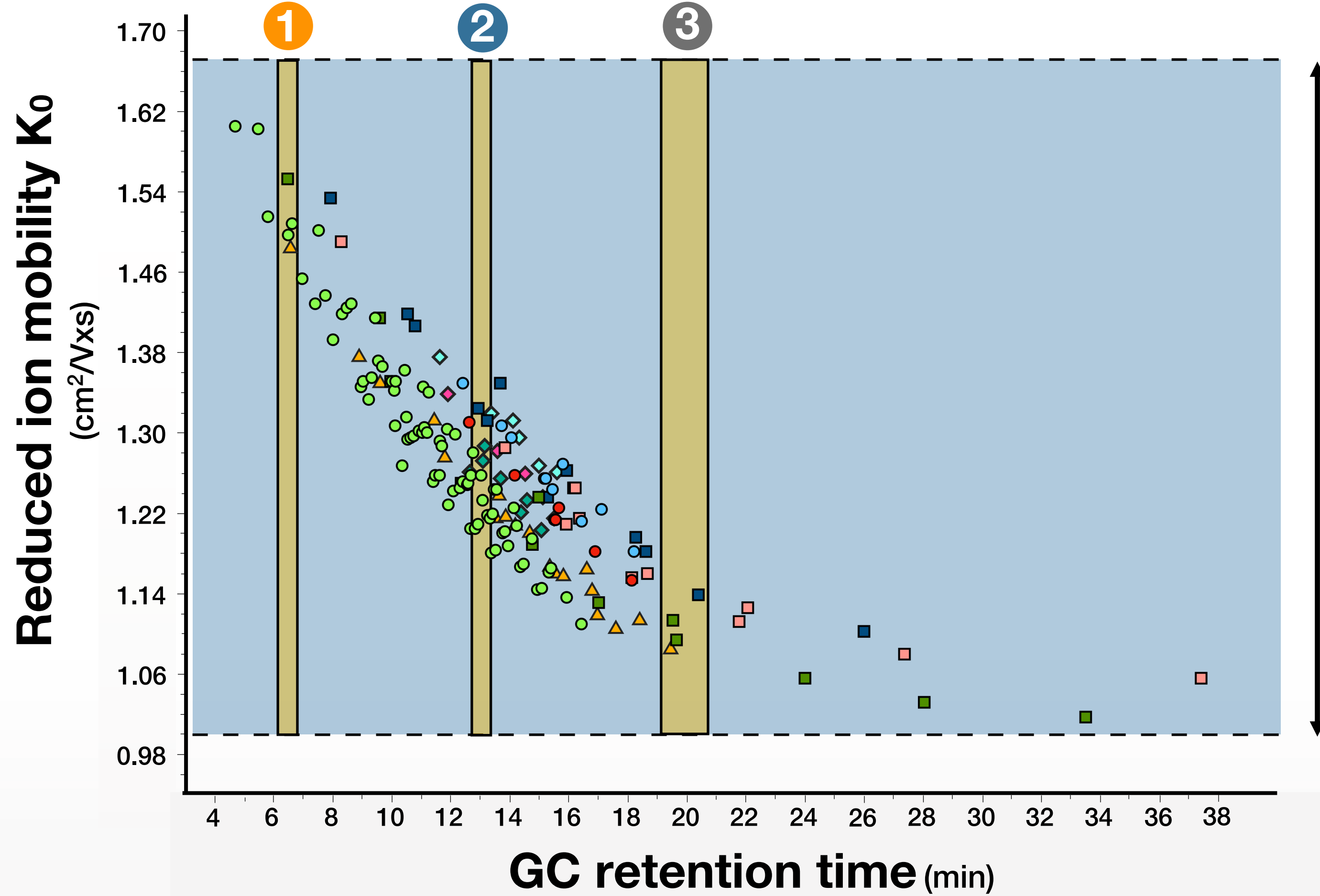
SWIM

Sliding Windows in Ion Mobility

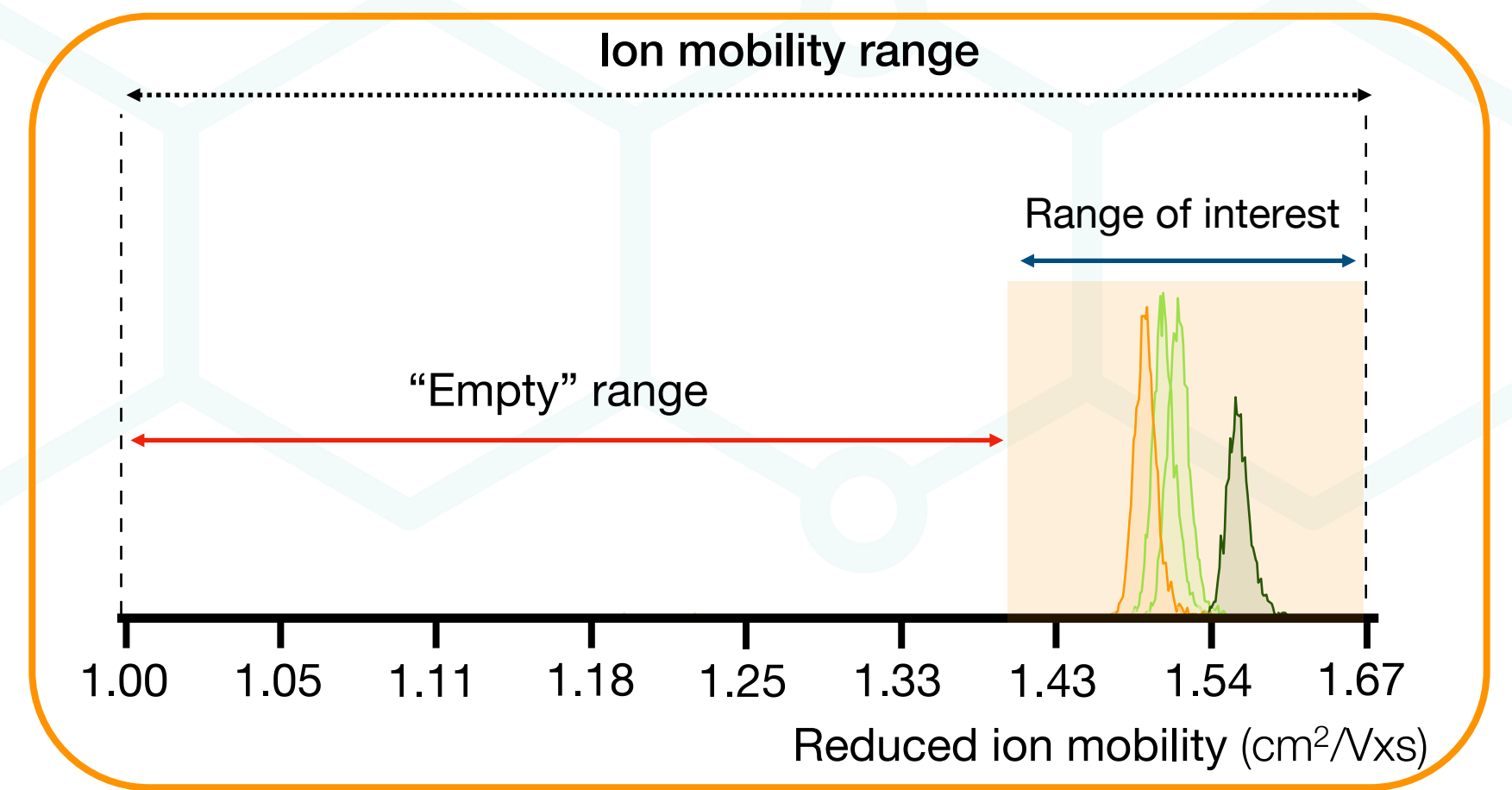
RT vs K correlation



Standard mode

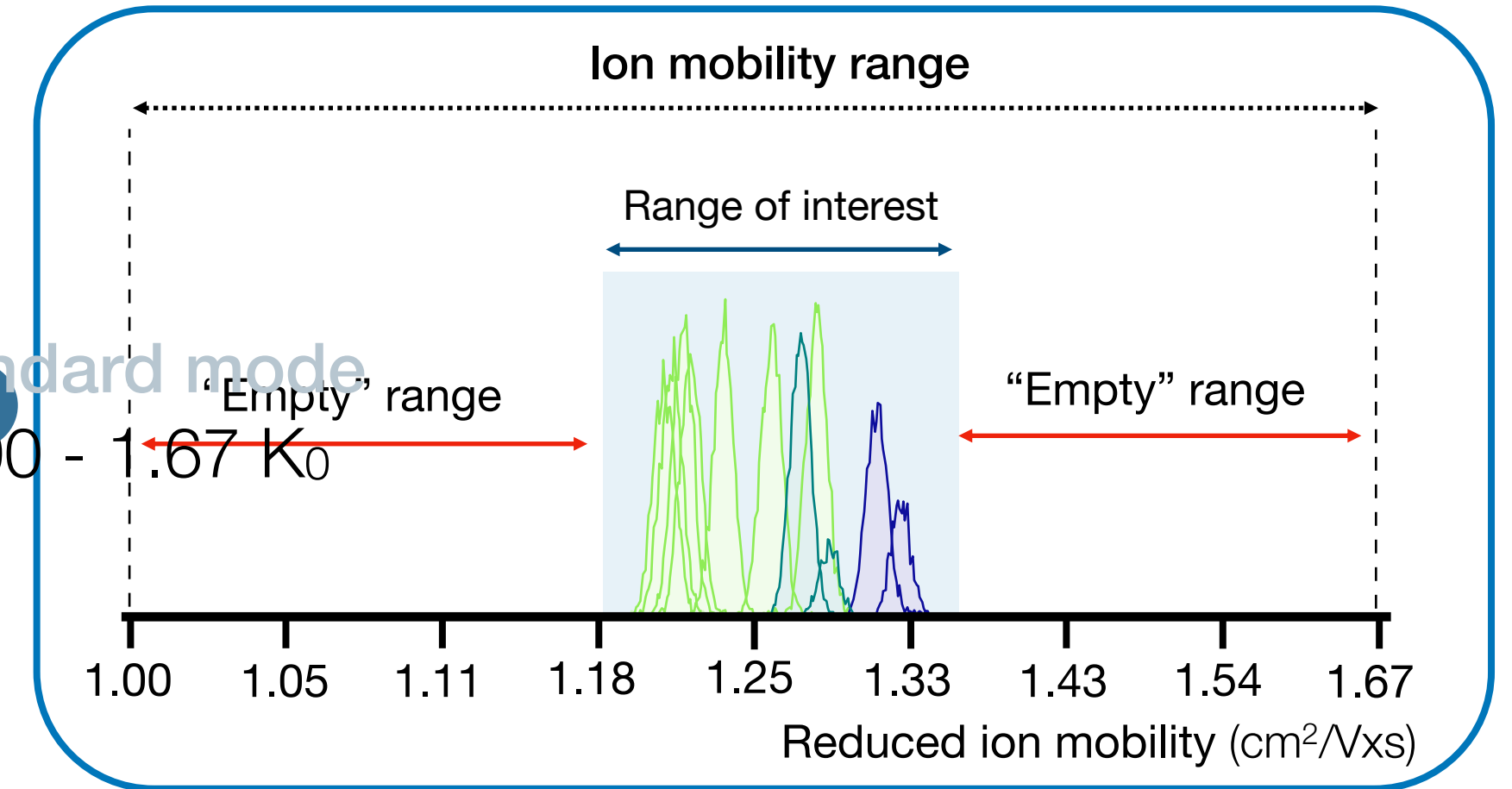


1

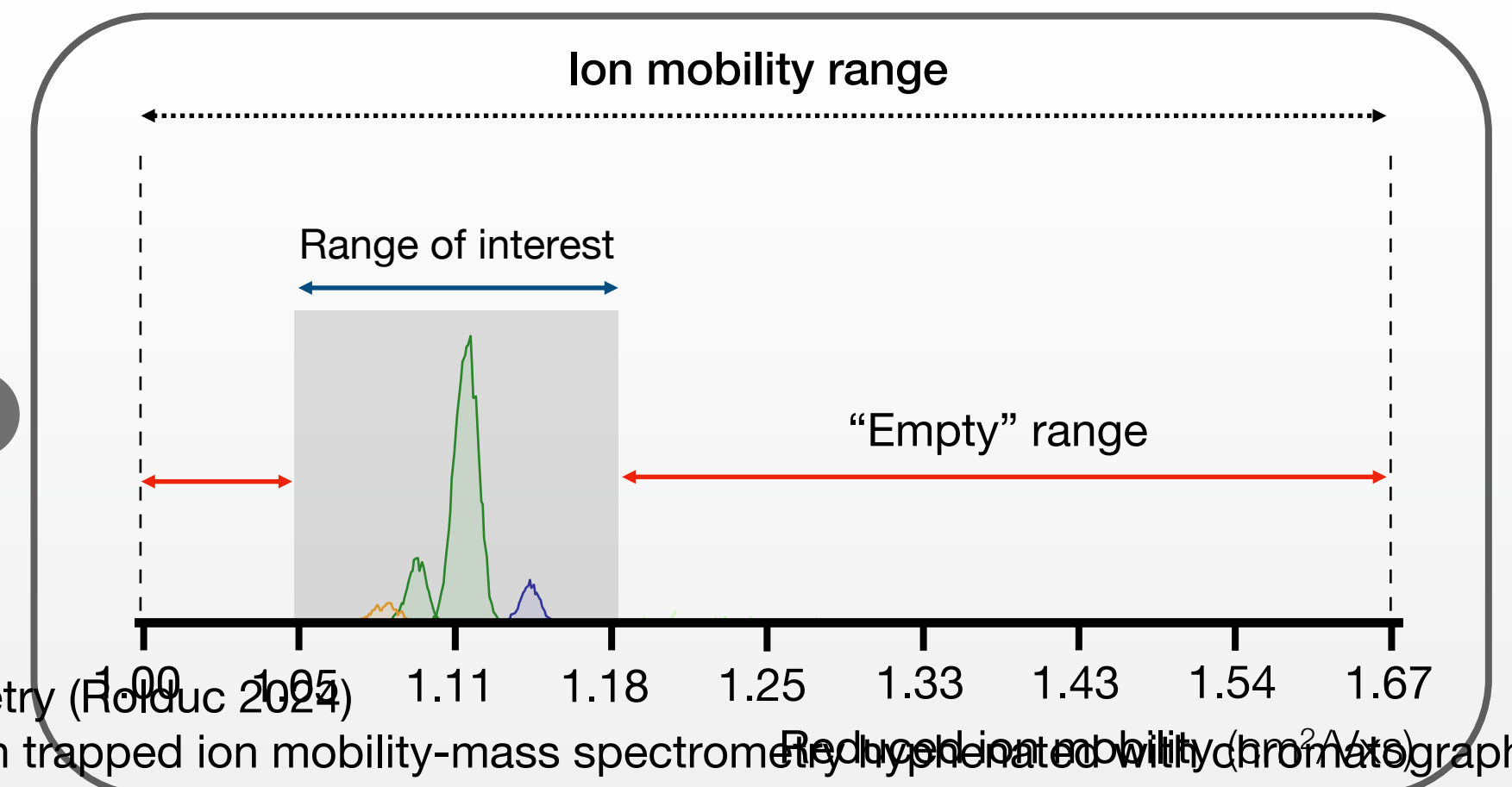


Standard mode

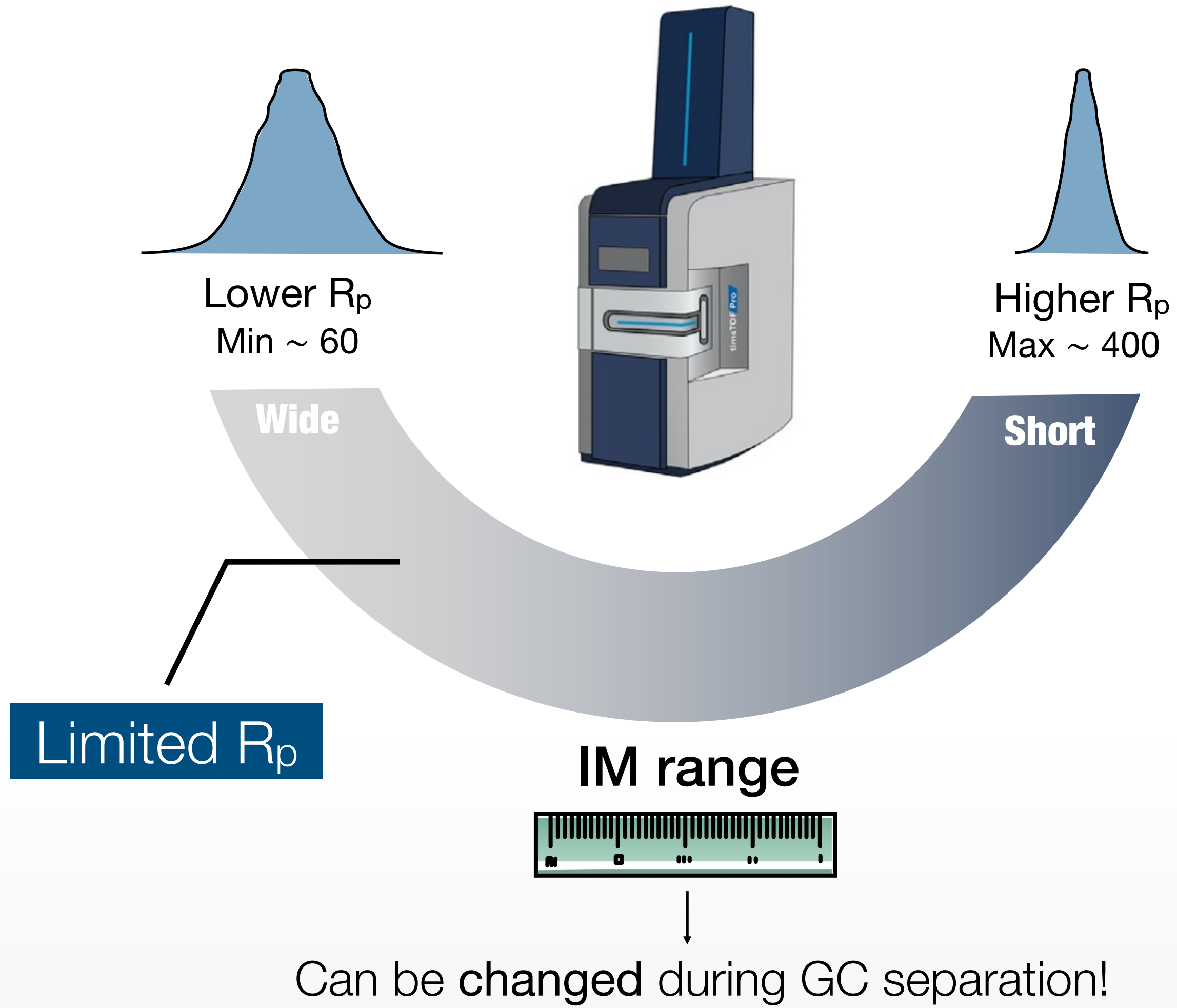
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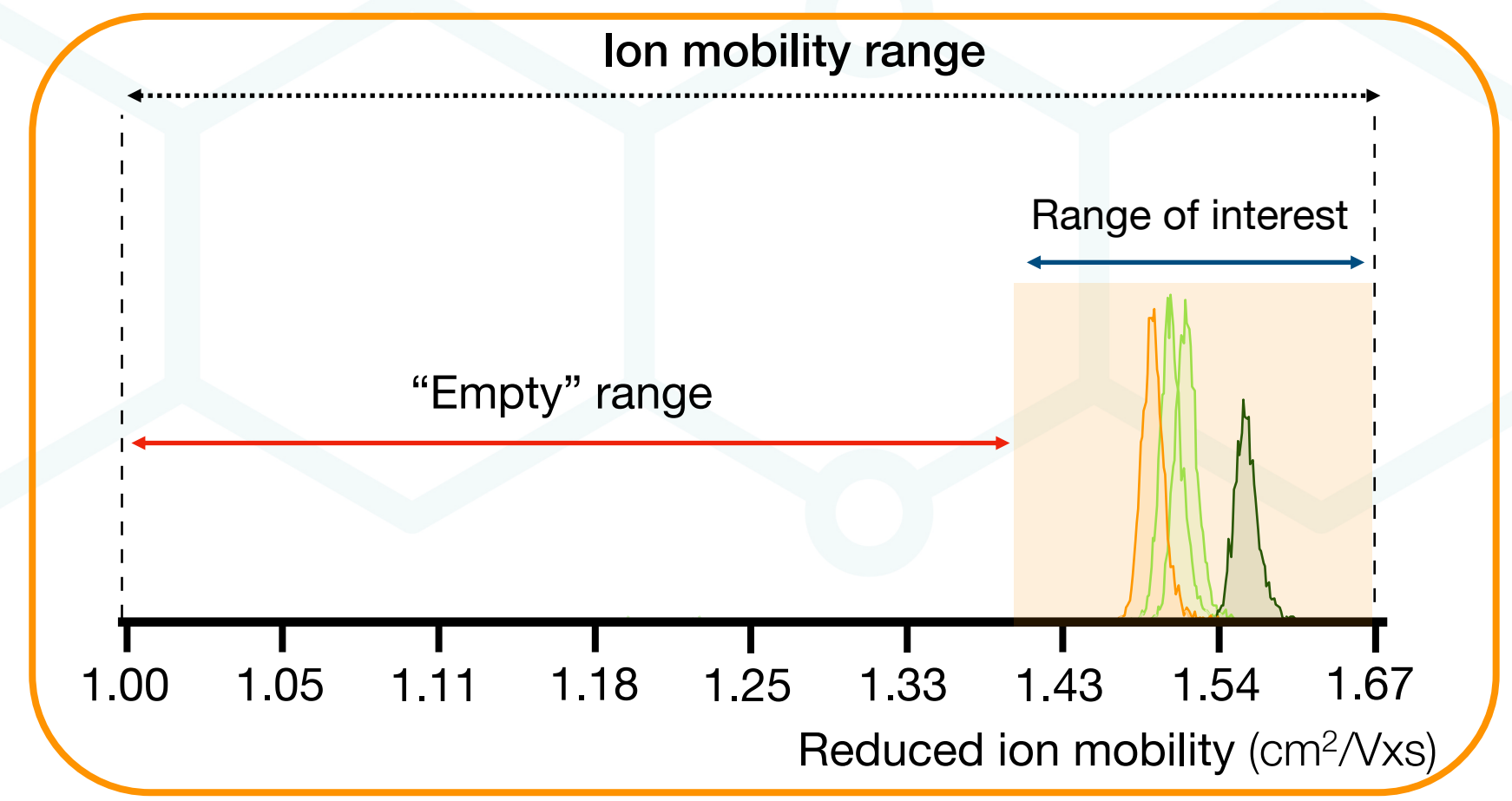
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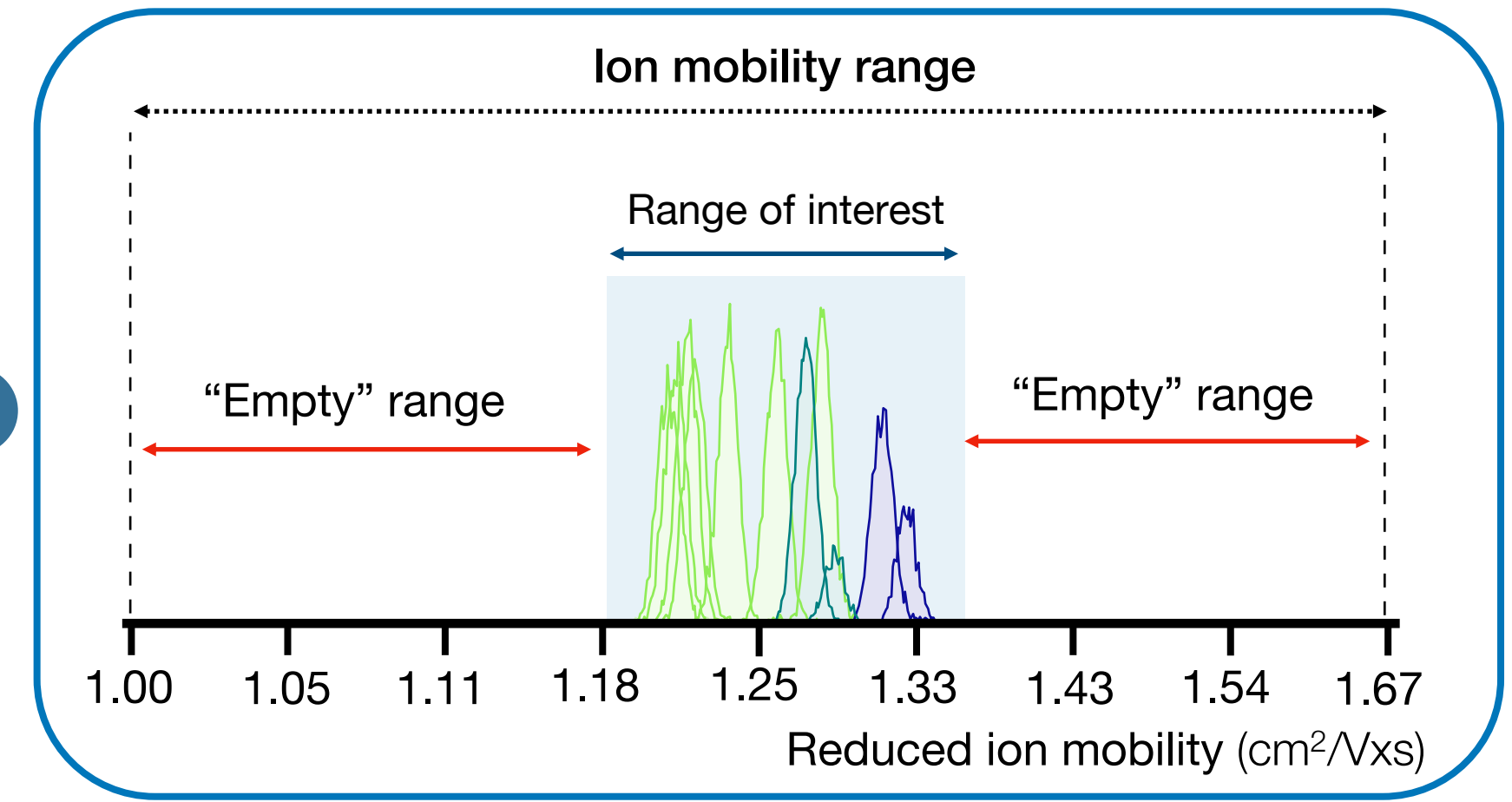
Standard mode



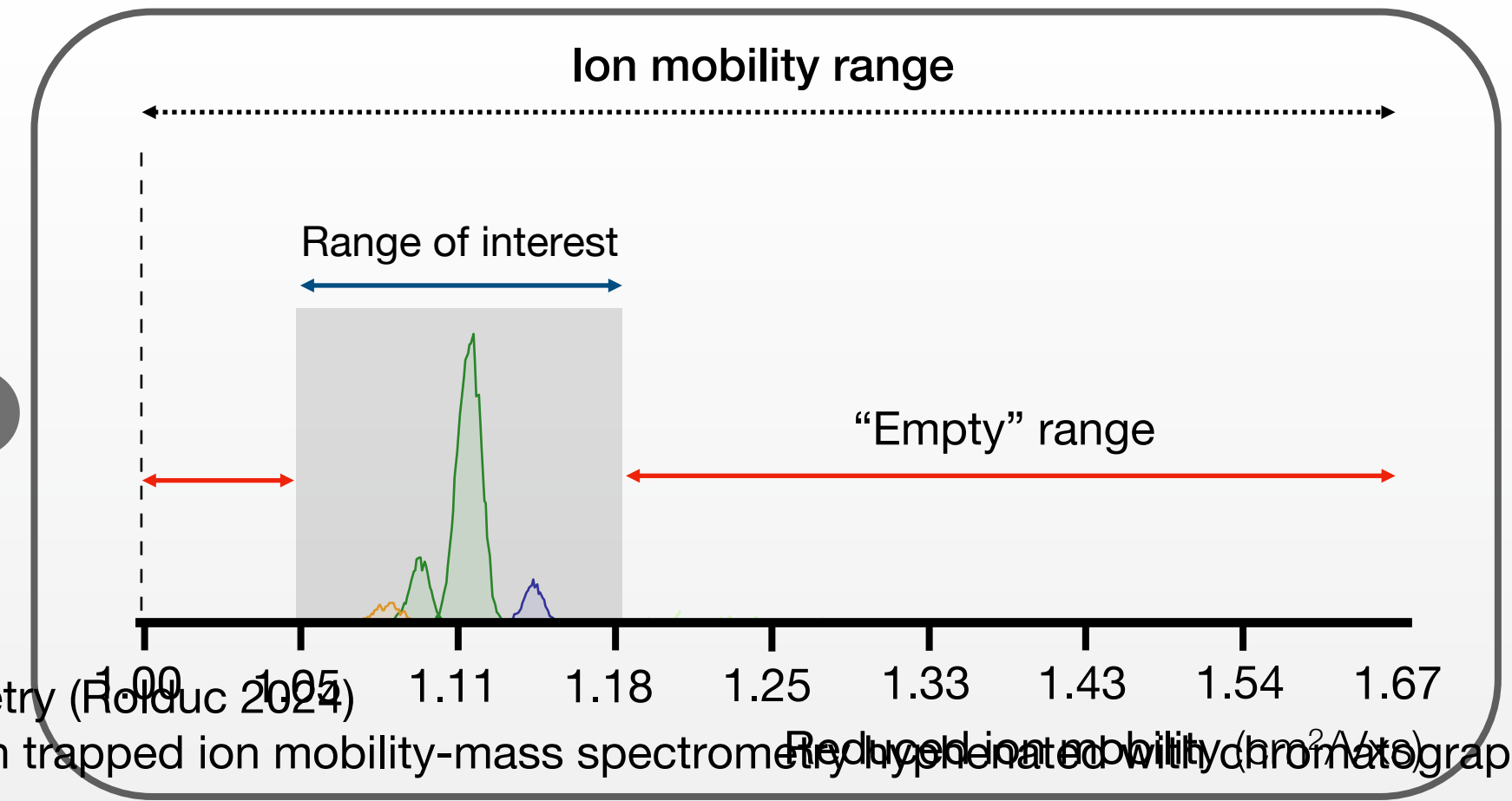
1



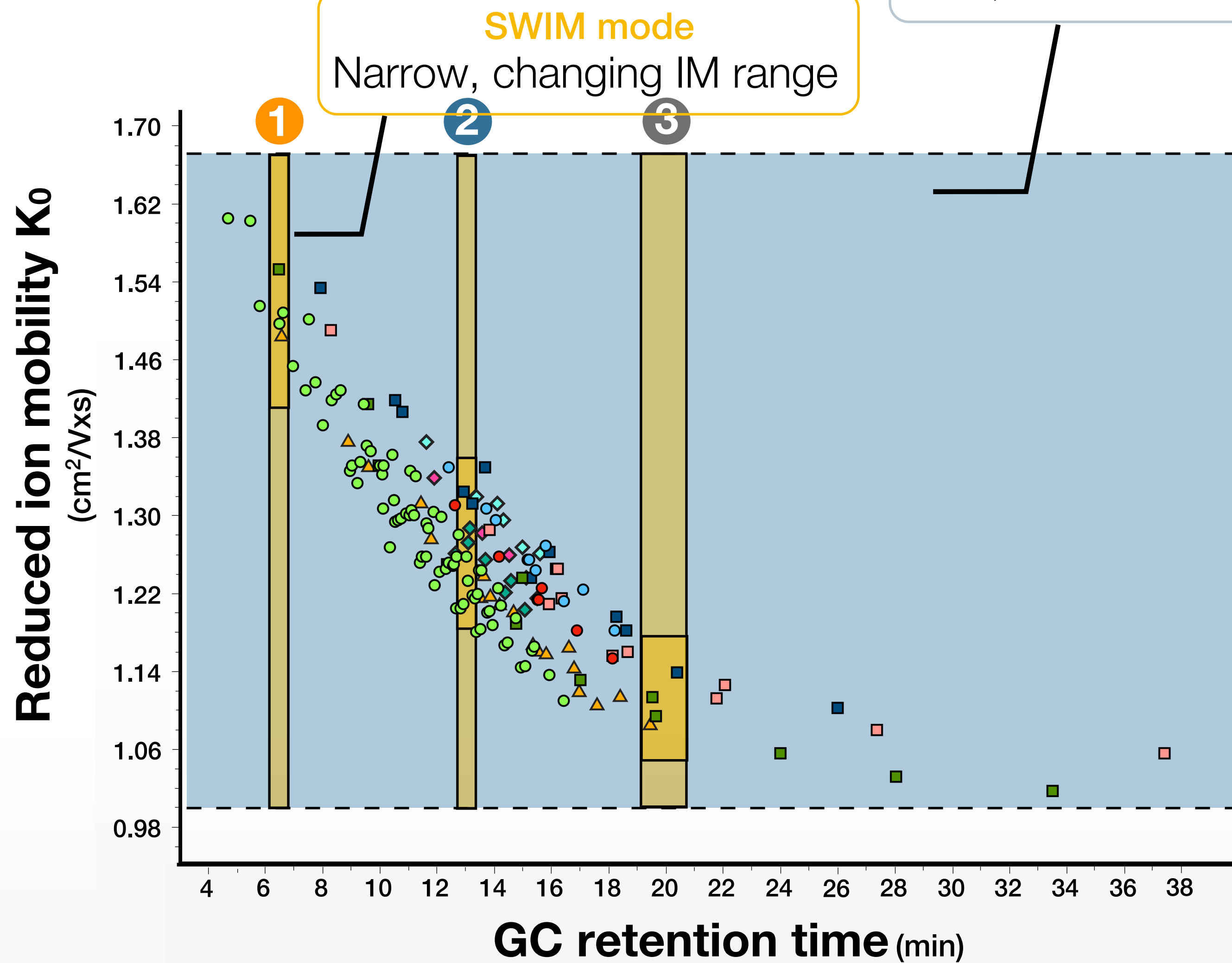
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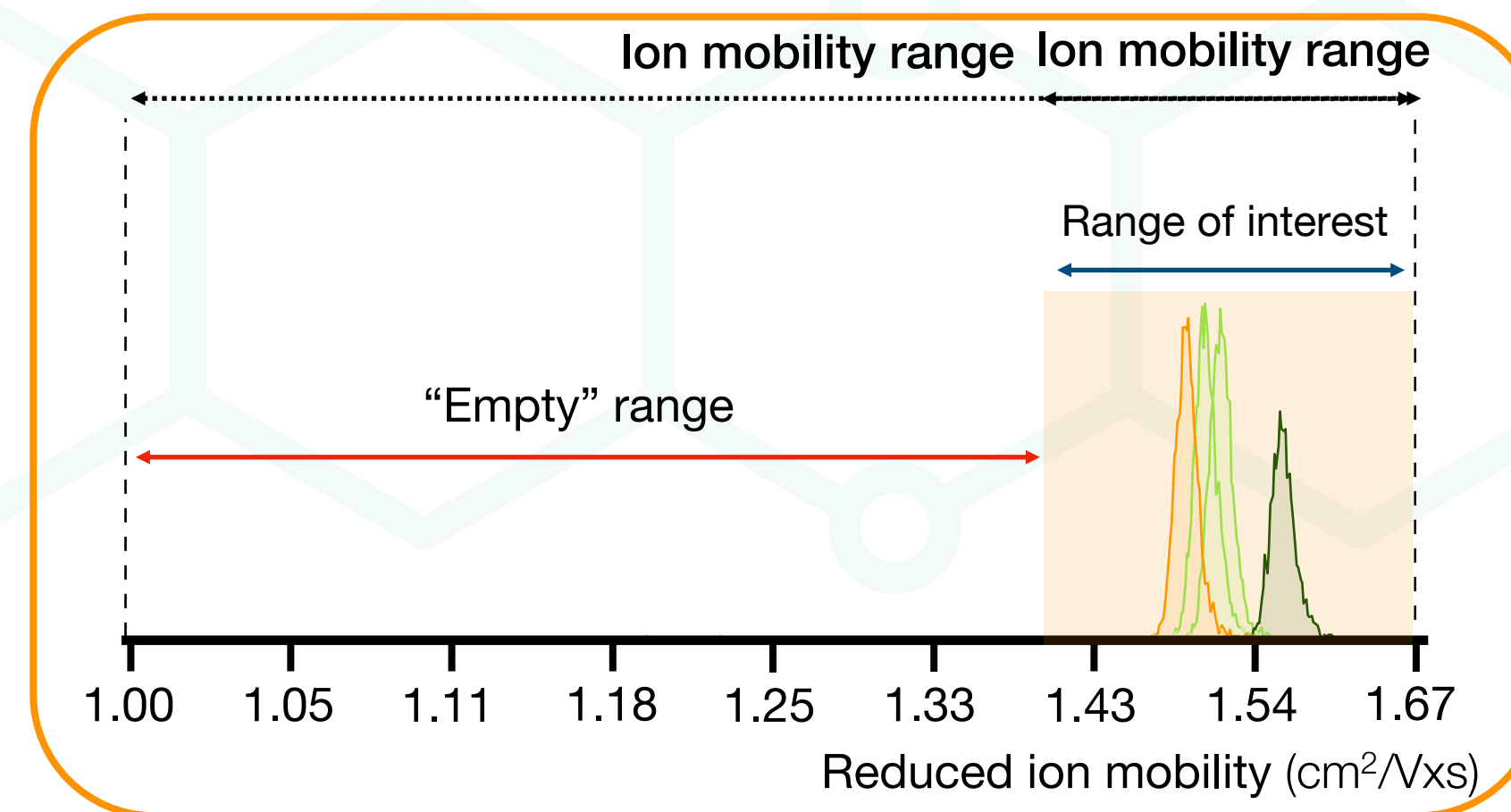
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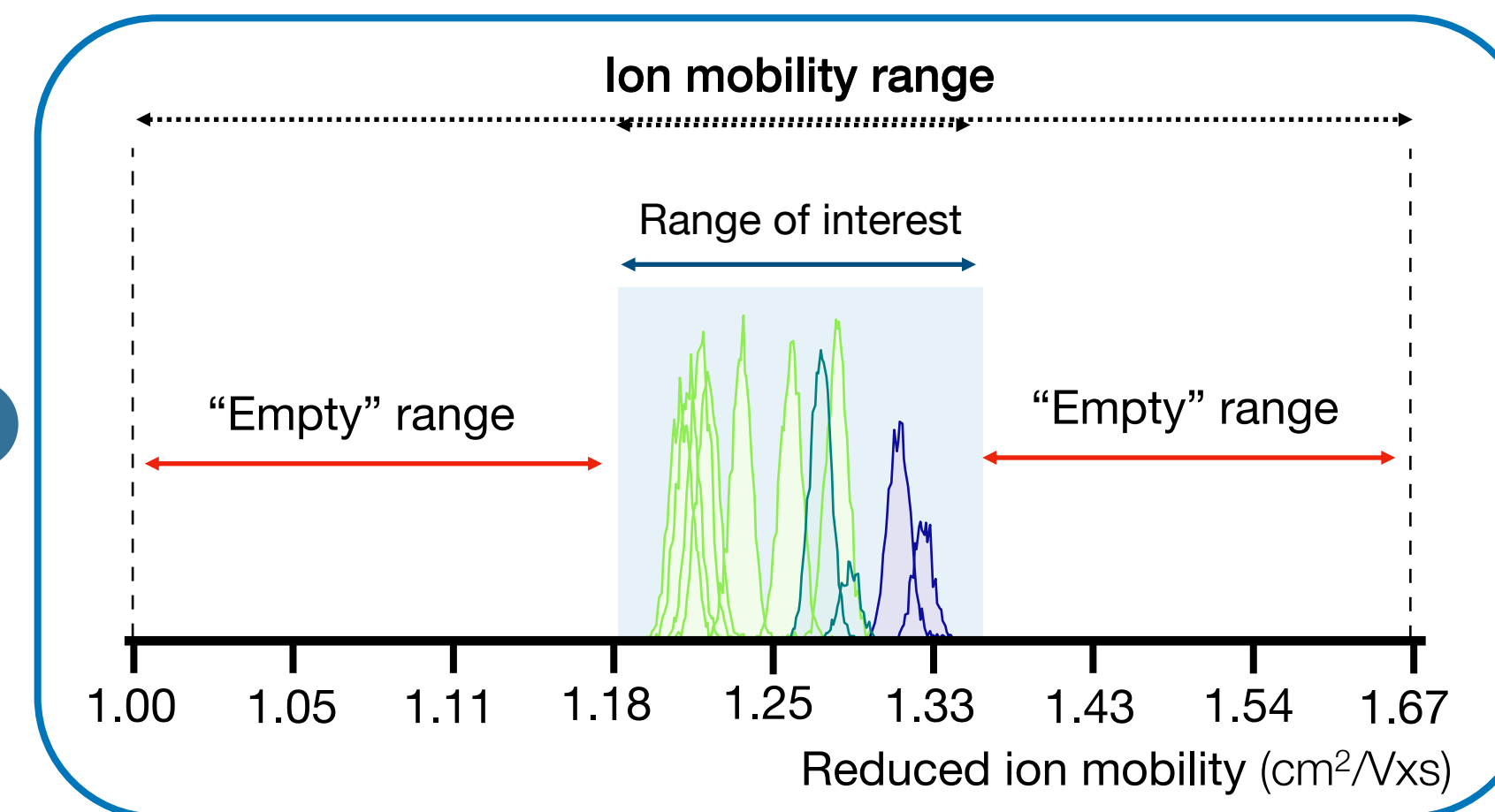
SWIM mode



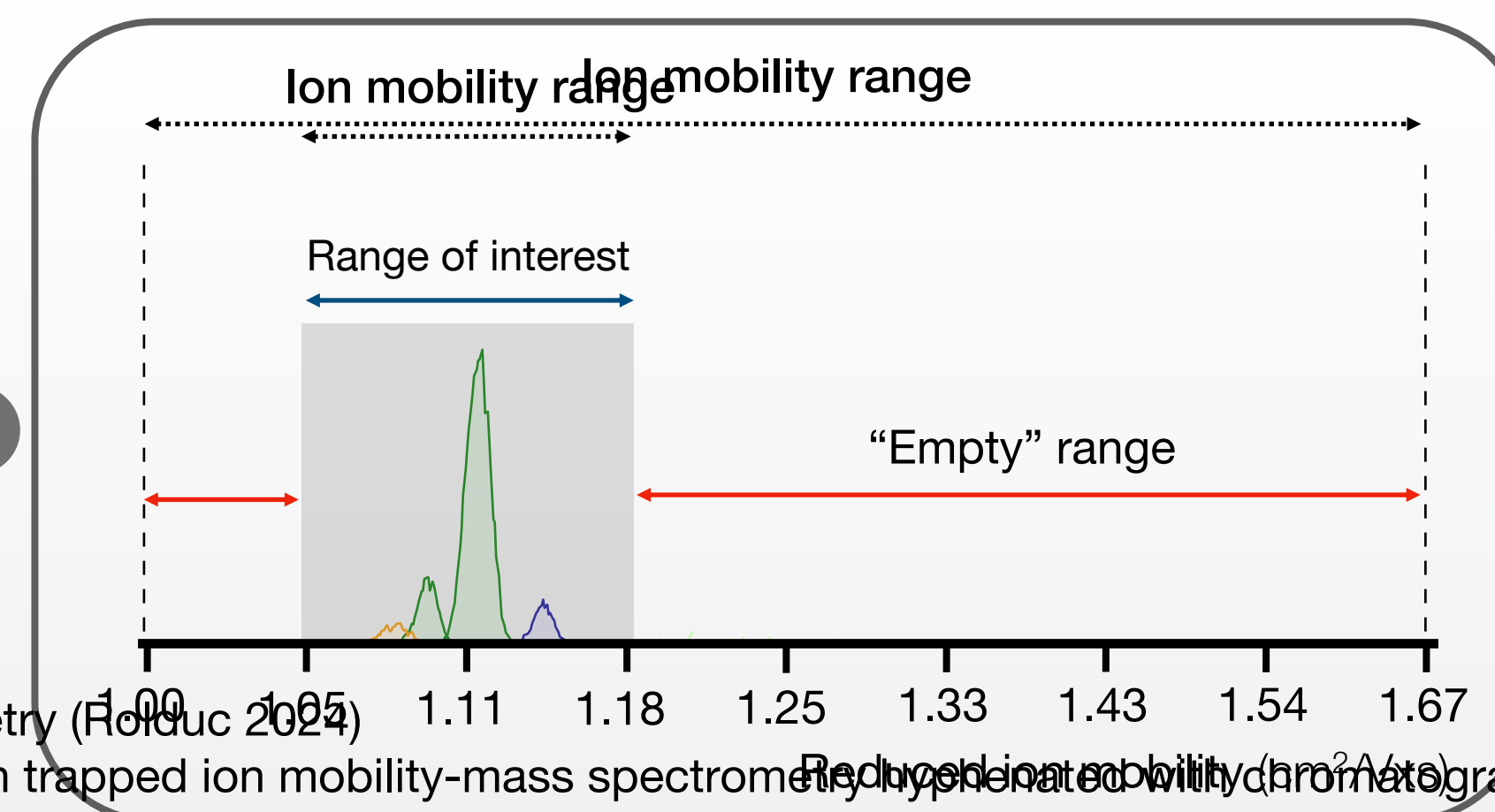
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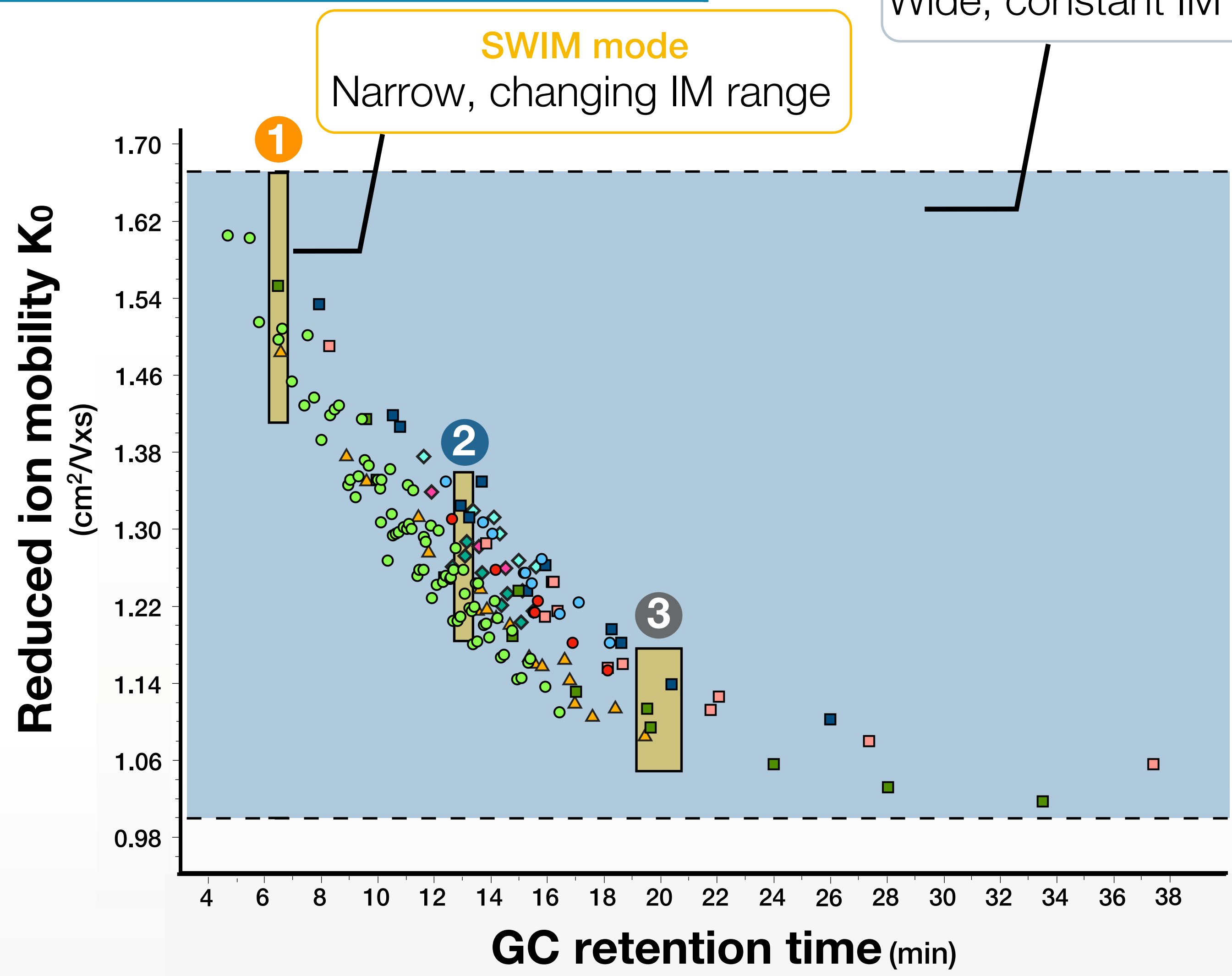
2



3

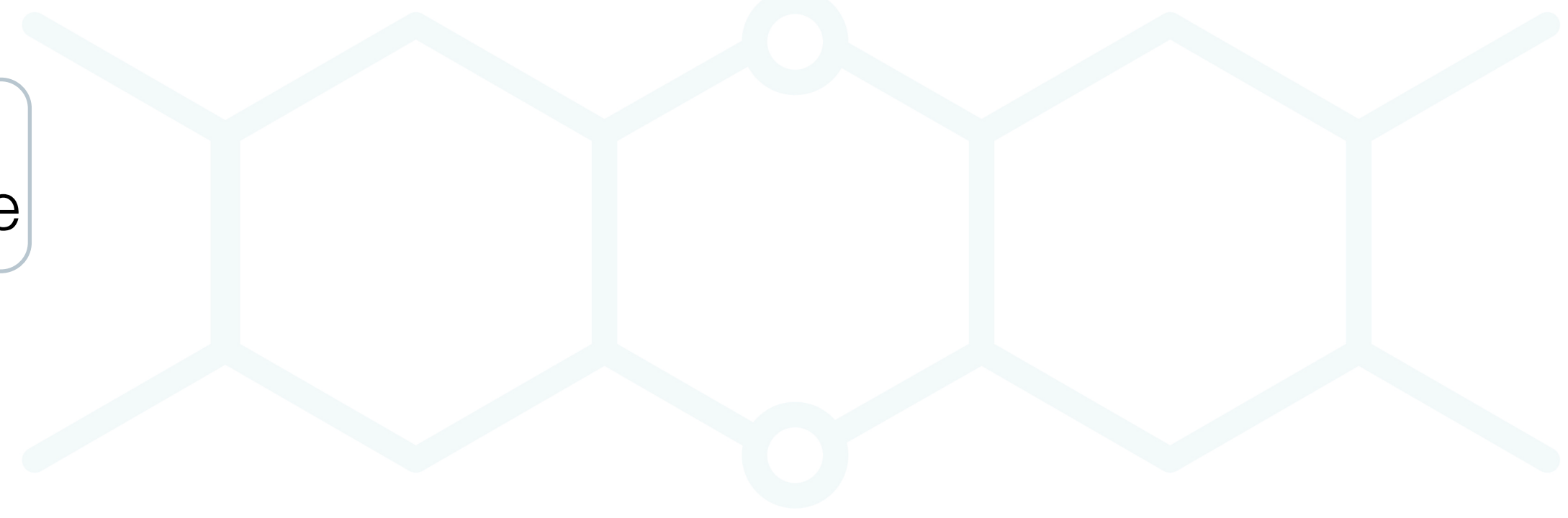


SWIM mode



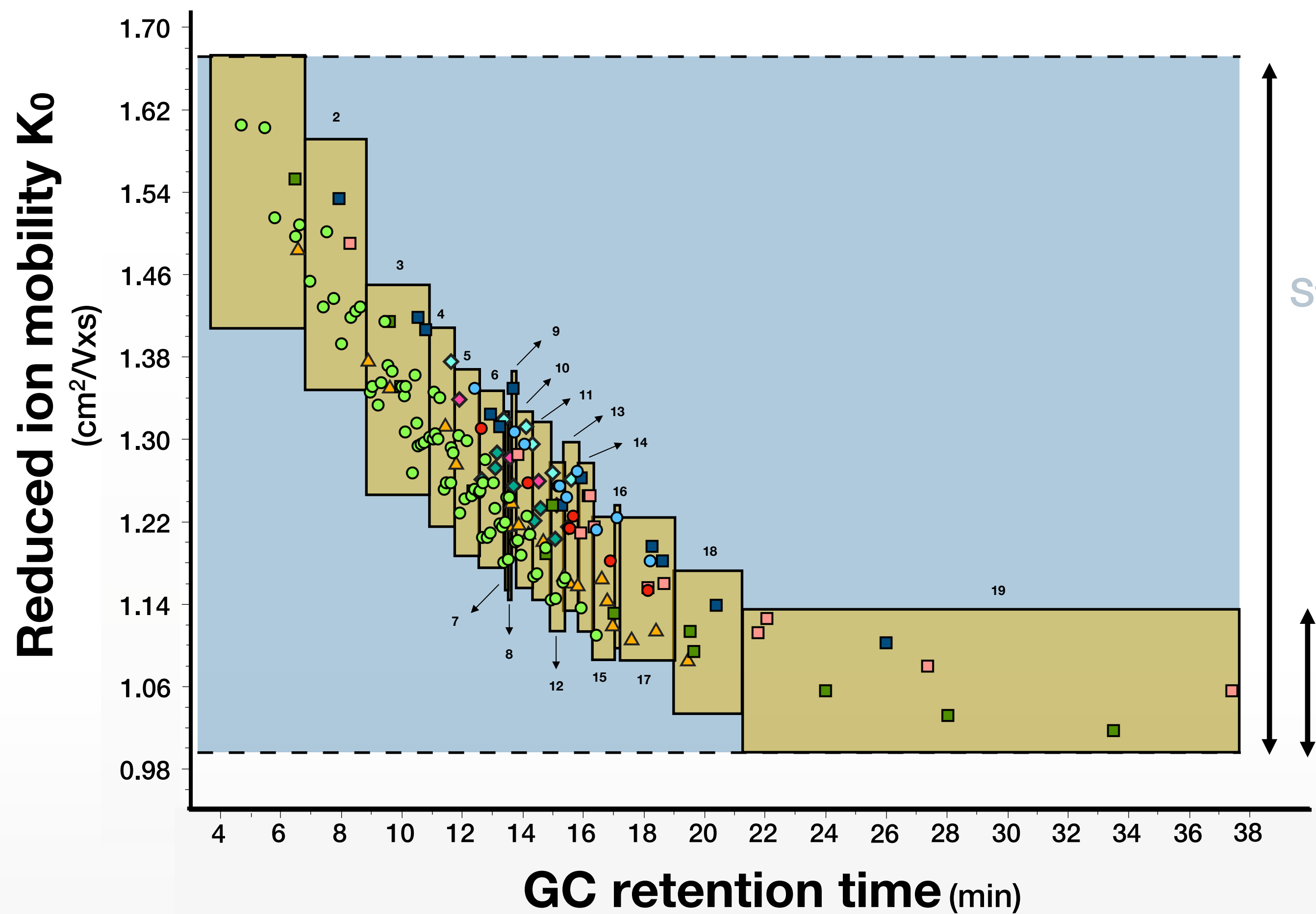
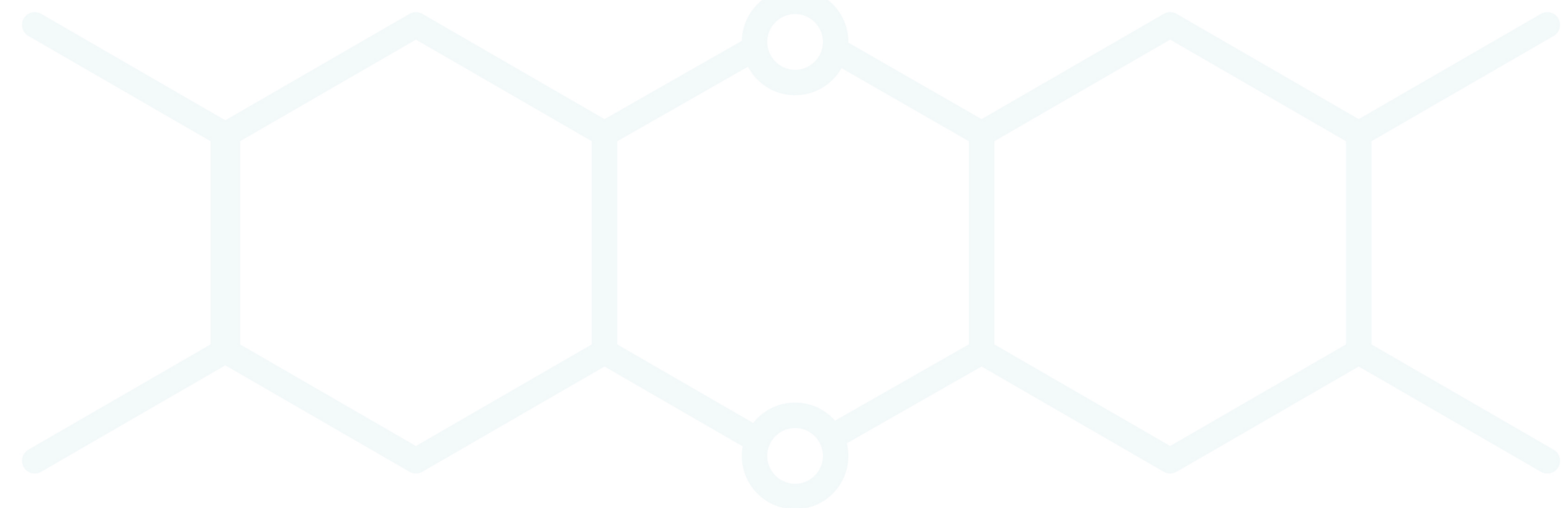
Standard mode
Wide, constant IM range

SWIM mode
Narrow, changing IM range



Sliding
Windows
Ion
Mobility

SWIM mode

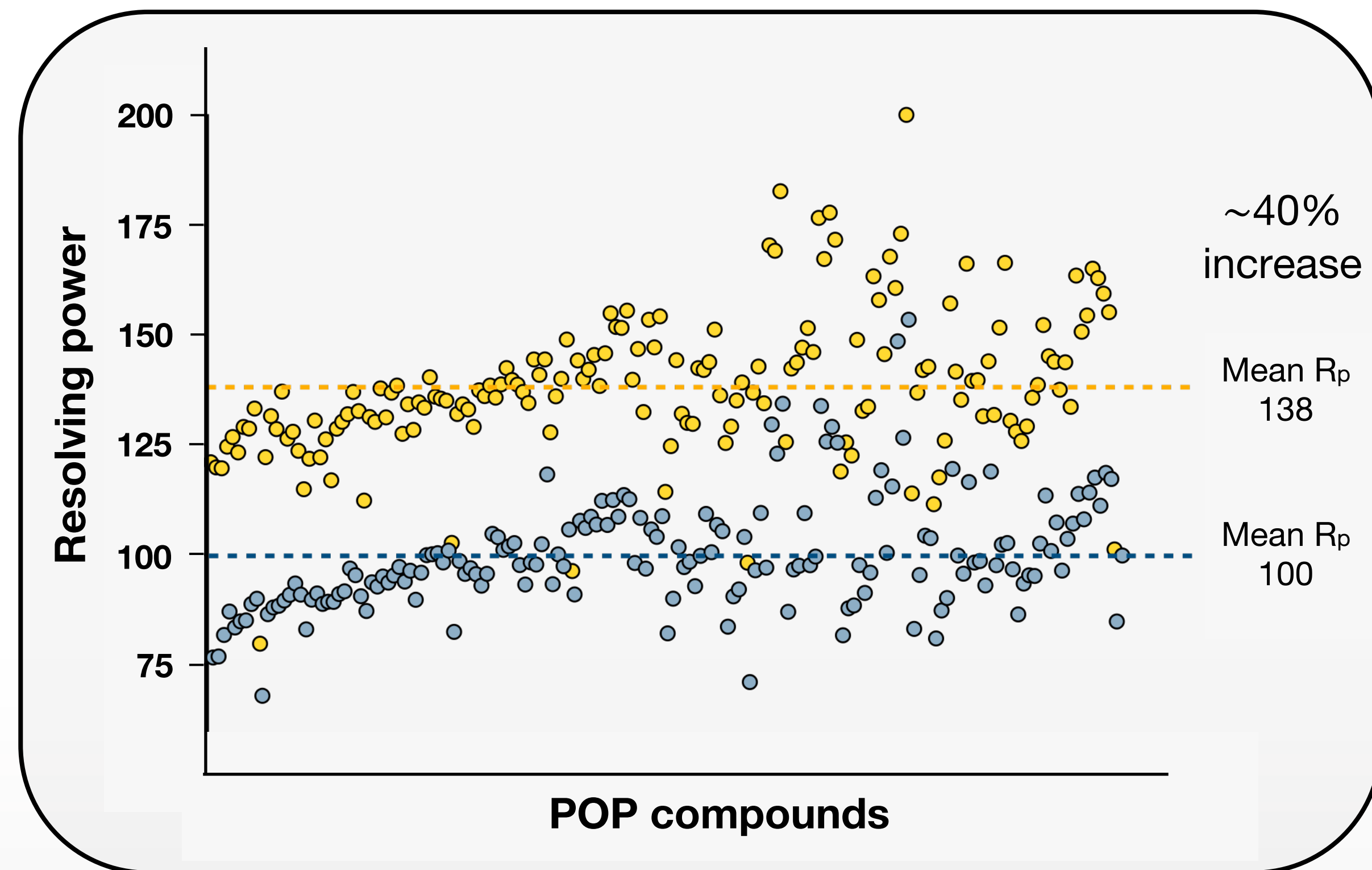
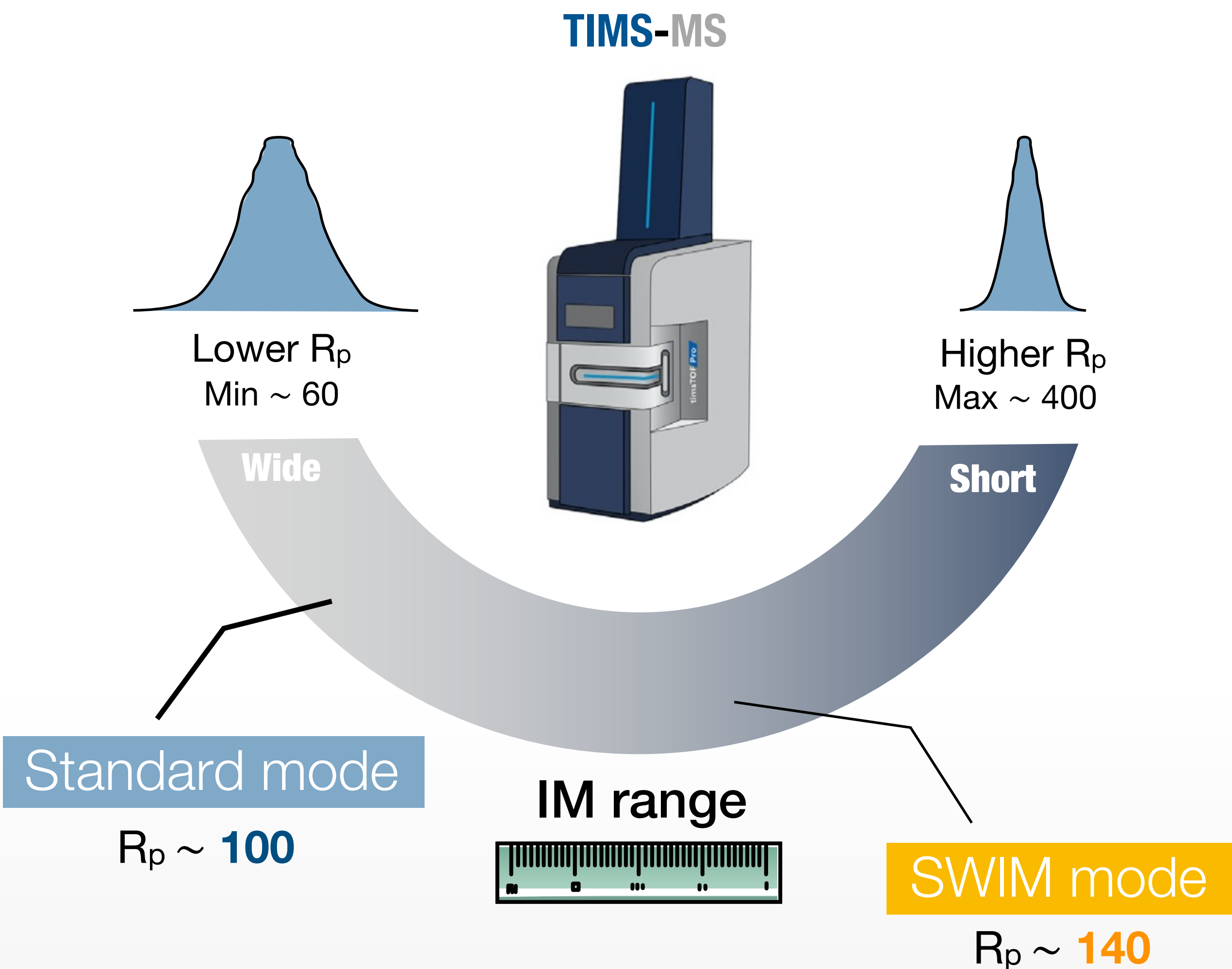


Standard mode

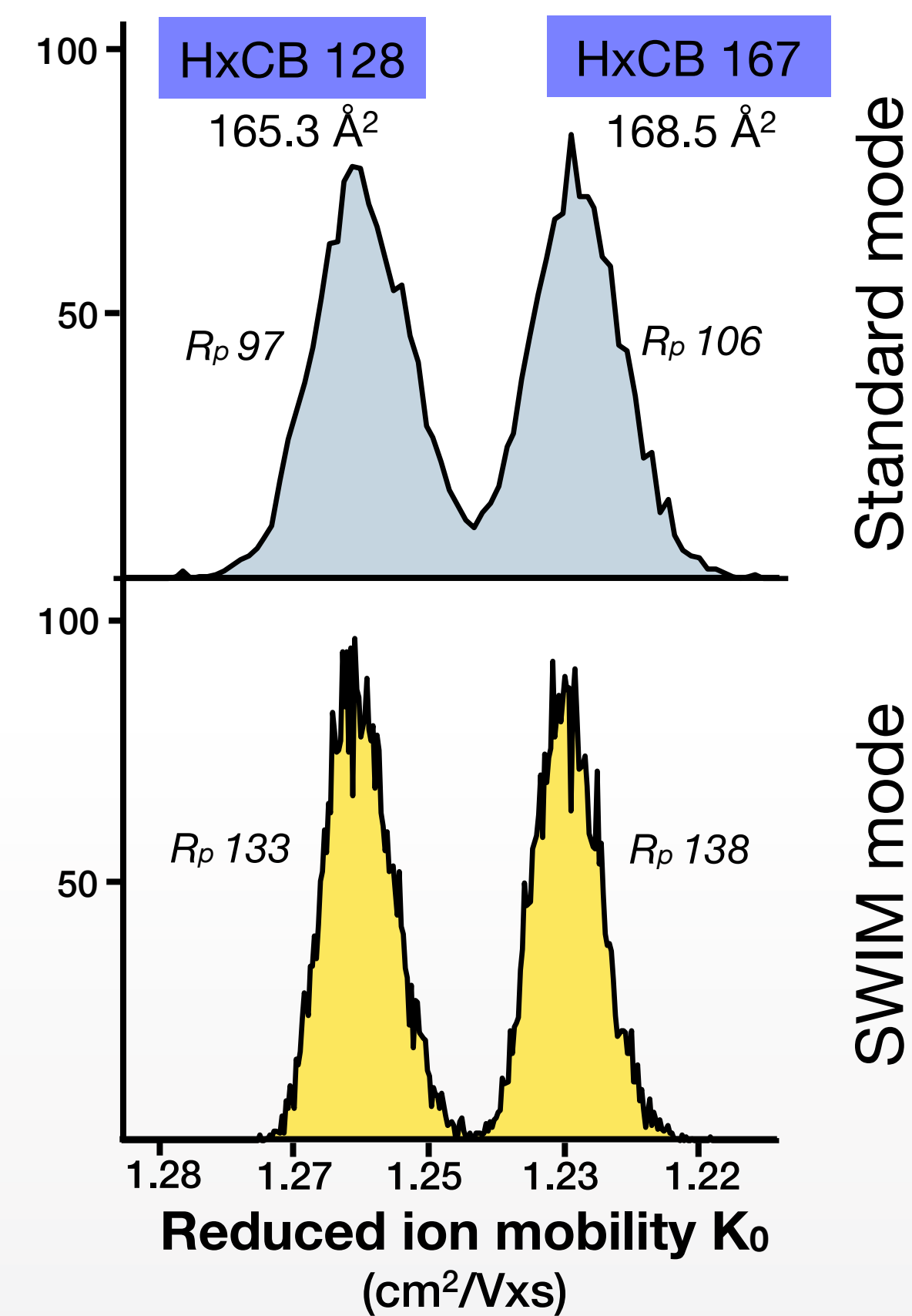
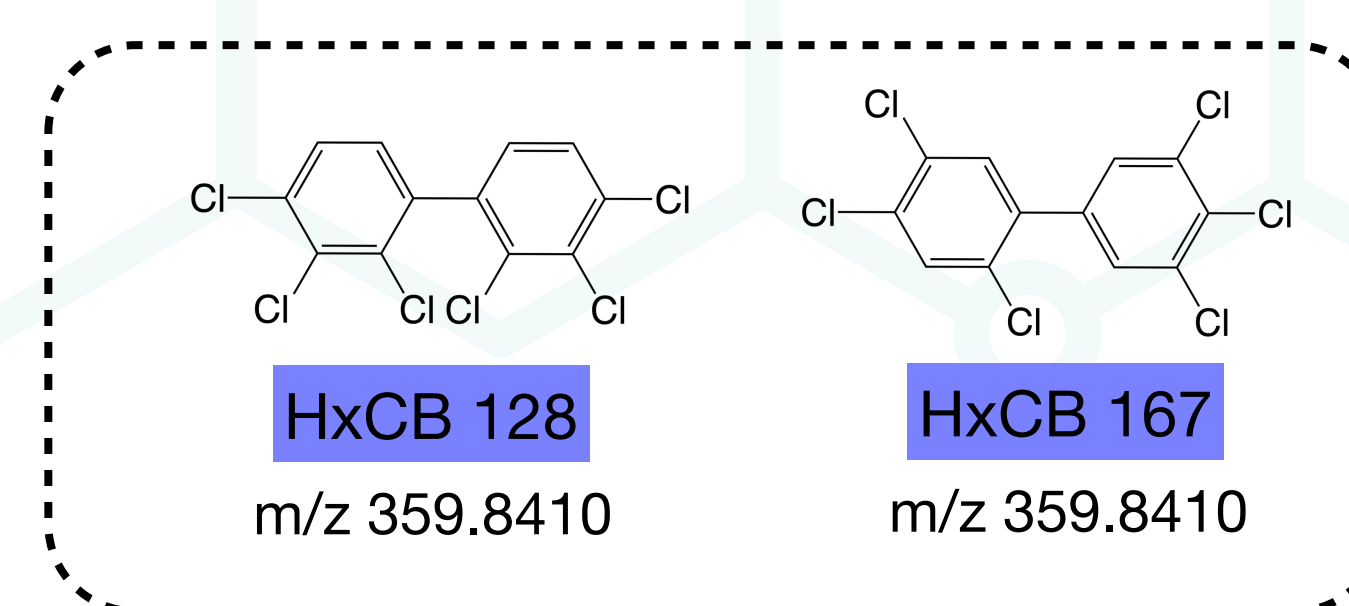
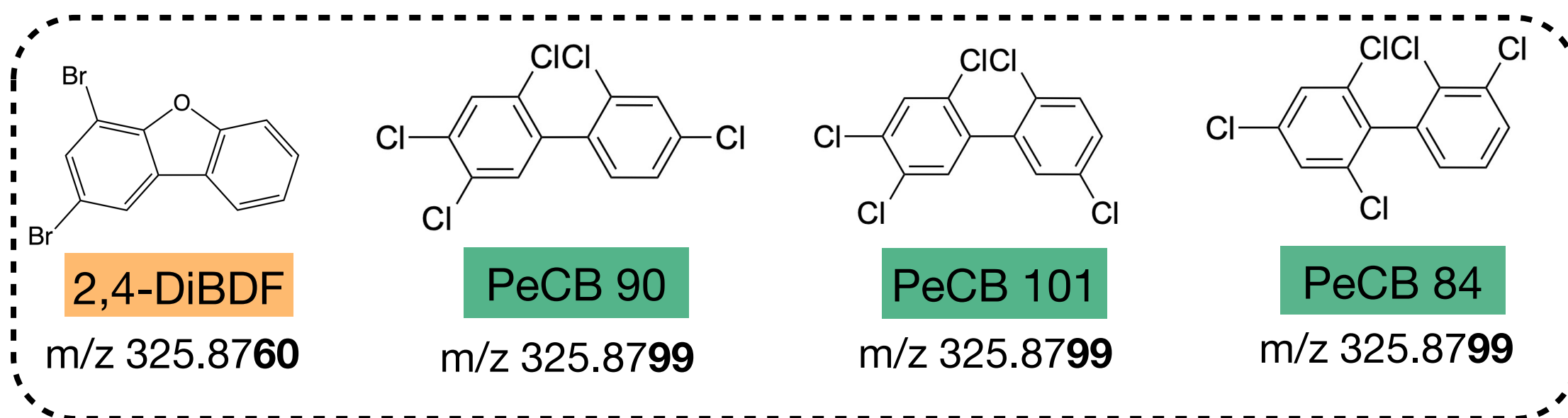
SWIM mode
~ 4x smaller

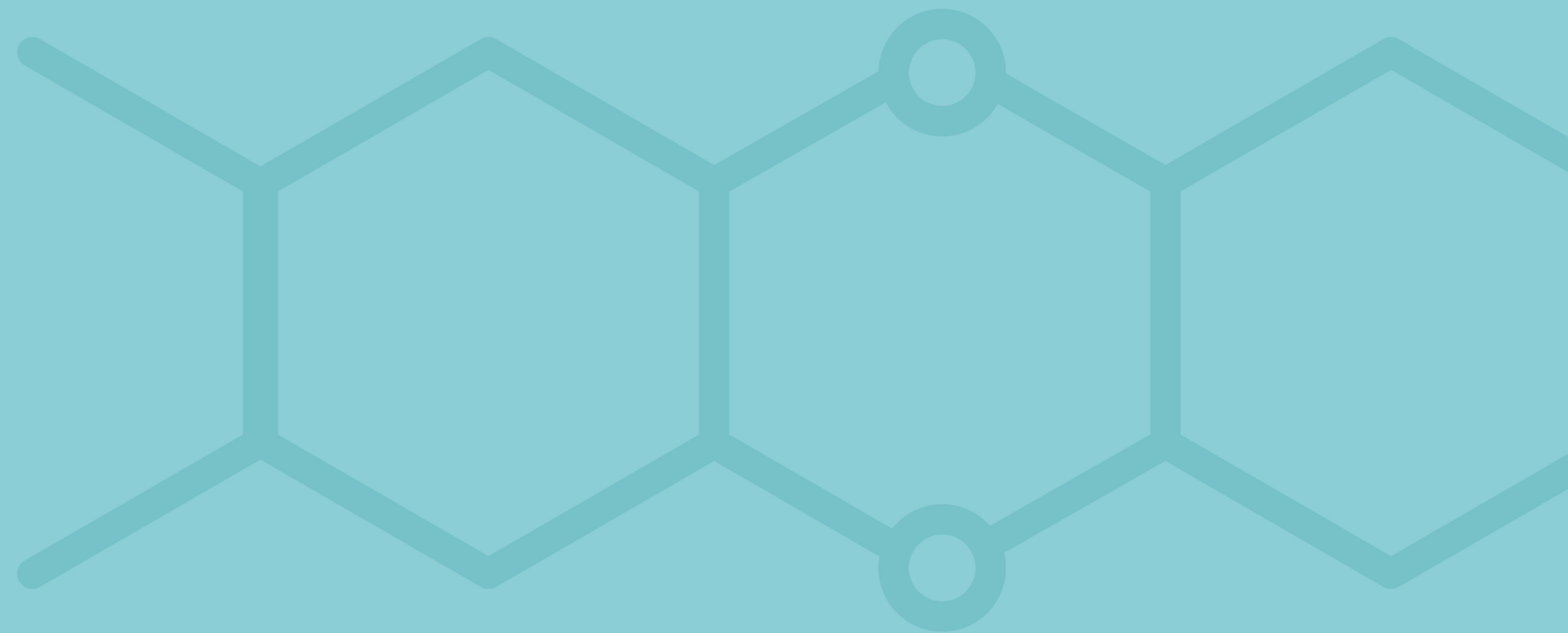
Sliding
Windows
Ion
Mobility

R_p improvement



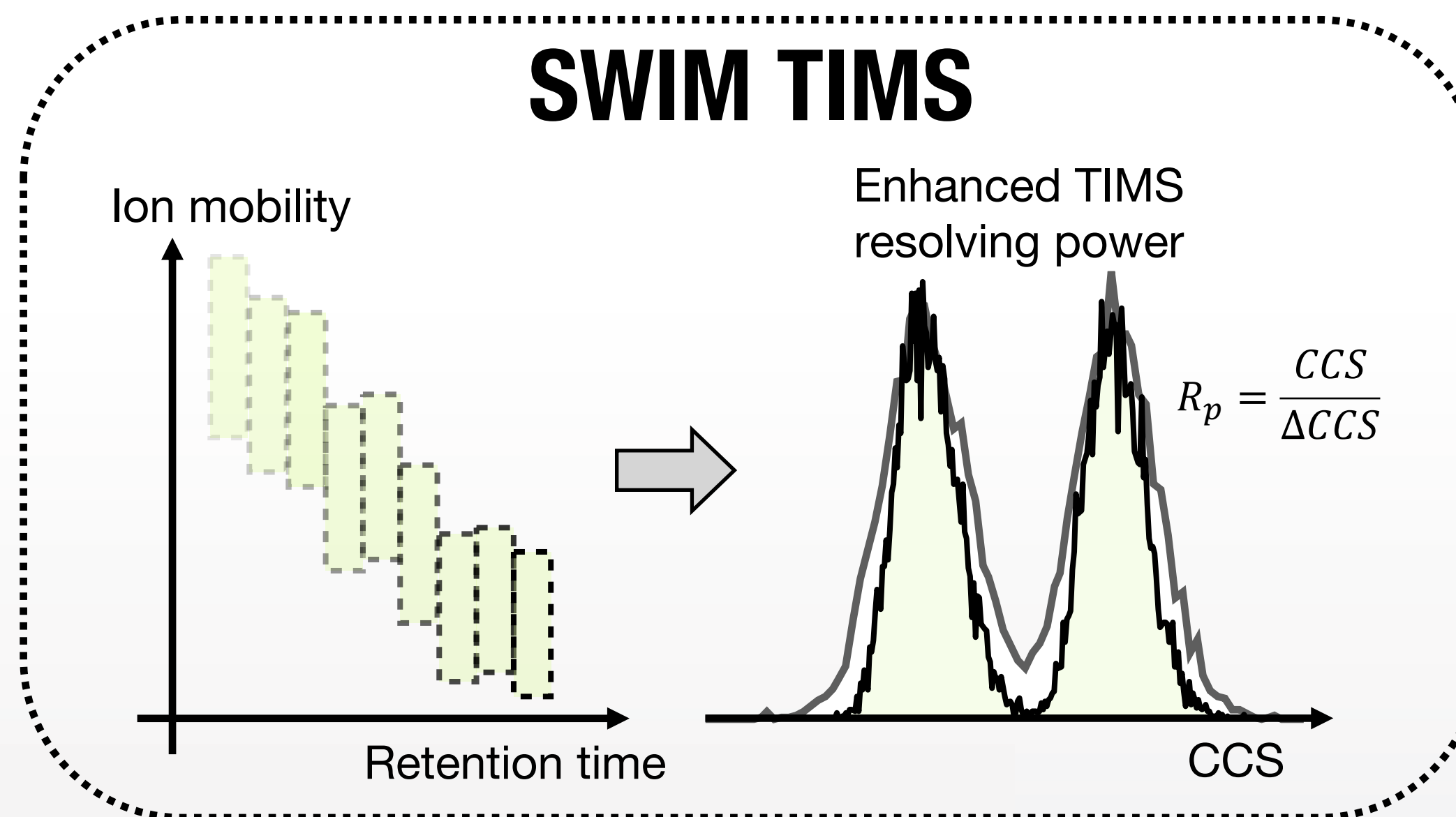
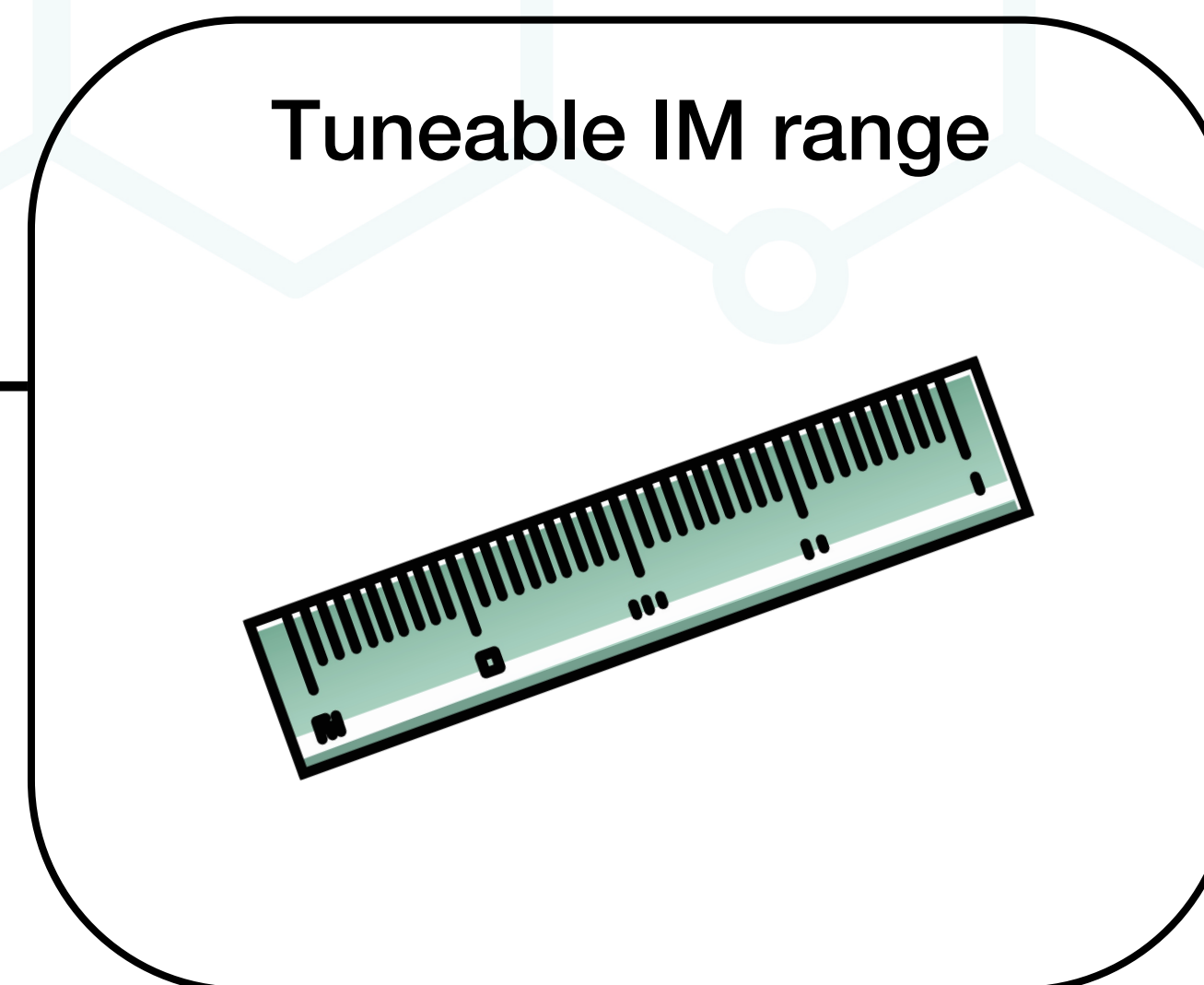
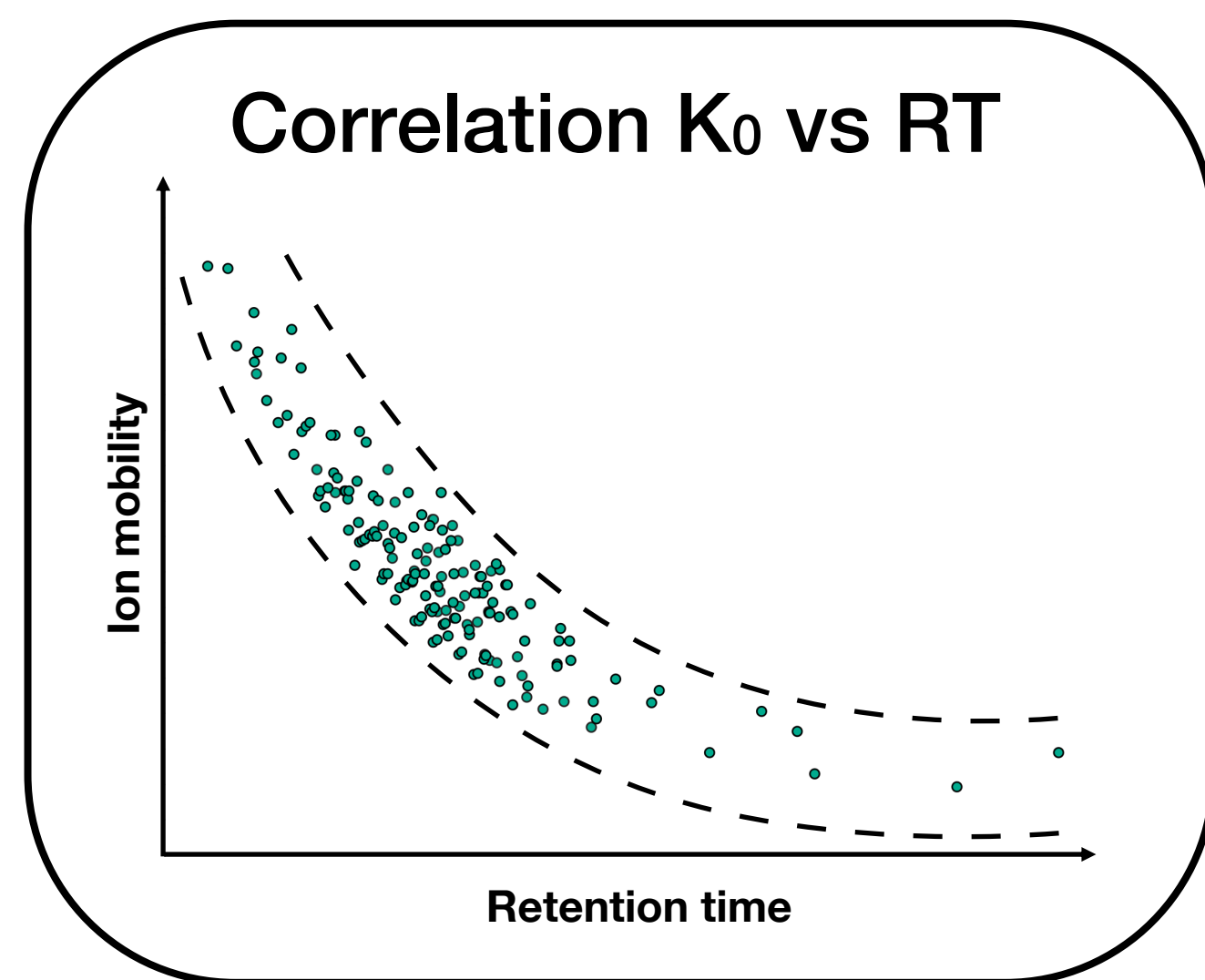
Selectivity improvement





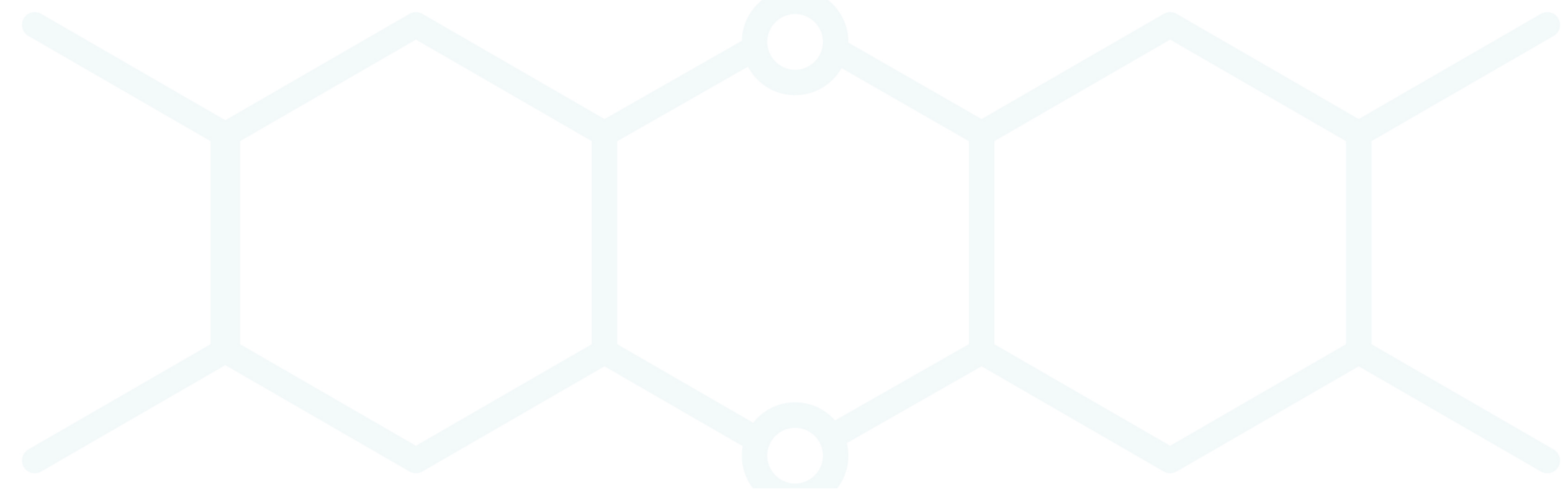
Conclusion

Summary



5th joint NVMS/BSMS conference on Mass Spectrometry (Rolduc 2024)

Hugo B. Muller et. al, "Sliding windows in ion mobility (SWIM): a new approach to increase the separation power in trapped ion mobility-mass spectrometry hyphenated with chromatography"



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Article

Sliding Windows in Ion Mobility (SWIM): A New Approach to Increase the Resolving Power in Trapped Ion Mobility-Mass Spectrometry Hyphenated with Chromatography

Hugo B. Muller, Georges Scholl, Johann Far, Edwin De Pauw, and Gauthier Eppe*



Cite This: *Anal. Chem.* 2023, 95, 17586–17594



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SSVM
SS
SS



LABORATORY

SPECTROMETRY



- ◉ Pr. Gauthier Eppe
- ◉ Georges Scholl
- ◉ Edwin de Pauw
- ◉ Johann Far
- ◉ Aurore Schneiders





Thank you