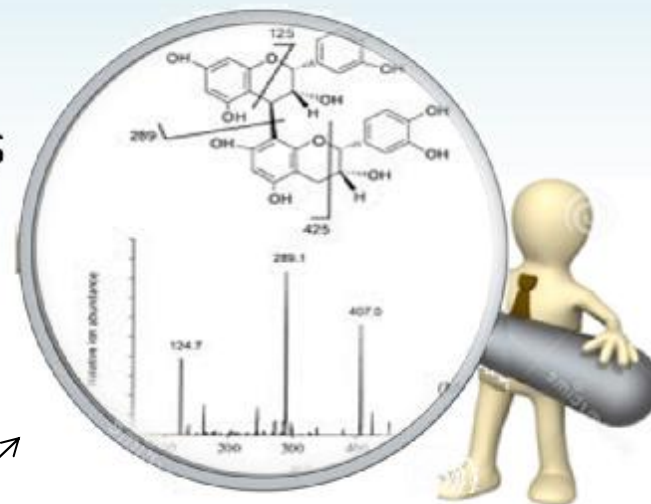
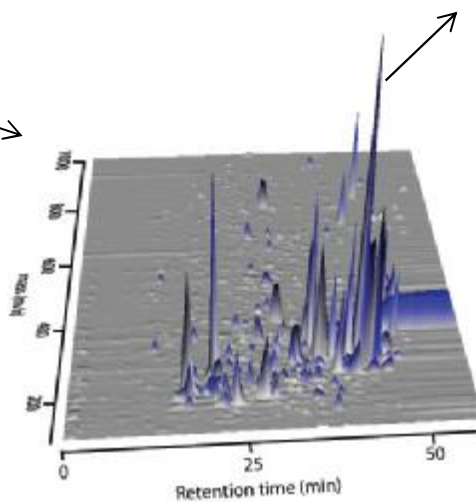
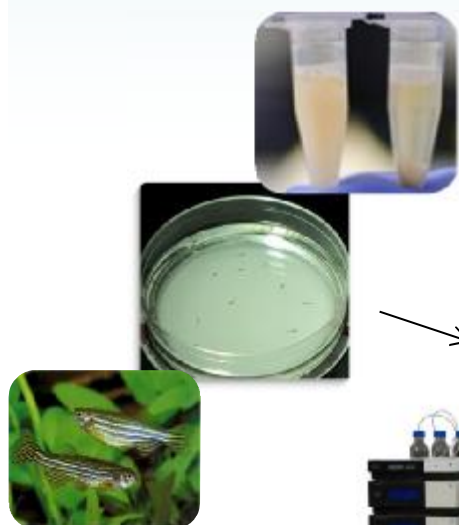


Study of the metabolism of zebrafish (danio rerio) embryo exposed to triclosan and benzotriazoles by HILIC-TOF-MS

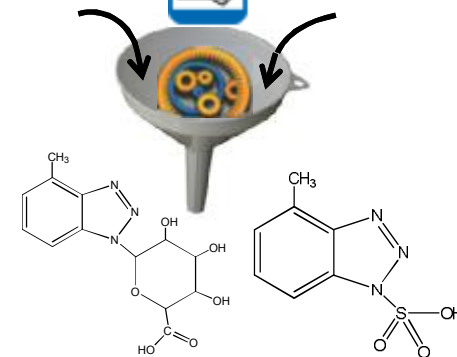
Damalas Dimitris



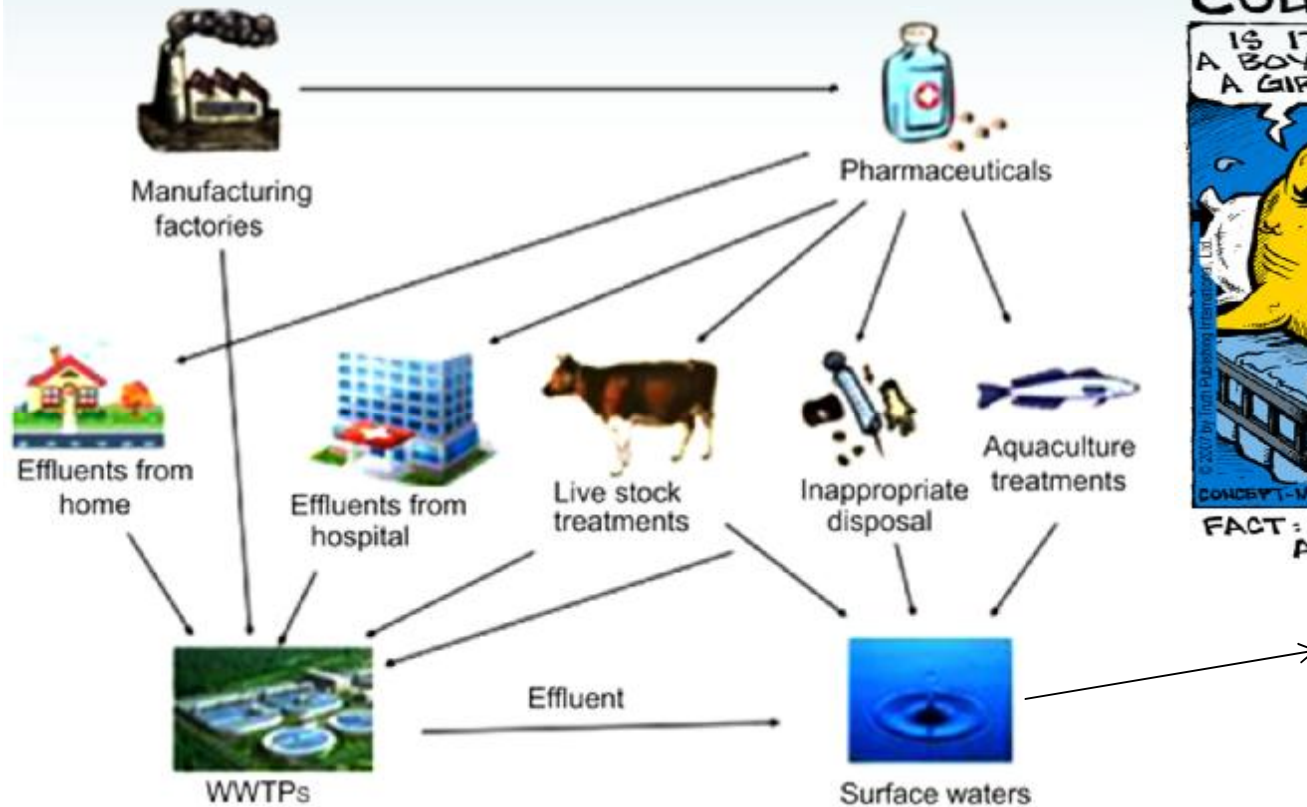
Non target screening

Suspect screening

Metabolic profiling



Aquatic environment contamination...



FACT: PHARMACEUTICALS DESTROY AQUATIC ECOSYSTEMS.



Bioaccumulation of xenobiotics and their bio-TPs in aquatic organisms

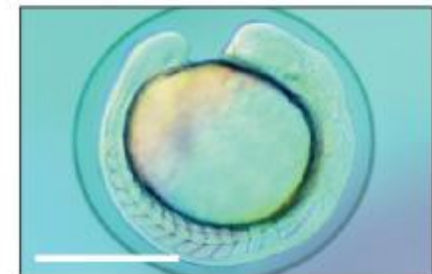
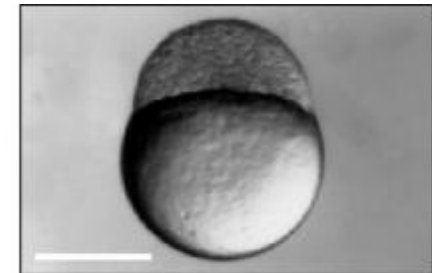
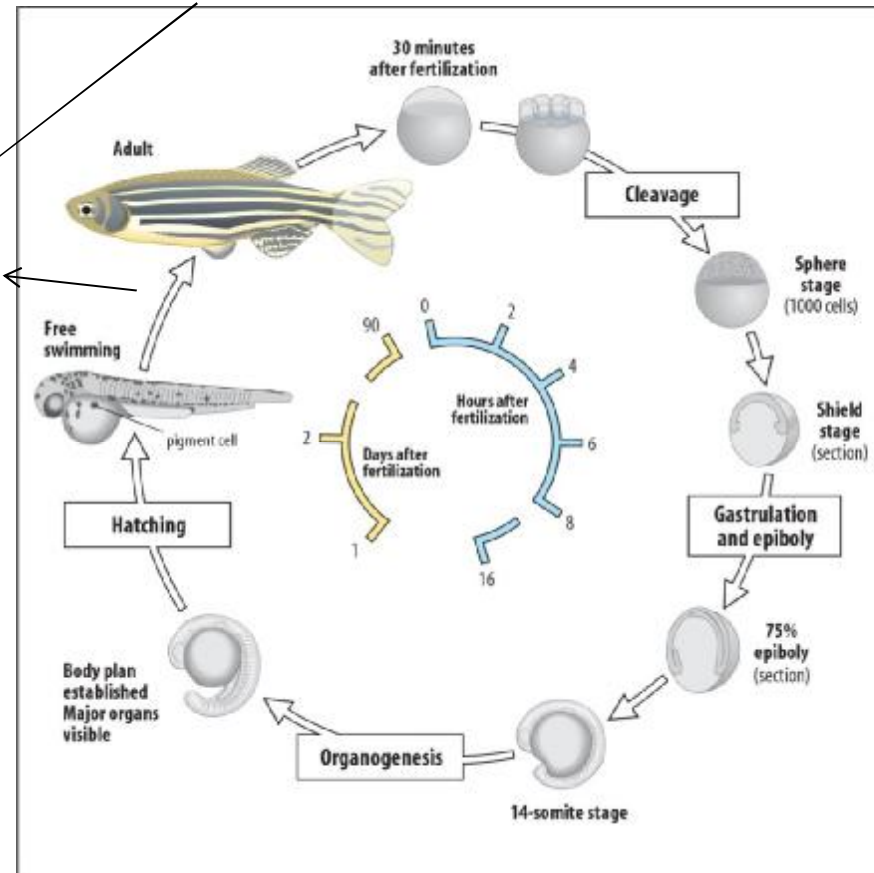
Xenometabolome = xenobiotics (unmodified) + bio-TPs

Endometabolome = endogenous organism metabolites

need for a model organism

- ❑ assess the toxicity of xenobiotics and their bio-TPs in aquatic organisms
- ❑ relate the toxic effect to metabolic phenotype variations
- ❑ evaluate the detoxification system of aquatic organisms

this is Zebrafish (*Danio rerio*) (96 hpf)



why *Zebrafish*...?

- ✓ Embryo and larval small size
- ✓ Rapid generation of large number of embryos
- ✓ Husbandry costs
- ✓ Recommended by the OECD for fish toxicity testing
- ✓ Similar xenobiotic metabolism pathways with those observed in mammals

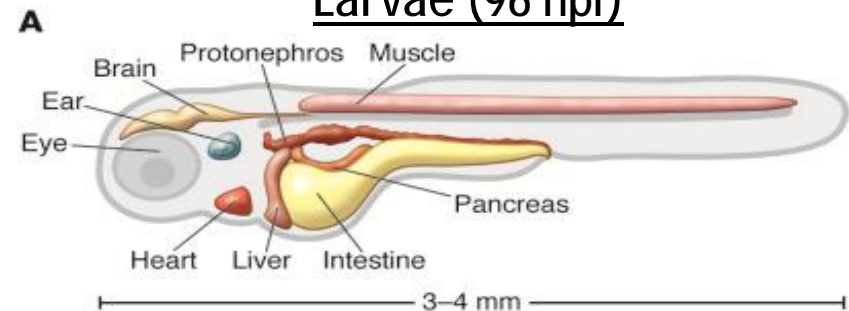
Ideal for keeping in the lab



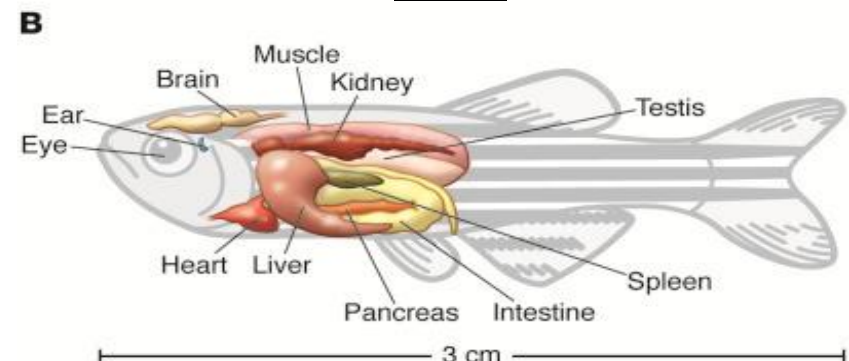
why 96 hpf...?

- ✓ The majority of major organs partially or fully formed at early life-stages
- ✓ Absorption of compounds from water across the skin at early life-stages

Larvae (96 hpf)



adult



experimental part

Incubation:



BTR

4-Me-BTR

5-Me-BTR

Triclosan

Control



~ 60 Zebrafish embryos (96 hpf) / petri

5 time intervals for each "exposure":



30s



2h



4h



8h



24h

each time interval sample in different petri: e.g. for BTR



30s



2h



4h



8h



24h

Time profiles observation

Estimation of skin adsorption

Short term effects

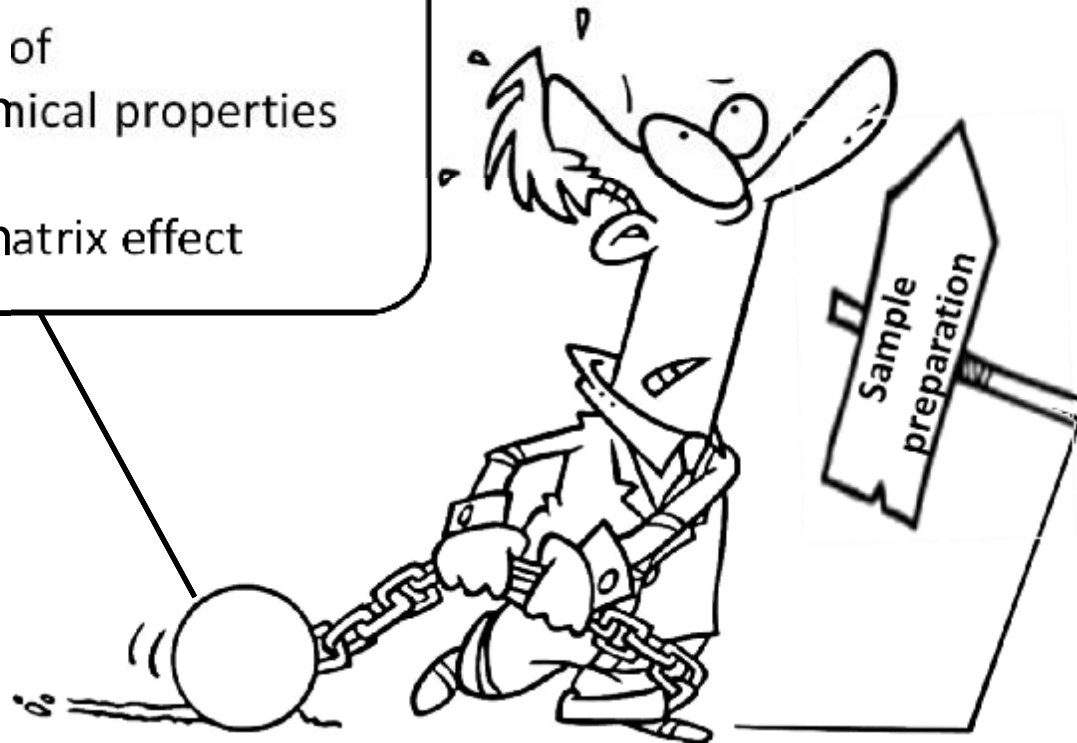
Long term effects

Sample preparation

- × Tissue quantity limitation (~ 15 mg/sample)
- × Wide range of physicochemical properties
- × Increased matrix effect

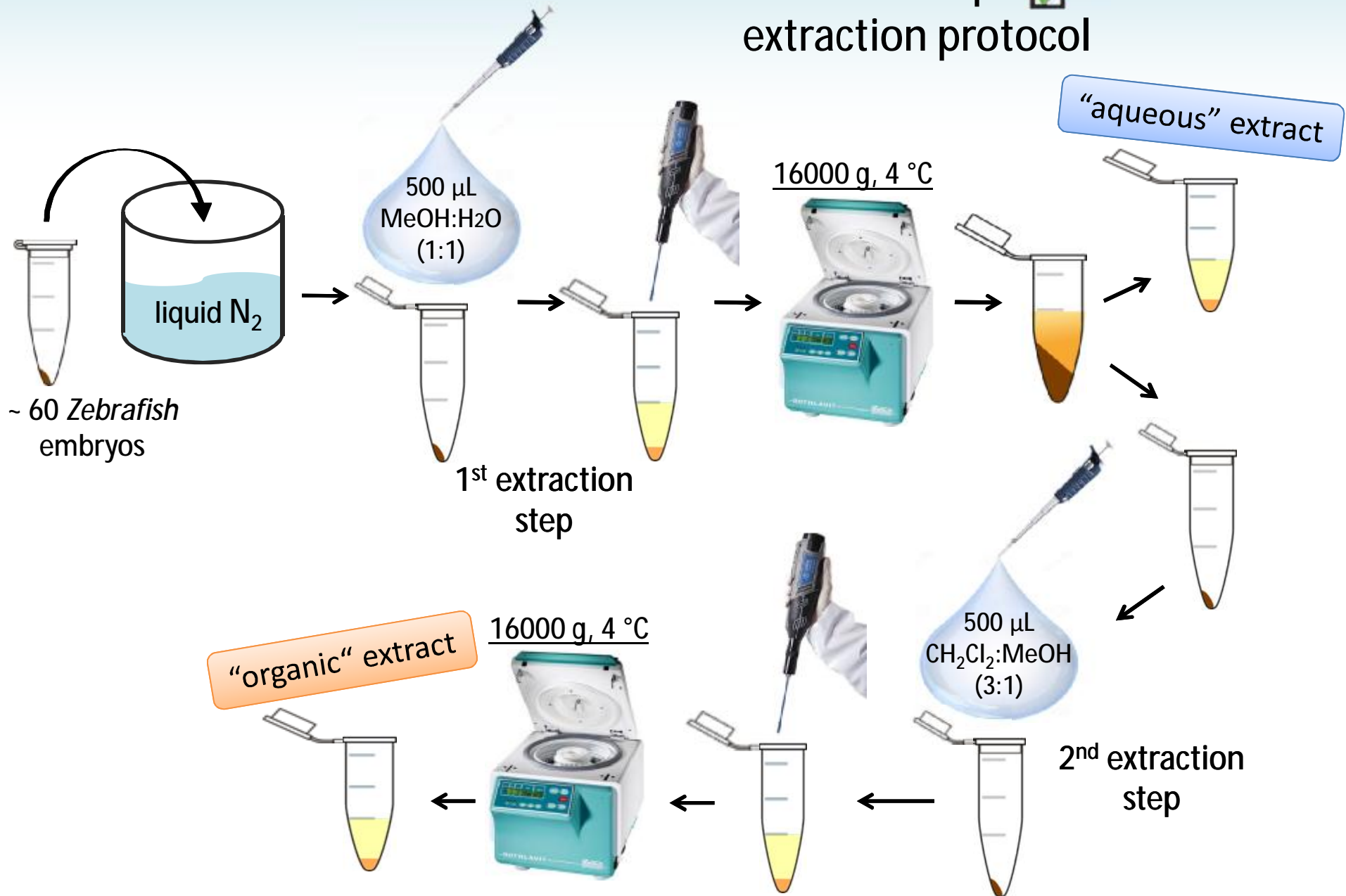


“two step” or “all in one”
extraction protocol



Sample preparation

"two step" extraction protocol



Evaluation part

Analysis

UHPLC-Q-TOF MS/MS

- **RPLC** (+/- ESI) (Acclaim C18)
- **HILIC** (+/- ESI) (Acquity BEH amide)

Data Acquisition modes

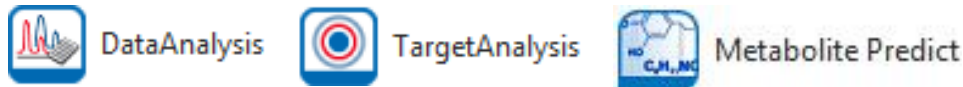
- Data-Independent (bb-CID)
- Data-Dependent (Auto-MS)

- Xenometabolome (low-medium polarity)
- Endometabolome (medium-high polarity)



Bio-TPs Identification

- Suspect Screening
(knowledge based approach)



- Non-target Screening
(treated/control comparison based)

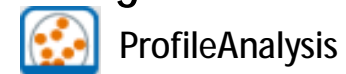


Metabolic profiling

- Targeted approach
(primary metabolites of interest)

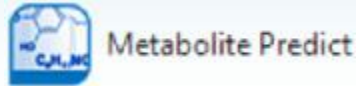


- Untargeted approach
(significant endogenous metabolic responses)



Suspect screening

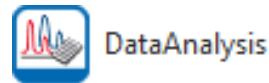
Suspect list compilation



(*in-silico* drug metabolism prediction tool)

.CSV

A	B	C	D
m/z	RT	sum formula	name
		C7 H7 N3	4 Me-BTR
		C7 H5 N3 O	4 Me-BTR-147
		C7 H7 N3 O	4 Me-BTR-149
		C8 H9 N3 O	4 Me-BTR-163
		C7 H7 N3 O2	4 Me-BTR-165



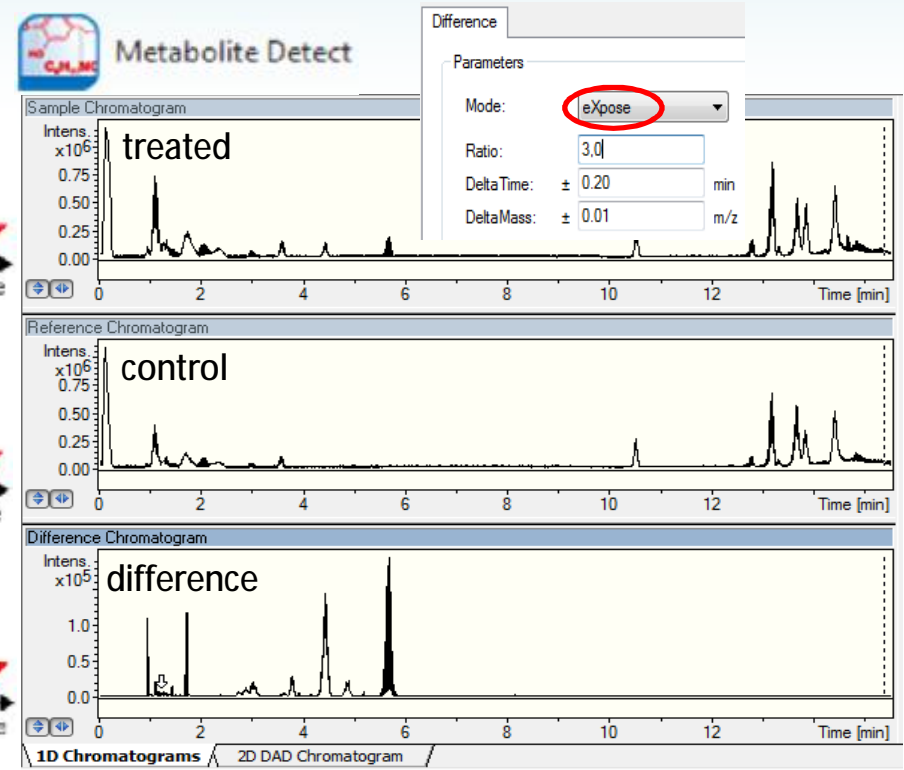
m/z → Tentative bio-TP

Criteria

- ✓ Accuracy ≤ 2 mDa
- ✓ Isotopic fit ≤ 100 mSigma
- ✓ Absence from control
- ✓ Time profile existence
- ★ Xenobiotic metabolism relevant

Non-target screening


Treated-control sample "comparison":



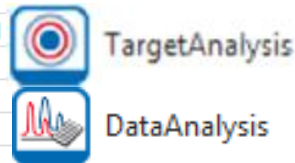
Example	Identification confidence	Minimum data requirements
	Level 1: Confirmed structure by reference standard	MS, MS ² , RT, Reference Std.
	Level 2: Probable structure a) by library spectrum match b) by diagnostic evidence	MS, MS ² , Library MS ² MS, MS ² , Exp. data
	Level 3: Tentative candidate(s) structure, substituent, class	MS, MS ² , Exp. data
C ₇ H ₇ N ₃ O ₂	Level 4: Unequivocal molecular formula	MS isotope/adduct
192.0757	Level 5: Exact mass of interest	MS

Targeted metabolic profiling

4 major classes of polar metabolites

- amines
 - aminoacids
 - organic acids
 - sugars
- standards available 

B	C	D
RT POS	sum formula	name
2	C6H6N2O	Nicotinamide
2.5	C7H8N4O2	Theobromine
2.5	C5H6N2O2	Thymine
2.5	C5H10O5	Xylose
2.55	C5H10O5	Arabinose
2.7	C6H10O4	Adipic acid
2.76	C5H6O4	Itaconic acid
3	C10H11NO3	2-methyl-hippuric acid
3.45	C10H16N2O3S	Biotin
3.8	C9H9NO3	Hippuric acid
4	C4H4N2O2	Uracil



Id	Cmpd.Name	Formula	Err [mDa]	mSigma	RT...	Area
+++	N-acetyl-histidine	C 8 H 11 N 3 O 3	-0.1	10.0	7.22	743052
+++	Alanine	C 3 H 7 N 1 O 2	0.3	3.8	7.50	11969
+++	Xanthine	C 5 H 4 N 4 O 2	0.1	2.7	6.00	12956
+++	Acetylcarnitine	C 9 H 17 N 1 O 4	0.2	6.1	7.05	1008280
+++	Inosine	C 10 H 12 N 4 O 5	-0.1	25.0	6.30	598996
+++	Uridine	C 9 H 12 N 2 O 6	0.2	16.2	5.30	55444
+++	Sarcosine	C 3 H 7 N 1 O 2	0.3	3.8	7.50	11969
++	Isoleucine	C 6 H 13 N 1 O 2	-0.5	5.7	6.40	7272
++	Monoisoamyla...	C 5 H 13 N 1	0.3	53.1	6.20	1894
++	Phenylalanine	C 9 H 11 N 1 O 2	0.4	21.1	6.90	1273
++	Proline	C 5 H 9 N 1 O 2	-0.5	n.a.	8.50	2335
++	Threonine	C 4 H 9 N 1 O 3	0.2	97.2	8.10	6839
++	Adipic acid	C 6 H 10 O 4	-0.5	38.5	2.70	2537

Untargeted metabolic profiling

Metabolic feature extraction  DataAnalysis

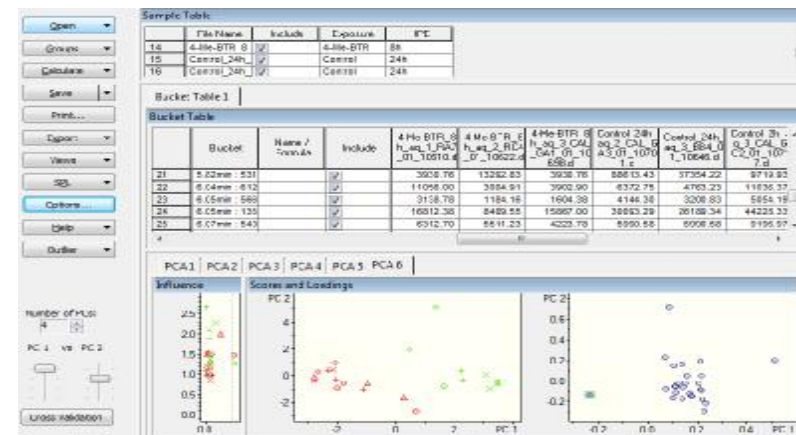
- Peak detection, peak alignment
- Find Molecular Features (FMF) Algorithm

Data pretreatment  ProfileAnalysis

- Normalization, scaling, missing values handling

Multivariate data analysis

- PCA  ProfileAnalysis



Why an additional separation mode?

× Double chromatographic run

× Laborious



× Time consuming

× Double data treatment

Bio-TPs Identification

Complementary metabolite separation technique to RPLC

Improved separation efficiency

- Better peak shape
- Smaller peak width

Orthogonality

- Elution in reversed order
- Enhance identification confidence



Improved detection sensitivity

- High organic content of mobile phase

Metabolic profiling

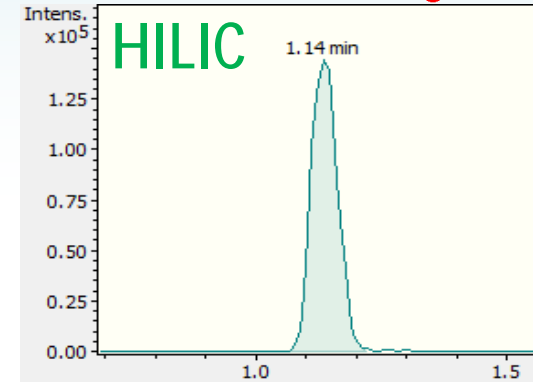
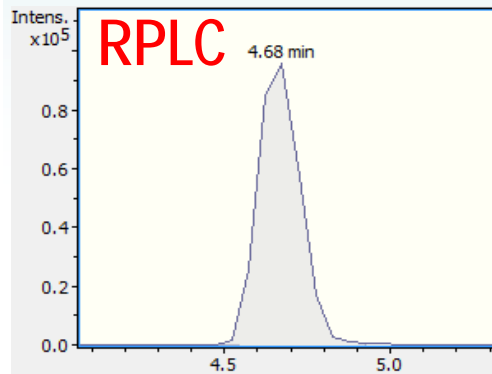
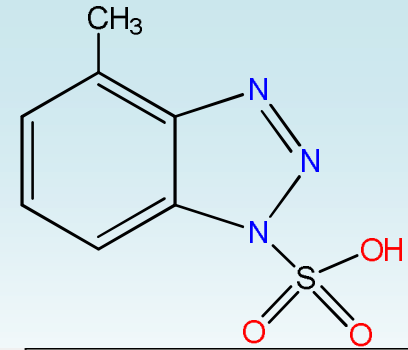
More comprehensive endometabolome coverage

- Adequate retention of highly polar primary metabolites (unretained in RPLC)

Examples (bio-TPs identification)

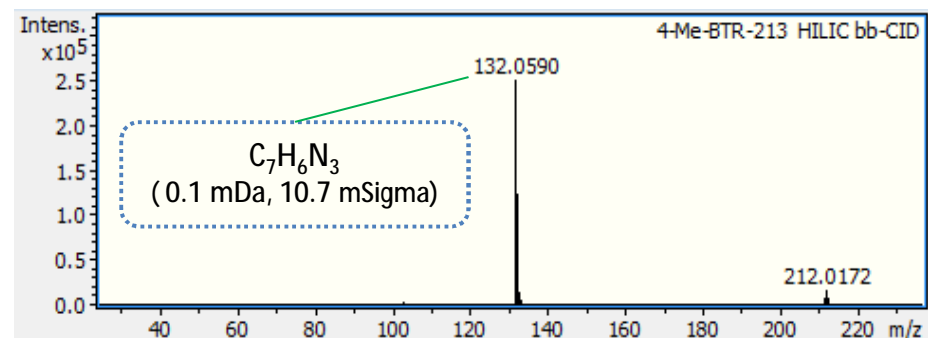
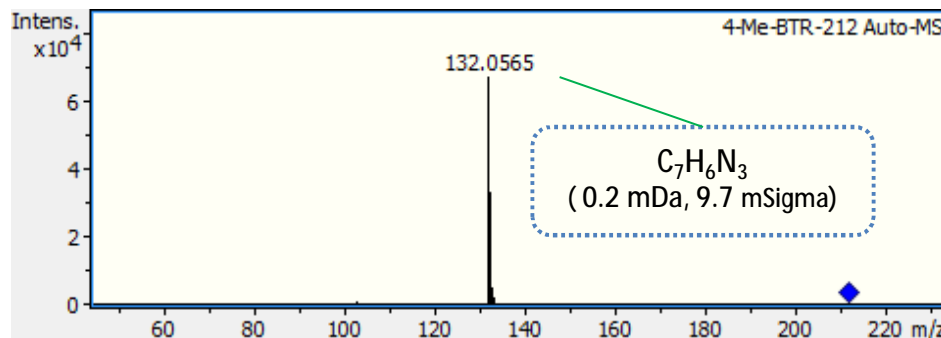
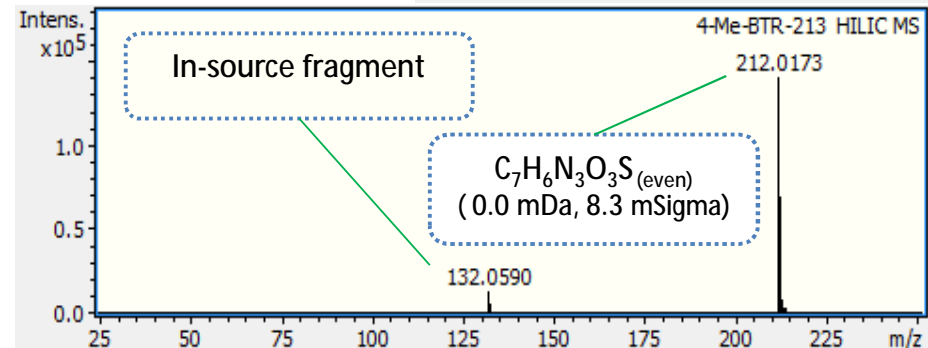
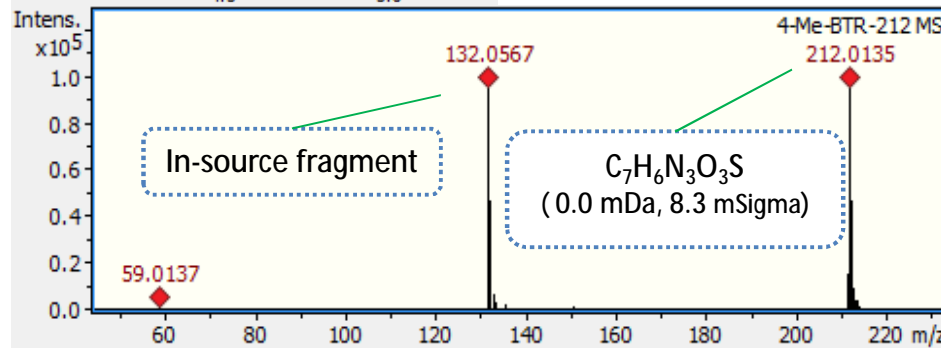
4-Me-BTR-N-sulfate

Negative



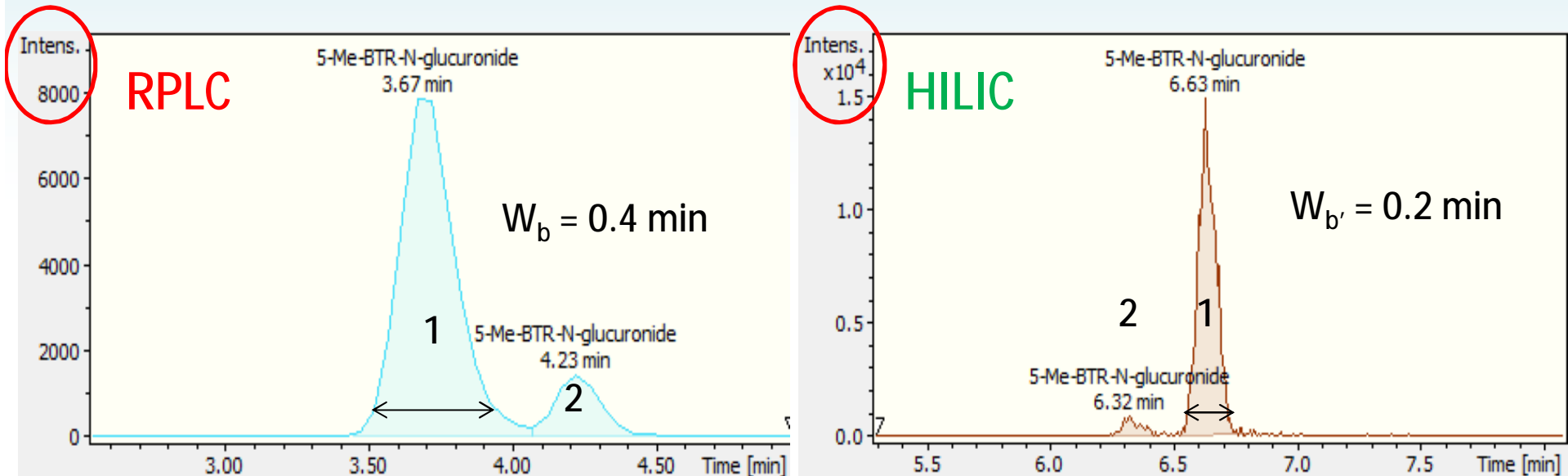
complementarity of
HILIC mode

✓ Identical MS and MS/MS spectra



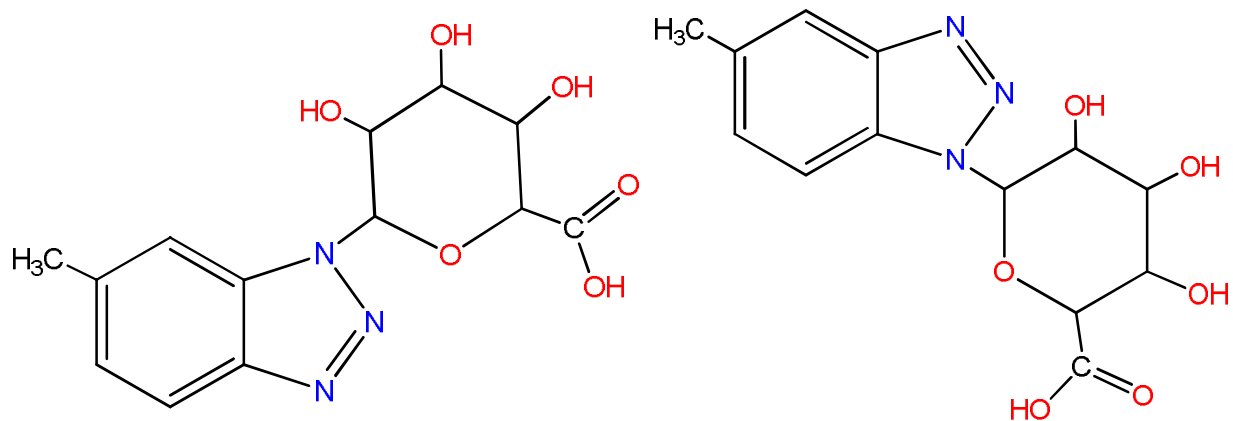
Examples (bio-TPs identification)

5-Me-BTR-N-glucuronide (2 isomers)



By **HILIC** mode

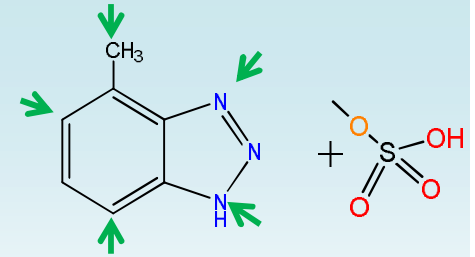
- ✓ Smaller peak width
- ✓ Greater sensitivity
- ✓ Reversed elution order



Examples (bio-TPs identification)

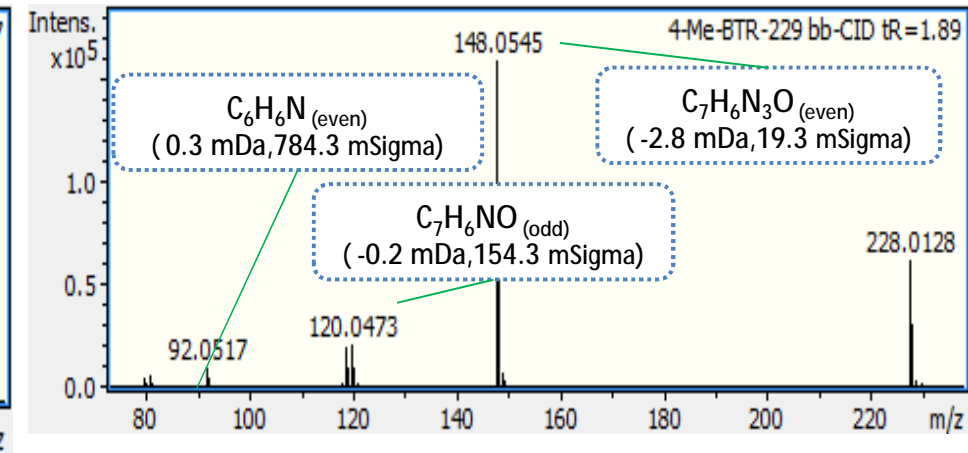
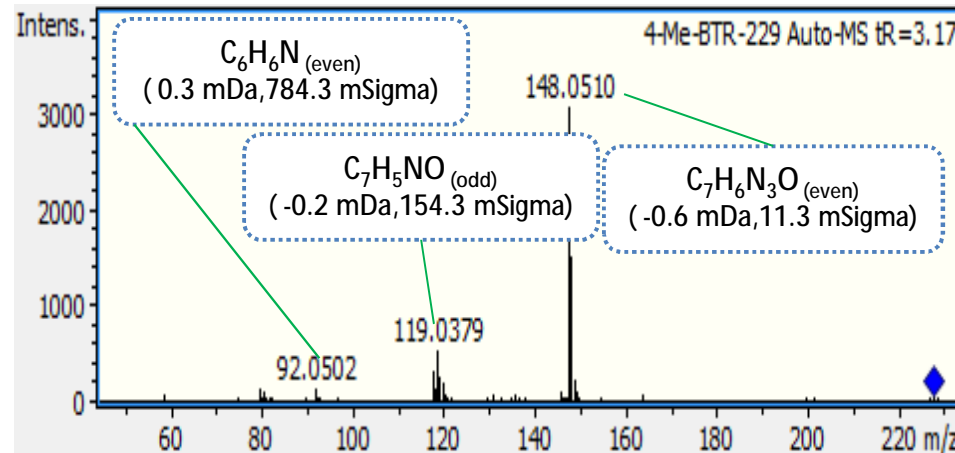
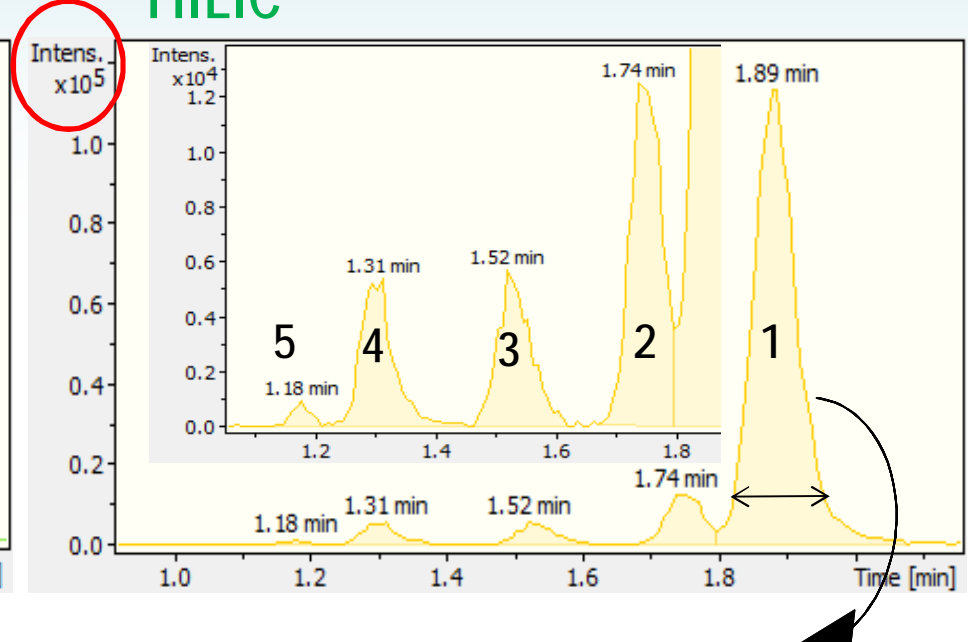
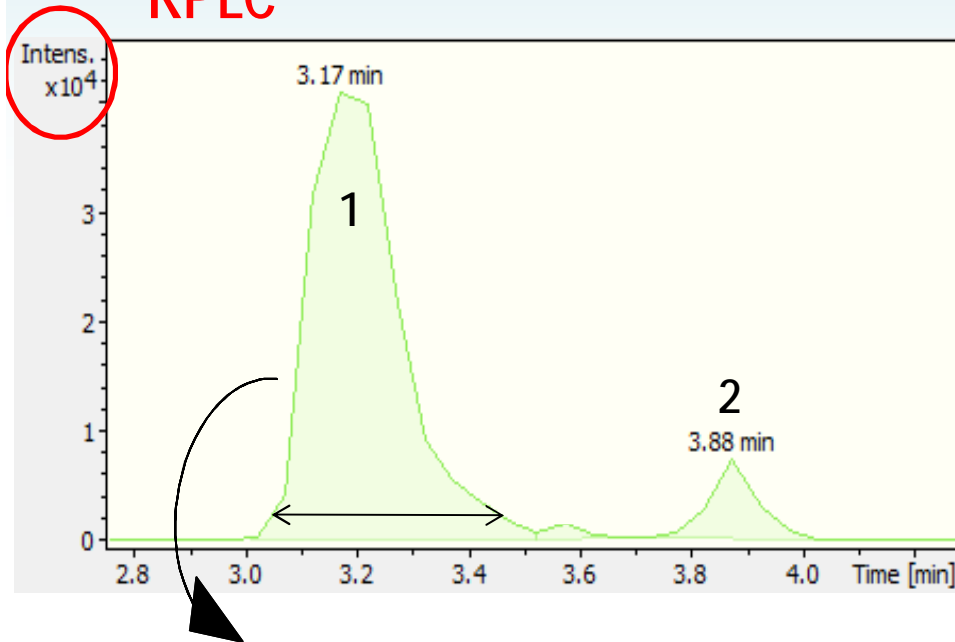
4-Me-BTR-O-sulfate (5 possible isomers)

Negative



RPLC

HILIC



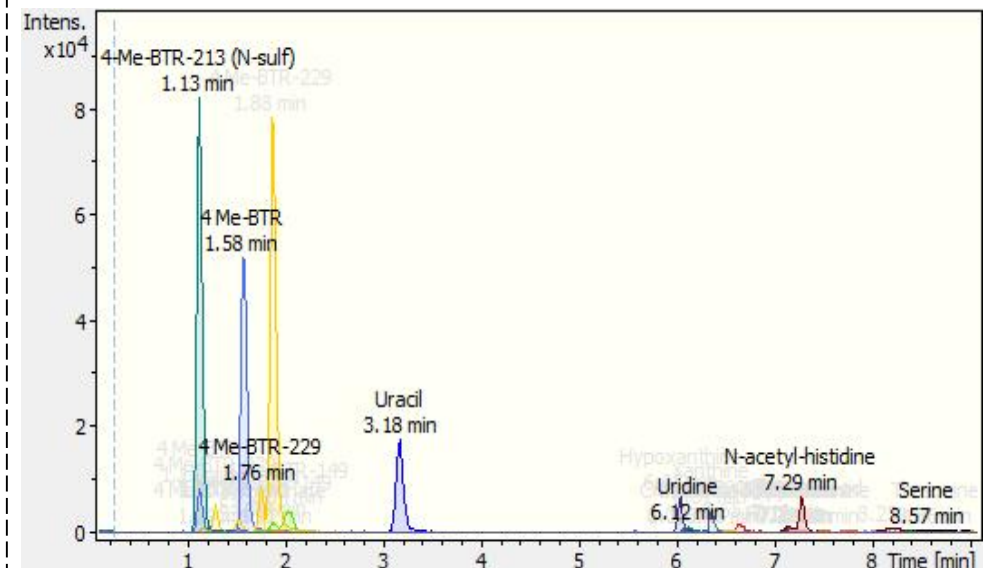
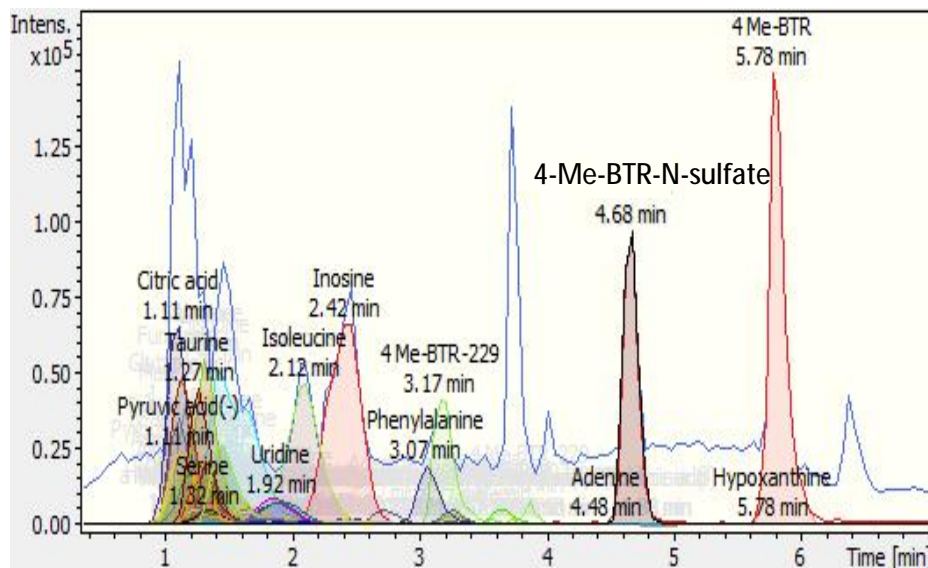
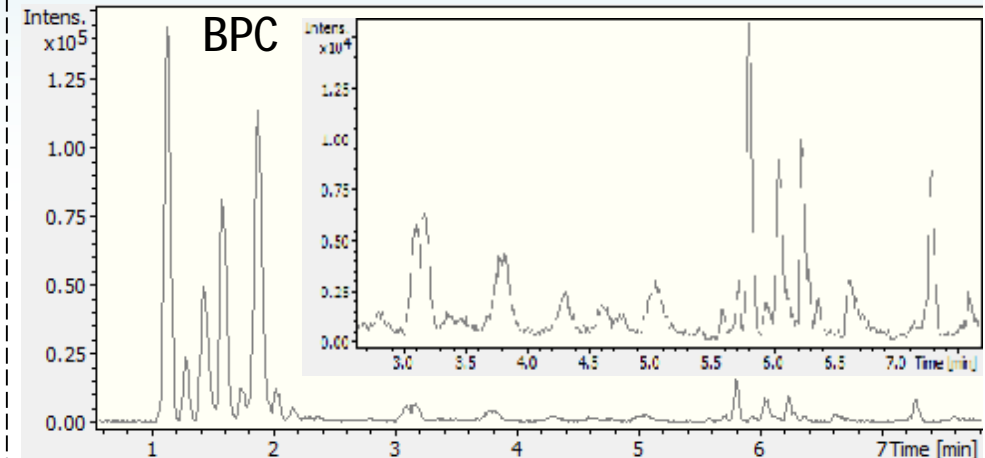
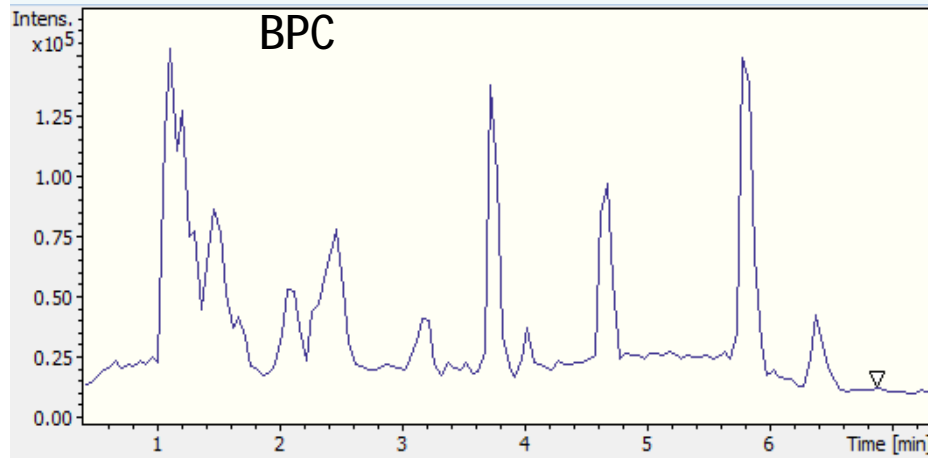
Examples (Targeted metabolic profiling)

ZFE treated with 4-Me-BTR

Negative

RPLC

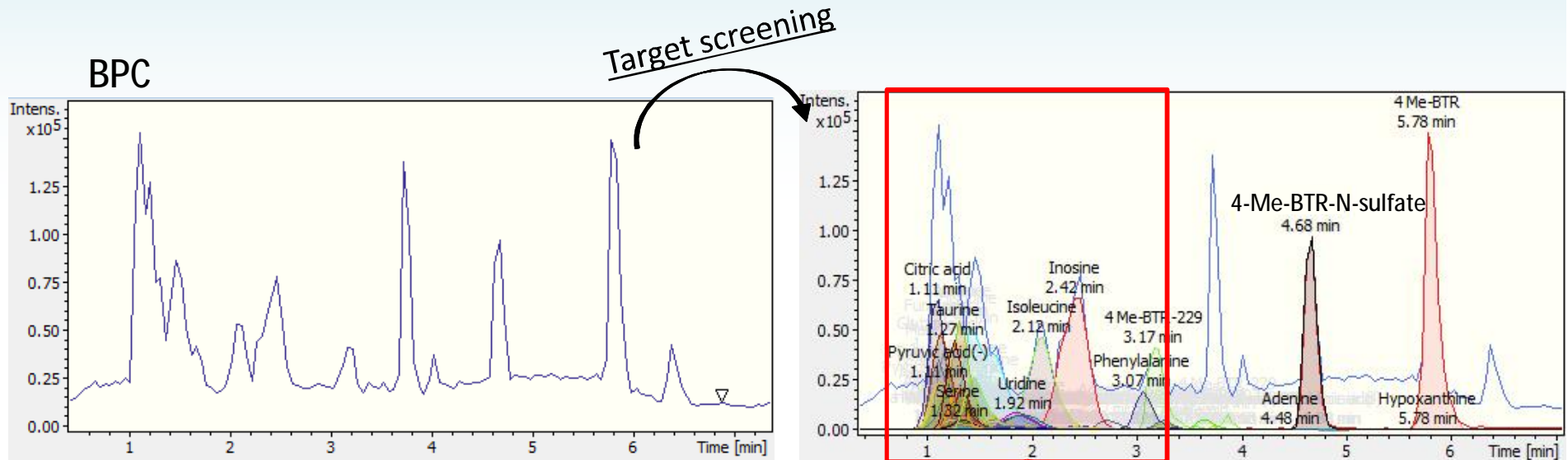
HILIC



Examples (Targeted metabolic profiling)

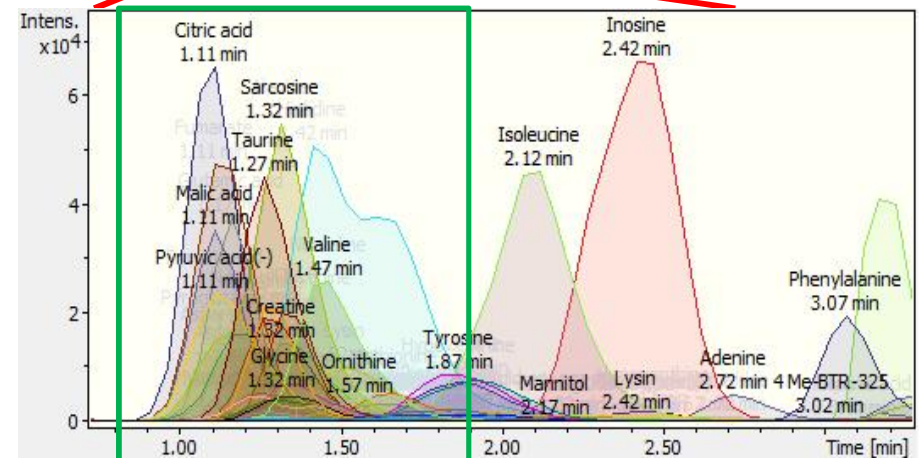
ZFE treated with 4-Me-BTR

RPLC - Negative



By RPLC mode

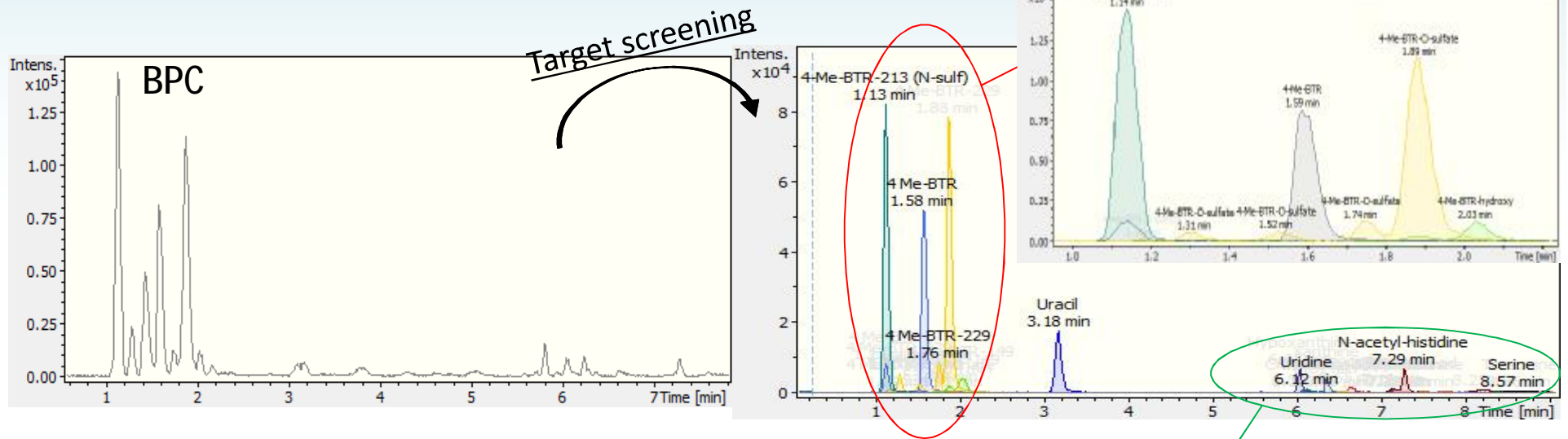
- × Majority of primary metabolites eluted in void volume
- × Co-elution
- × Wide peaks



Examples (Targeted metabolic profiling)

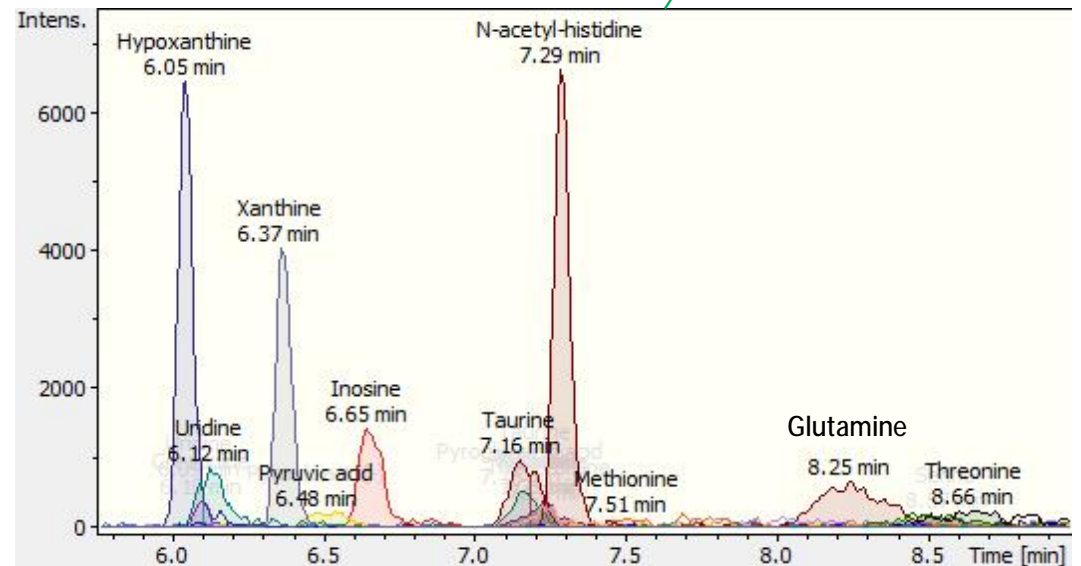
ZFE treated with 4-Me-BTR

HILIC- Negative



By HILIC mode

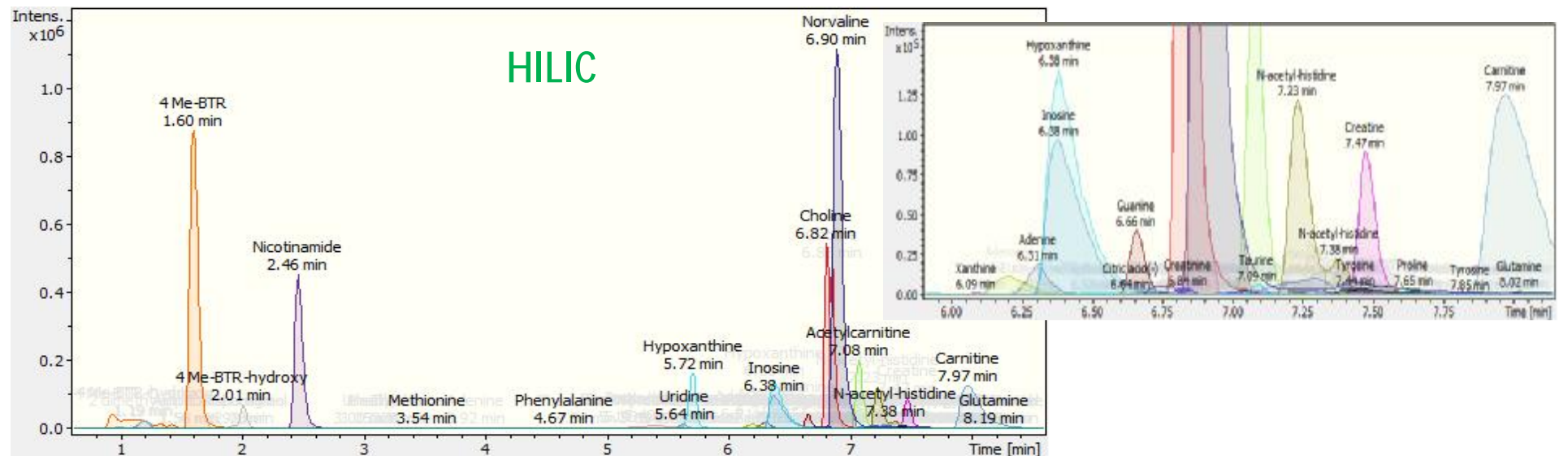
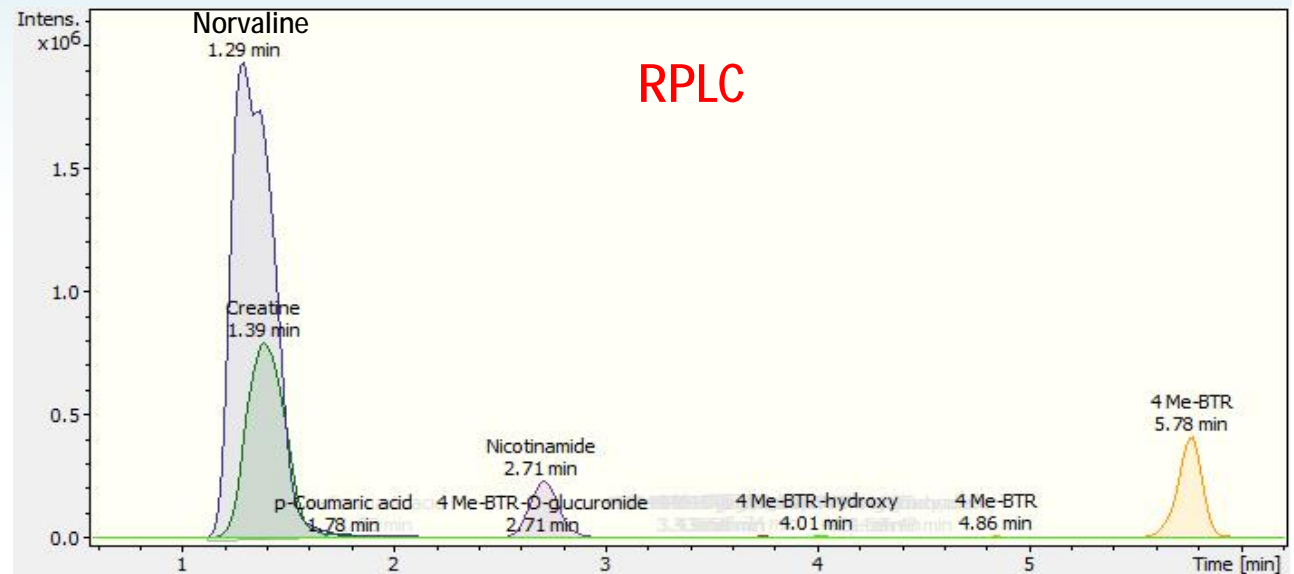
- ✓ Separation of primary metabolites
- ✓ Both xeno- and endometabolome coverage in one run



Examples (Targeted metabolic profiling)

ZFE treated with 4-Me-BTR

Positive



Conclusion

- ❑ Complementarity of **HILIC** mode to RPLC
- ✓ Improved separation efficiency and detection sensitivity
 - ✓ Orthogonality to RPLC
- ❑ Use in suspect and non-target for additional information
- ❑ Adequate retention of primary metabolites
- ❑ Identification of both endogenous and exogenous metabolites with a single separation mode

Acknowledgments



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<http://trams.chem.uoa.gr/>

<http://tremepol.chem.uoa.gr/>

<http://www2.env.aegean.gr/WaterMicropol/>



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