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|   |                         |   |   |  |  |
|---|-------------------------|---|---|--|--|
| <b>1. REPORT DATE (DD-MM-YYYY)</b><br>03/11/2015  |                         | <b>2. REPORT TYPE</b><br>Conference Publication |   | <b>3. DATES COVERED (From - To)</b><br>2014-2015                     |  |
| <b>4. TITLE AND SUBTITLE</b><br>Direct Measurement of the Isomerization Barrier of the Isolated Retinal Chromophore   |                         |   |   | <b>5a. CONTRACT NUMBER</b>   |  |
|   |                         |   |   | <b>5b. GRANT NUMBER</b>  |  |
|   |                         |   |   | <b>5c. PROGRAM ELEMENT NUMBER</b>                                    |  |
| <b>6. AUTHOR(S)</b><br>Jonathan Dilger, Lihi Musbat, Mordechai Sheves, Anastasia V. Bochenkova, David E. Clemmer and Yoni Tokor   |                         |   |   | <b>5d. PROJECT NUMBER</b>  |  |
|   |                         |   |   | <b>5e. TASK NUMBER</b>   |  |
|   |                         |   |   | <b>5f. WORK UNIT NUMBER</b>  |  |
| <b>7. PERFORMING ORGANIZATION NAME(S) AND ADDRESS(ES)</b><br>Naval Surface Warfare Center, Crane Division<br>Code WXP, Building 3323<br>300 Highway 361<br>Crane, IN 47522-5001   |                         |   |   | <b>8. PERFORMING ORGANIZATION REPORT NUMBER</b><br>NSWCCR/RDTR-15/57 |  |
| <b>9. SPONSORING / MONITORING AGENCY NAME(S) AND ADDRESS(ES)</b><br>Naval Innovative Science and Engineering Program  |                         |   |   | <b>10. SPONSOR/MONITOR'S ACRONYM(S)</b>                              |  |
|   |                         |   |   | <b>11. SPONSOR/MONITOR'S REPORT NUMBER(S)</b>                        |  |
| <b>12. DISTRIBUTION / AVAILABILITY STATEMENT</b><br>DISTRIBUTION STATEMENT A. Approved for public release; distribution is unlimited.   |                         |   |   |  |  |
| <b>13. SUPPLEMENTARY NOTES</b>  |                         |   |   |  |  |
| <b>14. ABSTRACT</b><br>Ion mobility spectroscopy (IMS) allows one to differentiate between different isomers of a given molecular ion according to their collisional cross-section. Using two stages of IMS (IMS-IMS) one can select a specific isomer, collisionally heat it and follow its isomerization pathways. Recently it has been shown that this technique allows one to determine internal energy barrier for isomerization. Here we apply the technique to the important case of the retinal protonated Schiff base (RPSB). Photoisomerization of the RPSB is the primary in animal vision. We find that the energy barrier for a single <i>cis-trans</i> isomerization is $0.64 \pm 0.05$ eV, which is significantly lower than that observed for the reaction within opsin proteins. Thus the protein has a significant role in increasing the barrier energy for thermal isomerization relative to the gas phase which lacks interaction with the RPSB counterion and steric constraints. High barrier energy is mandatory for efficient vision processes, otherwise thermal noise would overwhelm the signal originating from the photochemical isomerization. |                         |   |   |  |  |
| <b>15. SUBJECT TERMS</b><br>ion mobility spectrometry, mass spectrometry, retinal, chromophore, isomerization energy  |                         |   |   |  |  |
| <b>16. SECURITY CLASSIFICATION OF:</b><br>Unclassified  |                         |   | <b>17. LIMITATION OF ABSTRACT</b><br>UU | <b>18. NUMBER OF PAGES</b><br>1                                      | <b>19a. NAME OF RESPONSIBLE PERSON</b><br>Jonathan Dilger          |
| <b>a. REPORT</b><br>U   | <b>b. ABSTRACT</b><br>U | <b>c. THIS PAGE</b><br>U                        |   |  | <b>19b. TELEPHONE NUMBER (include area code)</b><br>1-812-854-1452 |

## Direct Measurement of the Isomerization Barrier of the Isolated Retinal Chromophore

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Anastasia V. Bochenkova<sup>E</sup>, David E. Clemmer<sup>B</sup> and Yoni Toker<sup>C,1</sup>

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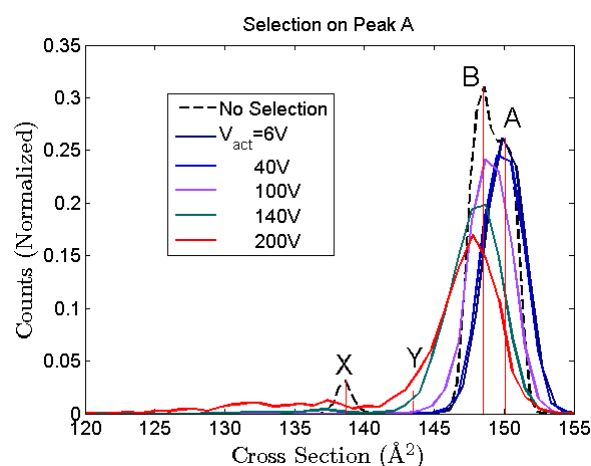
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**Synopsis** Energy barrier Heights for isomerization of the isolated retinal chromophore were measured using two stages of ion mobility spectroscopy (IMS-IMS).

Ion mobility spectroscopy (IMS) allows one to differentiate between different isomers of a given molecular ion according to their collisional cross-section. Using two stages of IMS (IMS-IMS) one can select a specific isomer, collisionally heat it and follow its isomerization pathways (See Fig. 1). Recently it has been shown that this technique allows one to determine internal energy barrier for isomerization [1].

Here we apply the technique to the important case of the retinal protonated Schiff base (RPSB) [2]. Photoisomerization of the RPSB is the primary in animal vision. We find that the energy barrier for a single *cis-trans* isomerization is  $0.64 \pm 0.05$  eV, which is significantly lower than that observed for the reaction within opsin proteins. Thus the protein has a significant role in increasing the barrier energy for thermal isomerization relative to the gas phase which lacks interaction with the RPSB counterion and steric constraints. High barrier energy is mandatory for efficient vision processes, otherwise thermal noise would overwhelm the signal originating from the photochemical isomerization.



**Figure 1.** Results of selection and activation when the selection is applied to peak A (the *all-trans* isomer), and activation is performed for different activation voltages,  $V_{act}$ . The dashed line corresponds to the IMS of the RPSB with no selection.

### References

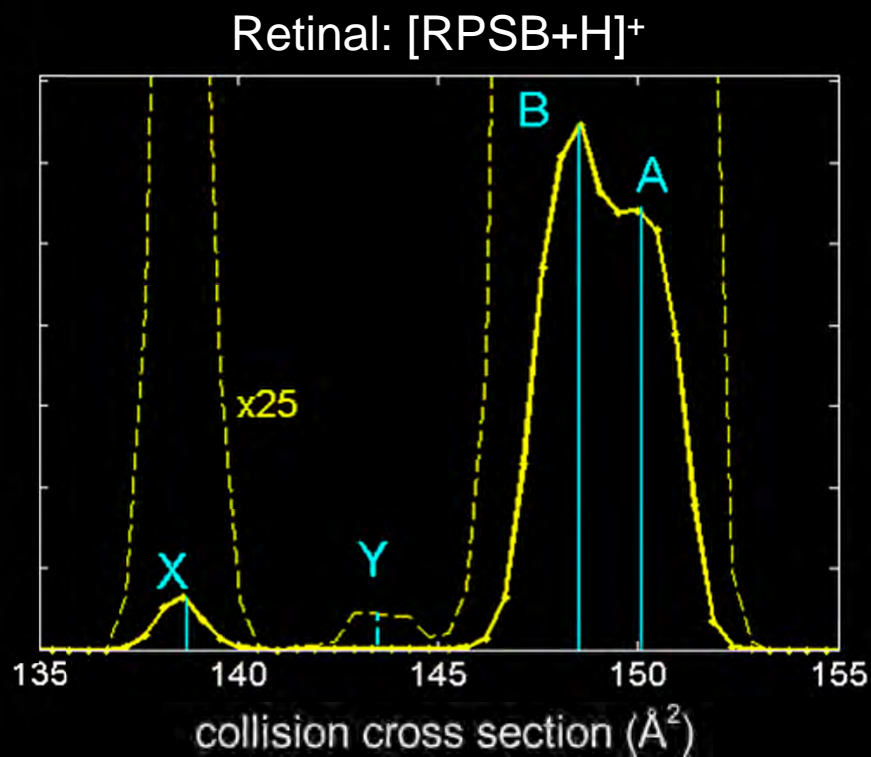
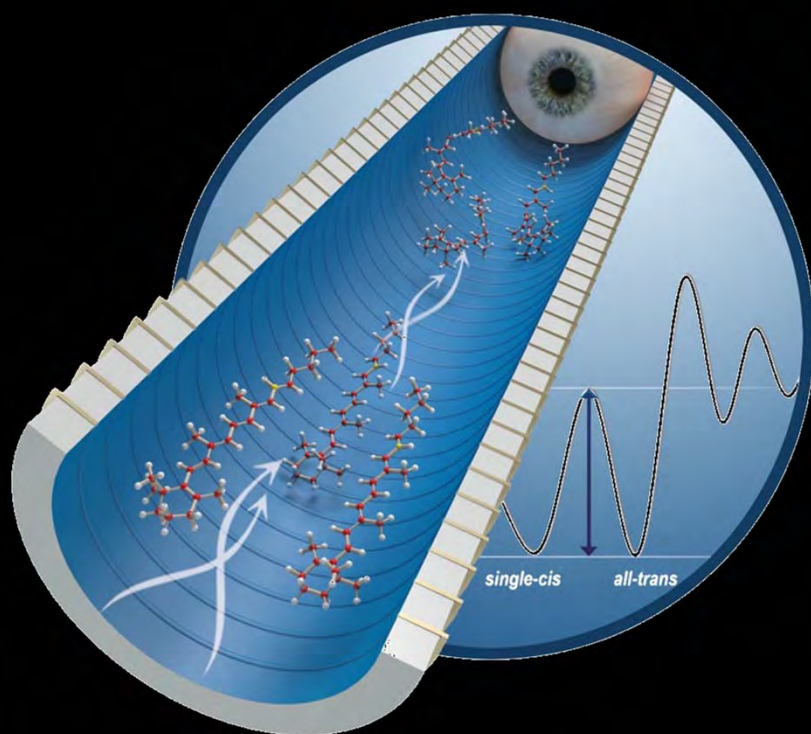
- [1] N. A. Pierson, S. J. Valentine, D. Clemmer 2015 Int. J. Mass. Spectrom, **377**, 646-654.
- [2] J. Dilger, Y. Toker *et al.* 2015 Ang. Chemie Int. Ed. **127**, 4830-4834.

<sup>1</sup>E-mail: [yonitoker@gmail.com](mailto:yonitoker@gmail.com)

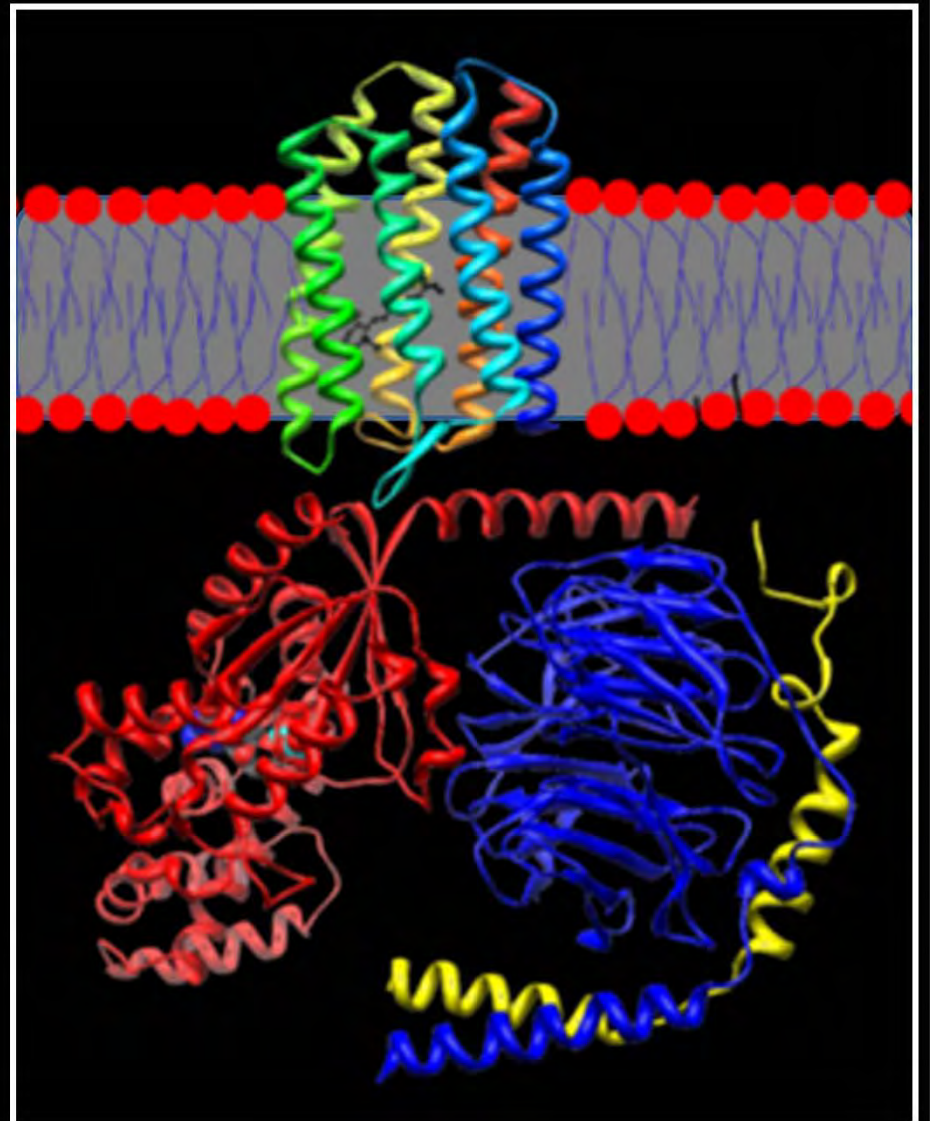
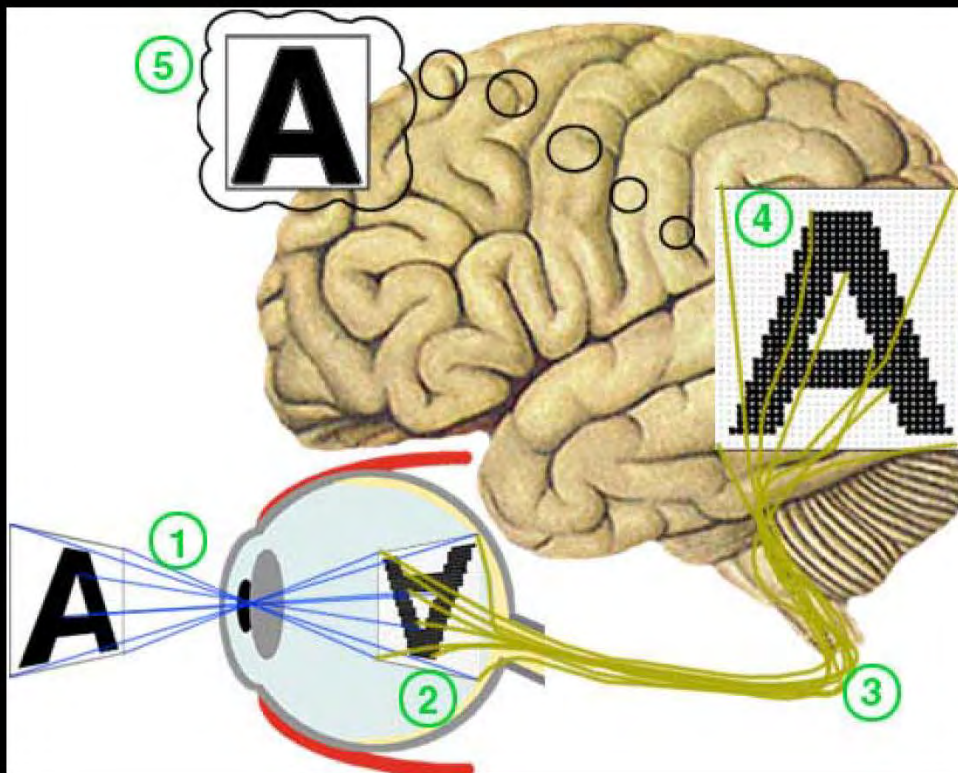


# Direct Measurement of the Isomerization Barrier of the Isolated Retinal Chromophore

Dr. Jonathan M. Dilger  
XXIX ICPEAC  
July 23, 2015

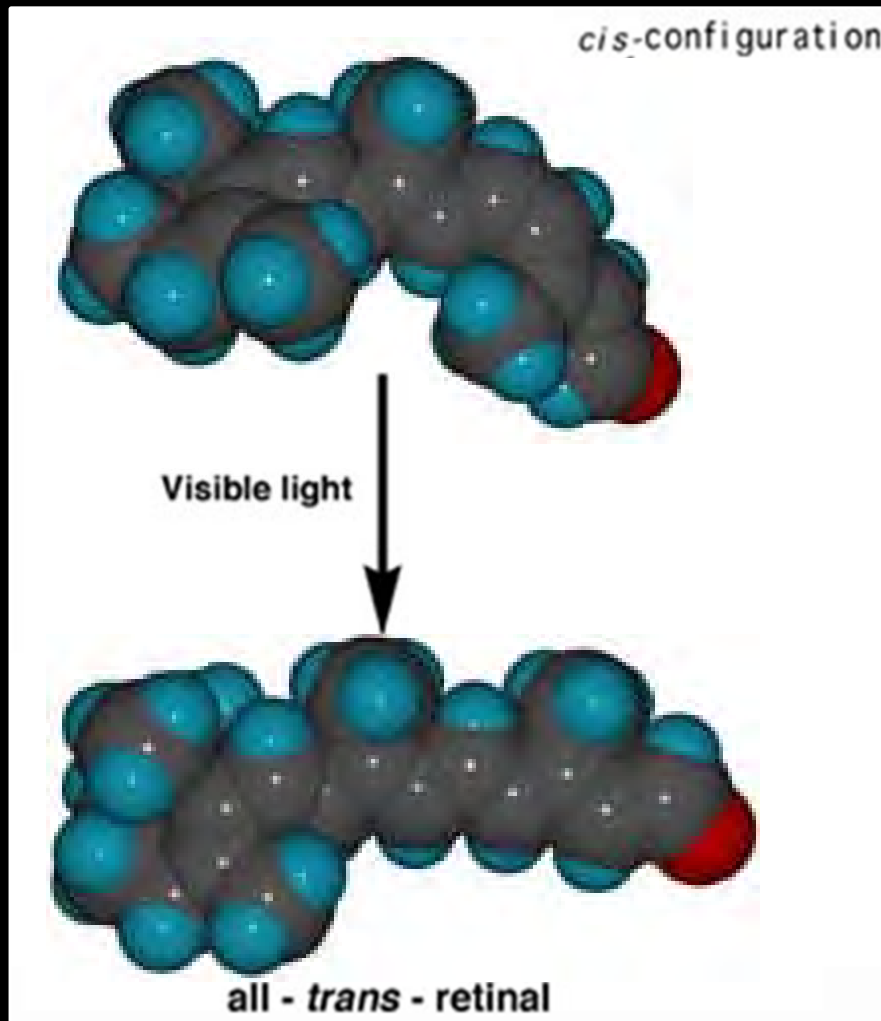


# Vision





# Light-induced Retinal Isomerization

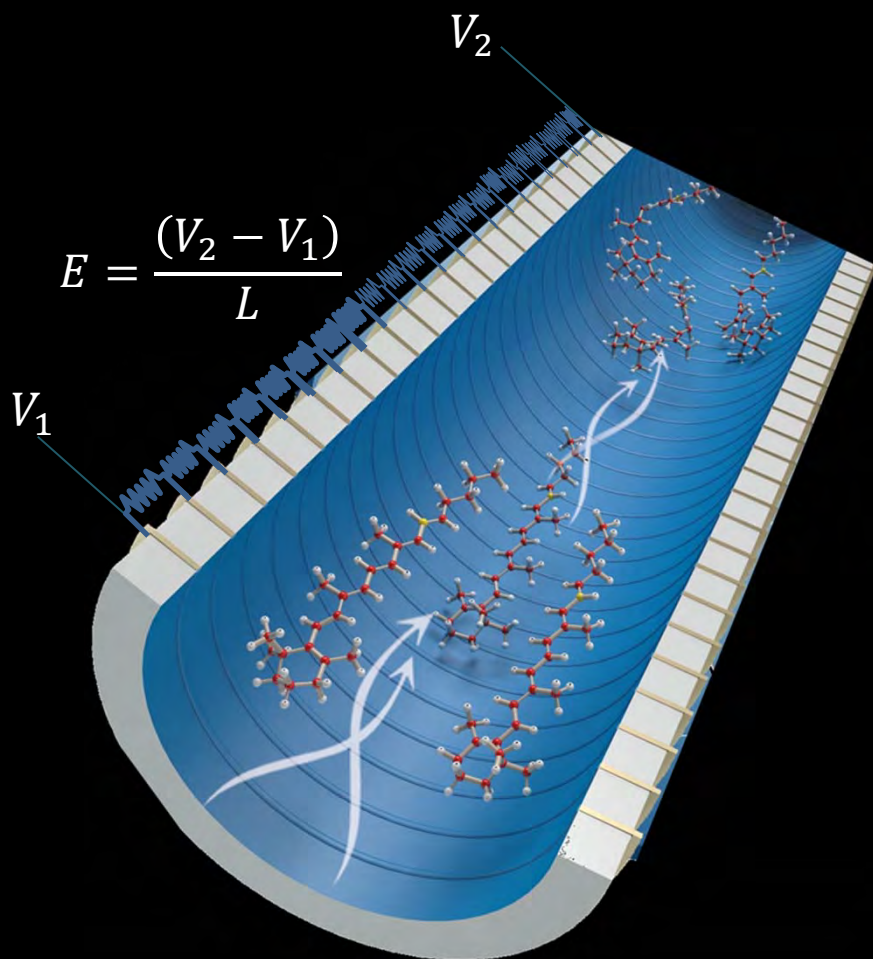
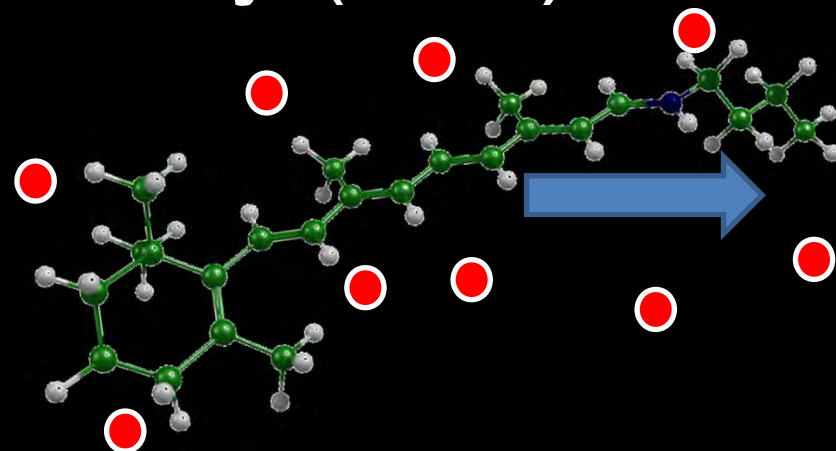


The top part of the diagram shows a retinal protein (represented by a multi-colored ribbon structure) embedded in a lipid bilayer membrane (represented by red and blue spheres and lines). A pink dashed line highlights the retinal chromophore. Below this, the protein is shown in a more disordered state, with the retinal chromophore in a different configuration, illustrating the isomerization process.

- Isomerization is ultrafast (<200 fs)
- Highly efficient (>60%)
- Specific

# Ion Mobility Spectrometry (IMS)

IMS pulls molecular ions with a small electric field (typically  $\sim 10$  V/cm) through a drift tube filled with gas



$$E = \frac{(V_2 - V_1)}{L}$$

The ions are accelerated by the electric field, and slowed down by the collisions, reaching an average drift velocity

$$v_d = \frac{L}{t_d} \quad K = \frac{v_d}{E}$$

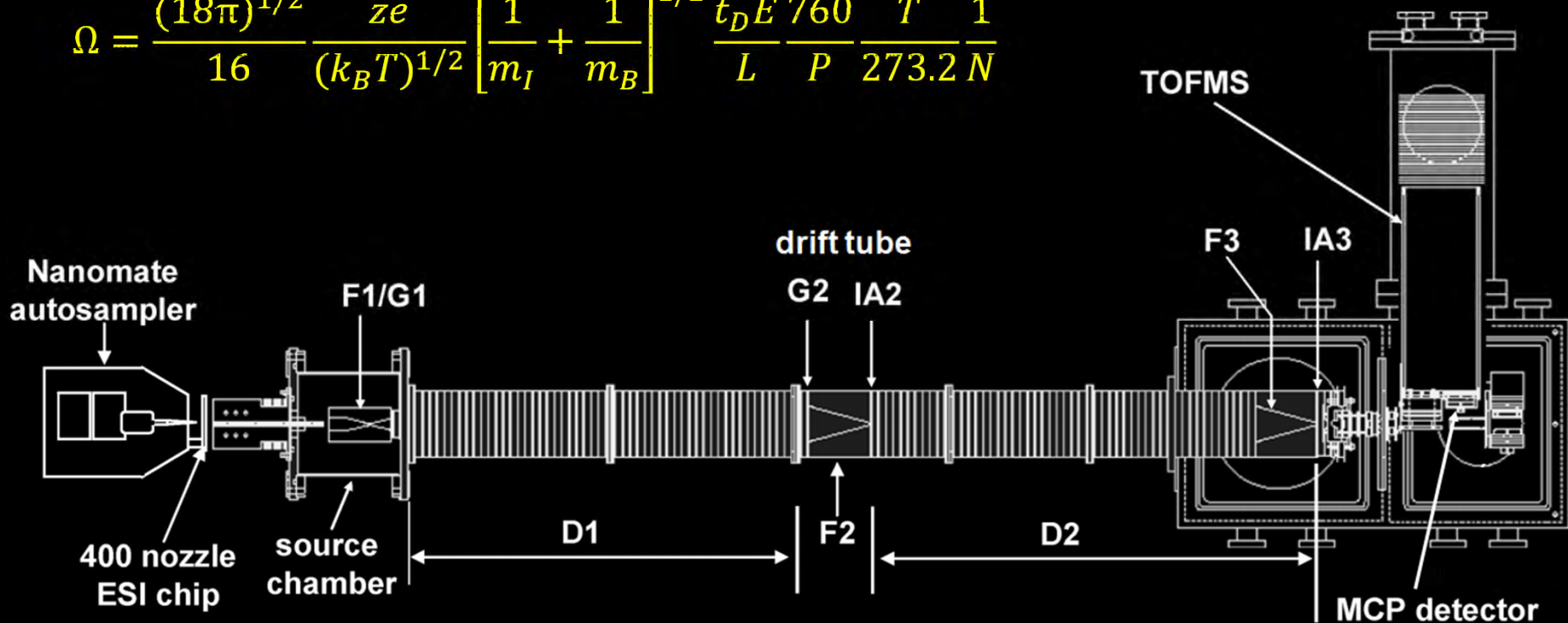
$$K = \frac{1}{\Omega} \frac{\sqrt{18\pi}}{16} \frac{ze}{\sqrt{k_B T \mu}} \frac{1}{N(T, P)}$$

# Theory and Instrumentation

$$v_D = KE \quad \text{Ion Mobility}$$

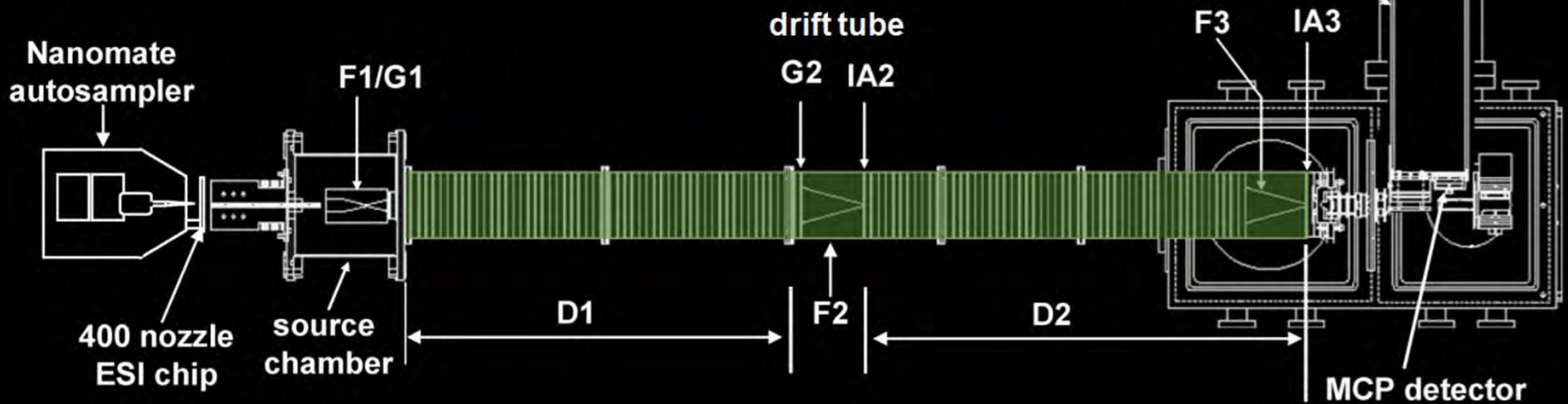
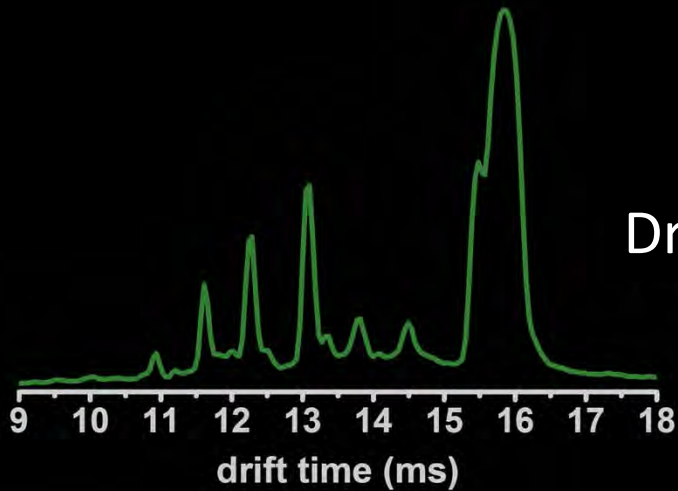
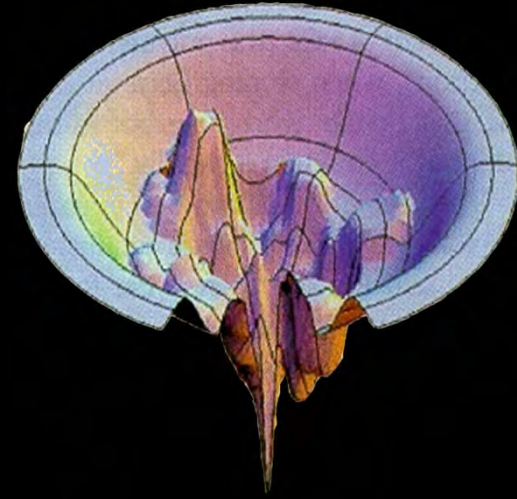
## Collision cross section

$$\Omega = \frac{(18\pi)^{1/2}}{16} \frac{ze}{(k_B T)^{1/2}} \left[ \frac{1}{m_I} + \frac{1}{m_B} \right]^{1/2} \frac{t_D E 760}{L P} \frac{T}{273.2 N}$$



Revercomb, H. E.; Mason, E. A. *Anal. Chem.* **1975**, *47*, 970–983  
Koeniger, et al. *Anal. Chem.* **2006**, *78*, 4161-4174

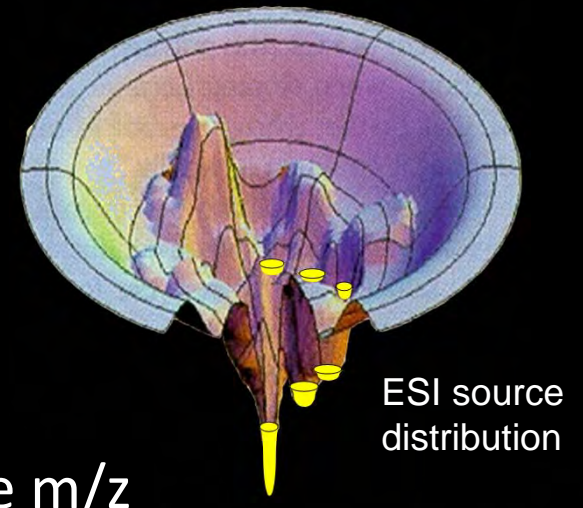
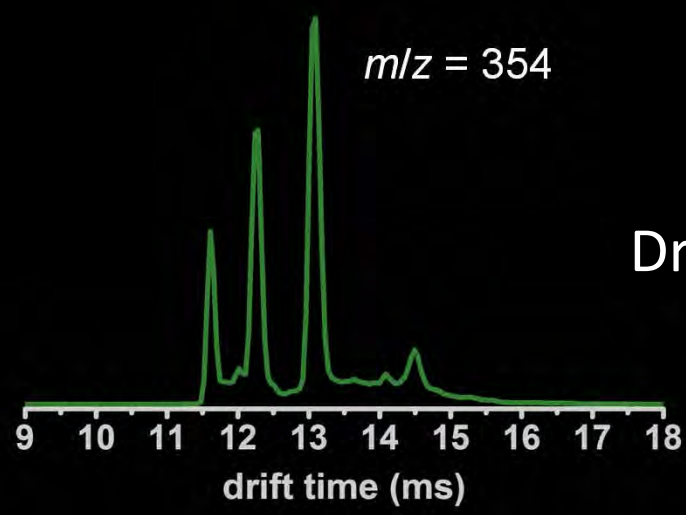
# IMS-MS: Bradykinin (BK)



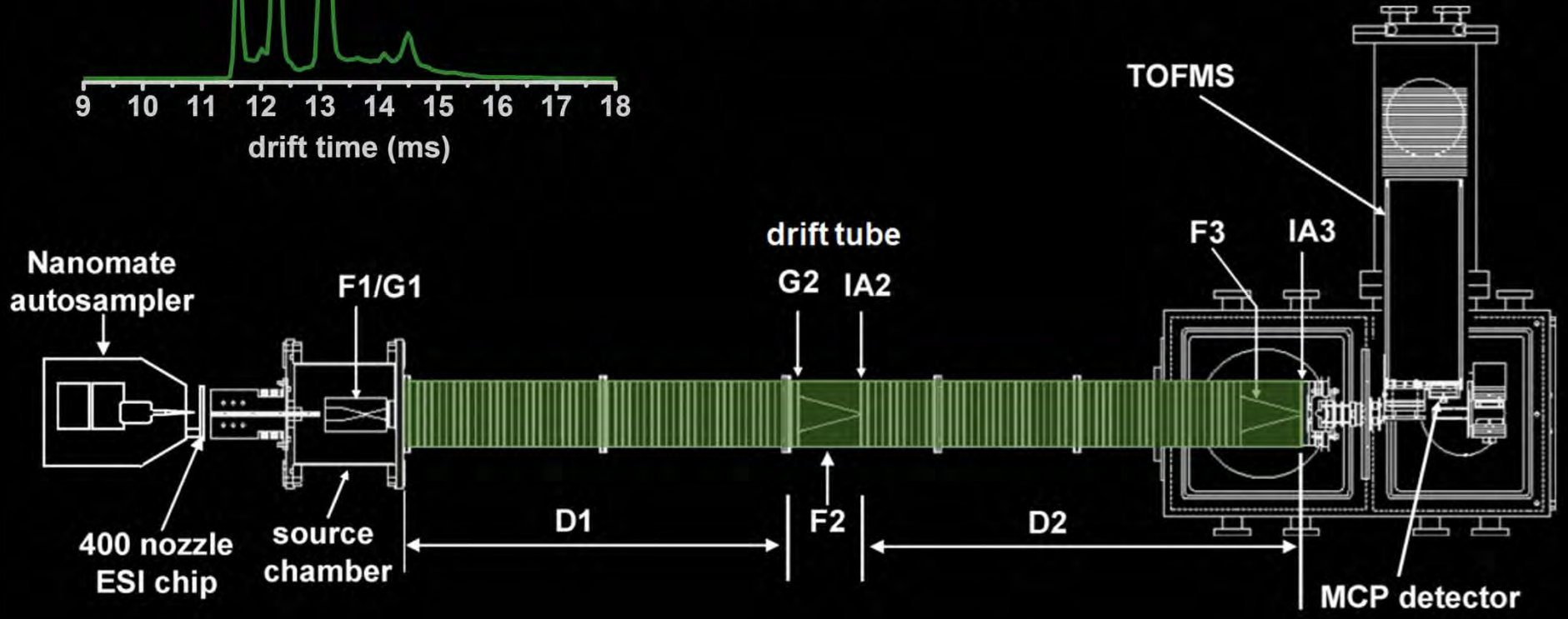
Surface modified from: Dill, K.A.; Chan, H. S. *Nature Structural Biology* 1997, 4, 10.



# IMS-MS: $[BK+3H]^{3+}$

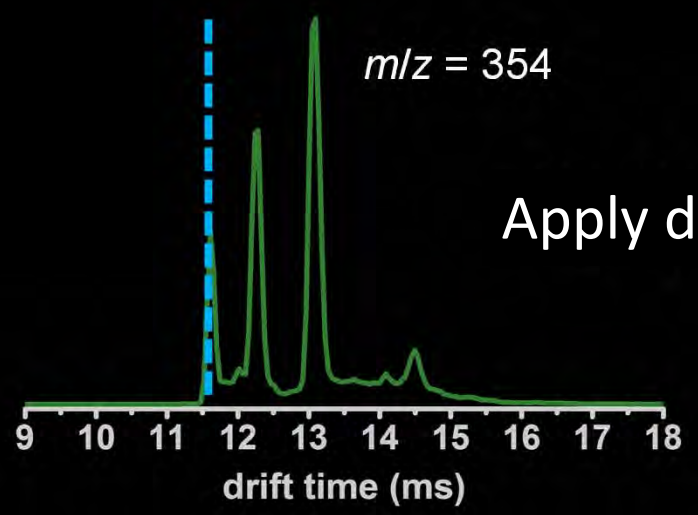


Drift profile of a single  $m/z$

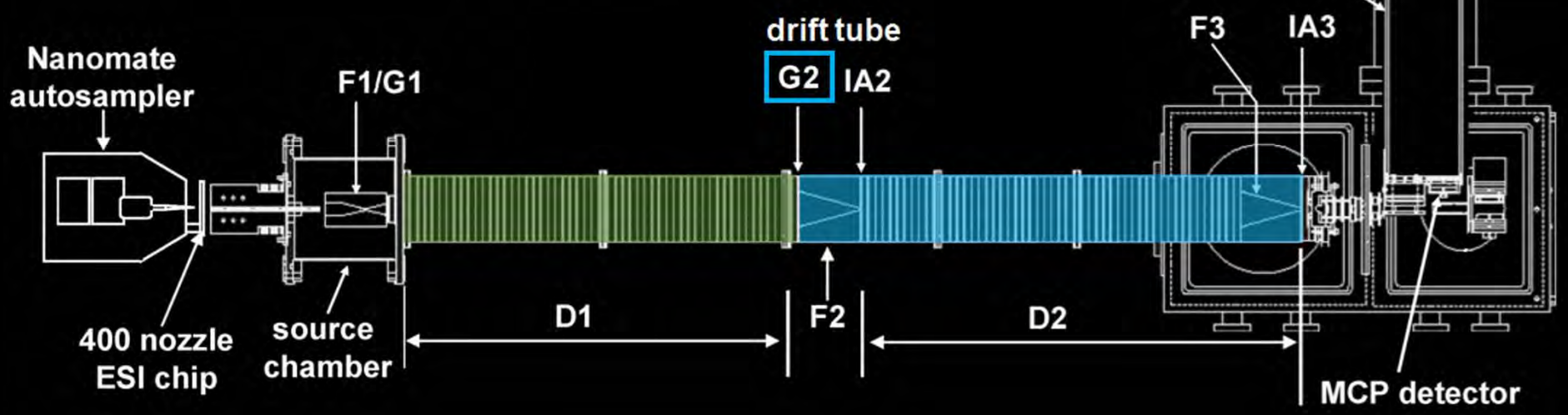
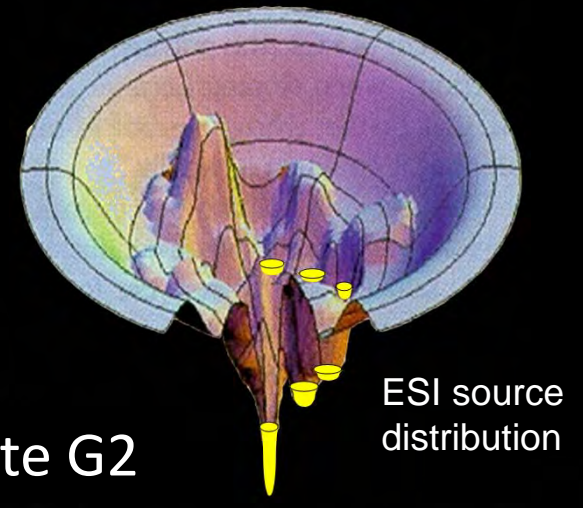


Surface modified from: Dill, K.A.; Chan, H. S. *Nature Structural Biology* 1997, 4, 10.

# IMS-MS: $[BK+3H]^{3+}$

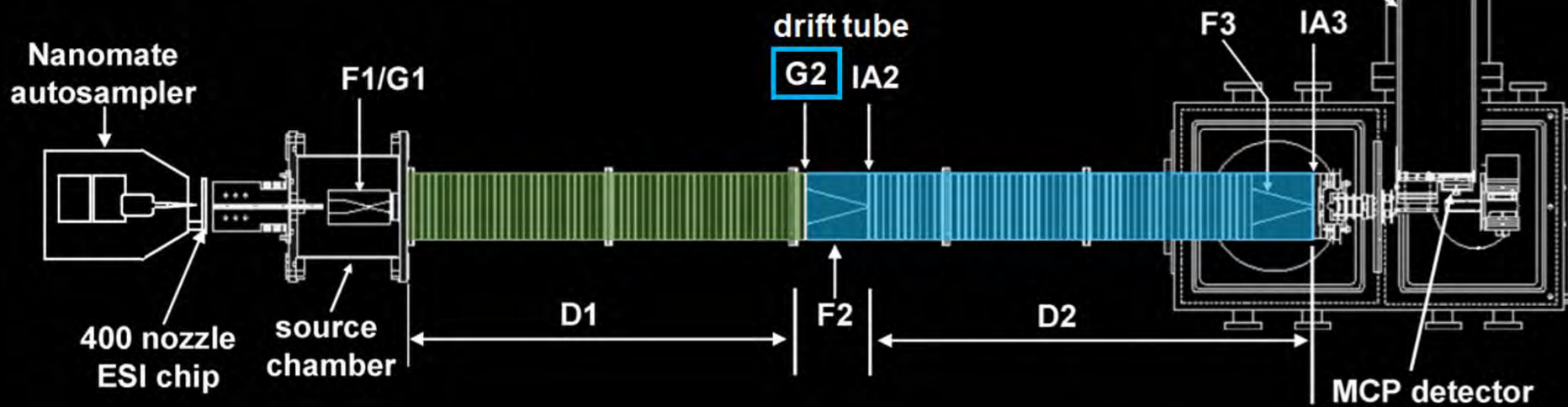
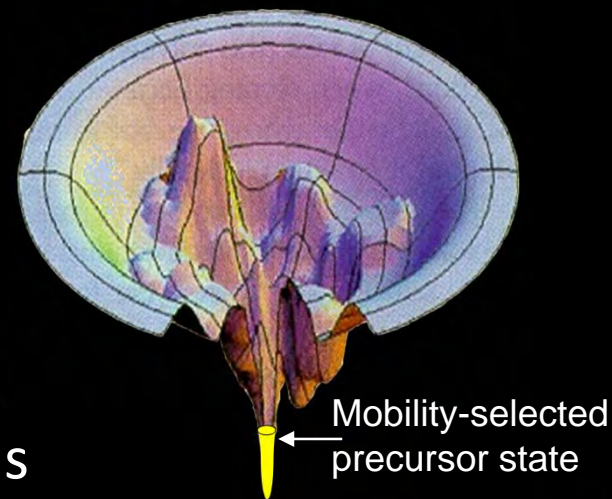
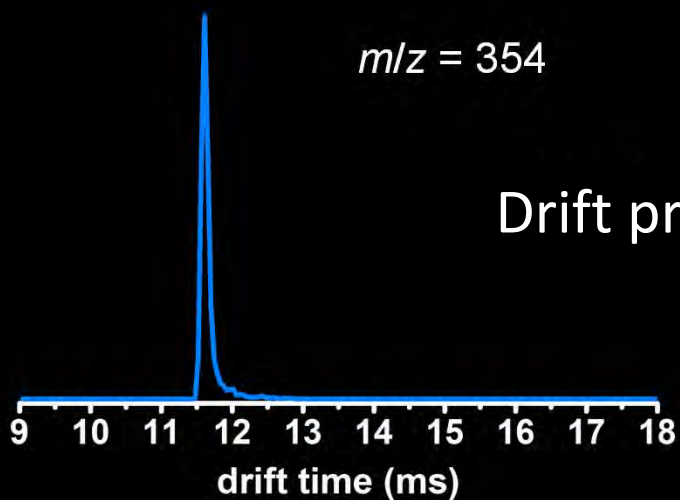


Apply delay pulse at ion gate G2



Surface modified from: Dill, K.A.; Chan, H. S. *Nature Structural Biology* 1997, 4, 10.

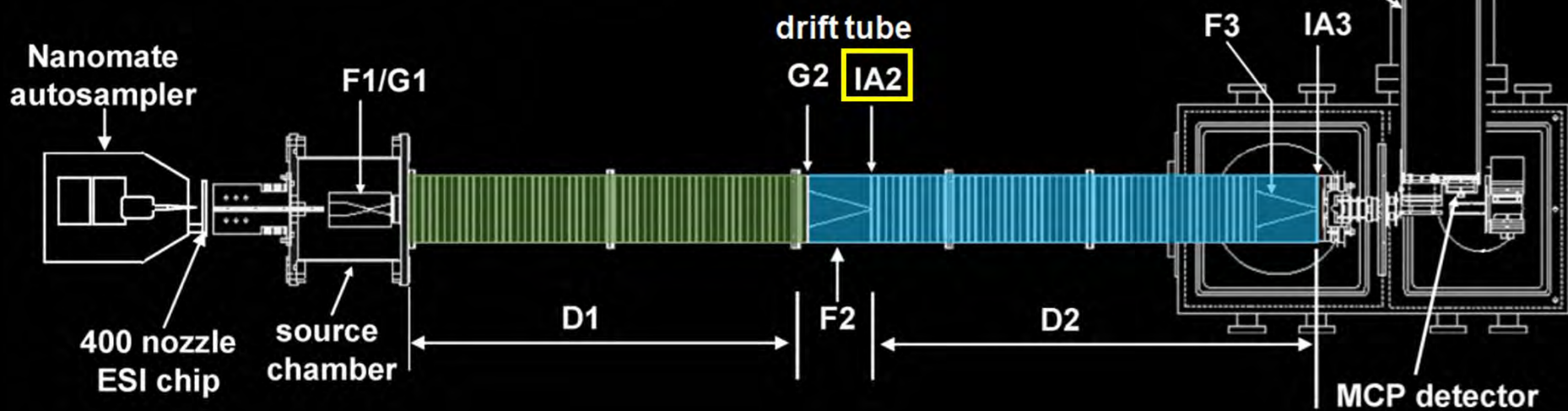
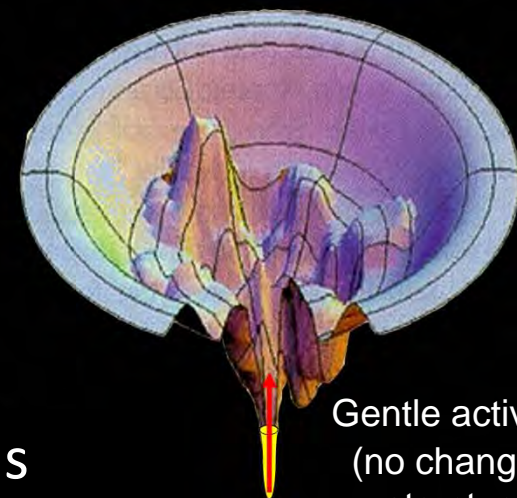
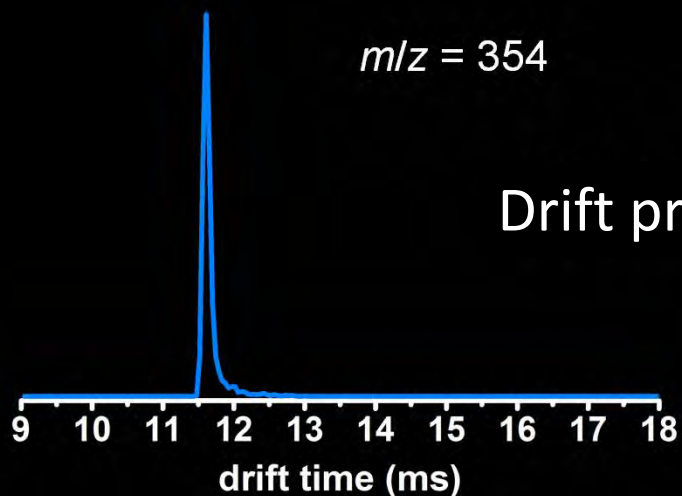
# IMS-IMS-MS



Surface modified from: Dill, K.A.; Chan, H. S. *Nature Structural Biology* 1997, 4, 10.



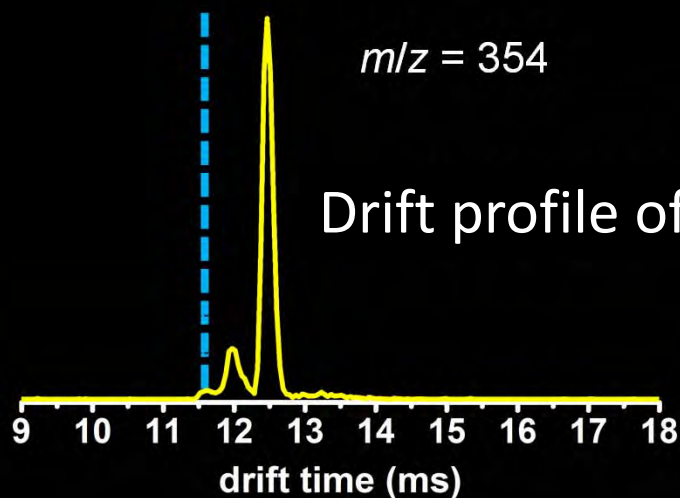
# IMS-IMS-MS



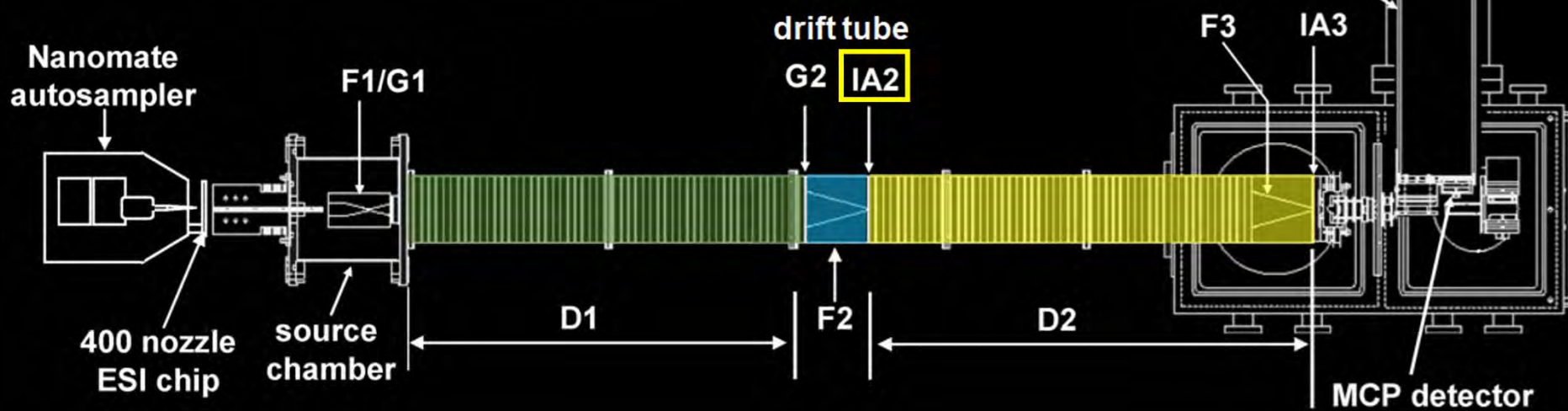
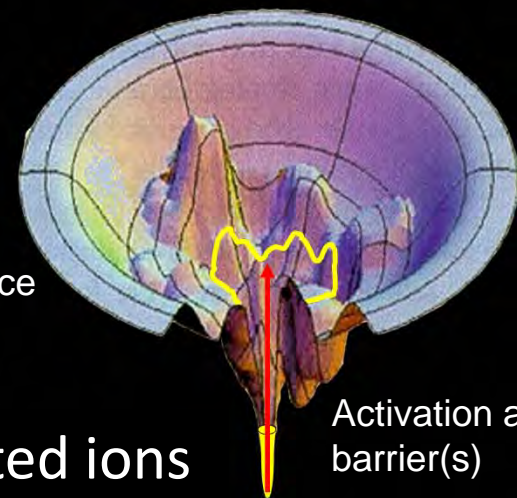
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# IMS-IMS-MS

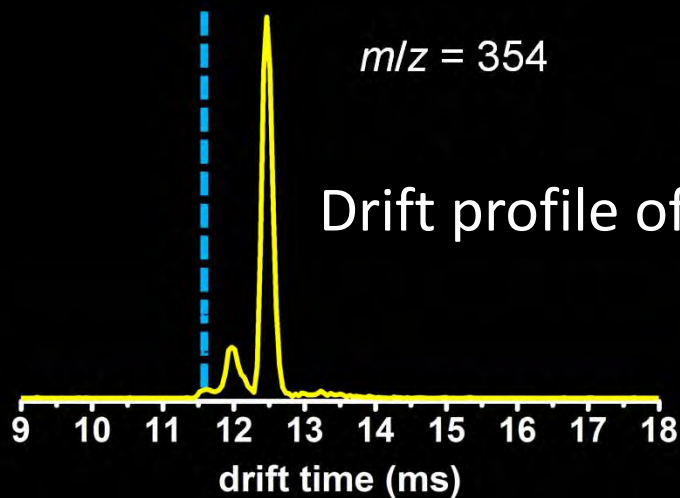


Sample conformational space

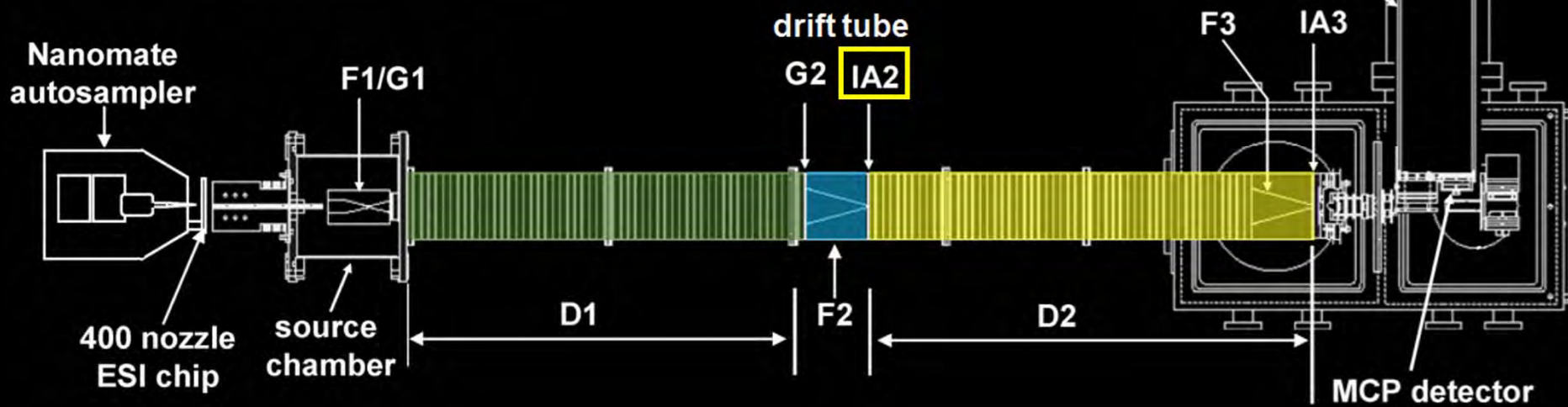
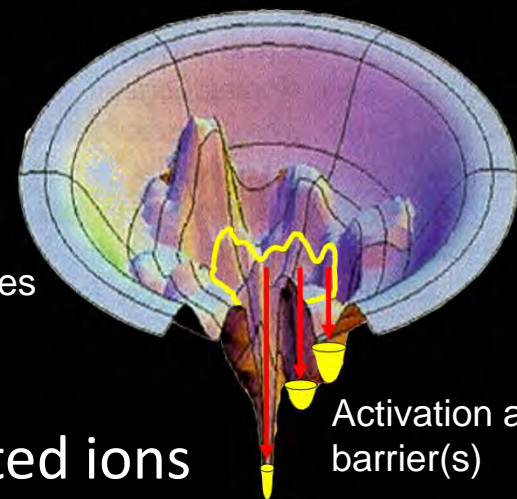


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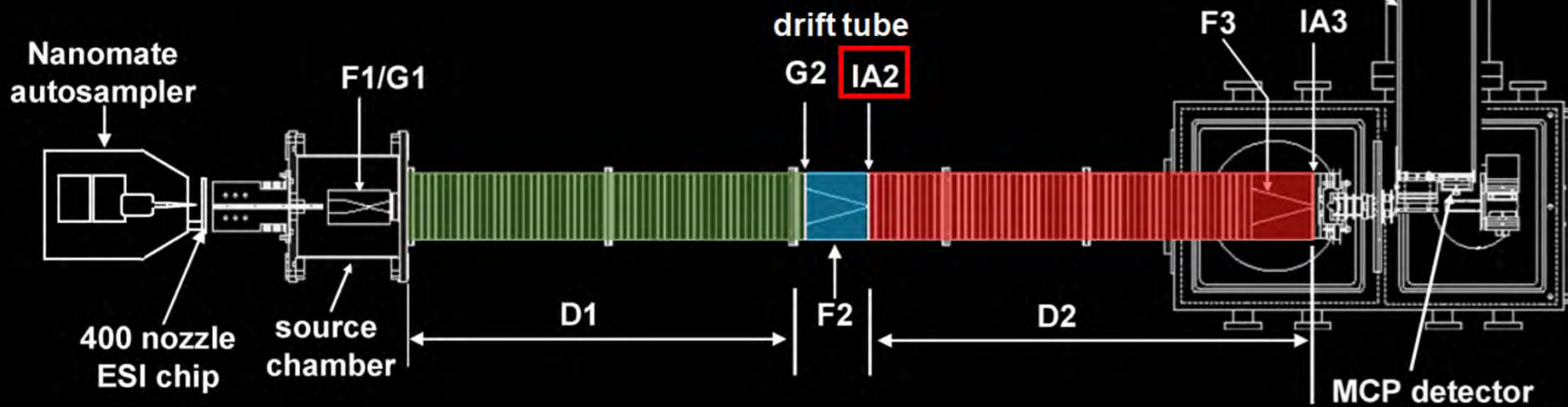
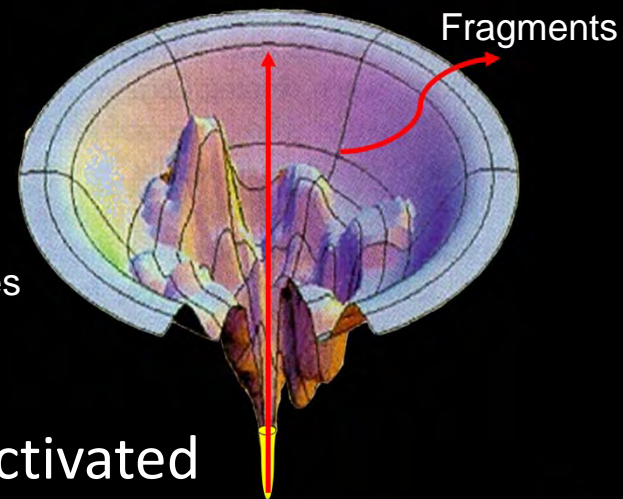
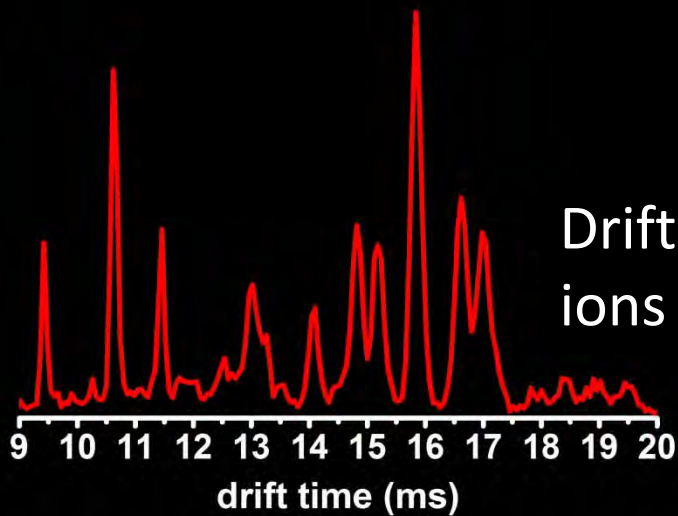


Create new population of states



Surface modified from: Dill, K.A.; Chan, H. S. *Nature Structural Biology* 1997, 4, 10.

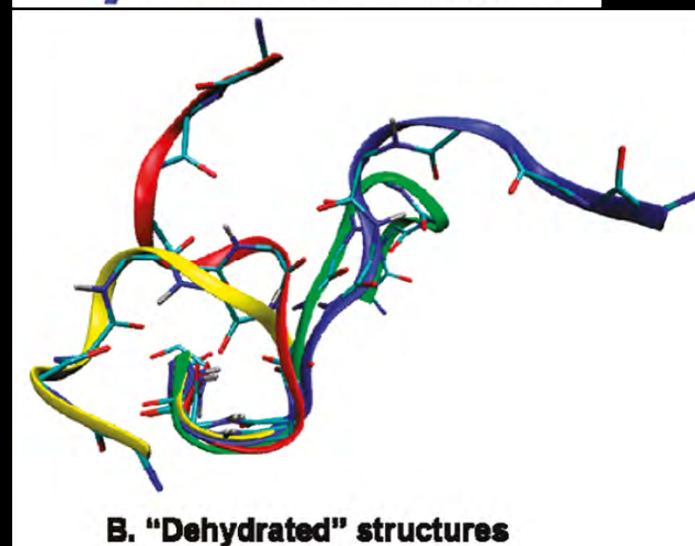
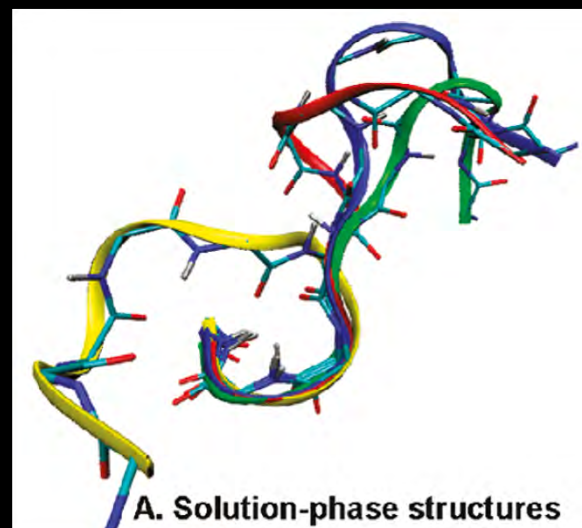
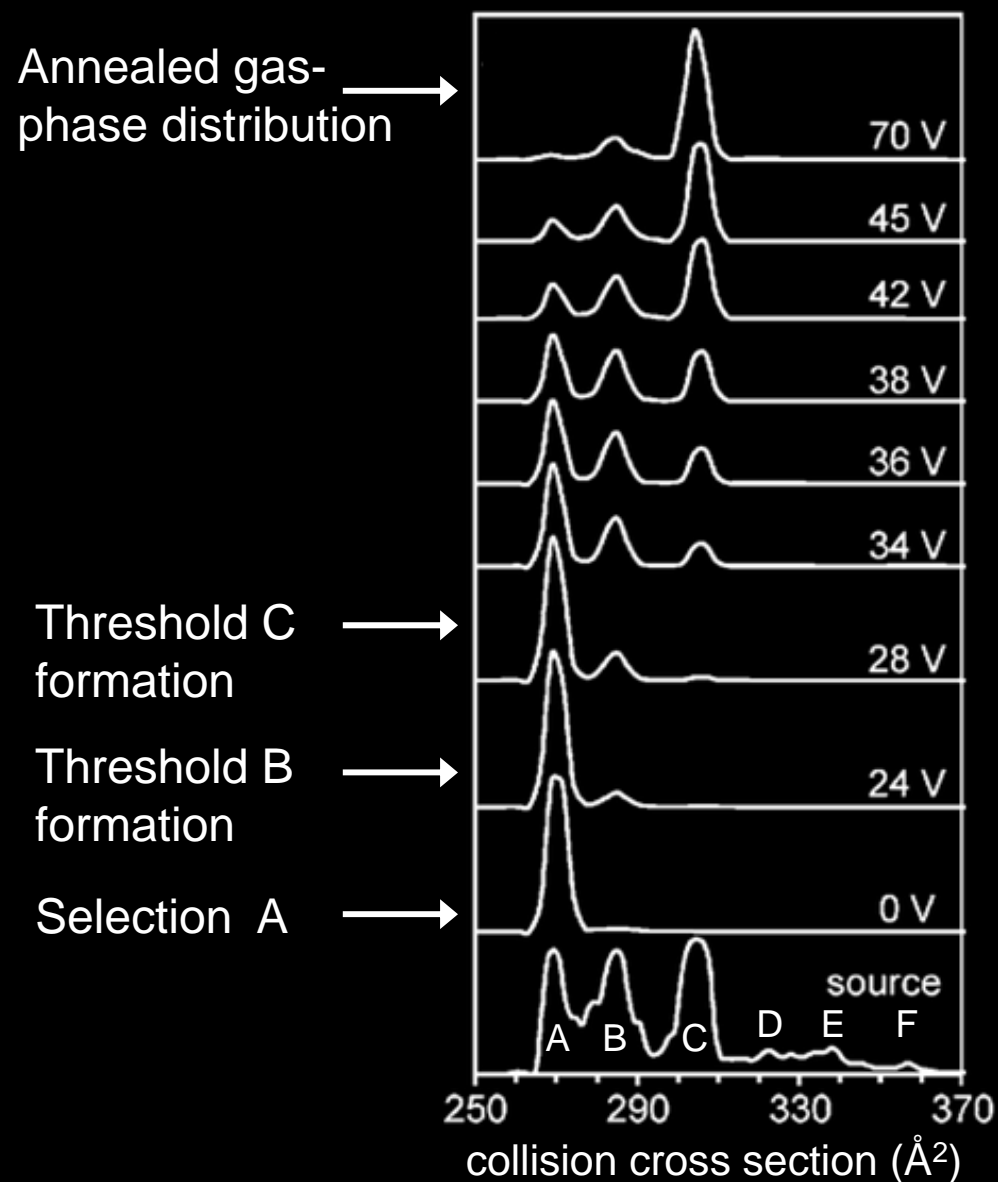
# IMS-IMS-MS



Surface modified from: Dill, K.A.; Chan, H. S. *Nature Structural Biology* 1997, 4, 10.



# Voltage-Resolved Selection and Activation of Conformer A

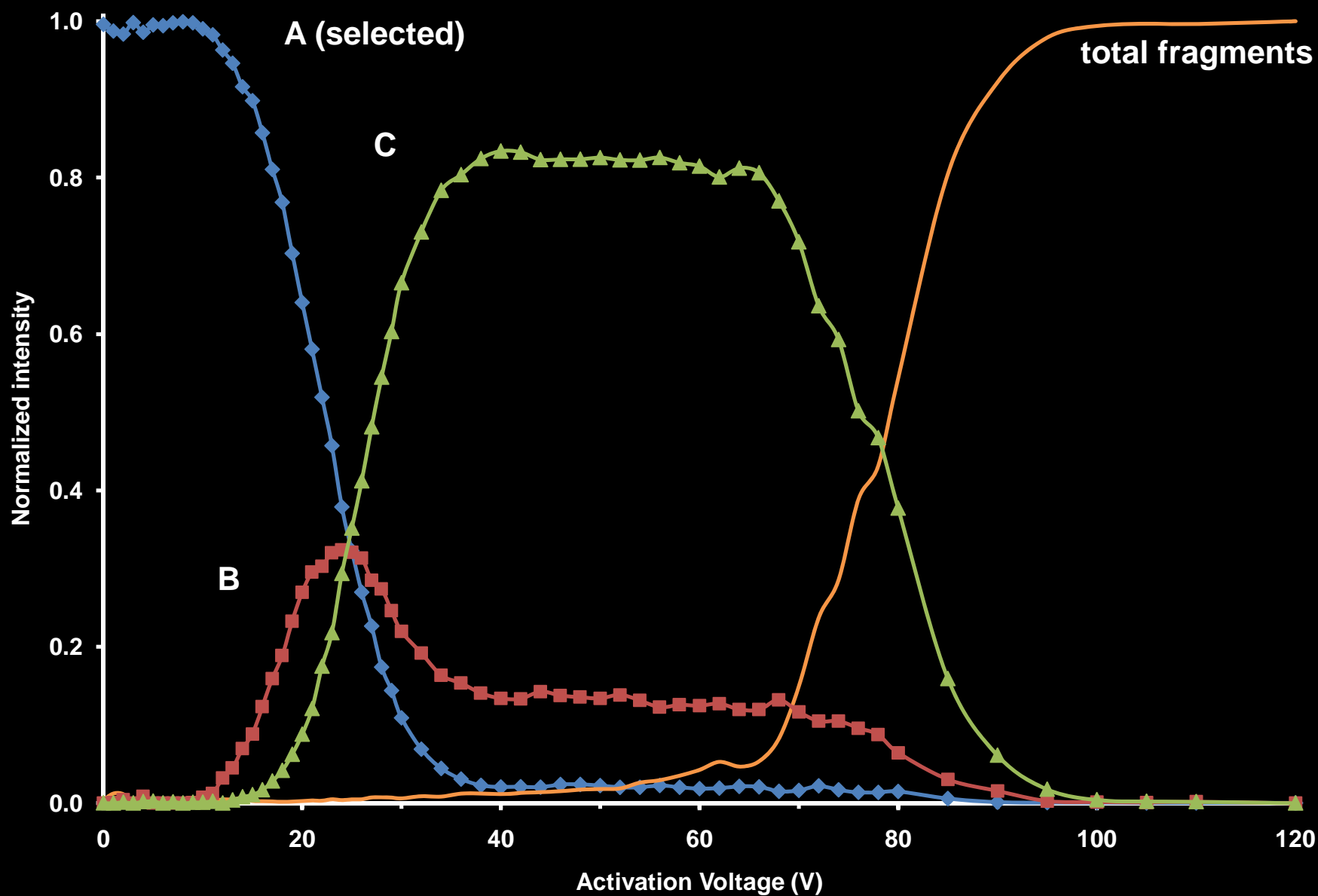


Pierson, N.A.; Valentine, S.J.; Clemmer, D.E. *J. Phys. Chem. B* **2010**, *114*, 7777–7783

Pierson, N.A.; Chen, L.; Valentine, S.J.; Russel, D.H.; Clemmer, D.E. *J. Am. Chem. Soc.* **2011**, *133*, 13810–13813

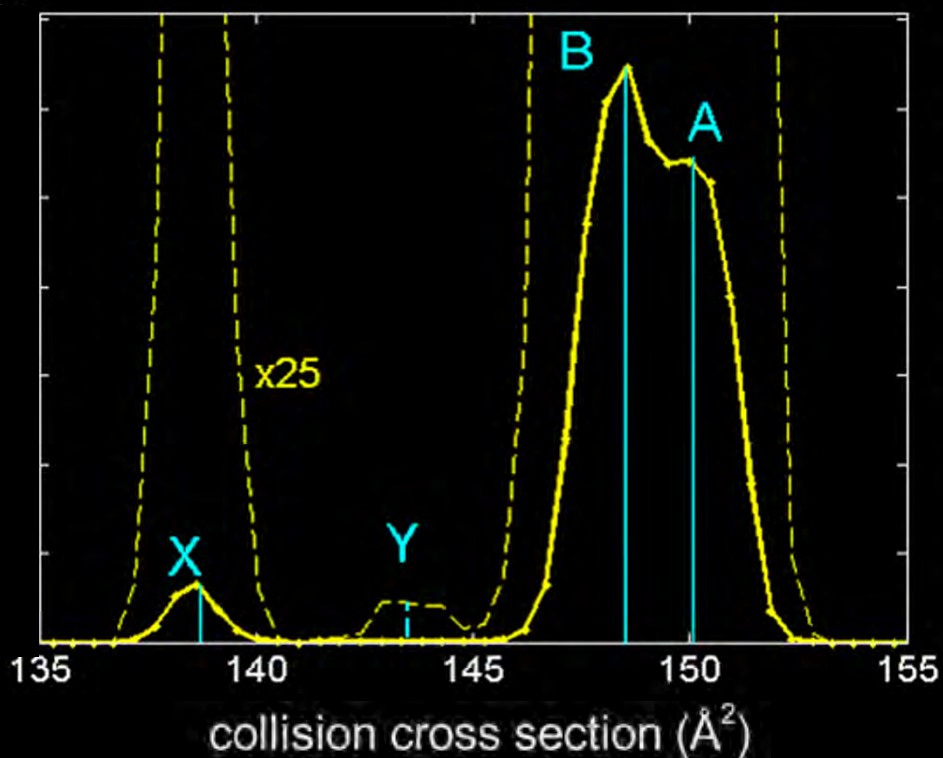


# Voltage-Resolved Selection and Activation of Conformer A



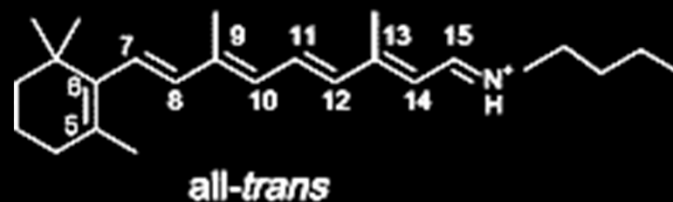
# IMS-MS: [RPSB+H]<sup>+</sup>

Retinal: [RPSB+H]<sup>+</sup>  
~340 amu



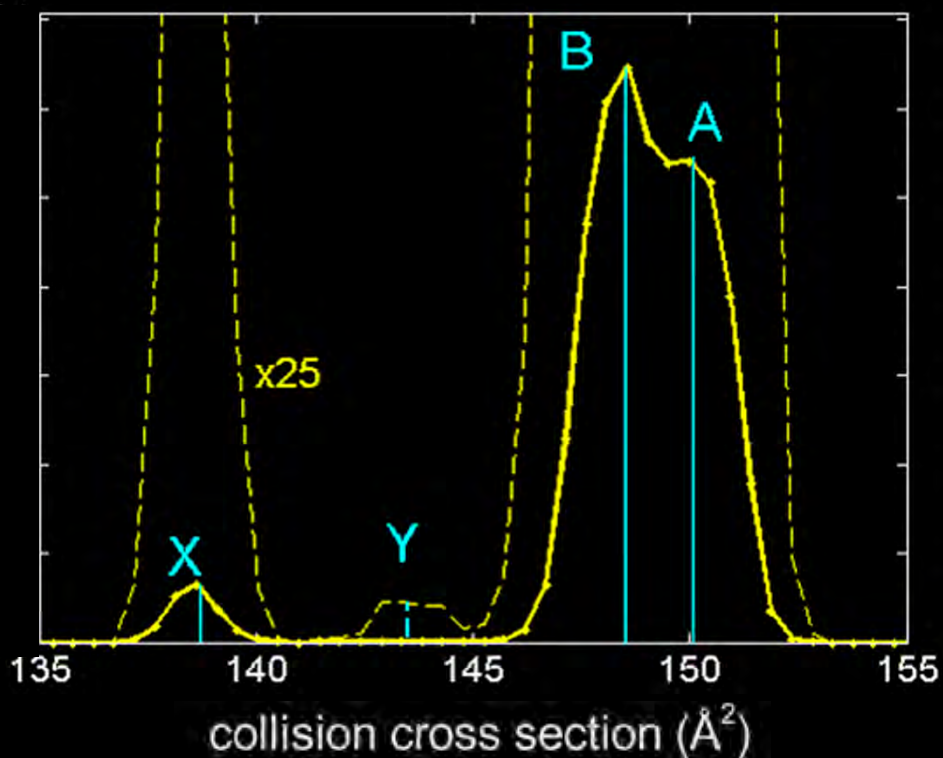
## Peak A

- largest measured ccs
- calculated ccs of the *trans*-RPSB within 5%



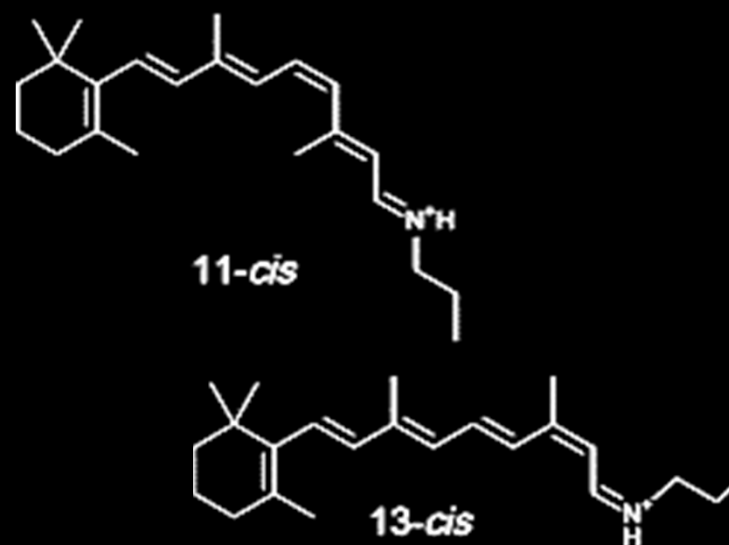
# IMS-MS: [RPSB+H]<sup>+</sup>

Retinal: [RPSB+H]<sup>+</sup>  
~340 amu



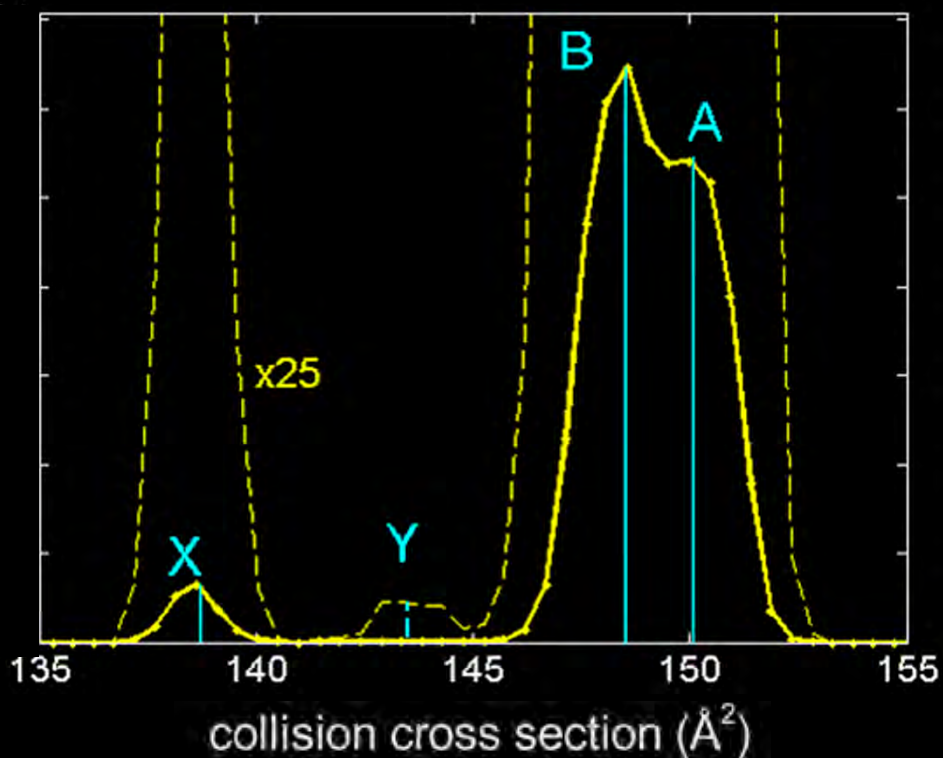
## Peak B

- most abundant peak in the distribution
- calculated ccs agree with multiple *cis*-RPSB geometries



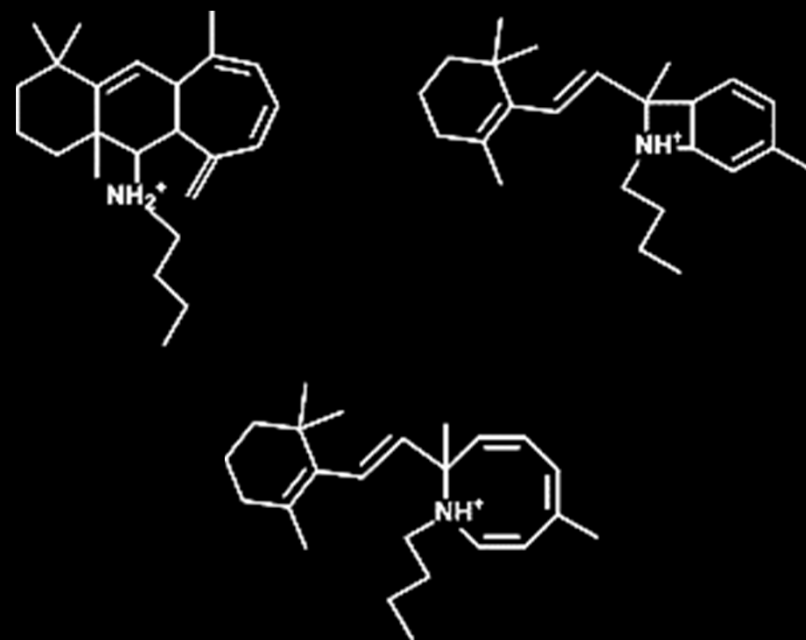
# IMS-MS: [RPSB+H]<sup>+</sup>

Retinal: [RPSB+H]<sup>+</sup>  
~340 amu



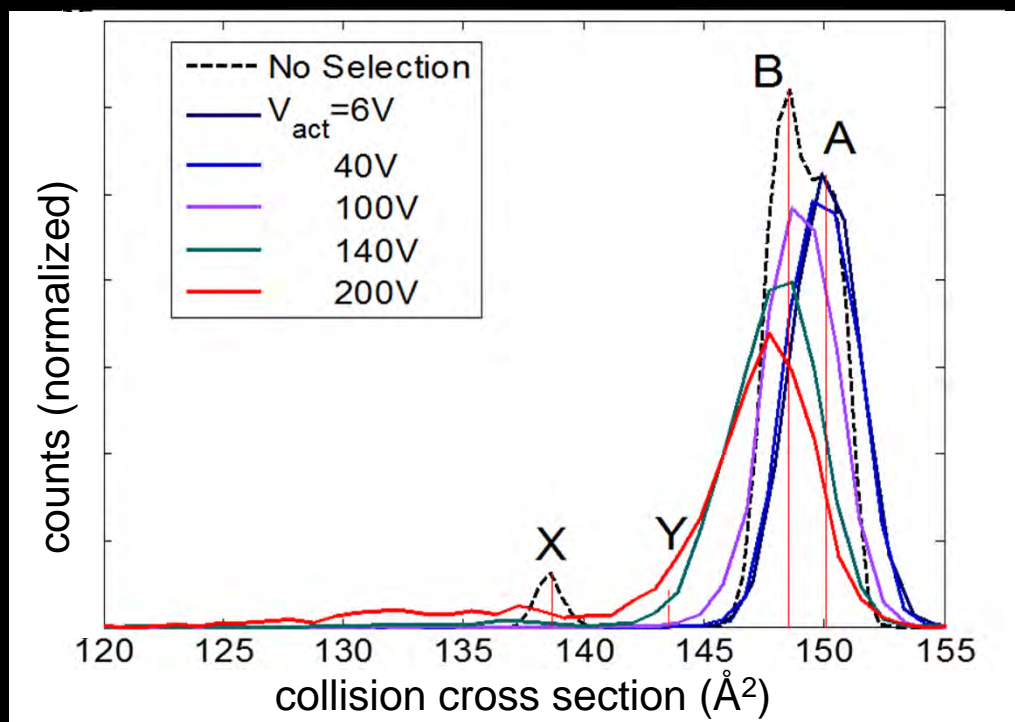
## Peaks X & Y

- multiple-*cis* bonds
- potentially cyclized





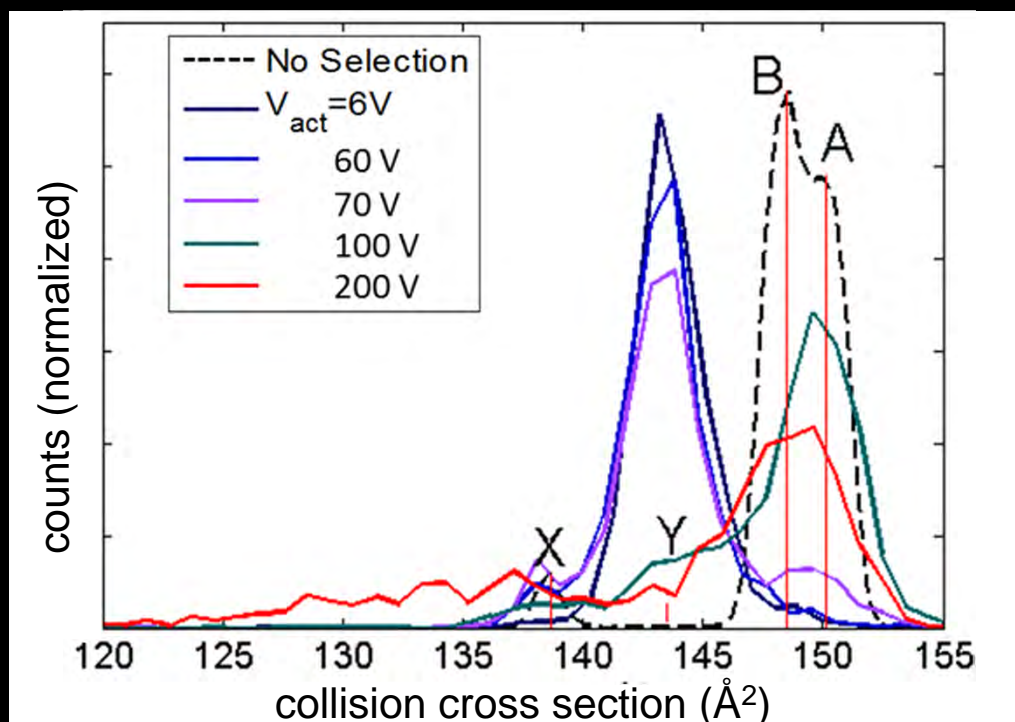
# IMS-IMS-MS: Peak A of $[\text{RPSB}+\text{H}]^+$



Activations were scanned in 10 V increments

Annealed gas-phase distribution shows a broad peak centered around Peak B

# IMS-IMS-MS: Peak Y of $[RPSB+H]^+$



Activations were scanned in 10 V increments

Annealed gas-phase distribution shows a broad peak centered around Peak B

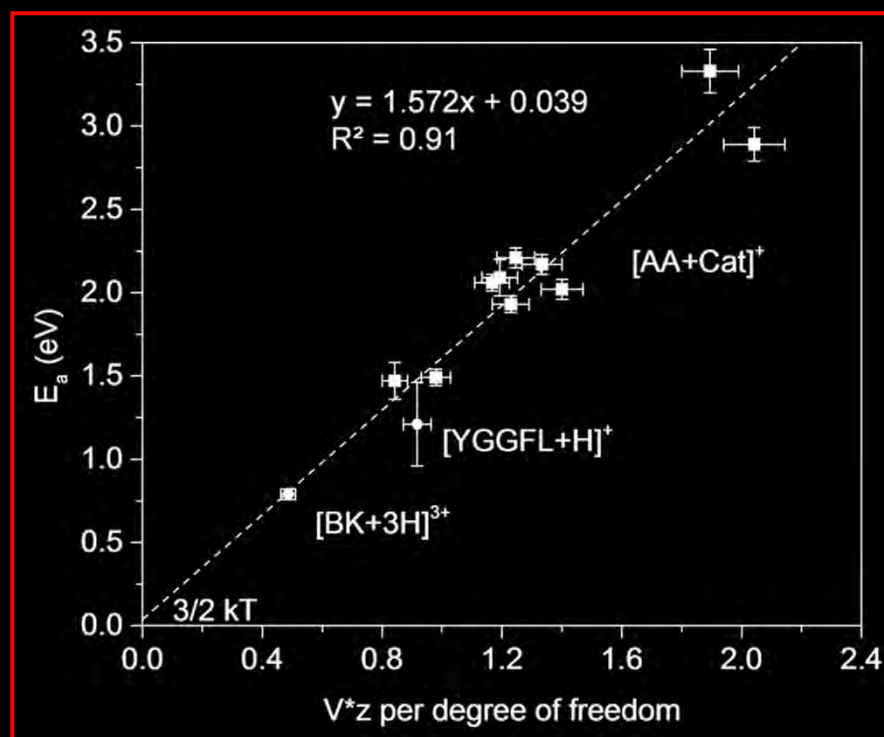
# Measuring Activation Energies by IMS–IMS

We observe pre-dissociation state-to-state transitions, but at what energies?

- Use of an external IA2 voltage-to-eV calibration by measuring well-characterized dissociation events

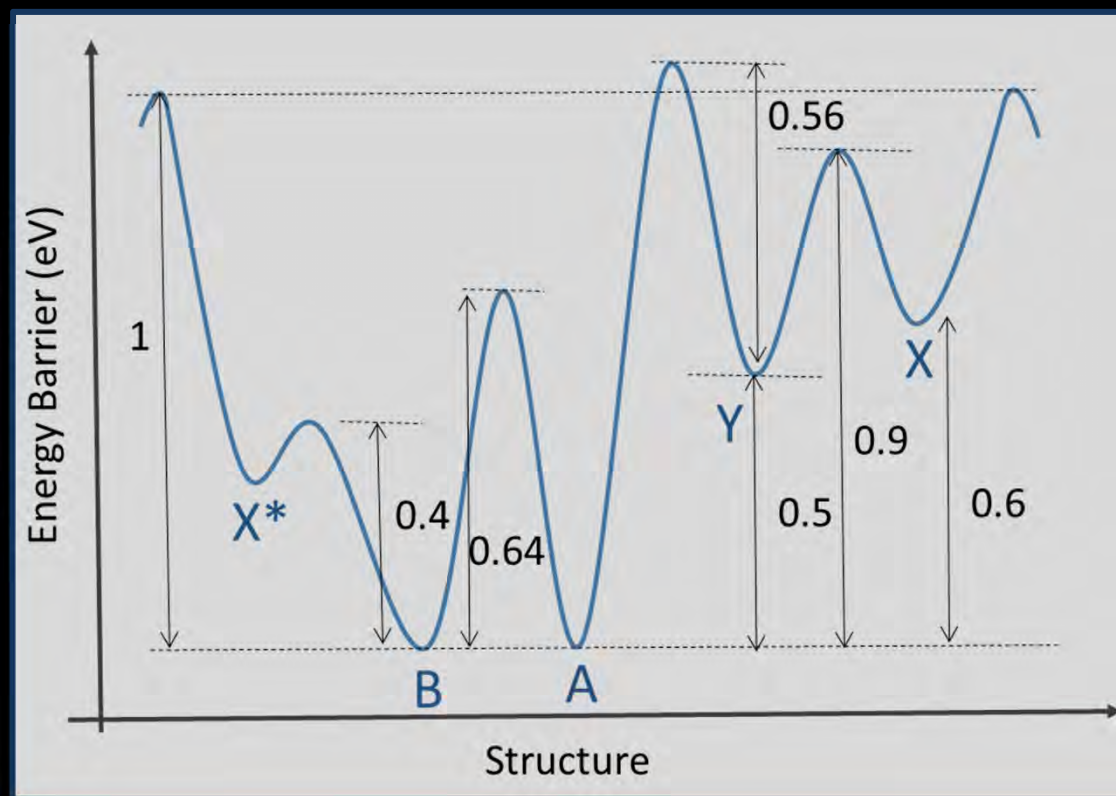
“Thermometer ion” systems:

| Ion                    | $E_a$ , eV          | IA2 Voltage $\cdot z$ |
|------------------------|---------------------|-----------------------|
| [Pro+K] <sup>+</sup>   | 1.49 ( $\pm 0.05$ ) | 47 ( $\pm 2.4$ )      |
| [Met+K] <sup>+</sup>   | 1.47 ( $\pm 0.11$ ) | 48 ( $\pm 2.4$ )      |
| [Asp+Na] <sup>+</sup>  | 2.02 ( $\pm 0.06$ ) | 63 ( $\pm 3.2$ )      |
| [Asn+Na] <sup>+</sup>  | 2.17 ( $\pm 0.06$ ) | 64 ( $\pm 3.2$ )      |
| [Glu+Na] <sup>+</sup>  | 2.06 ( $\pm 0.05$ ) | 63 ( $\pm 3.2$ )      |
| [Gln+Na] <sup>+</sup>  | 2.21 ( $\pm 0.06$ ) | 71 ( $\pm 3.6$ )      |
| [Pro+Na] <sup>+</sup>  | 1.93 ( $\pm 0.05$ ) | 59 ( $\pm 3.0$ )      |
| [Met Na] <sup>+</sup>  | 2.09 ( $\pm 0.11$ ) | 68 ( $\pm 3.4$ )      |
| [Pro Li] <sup>+</sup>  | 2.89 ( $\pm 0.10$ ) | 98 ( $\pm 4.9$ )      |
| [Met Li] <sup>+</sup>  | 3.33 ( $\pm 0.13$ ) | 108 ( $\pm 5.4$ )     |
| [YGGFL+H] <sup>+</sup> | 1.21 ( $\pm 0.25$ ) | 209 ( $\pm 10.5$ )    |
| [BK+3H] <sup>3+</sup>  | 0.79 ( $\pm 0.03$ ) | 219 ( $\pm 3.7$ )     |



# Measuring Activation Energies by IMS–IMS

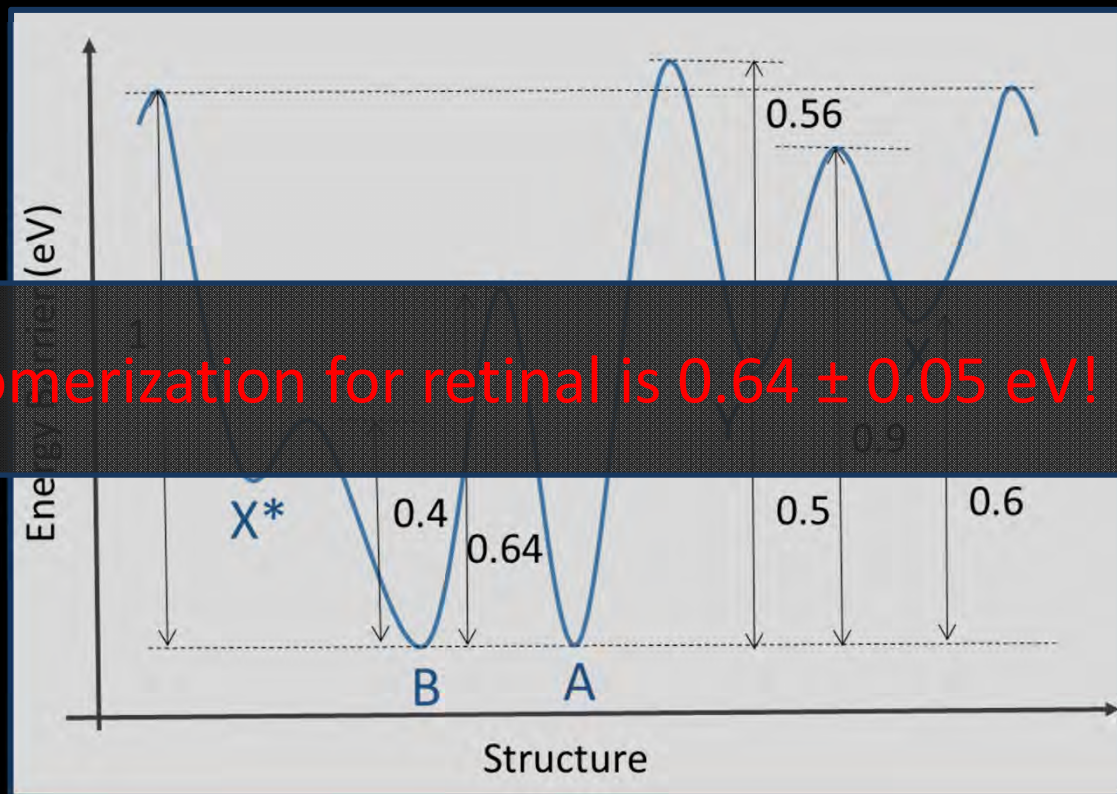
| Process | Barrier Energy (eV) |
|---------|---------------------|
| A→X     | 0.9 ( $\pm 0.05$ )  |
| B→X     | 0.4 ( $\pm 0.05$ )  |
| Y→A     | 0.56 ( $\pm 0.05$ ) |
| Y→B     | 0.56 ( $\pm 0.05$ ) |
| Y→X     | 0.5 ( $\pm 0.05$ )  |
| X→A     | 0.5 ( $\pm 0.05$ )  |
| X→B     | 0.5 ( $\pm 0.05$ )  |
| A→B     | 0.64 ( $\pm 0.05$ ) |
| A→B     | 0.64 ( $\pm 0.05$ ) |
| A→frag  | 1.0 ( $\pm 0.05$ )  |
| B→frag  | 1.0 ( $\pm 0.05$ )  |
| Y→frag  | 0.5 ( $\pm 0.05$ )  |
| X→frag  | 0.4 ( $\pm 0.05$ )  |





# Measuring Activation Energies by IMS–IMS

| Process | Barrier Energy (eV) |
|---------|---------------------|
| A→X     | 0.9 (±0.05)         |
| B→X     | 0.4 (±0.05)         |
| Y→A     | 0.56 (±0.05)        |
| Y→B     | 0.56 (±0.05)        |
| Y→X     | 0.5 (±0.05)         |
| X→A     | 0.9 (±0.05)         |
| X→B     | 0.5 (±0.05)         |
| A→B     | 0.64 (±0.05)        |
| A→frag  | 1.0 (±0.05)         |
| B→frag  | 1.0 (±0.05)         |
| Y→frag  | 0.5 (±0.05)         |
| X→frag  | 0.4 (±0.05)         |



Thus, a *single cis-trans* isomerization for retinal is  $0.64 \pm 0.05$  eV!

# Summary

- Isomerization barriers of isolated  $[RPSB+H]^+$  via IMS-IMS-MS
- Low energy barrier for a single *cis*→*trans* isomerization
  - Below the thermal isomerization of double bonds
  - Below measured barrier within rhodopsin proteins

Thus, the protein plays a significant role in raising the energetic barrier for photoisomerization of retinal

# Acknowledgements

**Bar-Ilan University:**  
Dr. Yoni Toker  
Lihl Musbat

**Indiana University:**  
Prof. David Clemmer  
Nicholas Pierson  
Matthew Glover

**Aarhus University:**  
Anastasia Bochenkova  
S. Brøndsted Nielsen

**Weizmann Institute:**  
Mordechai Sheves

**Funding:**  
NSWC Crane NISE/ 219  
Indiana University METACyt



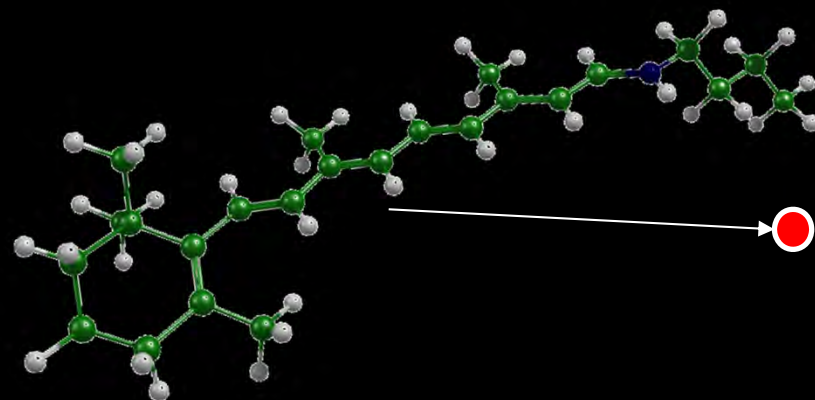
# Backup Slides



# Ion Mobility Spectrometry (IMS)

Study the shape of a molecule through collisions with neutral atoms/molecules

- Neutral atoms are as small as the features we want to study
- Collision energy can be set to be very small



↓

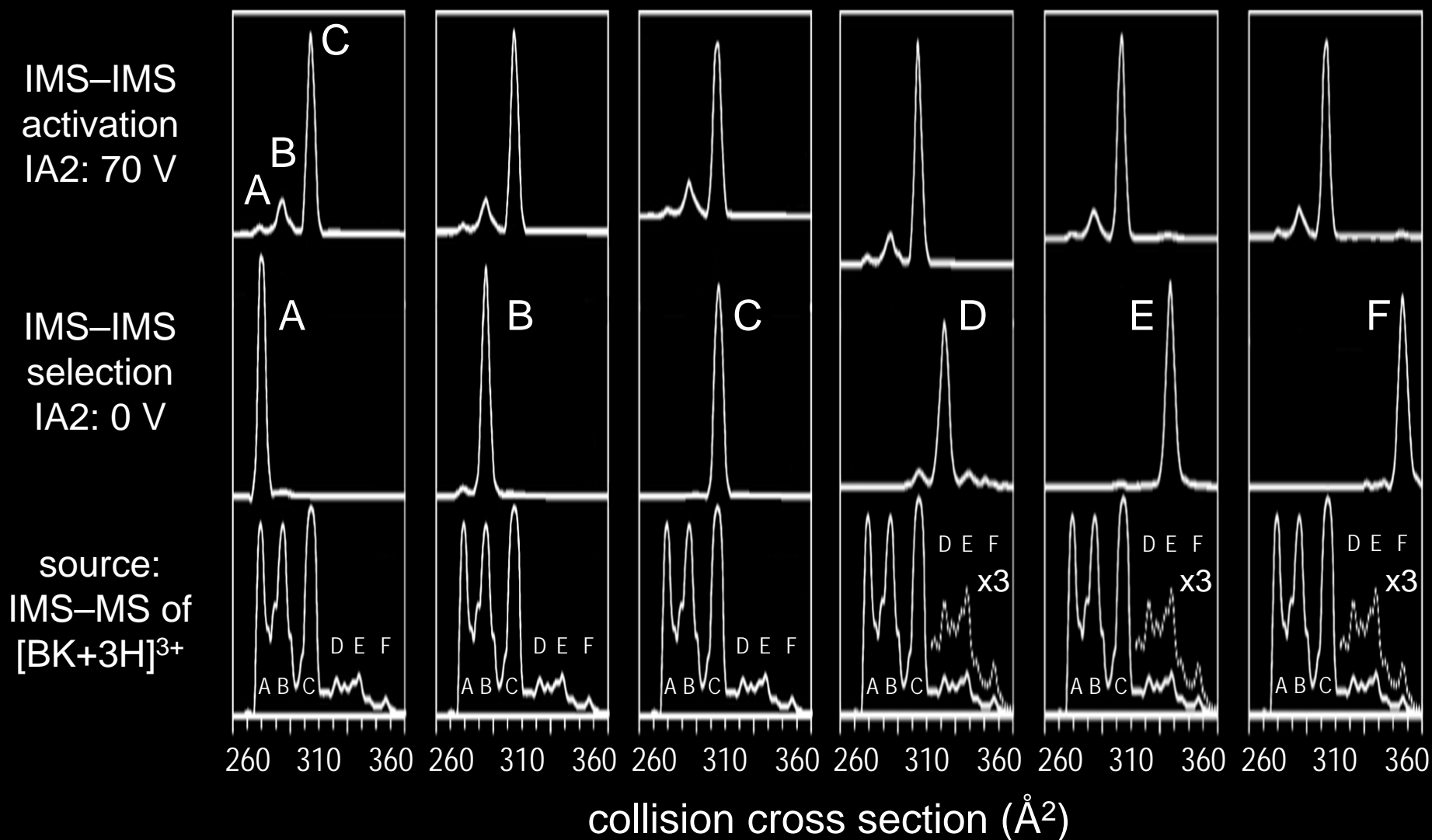
In order to study the structure

- And can also set to be large

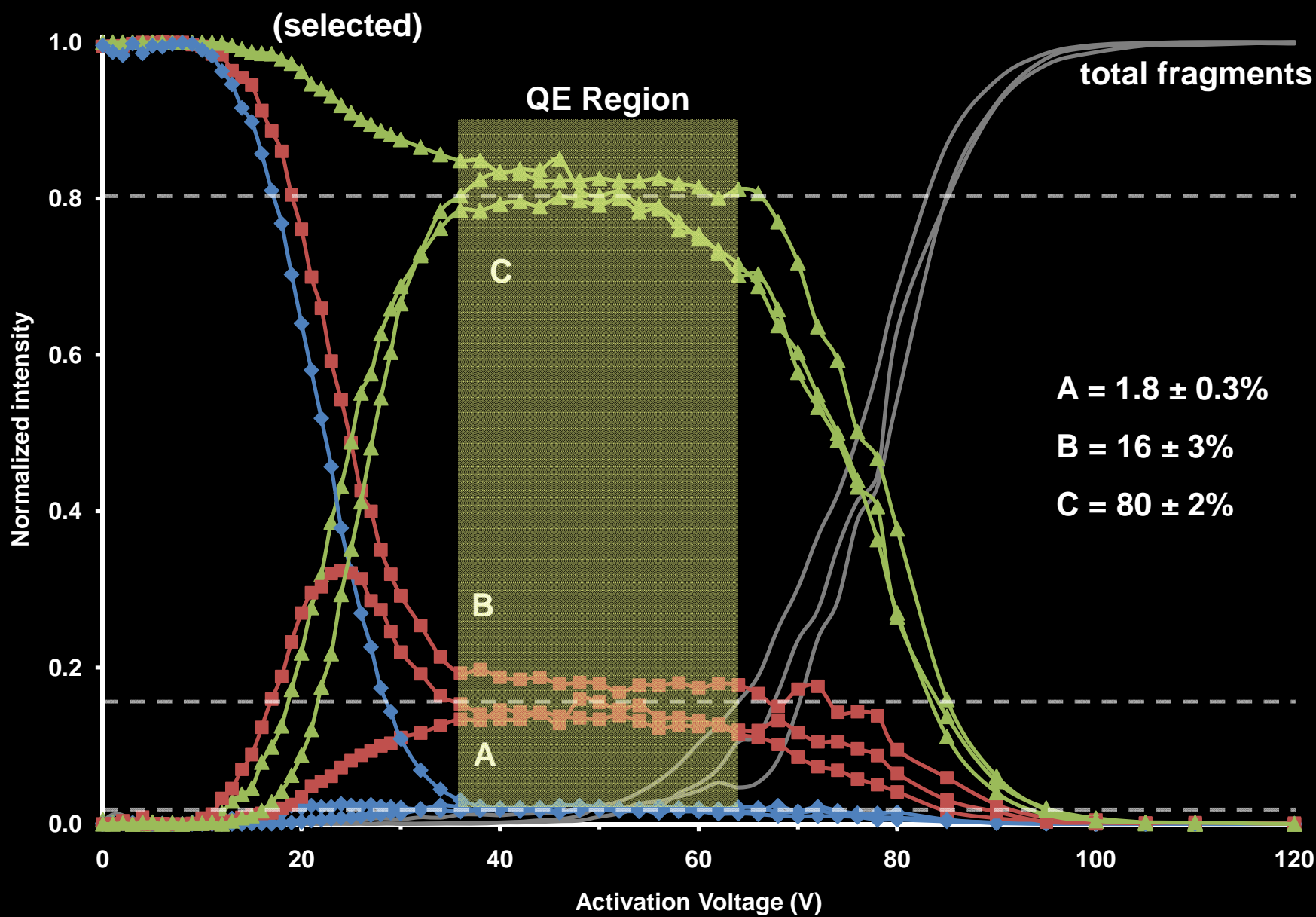
↓

In order to heat the molecule, cause it to isomerize, and eventually break apart.

# Gas-Phase Distributions of Bradykinin

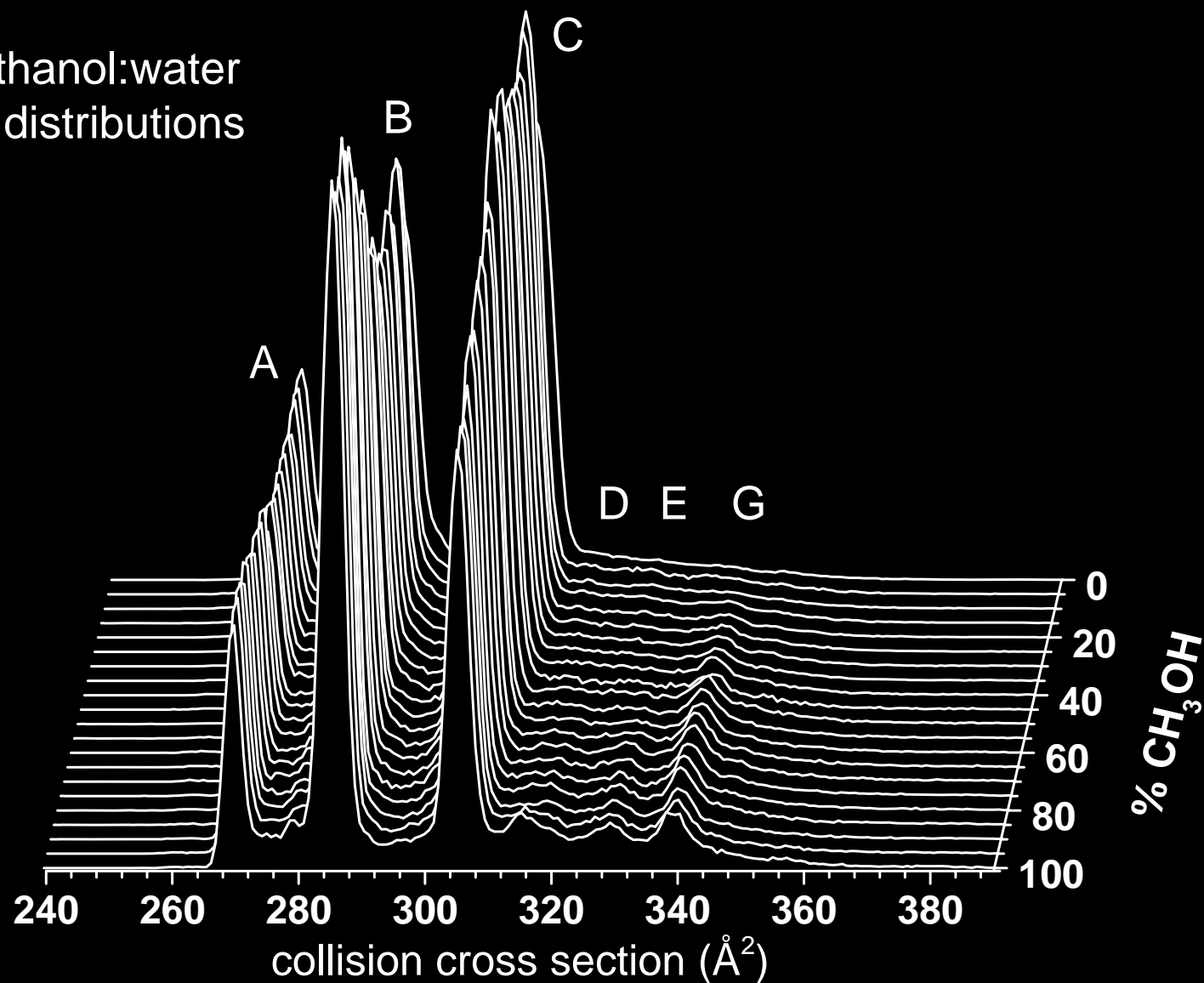


# Selection and Activation of Conformers A, B, and C



# ESI Solution Studies

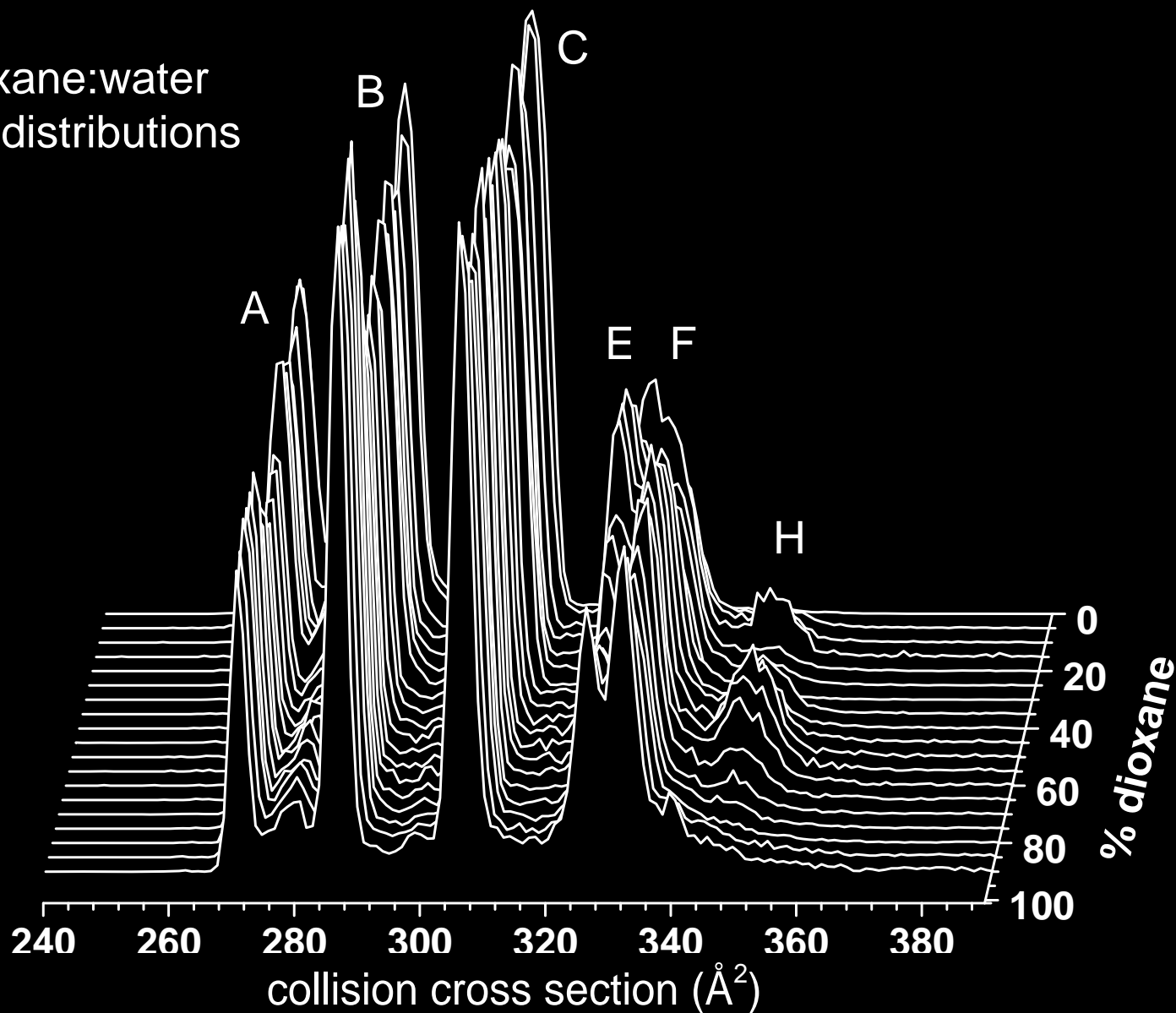
BK in methanol:water  
[M+3H]<sup>3+</sup> distributions



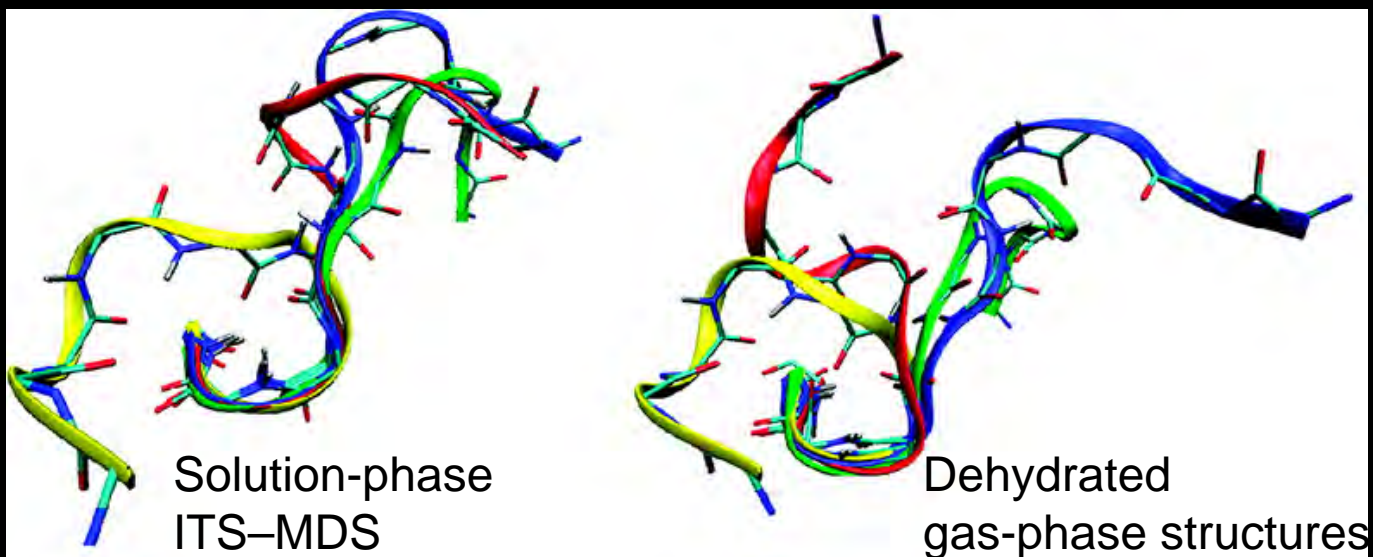


# ESI Solution Studies

BK in dioxane:water  
[M+3H]<sup>3+</sup> distributions

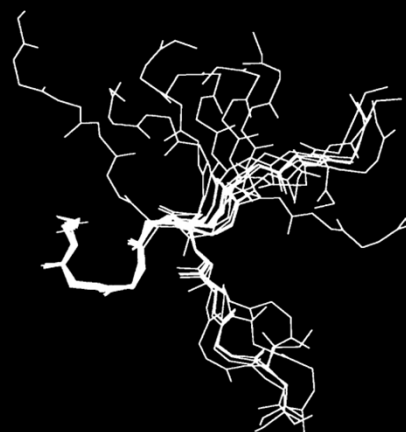
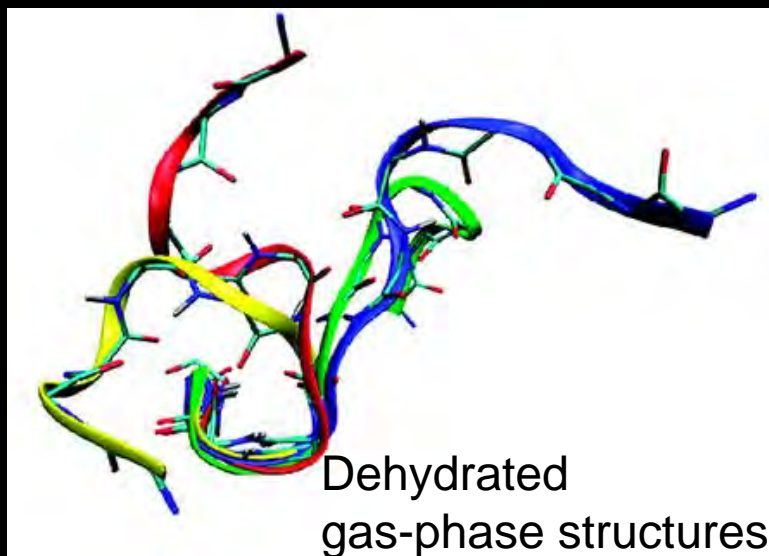


# Findings from BK Solution Scans

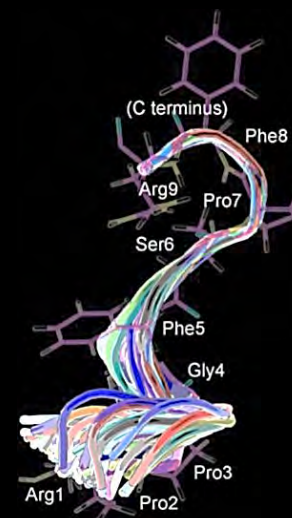


- Amino-terminal “unstructured” region consists of multiple, stable conformations
- Highly complementary to solution-phase characterization methods

# Findings from BK Solution Scans



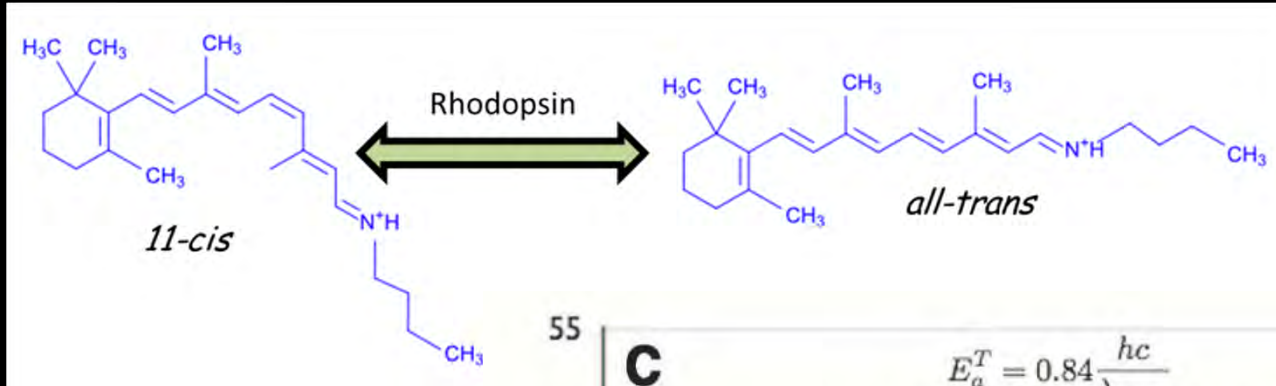
Young, J. K.; Hicks, R. P.  
*Biopolymers* **1994**, *34*, 611–623



Lopez, J. J. et al. *Angew. Chem. Int. Ed.* **2008**, *47*, 1668–1671

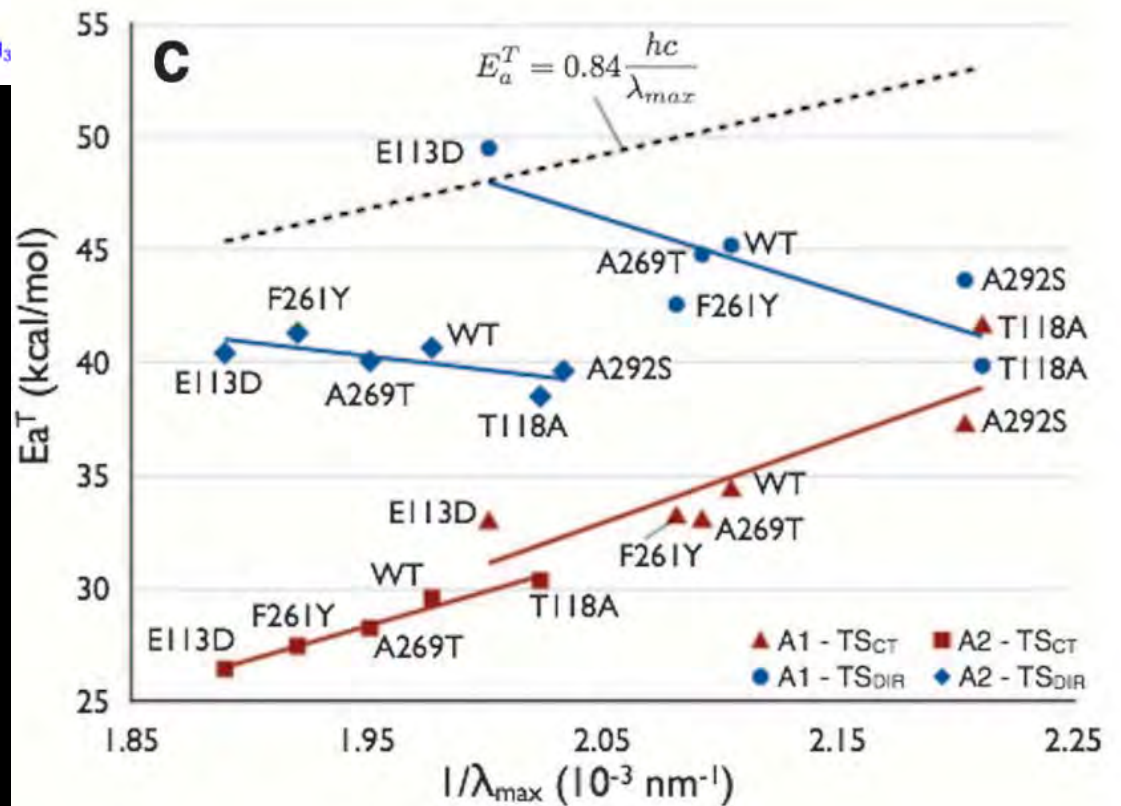
- Amino-terminal “unstructured” region consists of multiple, stable conformations
- Highly complementary to solution-phase characterization methods

# Barlow Correlation



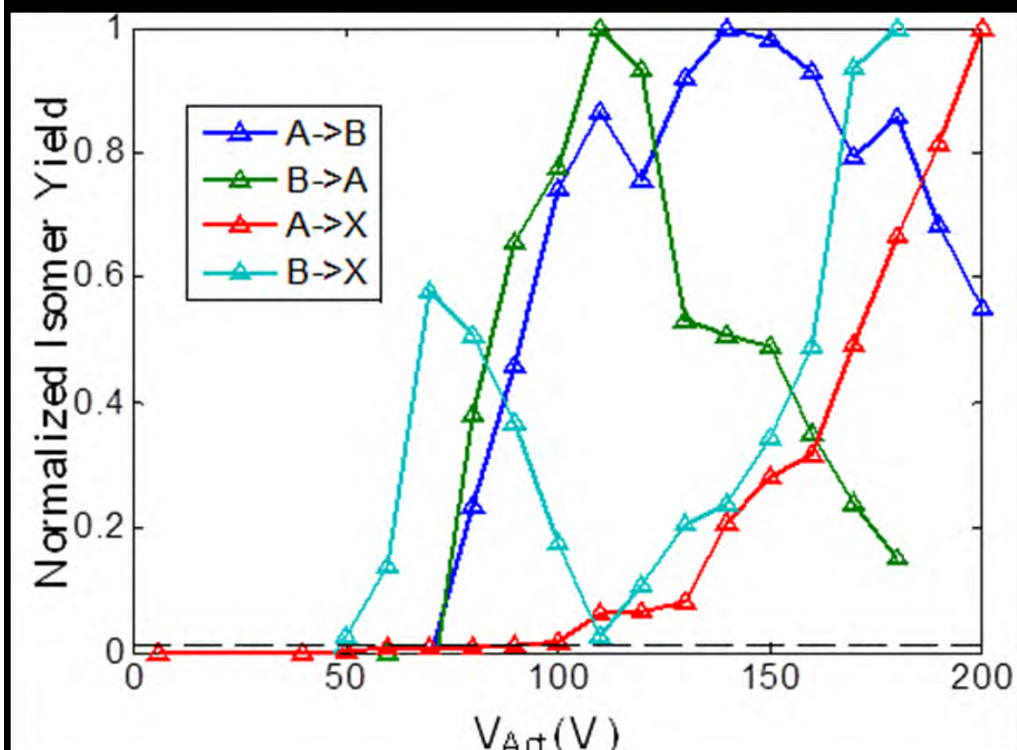
Experiment – Barrier energy in protein is ~1-1.2 eV, and inversely correlated with the absorption wavelength

Theory – ~1-2eV





# IMS-IMS-MS: [RPSB+H]<sup>+</sup>



- State-to-state conformational transitions
- Fragmentation pathway through a more compact, intermediate species