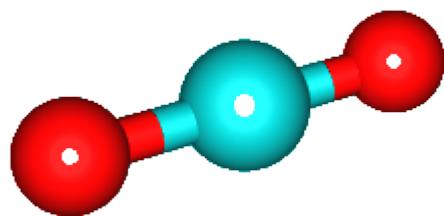


anti-sym

ω

>



sym

ω

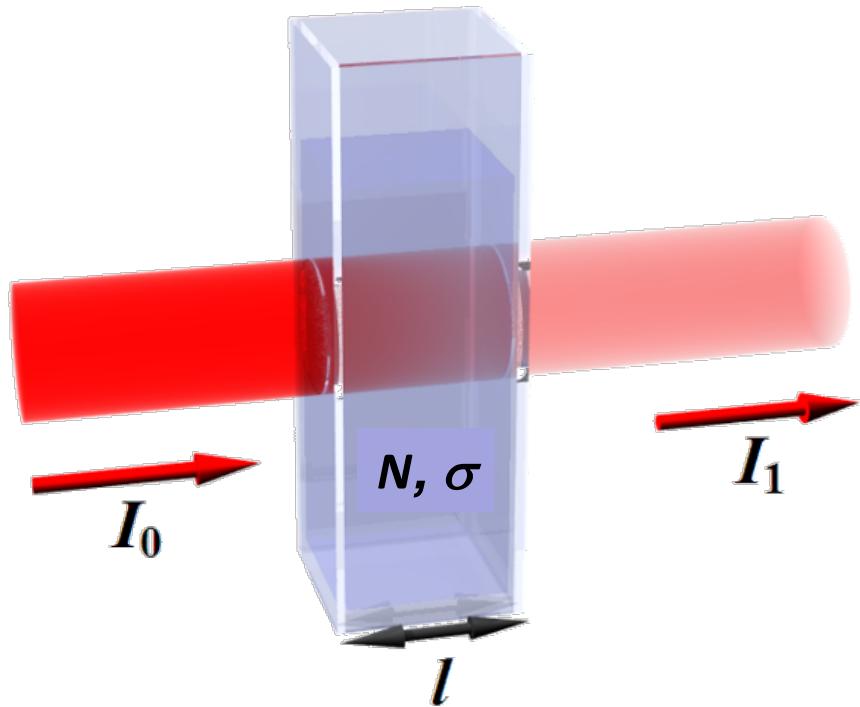
Combining IR spectroscopy with mass spectrometry

IR spectroscopy of extremely low-density samples

→ *Action spectroscopy in the IR*

- IR spectroscopy in molecular beams (lecture 1)
- IR spectroscopy of molecular ions (this lecture)
 - Combine IR spectroscopy with MS
 - IR spectroscopy with the sensitivity of MS
 - Analytical applications
 - Cryogenic ion spectroscopy
 - Dealing with conformational heterogeneity

Infrared spectroscopy



Typical values:

$$\sigma(\lambda) l N \sim 0.1 - 1$$

$$\sigma \sim 10^{-20} \text{ cm}^2$$

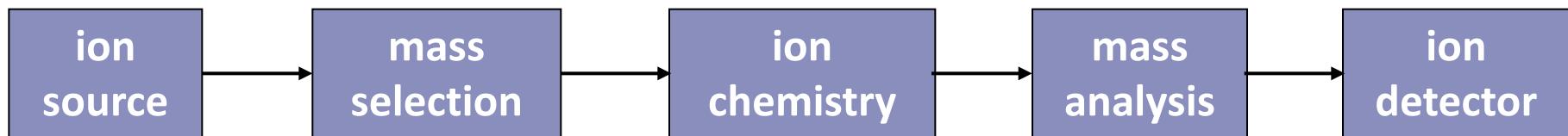
$$l \sim 10 \text{ cm}$$

$$\rightarrow N \sim 10^{19}$$

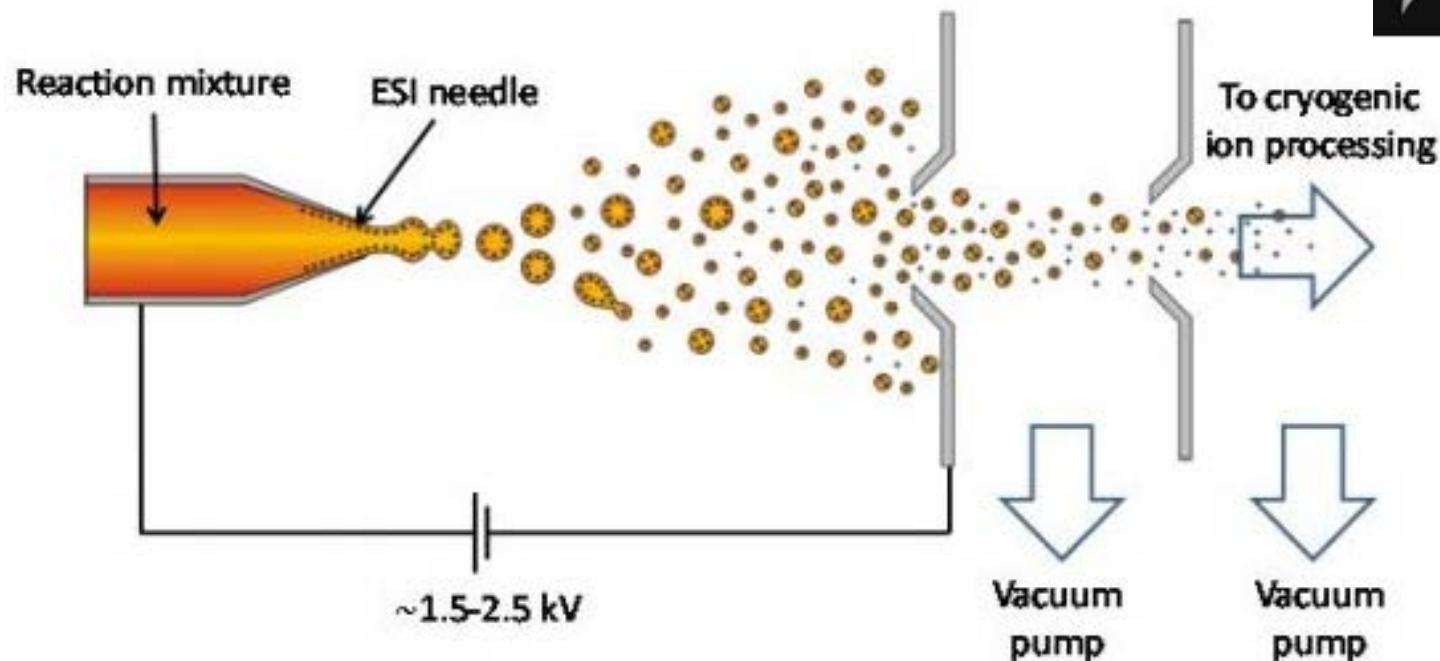
$$T(\lambda) = I_1 / I_0 = e^{-\sigma(\lambda) l N}$$

Lambert-Beer law

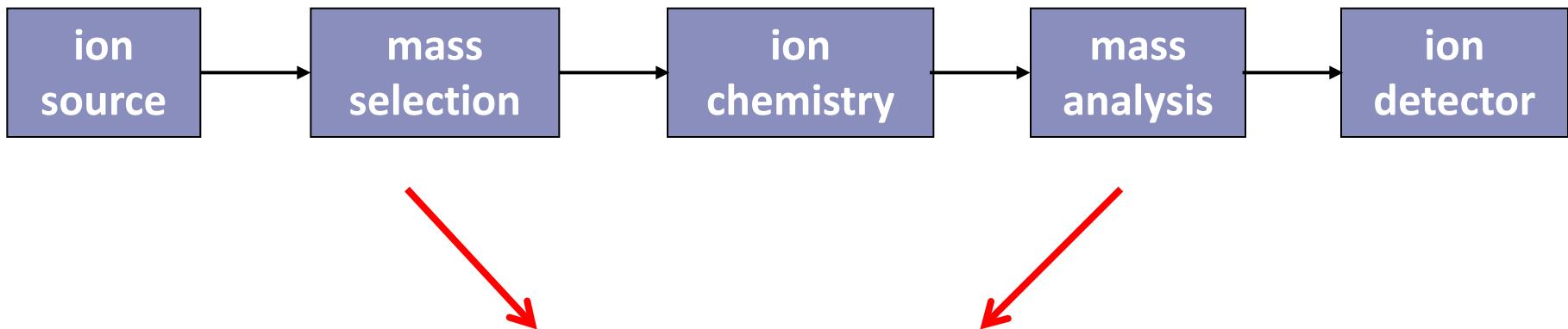
Tandem mass spectrometry



Electrospray Ionization (ESI)
John Fenn (NP Chemistry 2002)



Tandem mass spectrometry



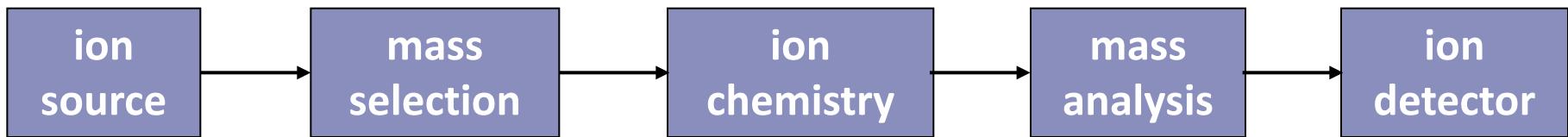
Electric fields

- Time of flight (TOF-MS)
- Quadrupole Mass Analyzer (QMS)
- Quadrupole ion traps

Magnetic fields

- Magnetic sector instruments
- Fourier Transform Ion Cyclotron Resonance (FTICR-MS)

Tandem mass spectrometry



Ion chemistry:

dissociation

collision induced (CID, CAD)

electron induced (ECD, ETD, EDD)

photon induced (IRMPD, BIRD, UVPD)

ion-molecule reaction

hydrogen/deuterium exchange (HDX)

ligand exchange

H⁺ transfer reaction

others

ion-ion reaction (ETD, PTR)

*ion storage
devices*

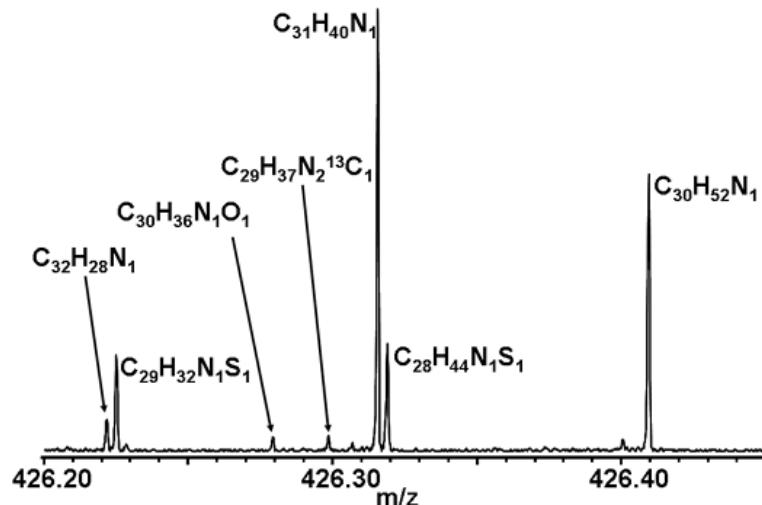
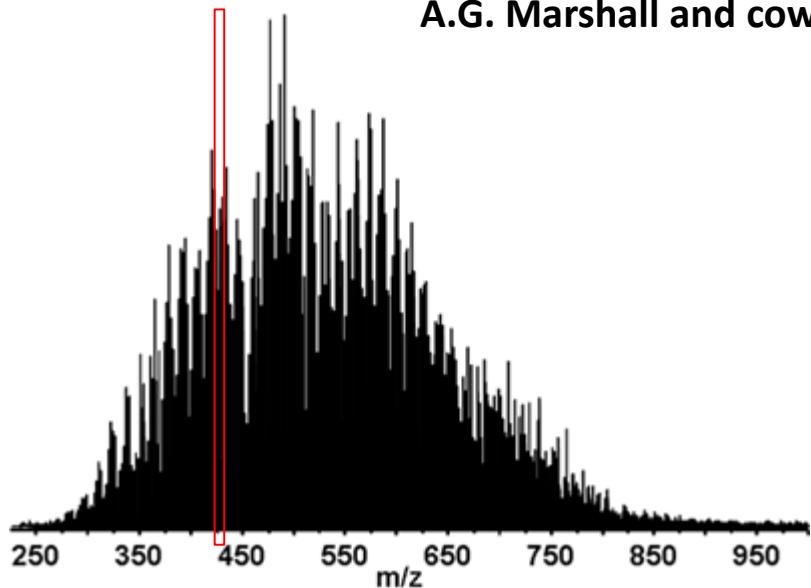
Tandem mass spectrometry (MS², MSⁿ): in space, in time

Mass spectrometry as analytical tool

- high sensitivity
- extremely high resolution

- metabolites
- environmental
- food analysis
- petroomics
- illicit drug testing
- proteomics
- glycomics

A.G. Marshall and coworkers, NHFML, Florida



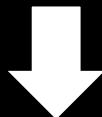
molecular weight → molecular formula → molecular structure ?

The large diversity of organic molecules

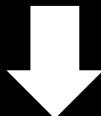
$C_{16}H_{10}N_2O_2$

MW = 262.074

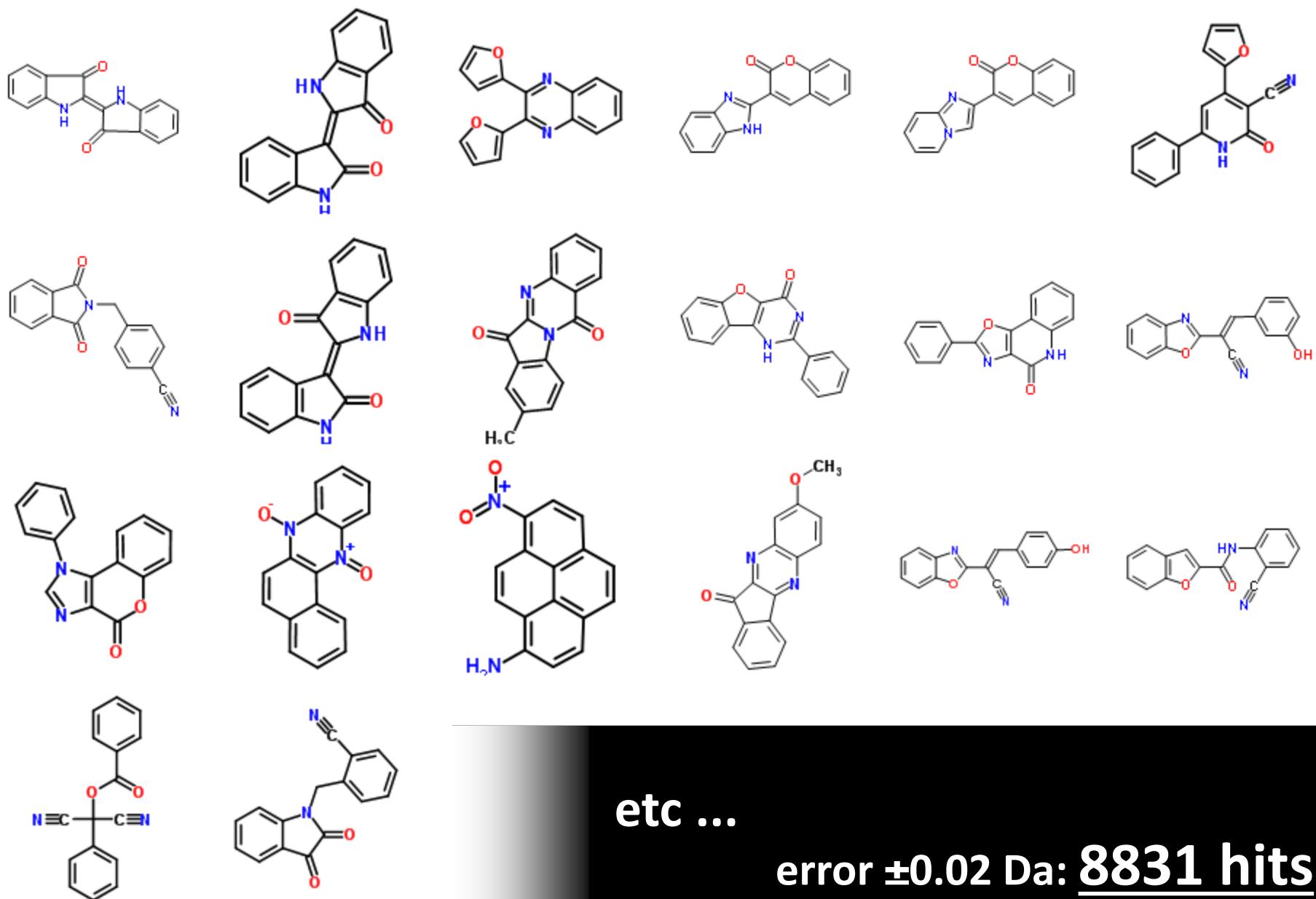
Search molecular formula
(= exact mass)



The screenshot shows the ChemSpider search interface. On the left, the ChemSpider logo is displayed with the tagline "Search and share chemistry". On the right, the Royal Society of Chemistry logo is visible.



227 known isomers

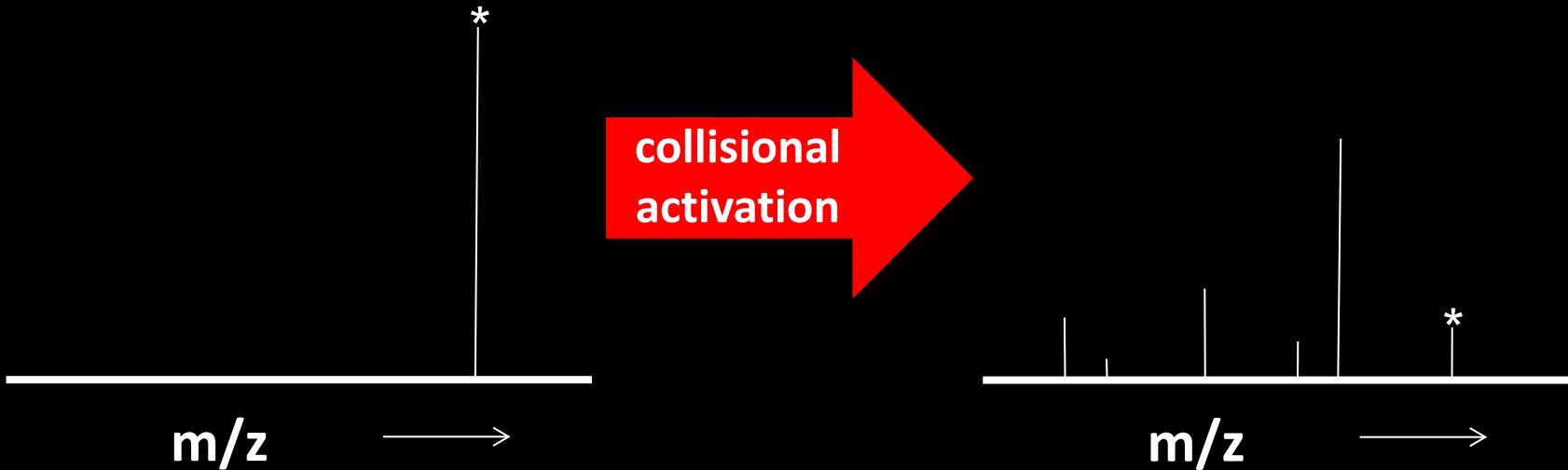


How many different structures can you build?



Molecular structure from MS

Collision induced dissociation (MS/MS)

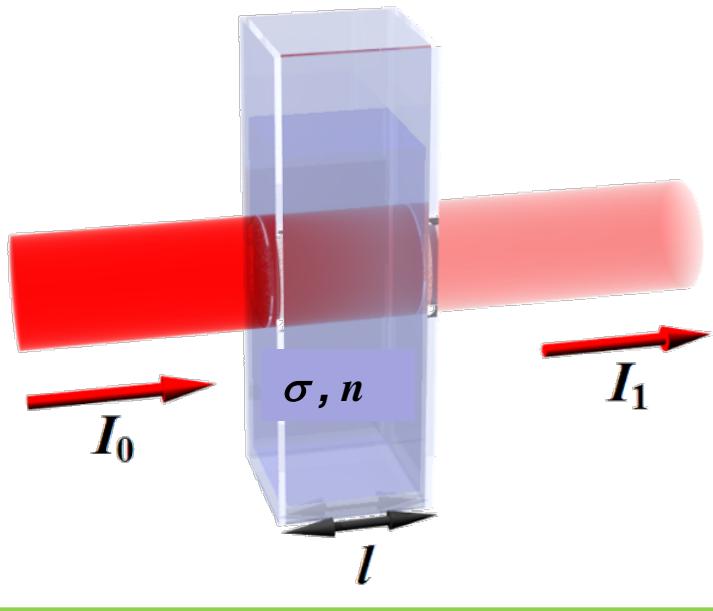


- Fragment spectrum platform dependent
- Fragment spectrum not predictable from *first principles*
- MS/MS database comparison
- Identify only *known unknowns*

Structural information from orthogonal methods

- retention time (LCMS)
- geometric cross section (ion mobility)
- # labile H-atoms (H/D exchange)
-
-
- IR spectroscopy
 - connectivity
 - intramolecular interactions
 - predictable by QC
 - database independent

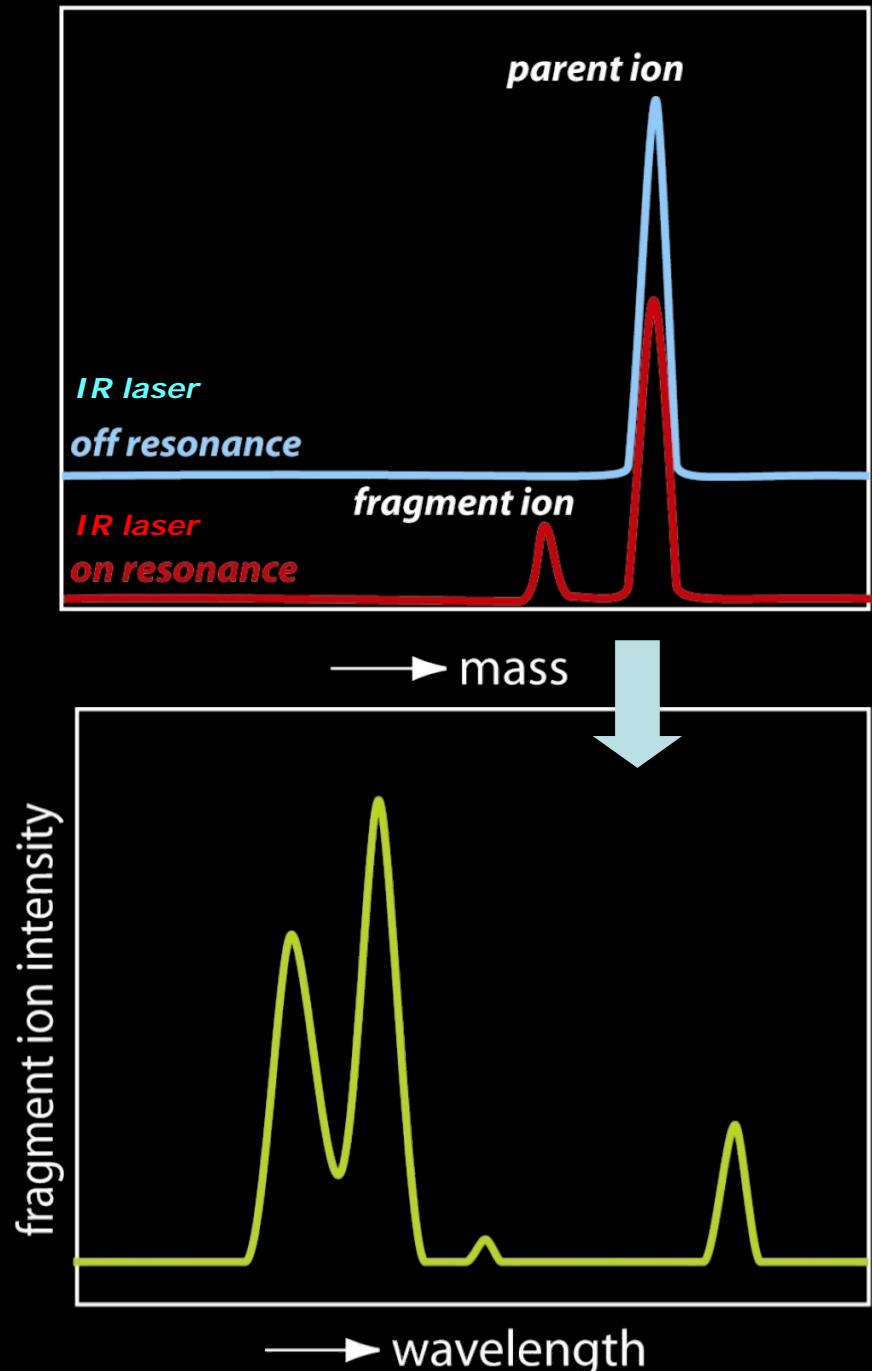
Can we record an infrared spectrum of the ions?



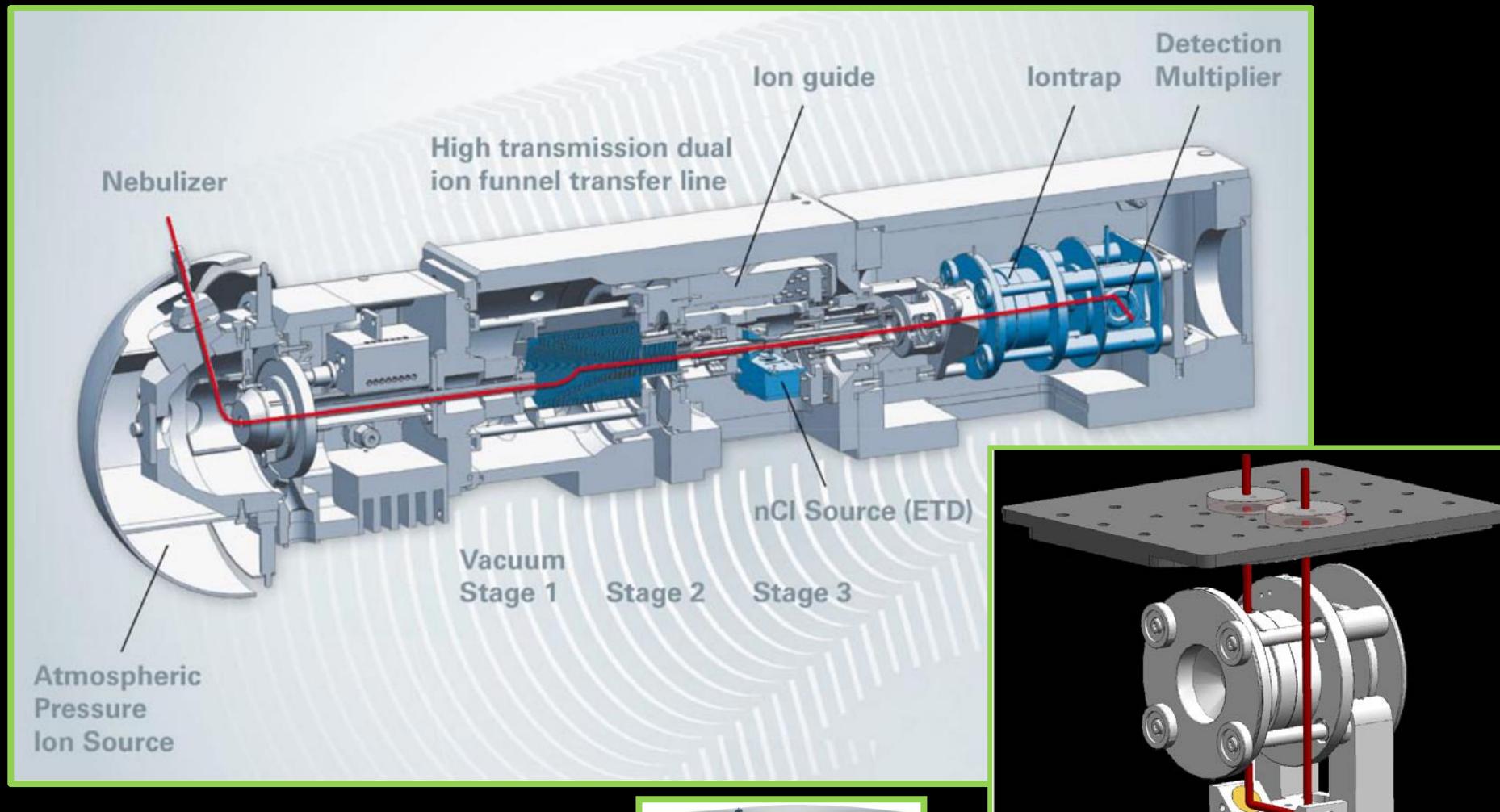
$$T(\lambda) = I_1/I_0 = e^{-\sigma(\lambda)nl}$$

$n_{\text{ion}} < 10^6 \text{ cm}^{-3}$

$< 10^{-12} \text{ mbar}$



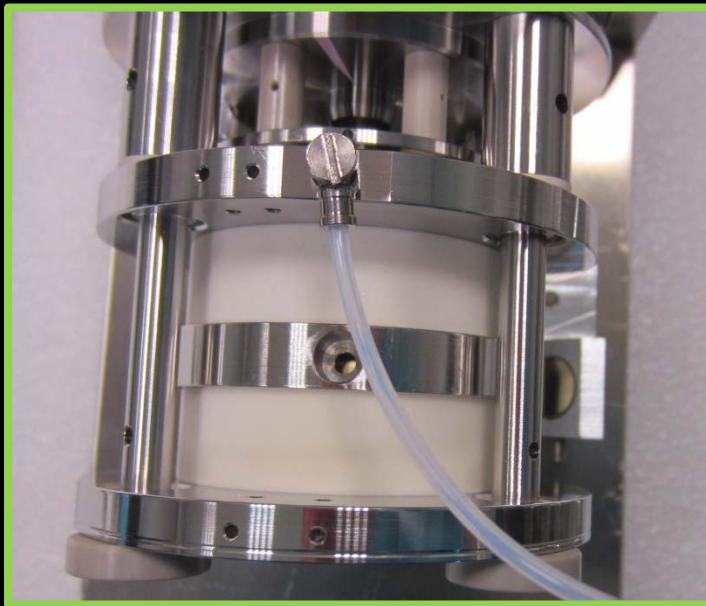
Experimental: modified Bruker Amazon Speed ETD



Thanks Christoph Gebhardt et al.
at Bruker!



Experimental: modified Bruker Amazon Speed ETD



Application to biomarker discovery in metabolomics

264 known
isomers

Found 264 results

Search term: MF = 'C_{8}H_{8}O_{4}'

ChemSpider Search and share chemistry

Simple Structure Advanced History 1 2 3 4

ID	Structure	Molecular Formula	Molecular Weight
8155 			
532 			
15663			
12093			

Search Results for metabolite

Searching metabolite for C8H8O4 returned 13 results.

Did you mean c4h8o4
Displaying all 13 metabolites

Filter by metabolite status:
 Detected and quantified Detected but not quantified Expected but not quantified

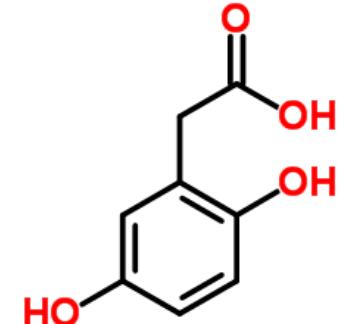
Filter by biofluid:
 Other Fluids Saliva Cerebrospinal Fluid Urine Blood

HMDB33129 3-Acetyl-4-hydroxy-6-methyl-2H-pyran-2-one
771-03-9

HMDB59713 3-Methoxysalicylic acid
2-hydroxy-3-methoxybenzoic acid

Example: homogentisic acid

13 known
metabolites



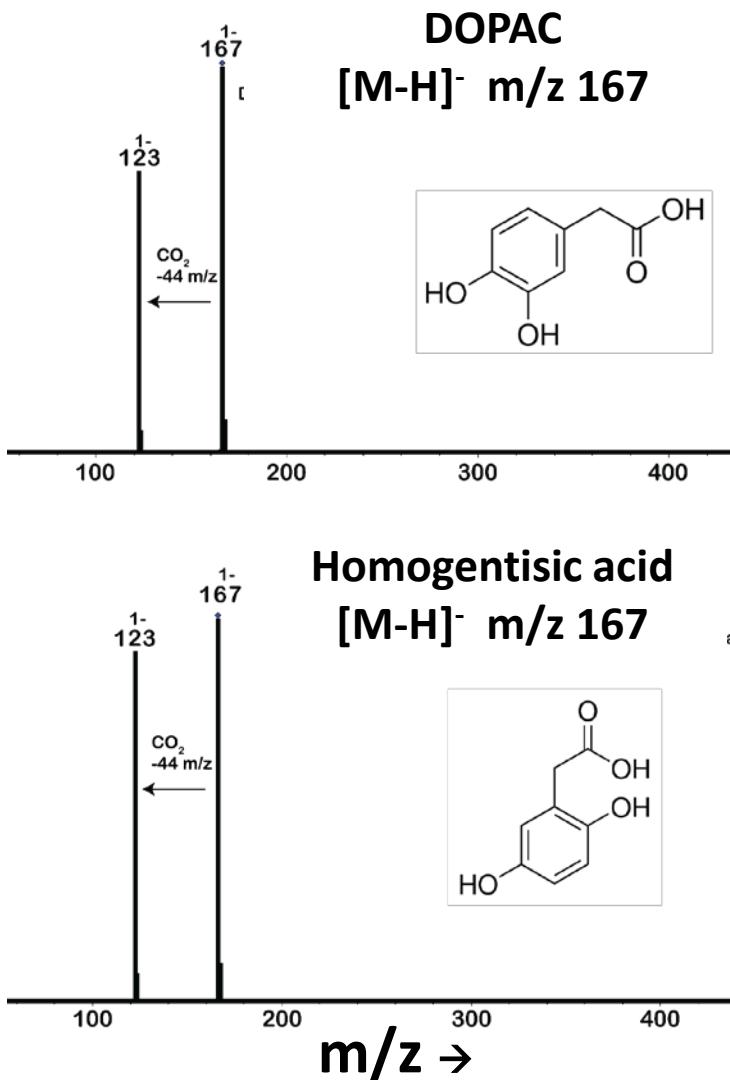
C8H8O4 m168



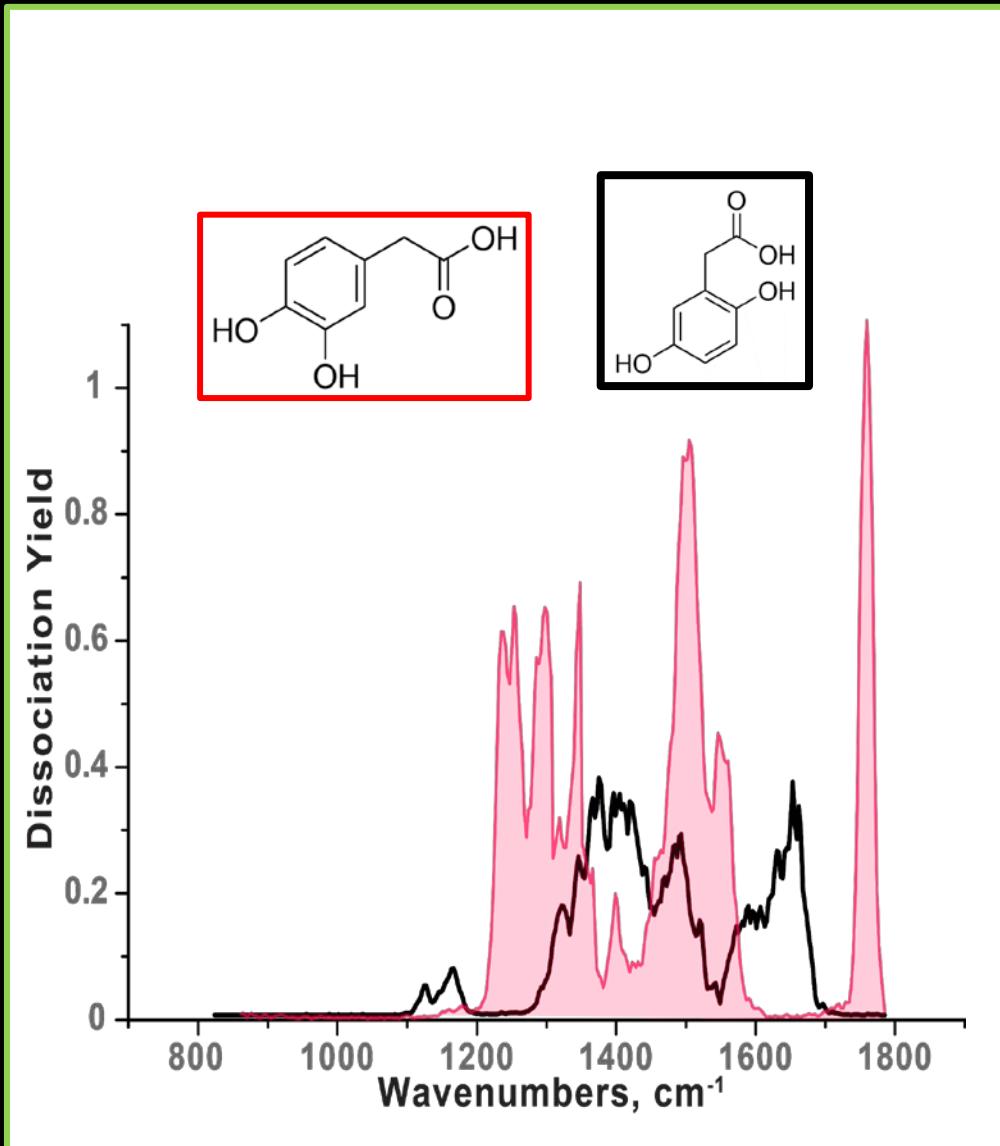
Collaboration with
Translational Metabolic
Laboratory at RU MC

Example: homogentisic acid

Tandem MS



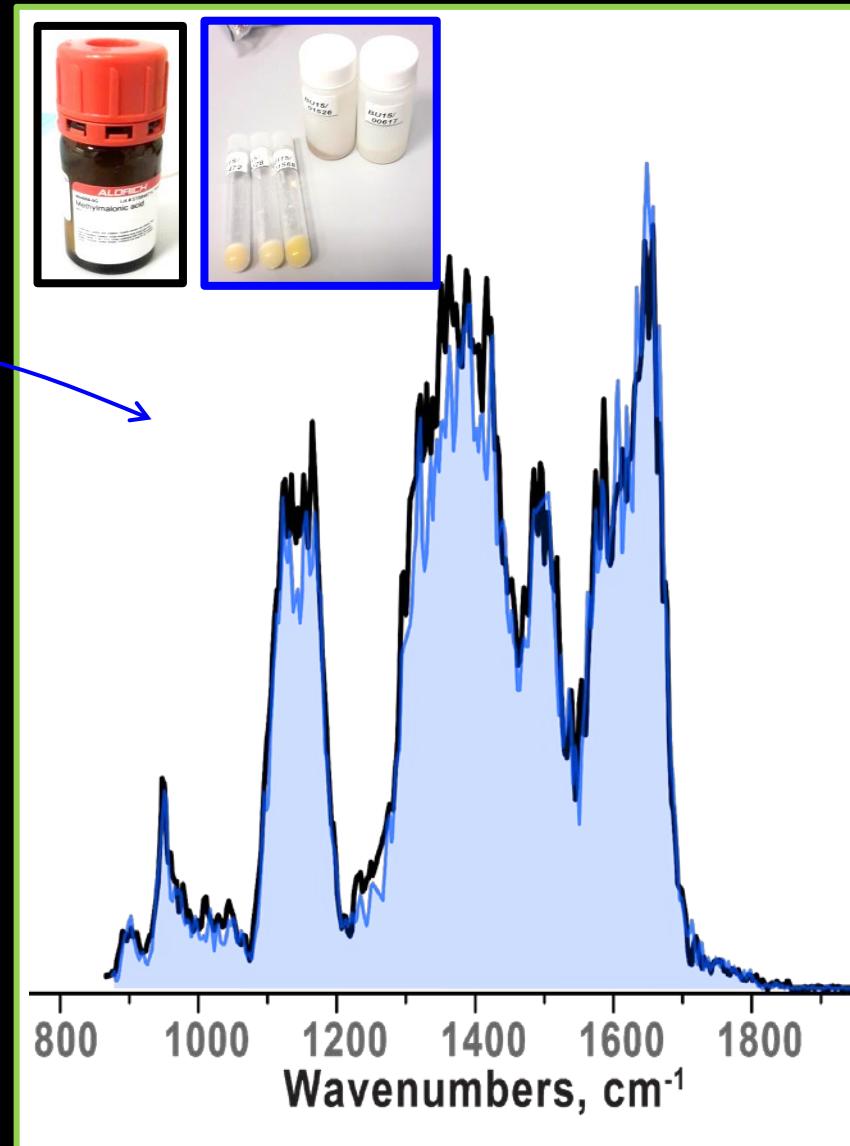
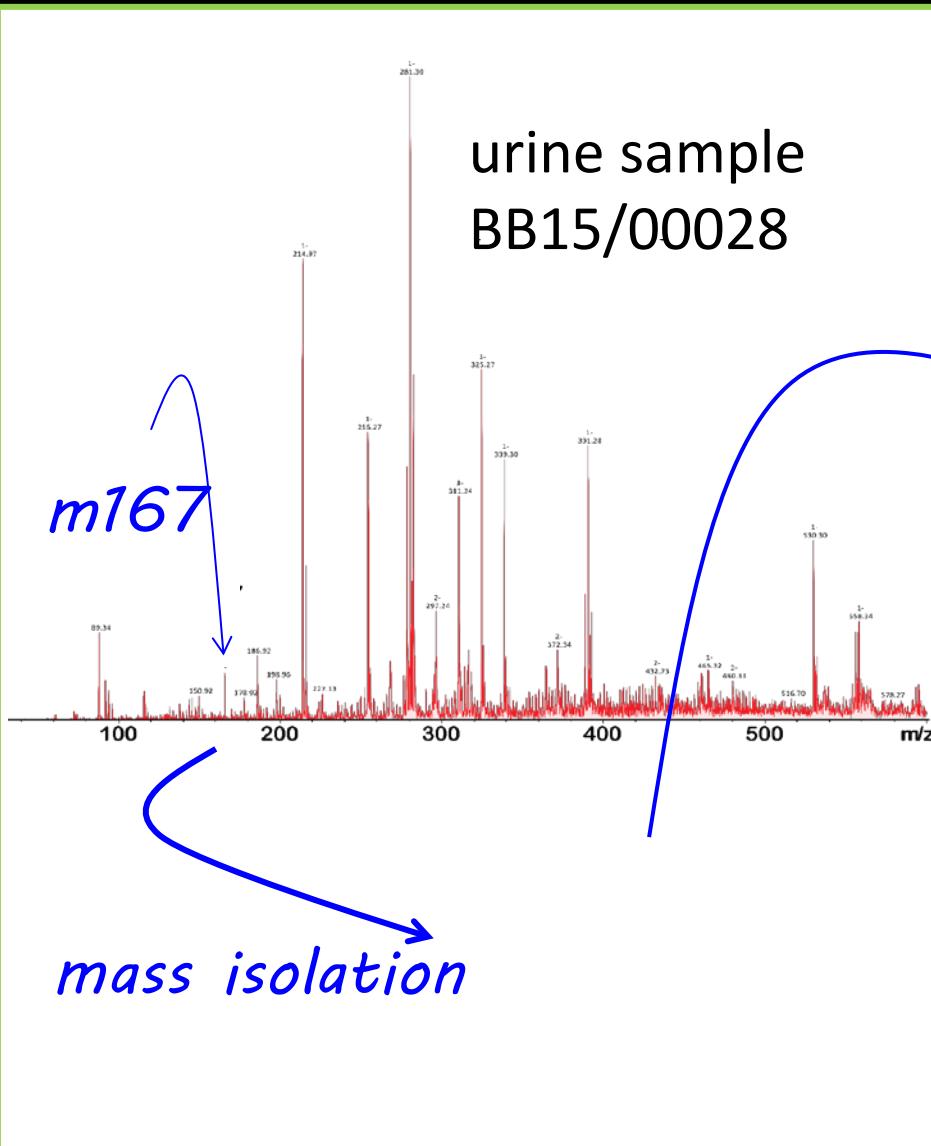
IR ion spectroscopy



Example: homogentisic acid

in a complex biological matrix

IR ion spectroscopy



Identification Inborn Errors of Metabolism

Collaboration with Translational Metabolic Laboratory

nature
genetics

ARTICLES

NANS-mediated synthesis of sialic acid is required for brain and skeletal development

Clara D M van Karnebeek^{1,2,34}, Luis Bonafe^{3,28}, Xiao-Yan Wen^{1,5,28}, Maja Tarallo-Graovac^{2,8}, Sara Balzano⁹, Béryl Royer-Bertrand^{3,7}, Angel Ashikov⁹, Livia Garavelli⁹, Isabella Mammì¹⁹, Licia Turrolla¹¹, Catherine Breen¹², Diana Iannuzzelli¹³, Valeria Coviello¹⁴, Philipp Heine¹⁵, Gen Nohimana¹⁶, Shoko Uchikawa¹⁷, Ryoko Yamashita¹⁸, Xavier Amiel¹⁹, Philippe Henain²⁰, Genoveffa Pichler²¹, Giovanna Sartori²², Jacob Boenigk²³, Ruth Harshman²⁴, Brian J Stevenson²⁵, Enrico Girardi²⁶, Giulio Superti-Furga^{2,21}, Tamirr Devan²⁷, Alissa Colbride²⁸, Jessie Halperin²⁸, Colin J Ross^{1,2,8}, Margot I Van Allen⁶, Andrea Rossi²², Udo F Engelke²³, Leo A J Kuijtemans²³, Ed van der Heet²³, Herma Renkens²¹, Arjan de Beuwer²³, Karin Huijbregts²³, Thorben Heiss²³, Thomas Boltje²³, Wyeth W Wasserman^{2,6}, Carlo Rivolta⁹, Sheila Unger²⁸, Dirk J Leefebur^{3,23}, Ron A Wevers^{23,29} & Andrea Superti-Furga^{3,27,29}



Radboudumc
university medical center

Next Generation Metabolic Screening Cerebrospinal fluid (CSF)

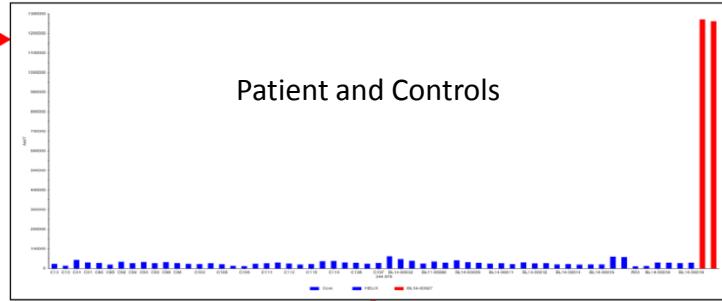
a i-resolution QTOF results

RI	Mass	RT
1	244.07902	0.73
2	204.08663	0.72
3	123.05511	1.38
4	219.11006	5.88
5	246.10811	0.78
6	168.06524	1.20
7	137.08057	0.76
8	138.05458	0.71
9	316.21164	4.78
10	99.04171	1.06
11	195.11299	4.80
12	221.01043	1.09
13	170.08089	1.74
14	220.97417	1.05
15	130.97859	1.07
16	429.31854	18.87
17	235.09380	5.77
18	206.10187	0.86
19	281.08261	1.10
20	327.10610	2.93

RI= position ranking intensity
Mass= measured mass
RT=retention time (min)

b

MS intensity plot of m/z 244.07902 in CSF of controls (blue) and the patient with NANS deficiency (red).



c

HMDB MS search results for 244.07902 m/z:
multiple compounds possible

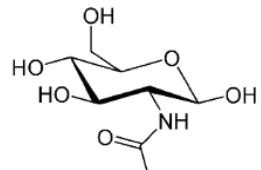
Compound	Name	Adduct	Adduct MW (Da)	Compound MW (Da)	Delta
HMDB01129	N-Acetylmannosamine	M+Na	244.079155	221.089937217	0.000135
HMDB00212	N-Acetylgalactosamine	M+Na	244.079155	221.089937217	0.000135
HMDB00215	N-Acetylglucosamine	M+Na	244.079155	221.089937217	0.000135

Three database hits are indistinguishable by both CID MS/MS and LC retention time

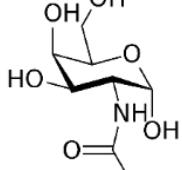
Identification Inborn Errors of Metabolism

Collaboration with Translational Metabolic Laboratory

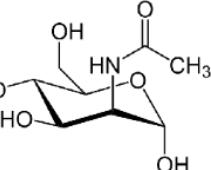
Possible database matches identified by metabolic screening



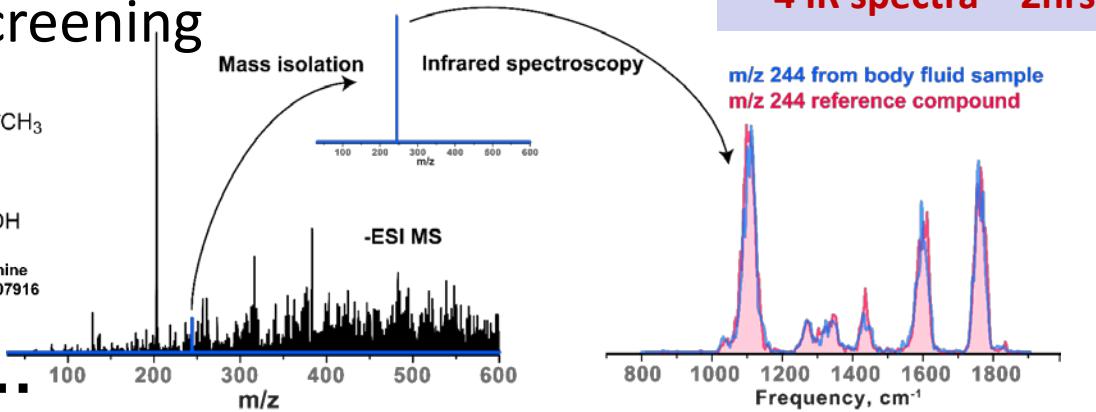
N-Acetylglucosamine
[M+Na]⁺ - m/z 244.07916



N-Acetylgalactosamine
[M+Na]⁺ - m/z 244.07916

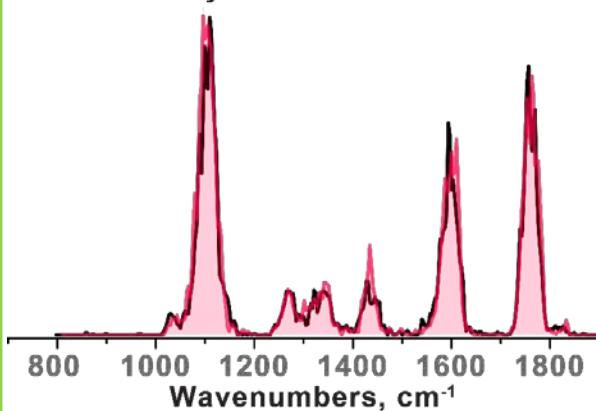


N-Acetylmannosamine
[M+Na]⁺ - m/z 244.07916



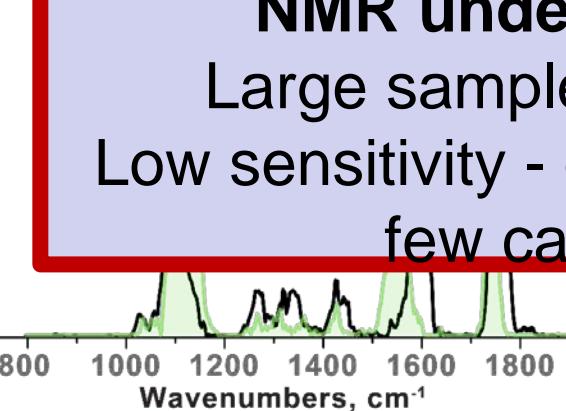
MS, MS/MS, LC, NMR...

— Sample VN021(Urine) - m/z 244
— N-acetylmannosamine



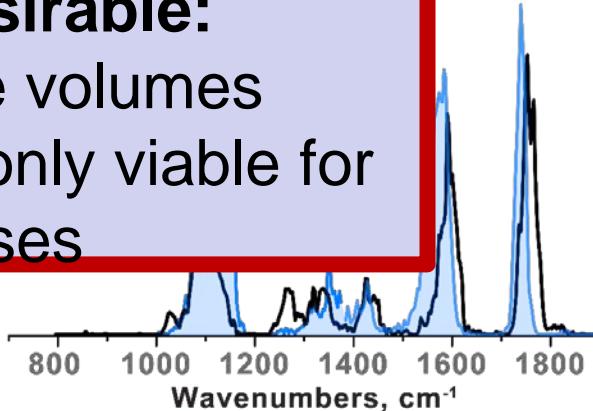
— Sample - VN021(Urine) - m/z 244

— N-acetylmannosamine



— Sample - VN021(Urine) - m/z 244

— N-acetylmannosamine



NMR undesirable:

Large sample volumes
Low sensitivity - only viable for
few cases

<10 microliters
blood/urine used!

4 IR spectra ~ 2hrs

IR multiple photon dissociation

IR photon energy << bond dissociation energy

Anharmonicity bottleneck

Manifestations of IRMPD

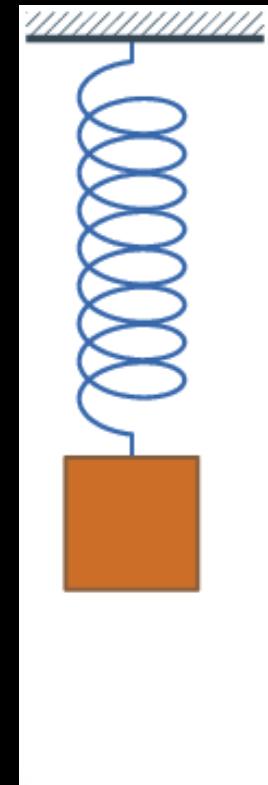
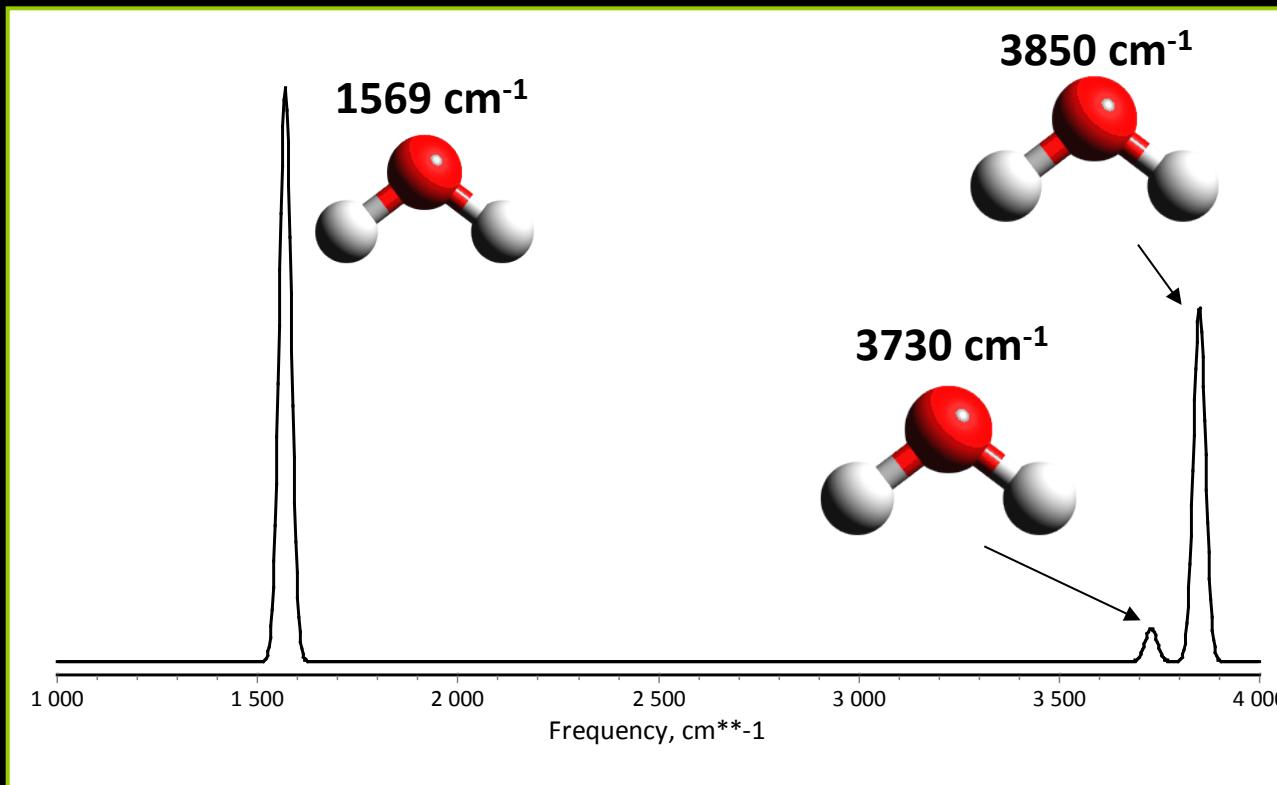
Vibrational structure of molecules

$3N - 6$ vibrational normal modes / frequencies

Complete orthogonal set

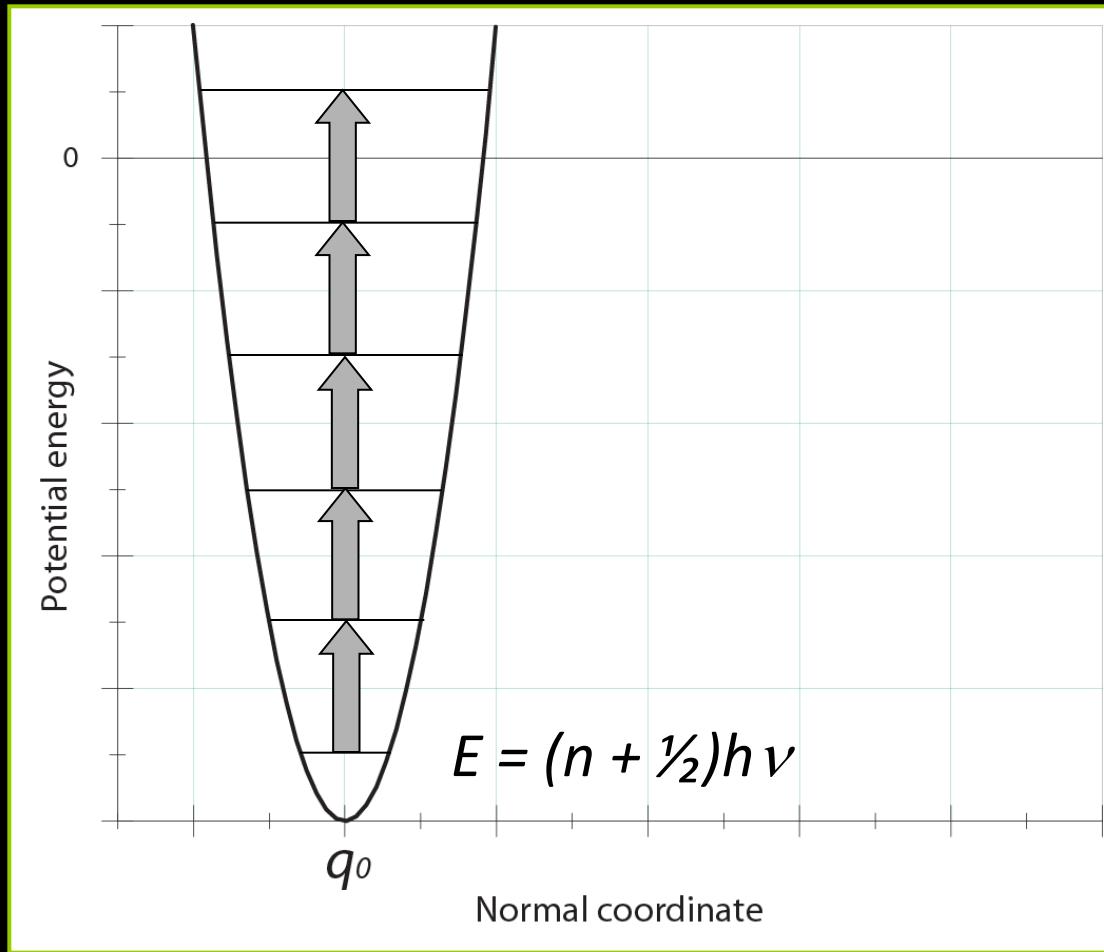
Vibrations are harmonic only approximately

$$F(z) = -kz$$



Vibrational structure of molecules

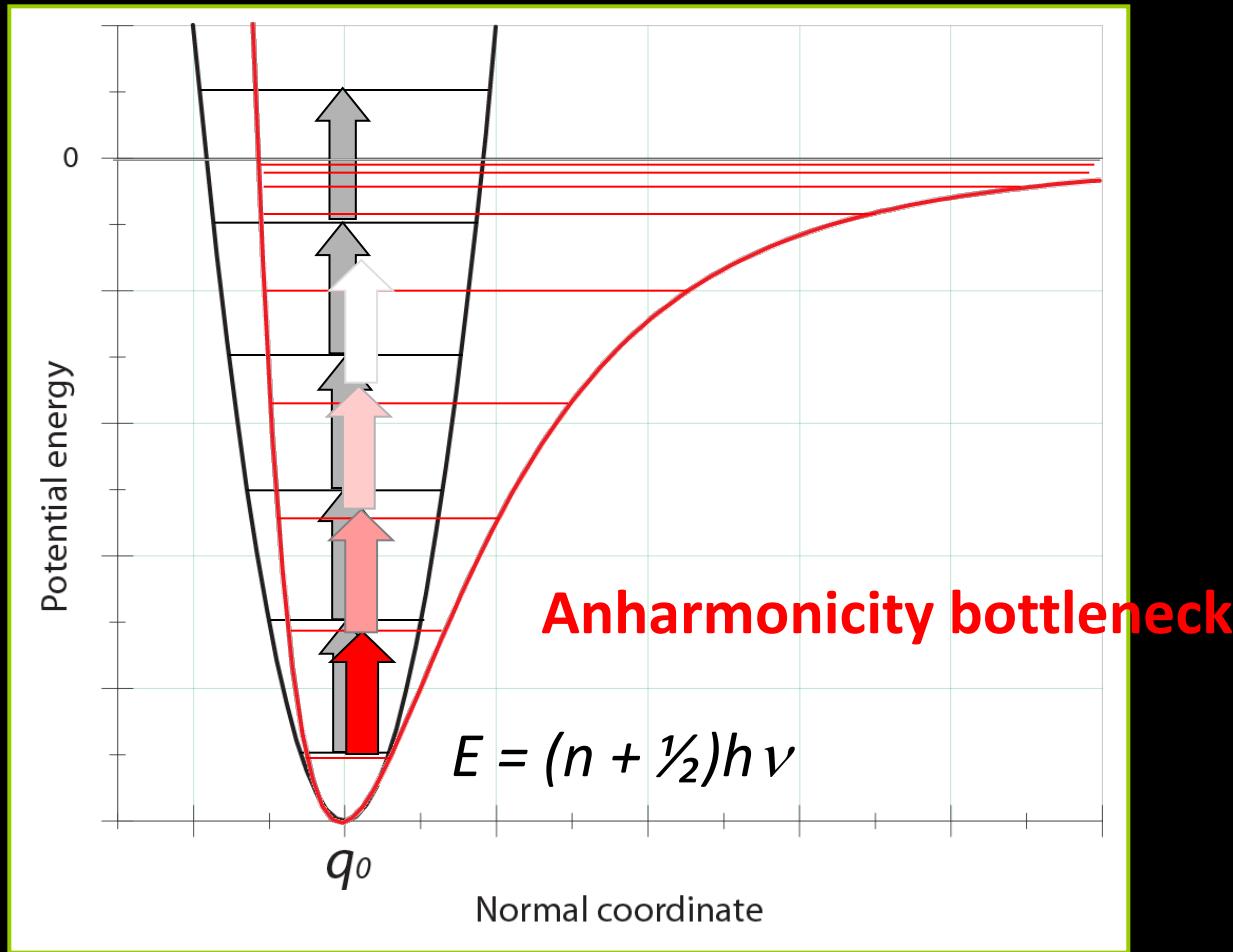
Harmonic potential → levels equidistant



Vibrational structure of molecules

Harmonic potential → levels equidistant

Anharmonic potential → levels converge to dissociation limit

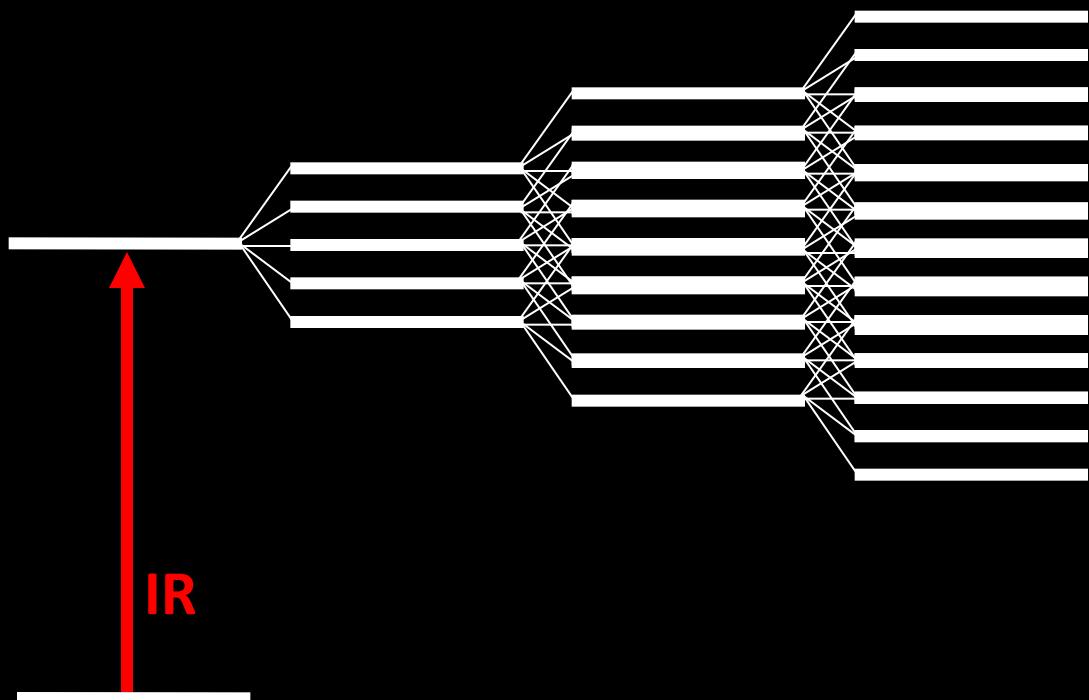


Vibrational structure of molecules

Vibrational levels coupled

Vibrational level density increases rapidly

Intramolecular Vibrational Redistribution (IVR)

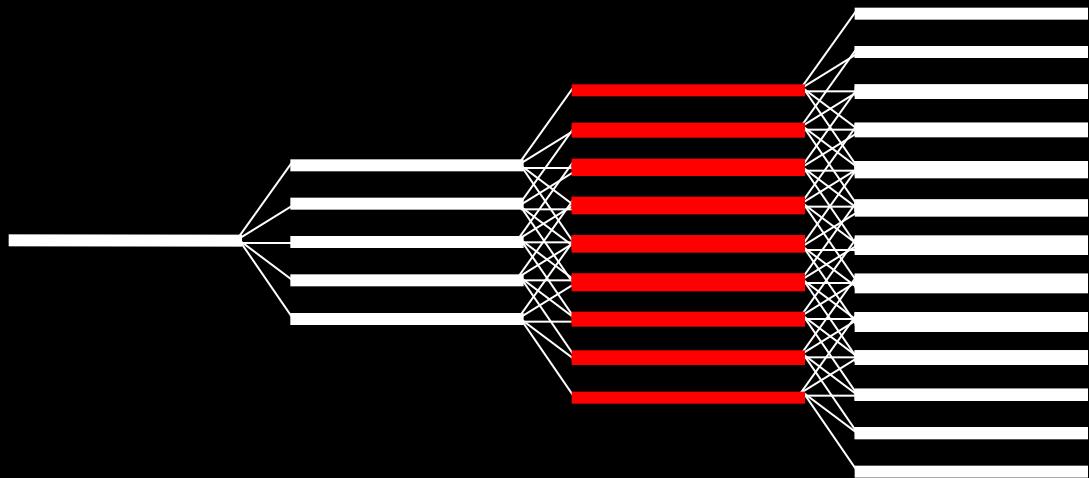


Vibrational structure of molecules

Vibrational levels coupled

Vibrational level density increases rapidly

Intramolecular Vibrational Redistribution (IVR)

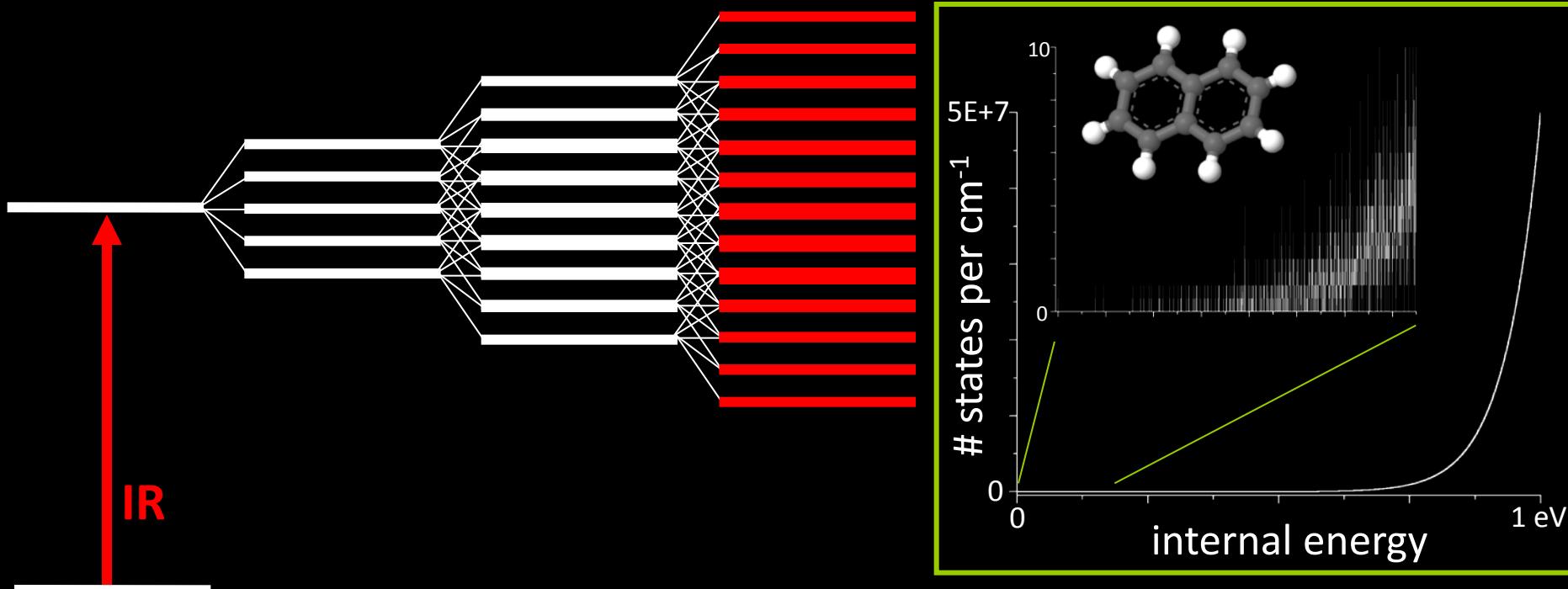


Vibrational structure of molecules

Vibrational levels coupled

Vibrational level density increases rapidly

Intramolecular Vibrational Redistribution (IVR)



Beyer Swinehart algorithm

Count # vibrational states per energy interval

$\text{nu}(i)$ i from 1 to $k=3N - 6$: *array containing the fundamental frequencies (as integers)*

$P(j)$ $j = 0$ to energy range of interest: *array to be filled up with # states per cm^{-1} interval. initialize as (1, 0, 0, 0, 0 ...)*

for $i = 1$ to k

 for $j = 1$ to 10 000 *calculate DoS up to 10 000 cm^{-1}*

$P(j) = P(j) + P(j - \text{nu}(i))$

 next j

next i

Example: $\text{nu}(1) = 3 \text{ cm}^{-1}$; $\text{nu}(2) = 4 \text{ cm}^{-1}$; $\text{nu}(3) = 5 \text{ cm}^{-1}$
 $P(j=0 - 24)$

init

(1,0)

nu=3

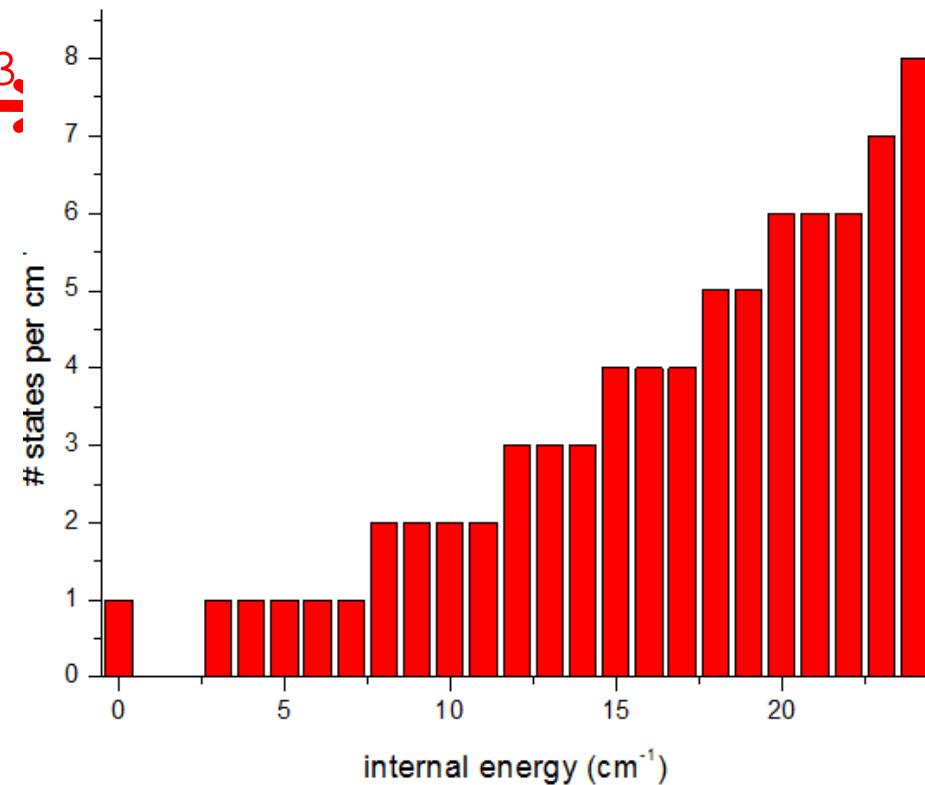
(1,0,0,1,0,0,1,0,0,1,0,0,1,0,0,1,0,0,1,0,0,1,0,0,1)

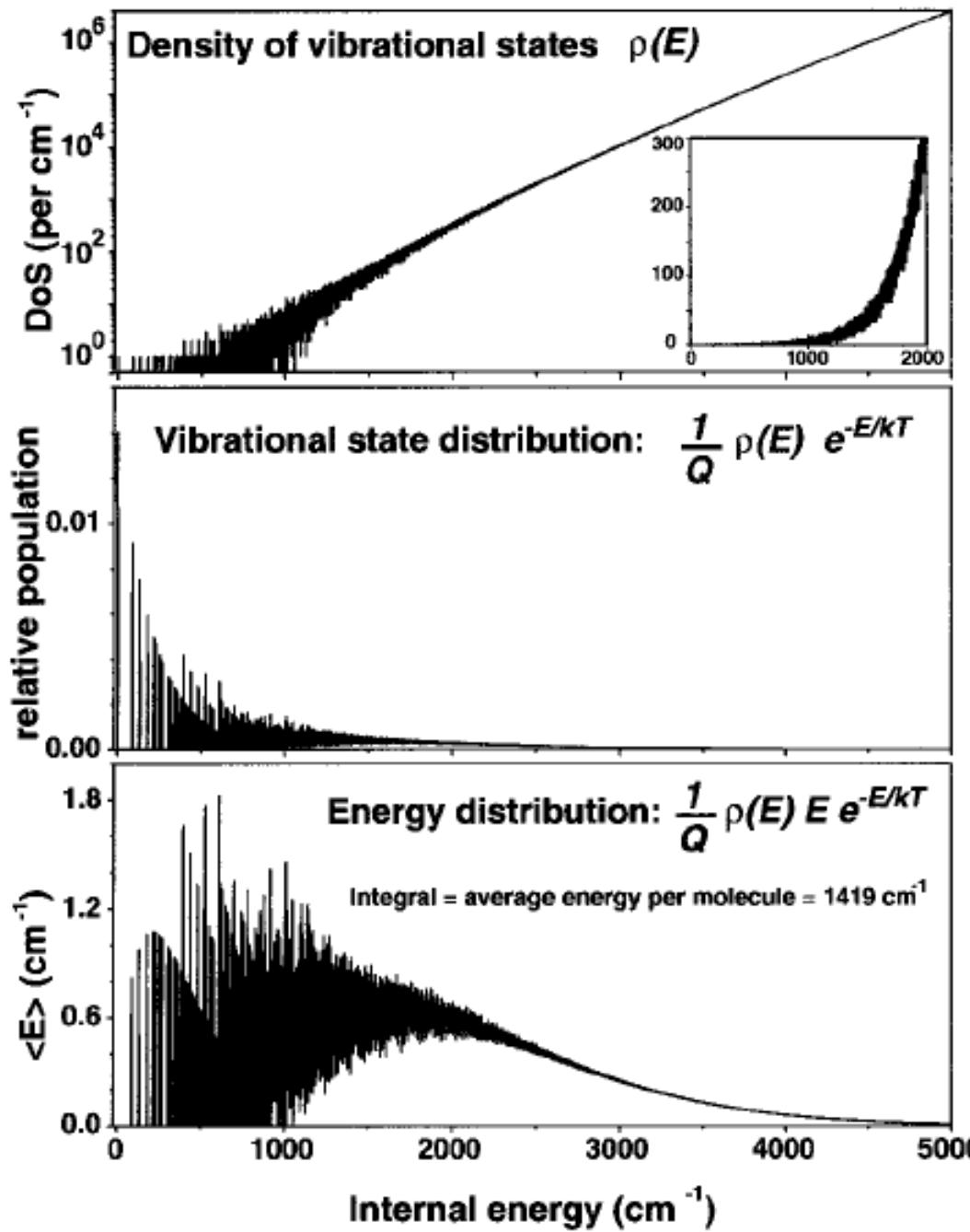
nu=4

(1,0,0,1,1,0,1,1,1,1,1,1,2,1,1,2,2,2,1,2,2,2,2,2,2,3)

nu=5

(1,0,0,1,1,1,1,1,2,2,2,2,2,3,3,3)



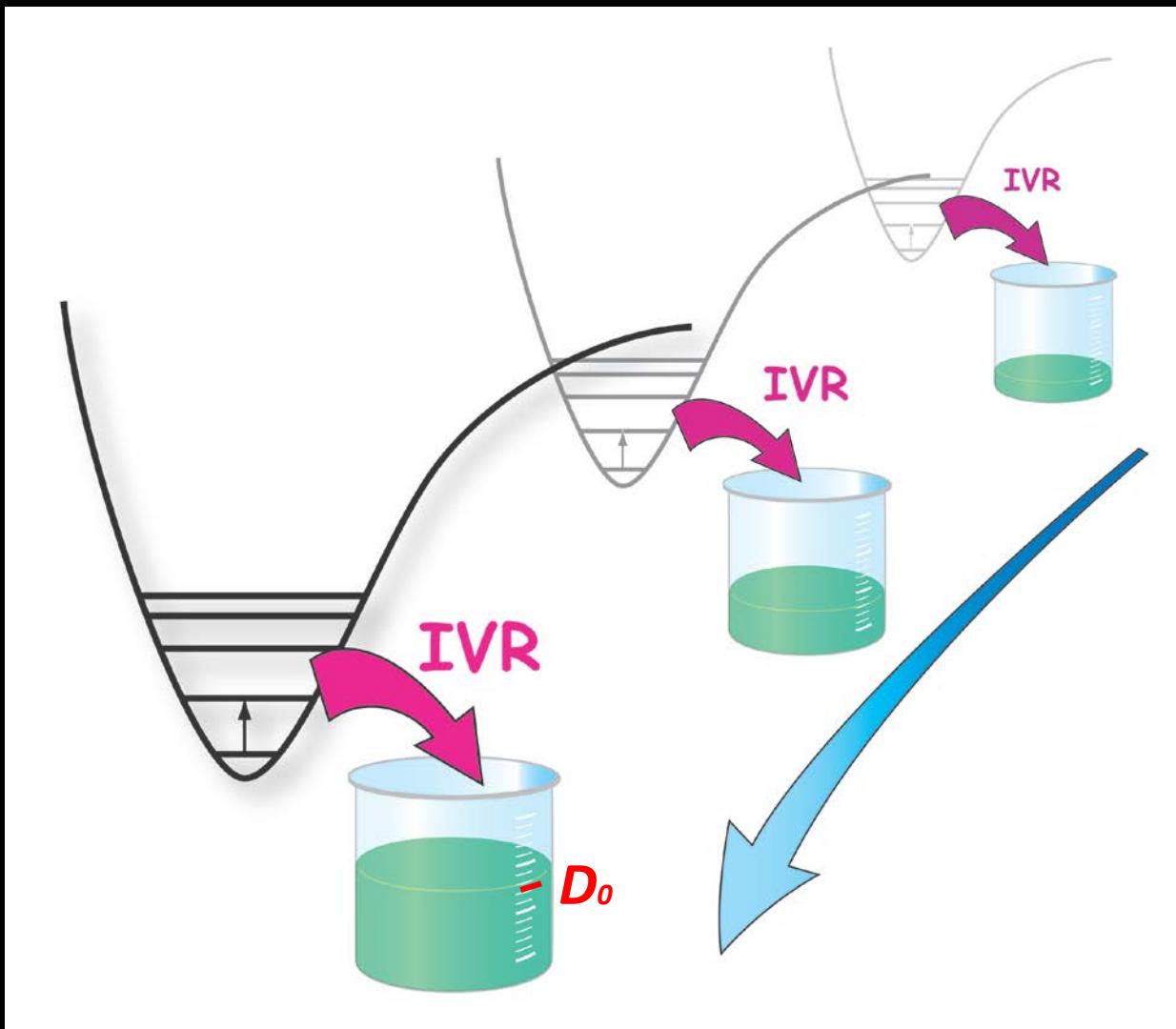


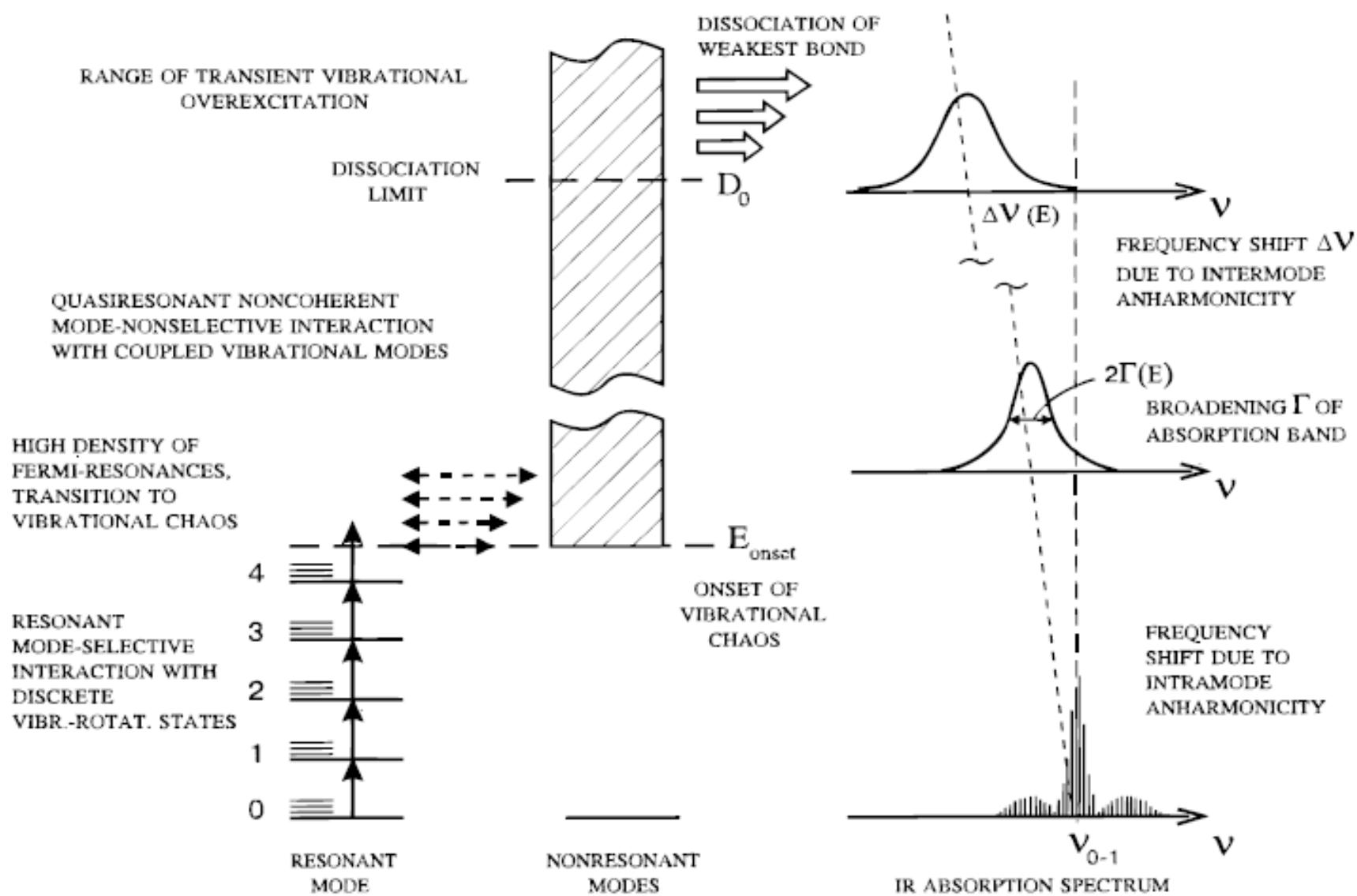
$$Q = \sum_{E=0}^{\max} \rho(E) e^{-E/kT}$$

partition function

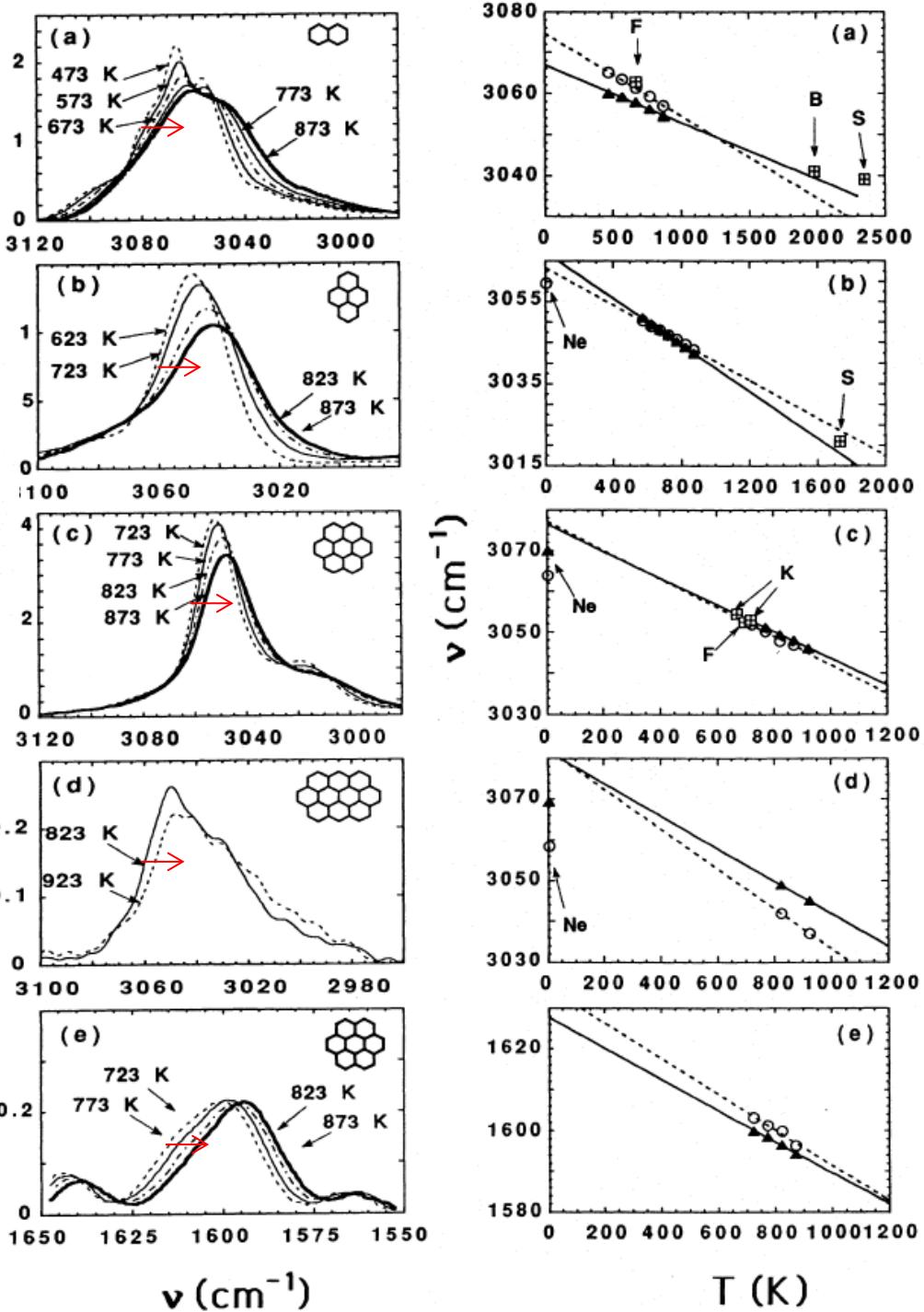
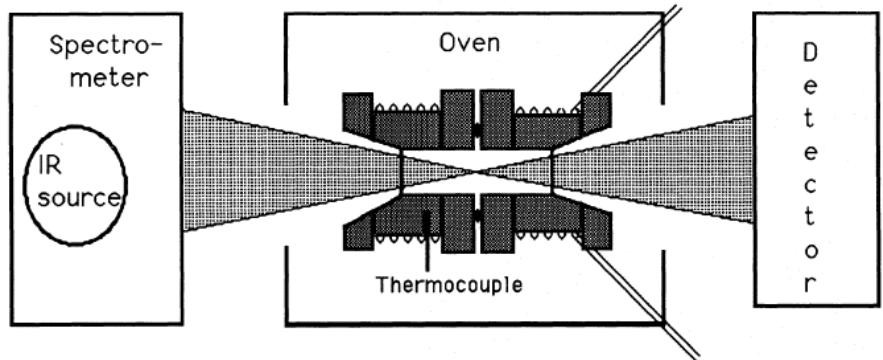
IVR mediated multiple photon excitation

- Anharmonicity bottleneck avoided
- Moderate red-shift of transition





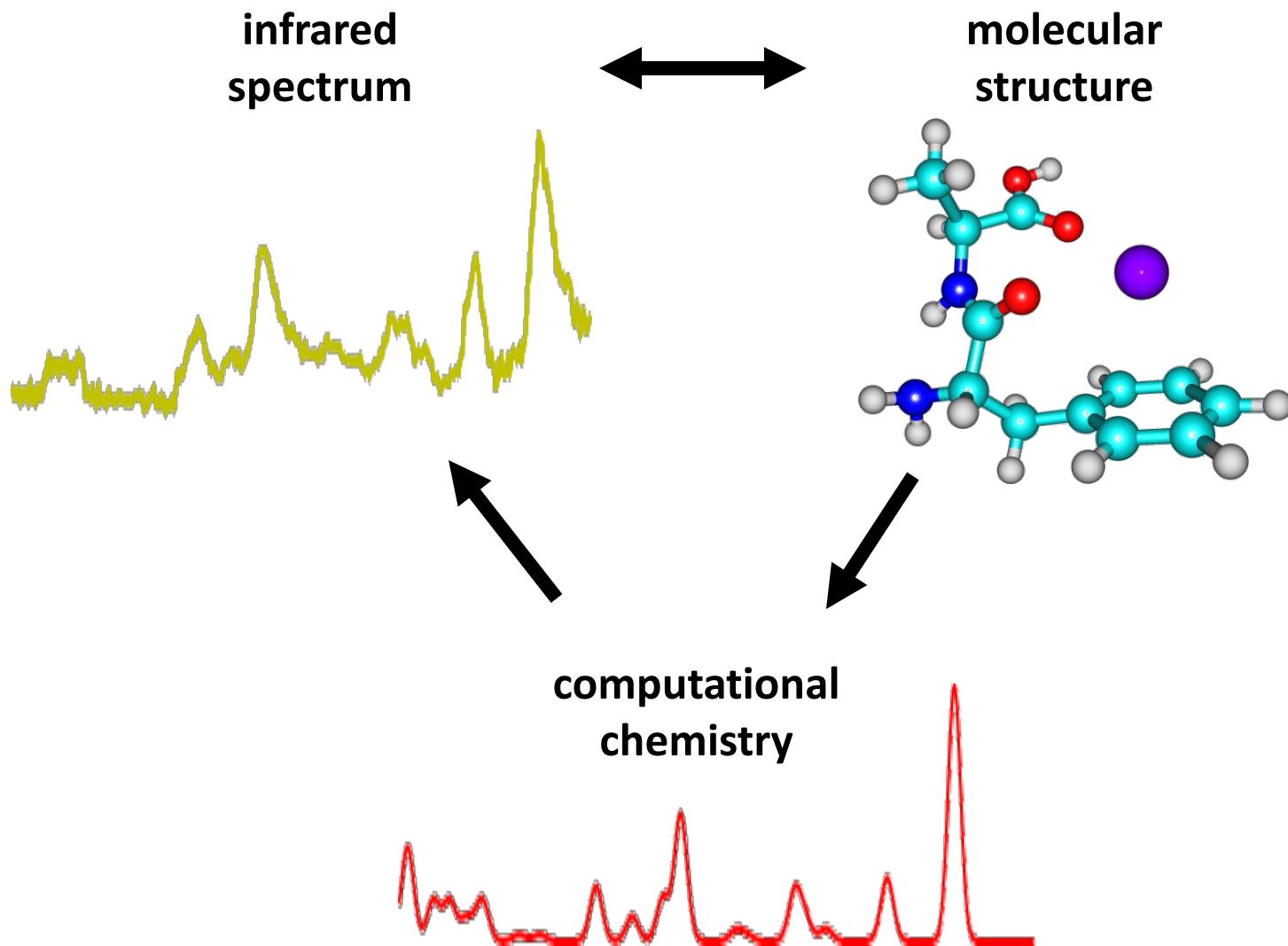
IR spectra as function of T



Red shift with increasing T due to anharmonicity

Infrared spectroscopy – molecular structure

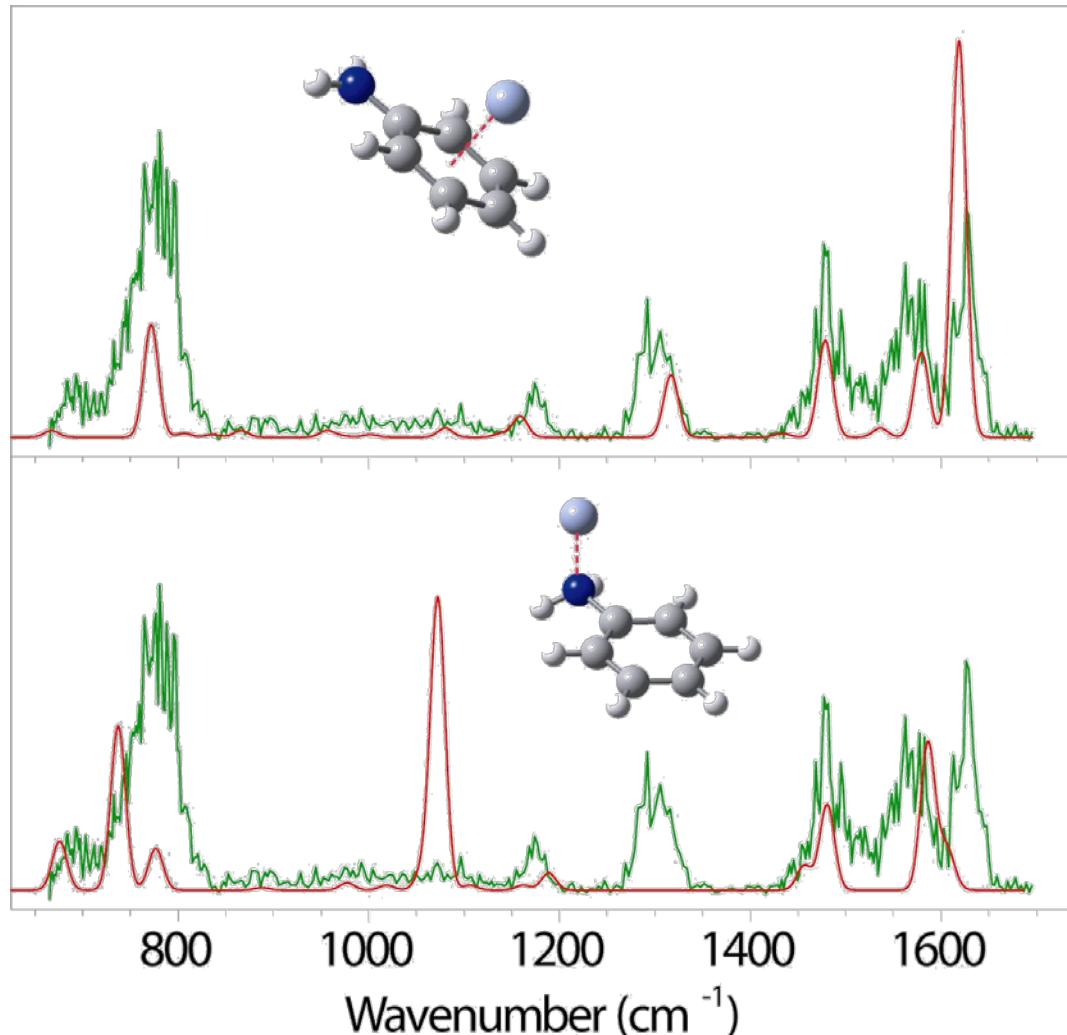
characteristic vibrations



$\text{Cr}^+\text{aniline}$: ring or nitrogen bound ?

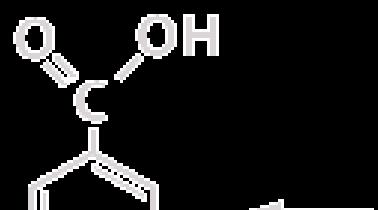
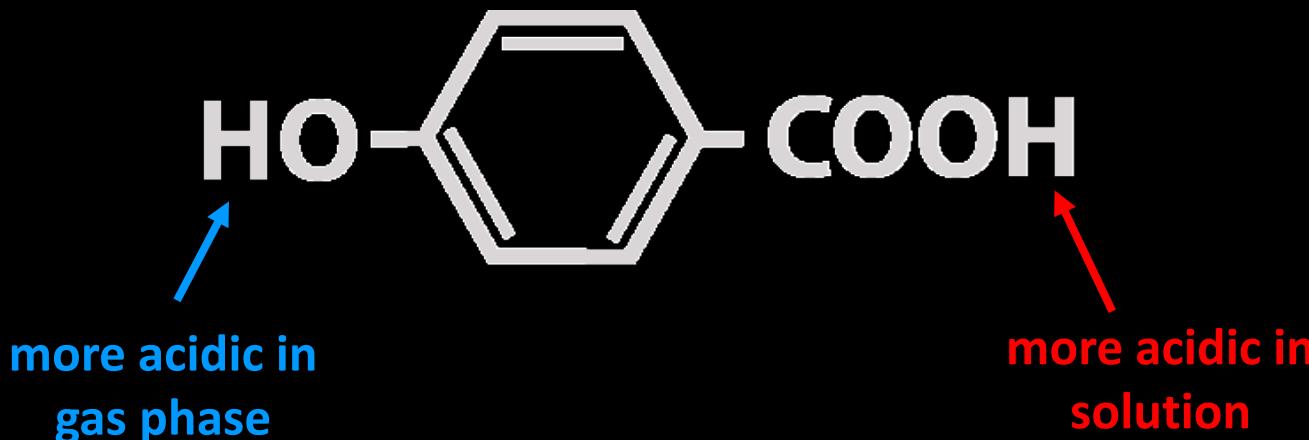
B3LYP: N-bound ($\Delta E = 7.2 \text{ kJ/mol}$)

MP1PW91: ring-bound ($\Delta E = 7.0 \text{ kJ/mol}$)

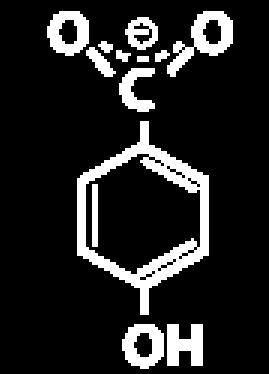
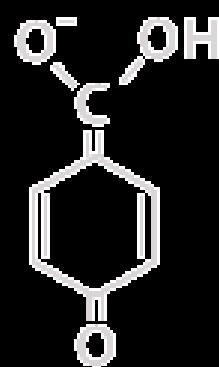


Site of deprotonation

para-hydroxy benzoic acid

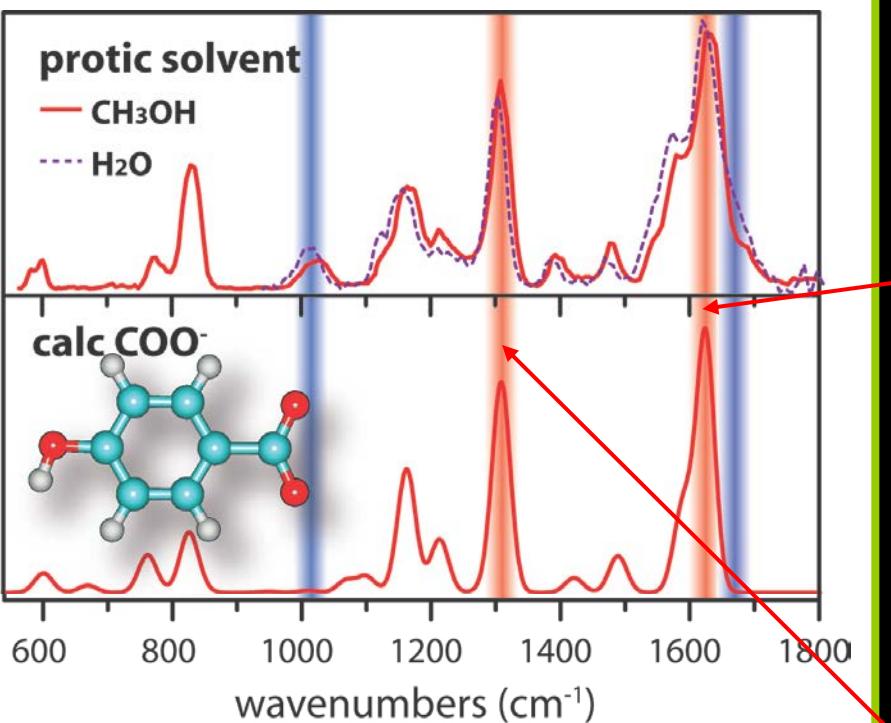


phenoxide

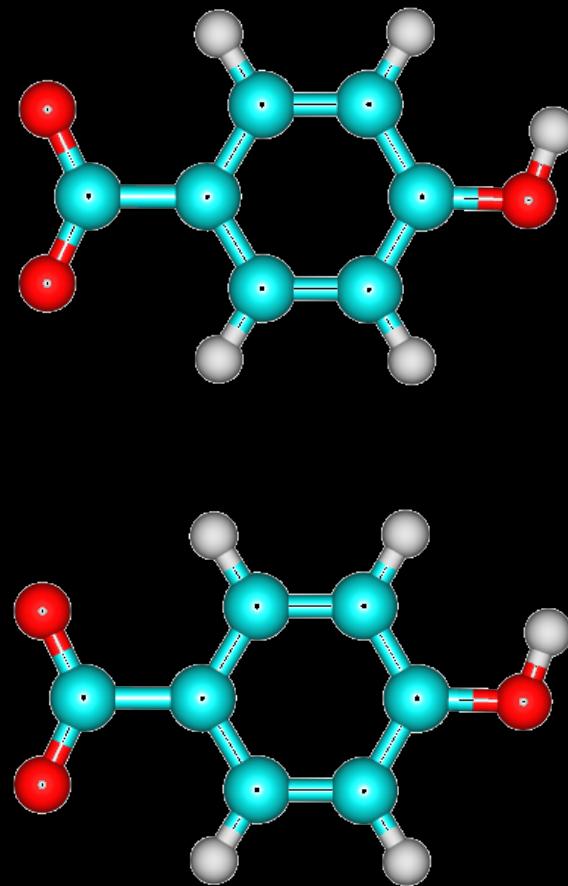


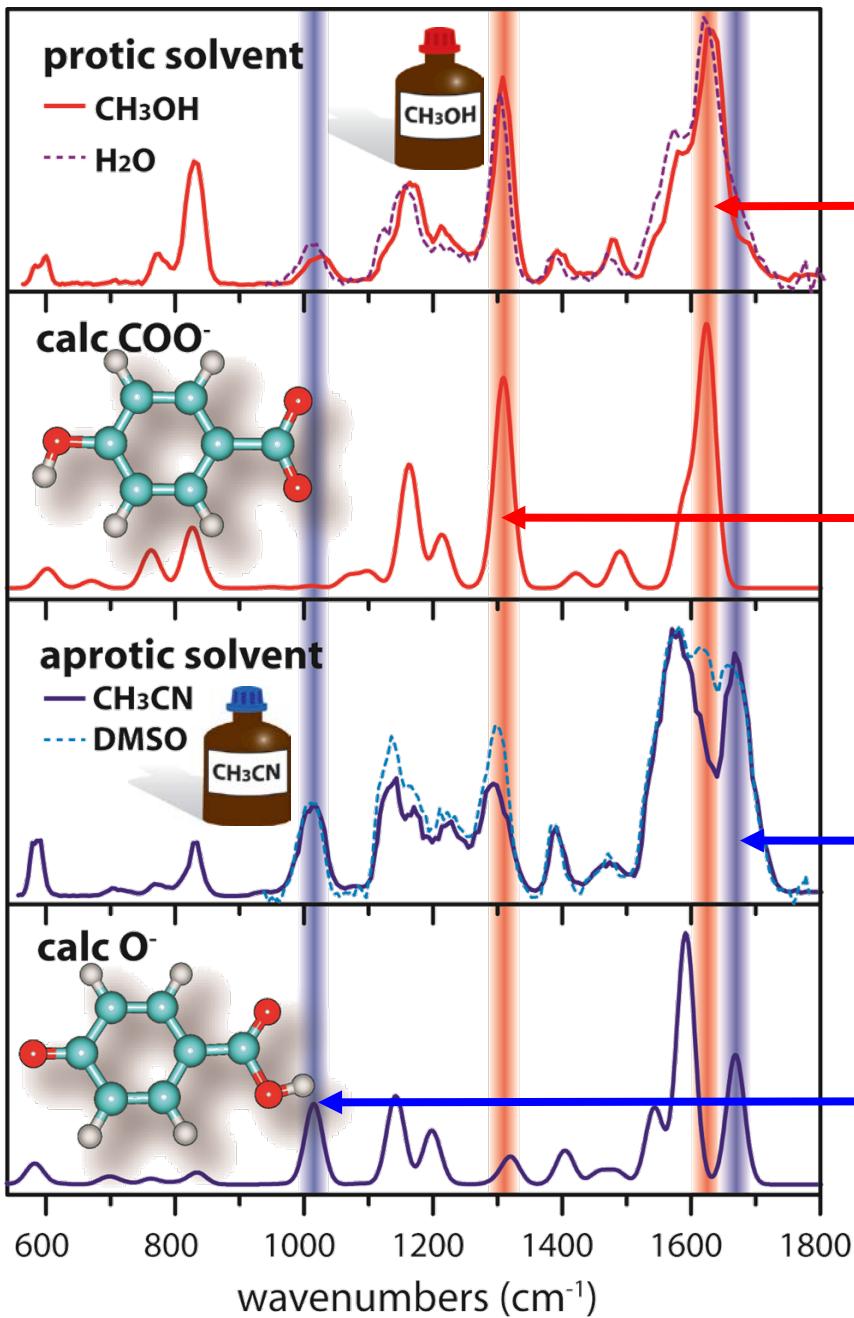
carboxylate

-33 kJ/mol

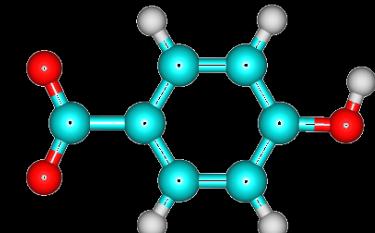


Site of deprotonation

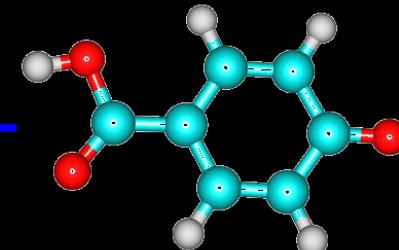
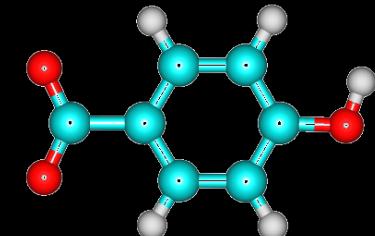




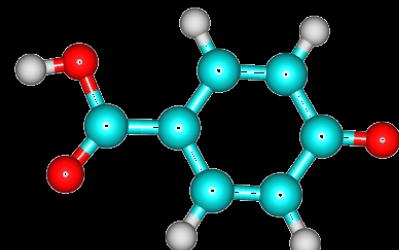
Site of deprotonation



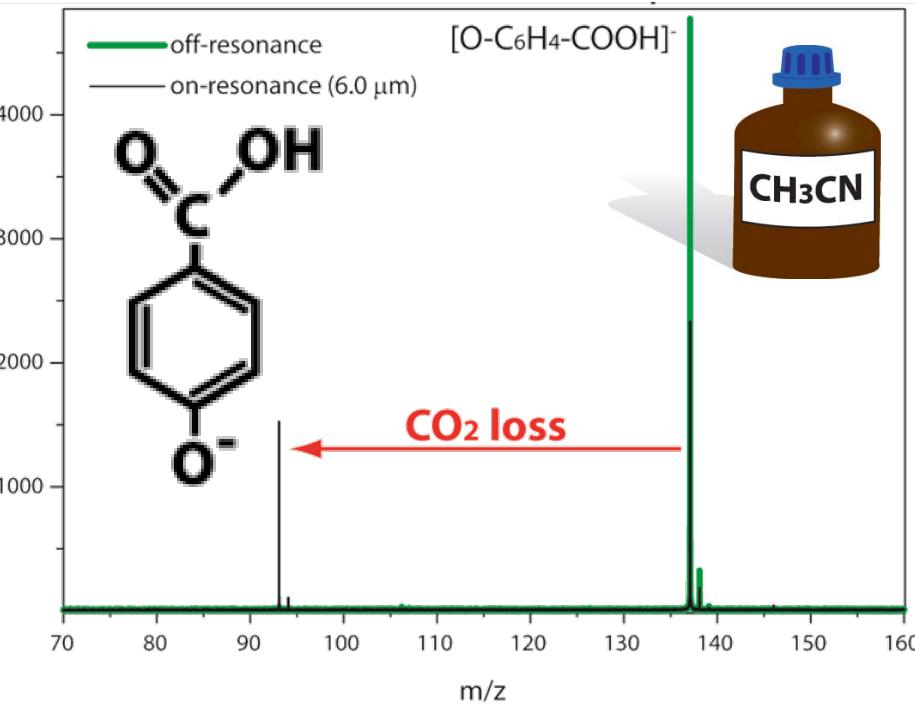
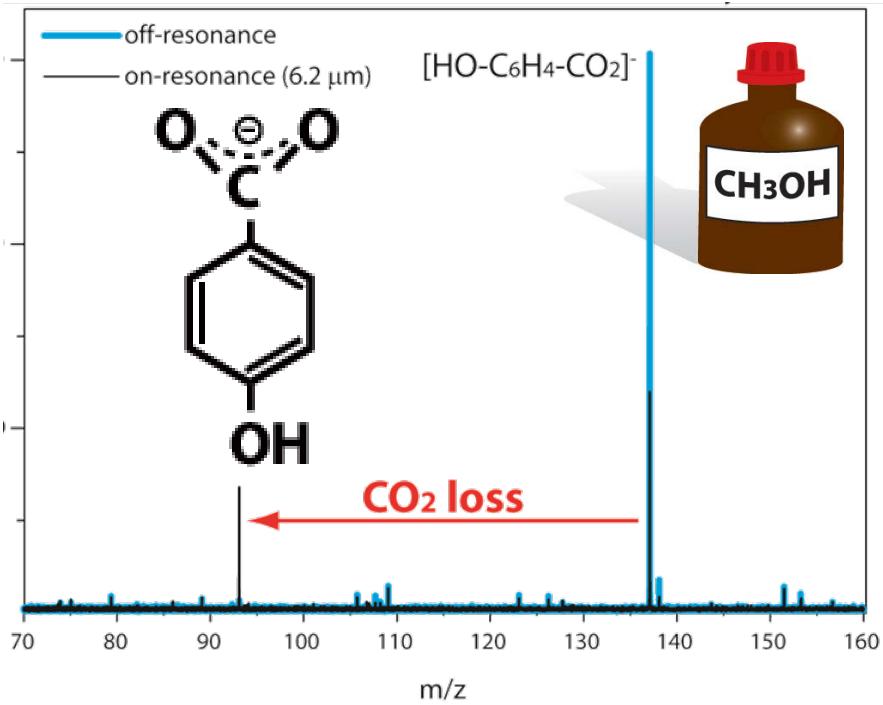
carboxylate



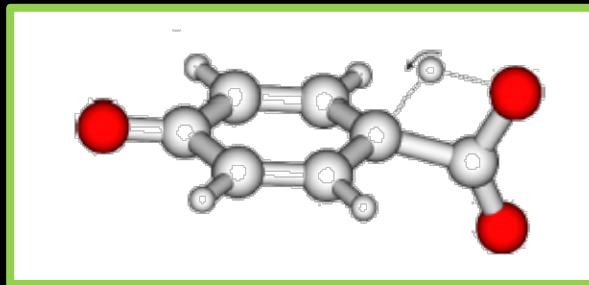
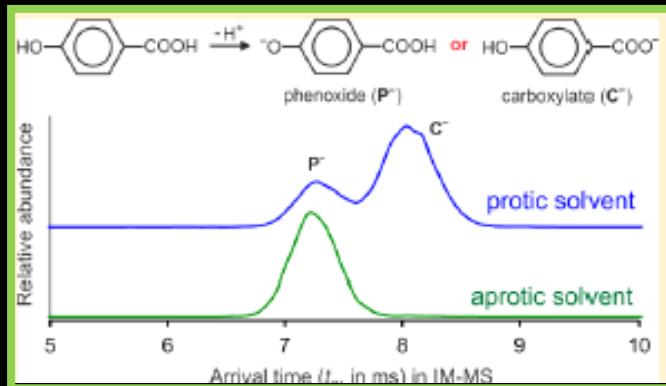
phenoxide



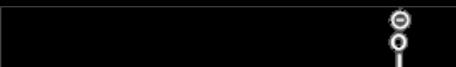
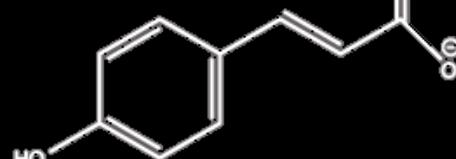
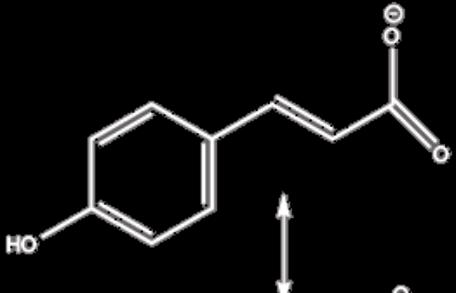
Mass spectra for *p*-HBA



Tandem MS can be deceiving in structure determination !

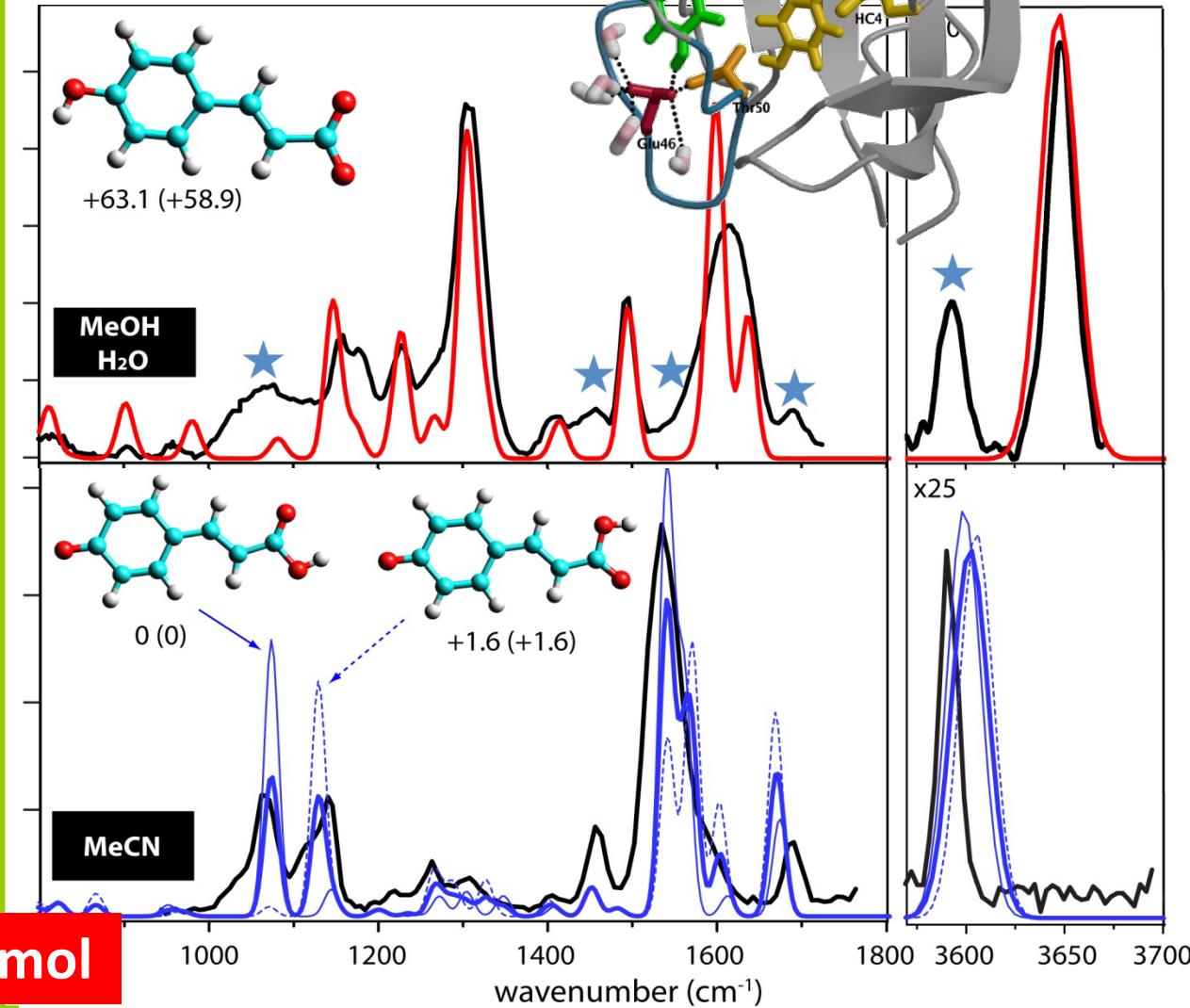


Deprotonation site: chromophore of PYP

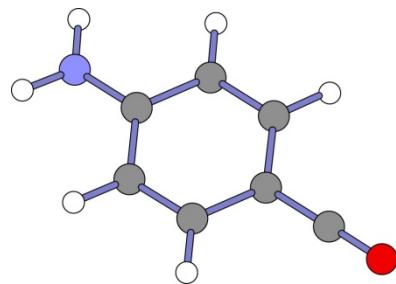


-60 kJ/mol

JPC Lett 2012, 3, 2259

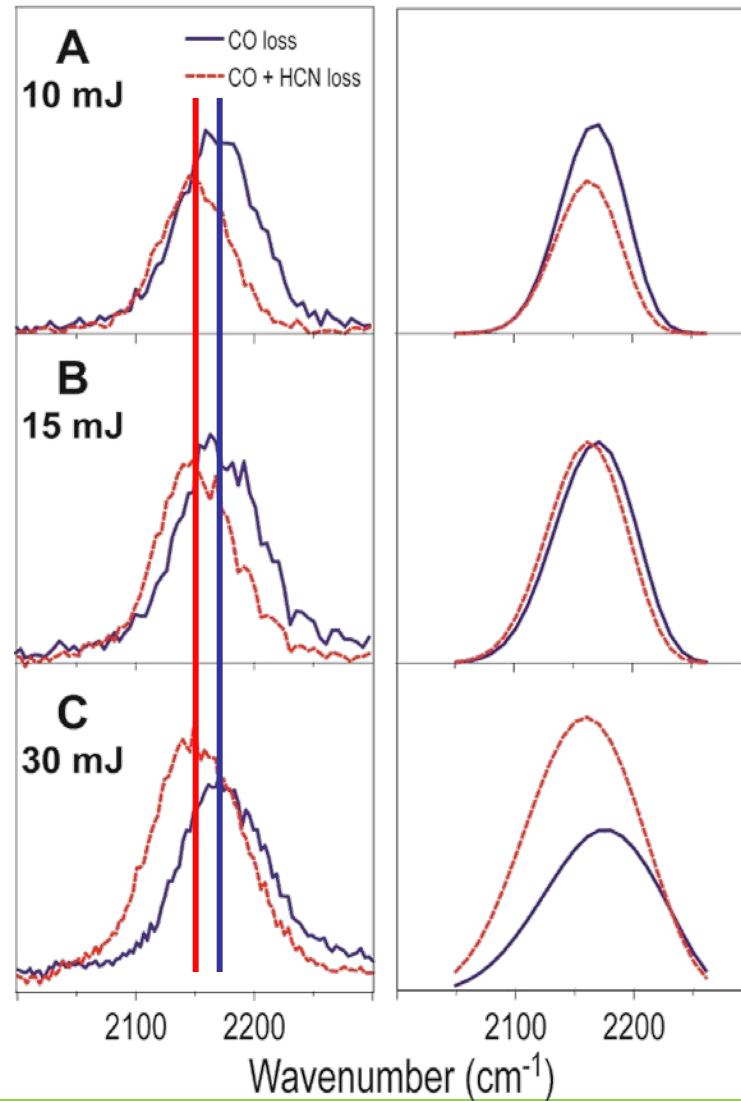
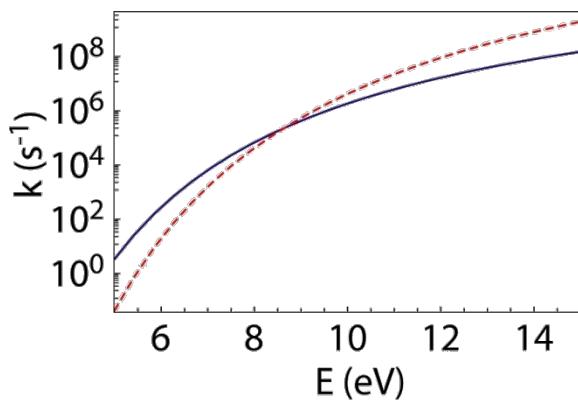


Exit channel dependent IRMPD spectra



para-amino benzoyl ion

CO loss 3.5 eV
CO+HCN loss 4.9 eV

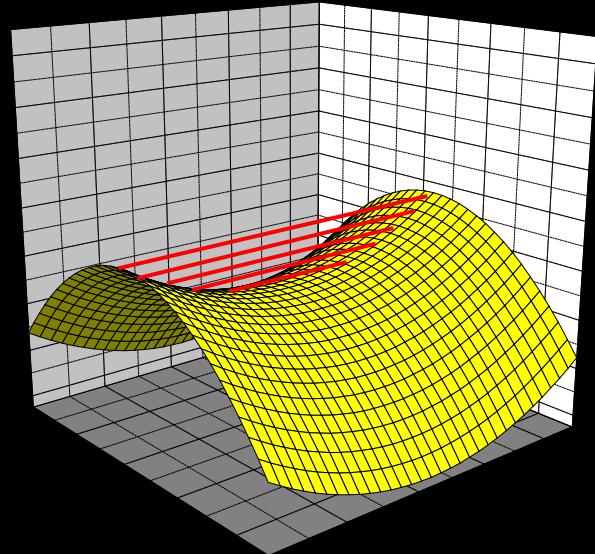


Unimolecular dissociation – transition state theory

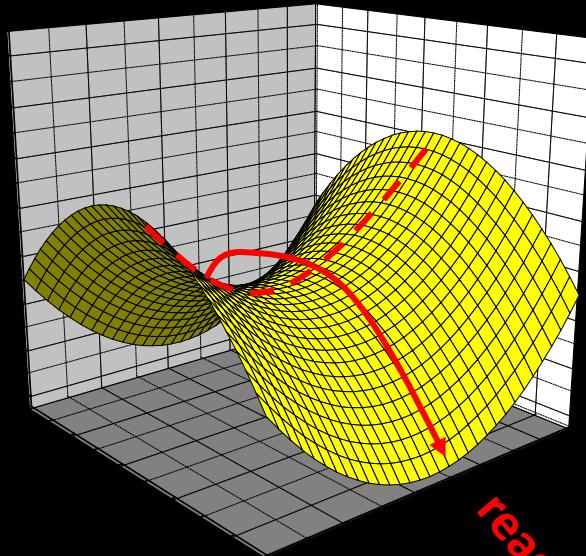


Unimolecular dissociation – transition state theory

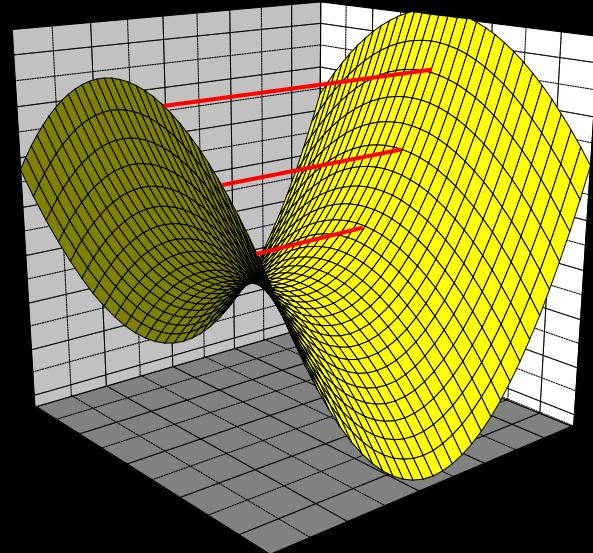
Transition state: maximum along 1 coordinate
minimum along other coordinates



Loose TS
High state density
High entropy



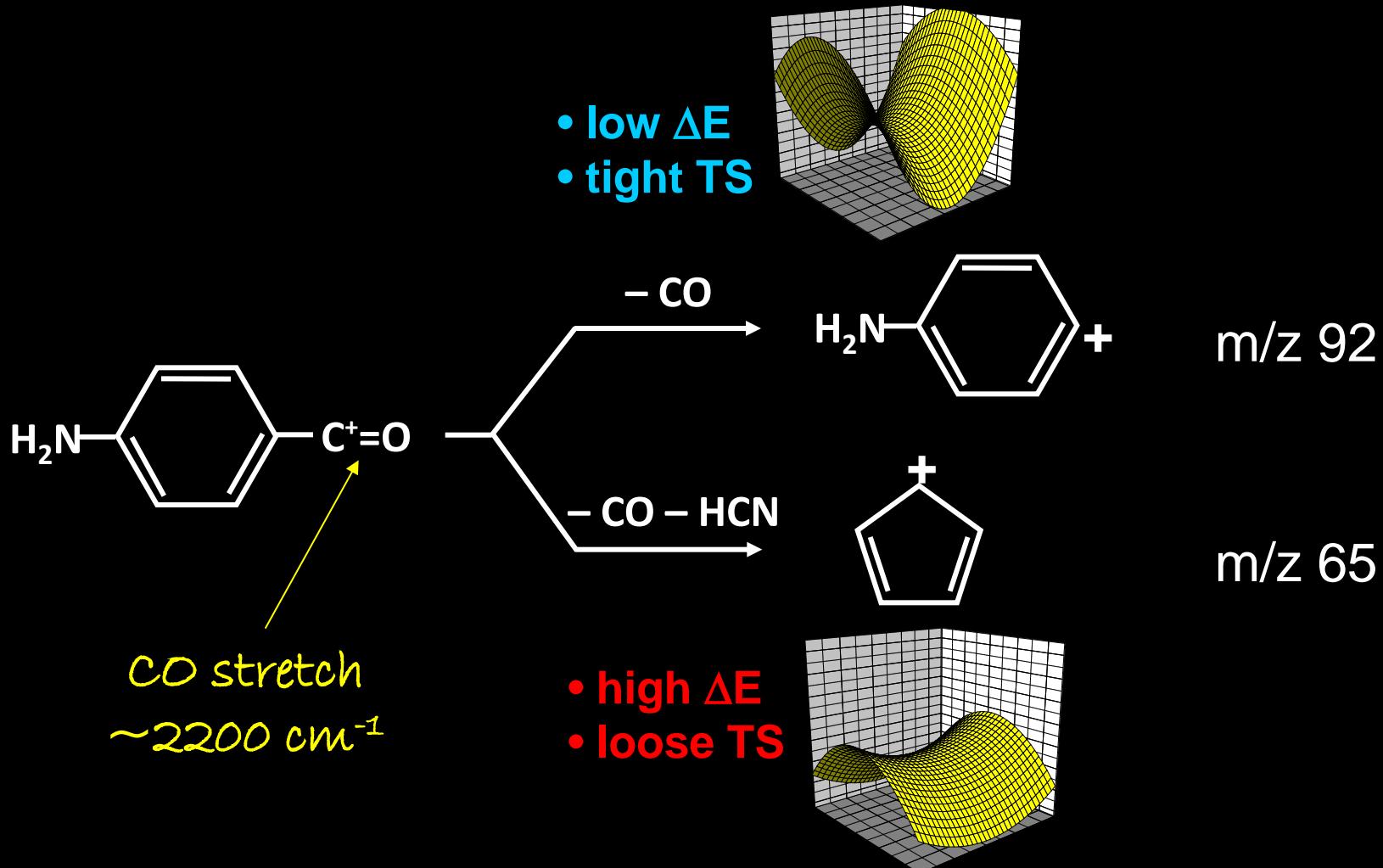
free energy
 $\Delta G = \Delta E - T\Delta S$



reaction coordinate

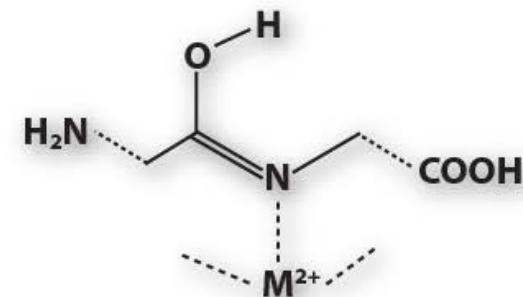
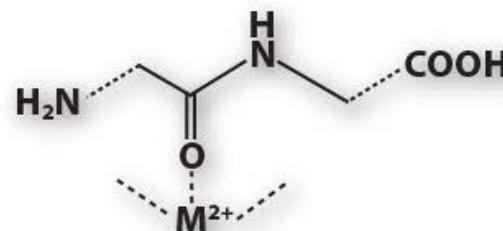
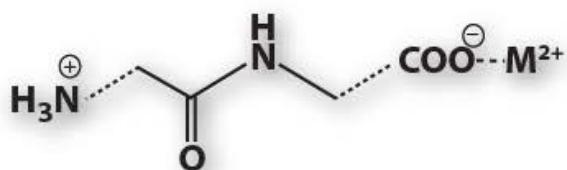
Tight TS
Low state density
Low entropy

IRMPD spectra of *p*-ABz⁺



Metal-ion peptide binding

How peptides chelate metal ions in the gas phase

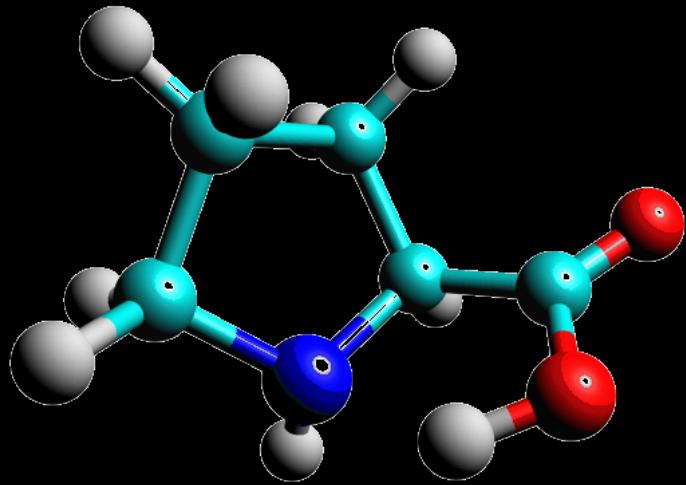


**salt bridge
(zwitterion)**

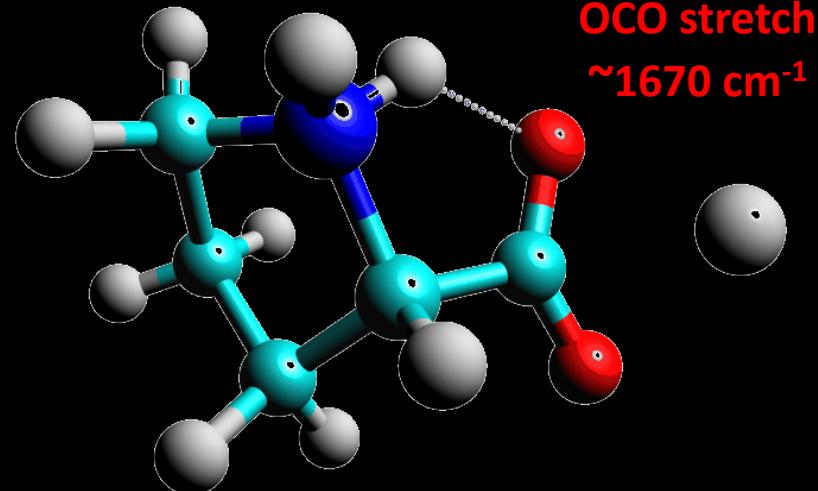
**charge solvated
(‘keto’)**

**iminol
(‘enol’)**

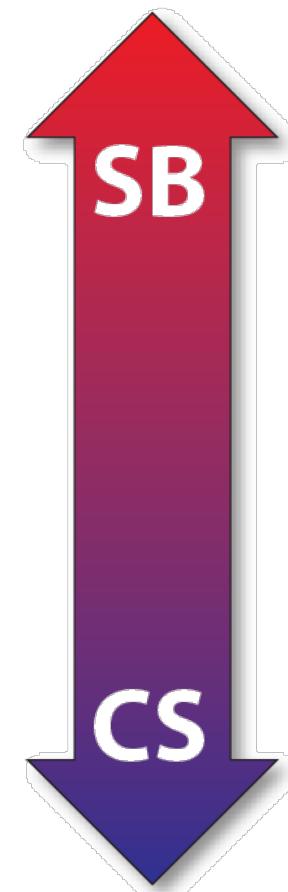
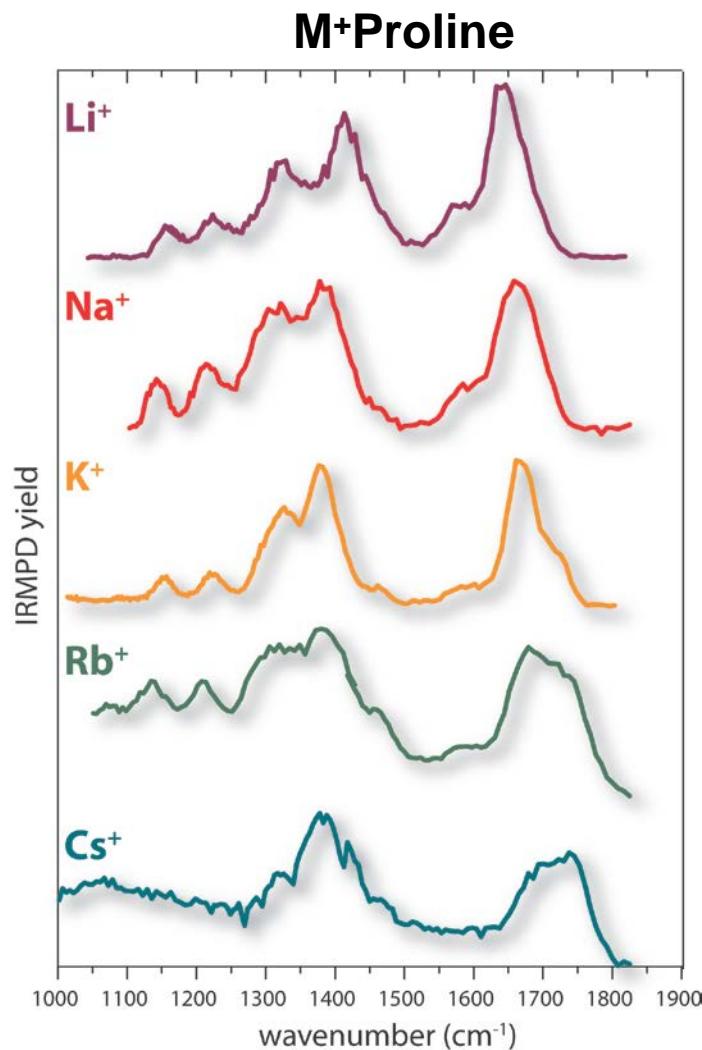
Charge-solvation or salt-bridge? M^+ Proline



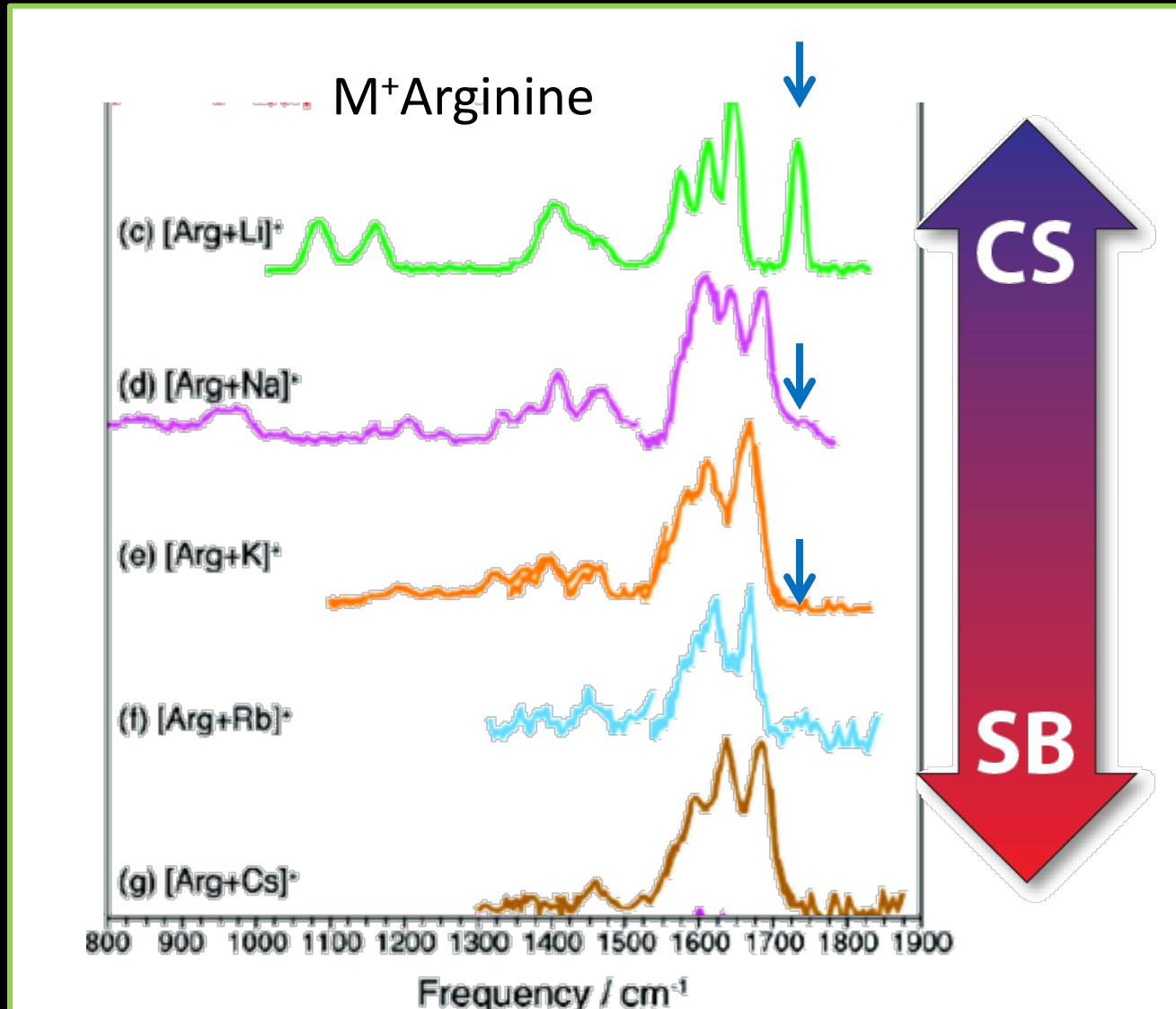
charge solvated
CO stretch
 $\sim 1740 \text{ cm}^{-1}$



Coordination: trends with metal ion size



Coordination: trends with metal ion size



Coordination: trends with metal ion size



- Smaller ion:
 - higher charge density, more polarizing
 - induces charge separation more easily
 - tends to favor SB

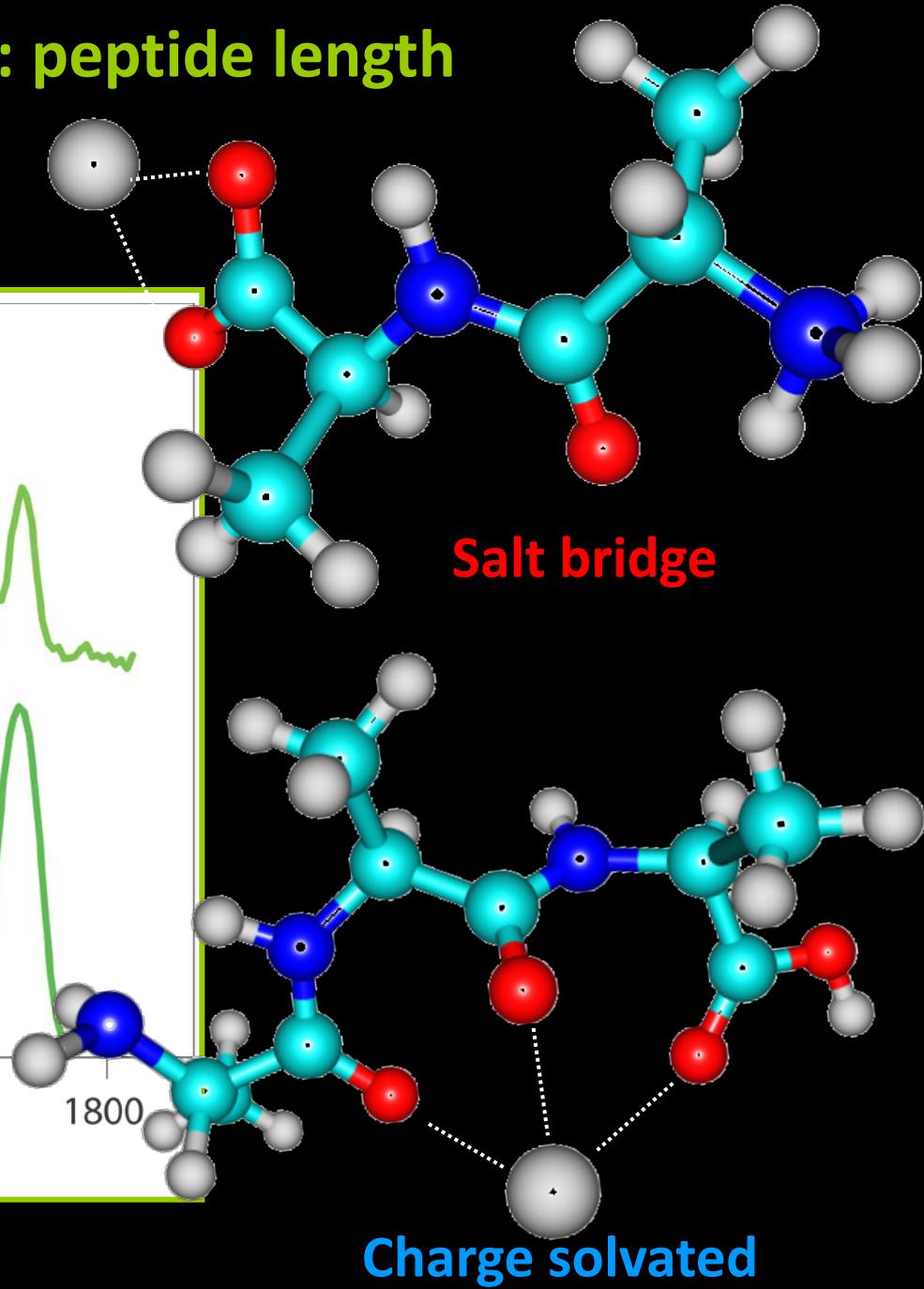
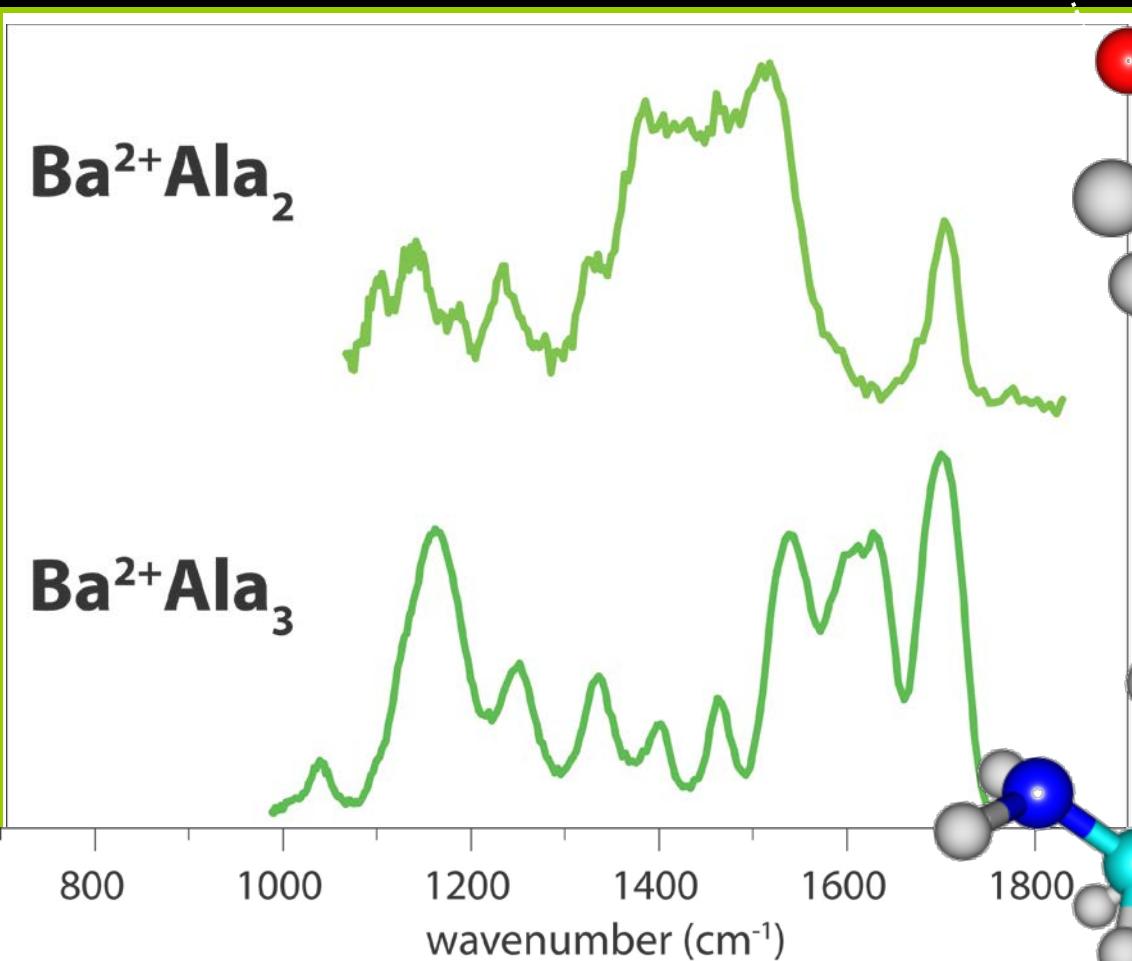
dominates for
aliphatic AA



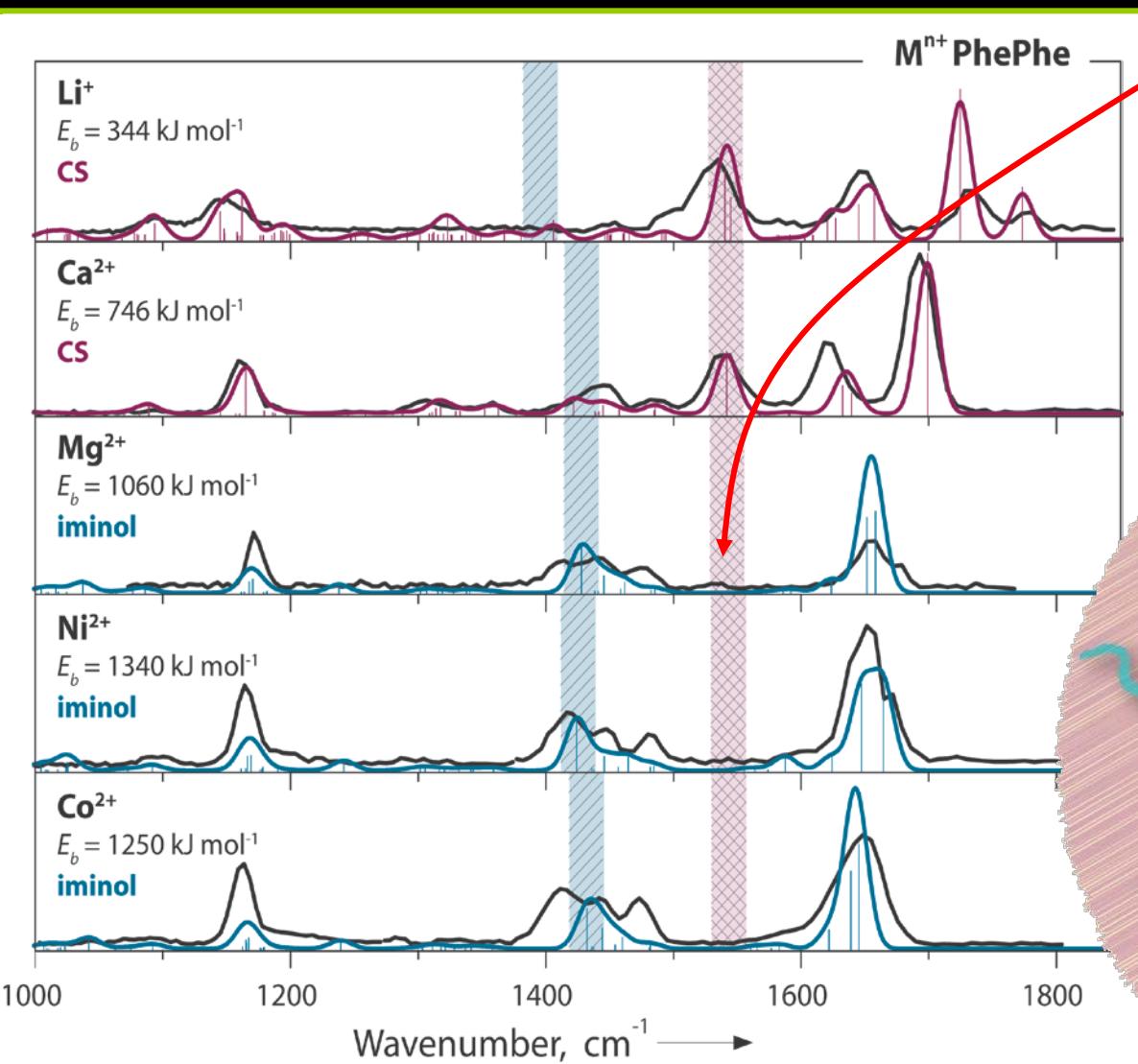
- Smaller ion:
 - smaller ionic radius
 - sterically easier to solvate from all sides
 - tends to favor CS

dominates for
non-aliphatic AA

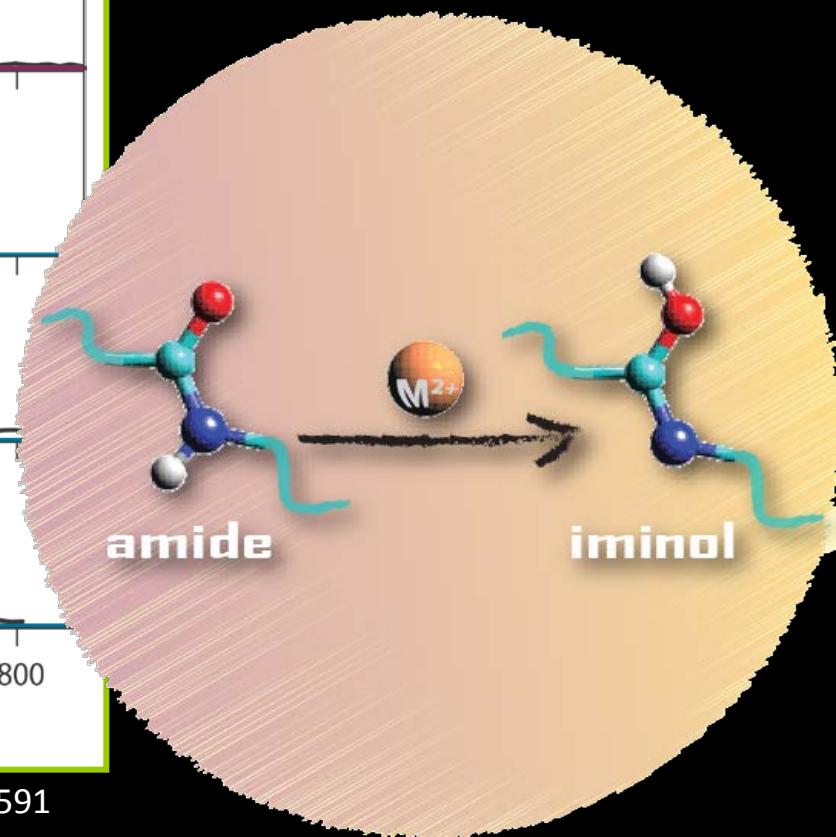
Coordination: peptide length



The iminol motif



No Amide II band
Strongly binding metals
Keto-enol tautomerization



ion chemistry: characterizing ion reactions

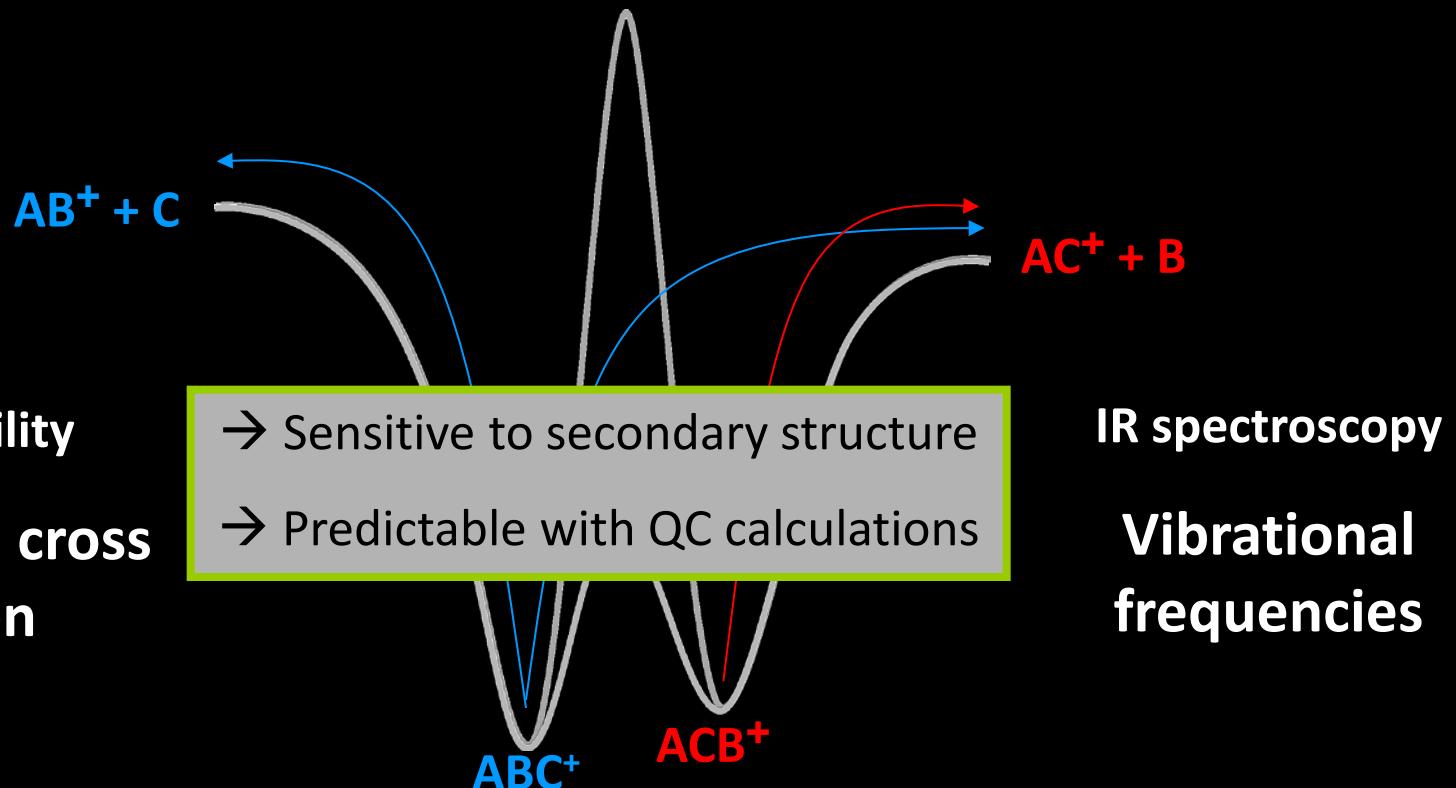
- Molecular structure determination
- Identification

Collision induced
dissociation

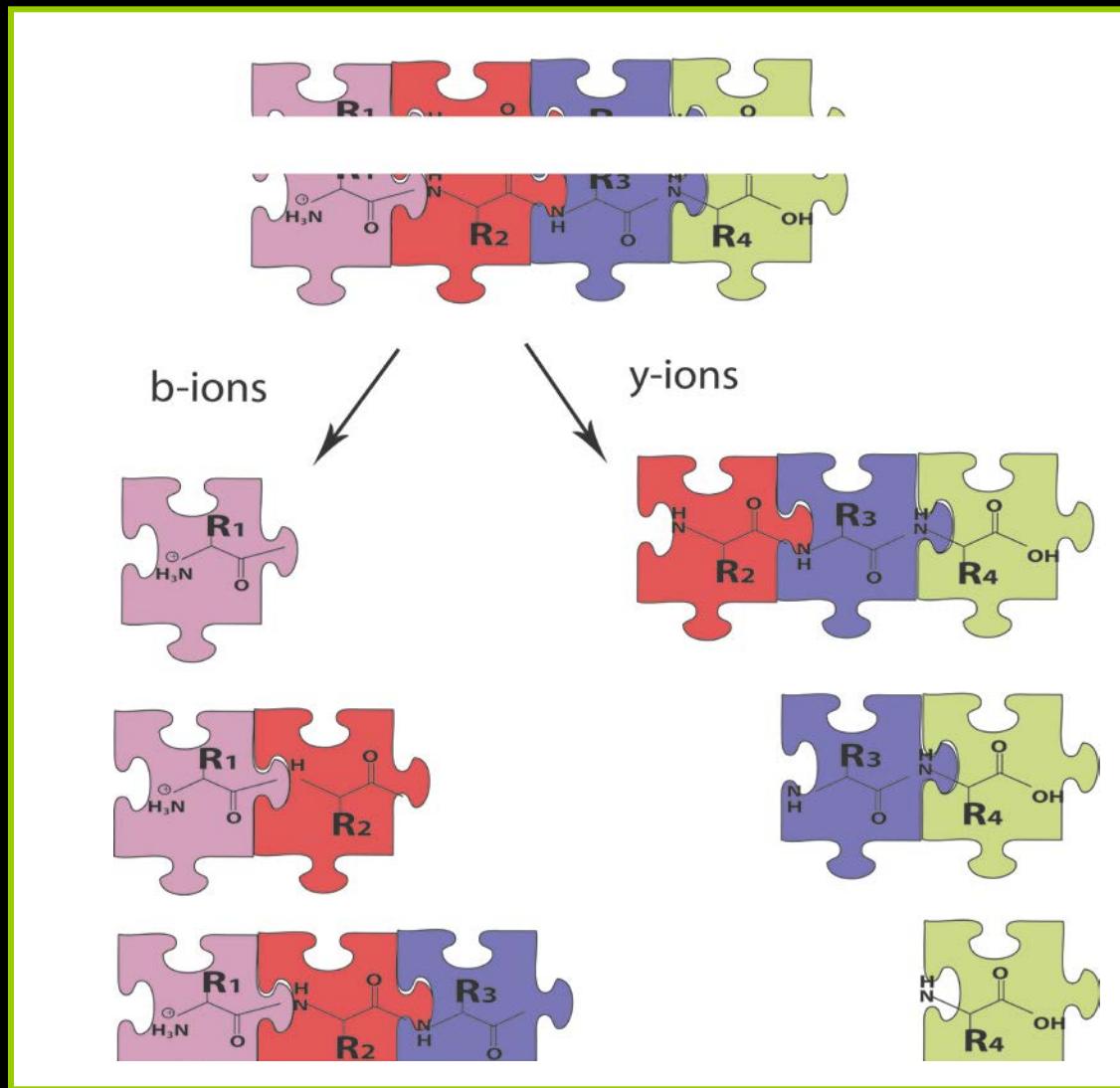
Ion-molecule reaction

H/D exchange

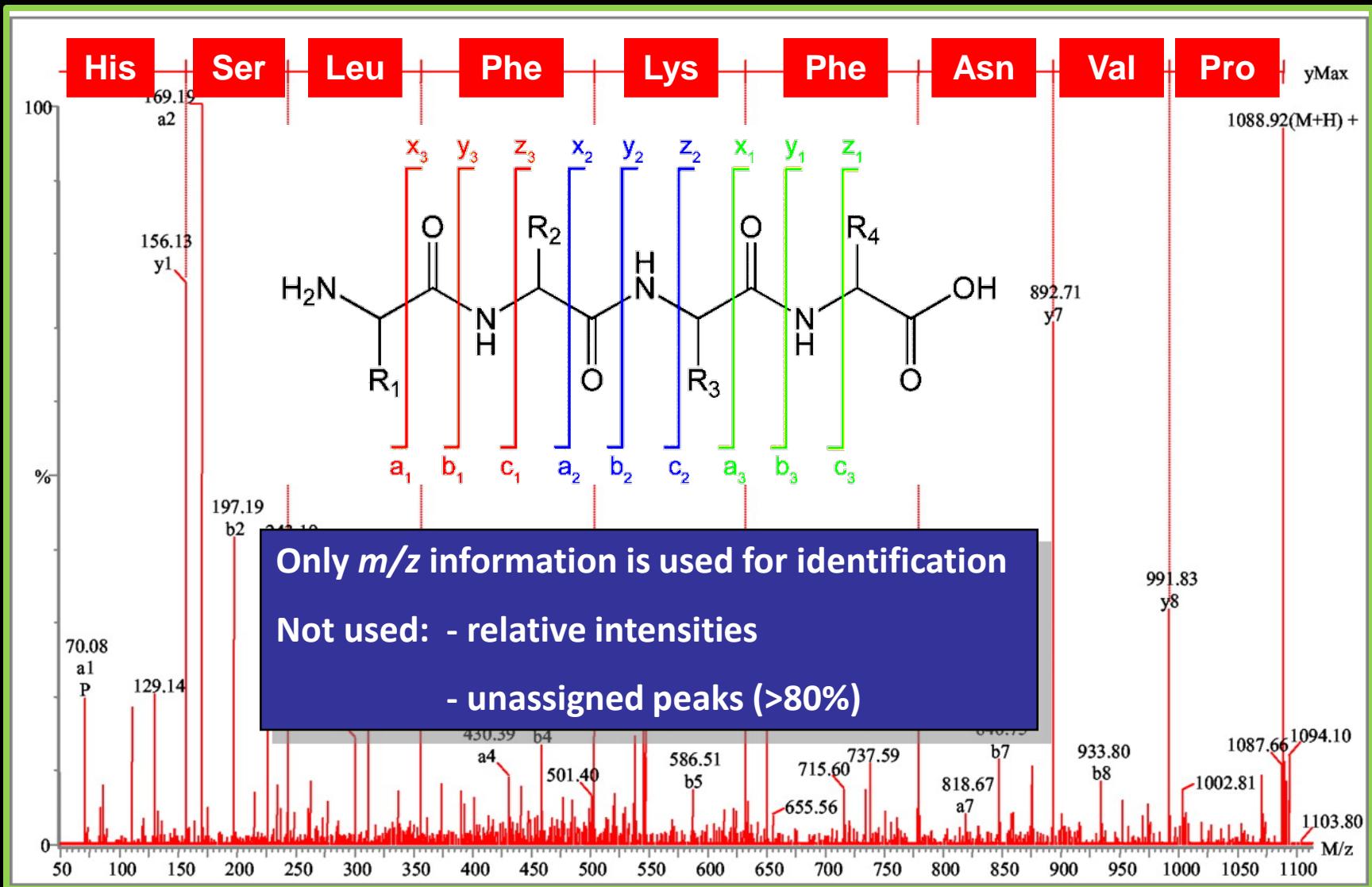
Based on unknown reaction mechanisms



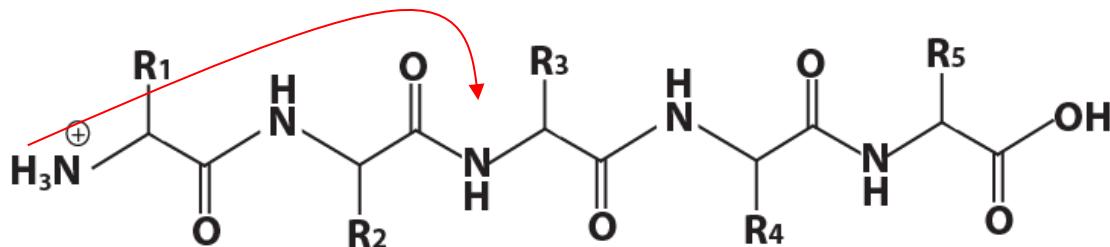
Peptide sequencing by mass spectrometry



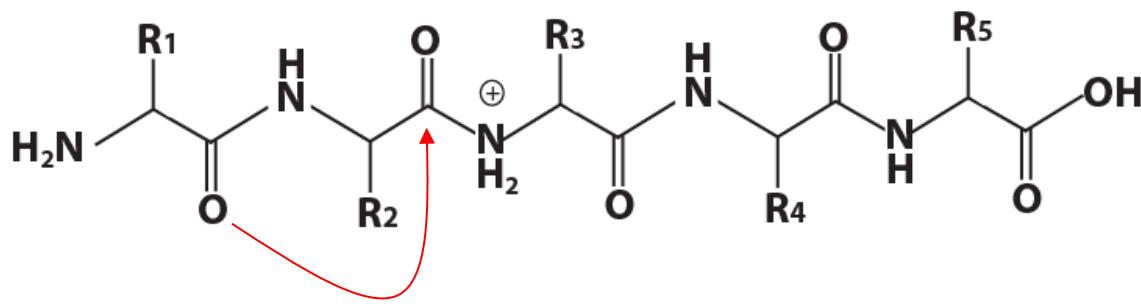
Peptide sequencing by mass spectrometry



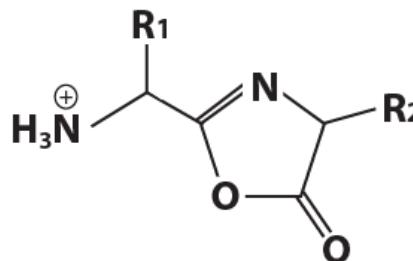
b/y fragmentation pathway



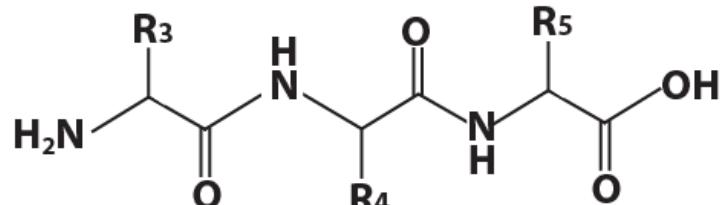
mobile
proton



nucleophilic
attack



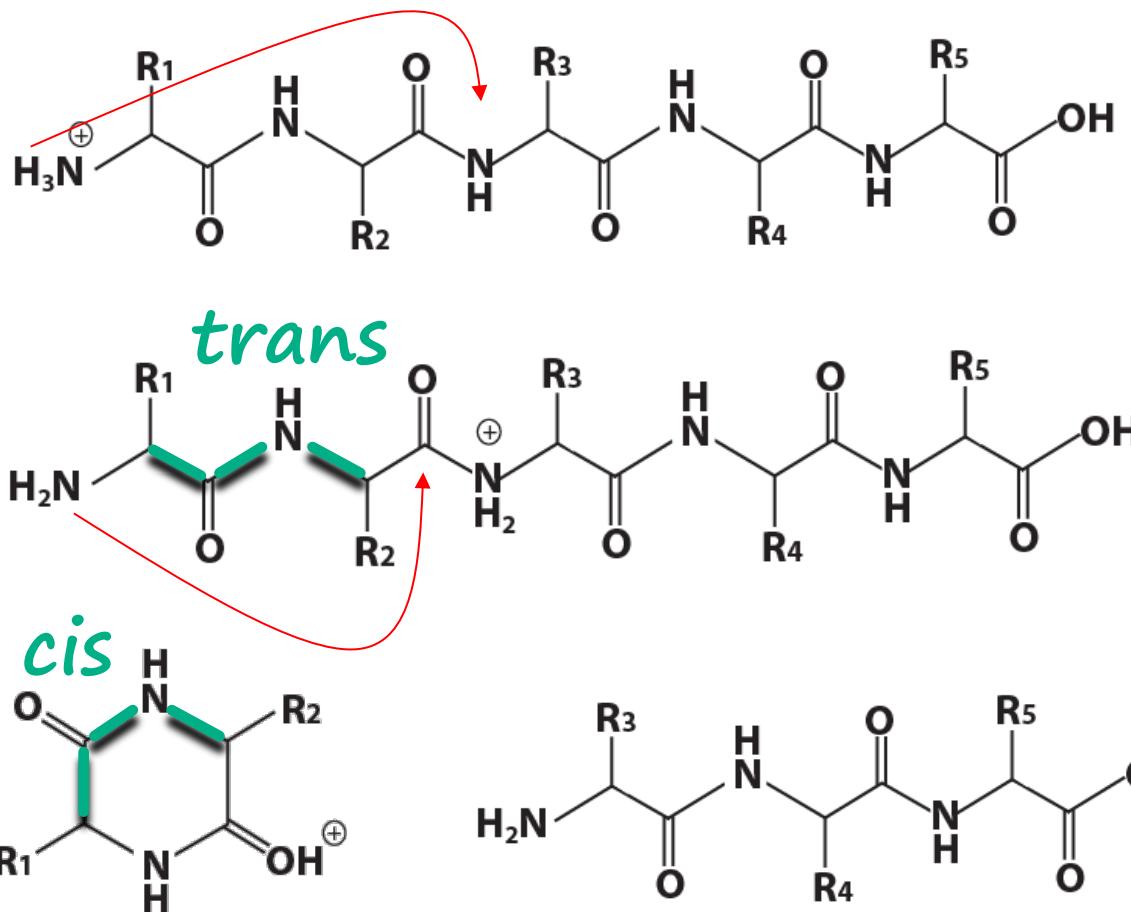
b-fragment: oxazolone



y-fragment: truncated peptide)

amide bond
cleavage

Alternative *b/y* pathway: N-terminus as nucleophile



mobile
proton

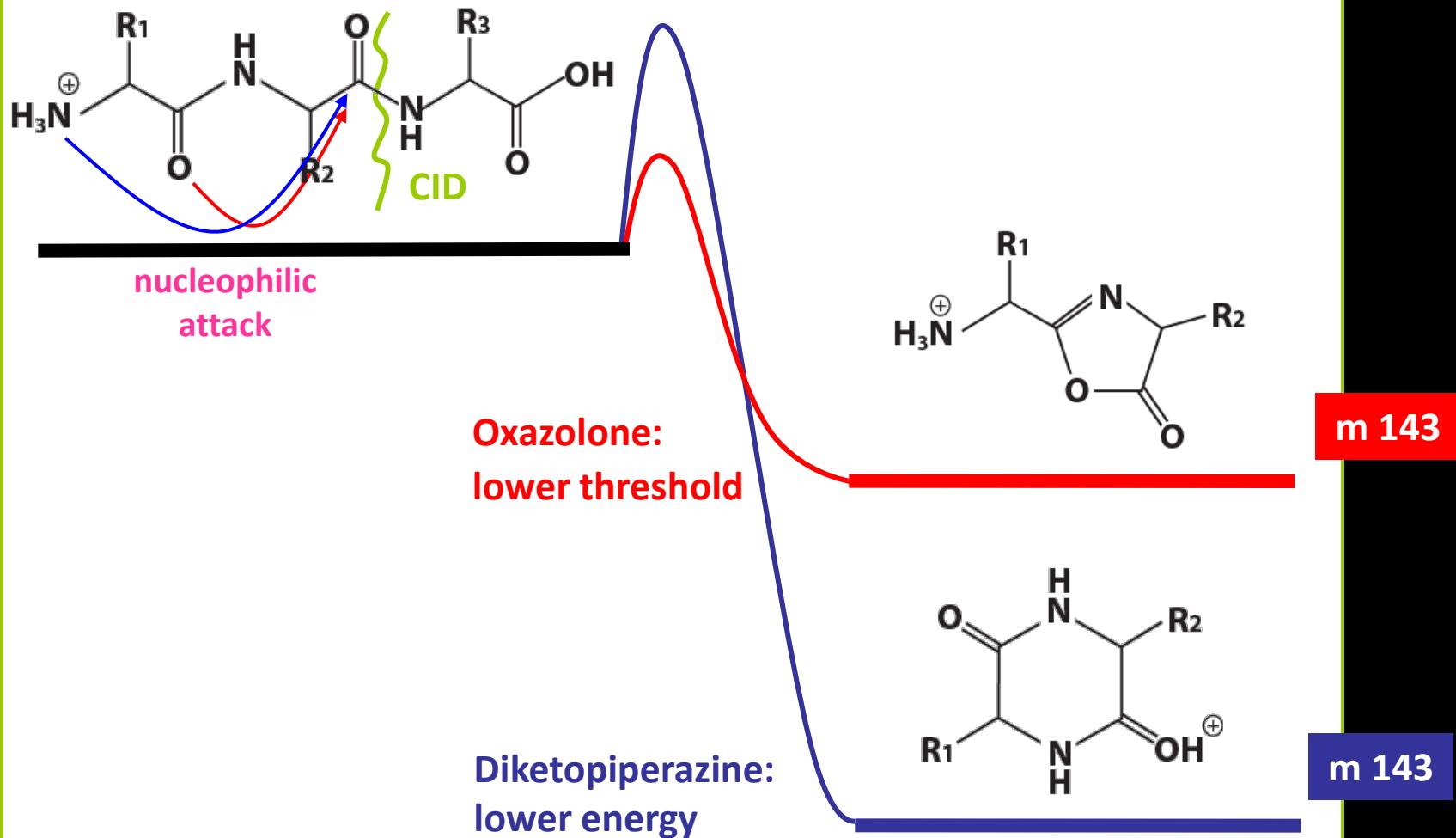
nucleophilic
attack

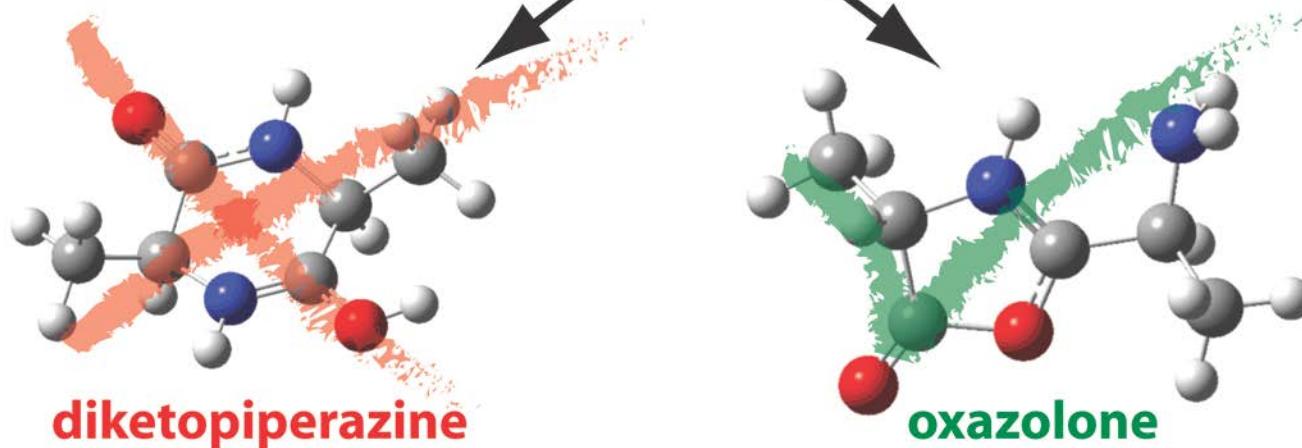
amide bond
cleavage

b-fragment: diketopiperazine (*y*-fragment: truncated peptide)

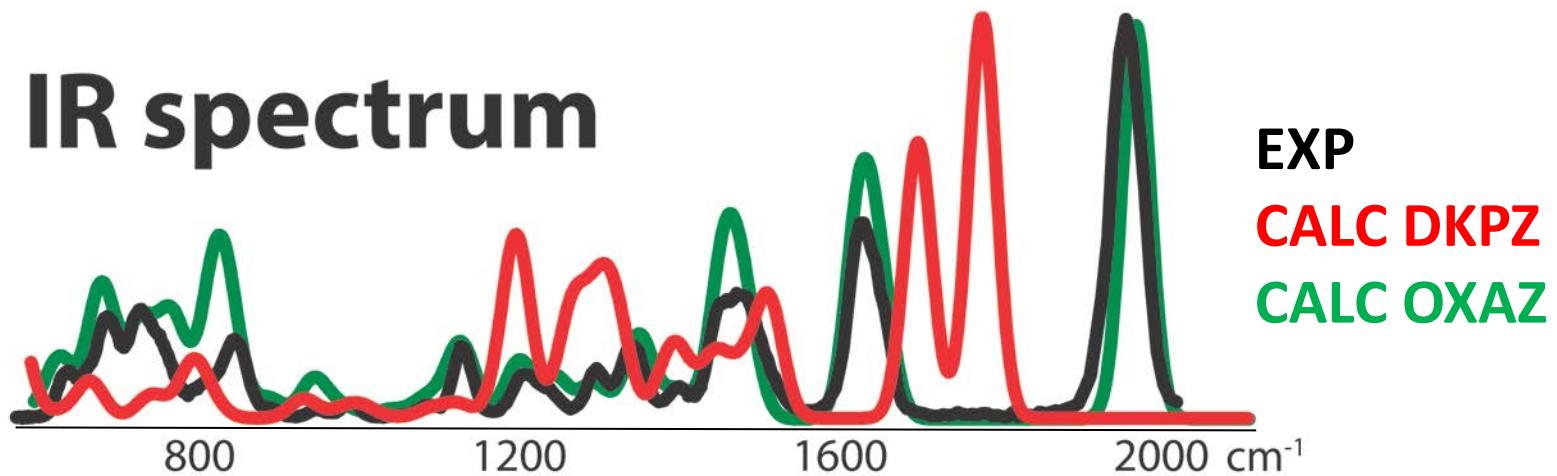
Lower in energy than oxazolone !

Peptide fragmentation: *b*-type ions

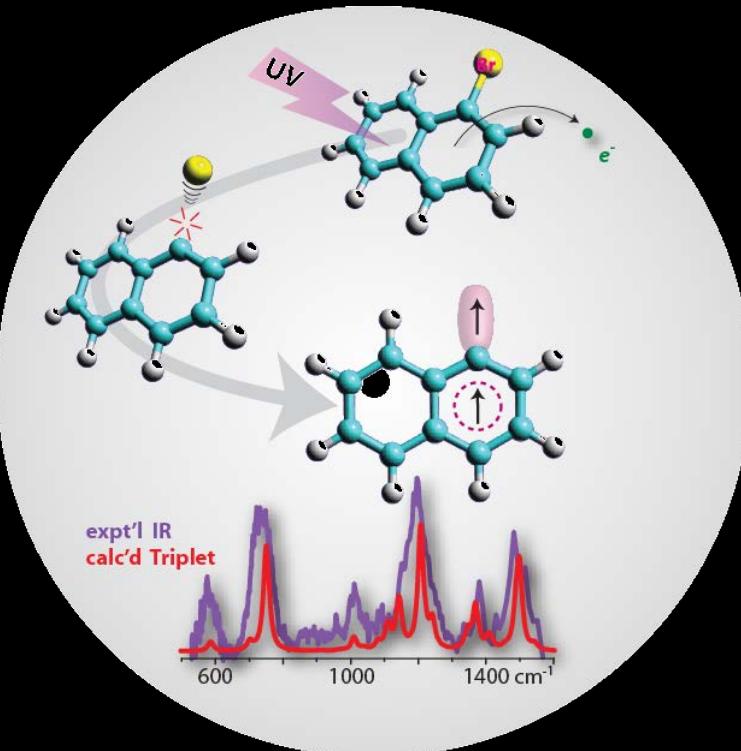




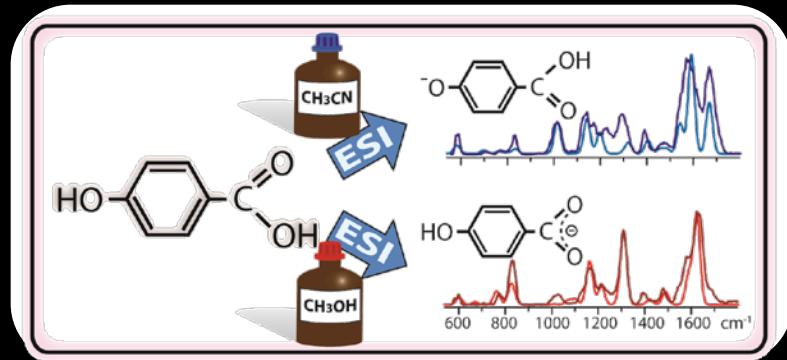
IR spectrum



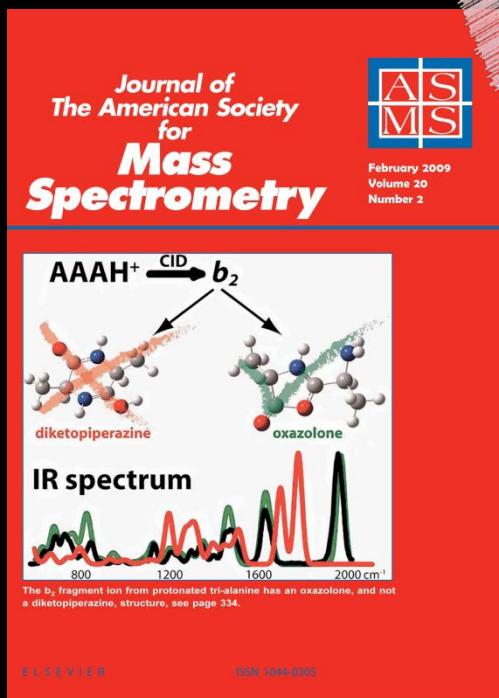
ion spectroscopy → ion structure



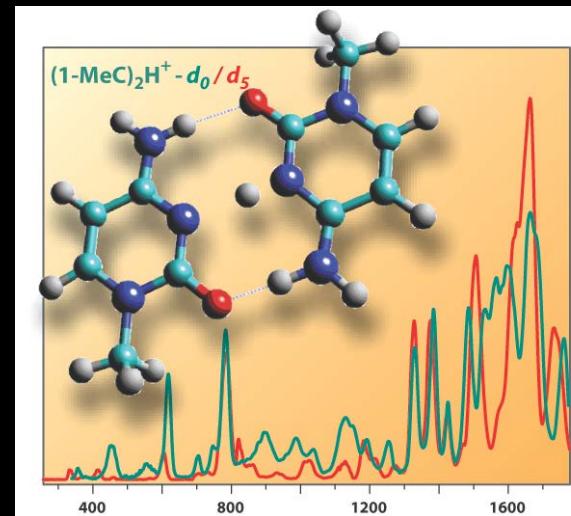
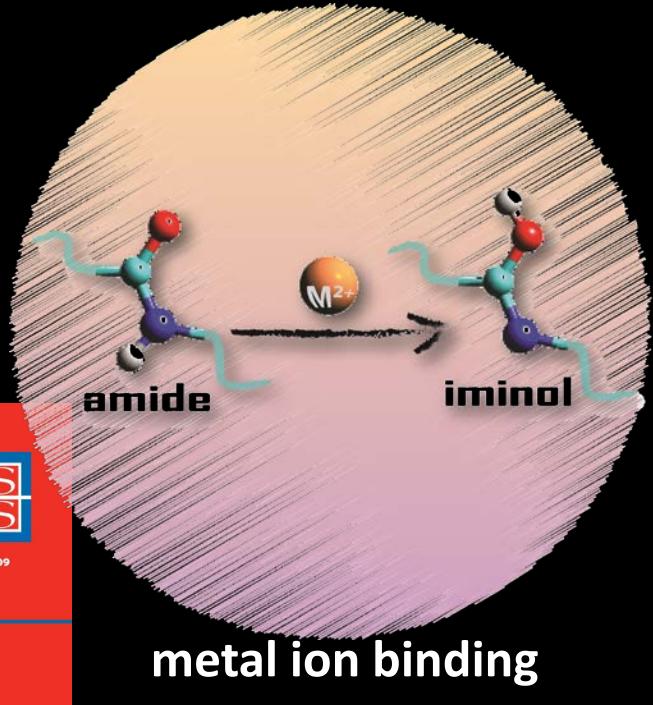
electronic state aryl cations



deprotonation & tautomerization

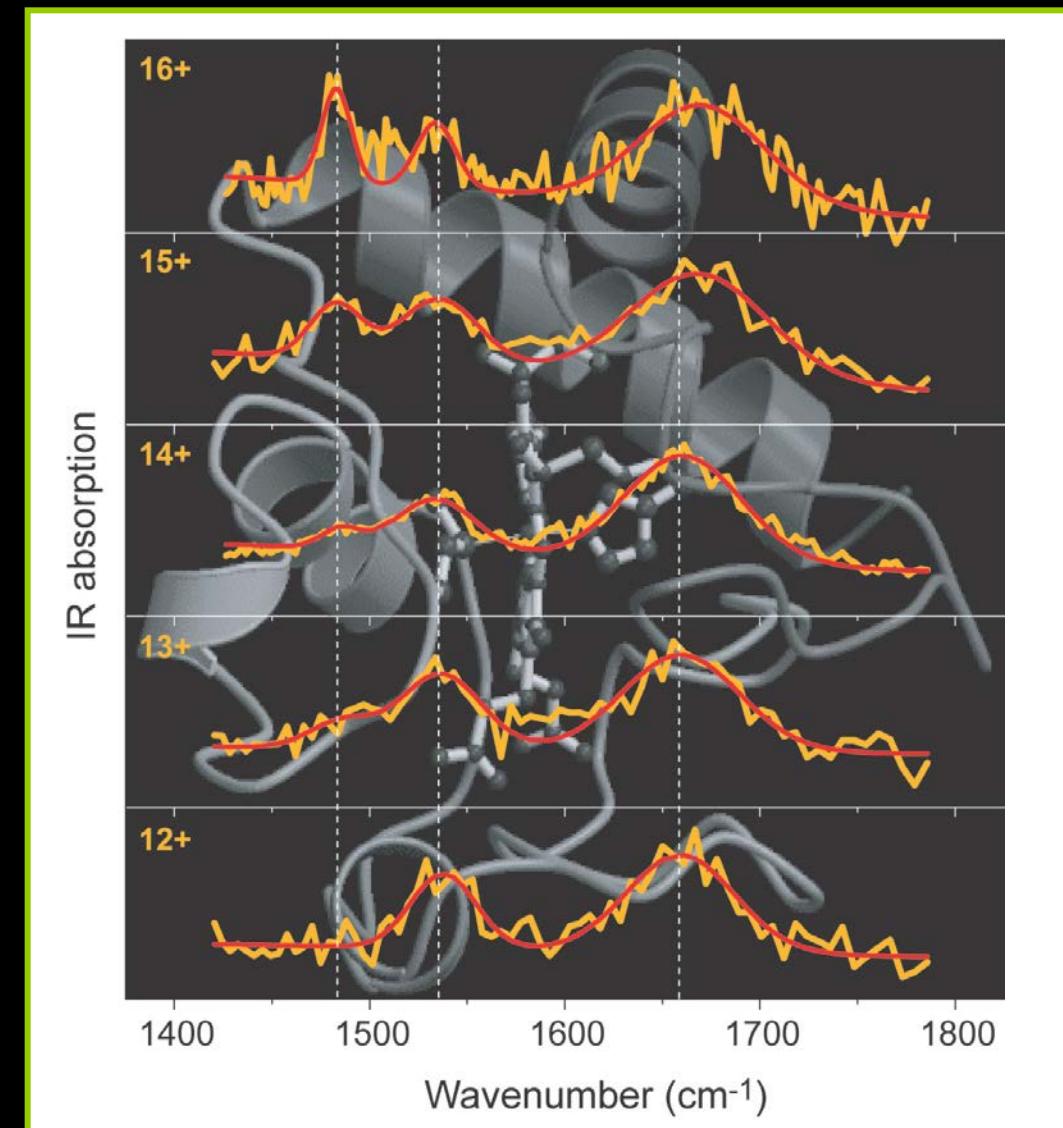


peptide fragment
structures



proton-bound dimers

Biochemistry: IR spectra of proteins



Cytochrome C

~12.5 kDa

Amide I/II bands

Charge-state resolved

No DFT spectra

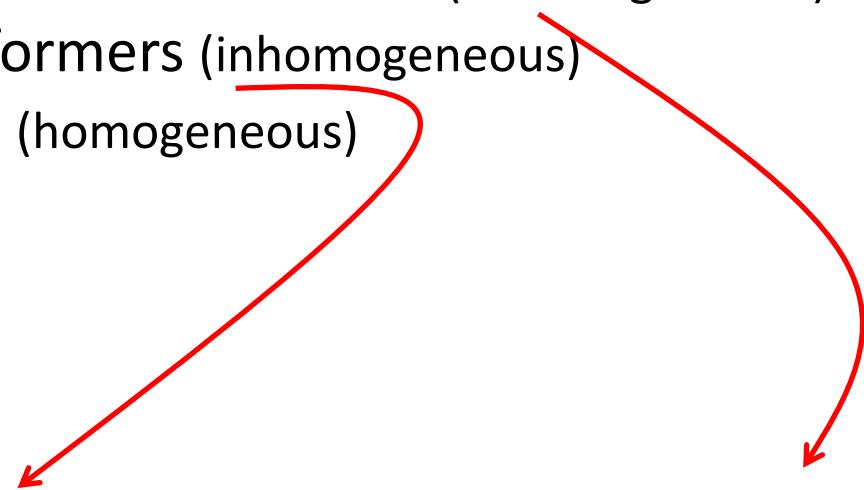
Cryogenic ion spectroscopy

Sources of spectral broadening

- Multiple thermally populated lower states (inhomogeneous)
- Presence of multiple conformers (inhomogeneous)
- Overlap of spectral bands (homogeneous)
- Lifetime (homogeneous)

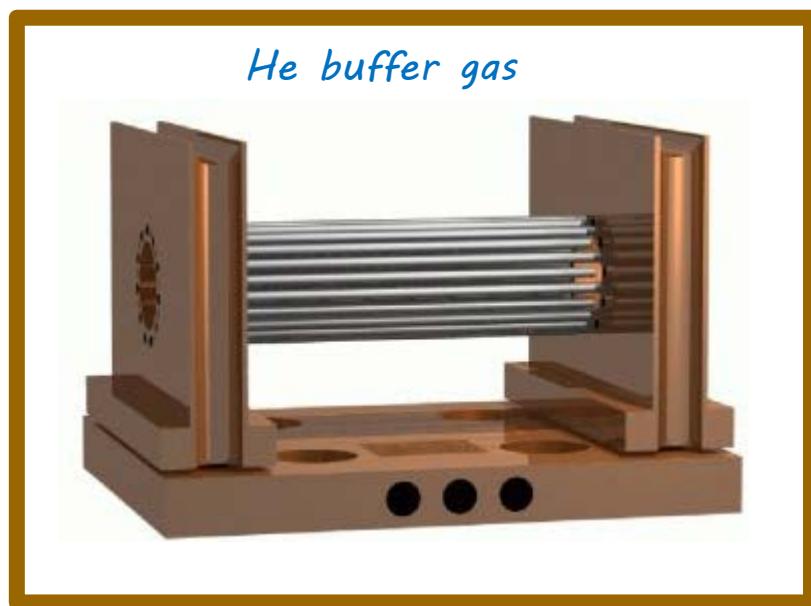
Double resonance methods

Cooling

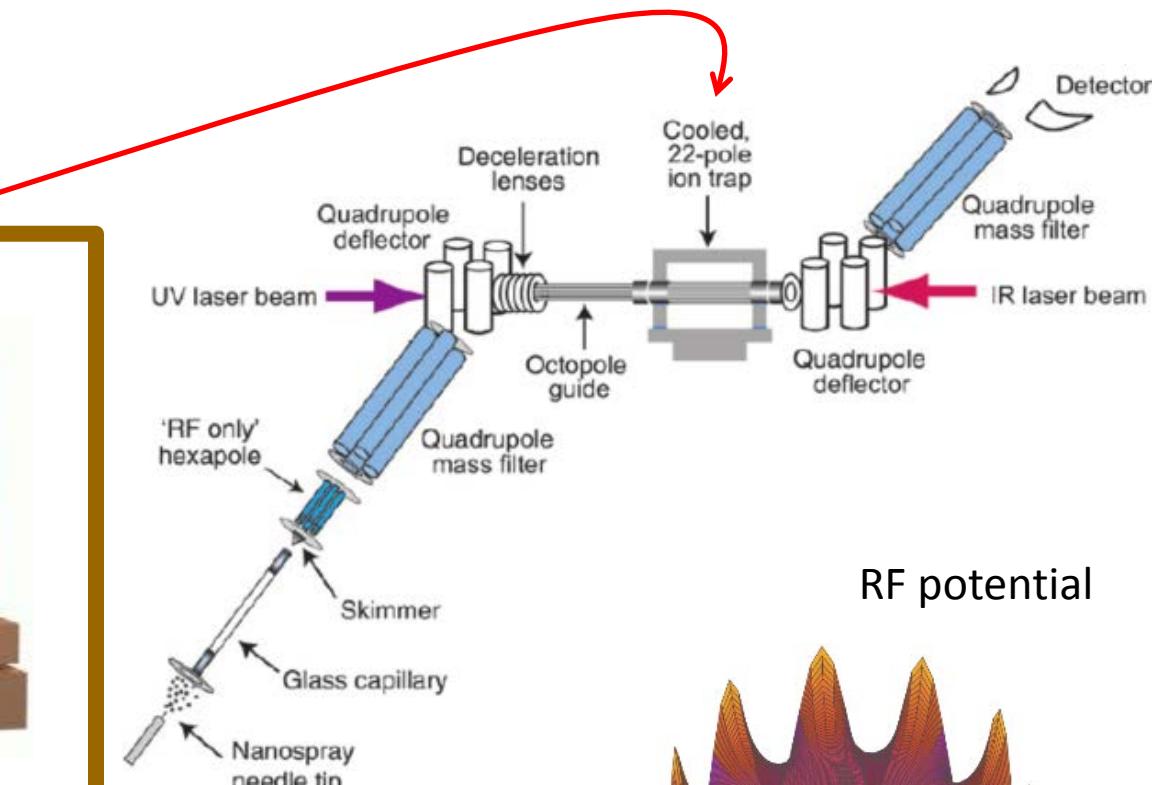


Cryogenic ion spectroscopy

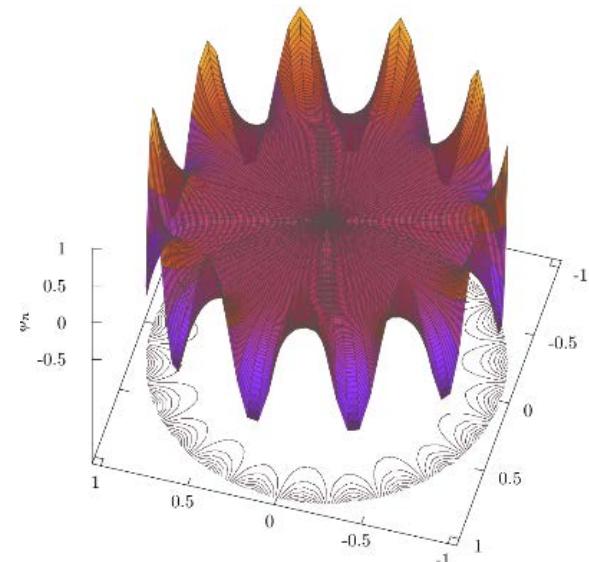
Buffer gas cooling



LHe Cryostat



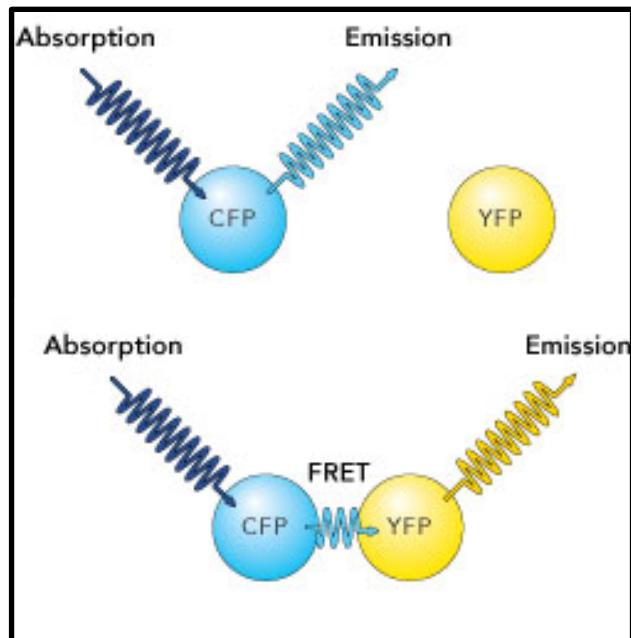
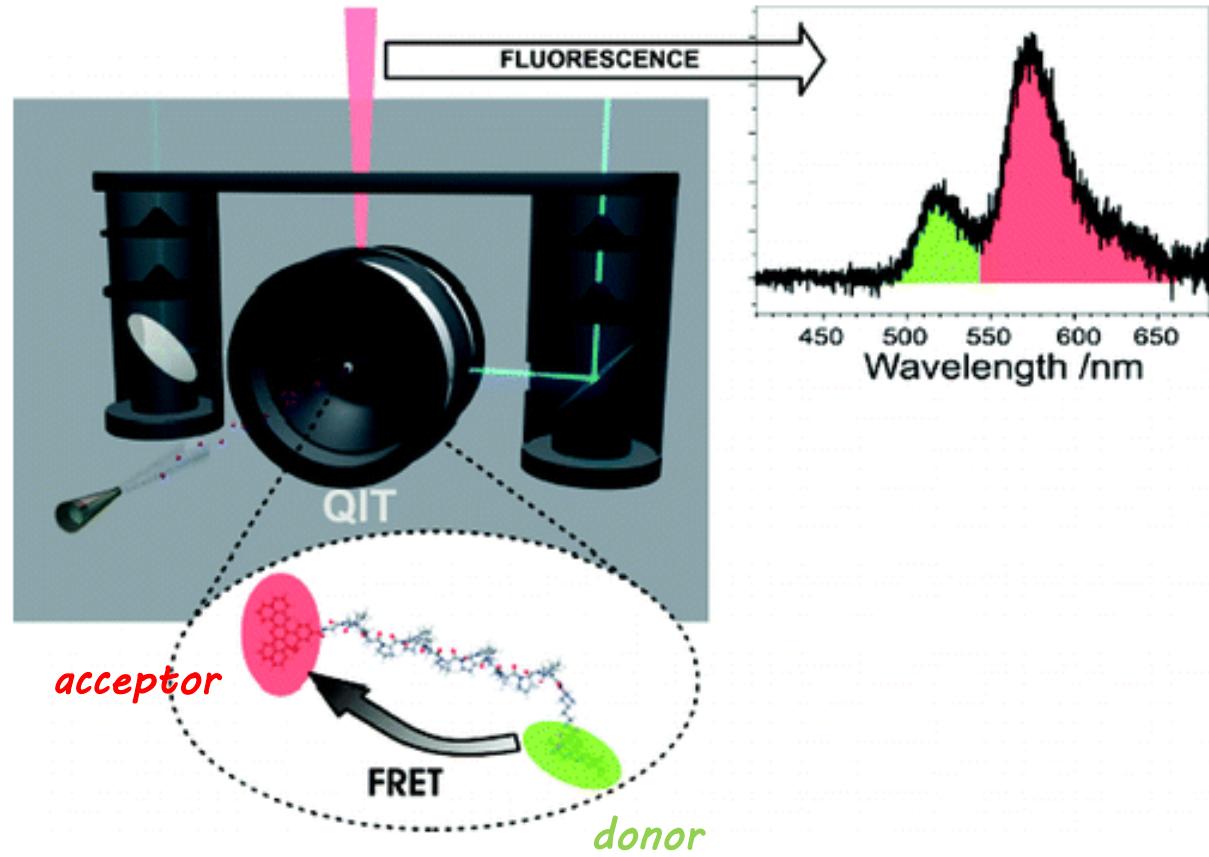
RF potential



Cryogenic ion spectroscopy

Detection for IR or UV spectrosopies

- Fluorescence (LIF)

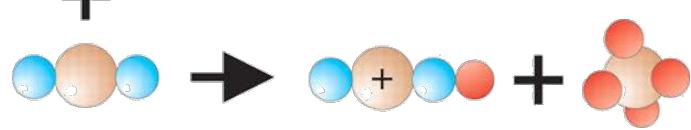
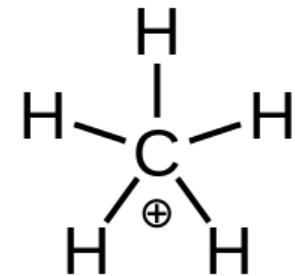
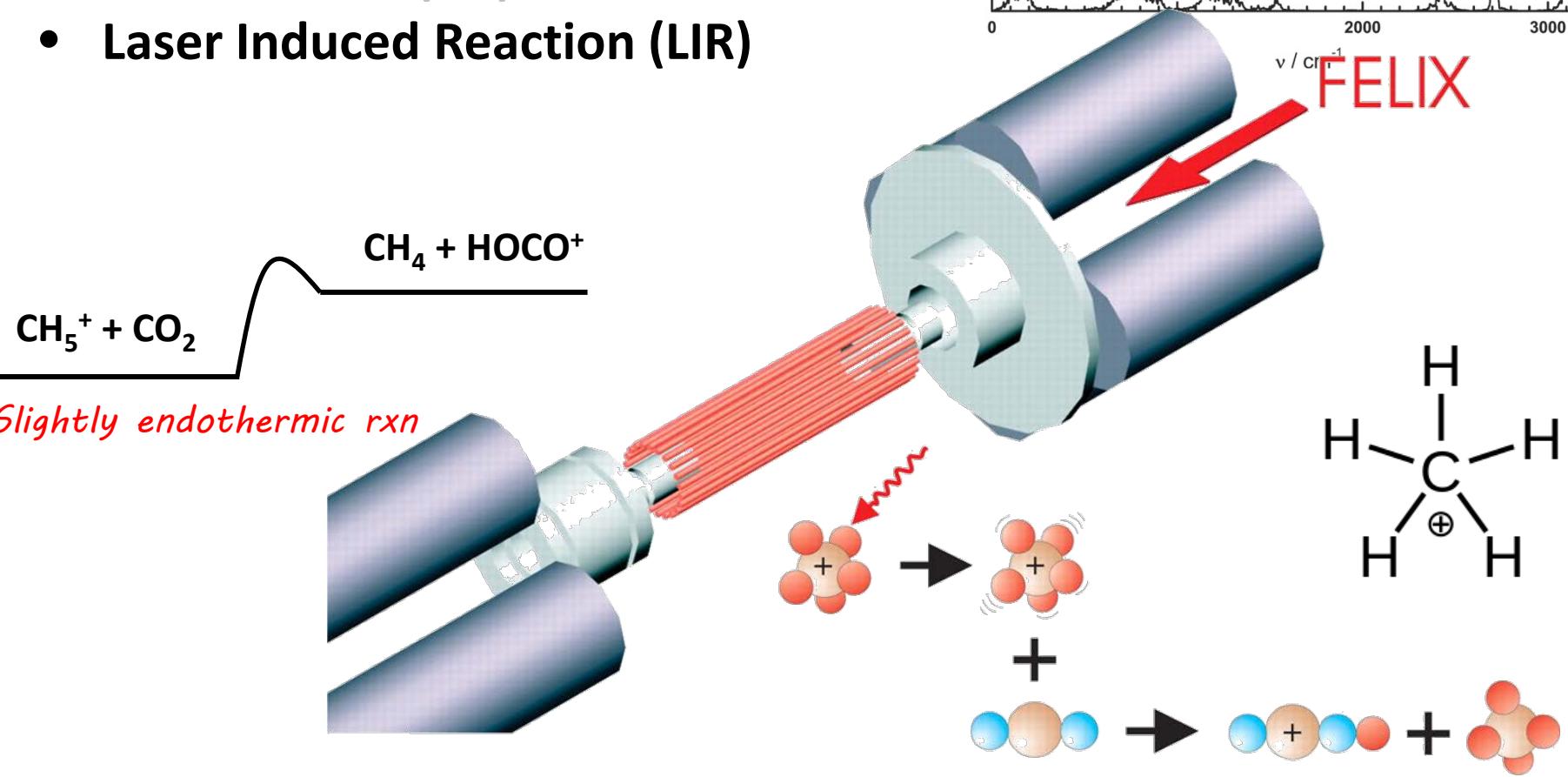
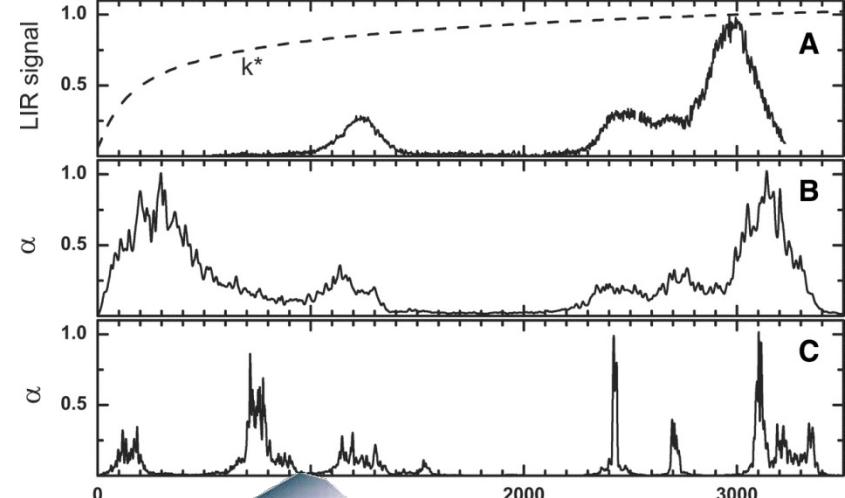


Jockusch et al. *J. Am. Chem. Soc.*, 2010, 132, 16156

Cryogenic ion spectroscopy

Detection for IR or UV spectroscopies

- Fluorescence (LIF)
- Laser Induced Reaction (LIR)



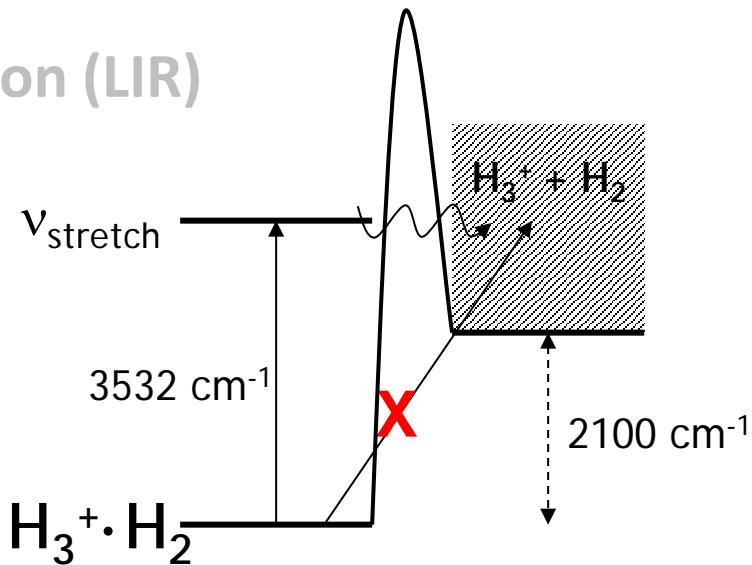
Asvany et al. *Science* 2005;309:1219

Cryogenic ion spectroscopy



Detection for IR or UV spectrosopies

- Fluorescence (LIF)
- Laser Induced Reaction (LIR)
- Messenger



Yuan T Lee

The vibrational predissociation spectroscopy of hydrogen cluster ions^{a)}

M. Okumura, L. I. Yeh,^{b)} and Y. T. Lee

Materials and Molecular Research Division, Lawrence Berkeley Laboratory, and Department of Chemistry,
University of California, Berkeley, California 94720

Weakly attached “messengers”



Infrared Spectra of the Solvated Hydronium Ion: Vibrational Predissociation

Spectroscopy of Mass-Selected $\text{H}_3\text{O}^+\cdot(\text{H}_2\text{O})_n\cdot(\text{H}_2)_m$

system of interest messenger

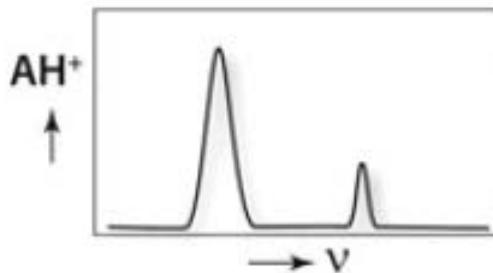
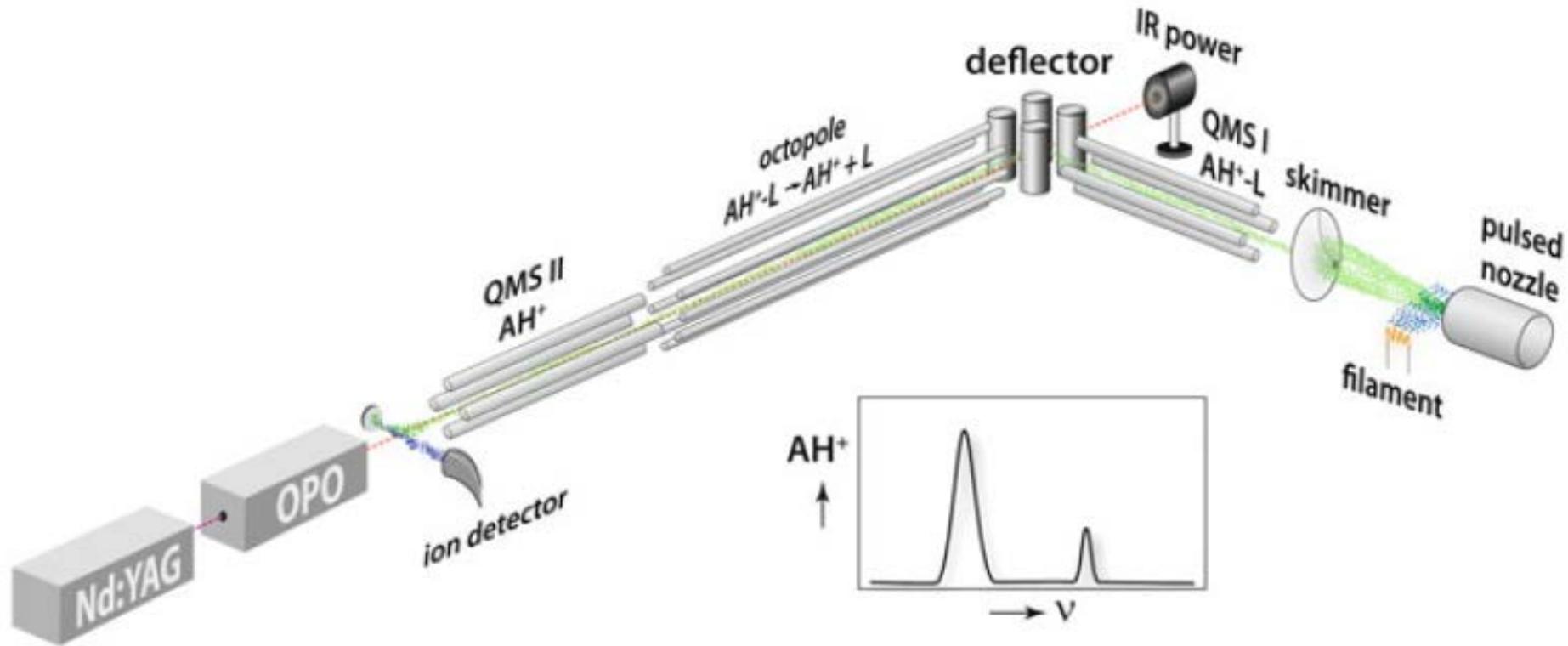
M. Okumura,[†] L. I. Yeh,[‡] J. D. Myers,[‡] and Y. T. Lee*

Materials and Chemical Sciences Division, Lawrence Berkeley Laboratory, and Department of Chemistry,
University of California, Berkeley, California 94720 (Received: March 6, 1989;
In Final Form: November 9, 1989)

J. Phys. Chem. 94, 3416 (1990)

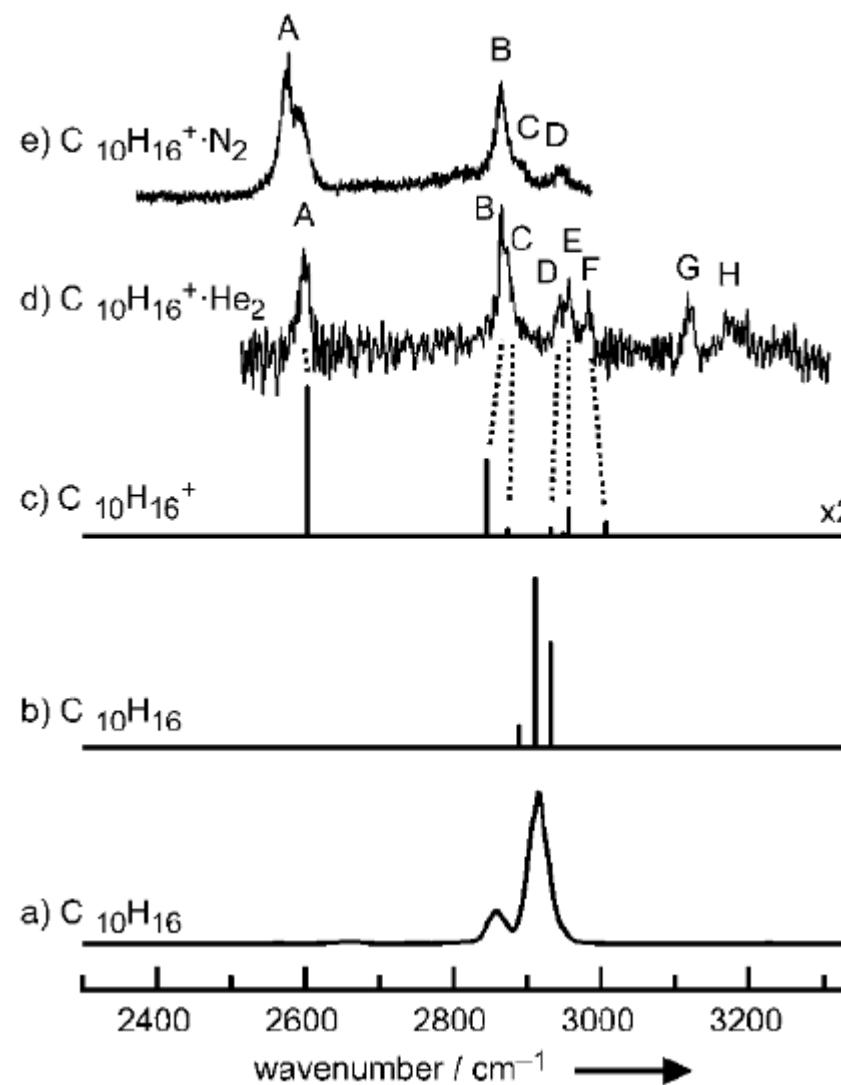
This technique cannot be applied directly to the hydrated hydronium ions, which are bound far more strongly than the H_n^+ clusters. A single infrared photon exciting an OH stretching vibration cannot dissociate these clusters.

We overcome this problem by attaching an additional atom or molecule to the cluster. By choosing a “messenger” that is very weakly attached to the hydrate cluster, the vibrations of the hydrate itself will only be slightly perturbed. When we excite an OH stretch of the hydrate, the messenger atom will detach by vibrational predissociation. The messenger thus acts as a mass label, allowing us to use vibrational predissociation to probe the low-resolution infrared spectra of a large variety of previously unobserved ions. Like a spy, its role is to gather information as unobtrusively as possible.



Infrared Spectrum and Structure of the Adamantane Cation: Direct Evidence for Jahn–Teller Distortion**

Alexander Patzer, Markus Schütz, Thomas Möller, and Otto Dopfer*



Angew. Chem. Int. Ed. 2012, 51, 4925–4929

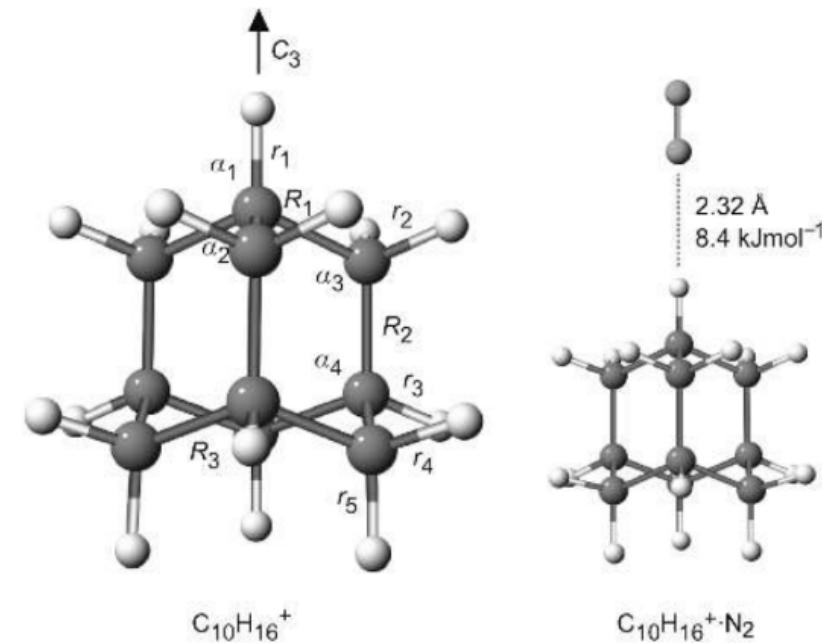


Figure 1. Structures of $\text{C}_{10}\text{H}_{16}^+$ and the most stable $\text{C}_{10}\text{H}_{16}^+\cdot\text{N}_2$ dimer calculated at the B3LYP/cc-pVDZ level. Relevant structural parameters are listed in Table T1 in the Supporting Information.

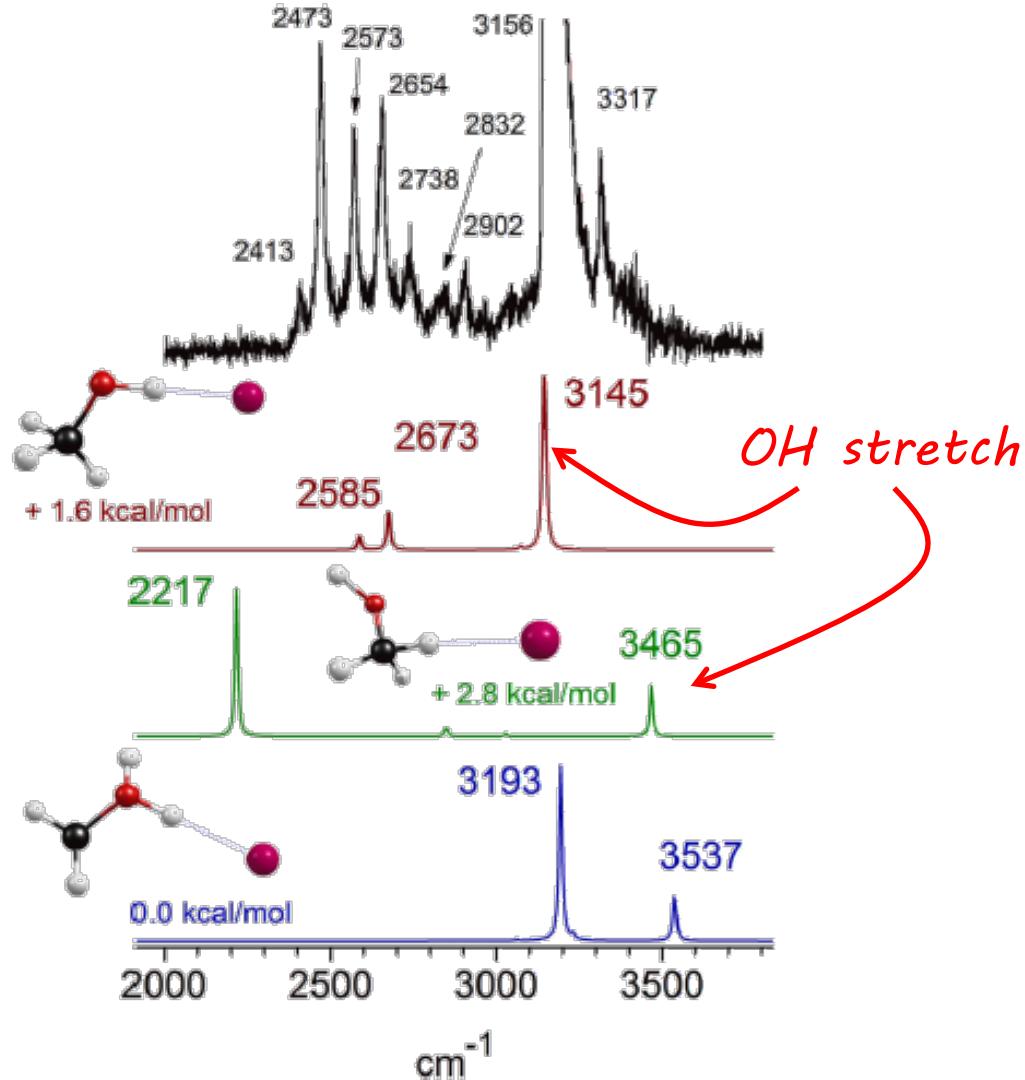
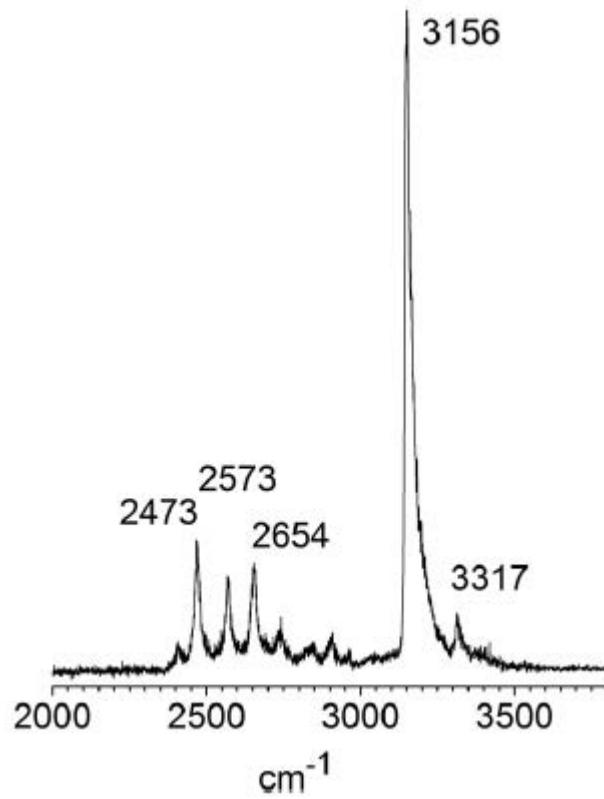
Infrared spectroscopy of the methanol cation and its methylene-oxonium isomer

J. D. Mosley,^{1,a)} J. W. Young,^{1,b)} M. Huang,² A. B. McCoy,^{2,c)} and M. A. Duncan^{1,c)}

¹Department of Chemistry, University of Georgia, Athens, Georgia 30602, USA

²Department of Chemistry and Biochemistry, The Ohio State University, Columbus, Ohio 43210, USA

Methanol radical cation Ar messenger



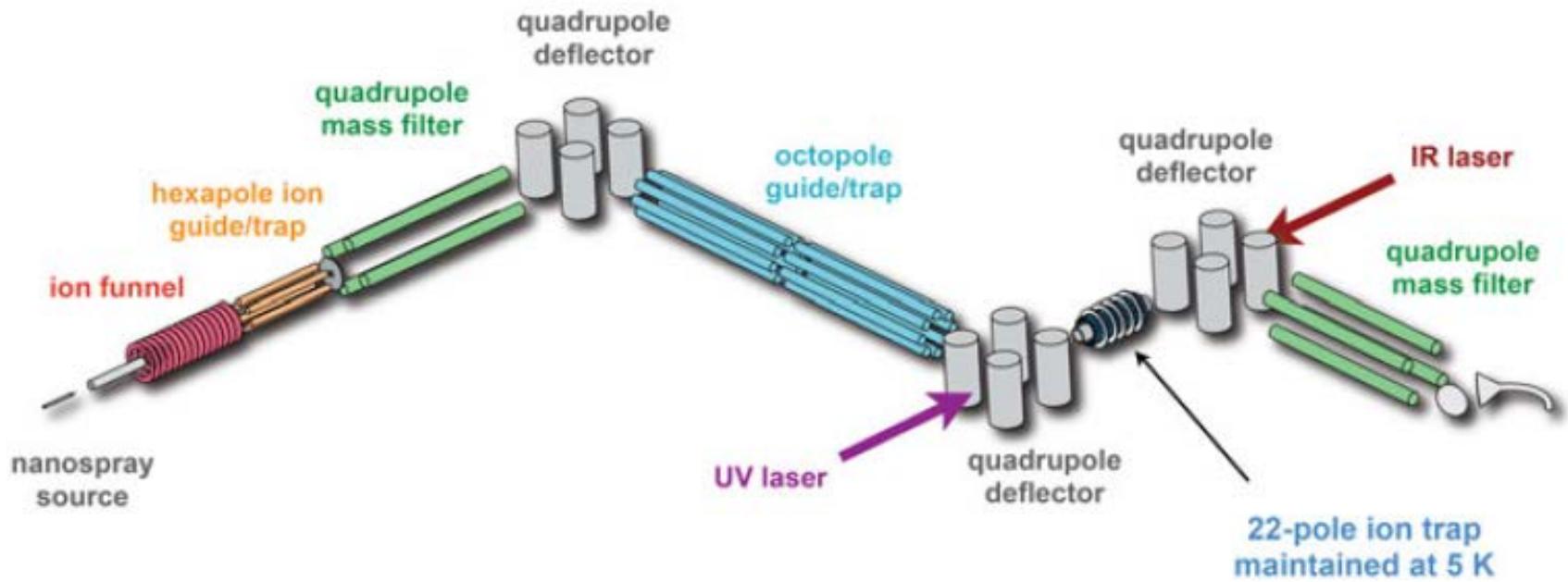


Fig. 7 The second generation Lausanne cold-ion photofragment spectrometer with a 22-pole ion trap [131]

Rizzo group, EPFL

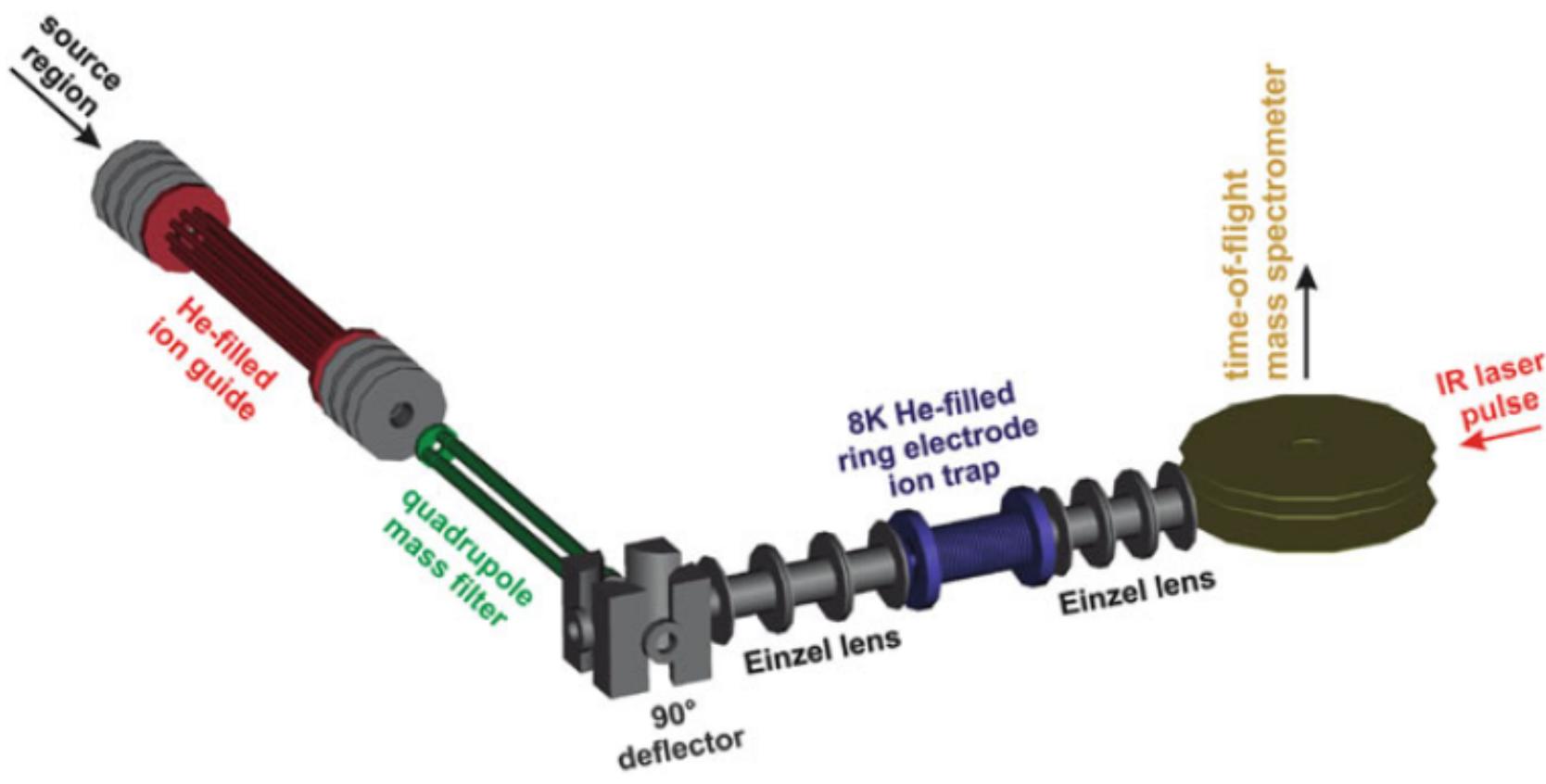


Fig. 8 Second-generation ion trap machine from the Asmis group [134]. The ion trap in this case is a ring-electrode trap, and fragment mass analysis is performed in a time-of-flight mass spectrometer. Reproduced with permission from [134]. Copyright (2009) ACS

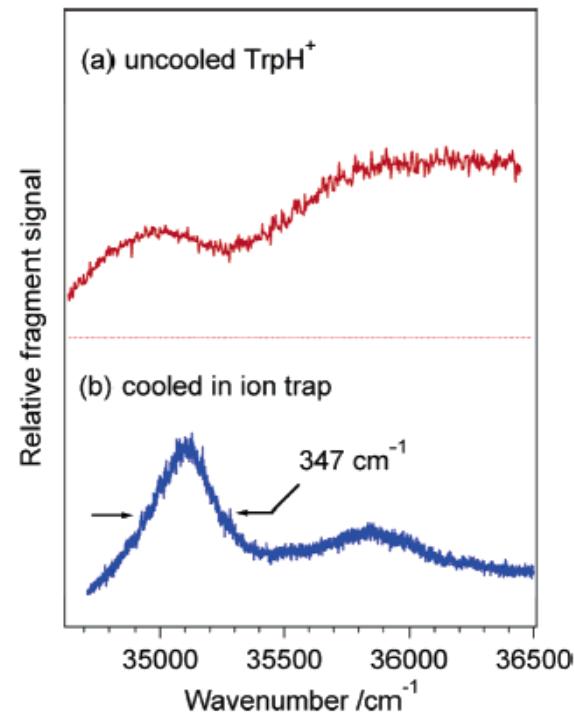
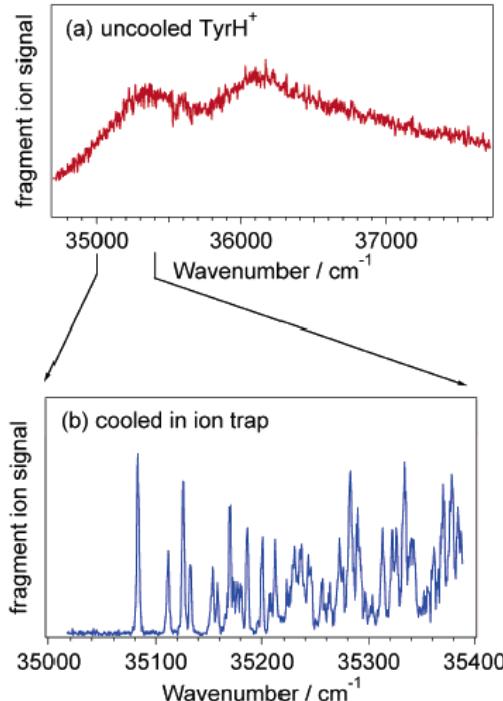
Asmis group, FHI Berlin

Cryogenic ion spectroscopy

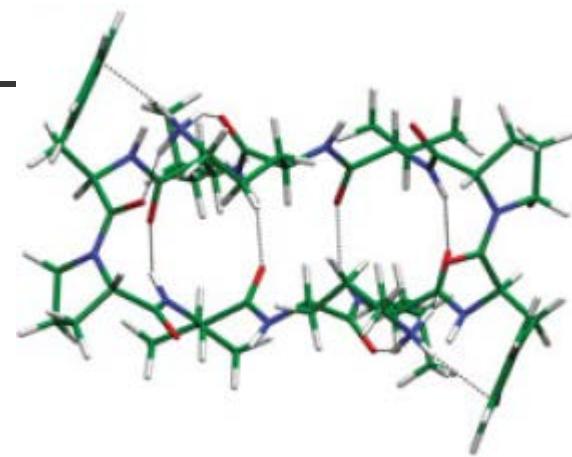
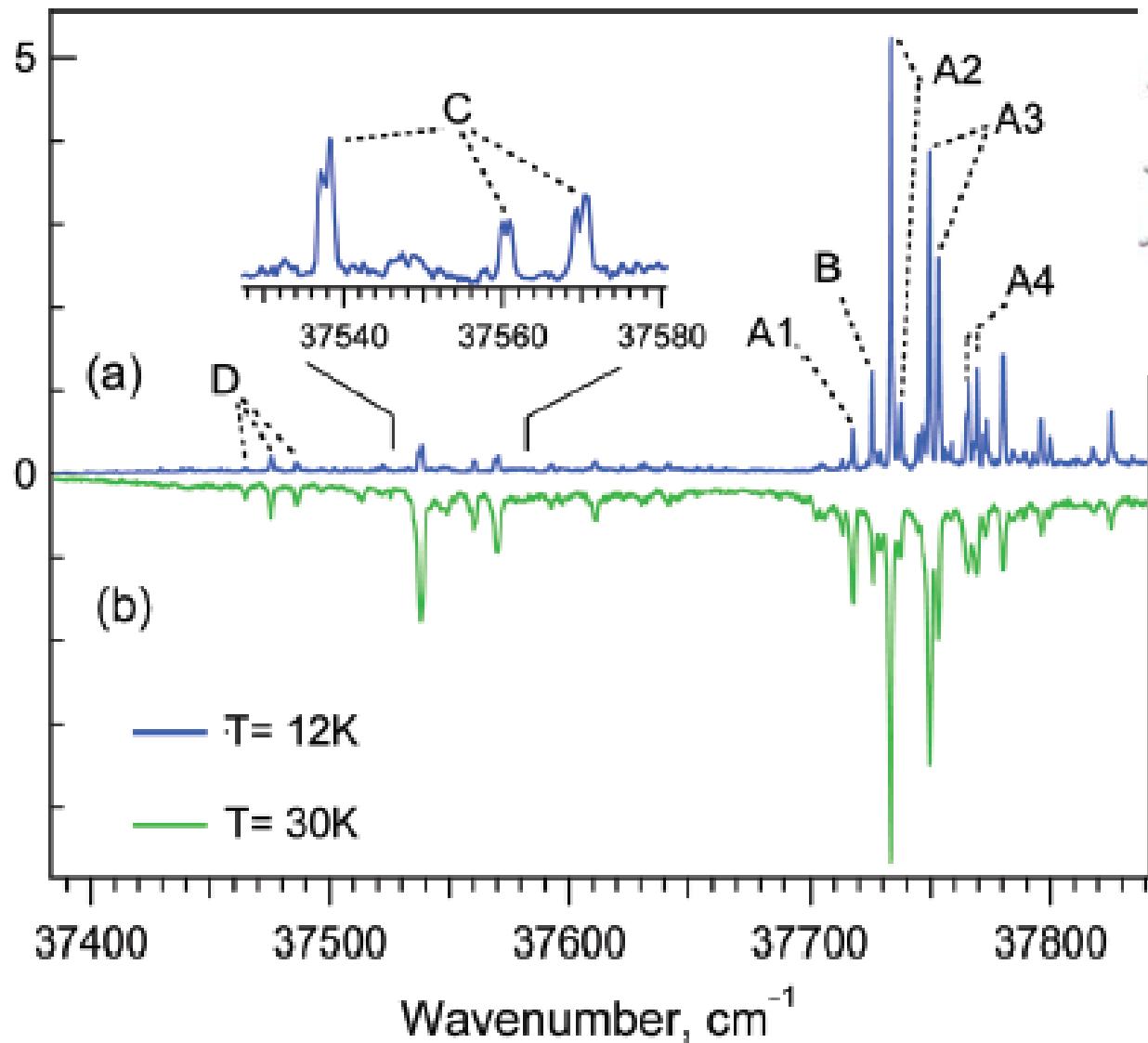
Detection for IR or UV spectroscopies

- Fluorescence (LIF)
- Laser Induced Reaction (LIR)
- Messenger
- UV photodissociation

1. Electronic excitation
2. Internal conversion
3. Vibrational excitation
4. Dissociation
5. Detect fragment ion m/z

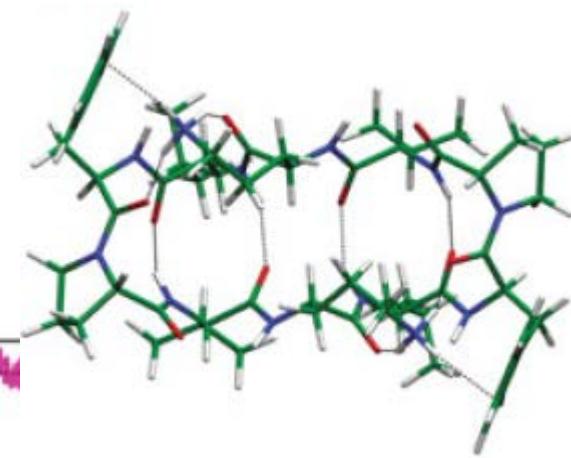
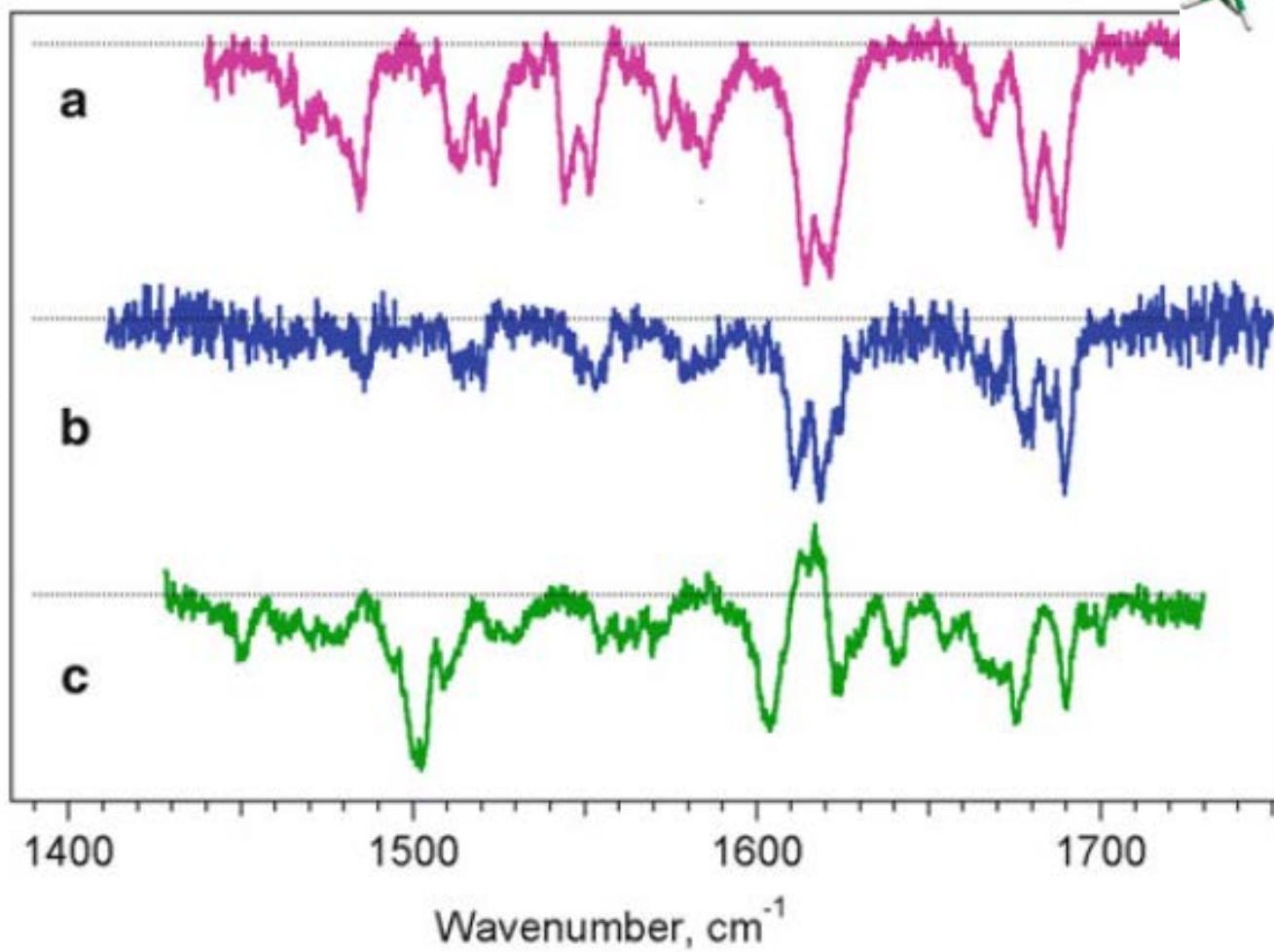


Fragment yield, %



Gramicidin S

Relative ion signal depletion

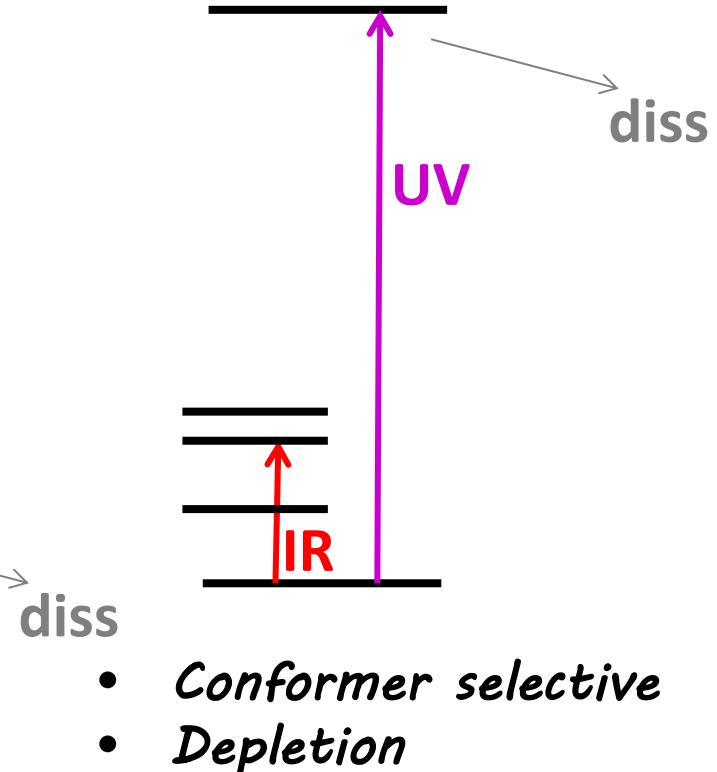
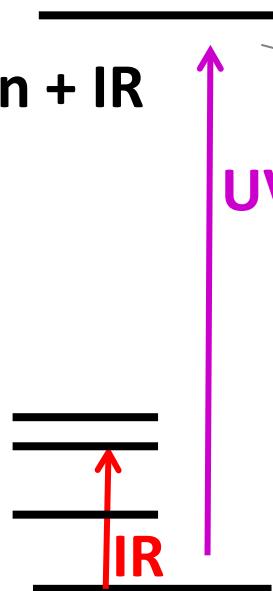


Gramicidin S

Cryogenic ion spectroscopy

Detection for IR or UV spectroscopies

- Fluorescence (LIF)
- Laser Induced Reaction (LIR)
- Messenger
- **UV photodissociation + IR**

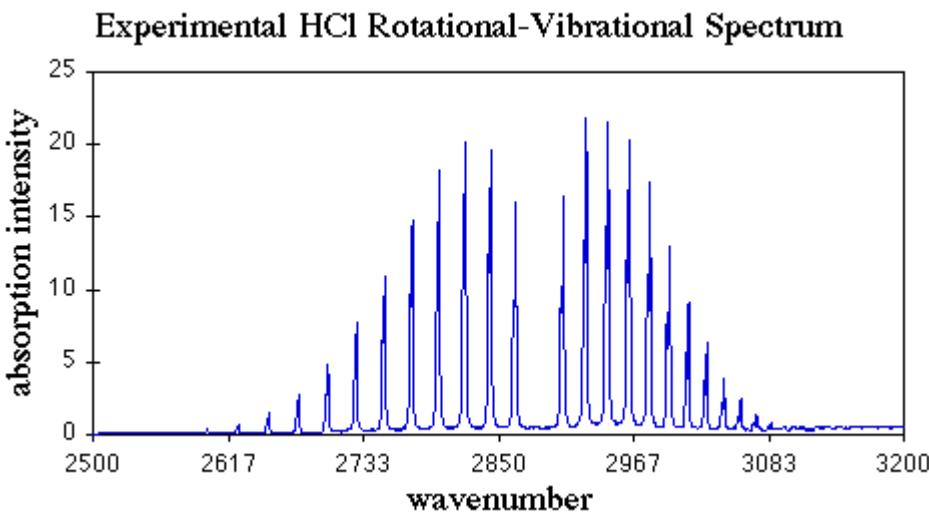


- *Not conformer selective*
- *Gain*

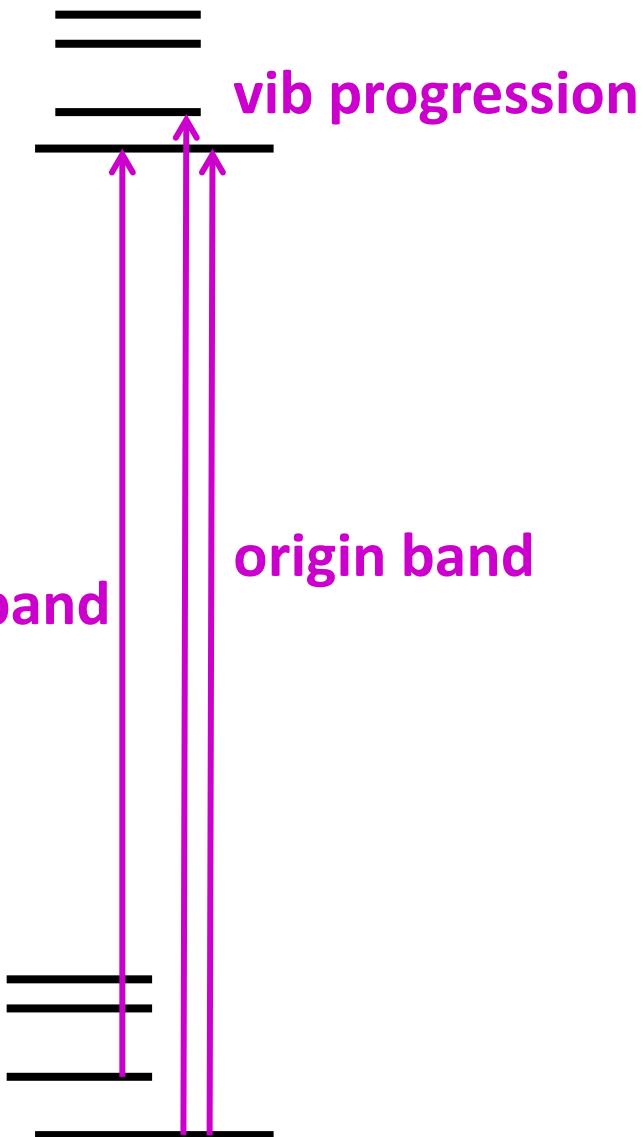
Cryogenic ion spectroscopy

Determination of the ion temperature

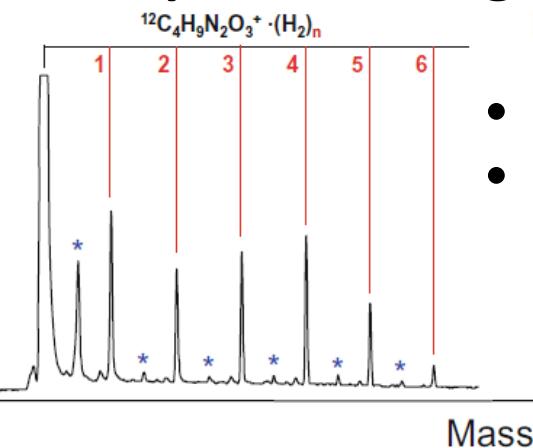
- Clustering (with He) observed?
- Rotational resolution: highest J observed
- Rotational envelope
- Hot bands observed



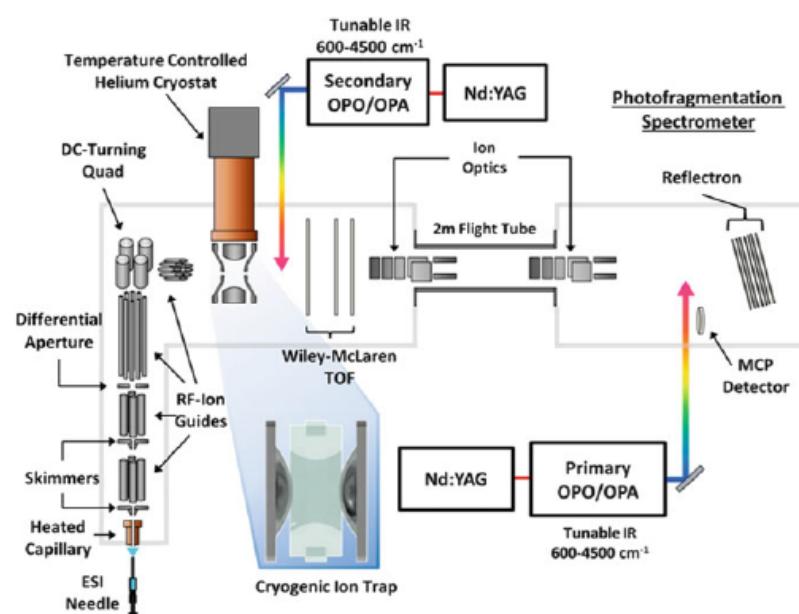
$$\text{rotational: pop} \sim (2J+1)\exp[-E_J/kT]$$



Example: Messenger (H_2)

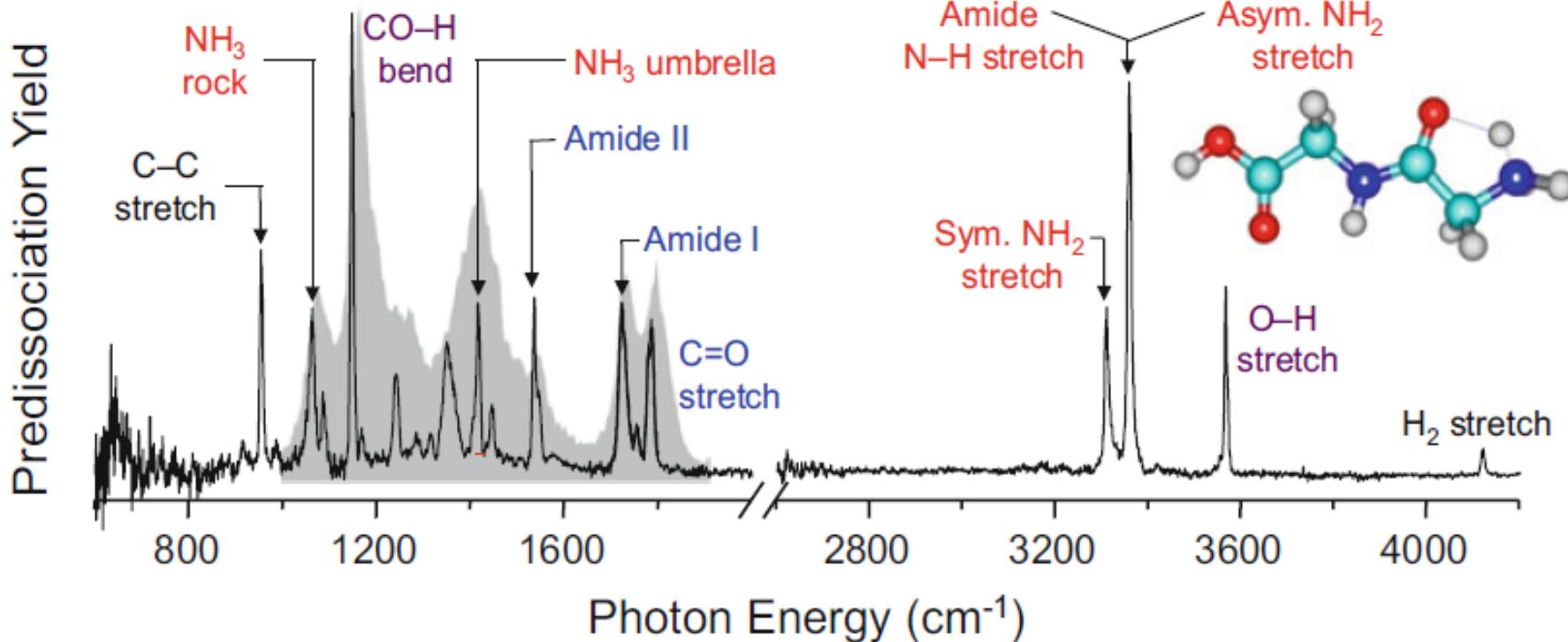


- no UV chromophore
- no conformer select



M.A. Johnson & co.

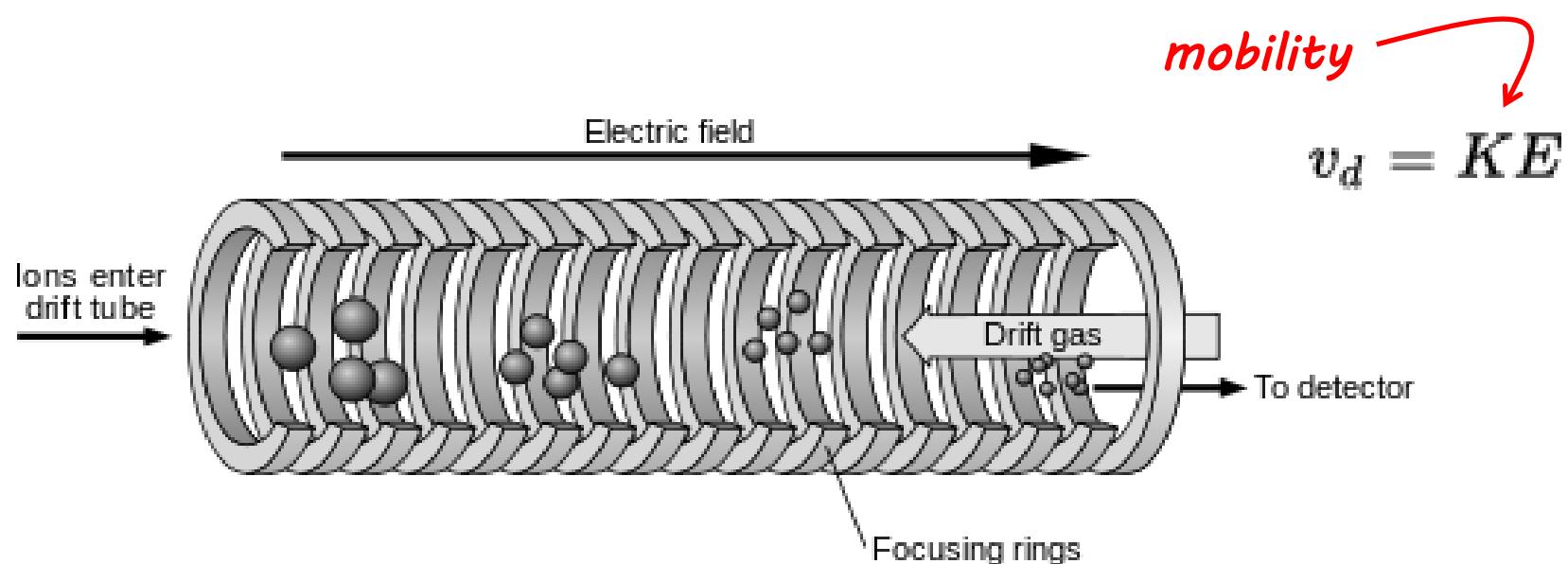
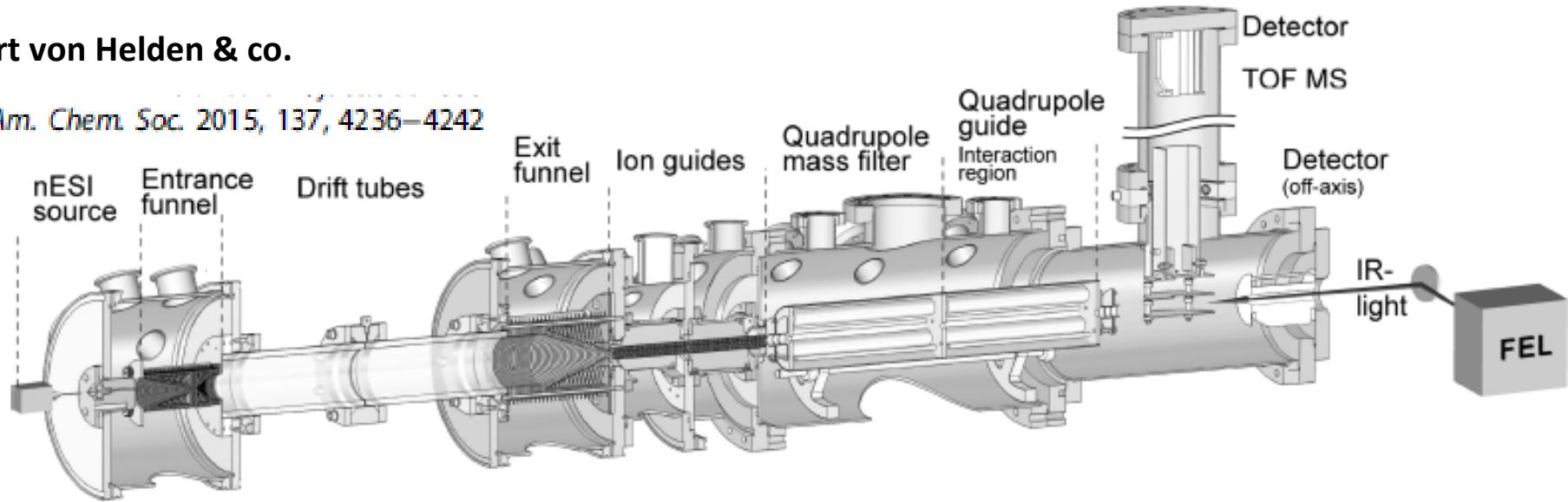
ACCOUNTS OF CHEMICAL RESEARCH ■ 202–210 ■ 2014 ■ Vol. 47,



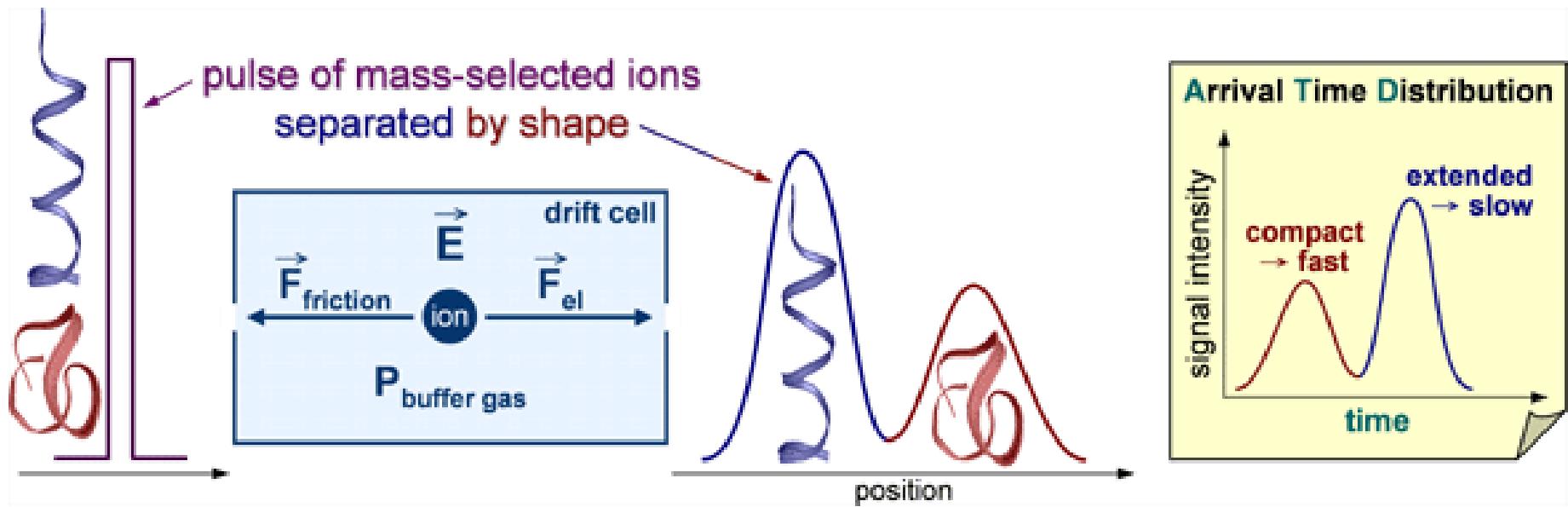
Dealing with conformational heterogeneity: ion mobility separation

Gert von Helden & co.

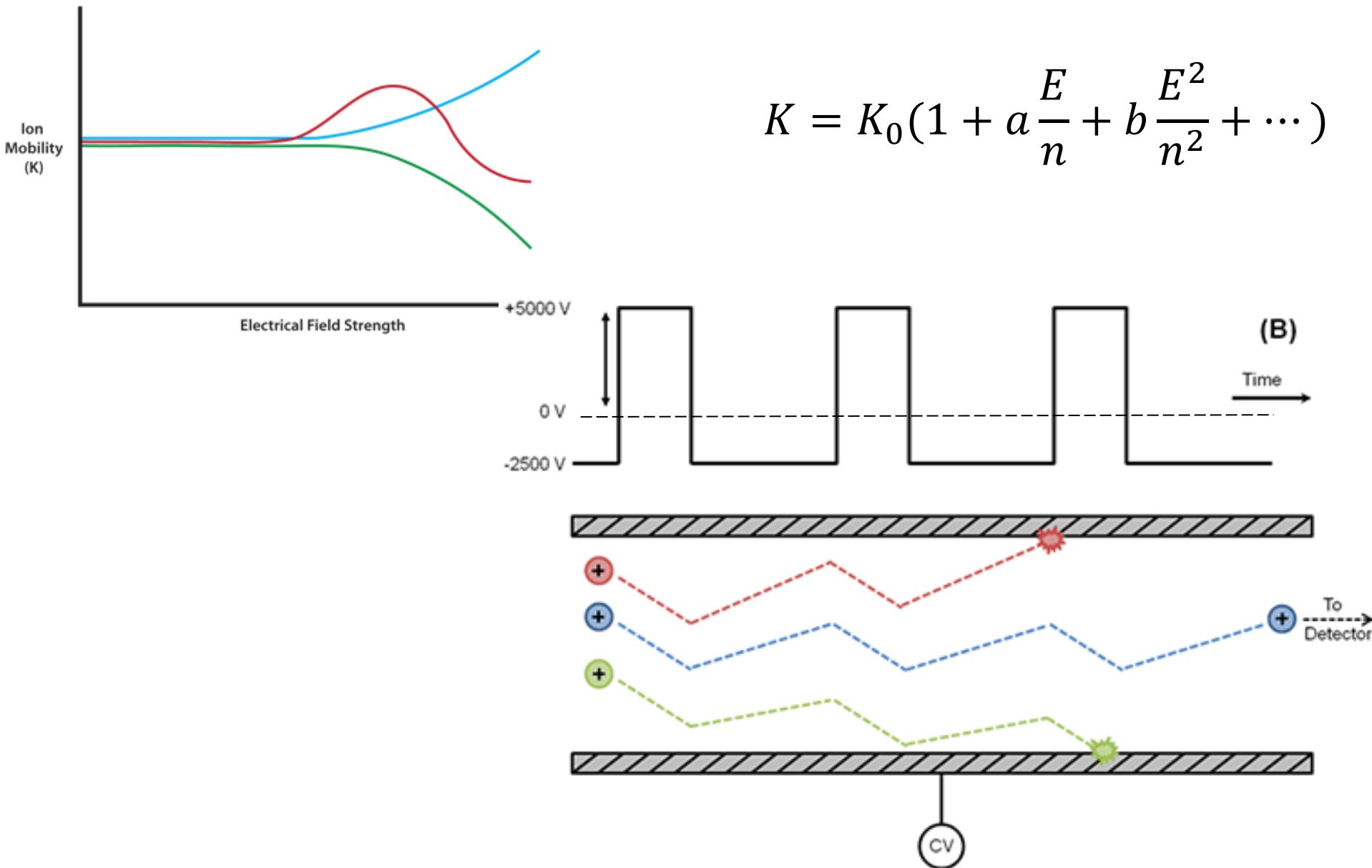
J. Am. Chem. Soc. 2015, 137, 4236–4242



ion mobility spectrometry (IMS)



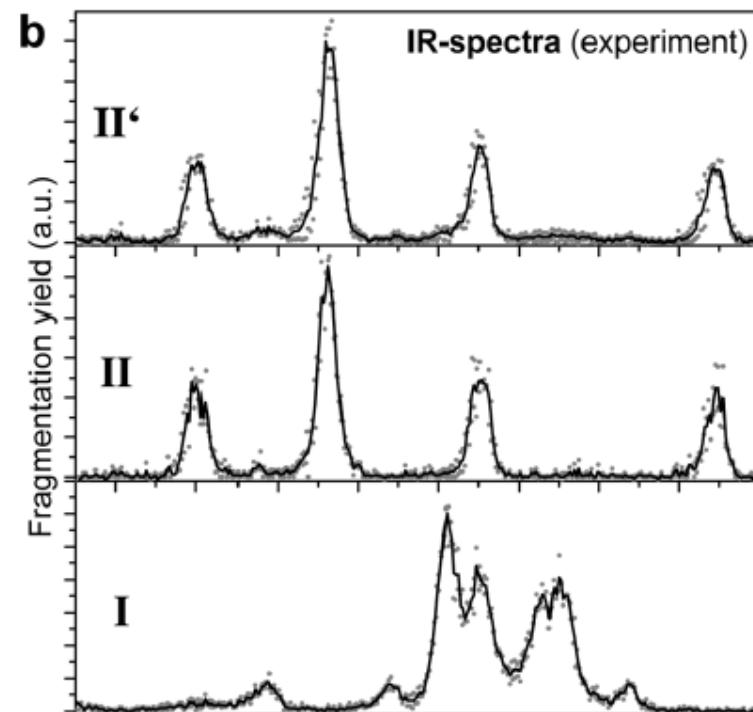
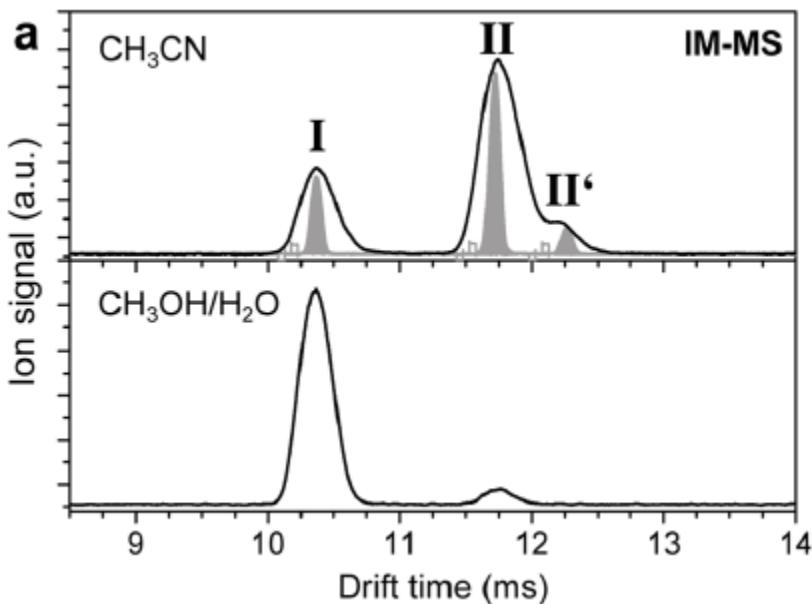
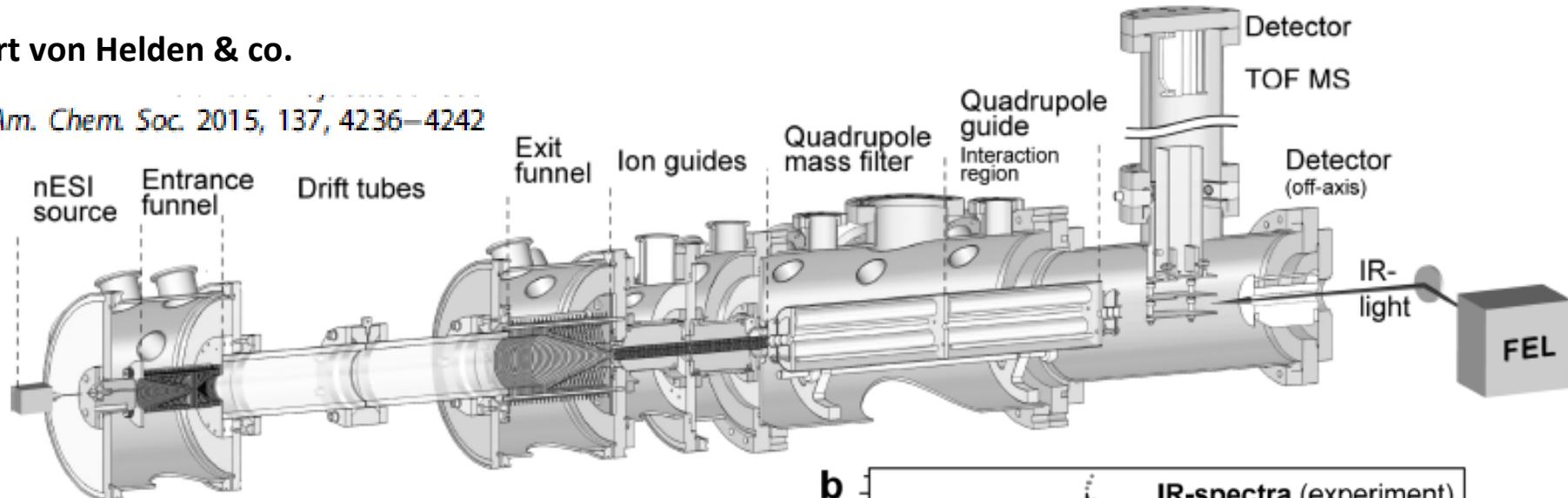
Differential ion mobility spectrometry (DIMS)



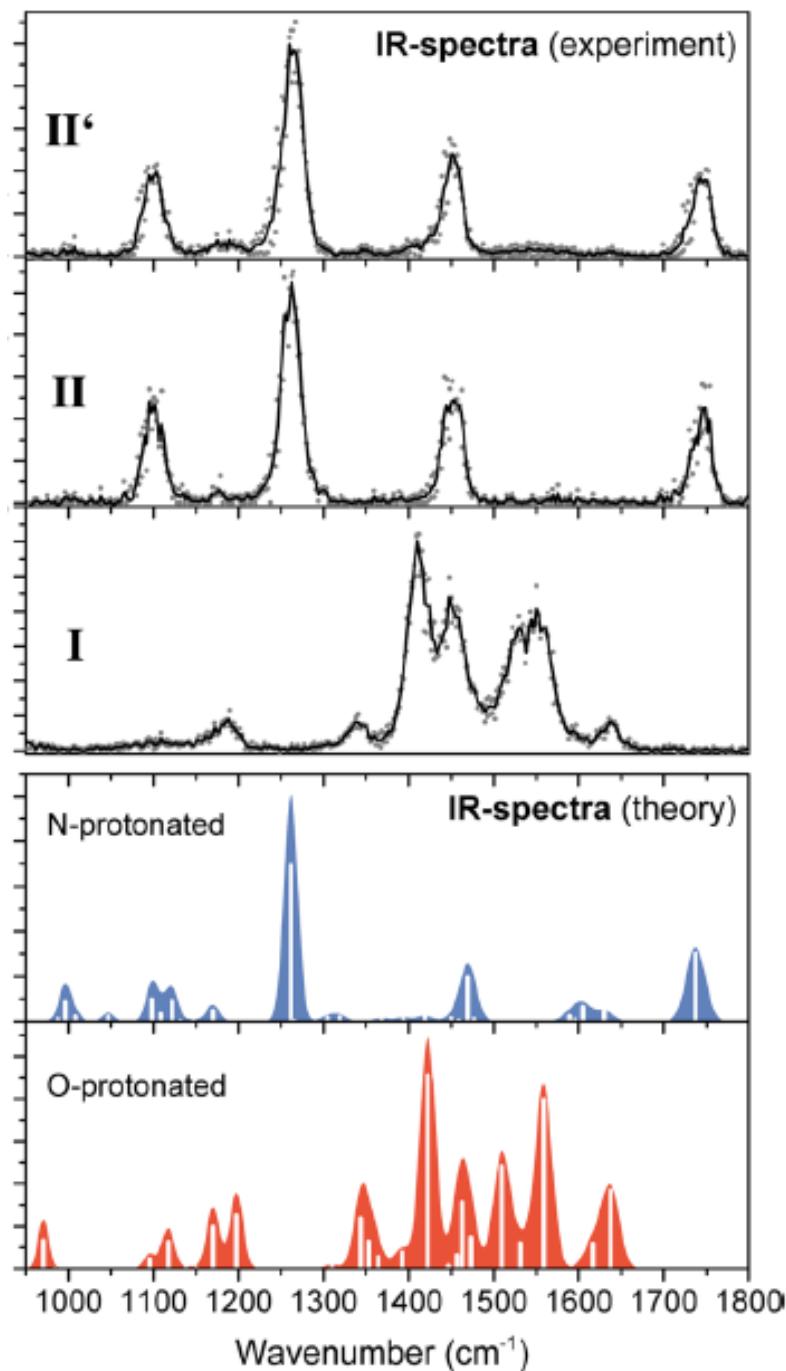
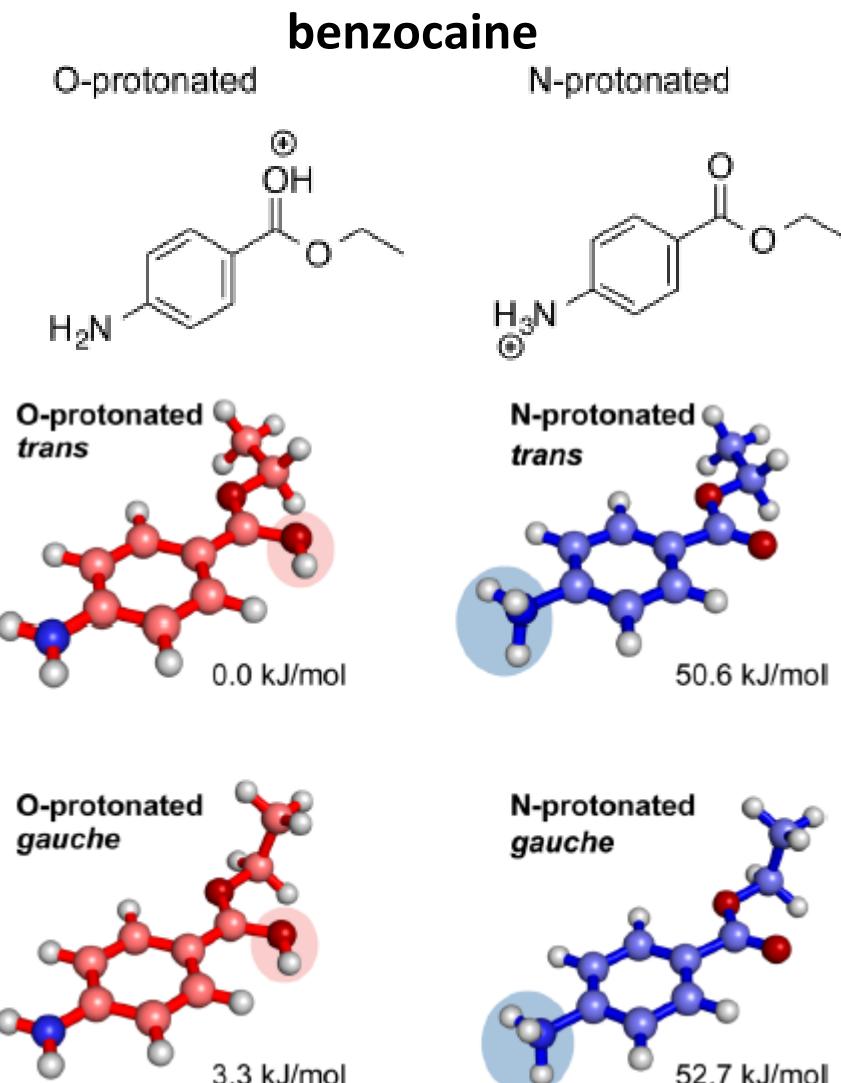
Dealing with conformational heterogeneity: ion mobility separation

Gert von Helden & co.

J. Am. Chem. Soc. 2015, 137, 4236–4242



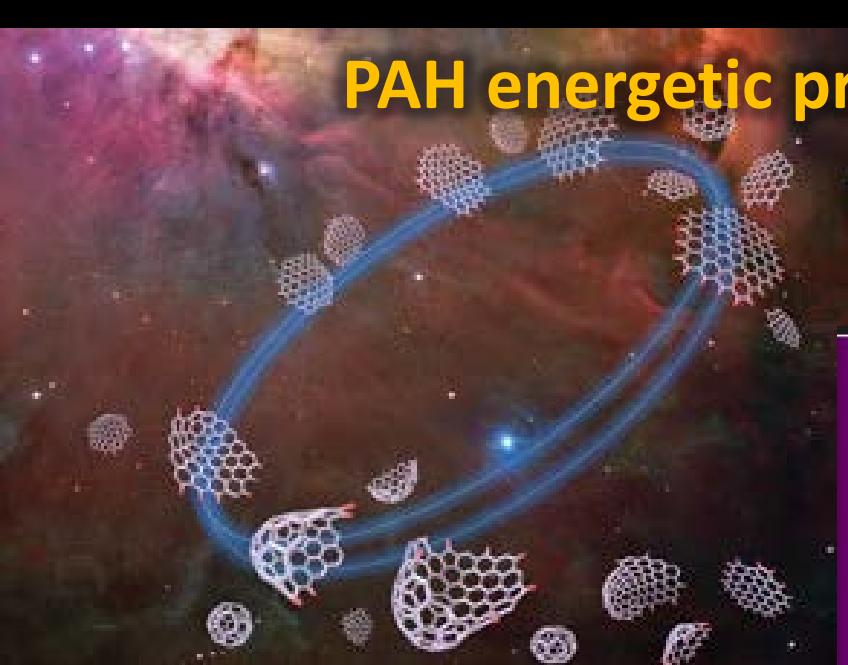
Conformer (protomer) selected IR spectroscopy



IR spectroscopy and chemistry of ionized polycyclic aromatic hydrocarbons (PAHs)

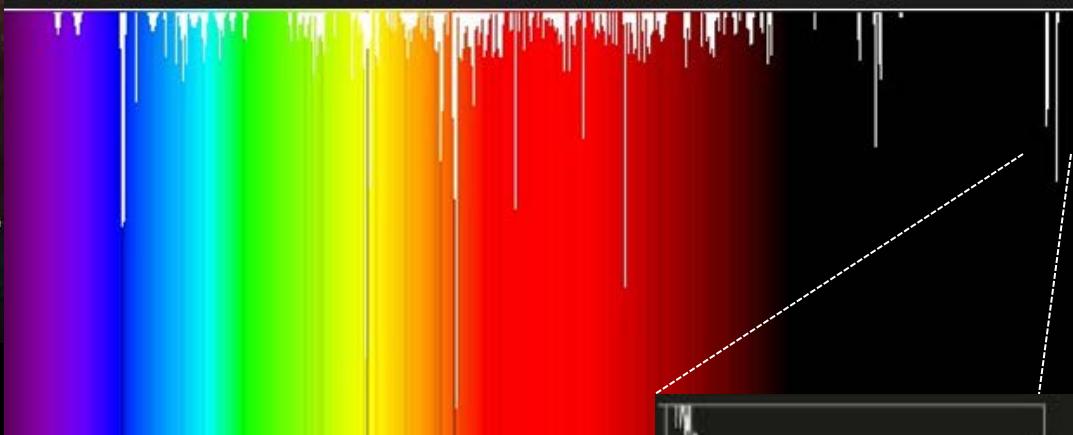
Applications in astrochemistry

PAH energetic processing and fullerenes



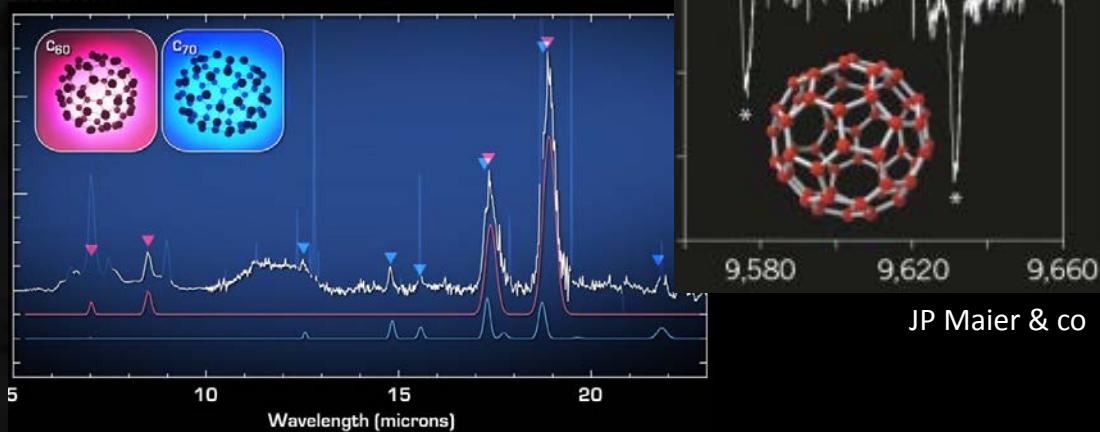
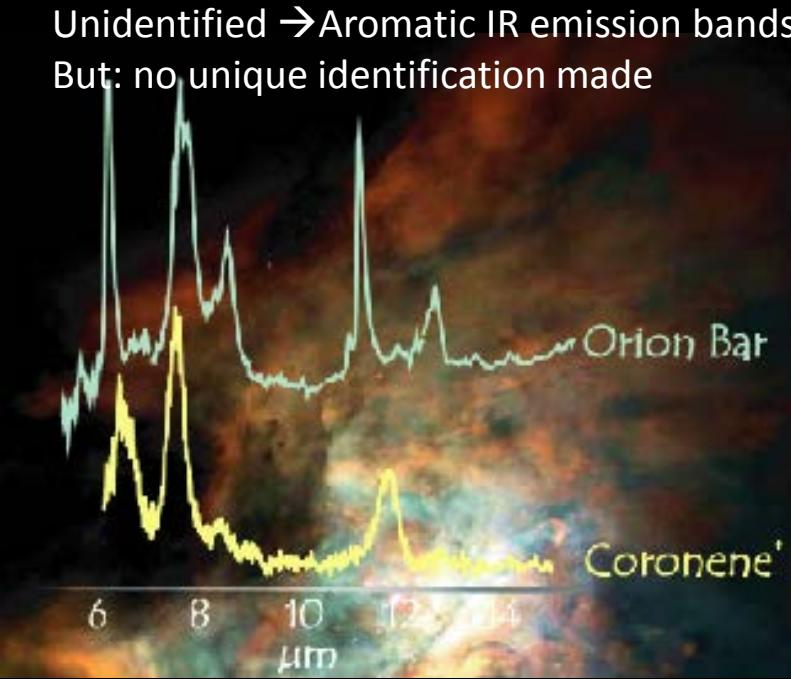
Diffuse Interstellar Bands (DIBs)

Recent identification of C₆₀ and C₇₀
More large carbon species?



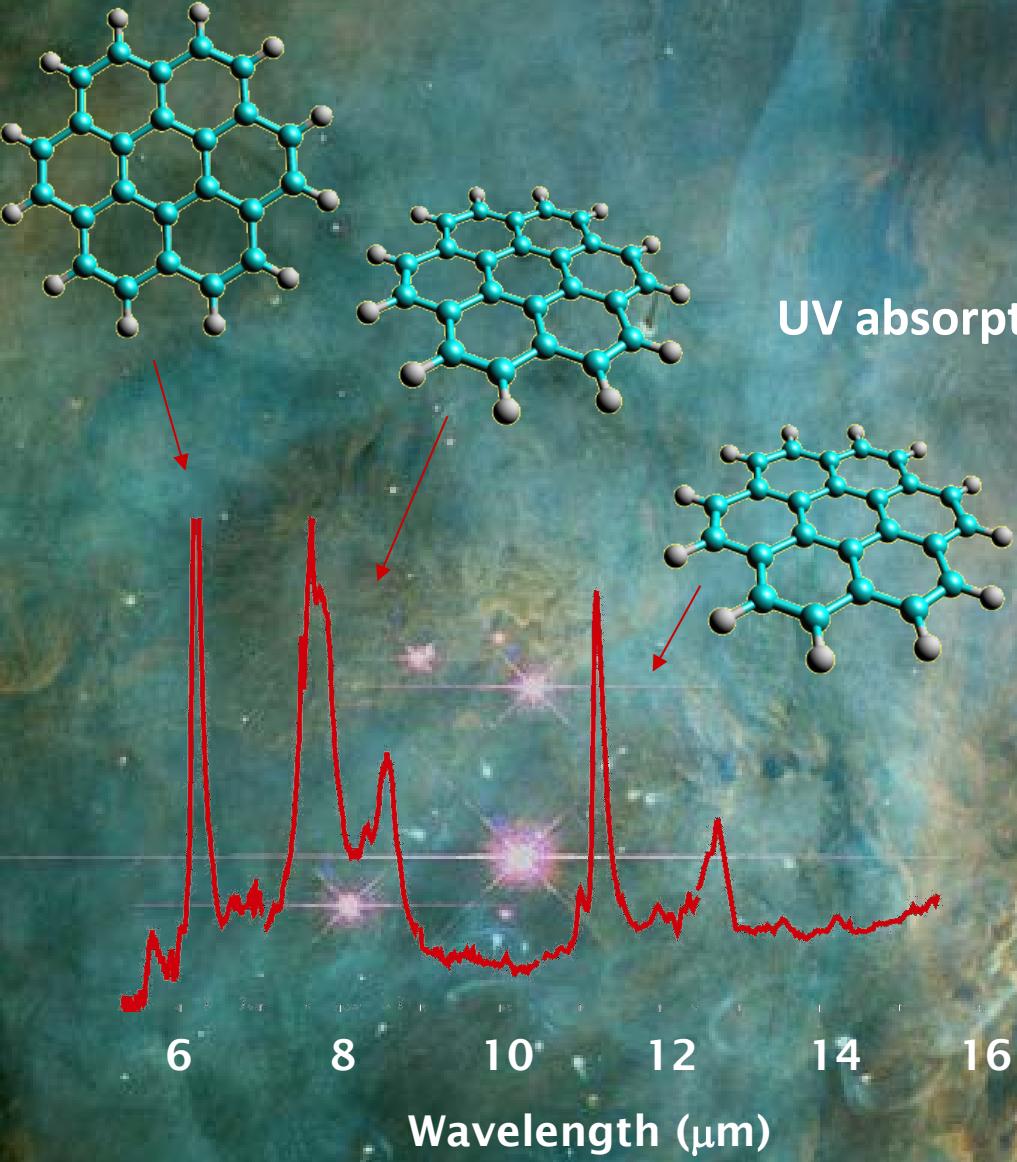
From UIRs to AIRs

Unidentified → Aromatic IR emission bands
But: no unique identification made



JP Maier & co

Unidentified infrared bands (UIRs)



Abundantly present

Observed in emission

UV absorption followed by IR radiative cooling

→ Polyaromatic species - PAHs

The Astronomer's Periodic Table
(Ben McCall)

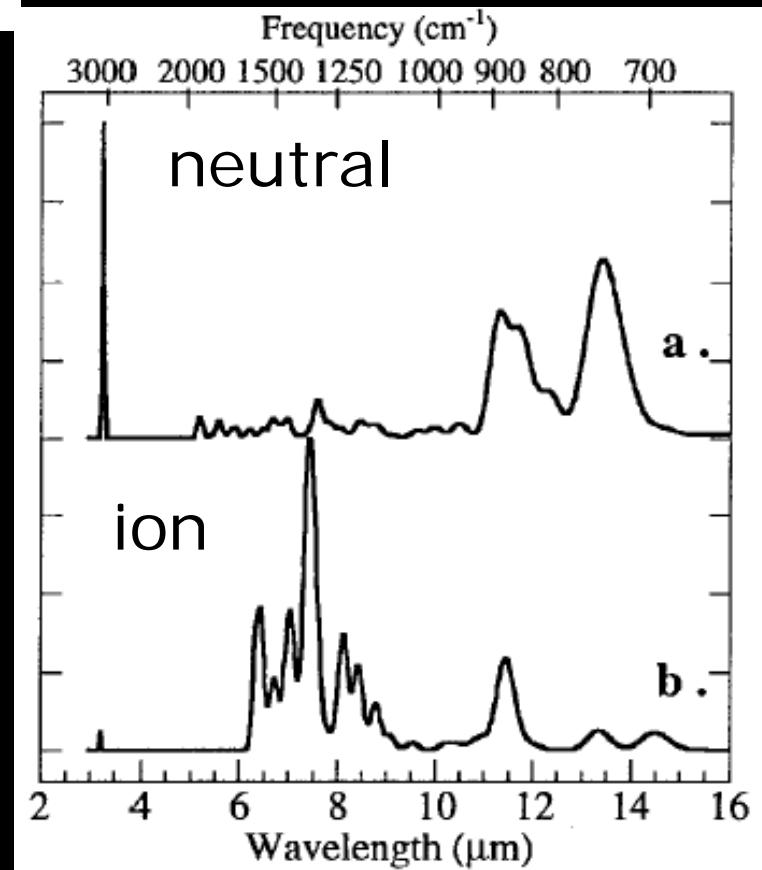
H	He
Mg	Si
C N O	S Ar

Neutral versus ionic PAHs

Pauzat, Talbi, Miller, DeFrees, Ellinger, JPC **96**, 7882 (1992)

Theoretical IR Spectra of Ionized Naphthalene

The main result of this study concerns the unexpected and striking behavior of IR intensities when comparing neutral and positively charged naphthalene. Hartree-Fock calculations show

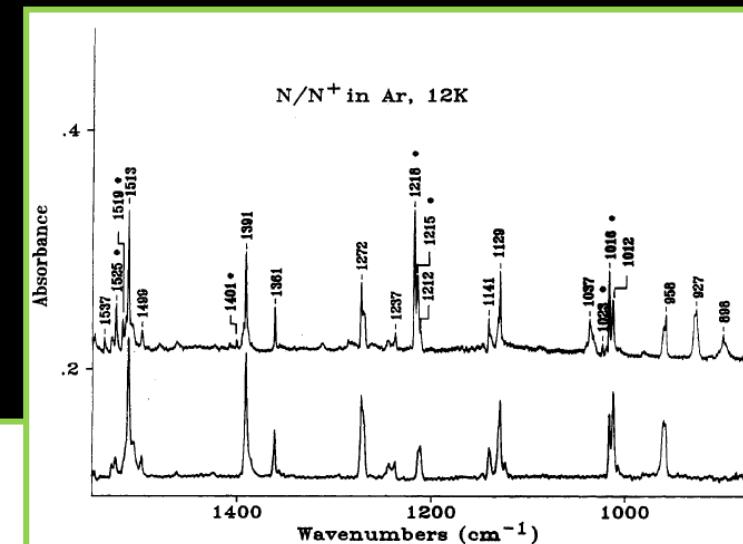
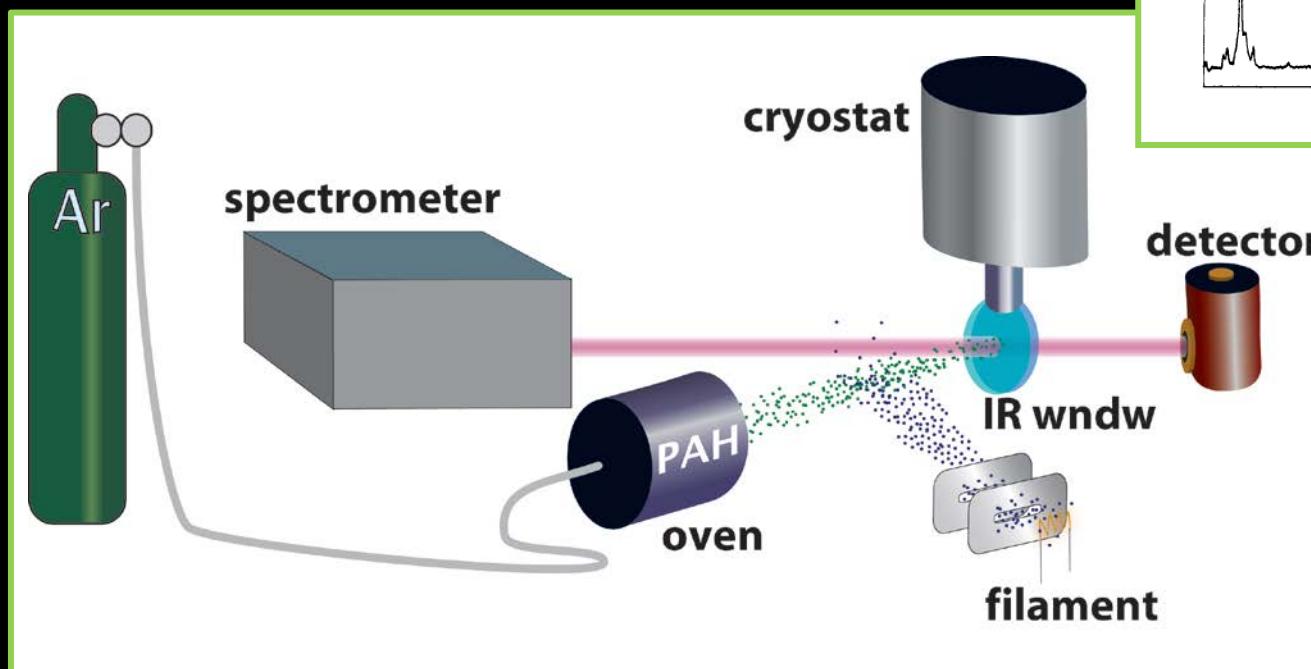


Allamandola, et al.
ApJ **511**, L115 (1999)

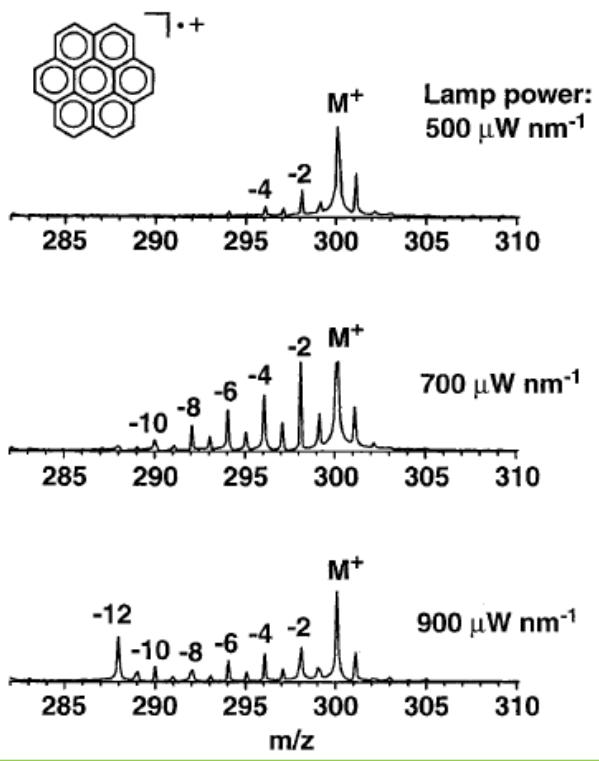
Neutral versus ionic PAHs

Infrared Spectrum of Matrix-Isolated Naphthalene Radical Cation

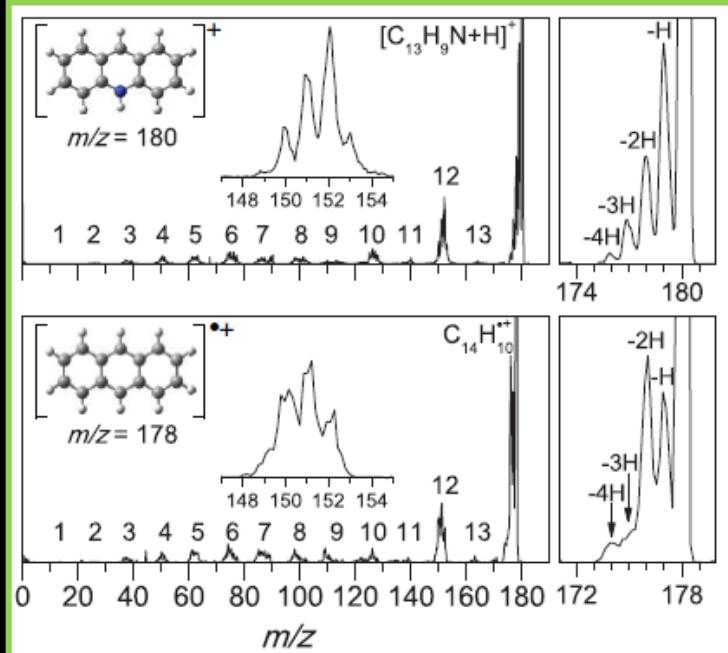
Szczepanski, Roser, Personnette, Eyring, Pellow, Vala,
JPC 96, 7876 (1992)



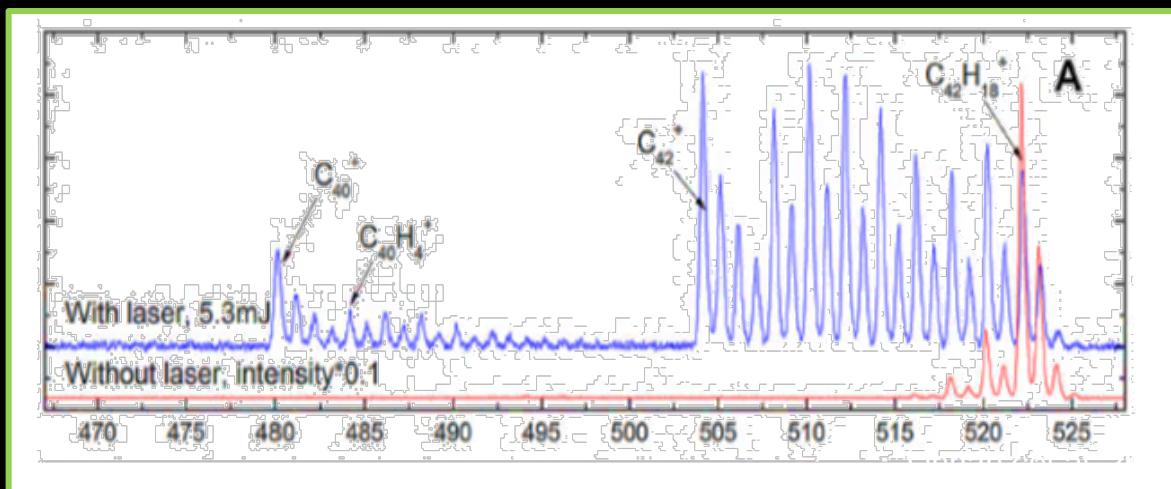
Hydrogen loss



Ekern, Marshall, Szczepanski, Vala
ApJ 1997, **488**, L39



Johansson, Zettergren, Holm, Haag, Nielsen, Wyer,
Kirketerp, Stochkel, Hvelplund, Schmidt, Cederquist
JCP 2011, **135**, 084304

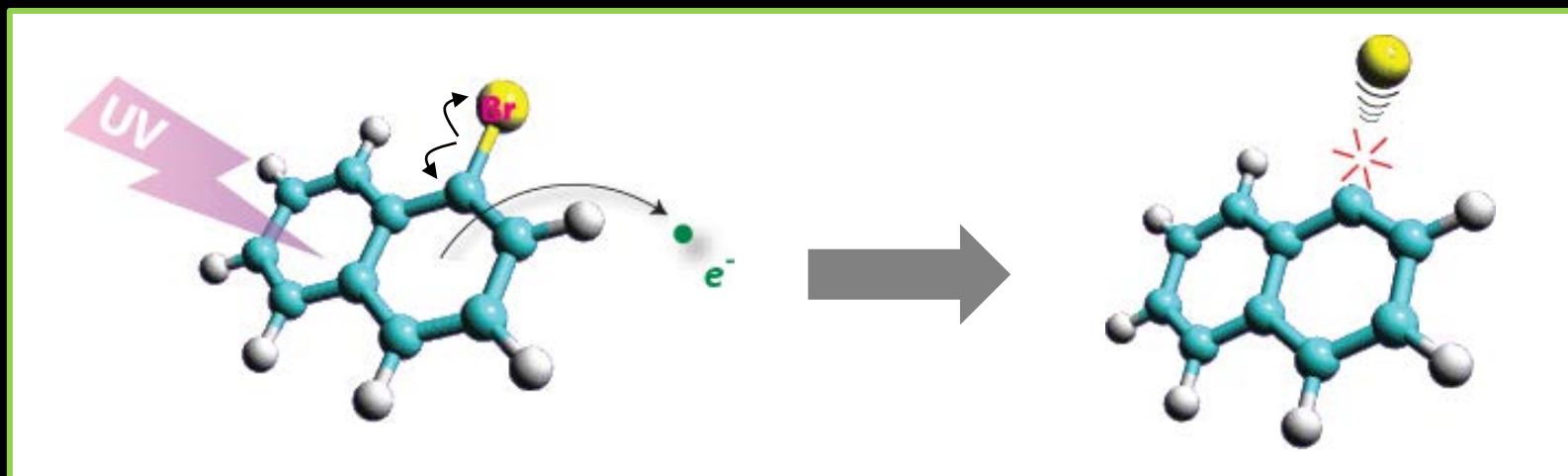
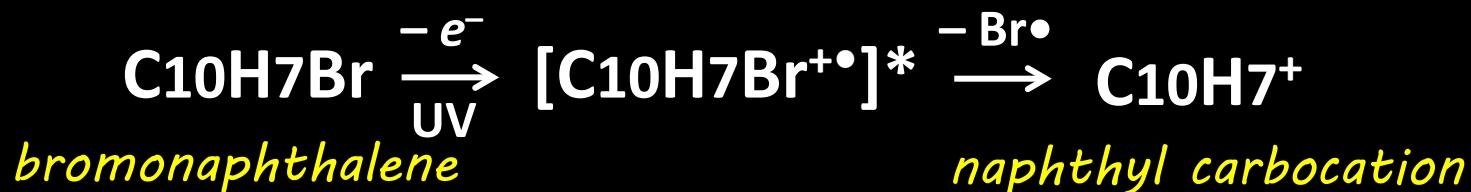


C₄₂H₁₈

H-loss from radical cation PAHs

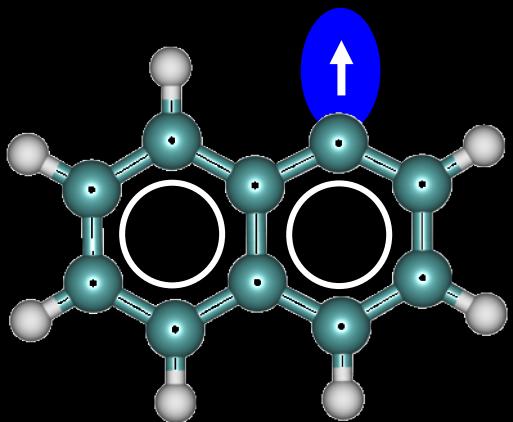
Aryl cations

- Carbocation
- Even-electron
- Closed shell?

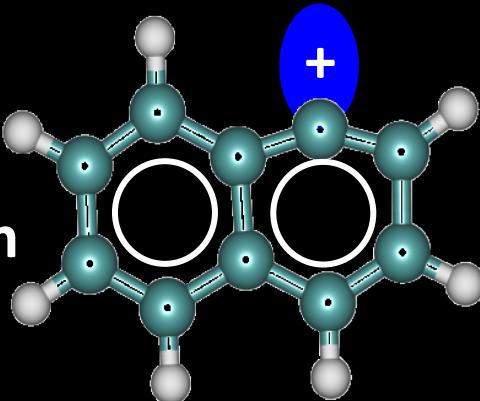


See e.g. Gotkis, Naor, Laskin, Lifshitz, Faulk, Dunbar, *JACS* **1993**, *114*, 7402

aryl cations: even-electron, but closed-shell?



remove
electron

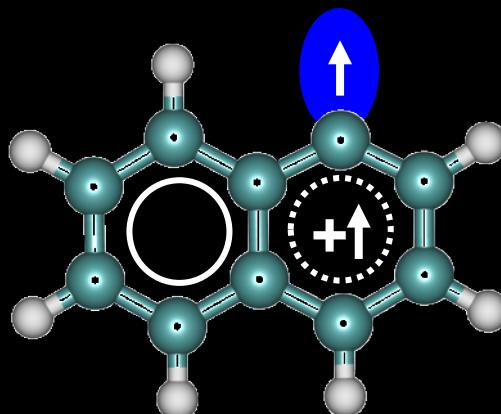


singlet: ... $\pi^{10}\sigma^0$

*localized charge
closed shell
sp hybrid distorts*

$$\Delta E(S - T) = 0$$

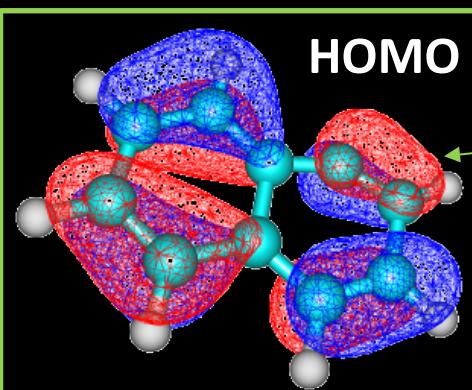
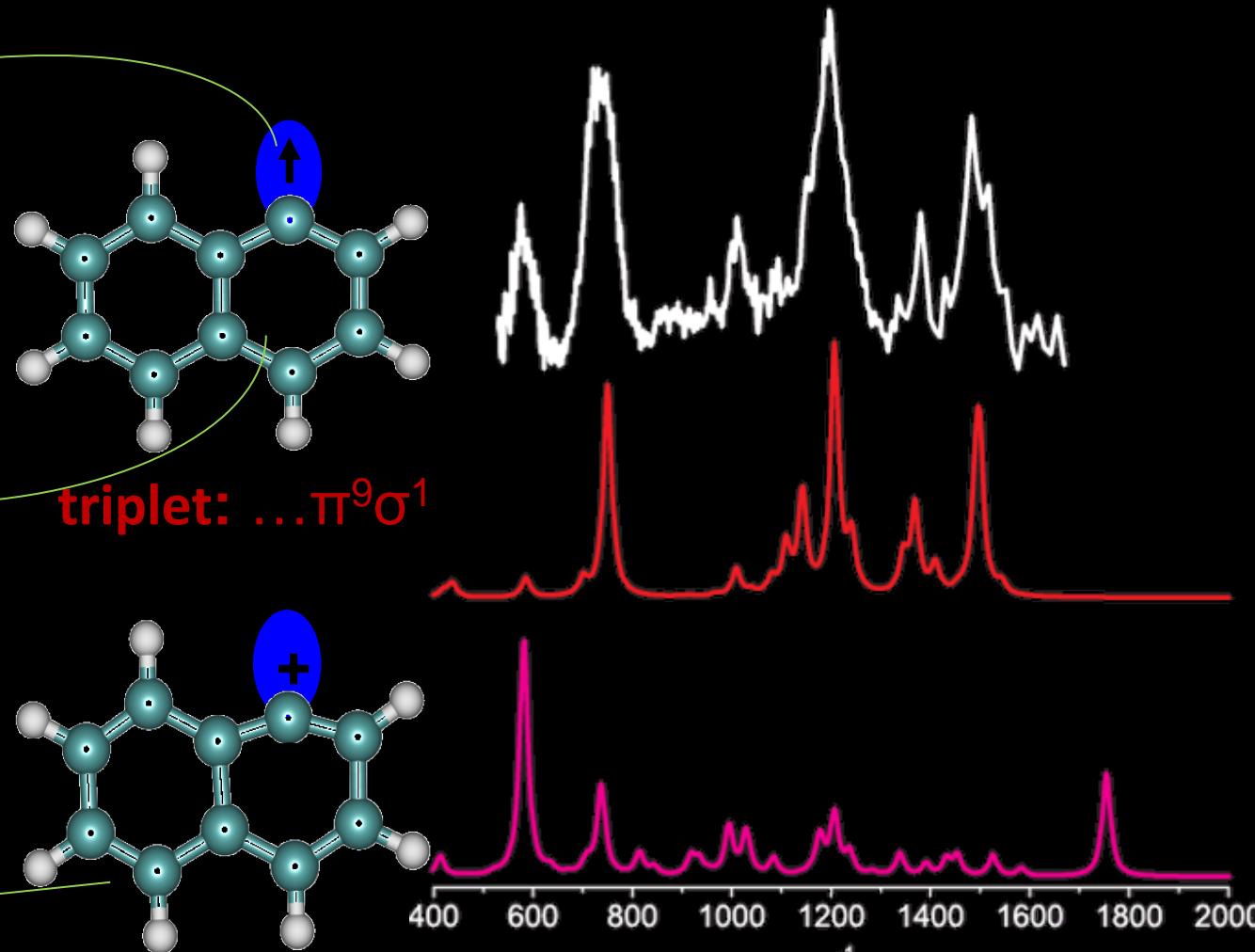
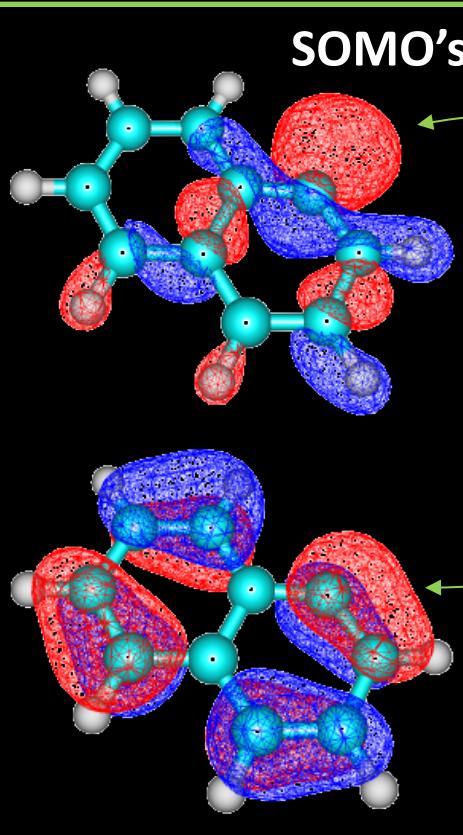
DFT level calculation



triplet: ... $\pi^9\sigma^1$

*delocalized charge
open shell
all sp², no distortion*

IR spectroscopy of the naphthyl cation

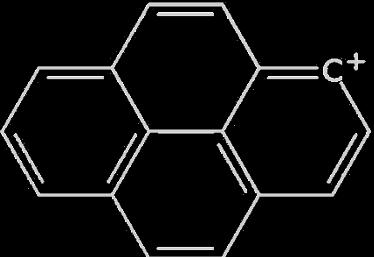


singlet: ... $\pi^{10}\sigma^0$

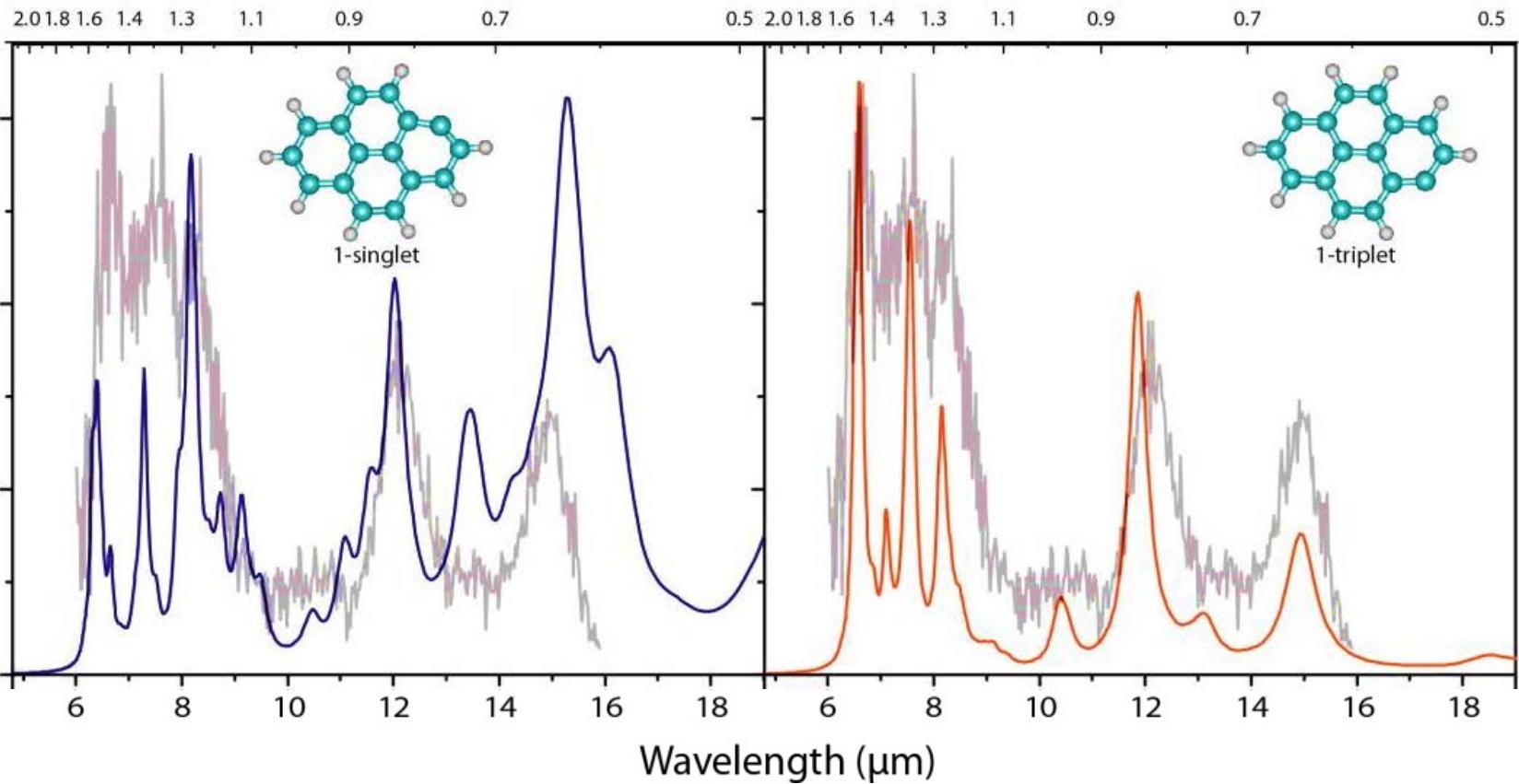
Alvaro Galve, Oomens, *Angew Chem Int Ed* 2011, 50, 7004

Alvaro Galve, Oomens, *Astrophys J* 2012, 746, 83

Larger PAHs



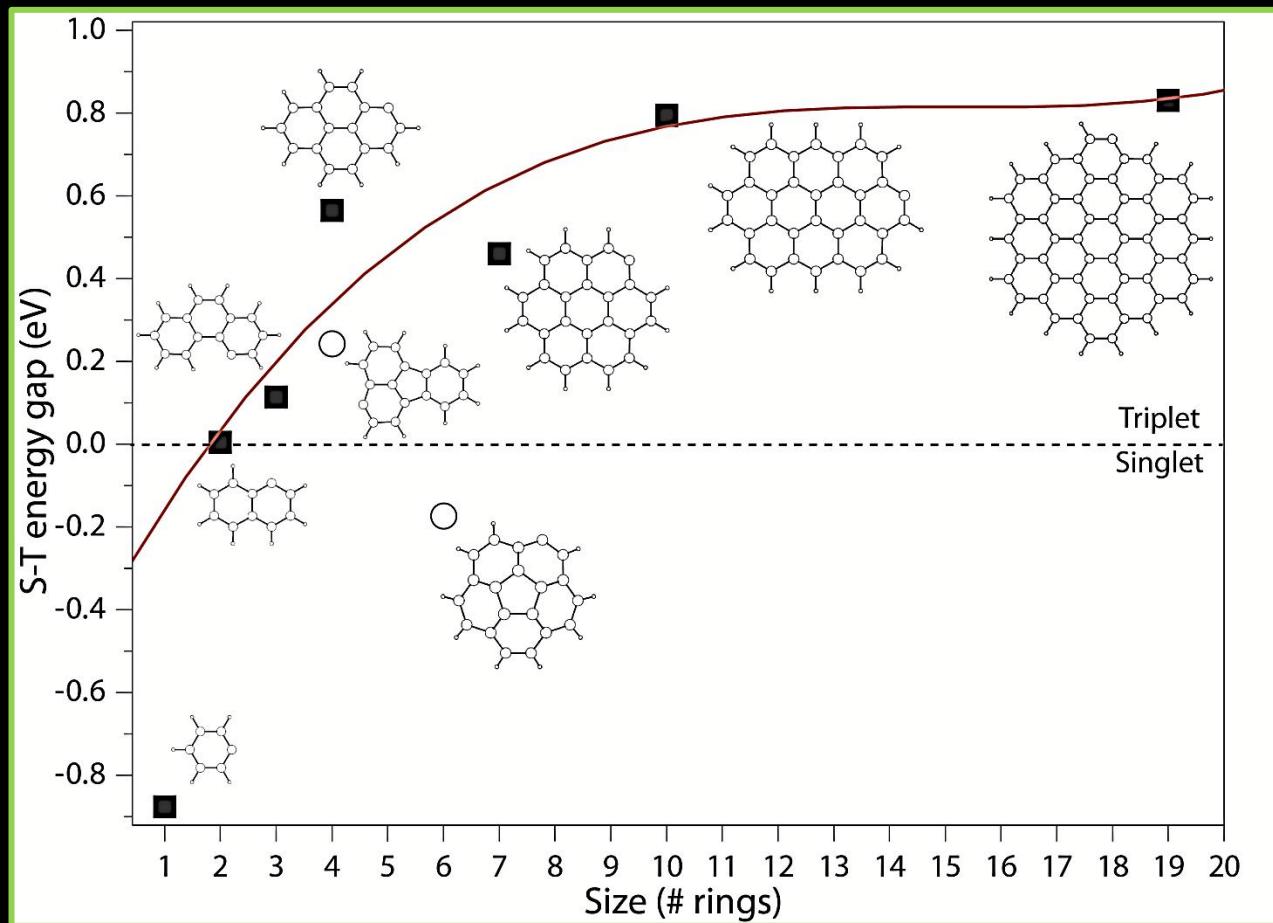
$$\Delta E(S - T) = +0.56 \text{ eV}$$



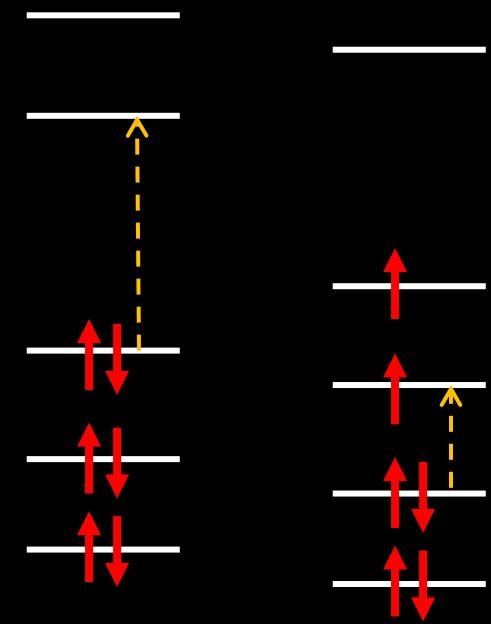
singlet

triplet

Aryl cations: triplet state more stable



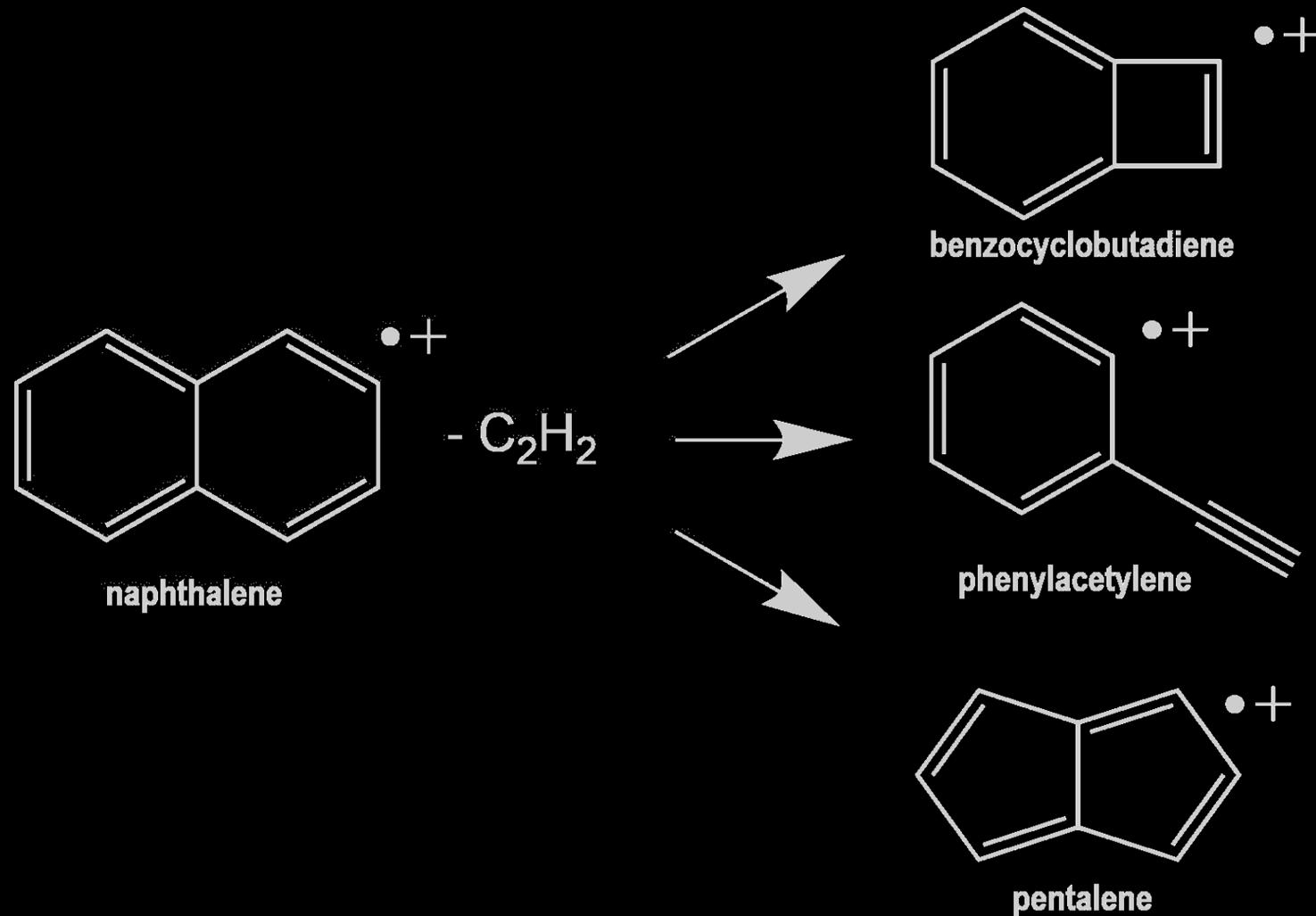
UV/vis spectra?



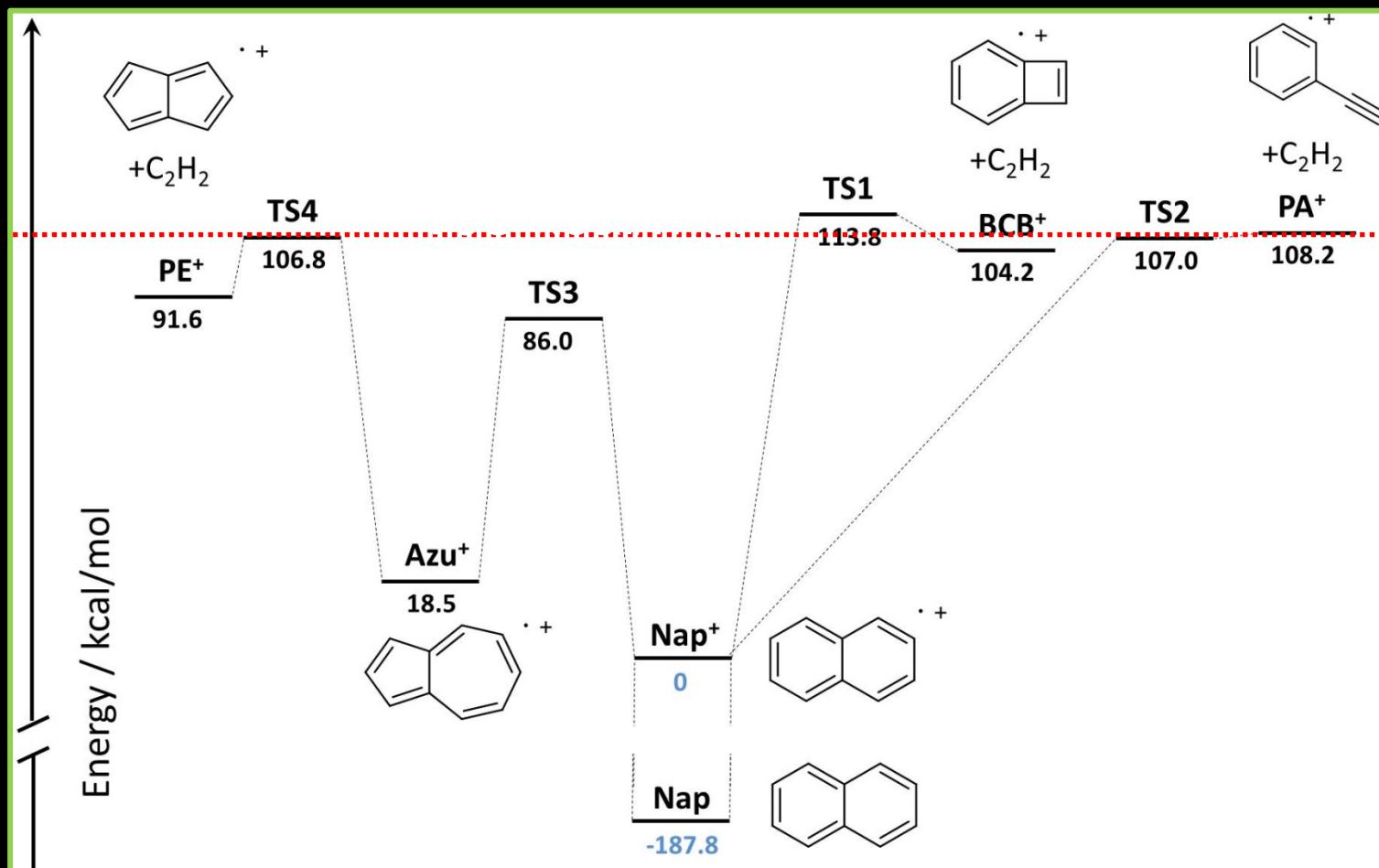
singlet
triplet

Alvaro Galve, Oomens, *Astrophys J* 2012, 746, 83

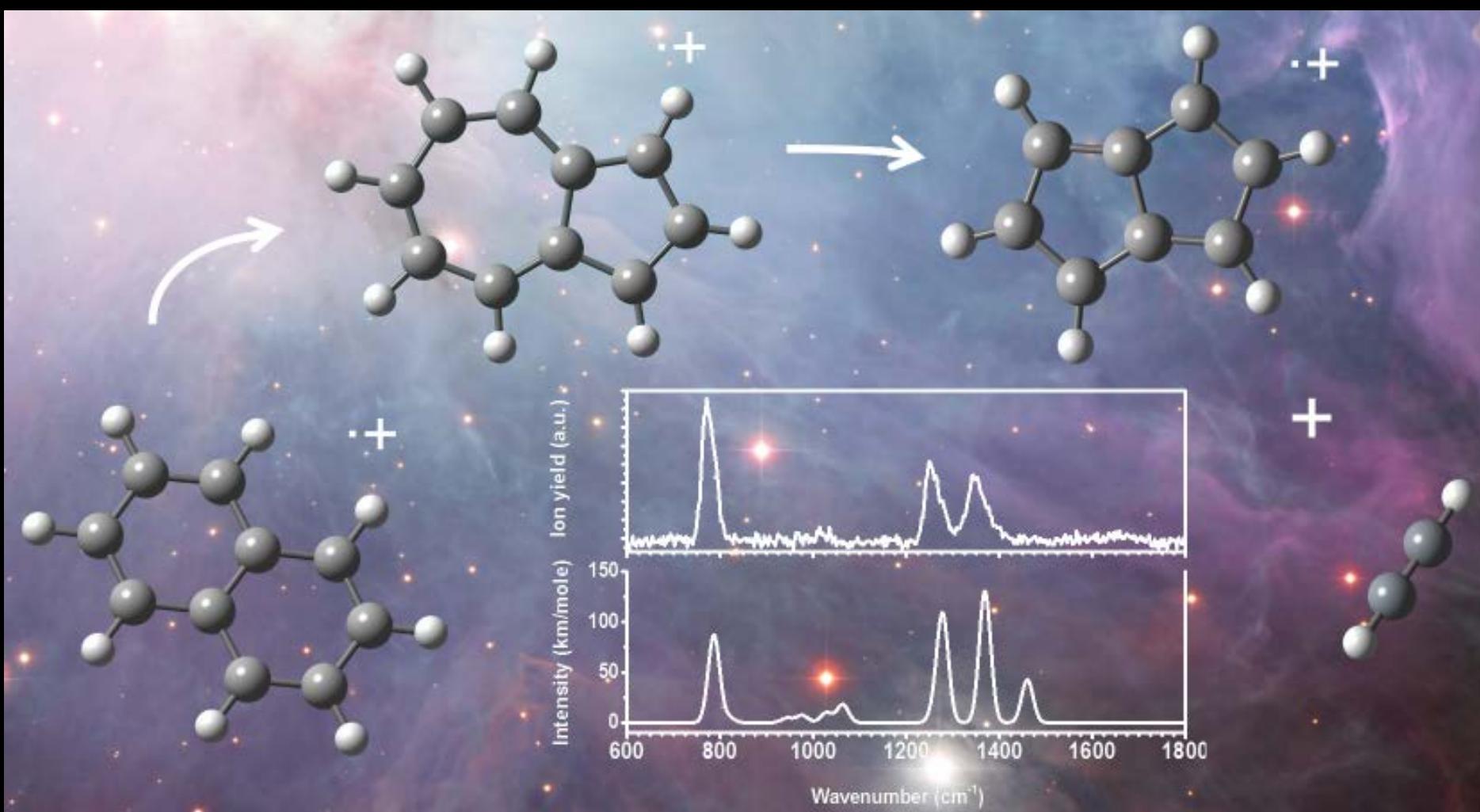
Naphthalene⁺ dissociation: C₂H₂-loss



Naphthalene⁺ Potential Energy Surface

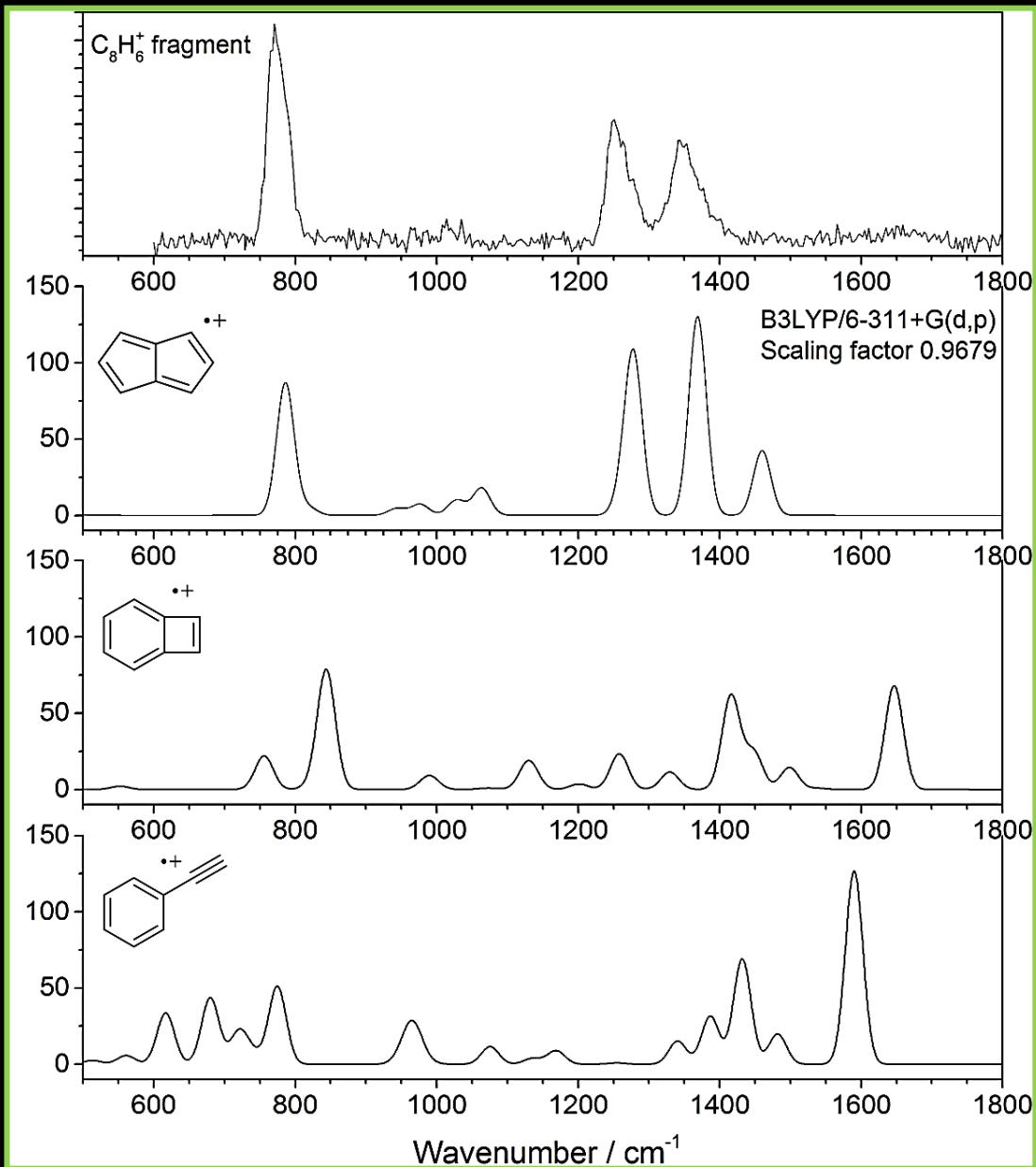


Spectroscopic product ion identification



Bouwman, de Haas & Oomens, *Chem. Commun.* 2016, 52, 2636-2638

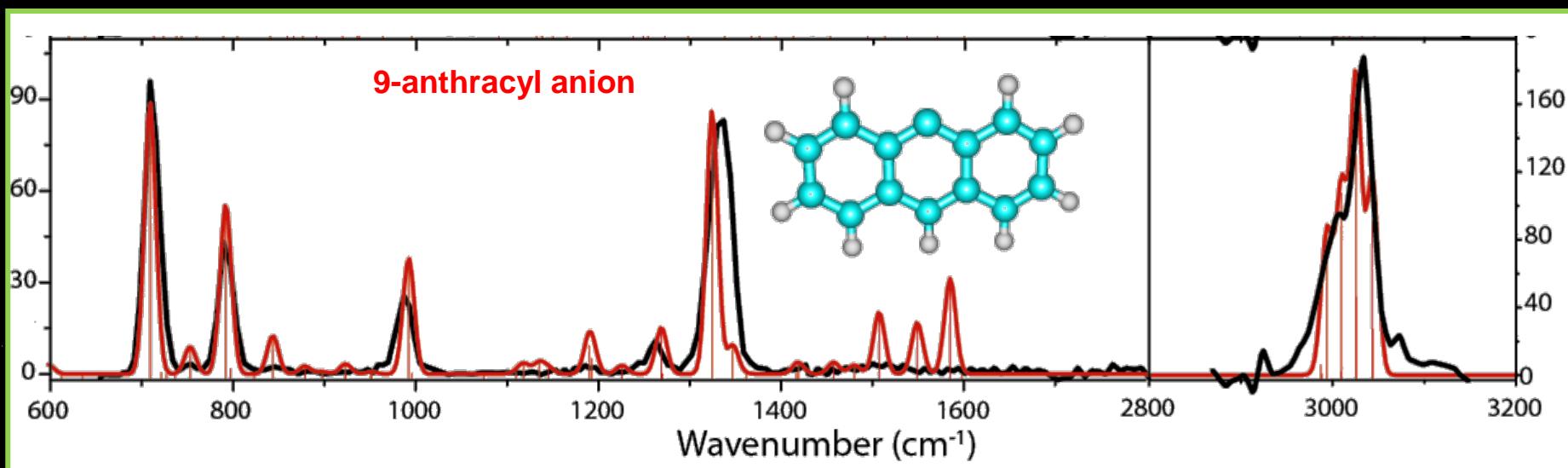
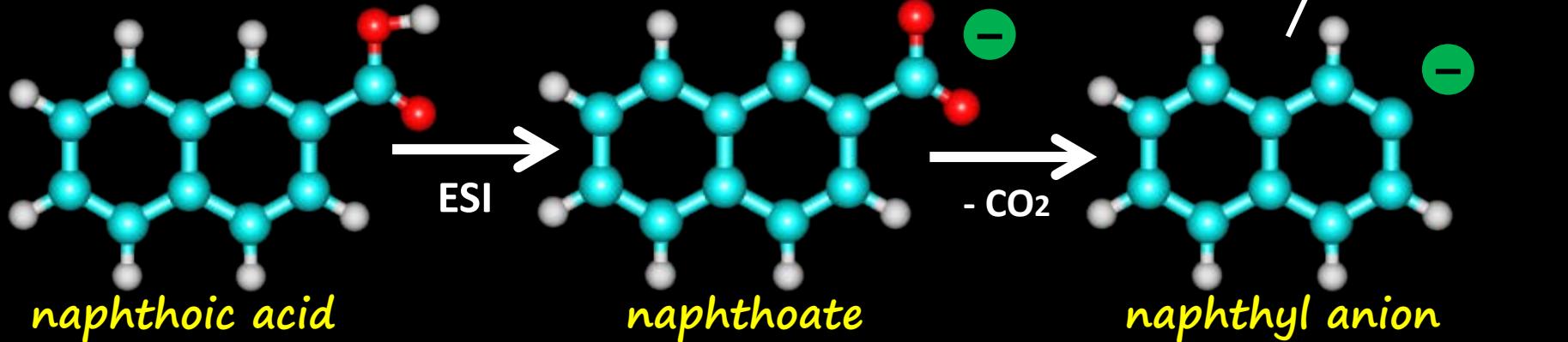
Spectroscopic product ion identification



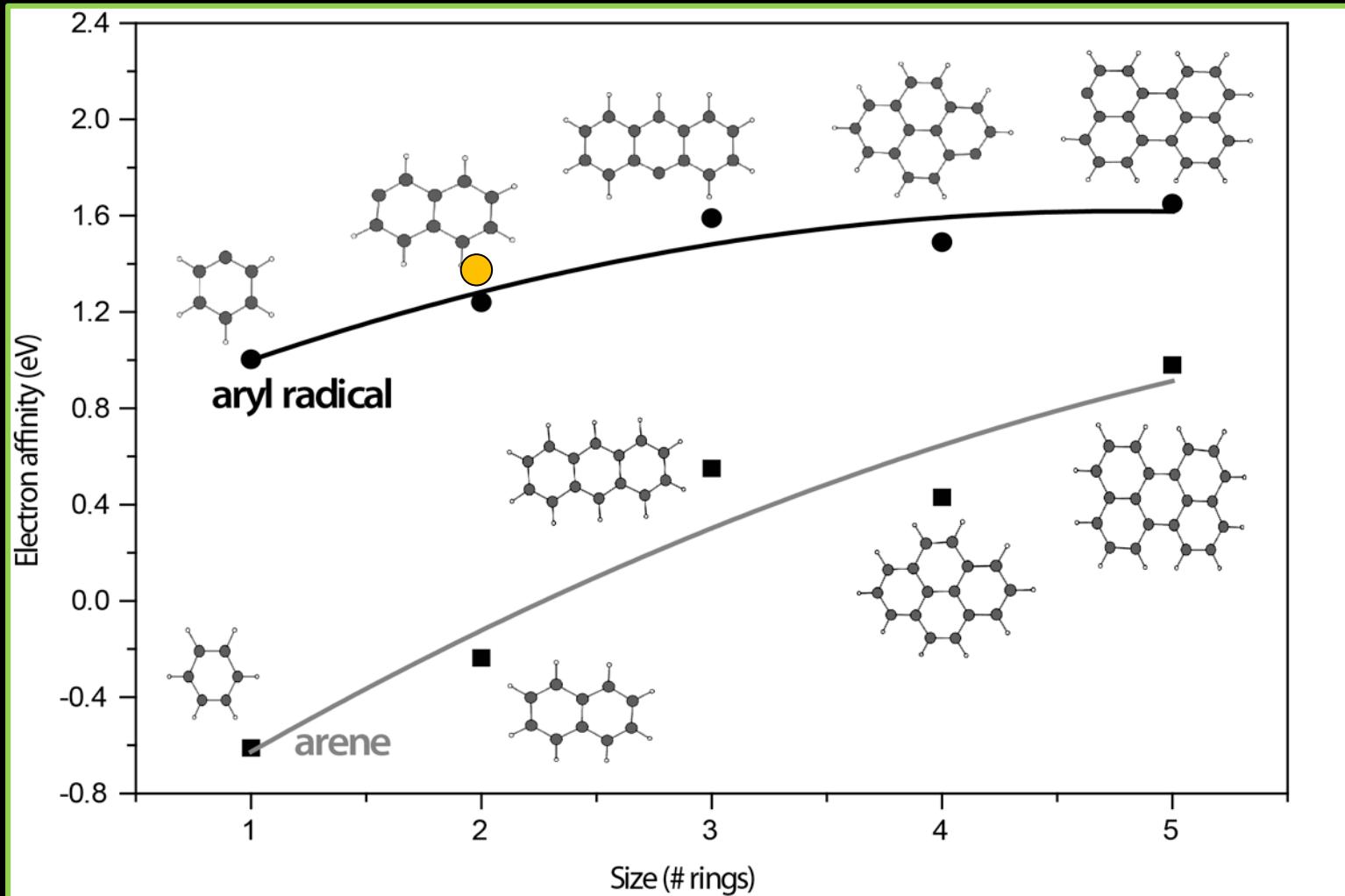
Facile formation of 5-membered ring species

Negatively charged PAHs

Negative ion ESI of PAH carboxylic acid



Electron affinities: radical vs deprotonated



- Exp value: 1.37 eV (Reed, Kass, *J. Mass Spectrom.* 2000, **35**, 534)

Deprotonated PAHs: large permanent dipole moment

	NAPH	ANTR	PHEN	PYR	TETR	CHRY	PERY	CORO
M	0.0	0.0	0.02	0.0	0.0	0.0	0.0	0.0
M ⁺	0.0	0.0	0.50	0.0	0.0	0.0	0.0	
	1.9	0.0	2.7	1.0	1.7	1.2	1.3	
MH ⁺								3.2
	2.0	3.7	3.7	3.5	5.0	5.7	6.5	
M ⁻	0.0	0.0	0.5	0.0	0.0	0.0	0.0	
	6.0	4.2	6.0	7.8	5.0	5.2	6.7	
[M-H] ⁻								9.9
	8.2	11.3	11.3	10.0	14.5	14.7	9.9	

Values in Debye

