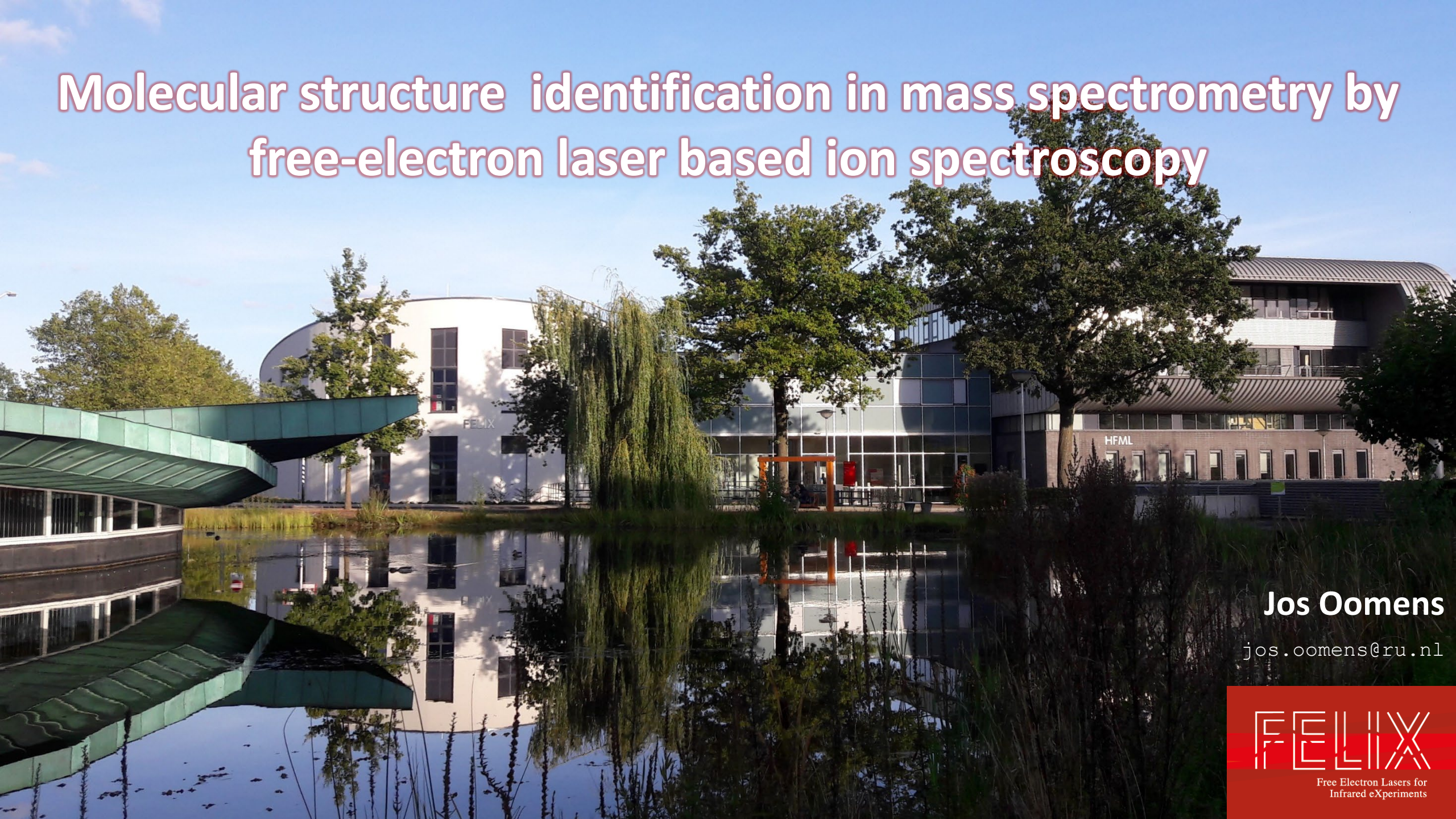


Molecular structure identification in mass spectrometry by free-electron laser based ion spectroscopy



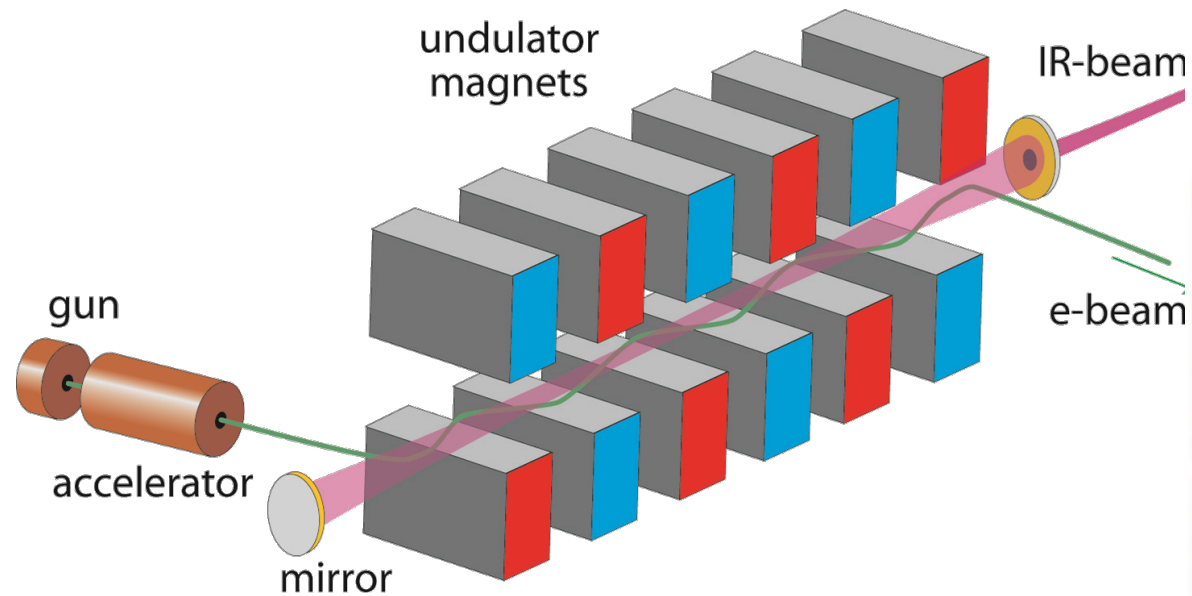
Jos Oomens

jos.oomens@ru.nl

FELIX

Free Electron Lasers for
Infrared eXperiments

FELIX – FREE ELECTRON LASER FOR INFRARED EXPERIMENTS



User facility
Wavelength tunable 2.8 – 150 μm
Pulse energy ~ 100 mJ per 5 μs pulse
FWHM bandwidth $>0.4\%$ of λ

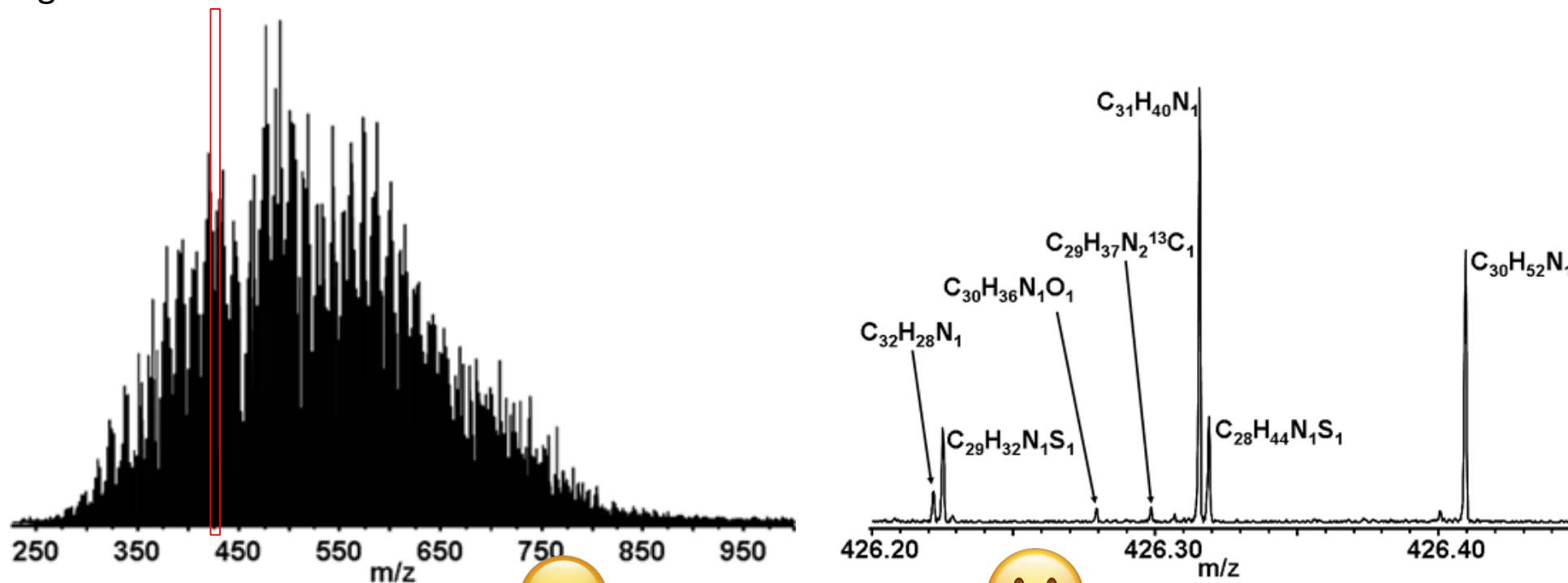
Open access user facility
www.ru.nl/felix



MASS SPECTROMETRY IN THE ANALYSIS OF COMPLEX MIXTURES

- High sensitivity
- High resolution

A.G. Marshall and coworkers, NHFML, Florida



molecular weight

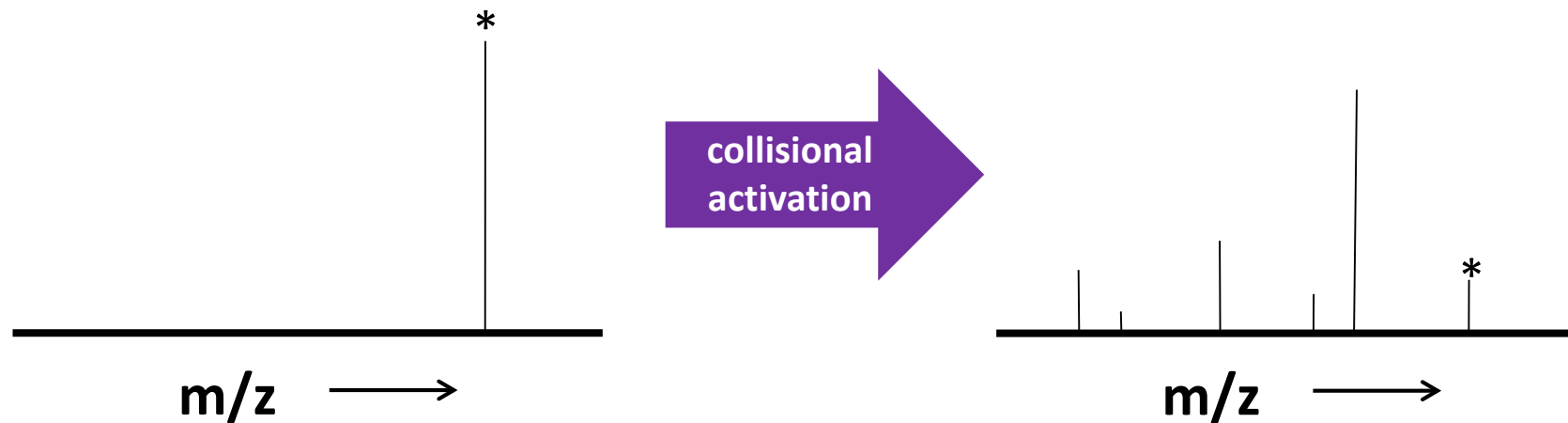


molecular formula



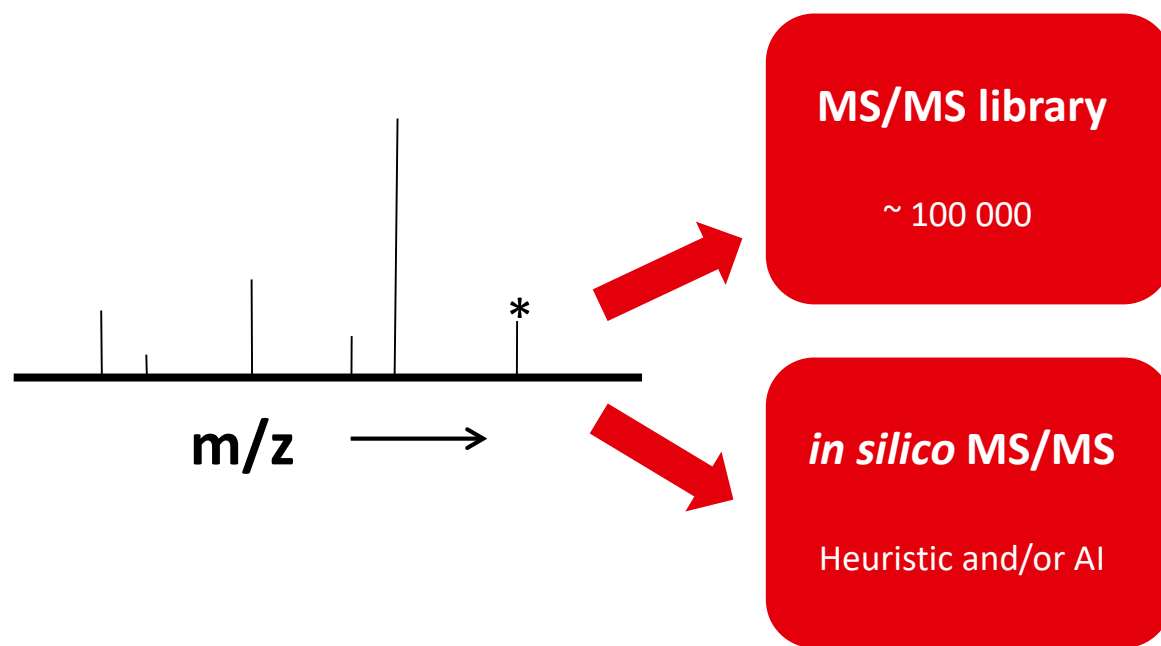
molecular structure

COLLISION-INDUCED DISSOCIATION MS/MS FOR SMALL MOLECULE IDENTIFICATION



- Fragment spectrum not predictable from *QM first principles*
- MS/MS library search
- Identify only *known unknowns*

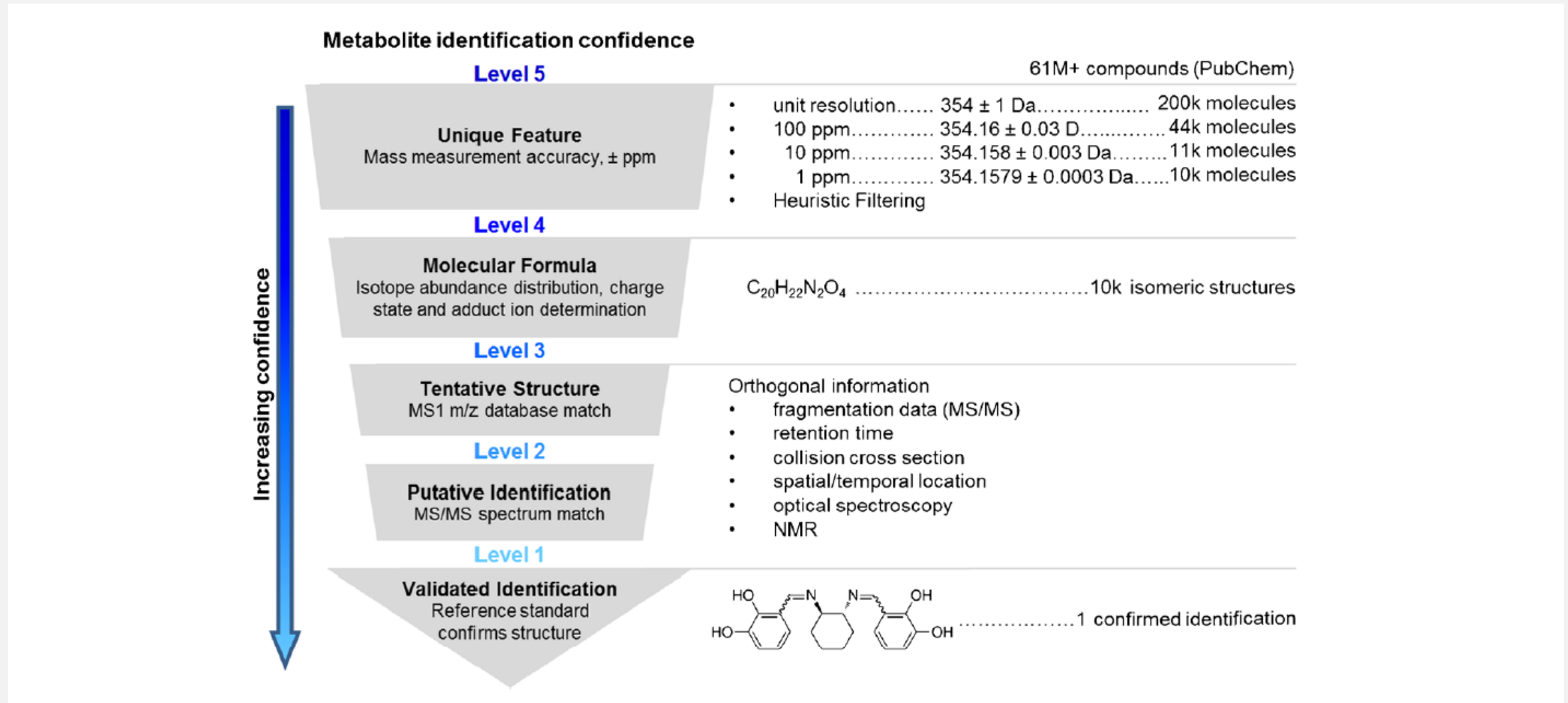
MS/MS IDENTIFICATION WORKFLOW



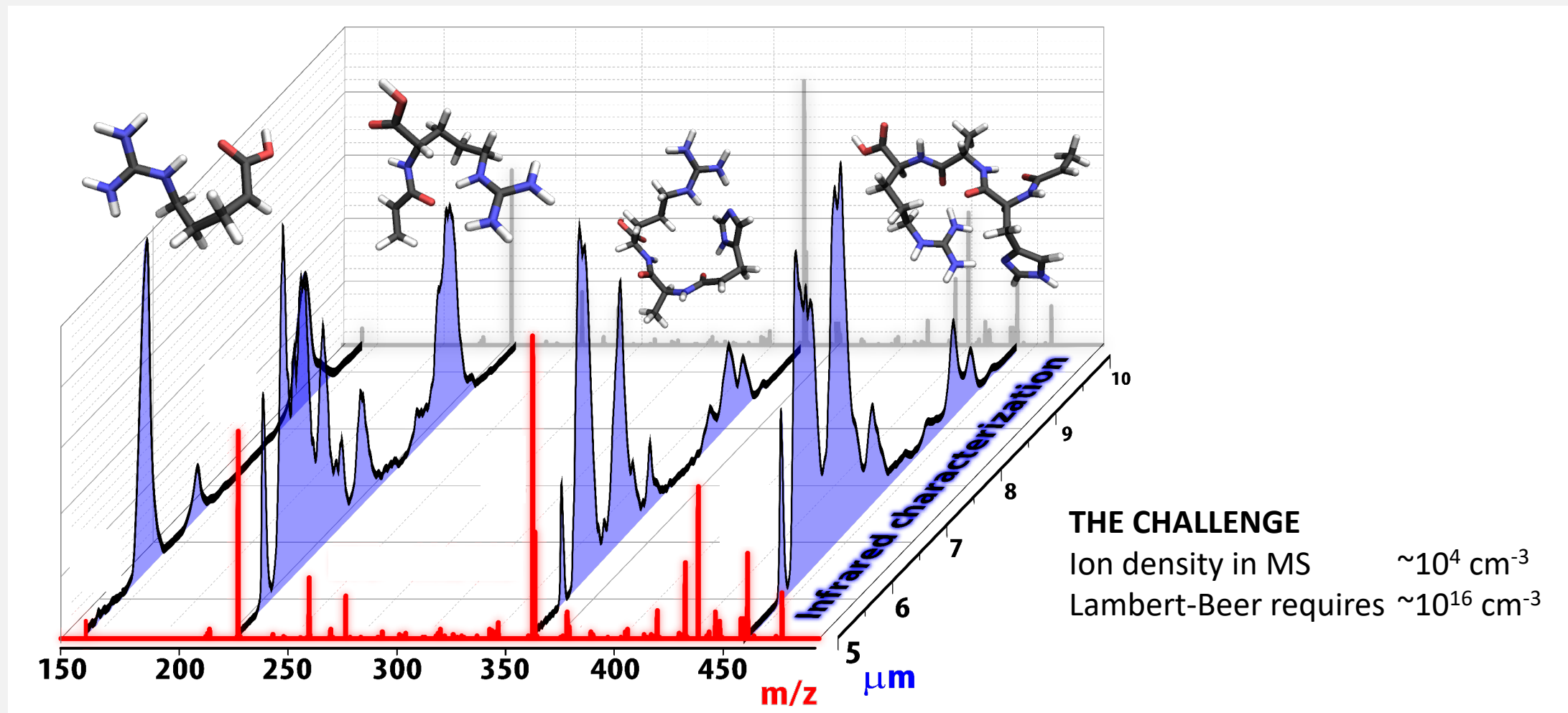
PubChem

| Collection | Live Count | Description |
|--|-------------|-------------------------------|
| Periodic Table of Elements | 118 | Interactive periodic table wi |
| Compounds | 115,056,553 | Unique chemical structures |

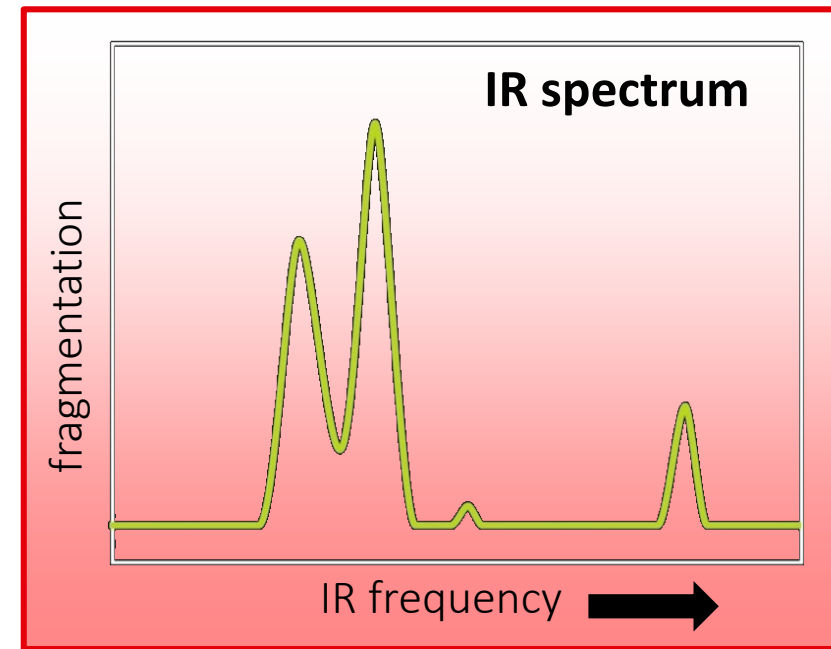
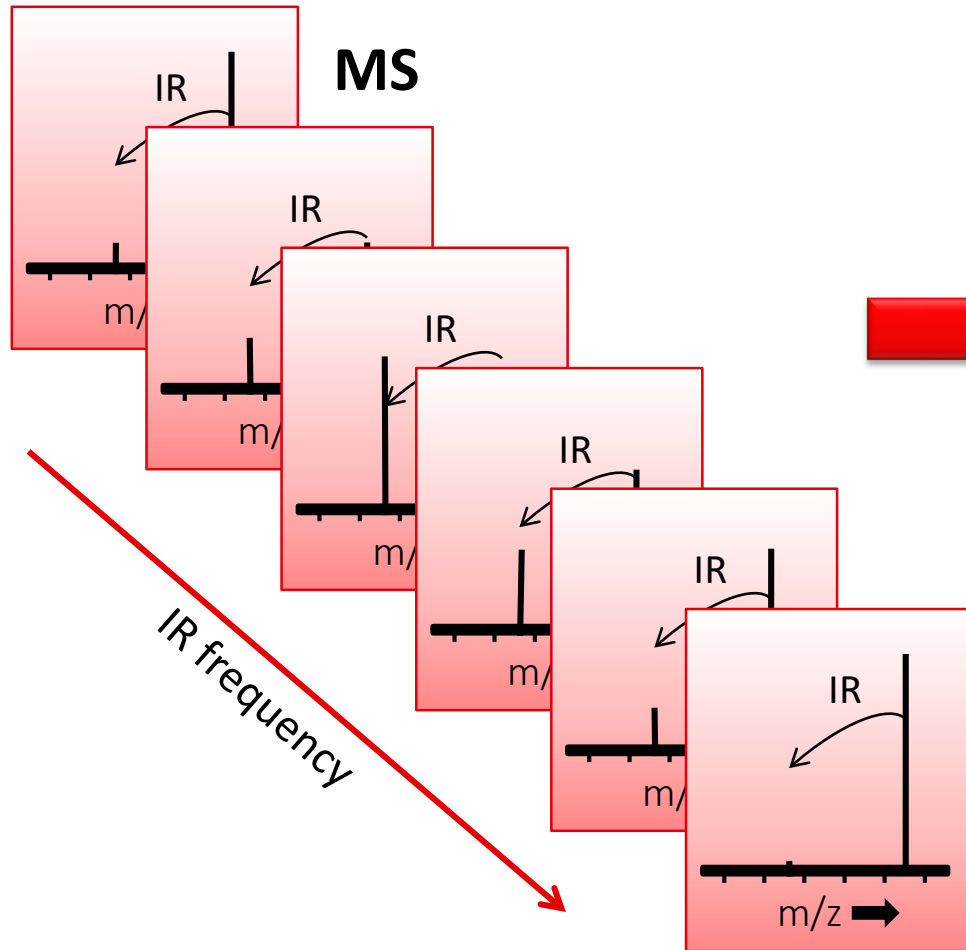
CONFIDENCE LEVELS IN MS-BASED MOLECULAR ID



INTEGRATE IR SPECTROSCOPY WITH MASS SPECTROMETRY



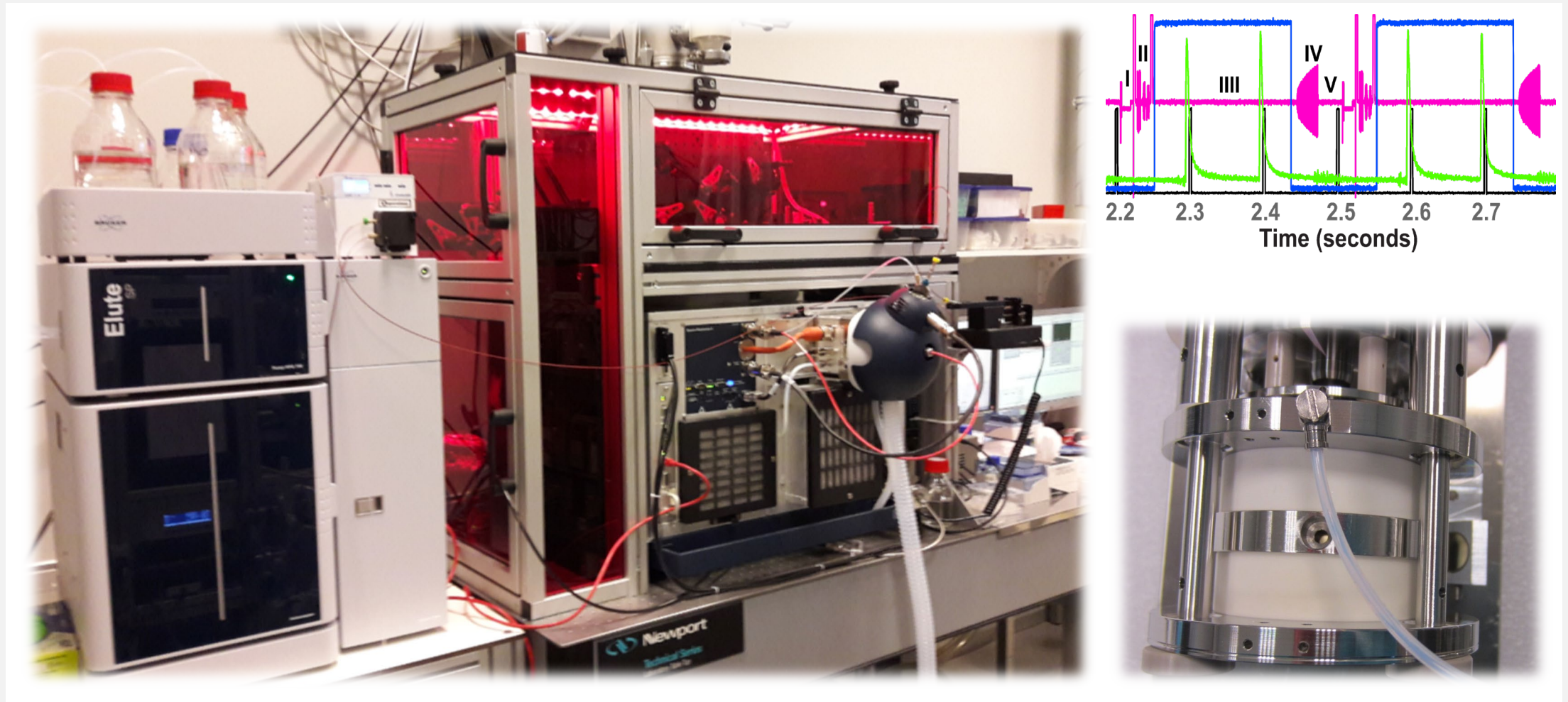
INFRARED ION SPECTROSCOPY (IRIS)



IR spectroscopy, but with

- selectivity of MS
- sensitivity of MS
- versatility of MS (LC, MS/MS, IMS)

EXPERIMENTAL: MODIFIED BRUKER AMAZON ION TRAP MASS SPECTROMETER



BIOMARKER DISCOVERY FOR METABOLIC DISEASES



TRANSLATIONAL METABOLIC LABORATORY AT RADBOUD UMC



Karlien Coene



Leo Kluijtmans



Udo Engelke



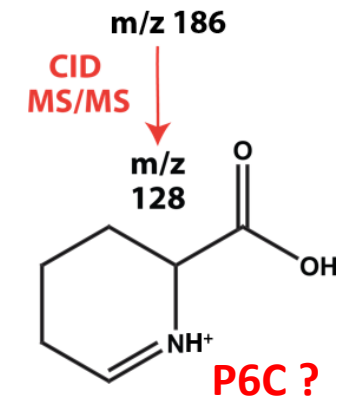
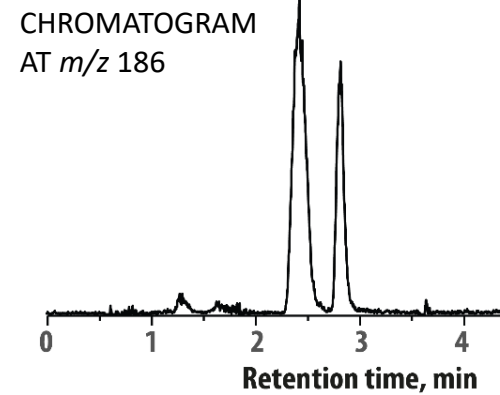
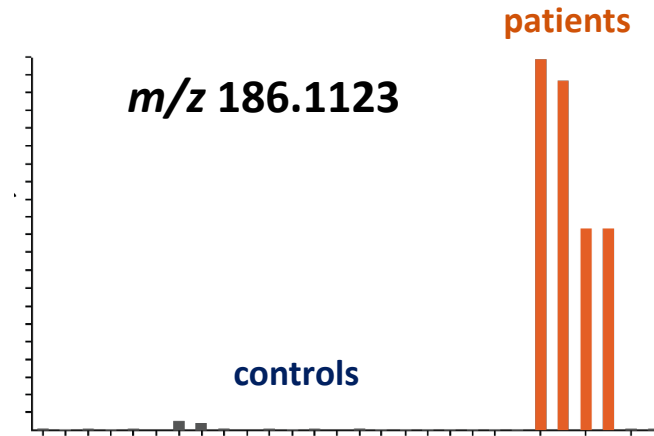
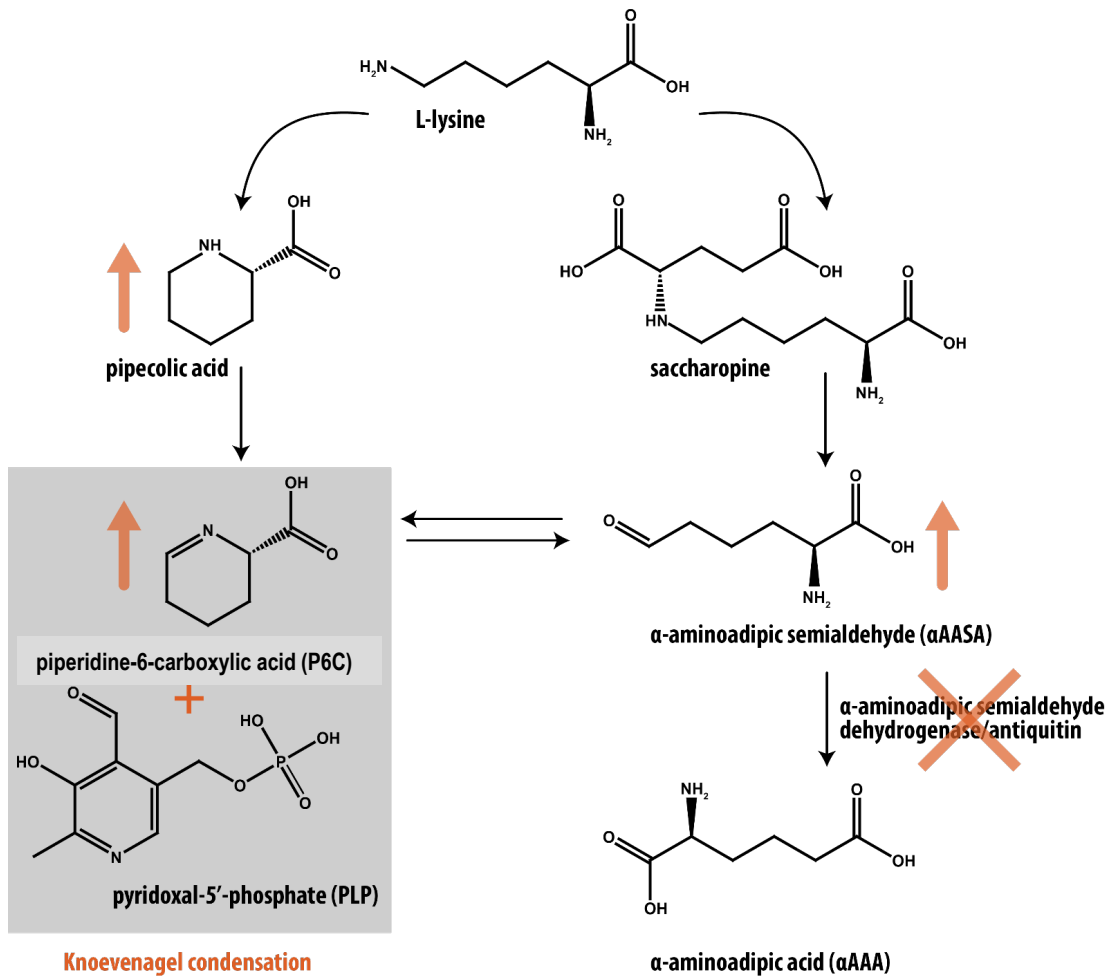
Ron Wevers



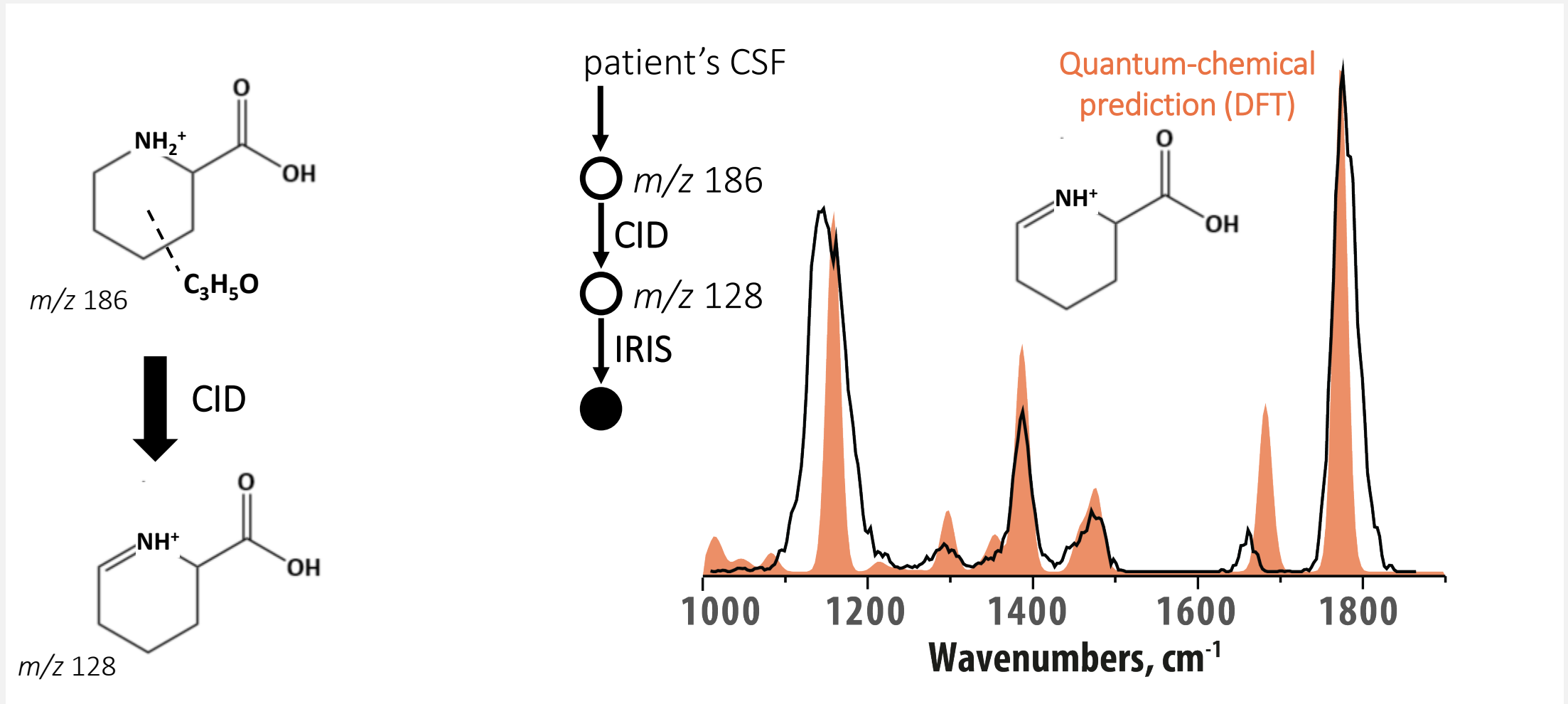
Dirk Lefeber

Radboudumc
university medical center

PYRIDOXINE DEPENDENT EPILEPSY (PDE)

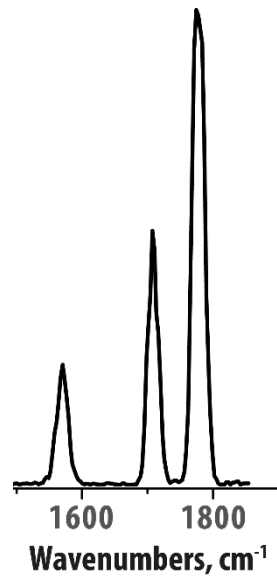


IRIS CONFIRMS THAT m/z 128 CID FRAGMENT IS PROTONATED P6C

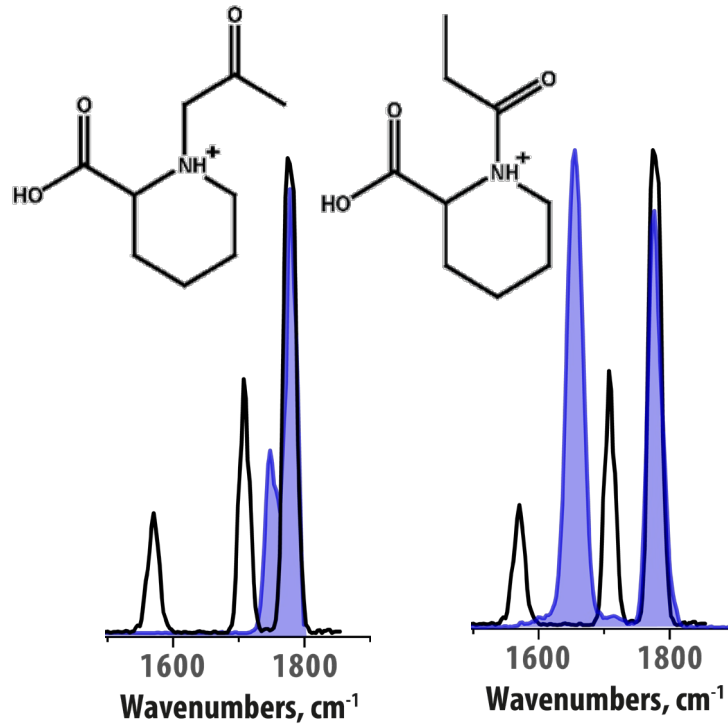


REFERENCE-FREE IDENTIFICATION OF m/z 186 BIOMARKER

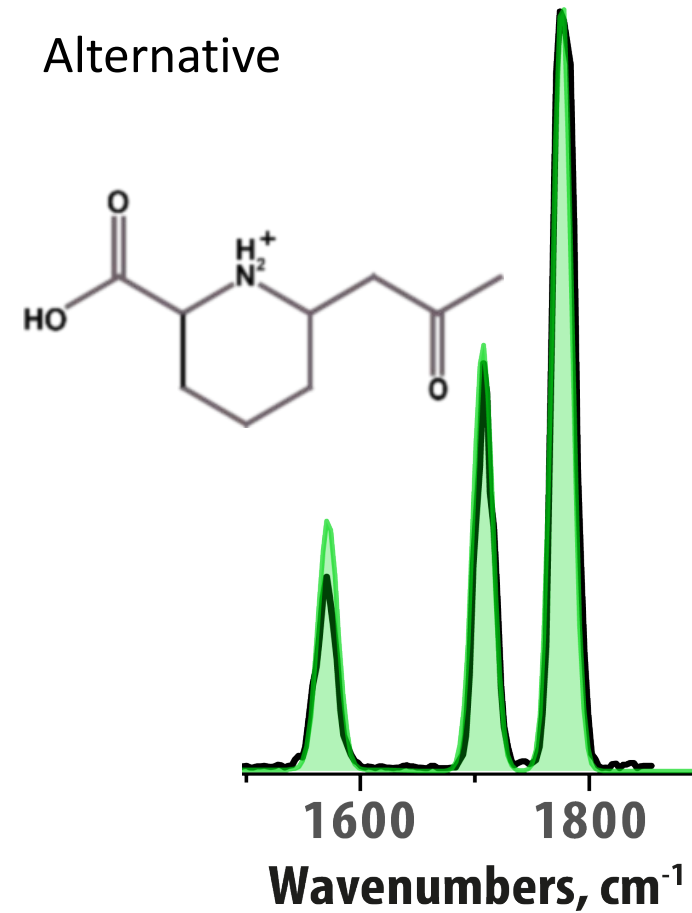
IR spectrum
unknown m/z 186



Two structures proposed

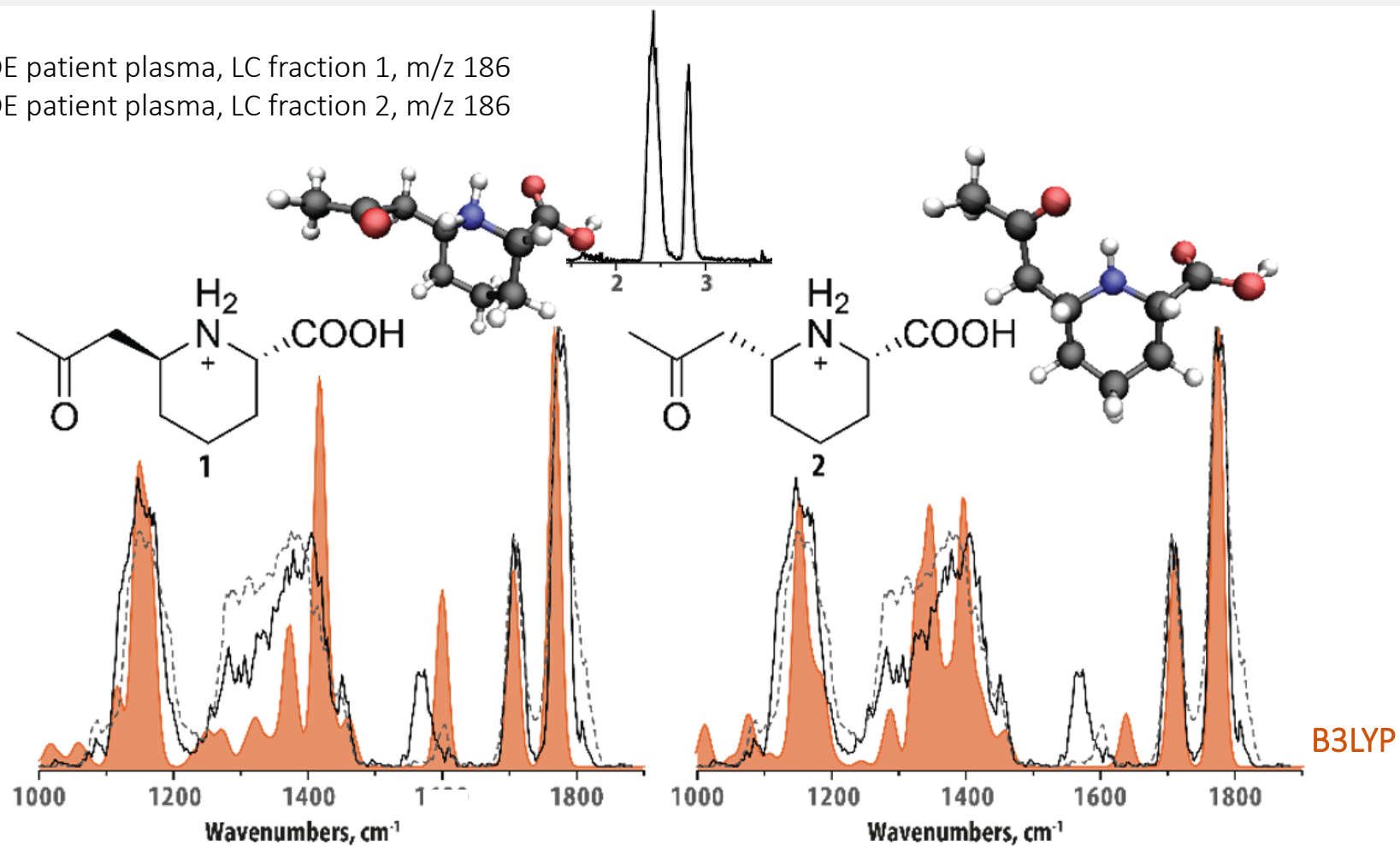


Alternative



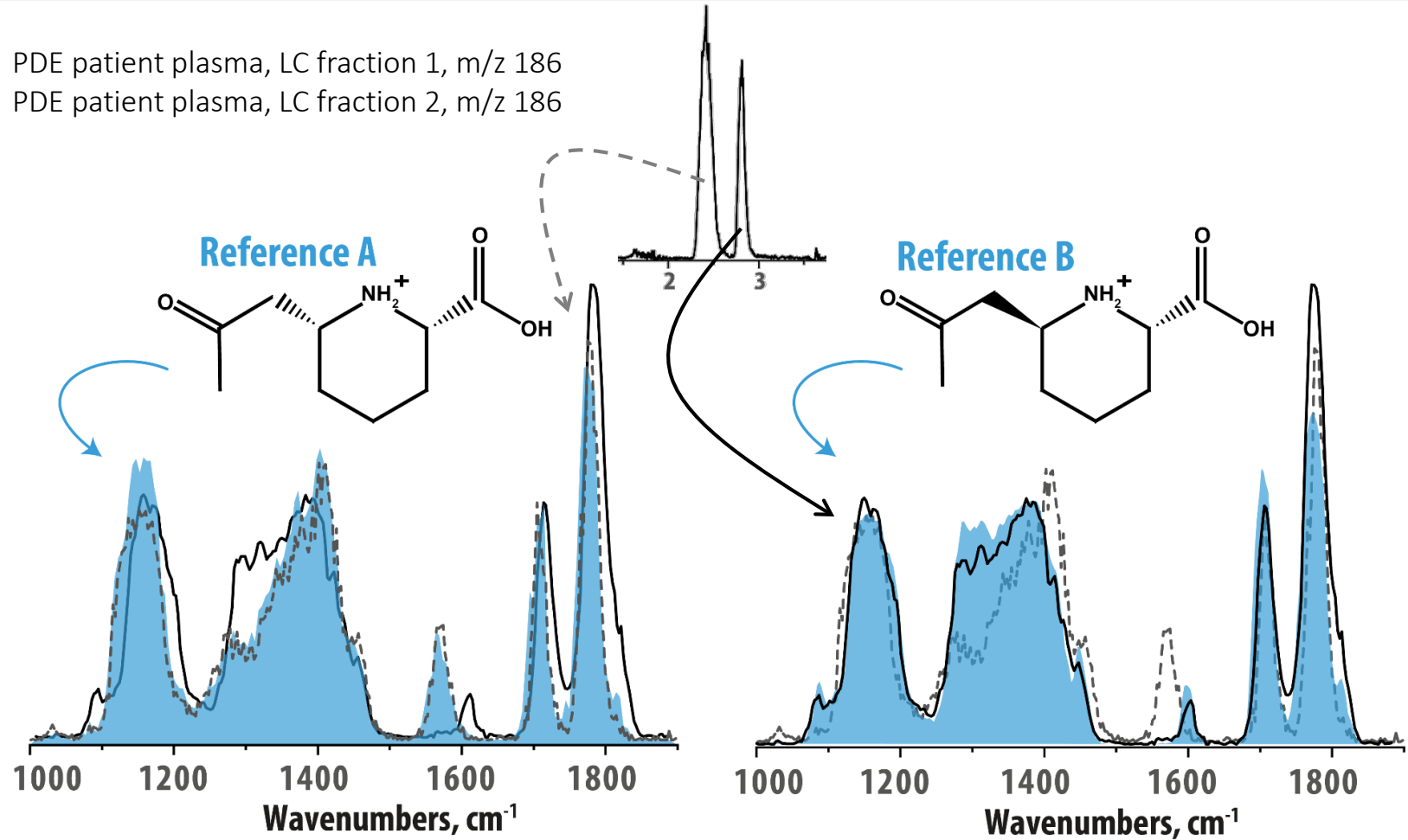
FULL IDENTIFICATION INCLUDING STEREOCHEMISTRY

----- PDE patient plasma, LC fraction 1, m/z 186
———— PDE patient plasma, LC fraction 2, m/z 186



FULL IDENTIFICATION (LEVEL 1) INCLUDING STEREOCHEMISTRY USING SYNTHESIZED STANDARDS

----- PDE patient plasma, LC fraction 1, m/z 186
———— PDE patient plasma, LC fraction 2, m/z 186

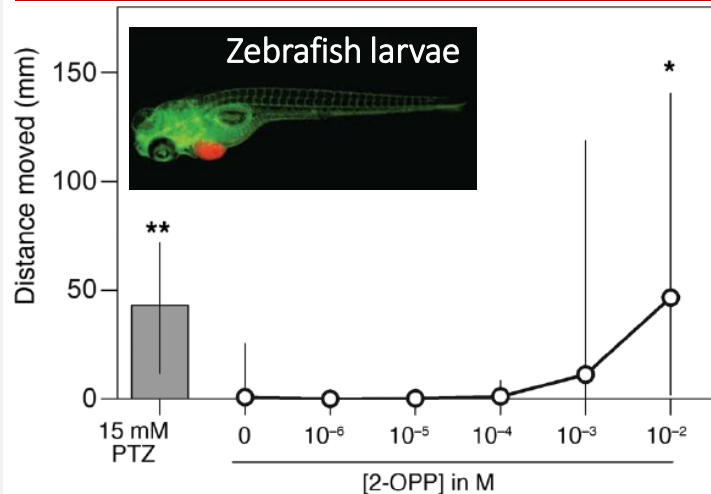


Thomas Boltje

METABOLITE IDENTIFICATION

- Inclusion in newborn screening programs
- Pathophysiology of PDE
- Treatment

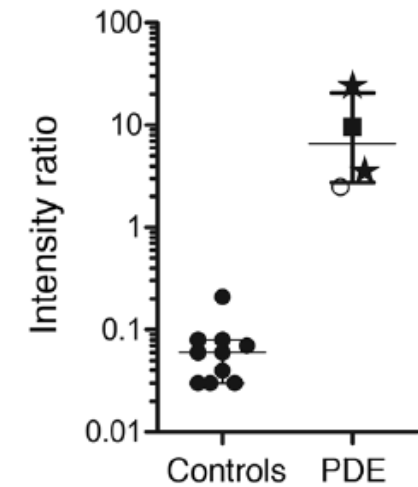
2-OPP induces epilepsy



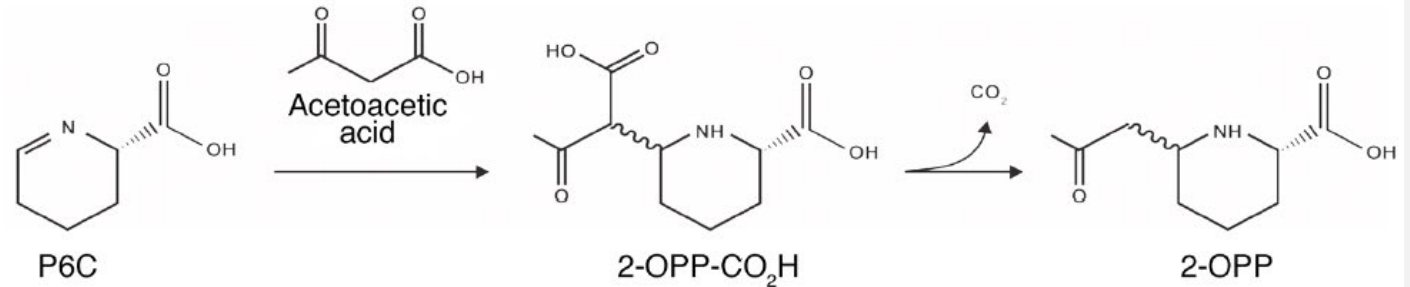
2-OPP is outstanding biomarker for PDE

| Feature | <i>m/z</i> | RT (min) | Fold change, |
|-------------------------------------|------------|----------|--------------|
| Biomarker A [M + H] ⁺ | 186.1123 | 2.33 | 200 |
| Biomarker B [M + H] ⁺ | 186.1123 | 2.55 | 145 |
| Biomarker C [M + H] ⁺ | 144.0652 | 3.05 | 45 |
| α-AASA [M - H] ⁻ | 144.0666 | 0.86 | 8 |
| P6C [M + H] ⁺ | 128.0706 | 0.86 | 9 |
| Pipecolic acid [M + H] ⁺ | 130.0861 | 1.04 | 3 |

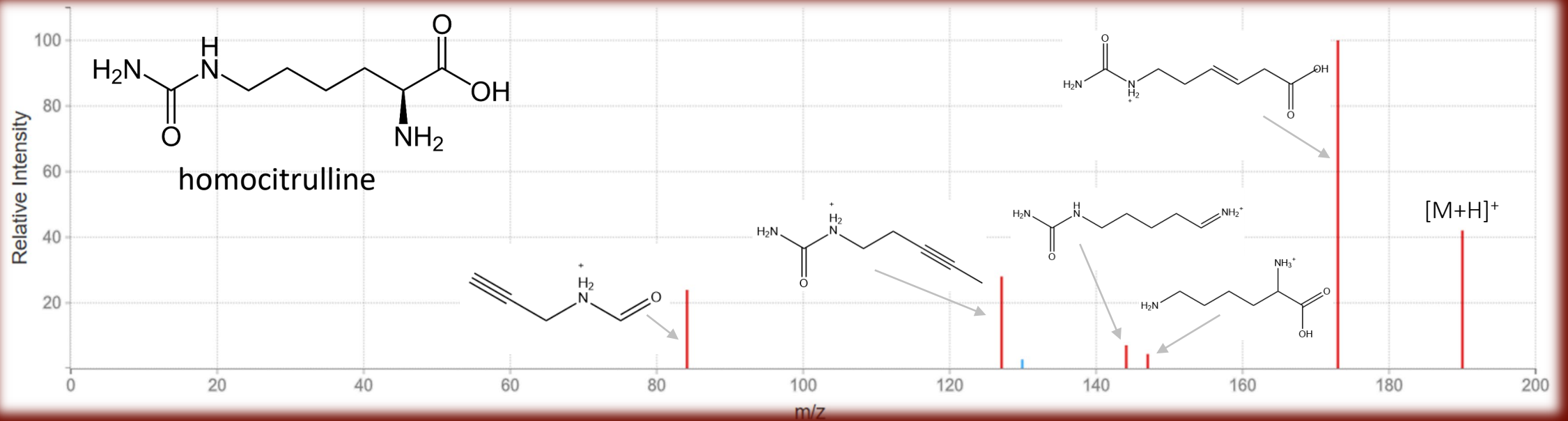
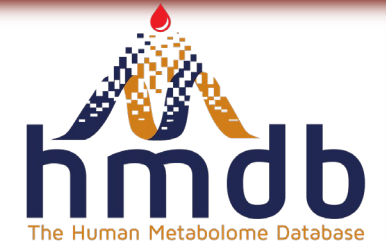
2-OPP in DBS



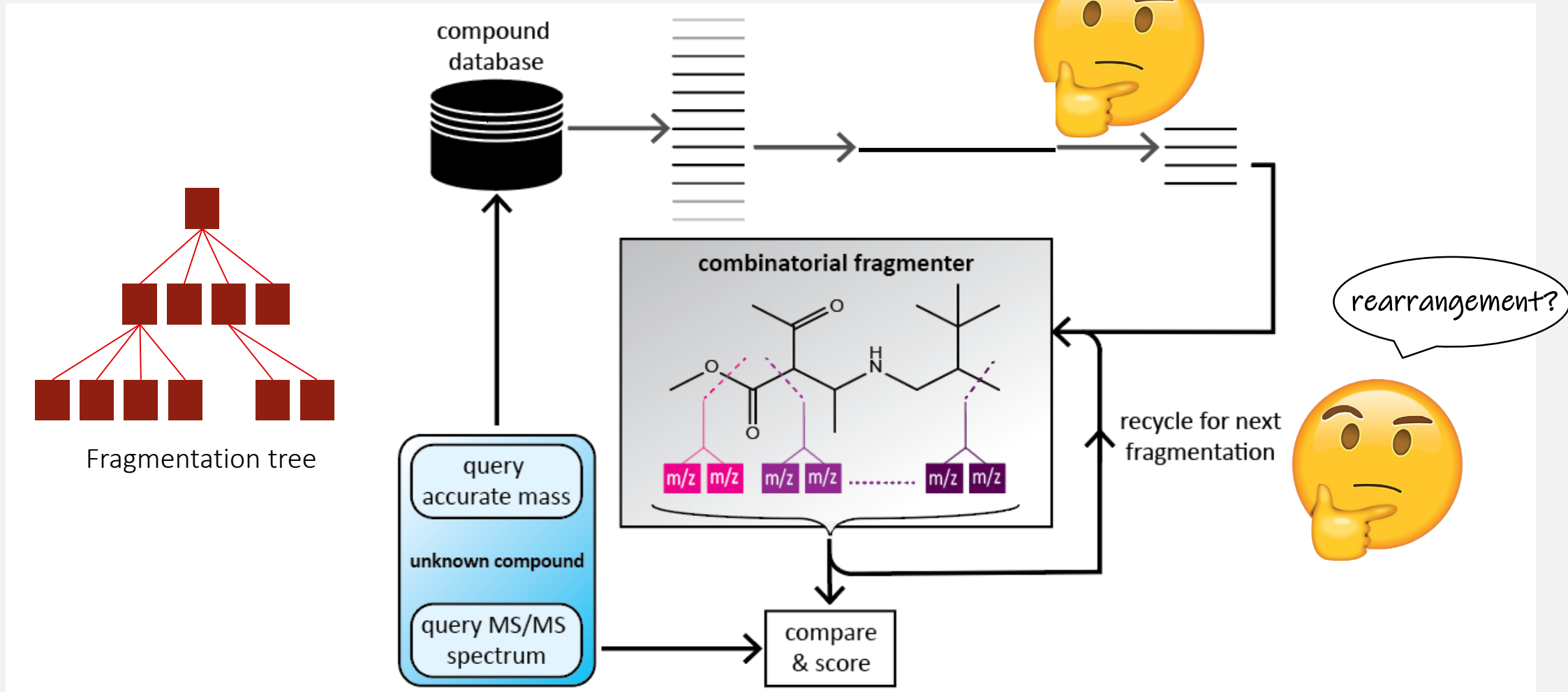
2-OPP is formed from P6C and AcAc



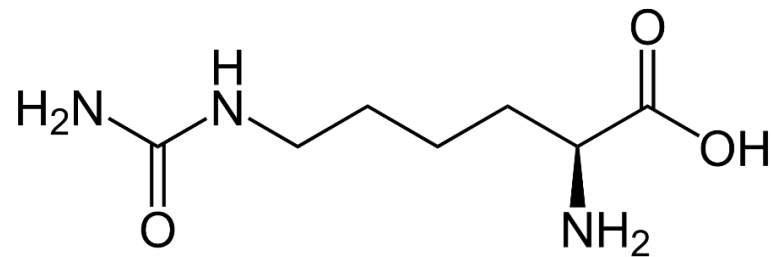
MS/MS LIBRARY ANNOTATIONS



WHY IS THIS IMPORTANT? ... *IN SILICO* FRAGMENTATION (COMBINATORIAL)



EXAMPLE: MS/MS FRAGMENT ION OF HOMOCITRULLINE AT m/z 127

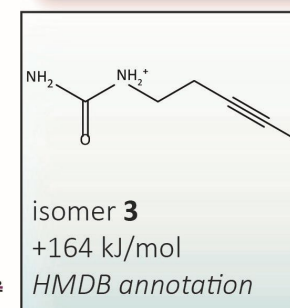
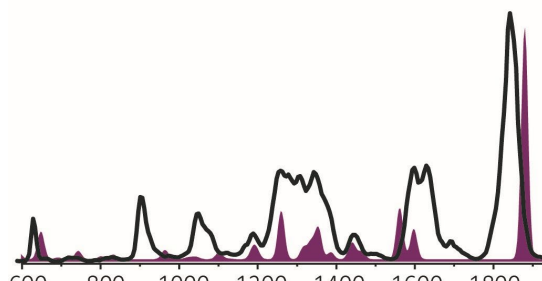
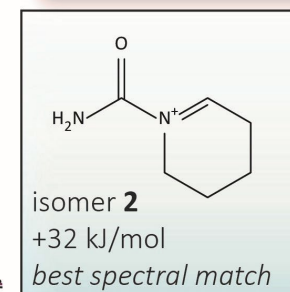
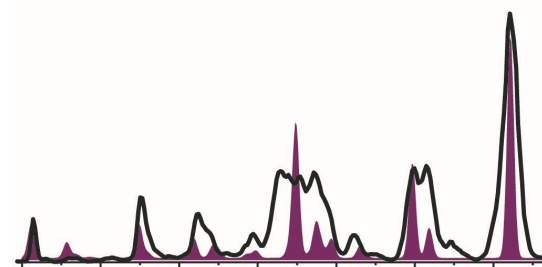
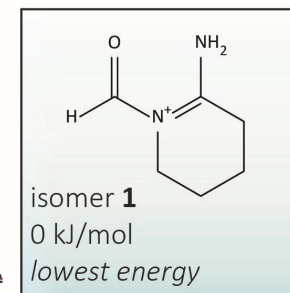
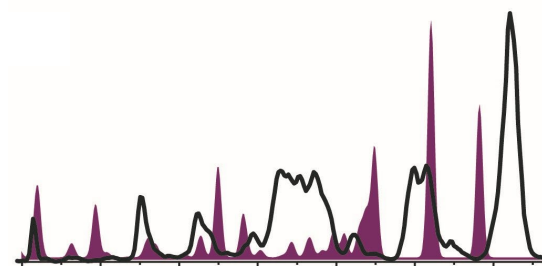


○ m/z 190

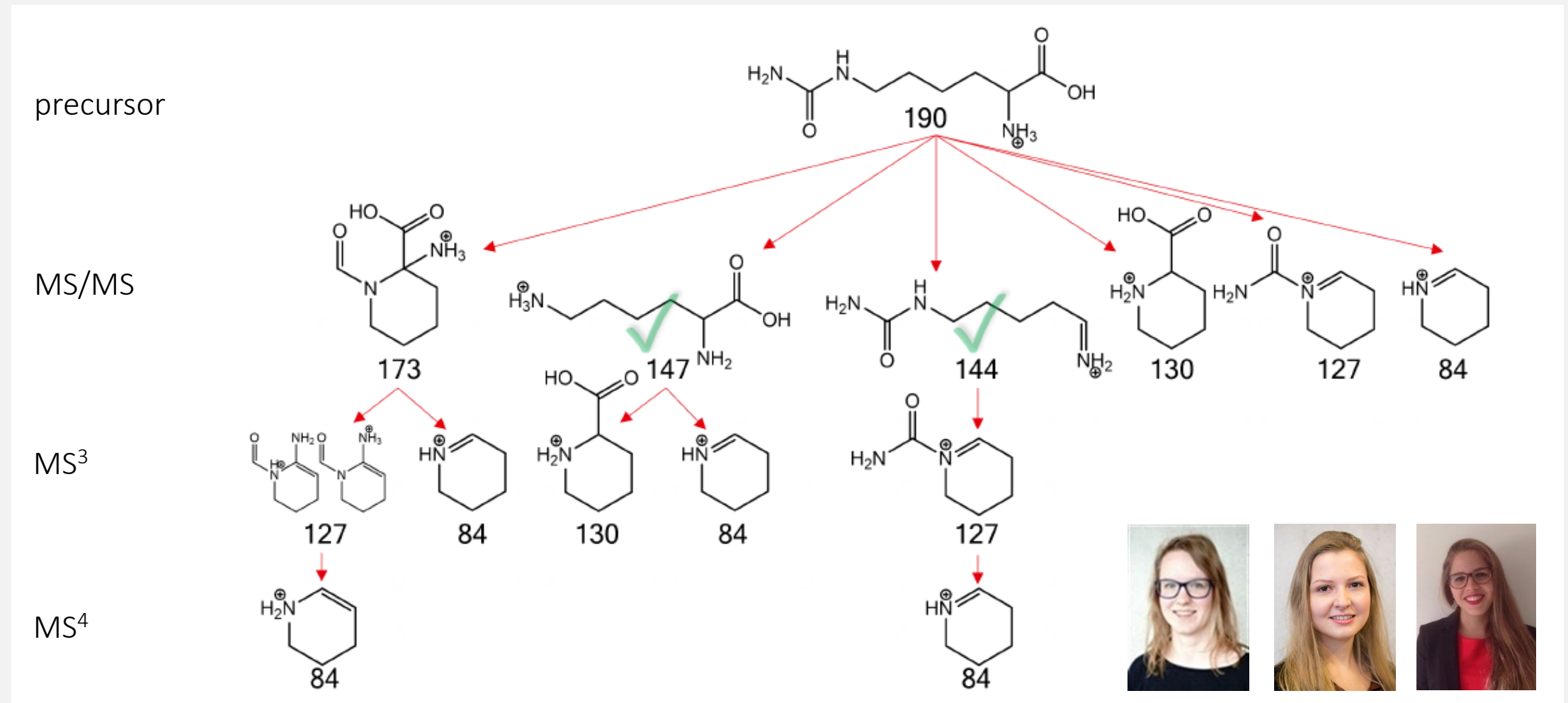
↓ CID

○ m/z 127

↓ IRIS



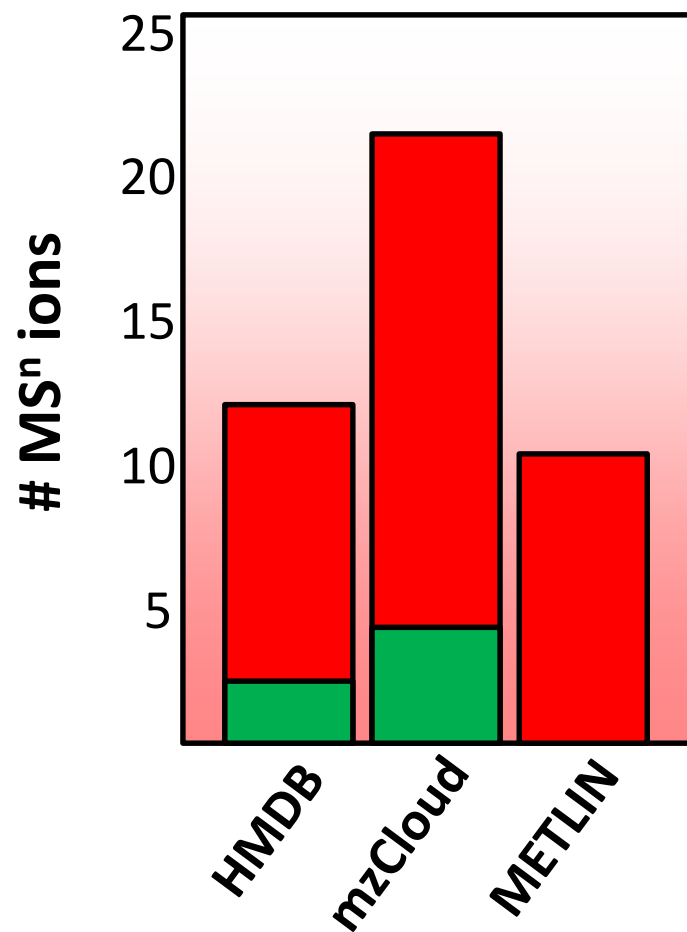
HOMOCITRULLINE FRAGMENTATION TREE



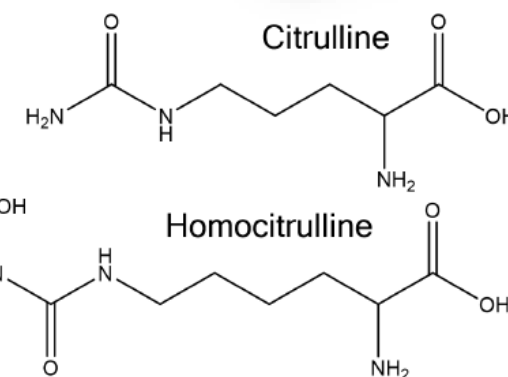
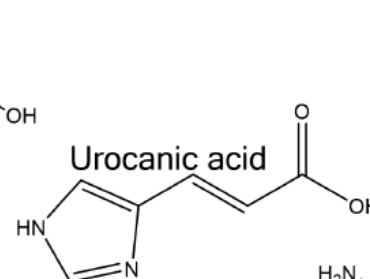
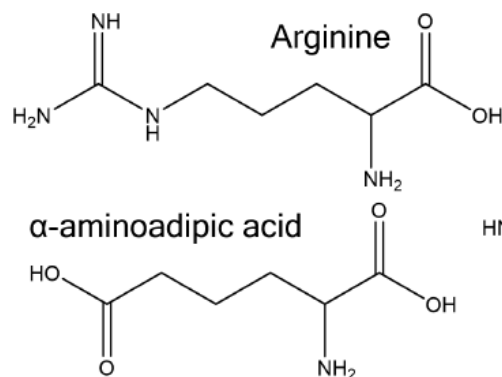
Lara van Tetering, Sylvia Spies, Quirine Wildeman

CONCLUSION: LIBRARY ANNOTATIONS ARE GENERALLY INCORRECT

an inconvenient truth ...



■ correct annotation
■ incorrect annotation



IRIS SPECTRA IN THE HMDB

HMDB Browse Search Downloads About Contact Us

Spectrum Details

HMDB ID: HMDB0000860
Compound name: Phenylpropionylglycine
Spectrum type: IR Ion Spectrum
Adduct: [M+Na]⁺

Spectrum View

Spectra Viewer Instructions...

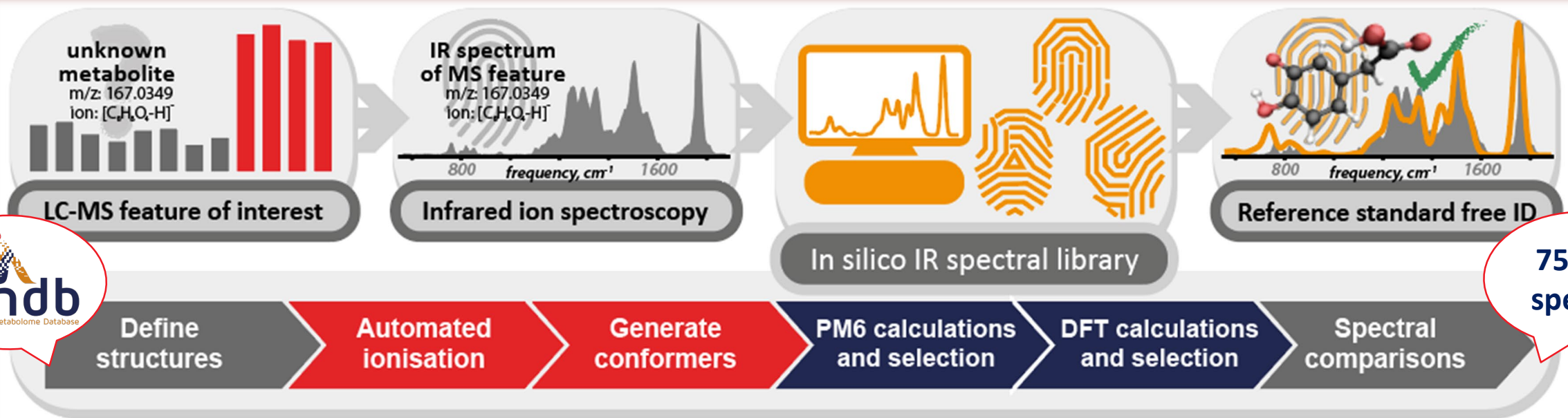
- Experimental

Experimental Conditions

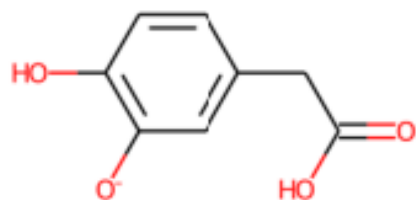
HMDB ID: HMDB0000860
Spectrum type: IR Ion Spectrum
Adduct: [M+Na]⁺
Instrument Type: Bruker AmaZon Speed Quadrupole Ion Trap
Laser Power: 20-160 mJ
Number of Pulses: 1

www.hmdb.ca

AN AUTOMATED WORKFLOW FOR IRIS-BASED IDENTIFICATION



AUTOMATIC FINDING OF THE CORRECT ISOMER



DOPAC, C₈H₉O₄

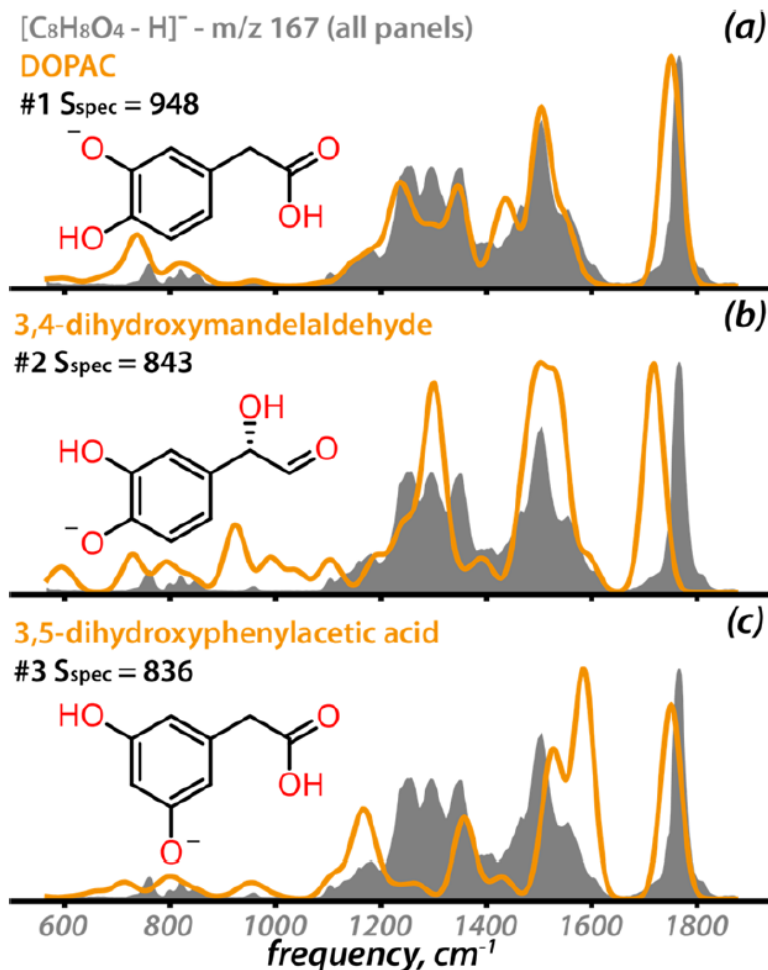
m/z 167 (- ESI)

18 isomers in HMDB

16 deprotonatable

Result:

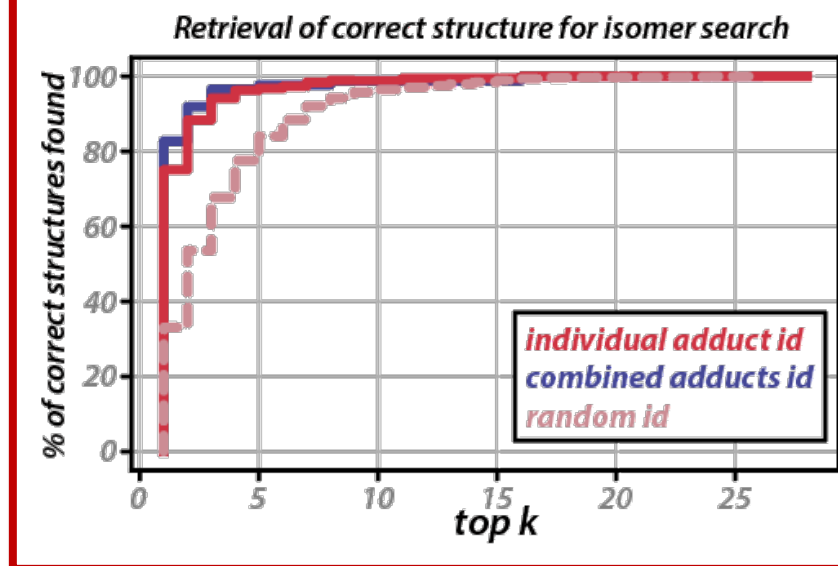
DOPAC returned as #1 match



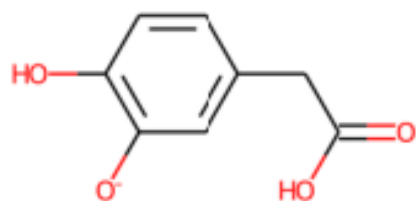
Spectral similarity

$$S_{spec} = 1000 \cdot \frac{a \cdot b}{|a||b|} = 1000 \cdot \frac{\sum_{i=1}^n a_i b_i}{\sqrt{\sum_{i=1}^n (a_i)^2} \sqrt{\sum_{i=1}^n (b_i)^2}}$$

For 189 IRIS spectra from 89 metabolites



AUTOMATIC FINDING OF THE CORRECT ISOMER



DOPAC, C₈H₉O₄

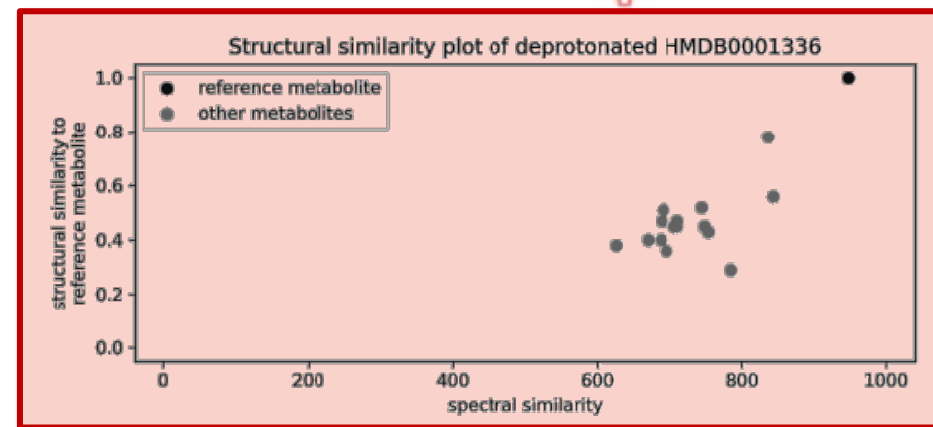
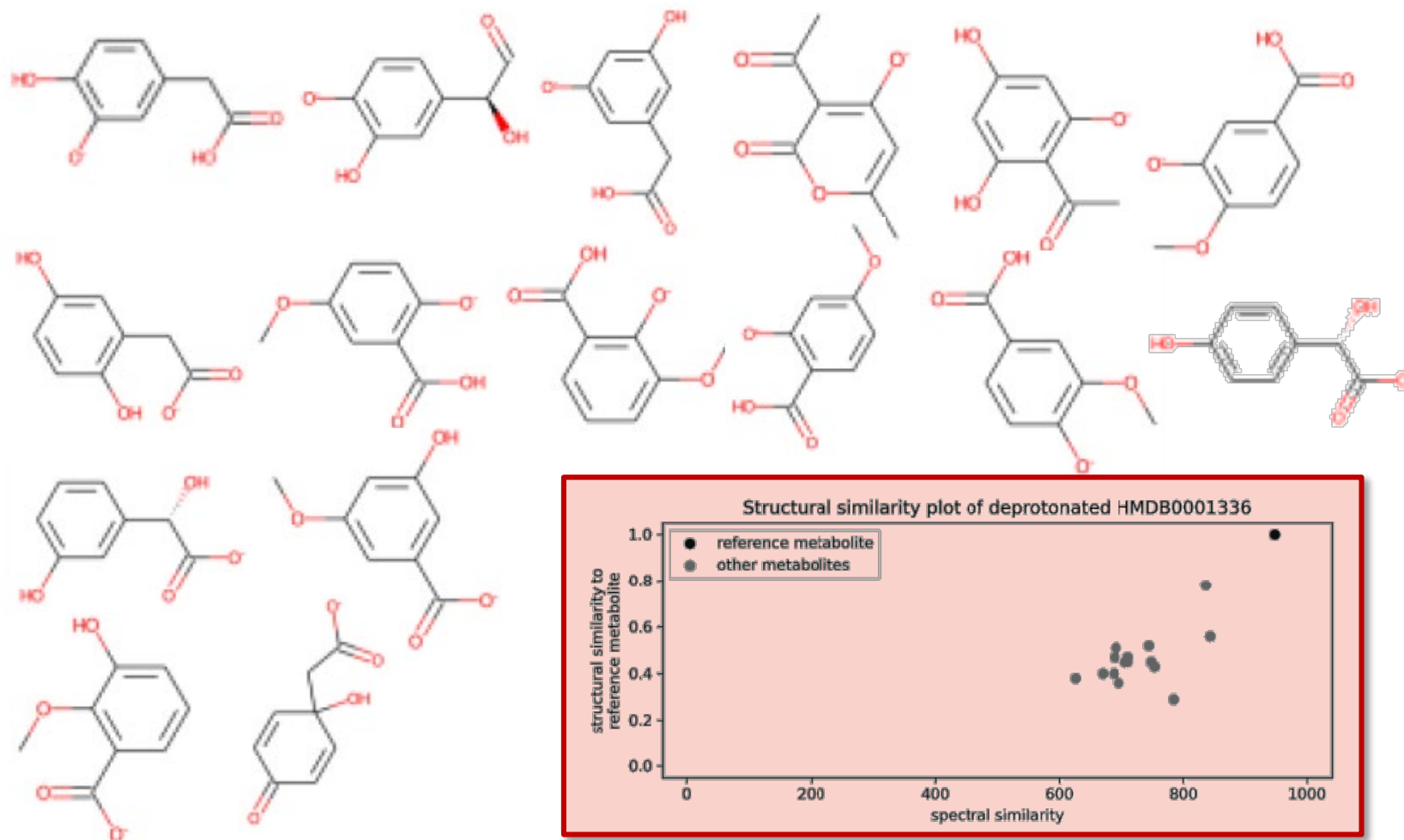
m/z 167 (- ESI)

18 isomers in HMDB

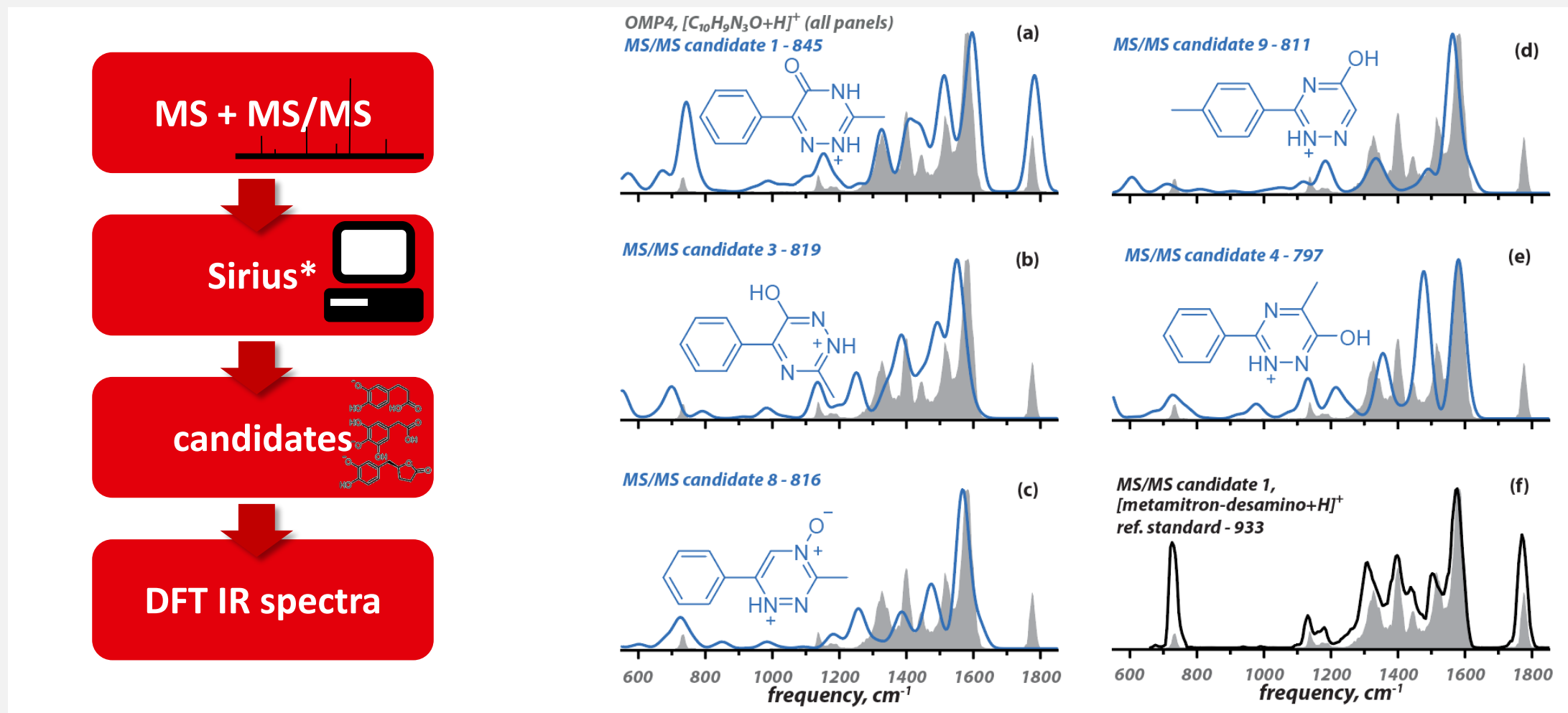
16 deprotonatable

Result:

DOPAC returned as #1 match



COMBINED MS/MS + IRIS IDENTIFICATION



* Dührkop, Fleischauer, Ludwig, Aksenov, Melnik, Meusel, Dorrestein, Rousu, Böcker, *Nature Meth.* 2019, 16, 299

CONCLUSION AND OUTLOOK

Combine with MS toolbox

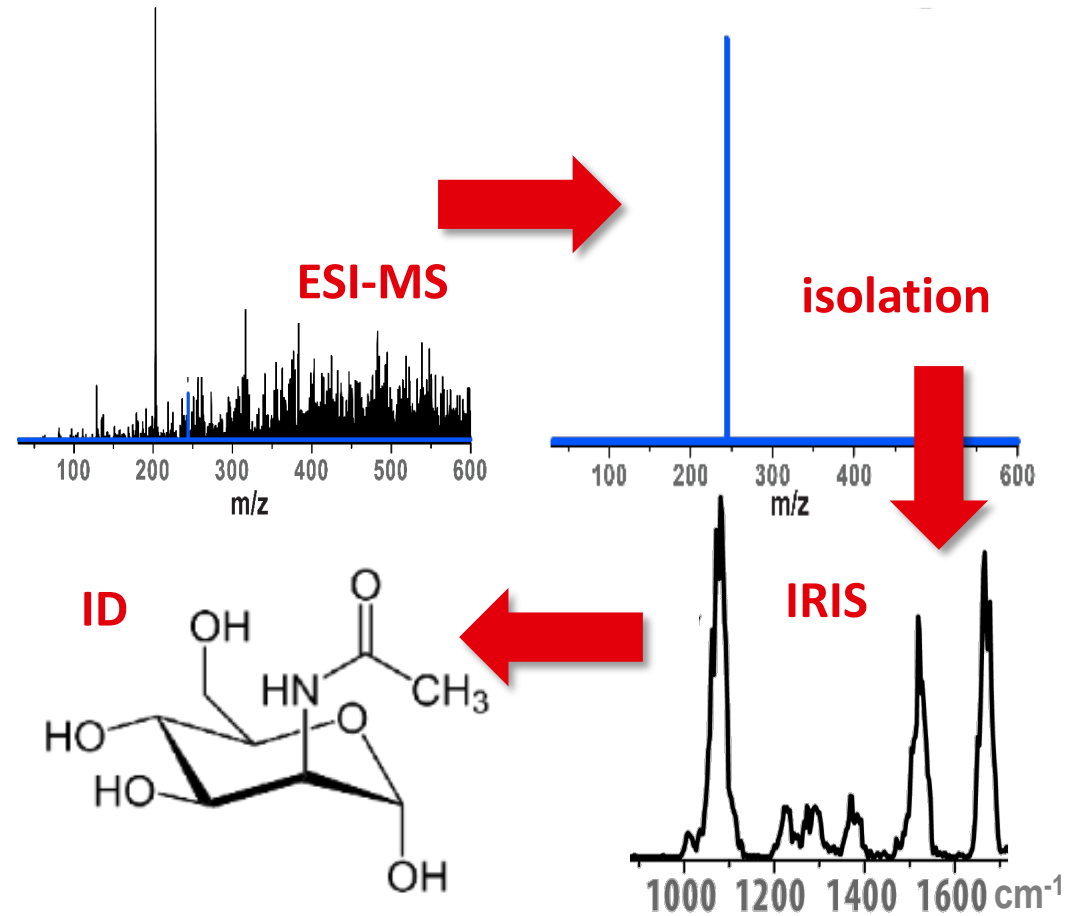
- Ion mobility & LC separation
- Accurate mass determination
- MALDI imaging

New analytical applications

- Environmental: water contaminants, air pollutants
- Forensics: novel psychoactive substances
- Drug metabolism
- Synthetic/organic chemistry

New methodologies

- 2-color
- Strategies for rapid identification
- Benchtop IRIS



Acknowledgements

Molecular ID Lab @ FELIX

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Jelle Schuurman
Laura Finazzi
Teun van Wieringen
Lara van Tetering
Renske Griepink

FELIX

Prof. Britta Redlich
FELIX staff

Bruker

Christoph Gebhart
Chris Wootton

Radboudumc

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Udo Engelke

Organic Chemistry Dept

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Prof. Floris Rutjes

University of Alberta

Prof. David Wishart
Vasuk Gautam

KWR

Dennis Vughs
Andrea Brunner

