
oloBion
OMICS BIOSCIENCE LAB

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About oloBion

oloBion is a science-based CRO providing cutting-edge OMICS services to private companies and academia.

Our mission is to help our customers gain new insights into organisms and the mode of action and composition of their products or technology with our multi-omics platform

With state-of-the-art instrument technology and our expert team, we deliver detailed reports revealing the chemistry behind life.





Parc Científic de Barcelona



House of Biohealth, Luxembourg



University of California, Davis

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Our Pillars and Commitment

01-**Technology**

State-of-the-art equipment based on mass spectrometry with ion mobility
Delivering high-resolution and reliable analytical performance.

02-**Science**

Method development with internationally renowned centers
Ensuring validated workflows and strong scientific rigor.

03-**Data**

Proprietary software for data processing and visualization
Transforming complex multi-omics outputs into clear, actionable insights.

04-**Quality**

Certified processes and rigorous quality controls
Standardized procedures, ISO-aligned practices, and consistent, reproducible results across all services.

Committed to sustainability, responsibility, and well-being
Integrating environmental care, fair practices, and a safe, people-centered working culture.

Certifications

Driven by Science.
Committed to Quality

TÜVRheinland CERTIFICADO
Sistema de Gestión ISO 9001:2015
www.tuv.com ID 9000036762

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Omics Services

+ 20 biological matrices: **Plasma**, **Stool**, **Skin**, **Cells**, **Plants**, **Soils**, **Bacteria**, **Algae**...

Targeted and Untargeted Methods

Metabolomics

Polar Molecules

- Small molecules: <1.200 Da
- Human, microbial, plants, drugs, etc.

200 - 1500 ID

Lipidomics

Apolar Molecules

- Lipidic fraction
- Detection of oxylipins
- Specific panels for fatty acids, ceramides, triglycerides and oxylipins

300 - 1000 ID

Proteomics

Proteins

- Analysis NextGen
- Includes low abundance proteins
- Includes GO biological processes

400 - 4000 ID

Ionomics

Elements

- Macro - and micro - elements
- Specific panels based on the study needs

1 – 50 E.

Caroteomics

Carotenes

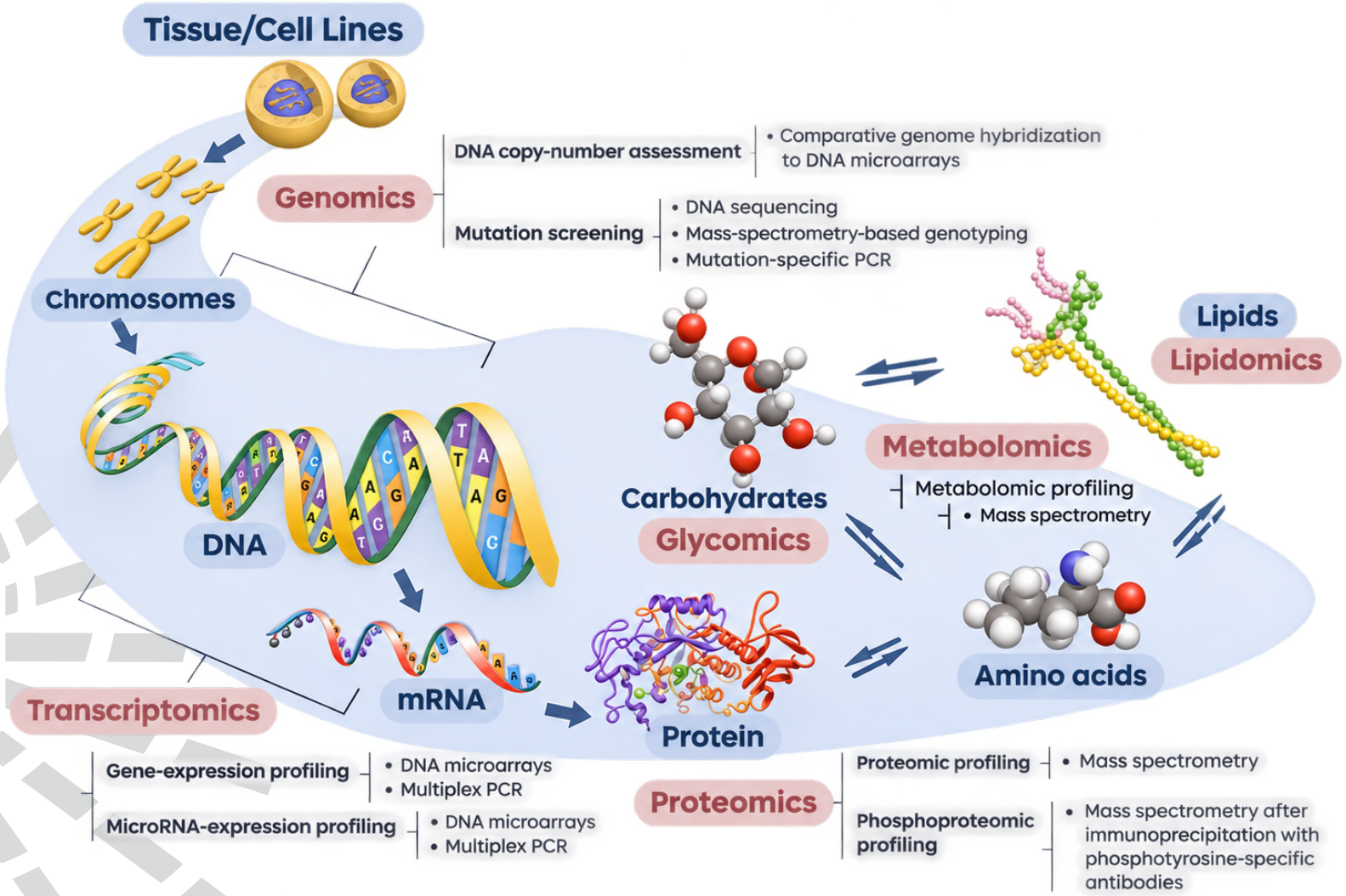
- Analysis of carotenes related to food

10 – 600 ID

Complementary services

Metagenomics, Nutritional Analysis, Method Development, *In vitro*, *In vivo*

Omics technology



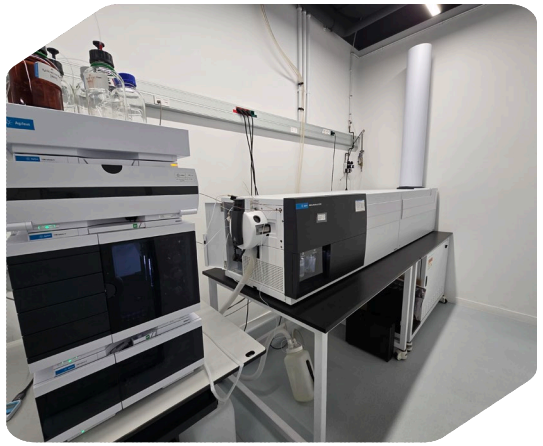
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State-of-the-art technology

LC/MS ZenoTOF 7600 Sciex



LC/IMS QTOF 6560 Ion Mobility Agilent



GC/MS QTOF 7200 Accurate-Mass Agilent



MP-AES 4210 Agilent



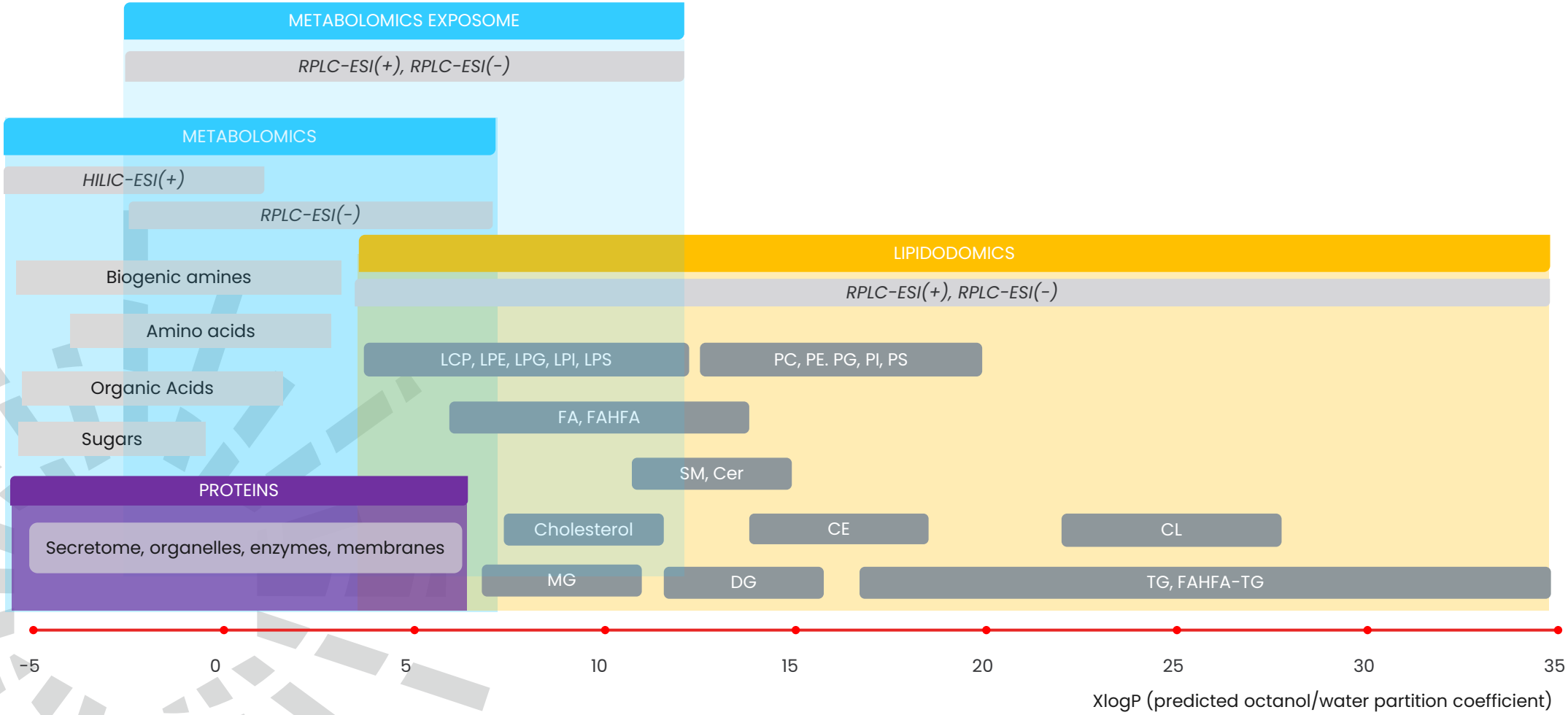
Technology Partners ↘

SCIEX

Agilent

LC-MS/MS Platform Range

Range coverage of subgroups of polar metabolites, lipids and proteins



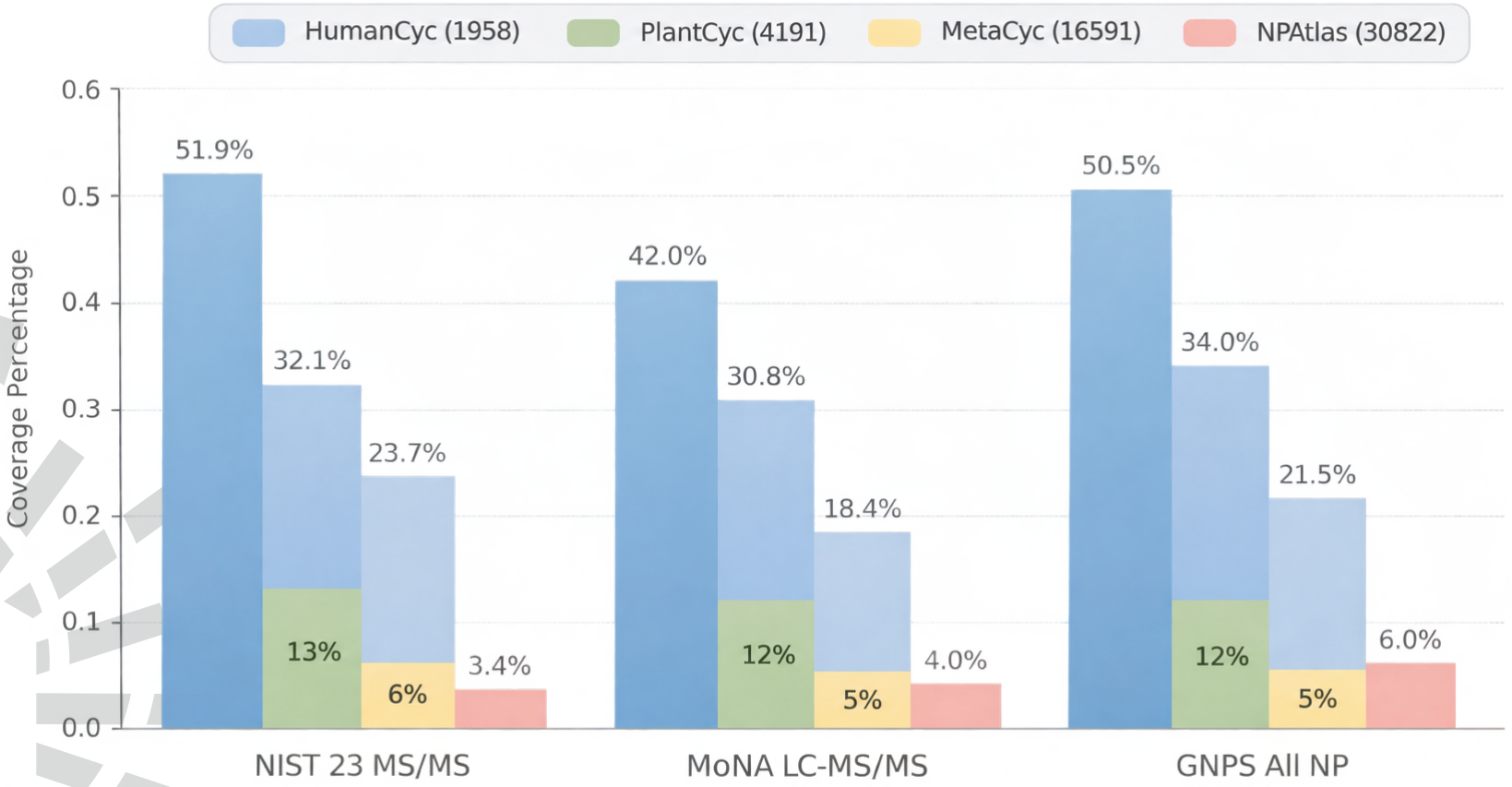






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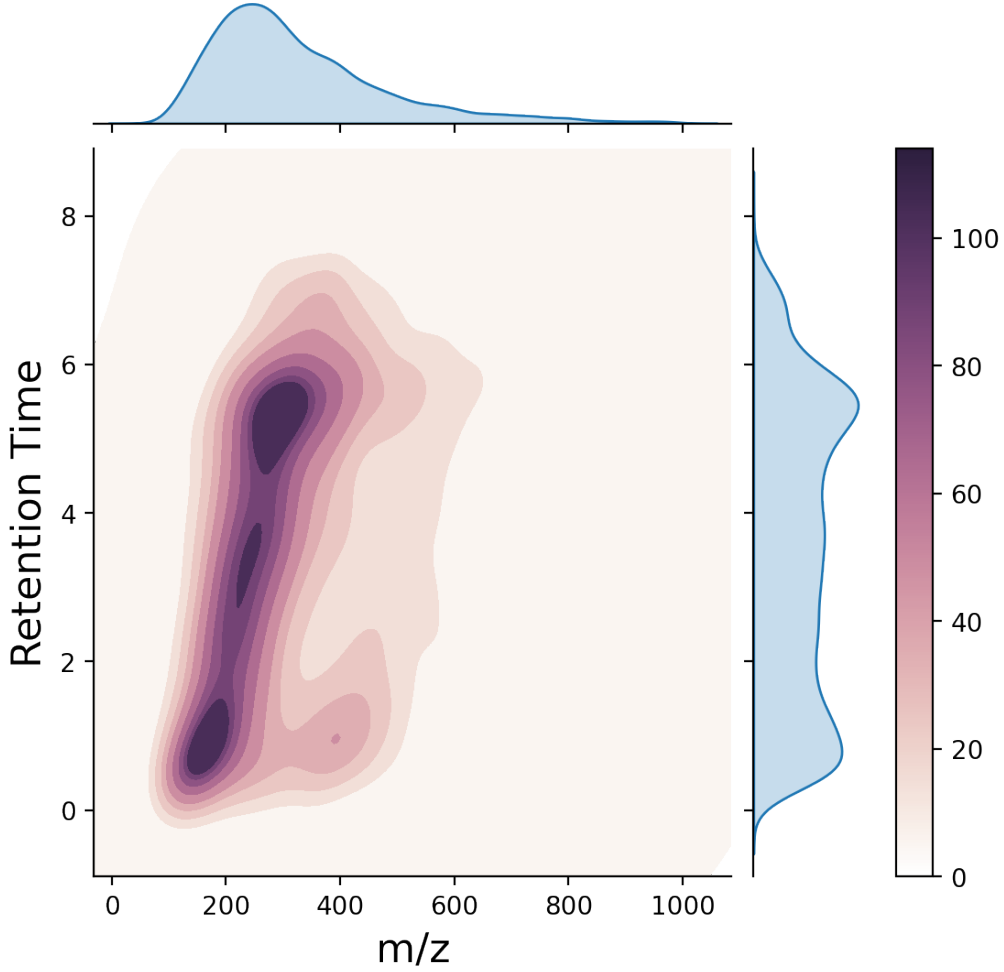
Compound spectral library LCMS



How identify a compound? ⟵

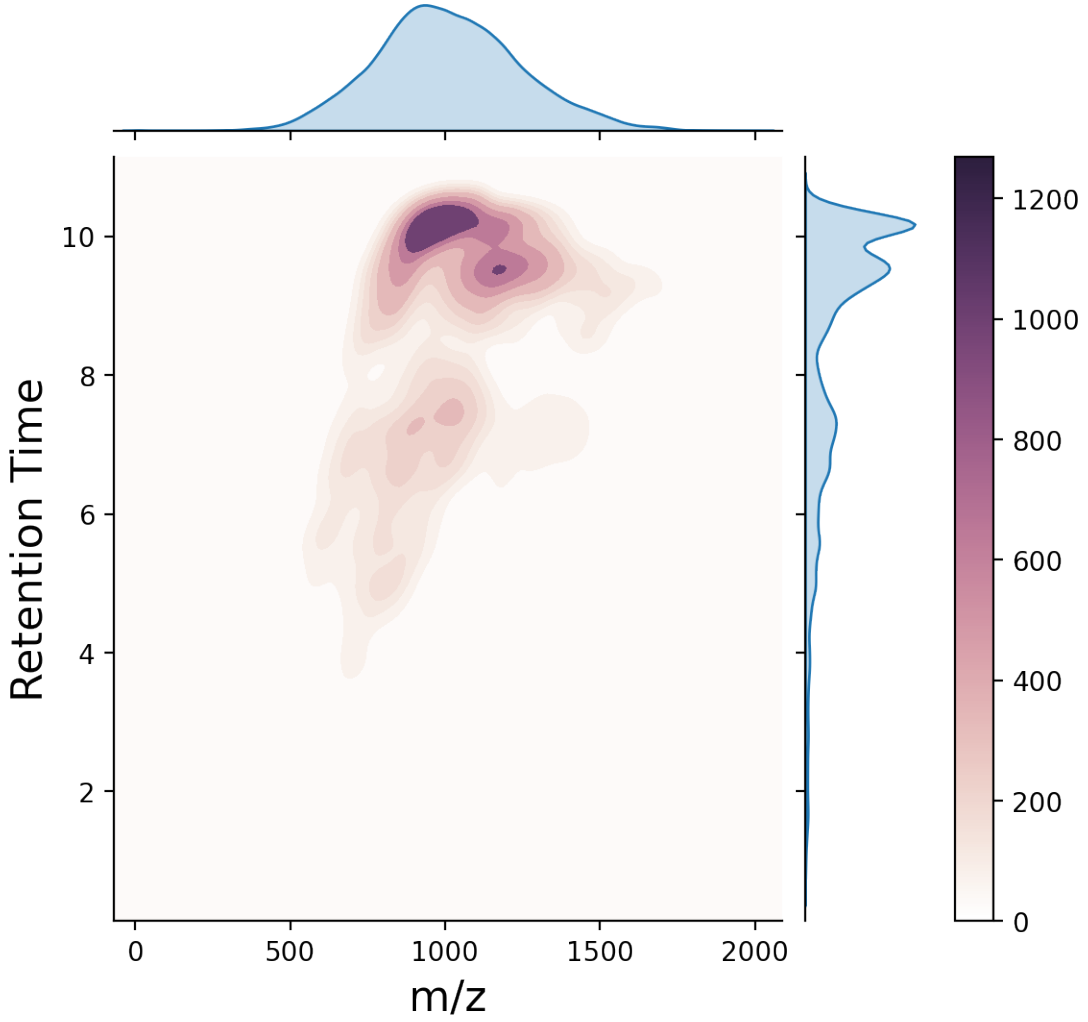
m/z-RT Overlaps METABOLOMICS

- We consider 26k compounds from NIST HR MS/MS with “typical” adducts and parsable structures
- Retention times were predicted using Retip 2
- m/z alone yields an excessive number of overlapping compounds, and this is why RT is important



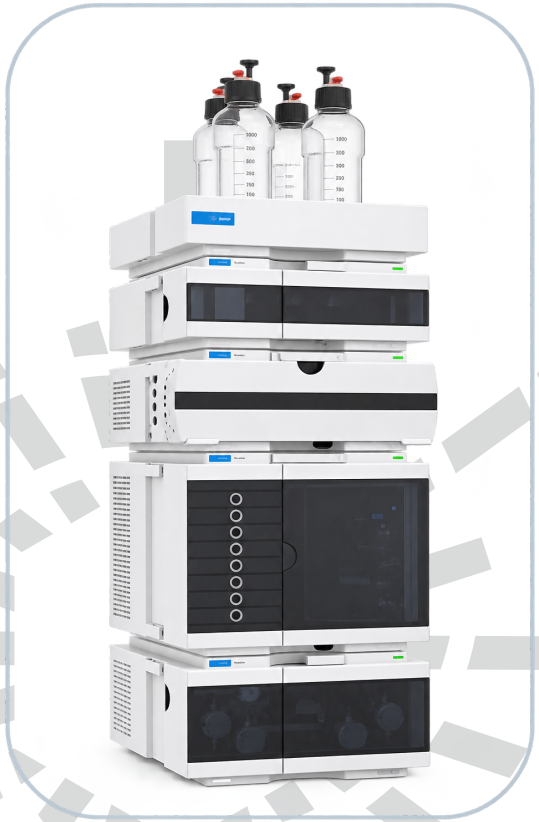
m/z-RT Overlaps LIPIDOMICS

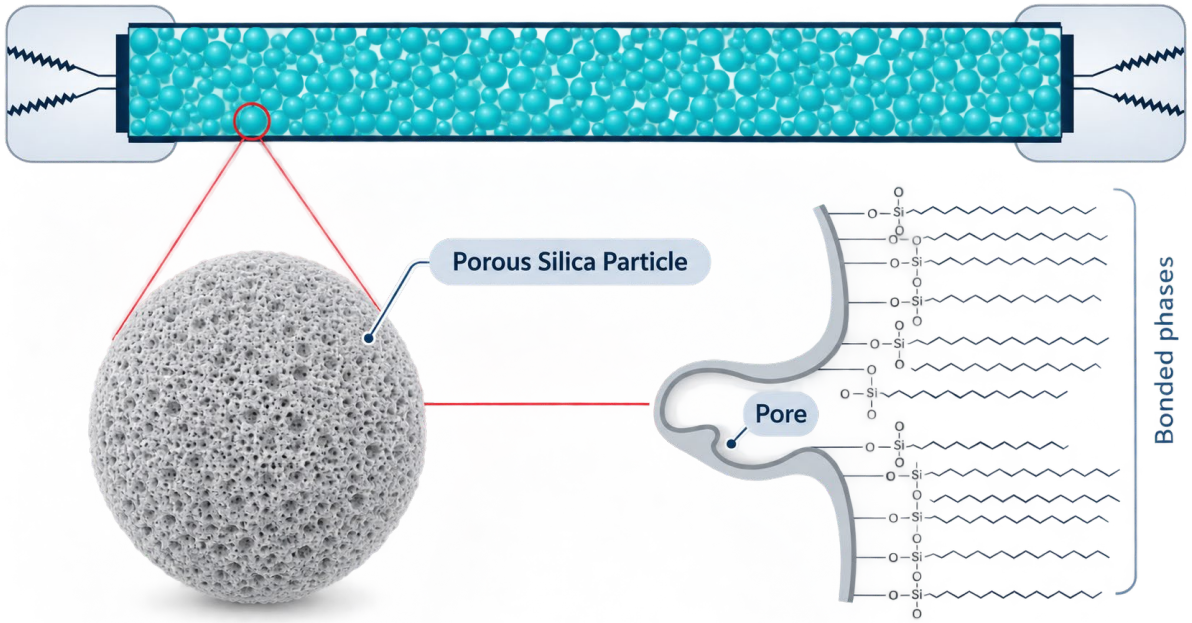
- We consider all the lipids included in MSDIAL4
- Retention times were predicted using Retip 2
- m/z alone yields an excessive number of overlapping compounds, while adding RT improve the distribution.



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4D-ID®: Retention Time prediction with Retip





analytical chemistry

pubs.acs.org/ac Article

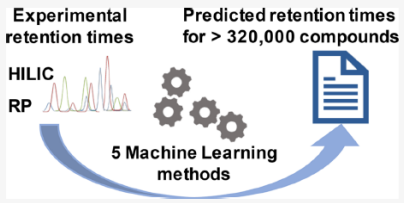
Retip: Retention Time Prediction for Compound Annotation in Untargeted Metabolomics

Paolo Bonini,* Tobias Kind, Hiroshi Tsugawa, Dinesh Kumar Barupal, and Oliver Fiehn*

Cite This: *Anal. Chem.* 2020, 92, 7515–7522 Read Online

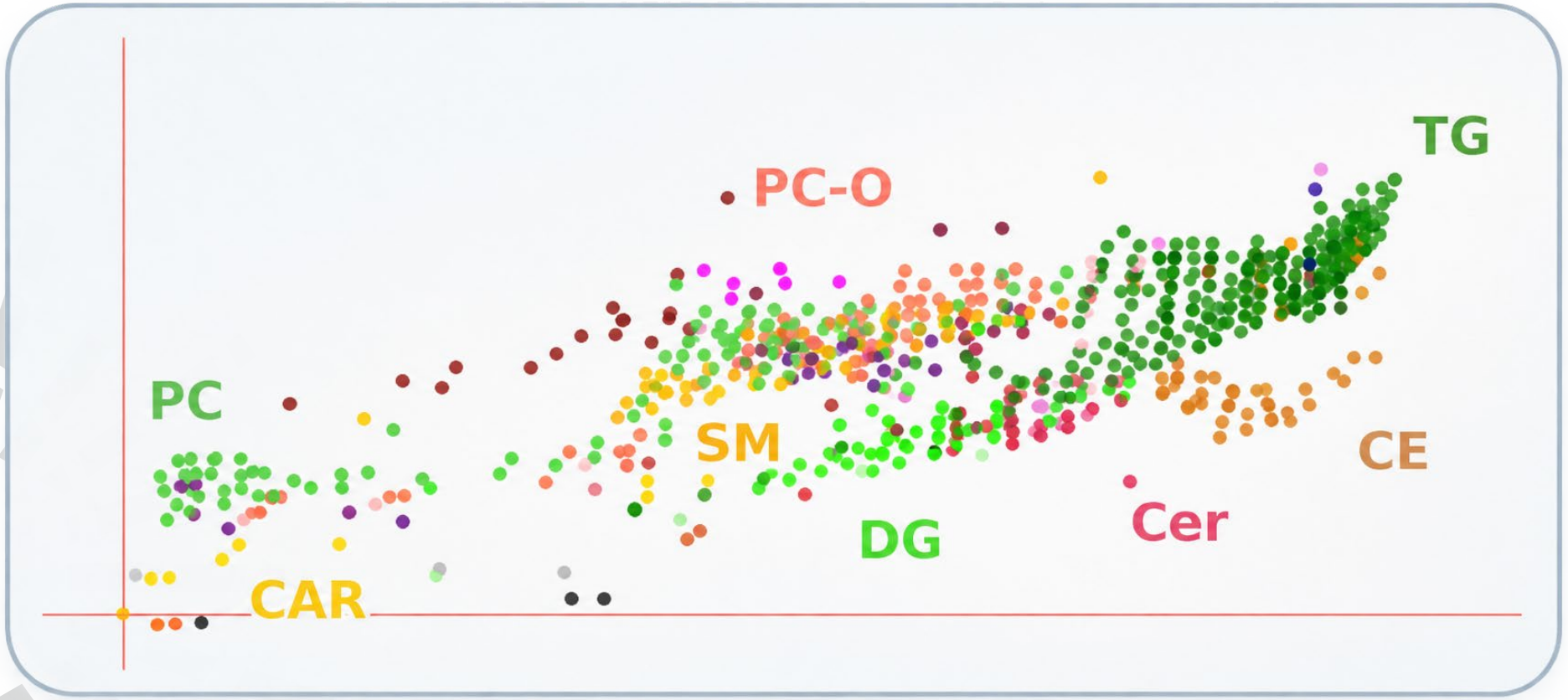
ACCESS | Metrics & More | Article Recommendations | Supporting Information

ABSTRACT: Unidentified peaks remain a major problem in untargeted metabolomics by LC-MS/MS. Confidence in peak annotations increases by combining MS/MS matching and retention time. We here show how retention times can be predicted from molecular structures. Two large, publicly available data sets were used for model training in machine learning: the Fiehn hydrophilic interaction liquid chromatography data set (HILIC) of 981 primary metabolites and biogenic amines,and the RIKEN plant specialized metabolome annotation (PlaSMA) database of 852 secondary metabolites that uses reversed-phase liquid chromatography (RPLC). Five different machine learning algorithms have been integrated into the Retip R package: the



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Overlapping lipids



What is collision induced dissociation (CID)?

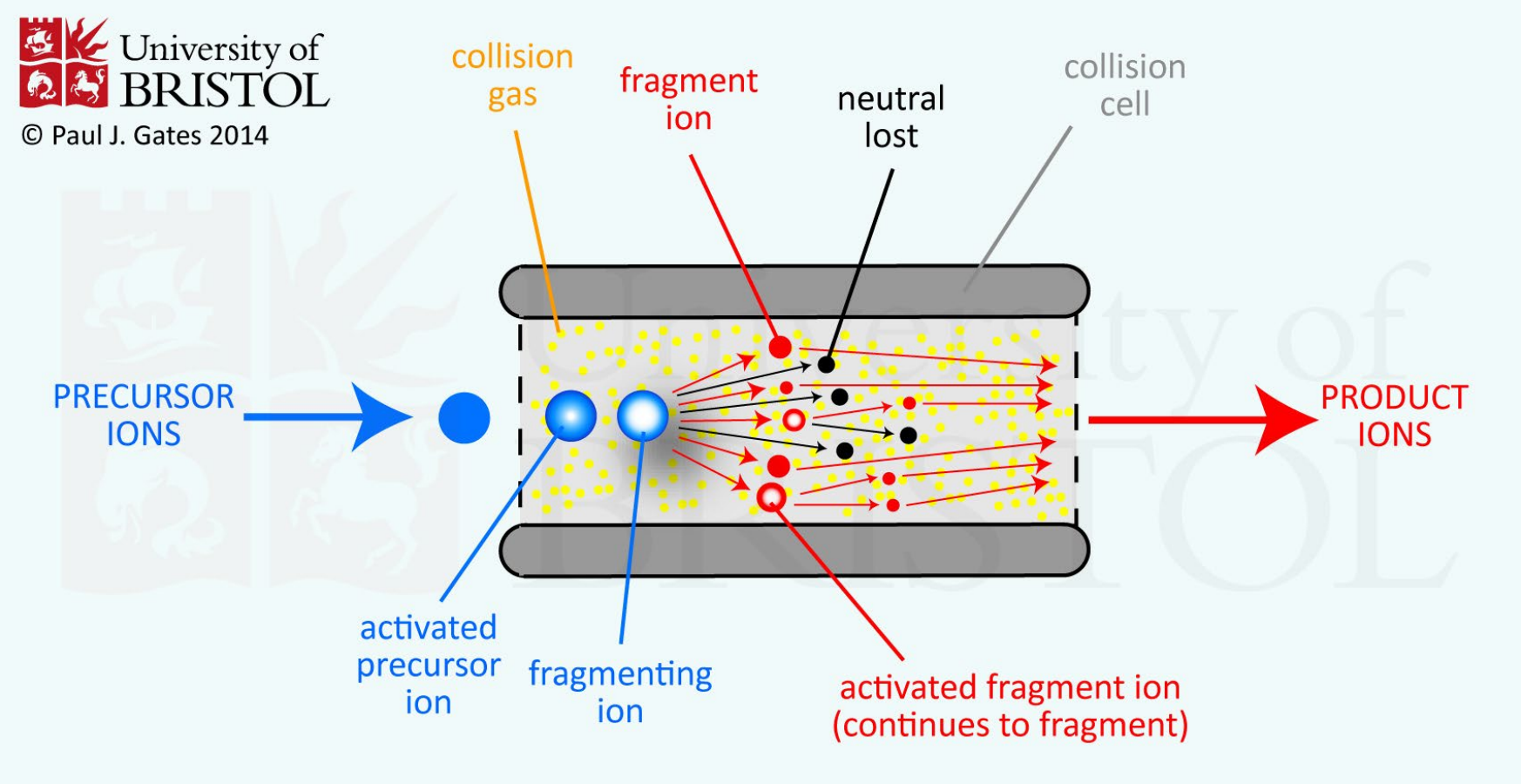
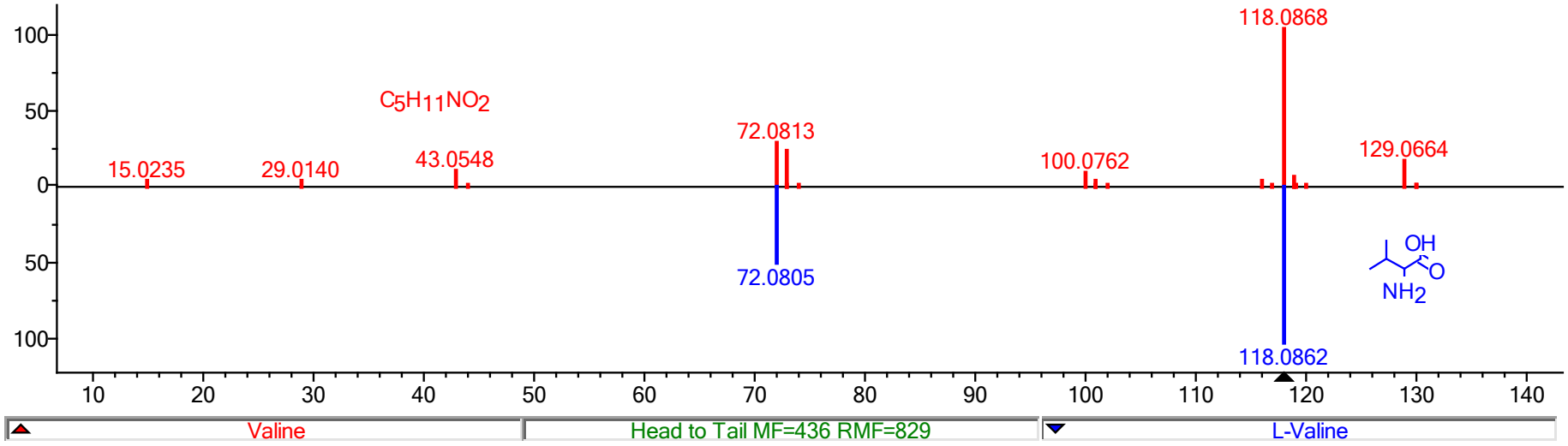
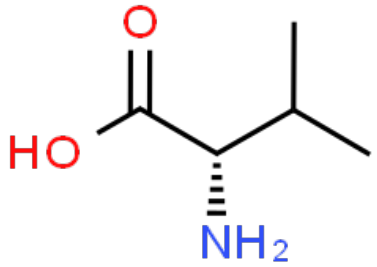


Figure: PJ Gates (2014) http://www.chm.bris.ac.uk/ms/cid.xhtml

In-silico MS/MS spectrum of valine compared to 5V HCD

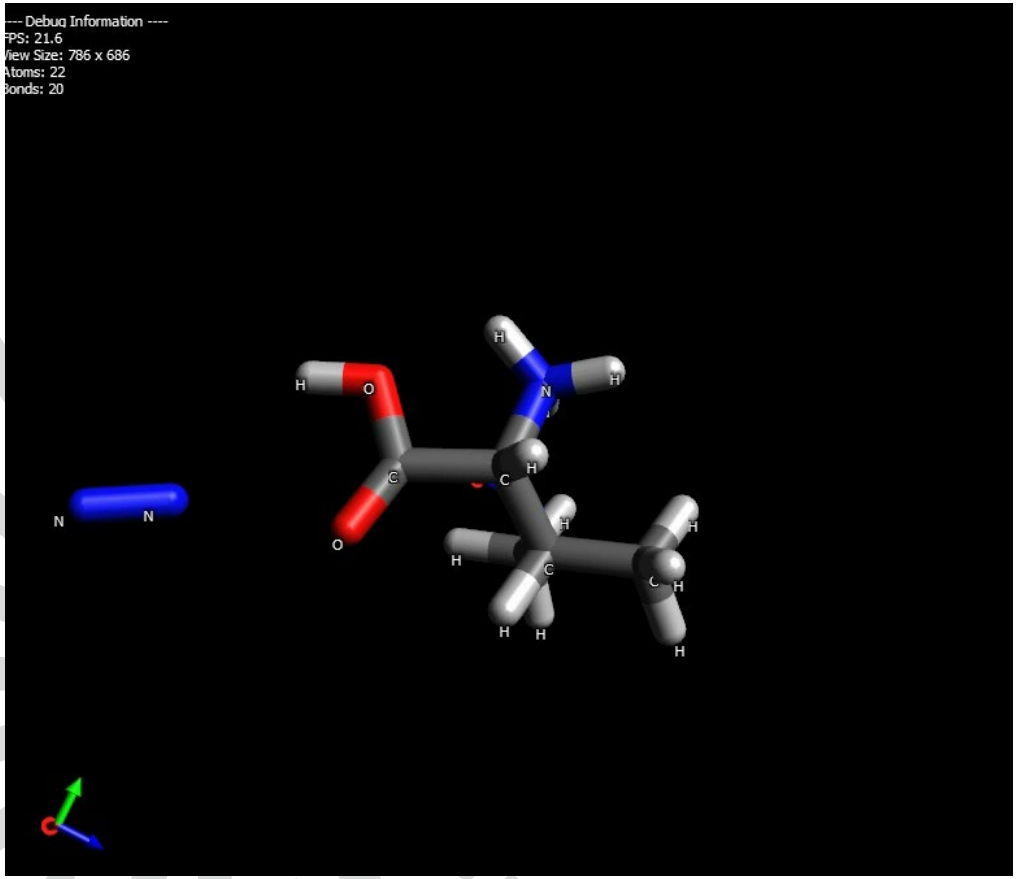




CID gas = N_2

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Gaining insights into fragmentations and rearrangements with trajectory investigations



Valine CID trajectory

CO = 27.994915 Da
H2O = 18.01056 Da

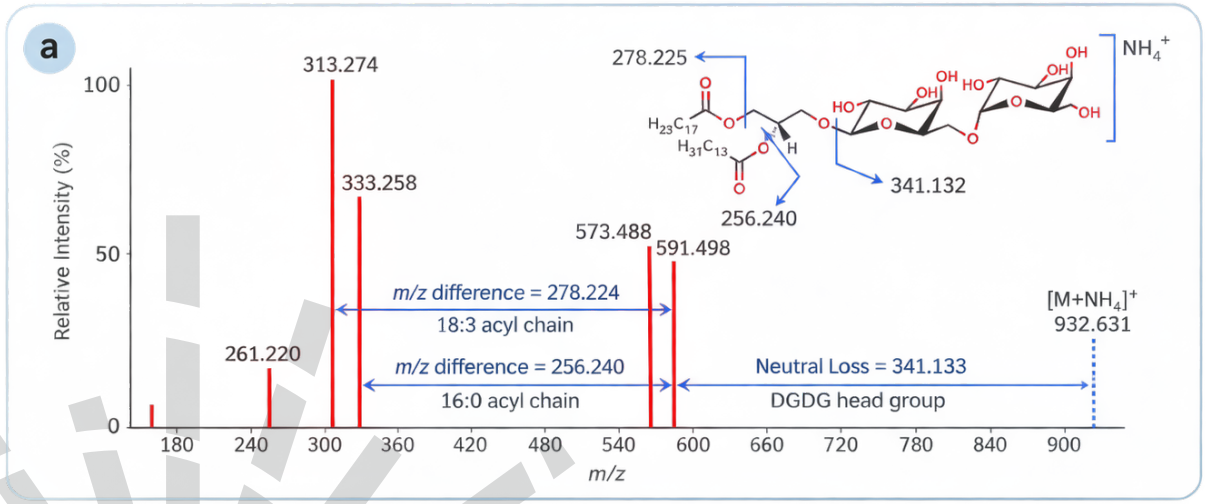
Loss = 46.00 Da

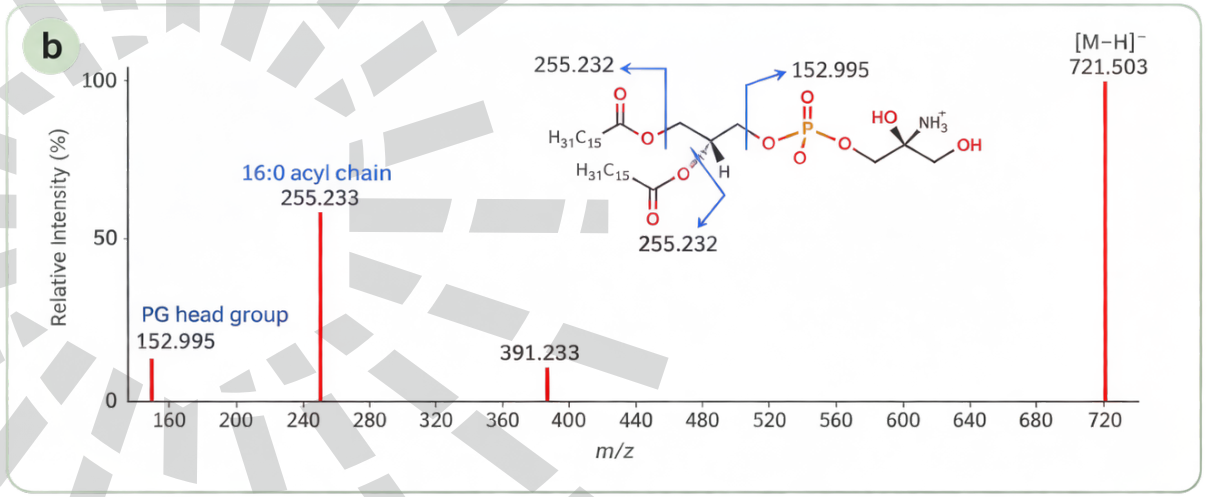
1. Many trajectories are sampled (144-400)

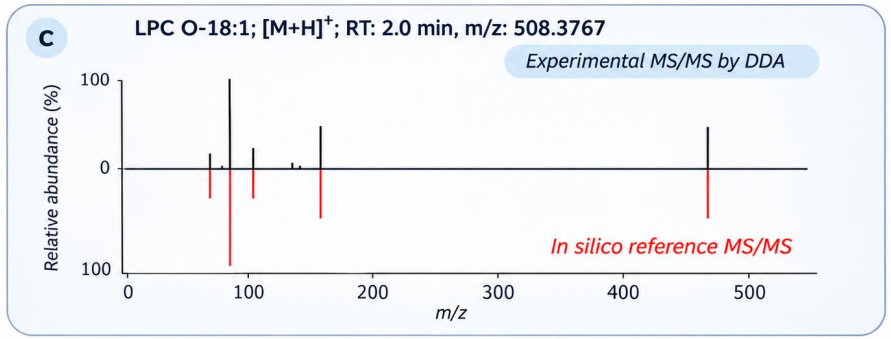
2. m/z values are calculated from accurate mass of ions

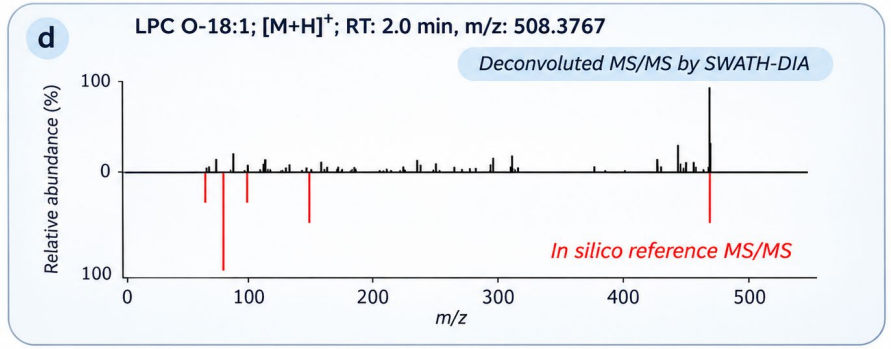
3. Abundances are calculated by averaging the ion count

The power of MSMS and SWATH

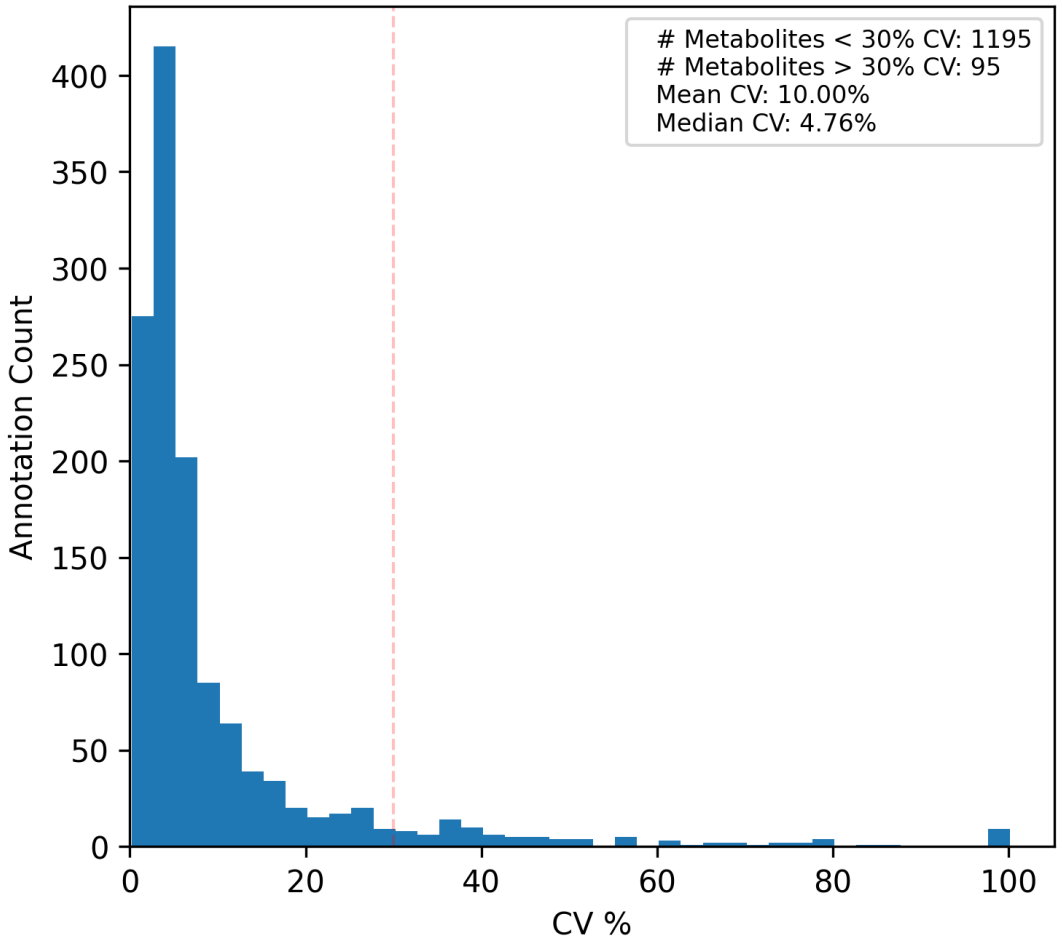








The CV problem



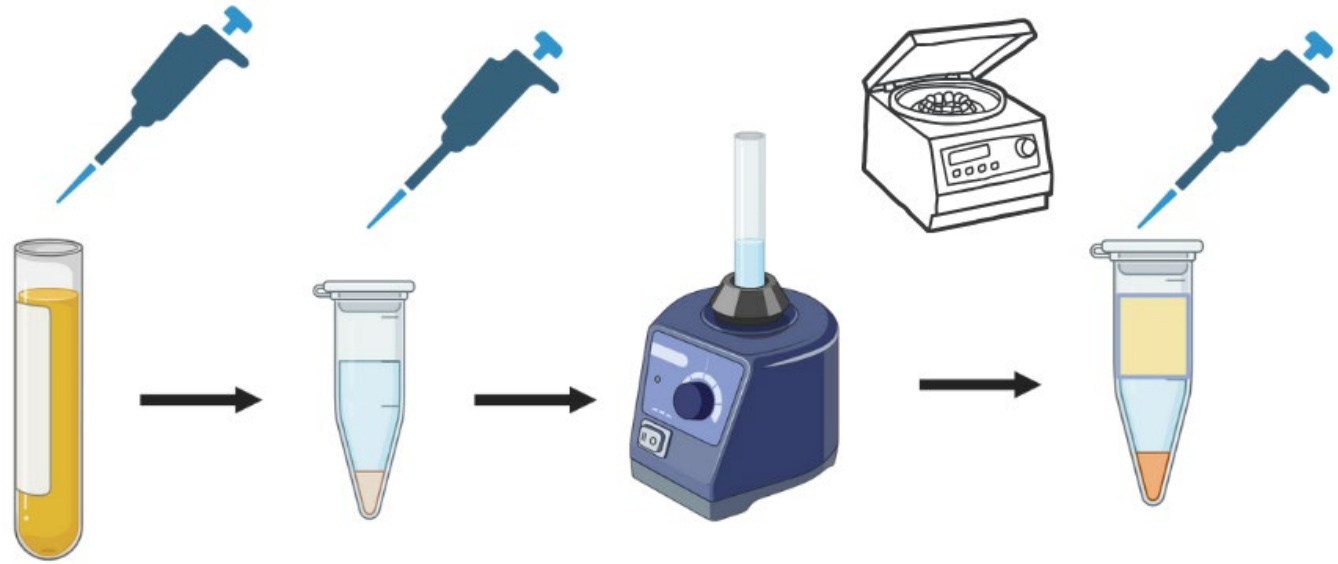
For a Technical CV of 0%
And a biological CV of 30%
SAMPLE SIZE= 8

For a Technical CV of 10%
And a biological CV of 30%
SAMPLE SIZE= 17

For a Technical CV of 20%
And a biological CV of 30%
SAMPLE SIZE= 25

Bi Phase extraction

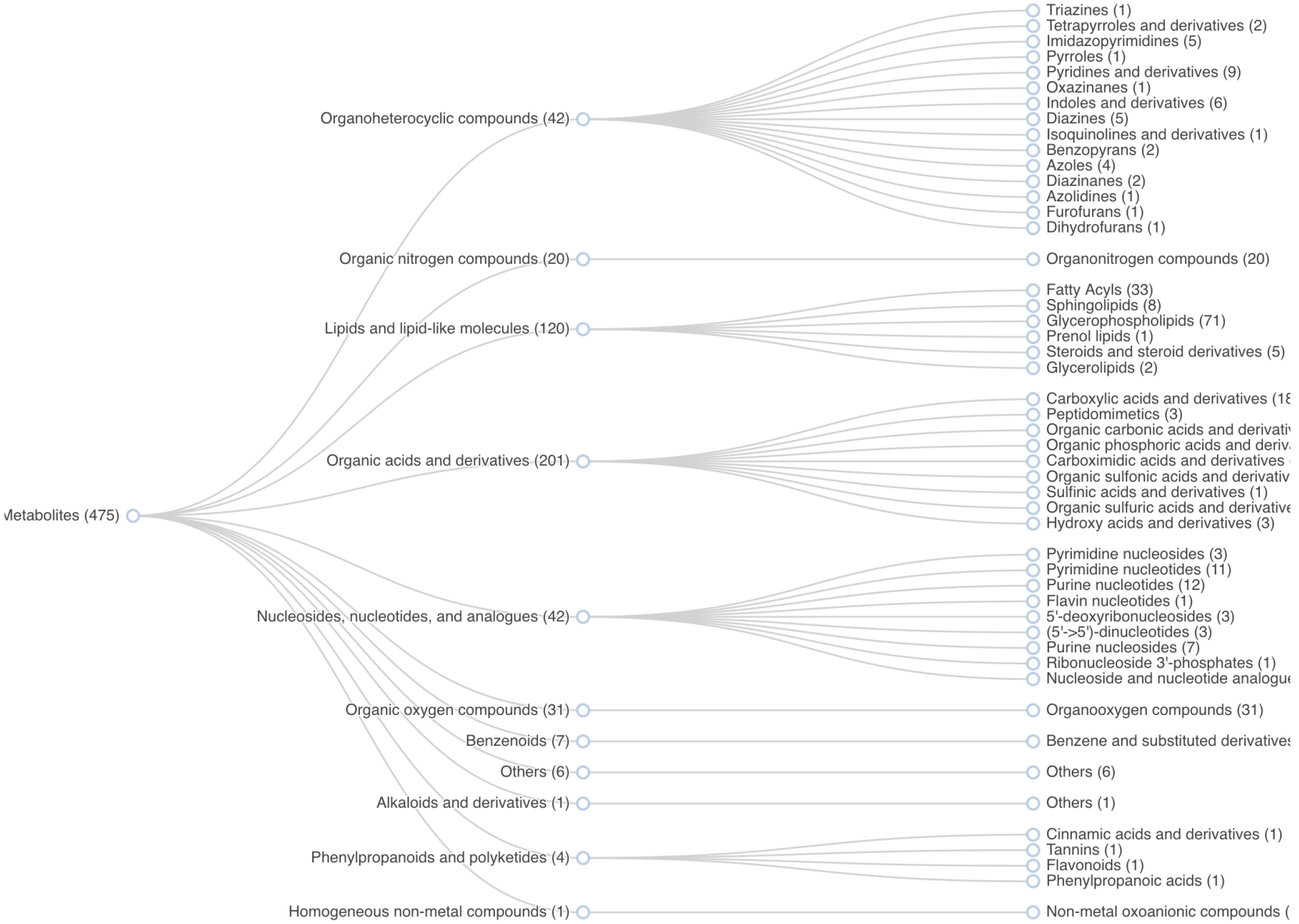
- Lipids
- Polar Metabolites
- Proteins



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METABOLOMICS

ClassyFire Supercl…	ClassyFire Class	Metabolites
11	48	466

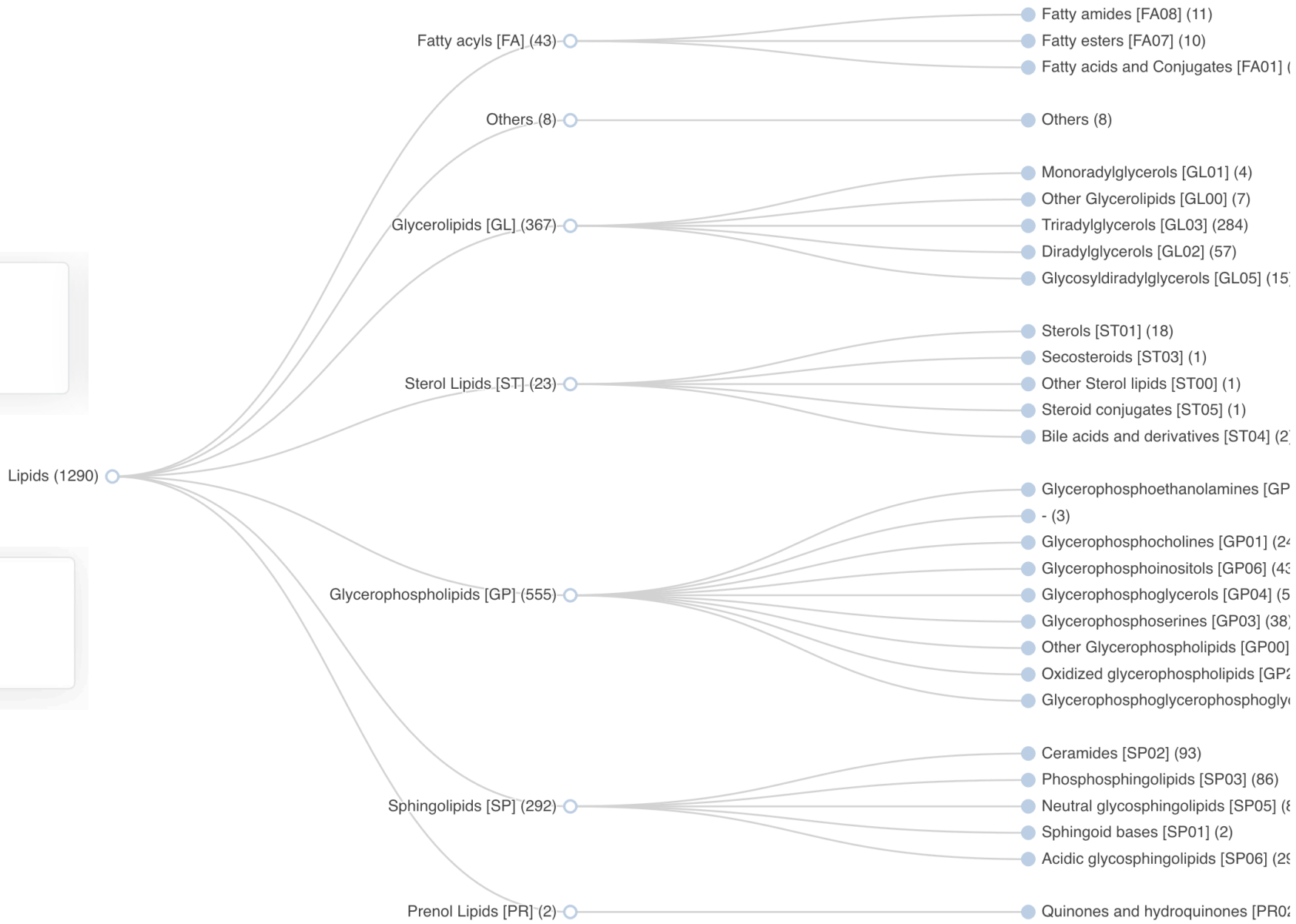


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LIPIDOMICS

Lipid categories	Lipid main classes
7	29

Lipid subclasses	Lipids
80	1289

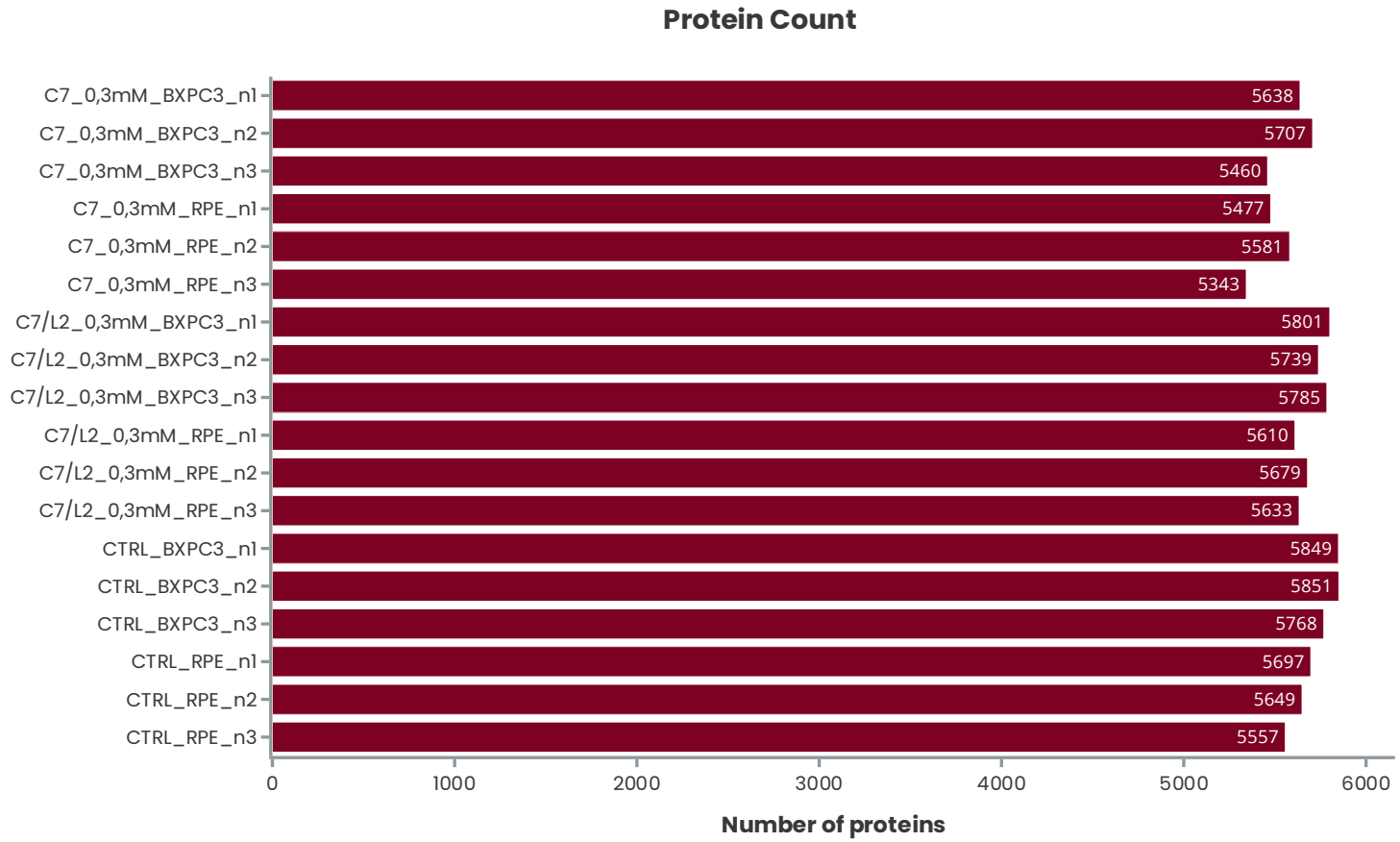


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PROTEOMICS

Protein Class	Family	Proteins	Proteins average across …
186	6345	6404	5656.89

Biological process	Pathway	Reactome	Samples
8987	149	2257	18



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oloMAP ®

Our solution for the interpretation and visualization of omics data



- **14K** Plant / Phytochemical
- **85K** Microbial
- **70K** Food
- **2K** Human
- **280K** Exposomics
- **1.890K** Lipidomics

oloMap® Portal

Our proprietary oloMAP® software allows us to identify compounds from data generated by our GC/MS and LC/MS instruments, as well as to generate advanced biostatistics reports.

oloMap® Data Base

The identifications of oloMAP® come from our database in which we have more than 1 million biomolecules

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oloMAP® Portal

Case Study Alzheimer. Mice Plasma. Lipidomics. “PCA”

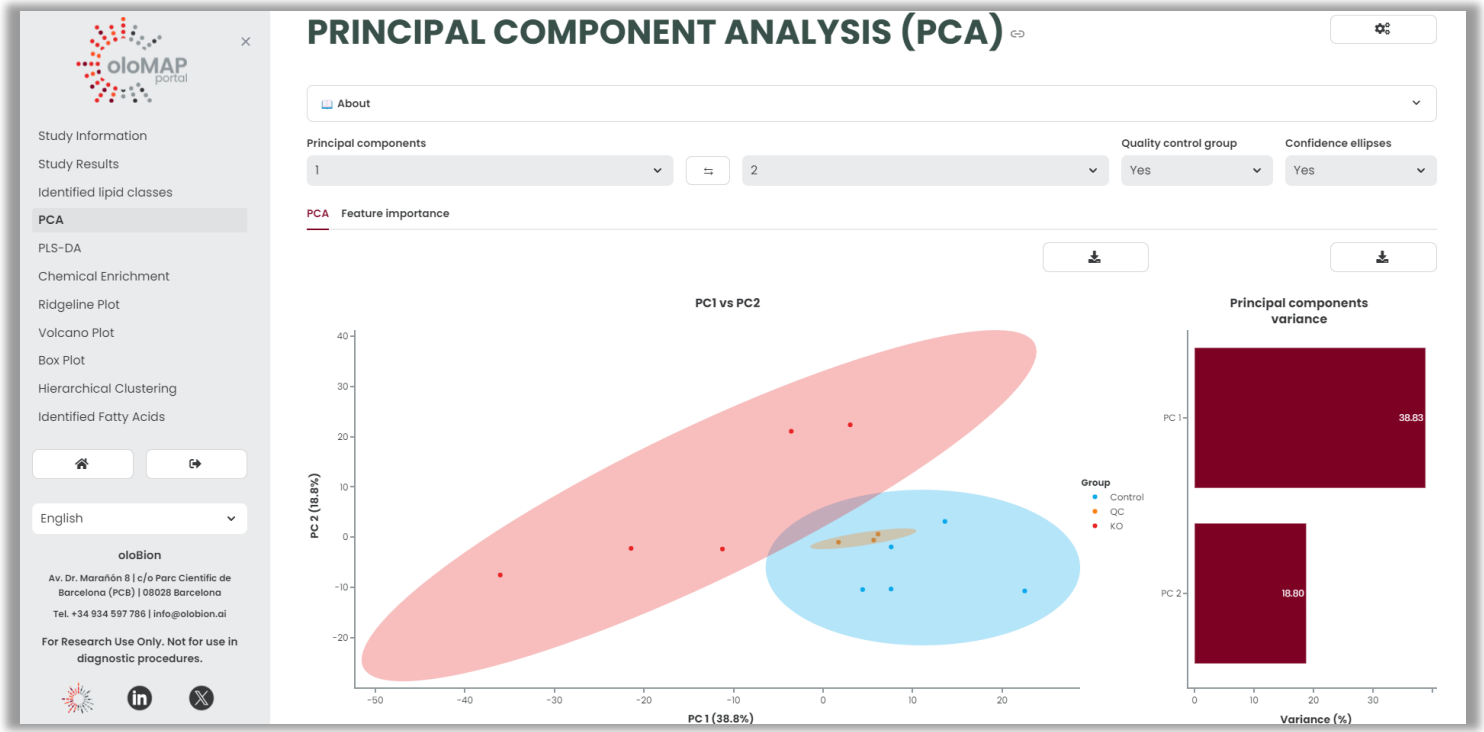
Hemi-control”

Alzheimer Model

Vs.

“WT-control”

Wild Type



Through the interactive reports of oloMAP, we can easily identify patterns or groups in omics data

oloBion

Turning samples into biological meaning

Contact
Assessing your needs and proposing the best approach

Submission
Submitting samples to oloBion

Analysis
Preparing, running, and processing samples

Report
Generating results report and providing support



Send us your samples, we take care of everything

What to expect

- Raw Data
- Compound annotation
- Chemical Ontology
- Quantification (relative or absolute)
- Biostatistical Analysis
- Functional analysis (e.g. pathways)
- Multi-omics analysis

What we deliver

- Secure online access to your results
- Ready-to-use tables and figures
- Exportable files for your own analysis

How to complement it

- Interpretation report
- Tailored recommendations for next experiments
- Scientific publication support
- Follow-up meeting



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