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Roundtable
Sample collection and preparation: impact on the
quality of the data
Veronica Ghini (CERM - UNIFI)

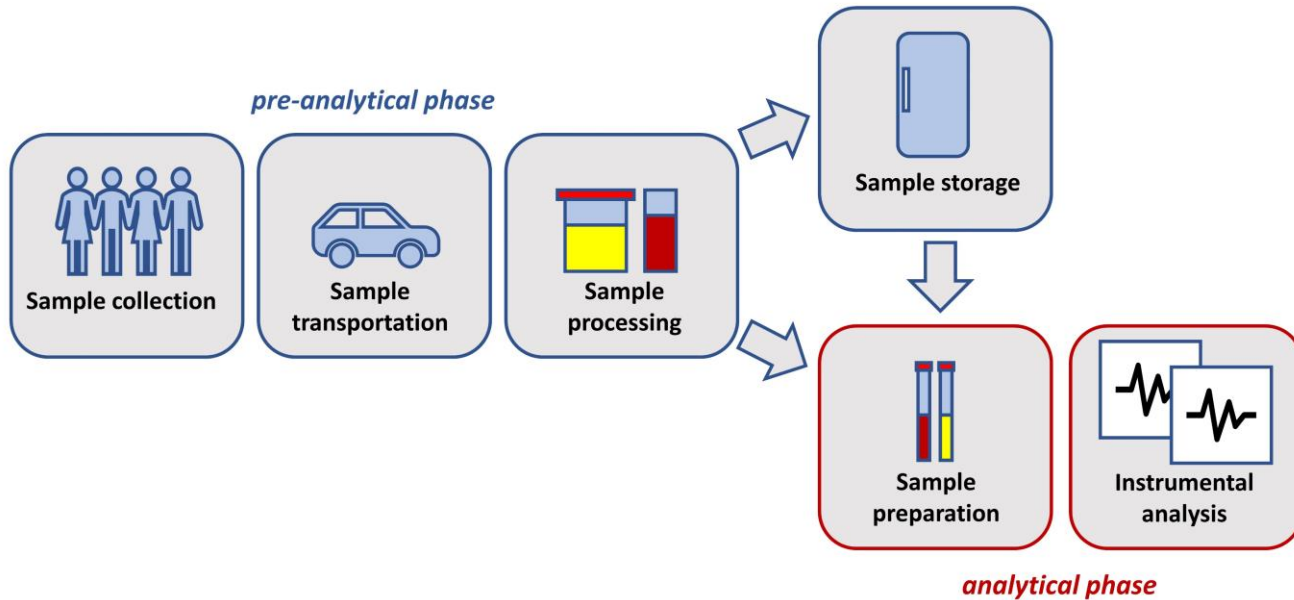


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Why SOPs are so important?

The preservation of the chemical composition (in terms of both nature and concentration of metabolites) of the “original” metabolome of a sample during the entire workflow that ends with metabolomic analysis represents a key factor in ensuring **highly accurate** and **reproducible** results.

Preservation of the original metabolome



Both phases comprise several steps that may influence the composition of the sample metabolome.

Degradation occurs along all steps (that inevitably occur prior to the actual laboratory analysis, starting from sample collection, to sample stabilization, transport, and storage

- Contaminations
- Enzymatic reactions
- Redox reactions
- ...

Validated and detailed procedures are required to reduce chemical changes in the metabolome as far as possible.

Evidenced-based SOPs



Within the EU SPIDIA and SPIDIA4P projects, NMR approaches to evaluate the impact of different pre-analytical treatments on the quality of urine and blood serum and plasma samples for metabolomics were developed.

SPIDIA

Problem: Wrong diagnosis due to instable patient samples

Solution: New technologies & standards secure high quality samples for reliable diagnosis



J Biomol NMR (2011) 49:231–243
DOI 10.1007/s10858-011-9489-1

ARTICLE

Standard operating procedures for pre-analytical handling of blood and urine for metabolomic studies and biobanks

Patrizia Bernini · Ivano Bertini · Claudio Luchinat · Paola Nincheri · Samuele Staderini · Paola Turano

Metabolomics (2015) 11:872–894
DOI 10.1007/s11306-014-0746-7



REVIEW ARTICLE

Standardizing the experimental conditions for using urine in NMR-based metabolomic studies with a particular focus on diagnostic studies: a review

Abdul-Hamid Emwas · Claudio Luchinat · Paola Turano · Leonardo Tenori · Raja Roy · Reza M. Salek · Danielle Ryan · Jasmeen S. Merzaban · Rima Kaddurah-Daouk · Ana Carolina Zeri · G. A. Nagana Gowda · Daniel Raftery · Yulan Wang · Lorraine Brennan · David S. Wishart

New BIOTECHNOLOGY 52 (2019) 25–34



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Full length Article

NMR for sample quality assessment in metabolomics

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Evidenced-based SOPs



A screenshot of the iTeh Standards website showing the technical specification CEN/TS 16945:2016. The page title is 'Molecular in vitro diagnostic examinations - Specifications for pre-examination processes for metabolomics in urine, venous blood serum and plasma'. The page includes a navigation bar with 'ABSTRACT', 'GERMAN', 'FRENCH', and 'SLOVENIAN' options. The abstract text reads: 'This Technical Specification covers the preanalytical phase and recommends the handling, documentation and processing of urine, venous blood plasma and serum intended for metabolomics analysis. This Technical Specification is applicable to metabolomics examinations and is of importance to biomedical laboratories, customers of laboratories, in vitro diagnostics developers and manufacturers, institutions and companies performing biomedical research, biobanks, and regulatory authorities. The adoption of the described procedures for the preanalytical phase make it possible to compare and evaluate the results obtained from metabolic profiling analysis.' To the right, there is a 'BUY STANDARD' section for the 'TECHNICAL SPECIFICATION' titled '-TS CEN/TS 16945:2016 - BARVE na PDF-str 17,18' in 'English language', which is '18 pages' long. A 'sale 10% off' badge is visible. The website footer includes 'Standards', 'About us', 'News', 'Taking part', 'Store', a search icon, a shopping cart icon, and 'EN' with a dropdown arrow. The ISO logo is also present in the bottom left corner of the screenshot.

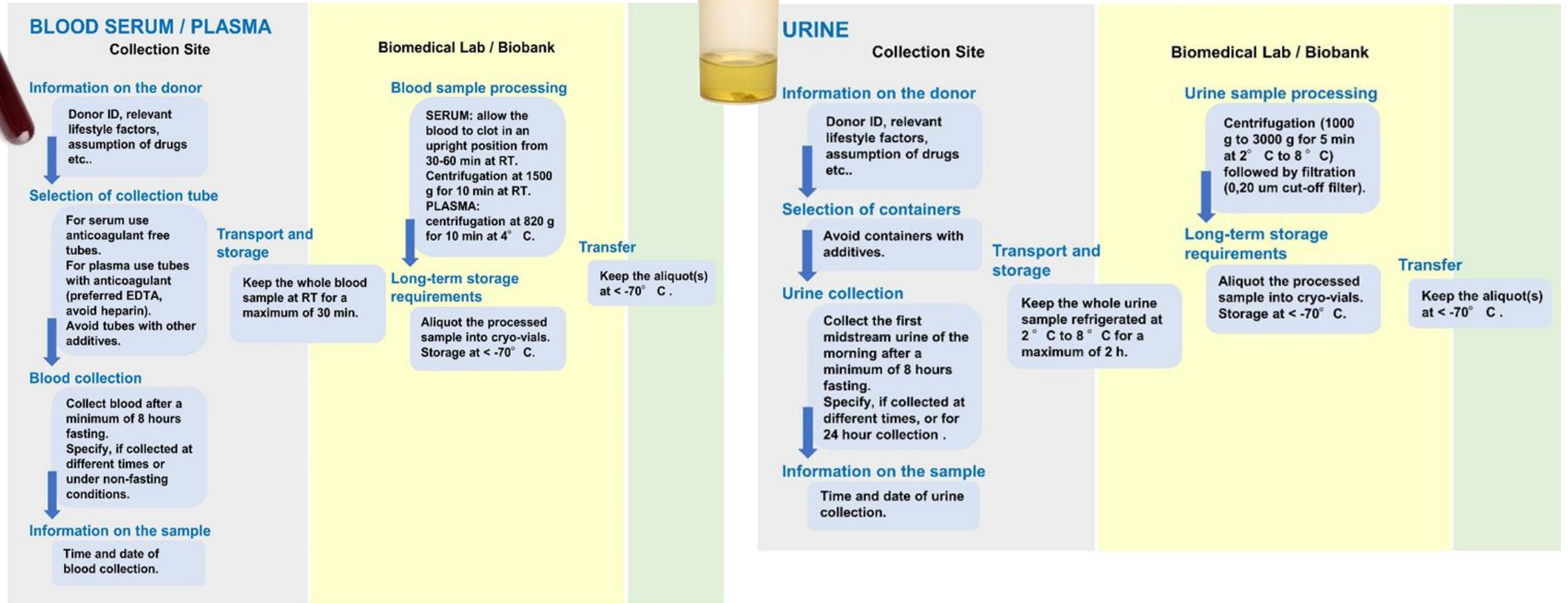


ICS > 11 > 11.100 > 11.100.10

ISO 23118:2021

Molecular in vitro diagnostic examinations —
Specifications for pre-examination processes in
metabolomics in urine, venous blood serum and plasma

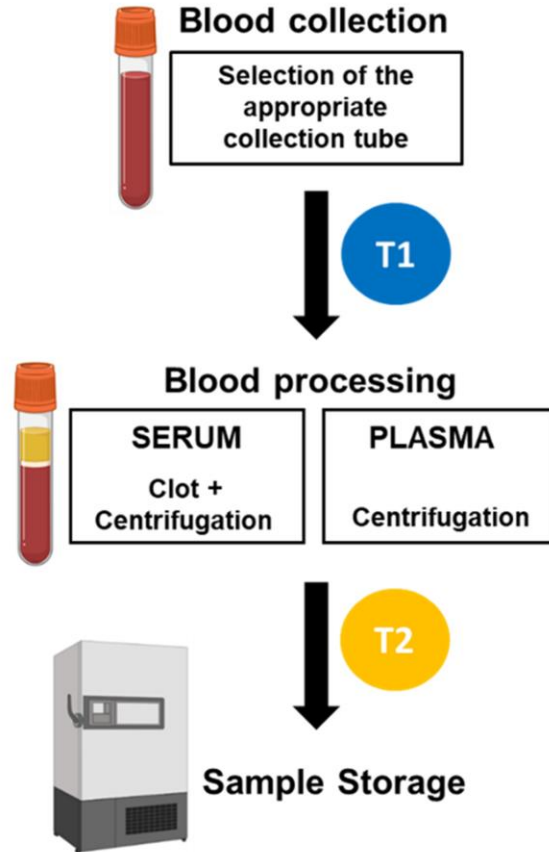
Evidenced-based SOPs



Transport and storage

Transport and storage

Blood- Critical steps along the preanalytical phase



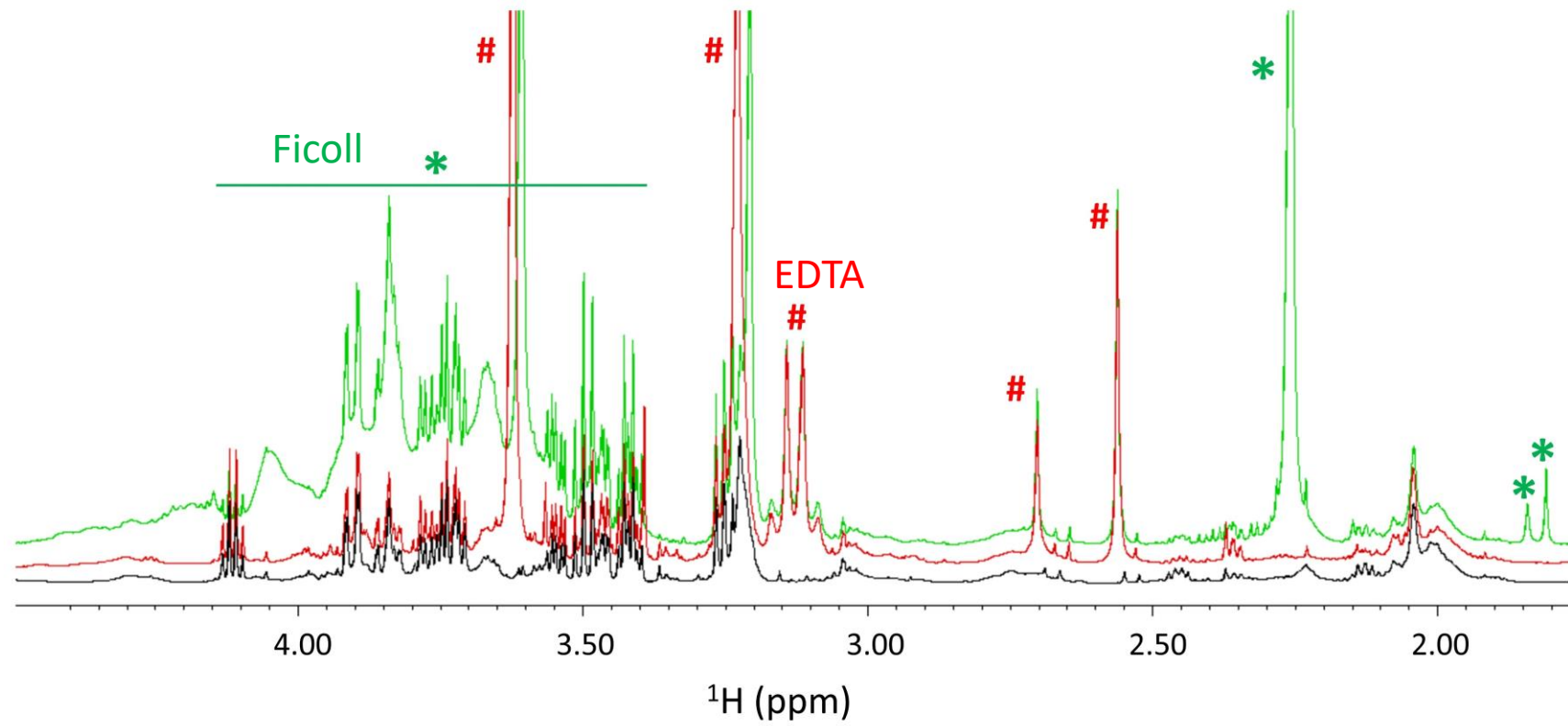
Factors influencing the stability of blood serum/plasma profiles over time:

Presence of cells

Oxidation reactions

Selection of the appropriate collection tube

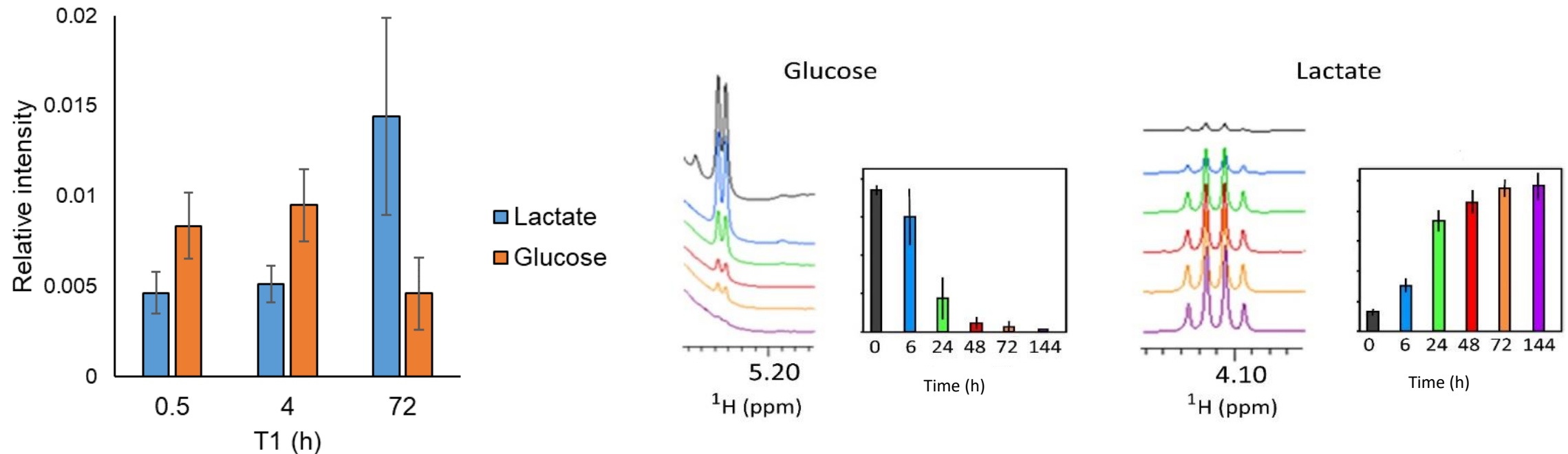
Avoid additives that could make difficult metabolite observation



Presence of cells. Critical step-T1

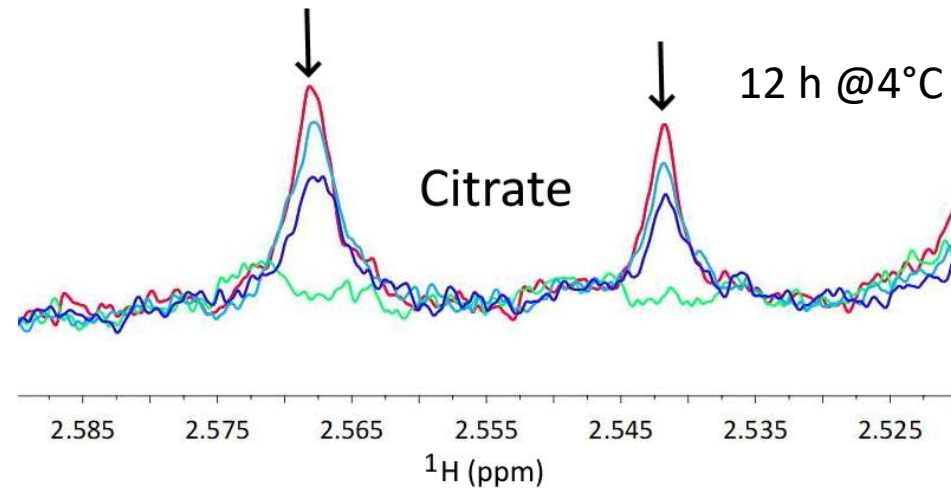
Cellular activity- main source of changes.

The processing should be initiated within 30 min after the blood collection in order to minimize these alterations.



Oxidation reactions. Critical step-T2

After blood processing, the sources of variation are attributable to **oxidation reactions** occurring under aerobic conditions that cause concentration changes of metabolites such as proline, citrate and lipoproteins

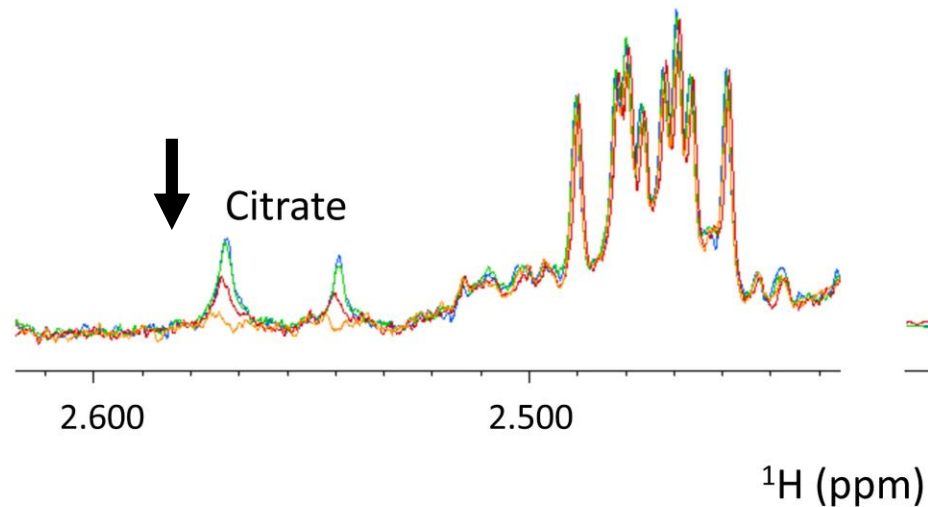


Serum sample maintained at 4°C for **0, 4, 8** and **12 h** after processing.

Freezing at -80°C immediately after serum obtainment is sufficient to quench this effect.

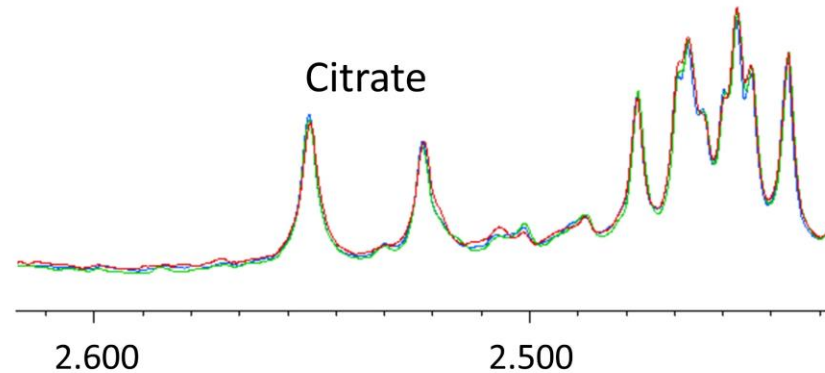
Long term storage at -80° C

A Citrate levels over time (12 h) at 4° C



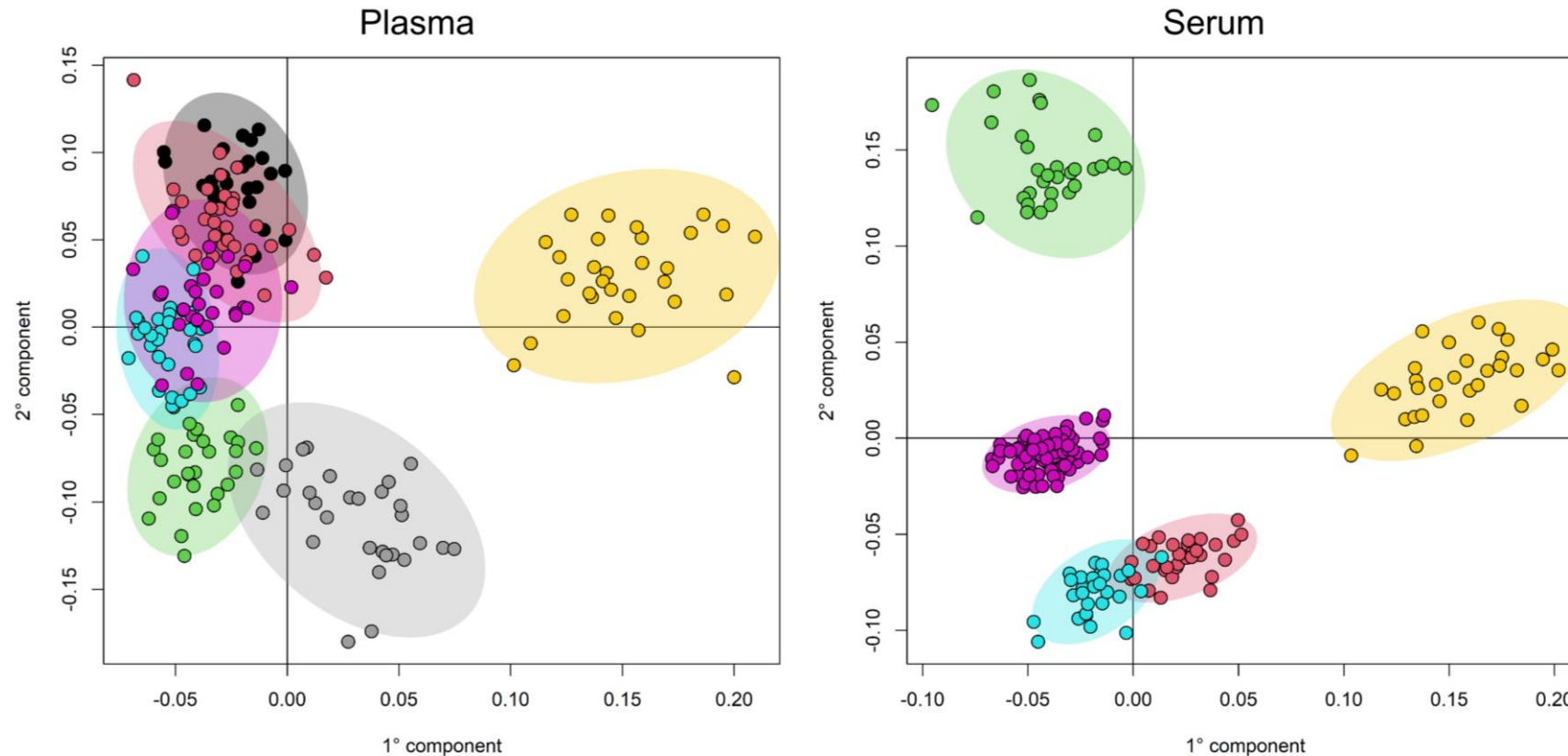
T0; 4h; 8h; 12 h

B Long-term storage at -80° C



The metabolic phenotype of urine samples was followed over 5-year storage. T0; 4 year-storage; 5 year-storage

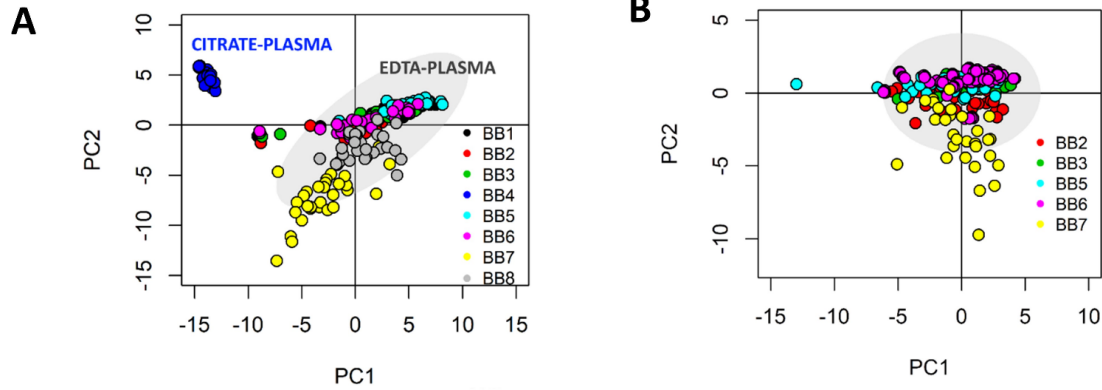
The problem of multicenter studies: plasma and serum from different biobanks



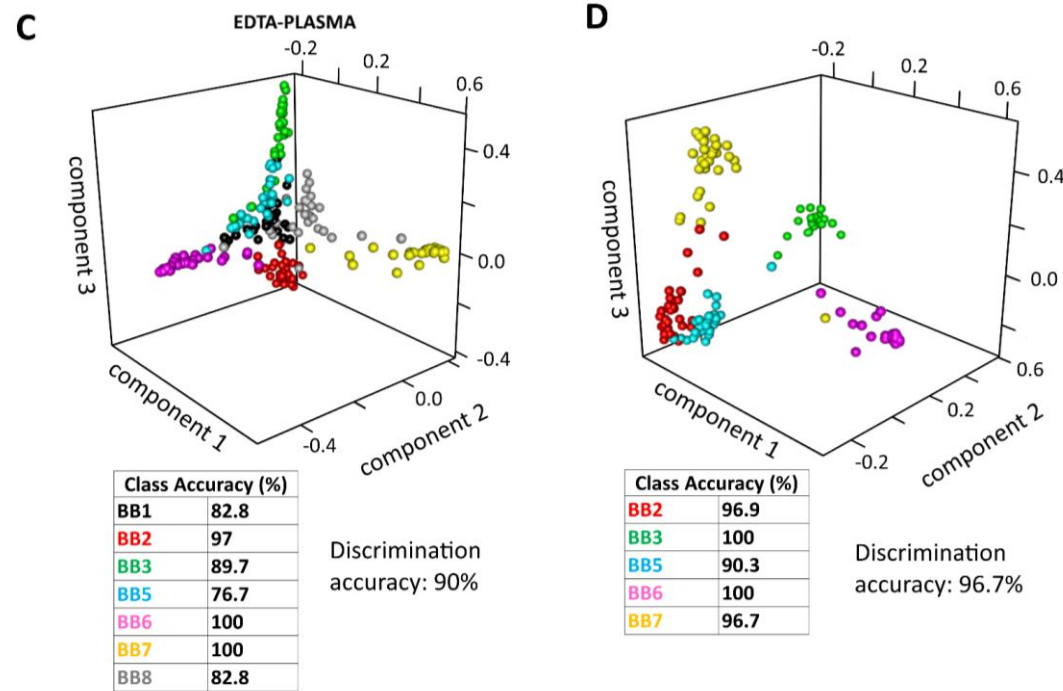
Ghini V., Abuja P.M., Polasek O., Kozera L., Laiho P., Anton G., et al. Impact of the pre-examination phase on multicenter metabolomic studies. 2022, *N Biotechnol*, 68, 37-47.

Ghini V., Abuja P.M., Polasek O., Kozera L., Laiho P., Anton G., et al. Metabolomic fingerprints in large population cohorts: Impact of pre-analytical heterogeneity. 2021, *Clin Chem*, 67(8), 1153–1155.

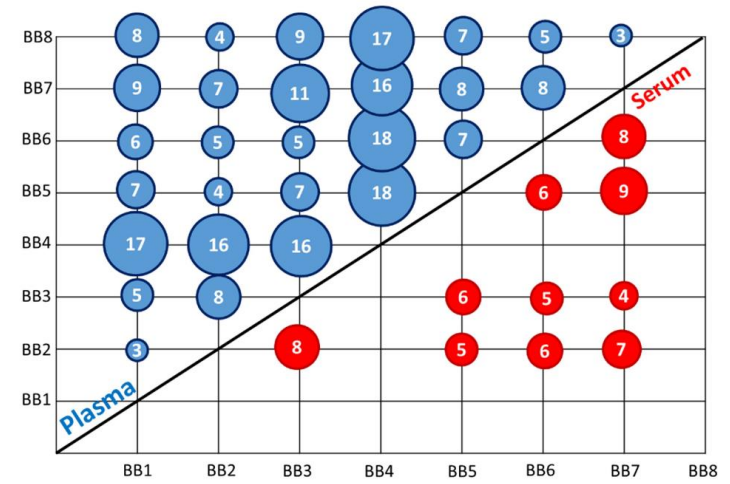
Multivariate analysis-PCA



Multivariate analysis-RF

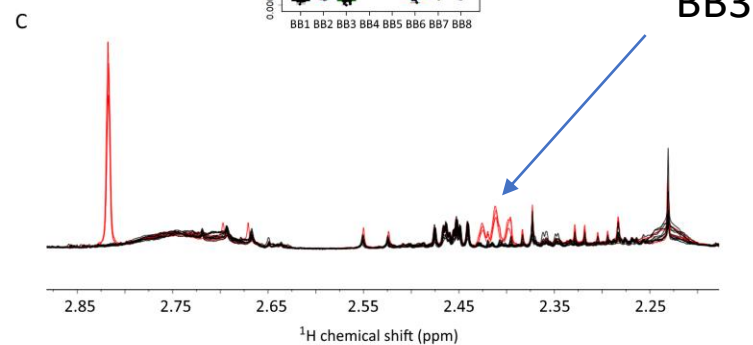
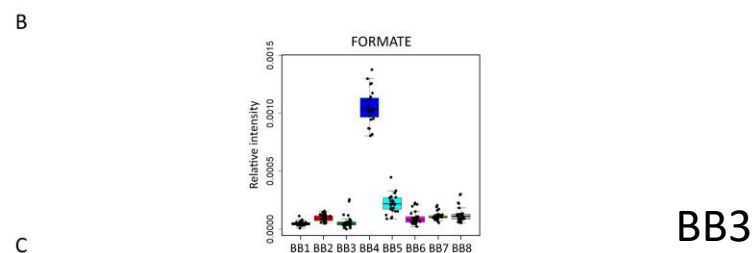
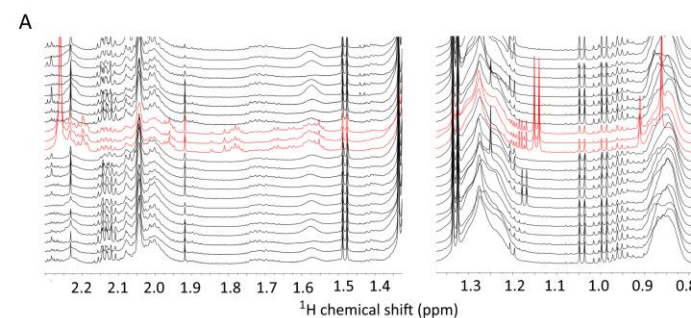
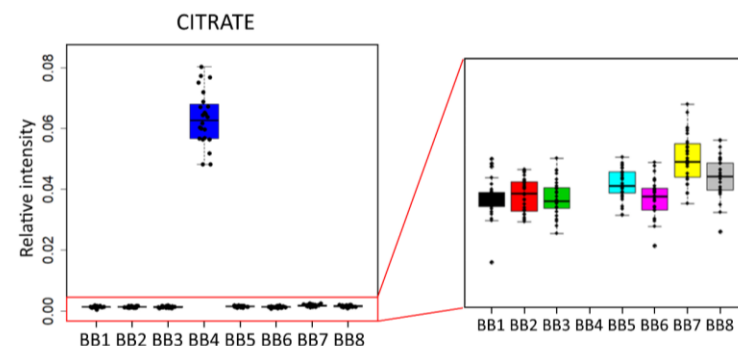


Univariate analysis



Collection tubes in the SOPs of different biobanks

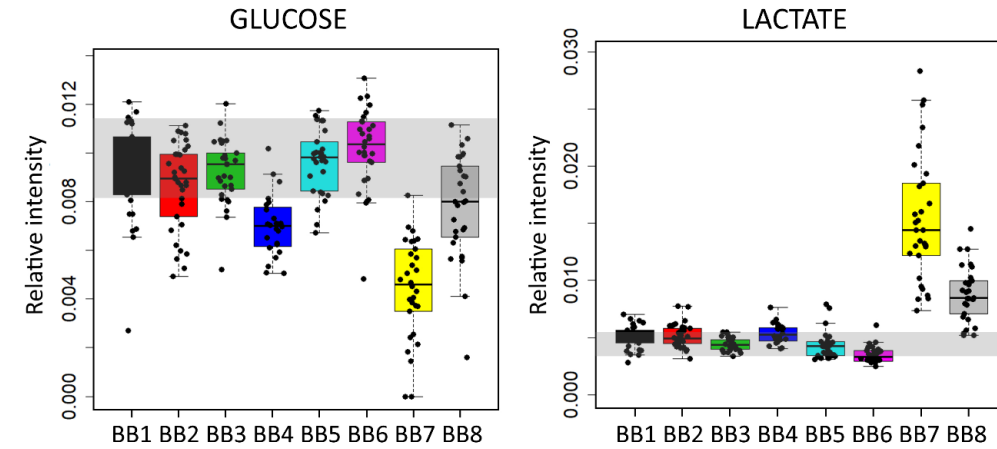
Biobank	Serum	Plasma
CEN/TS 16945:2016 / ISO 23118:2021	Anticoagulant free tubes with no other additives	Anticoagulant tubes with no other additives
BB1	-	EDTA-tubes (brand not specified)
BB2	Tubes with clot activator (brand not specified)	EDTA-tubes (brand not specified)
BB3	Tubes with separation gel and clotting activator (VACUETTE)	EDTA-tubes (VACUETTE)
BB4	-	Cell preparation tube with sodium citrate (BD)
BB5	Tubes with separation gel and clotting activator (SARSTED)	EDTA-tubes (SARSTED)
BB6	Tubes with separation gel and clotting activator (BD)	EDTA-K3 tubes (BD)
BB7	Tubes with separation gel and clotting activator (BD)	EDTA tubes (BD)
BB8	-	K2 EDTA tubes (brand not specified)



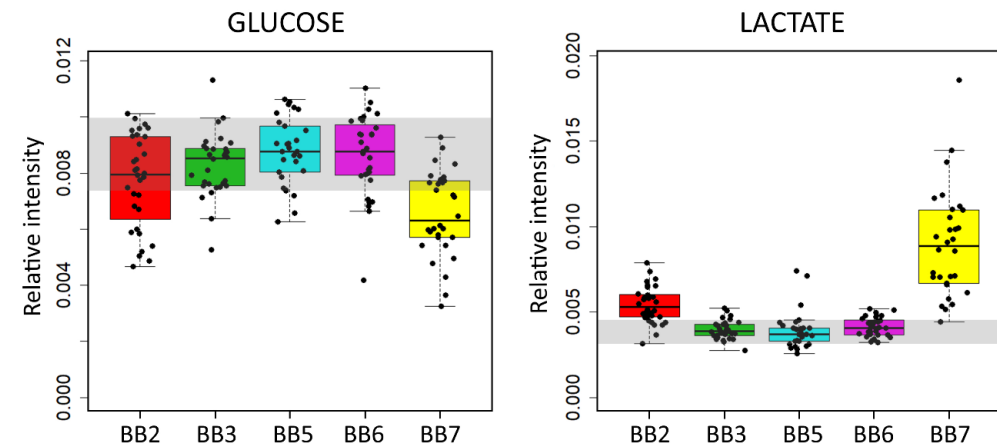
T1 in the SOPs of different biobanks

Biobank	T1
CEN/TS 16945:2016 / ISO 23118:2021	Max. of 30 min at RT
BB1	Max. of 30 min (T not specified)
BB2	Max. of 4 h (T not specified)
BB3	Max. of 60 min at RT
BB4	Max. of 120 min at RT
BB5	Max. of 30 min at RT
BB6	Max. of 2 h (T not specified)
BB7	Max. of 72 h at 4°C
BB8	Max. of 72 h at 4°C

Plasma



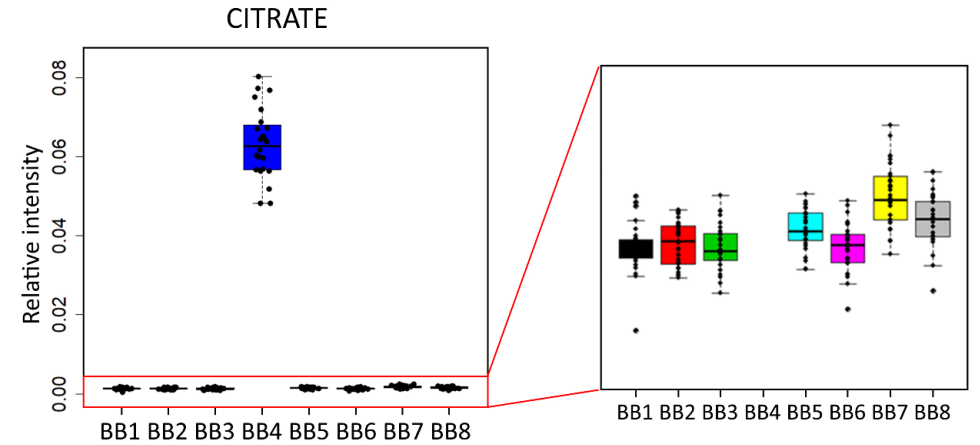
Serum



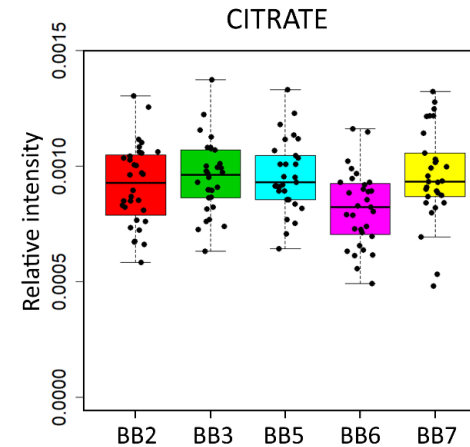
T2 in the SOPs of different biobanks

Biobank	T2
CEN/TS 16945:2016 / ISO 23118:2021	Immediate freezing
BB1	Not specified
BB2	Not specified
BB3	Not specified
BB4	Not specified
BB5	Put the tubes in ice water
BB6	dry ice at -80° C
BB7	Not specified
BB8	storage at +4 – 8° C then transfer to the storage straws within 2h

Plasma

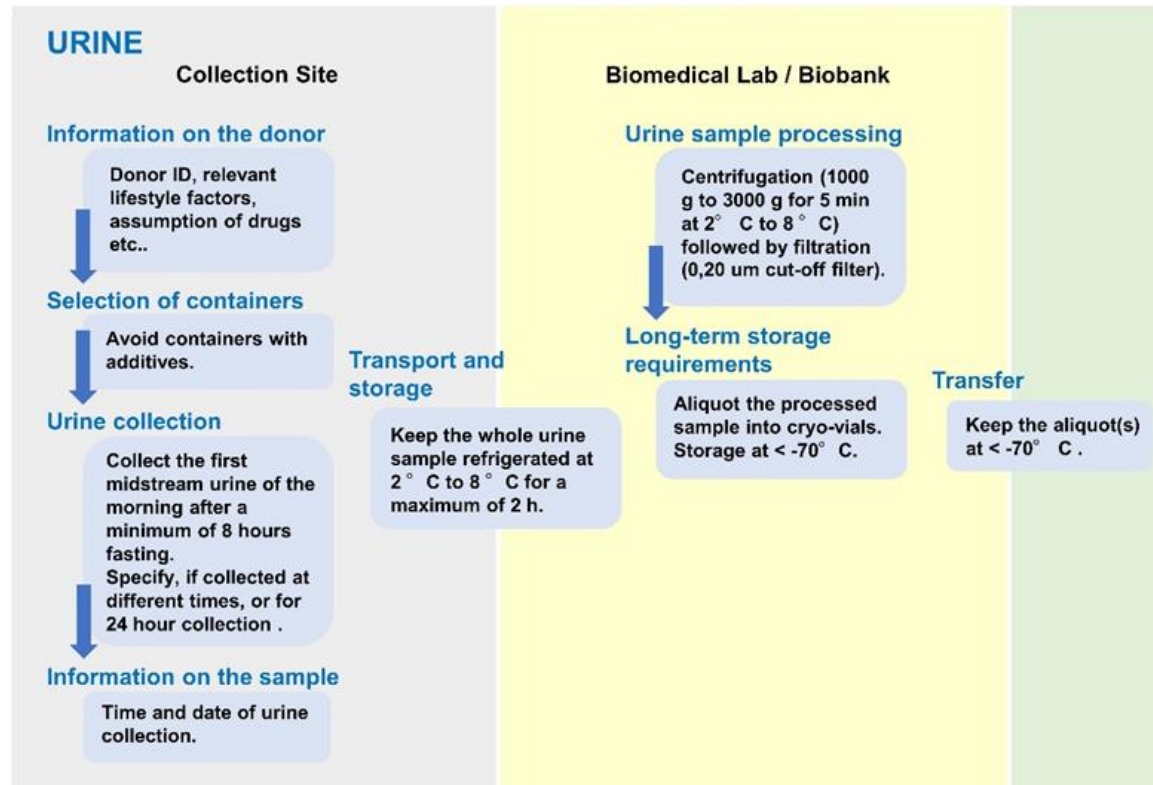


Serum





URINE SAMPLES



Factors influencing the stability of urine profiles over time:

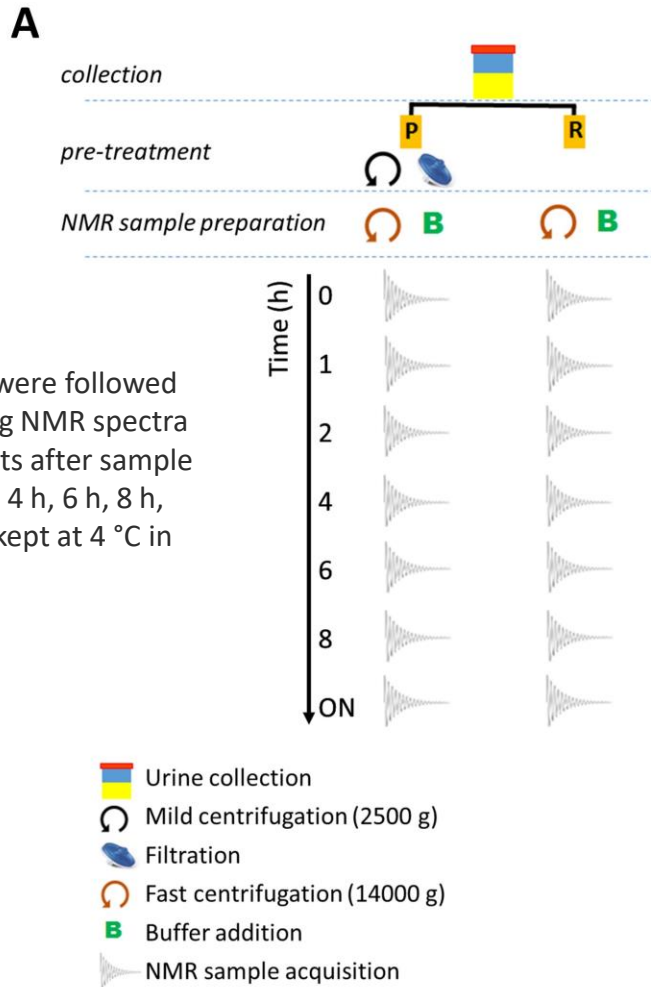
Presence of cells:

→ shift of signals over time

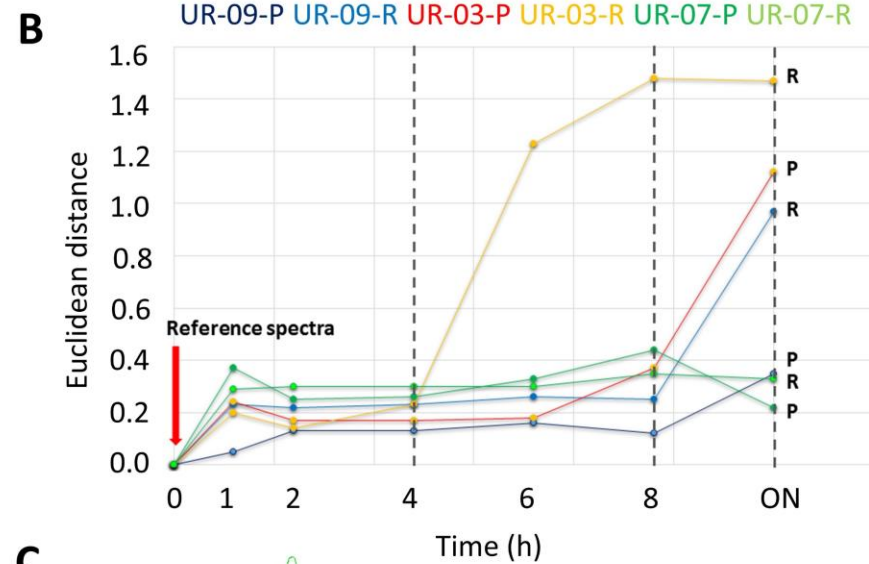
Chemical and enzymatic reactions

→ concentration changes over time

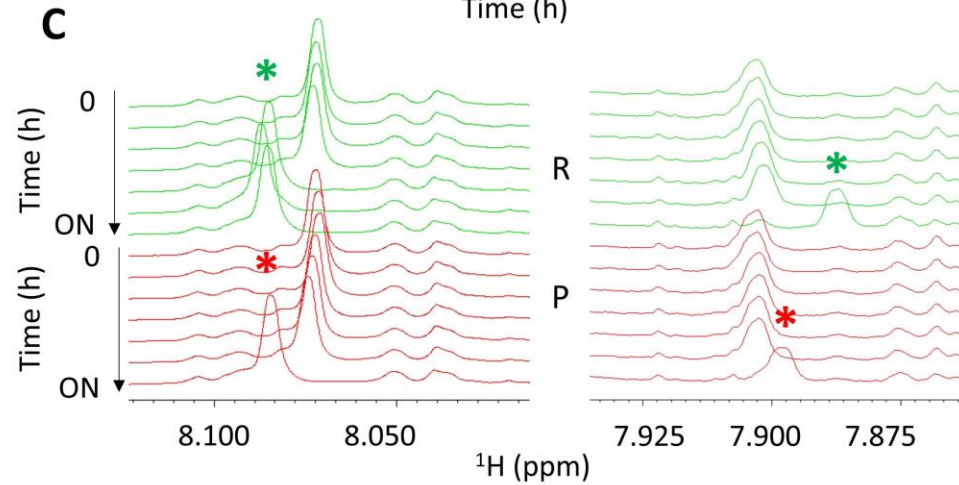
The presence of cells



The profiles of urine were followed over time by acquiring NMR spectra at different time points after sample collection (0, 1 h, 2 h, 4 h, 6 h, 8 h, 24 h). Samples were kept at 4 °C in between spectra.



UR-03: very high cellular contents
UR-09: modest
UR-07: low

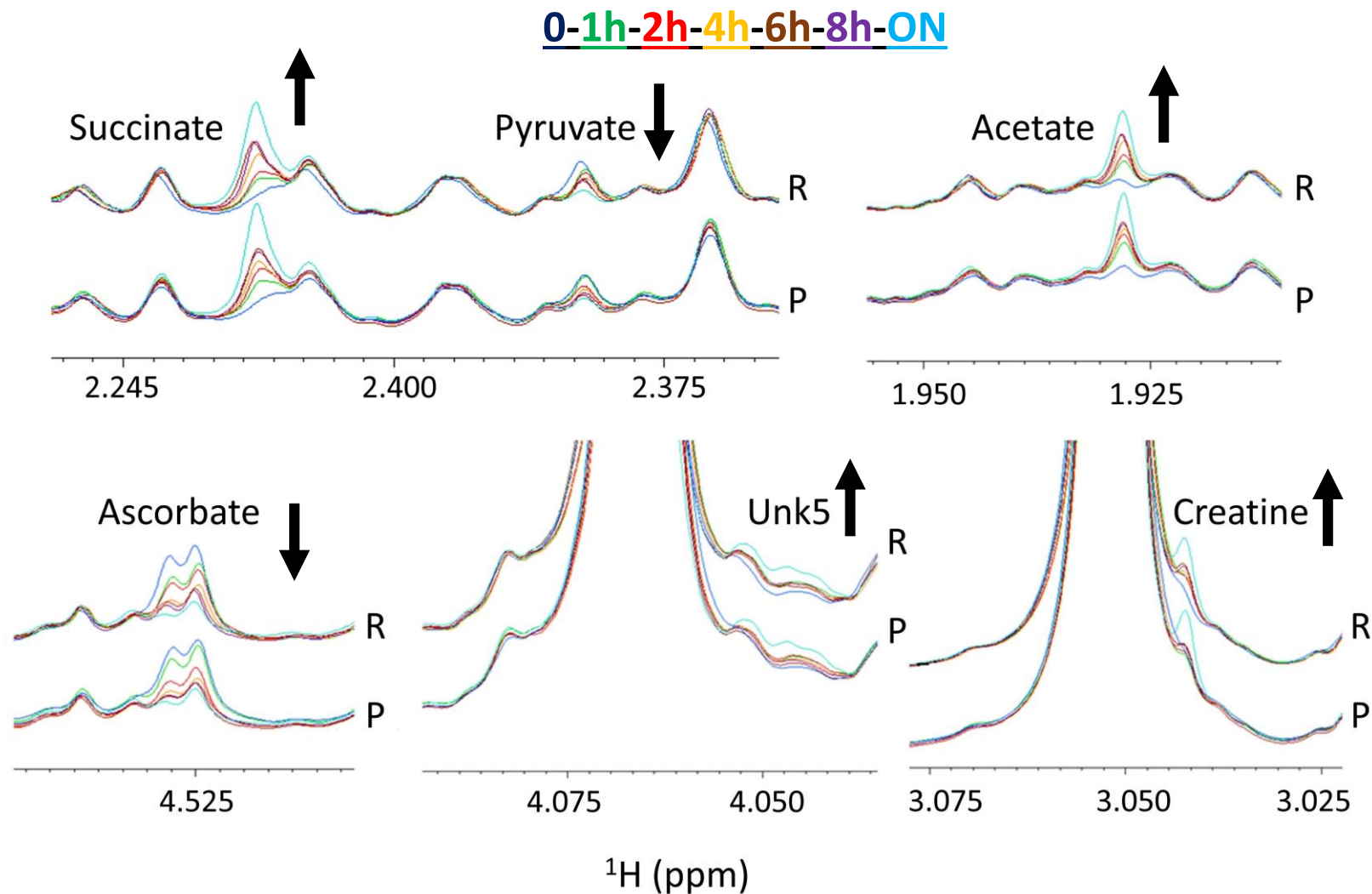


Mild centrifugation and/or filtration are strongly suggested to remove cells from urine

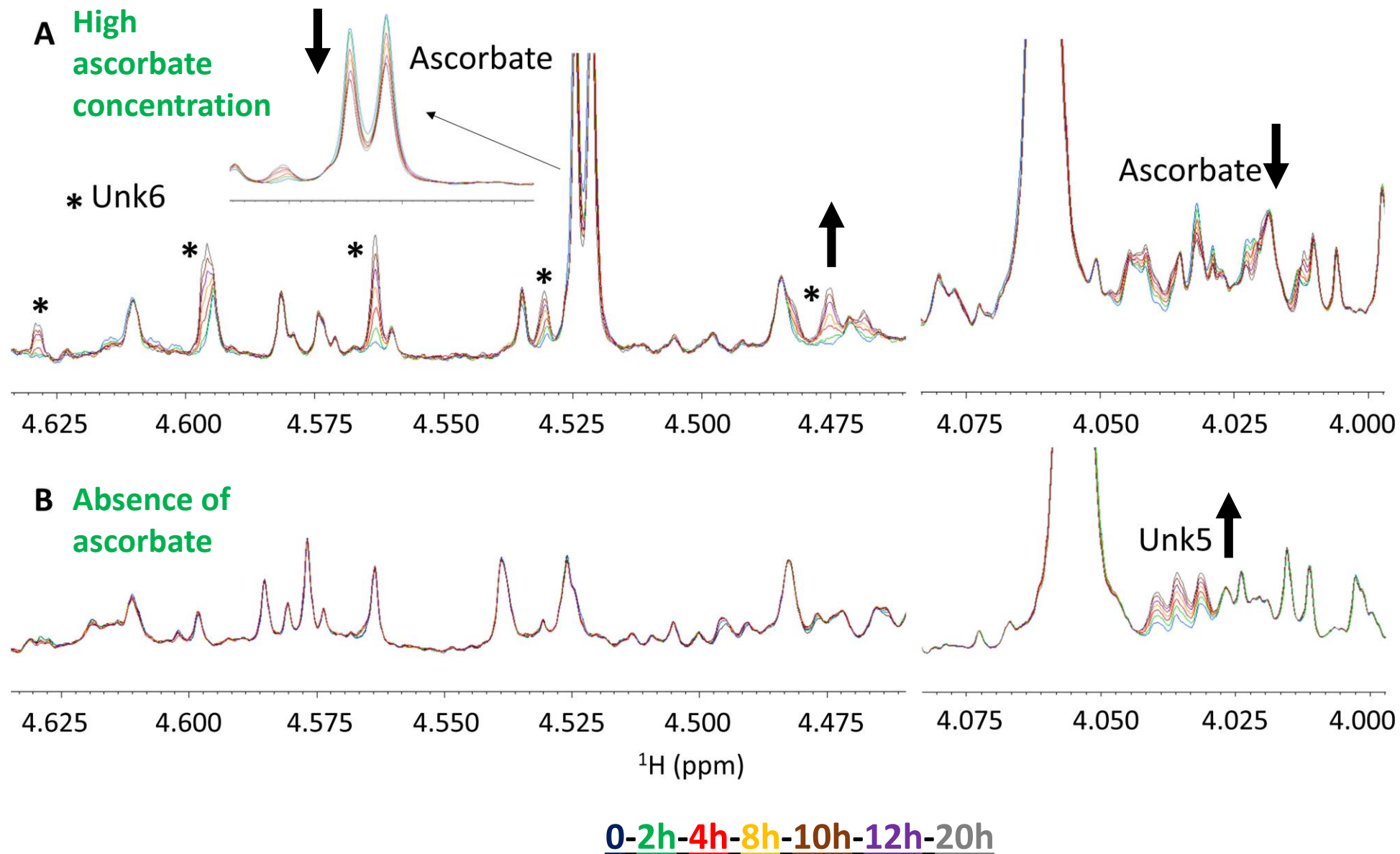
Chemical and enzymatic reactions

The metabolic profiles of 6 urine samples were followed for 24 h, acquiring an NMR spectrum every 2h; samples were kept at 4° C in between spectra

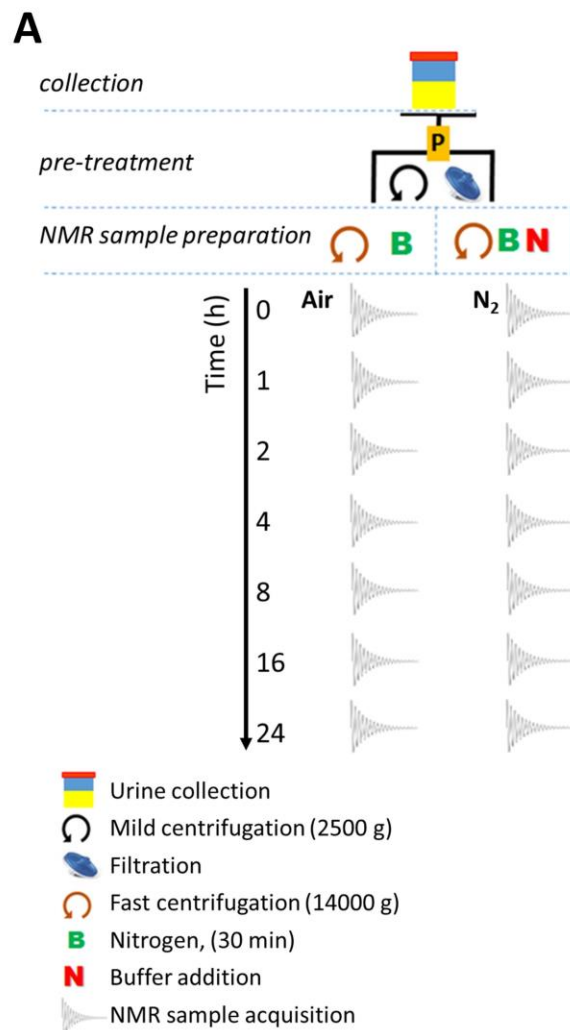
Metabolite	HMDB	Occurrence (%) presence/absence in the spectra	Chemical shift (ppm)	Changes
Acetate	HMDB0000042	100	1.92 (s)	↑
Unk2	-	70	2.17 (s)	↑
Unk3	-	70	2.18 (s)	↓
Pyruvate	HMDB0000243	100	2.38 (s)	↓
Succinate	HMDB0000254	100	2.40 (s)	↑
2-Oxoglutarate	-	100	2.44 (t) 3.00 (t)	↓
Creatine	HMDB0000064	100	3.04 (s) 3.93 (s)	↑
Creatinine	HMDB0000562	100	3.05 (s) 4.06 (s)	↓
Unk4	-	-*	3.35 (m)	↑
Ascorbate	HMDB0000044	14	3.74 (m) 4.01 (m) 4.51 (d)	↓
Unk5	-	-*	4.05 (t)	↑
Unk6 <i>ascorbic acid oxidation by- products</i>	-	-*	4.48 (t) 4.53 (s) 4.56 (s) 4.59 (s) 4.63 (s)	↑
Unk7	-	100	5.61 (d)	↓
Urea	HMDB0000294	100	5.80 (s)	↓



The patterns of changes correlated with the presence or absence of or absence of certain urinary metabolites. In particular, the presence/absence of ascorbate strongly influenced the changes overtime



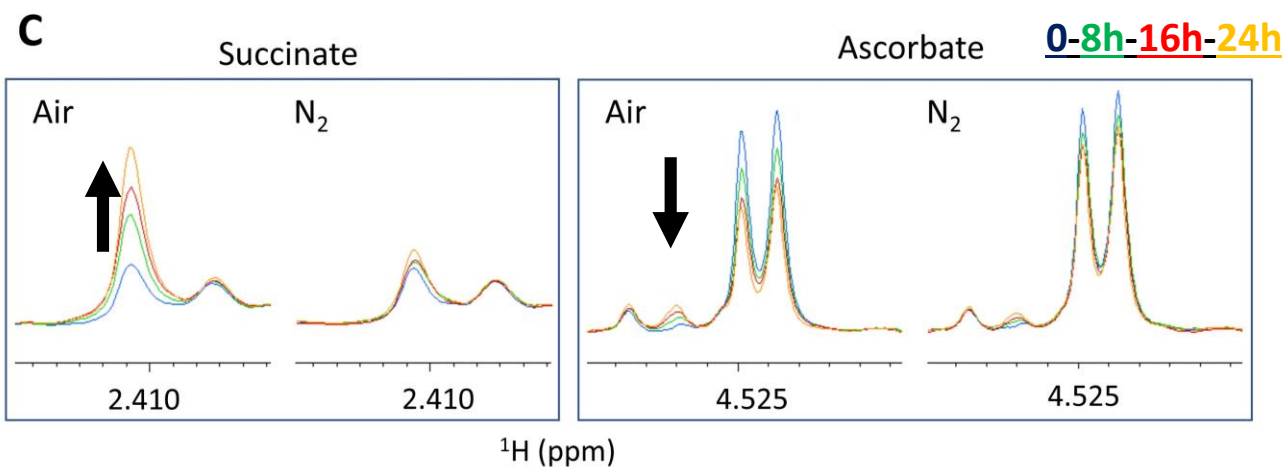
To investigate the nature of these changes, variations in the urine metabolome of 4 subjects were followed over time both under aerobic atmosphere and under an **inert atmosphere (N₂)**. During the intervals between experiments, the samples were kept at 4 °C and NMR spectra for each sample were acquired every 2 h for a total of 24 h.



B

Metabolites		Air (mean)	N ₂ (mean)
Acetate	↑	19.15%	7.9%*
Unk2	↑	7.6%	7.5%
Unk3	↓	5.9%	6.4%
Pyruvate	↓	13.6%	2.8%**
Succinate	↑	64.6%	15.9%*
2-oxoglutarate	↓	7.5%	1.5%*
Creatine	↑	20.5%	17.2%
Creatinine	↓	7.0%	7.0%
Unk4	↑	13.4%	8.3%*
Acorabate	↓	11.47%	4.3%*
Urea	↓	5.0%	0.5%*
Unk5	↑	33.3%	29.7%
Unk6	↑	49.0%	33.3%*
Unk7	↓	17.3%	16.7%

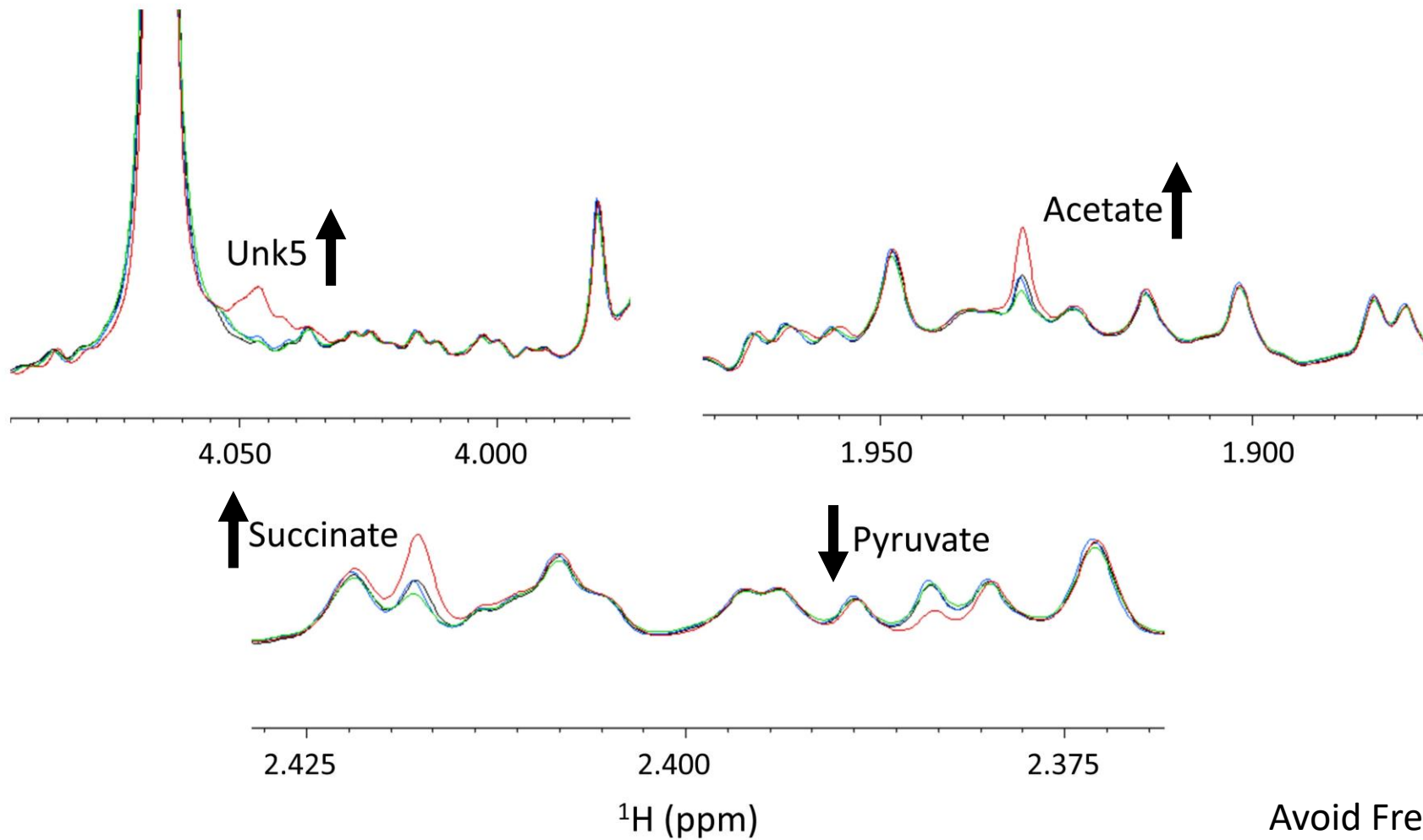
Under N₂, the urine metabolic profiles were more stable over time.



Chemical and enzymatic redox reactions are the main factors inducing changes in concentration levels of urinary metabolites. These effects cannot be avoided but can be reduced by maintaining the samples at low temperatures throughout the analytical and pre-analytical processes and reducing exposure to air.

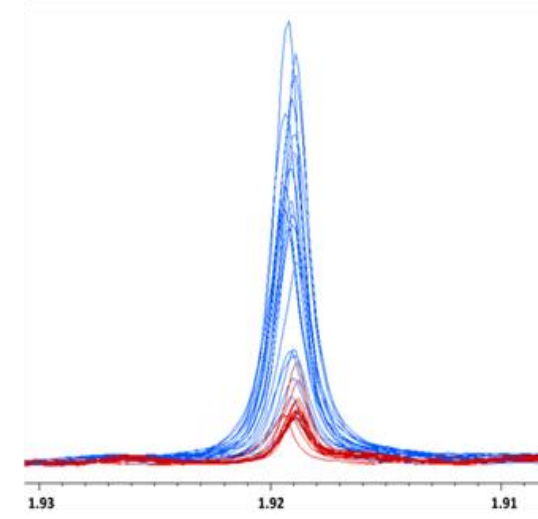
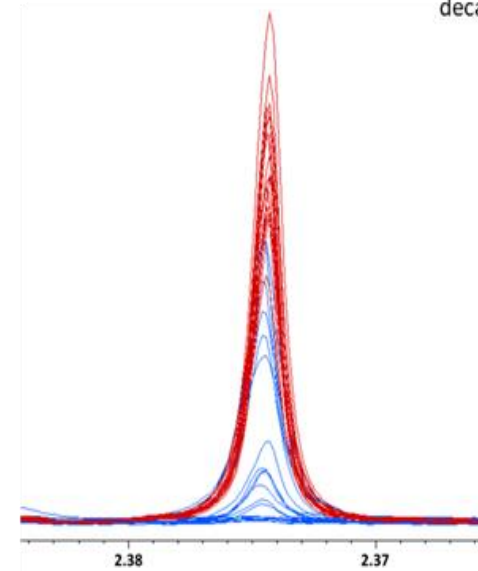
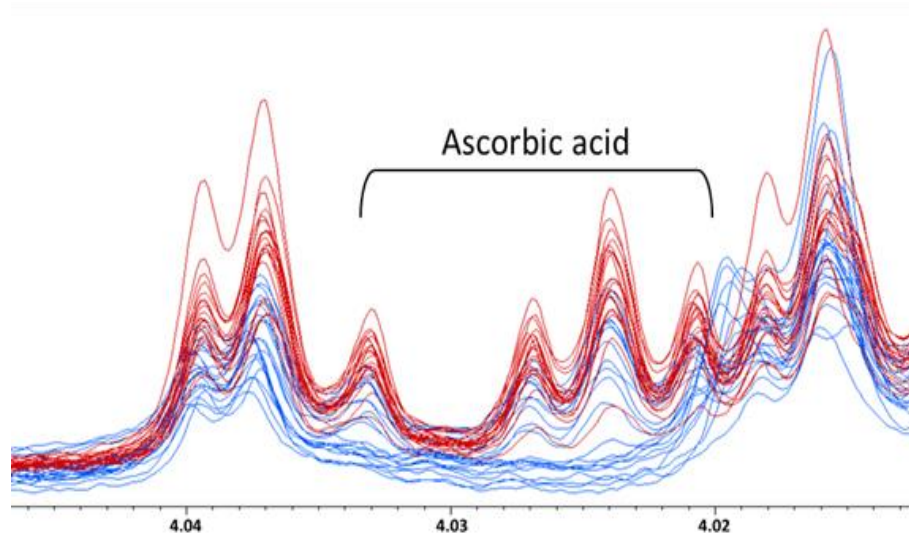
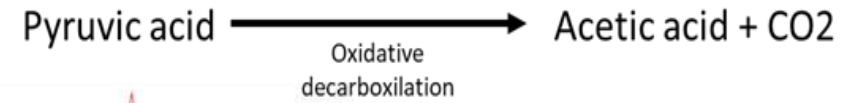
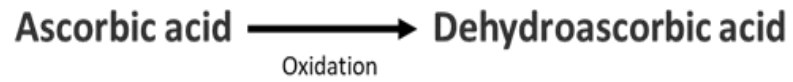
Reaction	Midpoint Reduction Potential at pH 7 (E _{m,7})
Acetate + CO ₂ → Pyruvate	-0.7 V
Succinate + CO ₂ + 2H ⁺ → 2-Oxoglutarate + H ₂ O	-0.6 V
Dehydroascorbic acid → Ascorbic acid	+0.06 V

Long-term storage at -80



The metabolic phenotype of urine samples was followed over 5-year storage. **T0**; **4 year-storage**; **5 year-storage**;
5 year-storage + 48 h at 4–6 °C

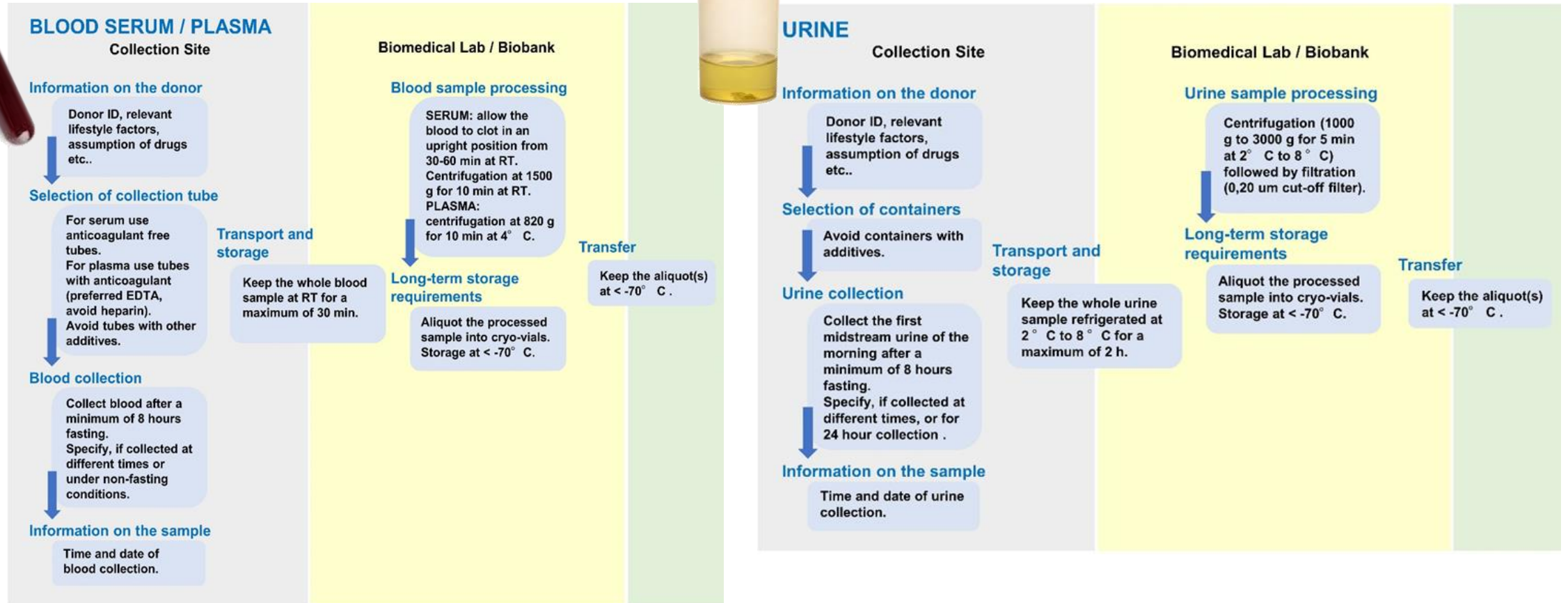
CSF - same reporters as in urine



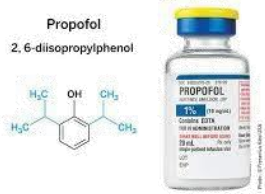
1H ppm

- Freezing > 1 h from collection
- Freezing within 1 h from collection

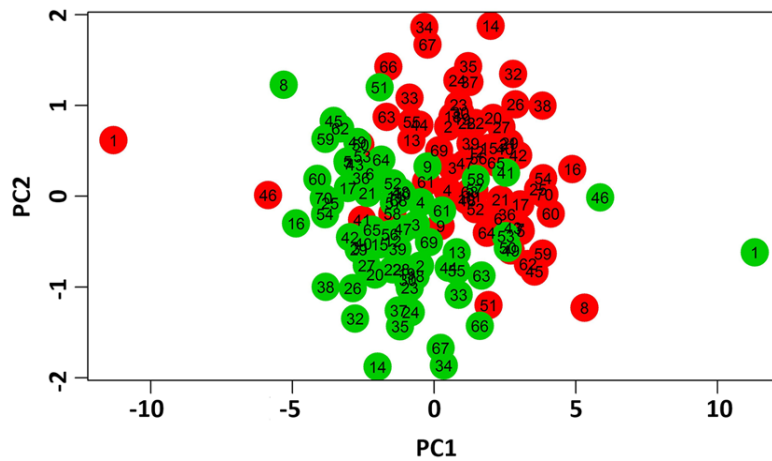
Information on the donor



The effect of anesthesia



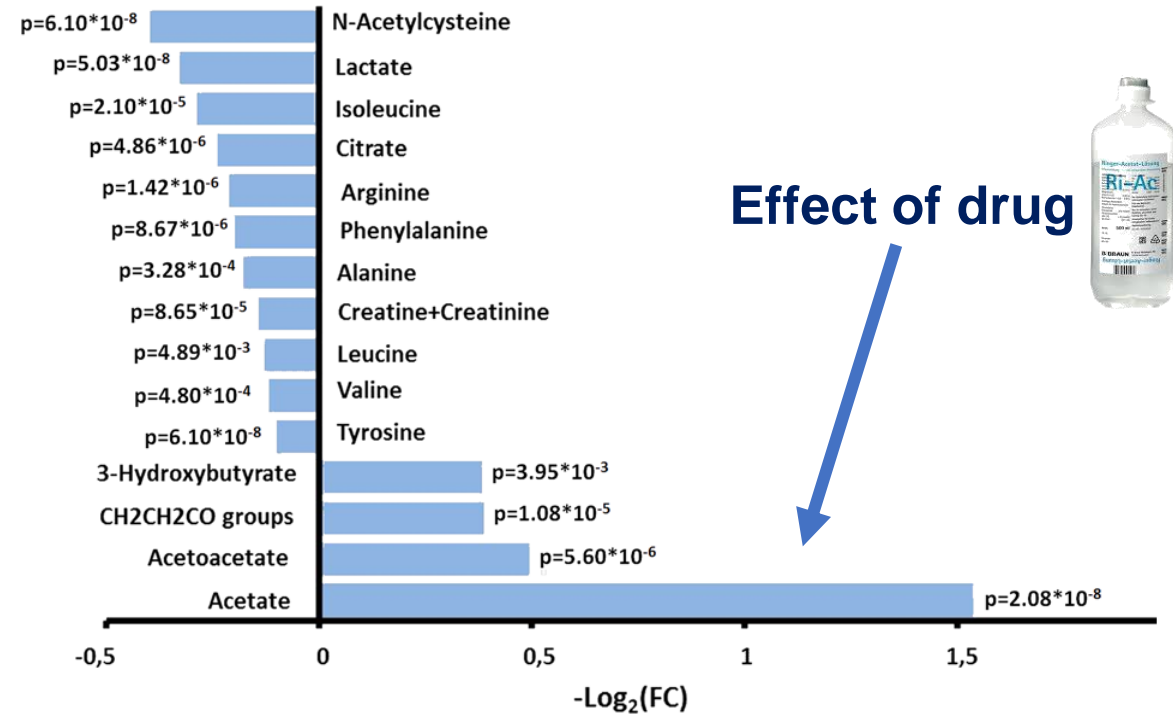
Pre- & post-anesthesia blood



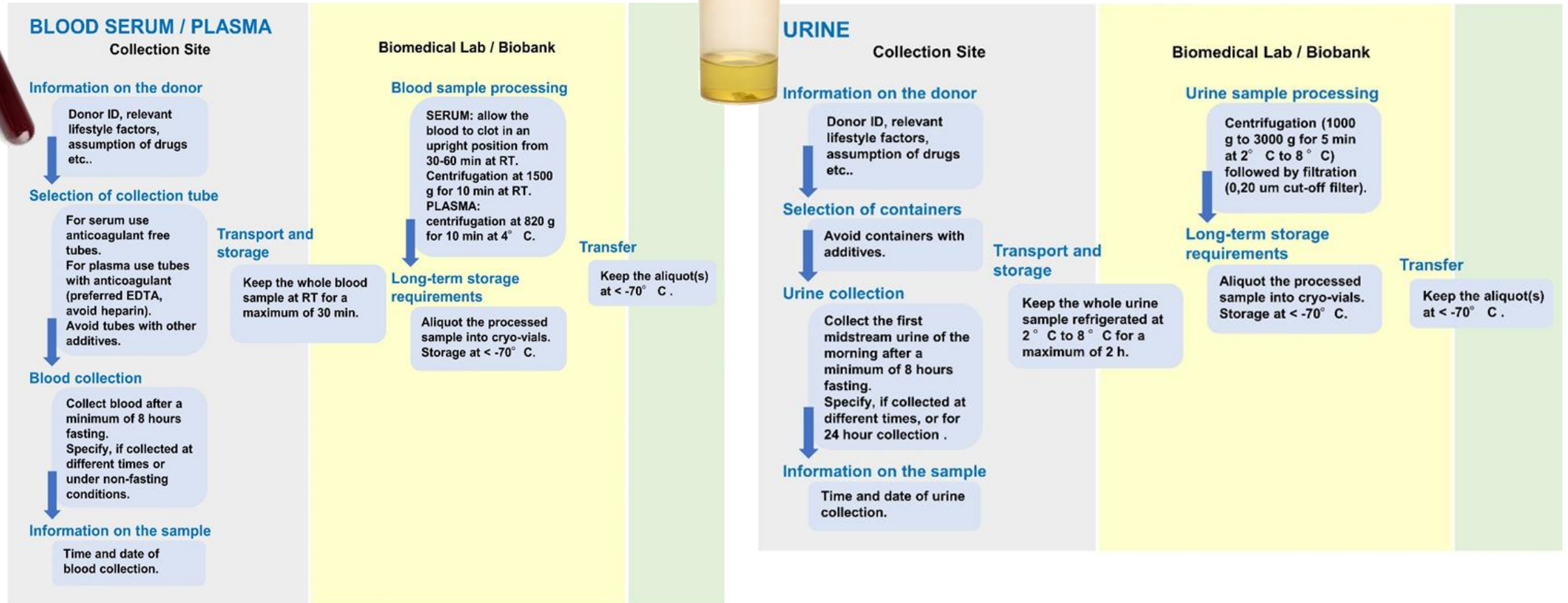
Discrimination accuracy
92.60%

Confusion matrix	Pre	Post
Pre	*92.6	7.4
Post	7.4	**92.6

- Avoid anesthesia
- Annotation of drugs administered to the patient

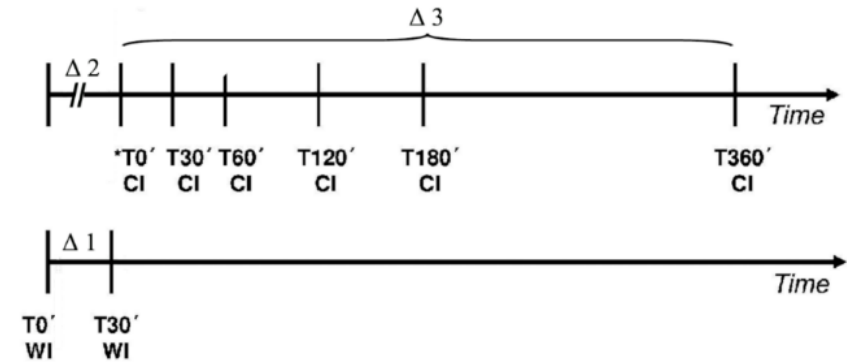


Information on the sample

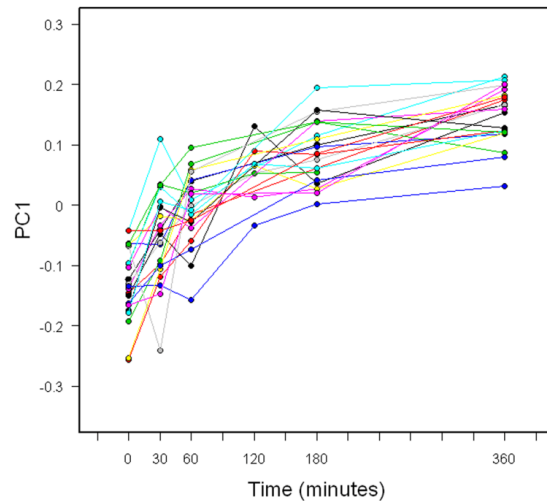


Human Liver: Cold and Warm Ischemia

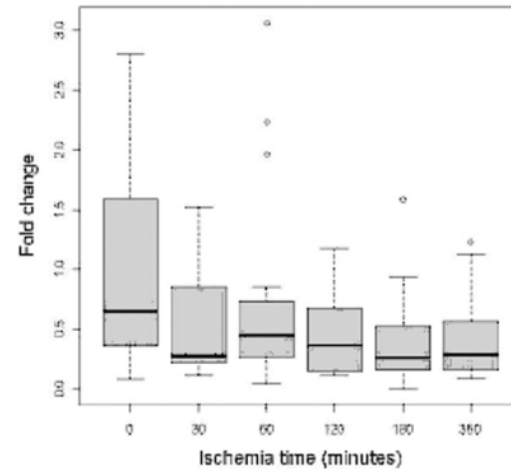
STUDY DESIGN



Individual NMR profile changes during CI



Acetate

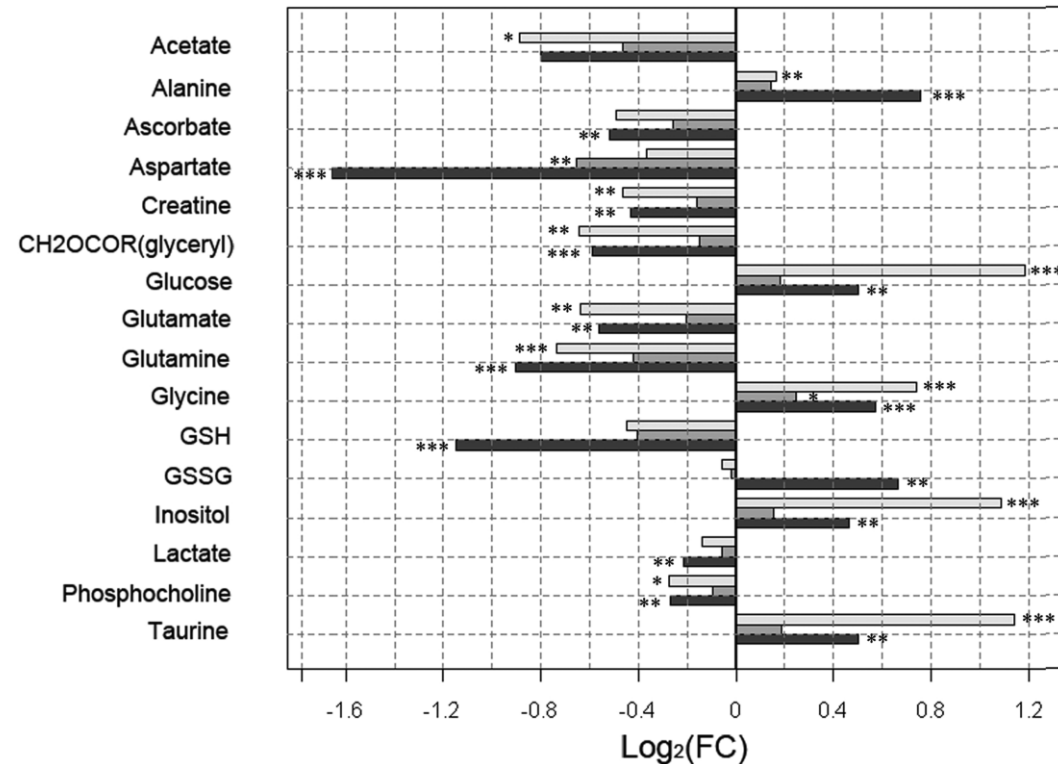


Mean intensity changes of metabolites during CI

- Annotation of the ischemia time

GSH/Gln consumption

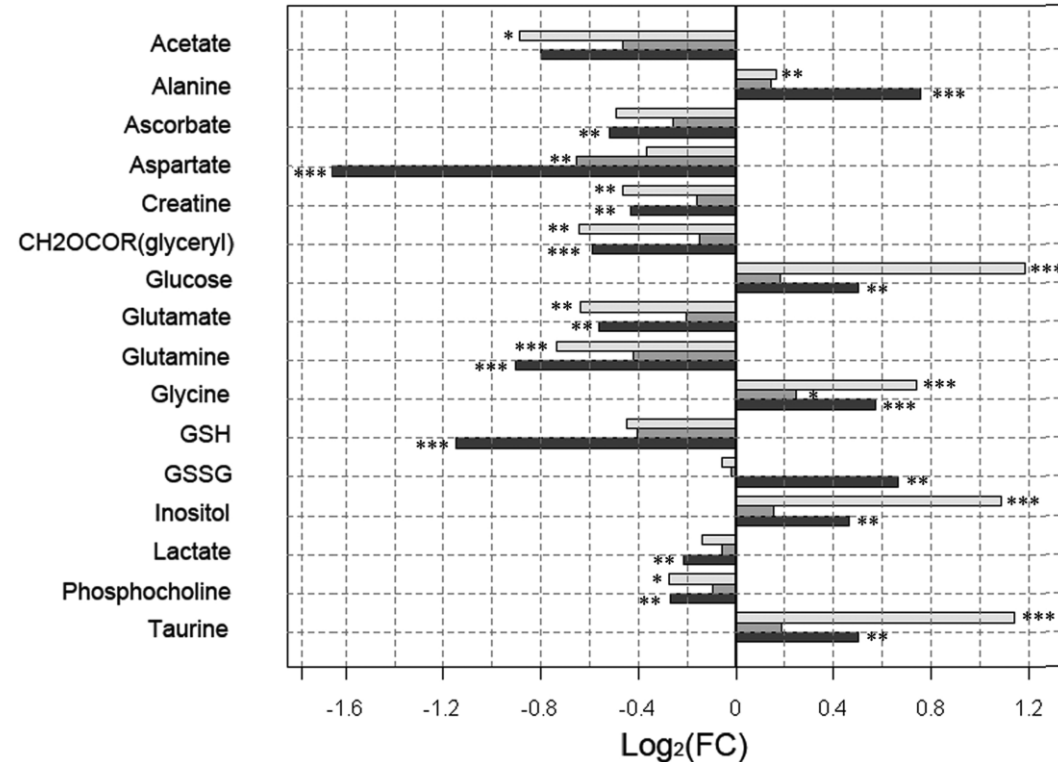
- **Oxidative stress** associated with ischemia was the likely cause for the consumption of the antioxidant **GSH** (and the concomitant production of **GSSG**).
- Consumption of **glutamine**, a GSH precursor, was also observed.
- GSH consumption was much more prominent at prolonged CI times compared to T30'WI, suggesting that in CI non-enzymatic reactions, such as those in which GSH acts as a reactive-oxygen-species scavenger, may be dominant over enzymatic reactions.



log₂ (T360' CI/T0' CI) in black
log₂ (T30' WI/T0' WI) in light grey
log₂ (T30' CI/T0' CI) in dark grey

Glucose, taurine inositol

- **Glucose** increase during ischemia possibly reflected glucose uptake by the cells and changes in glycogenolysis or gluconeogenesis.
- **Taurine**, a robust apoptotic biomarker, increased mainly in WI.
- **Inositol**, which regulates many cellular processes in eukaryotes, including stress responses and apoptosis also increased
- Changes in taurine and inositol were strongly correlated.



log₂(T360' CI/T0' CI) in black
 log₂(T30' WI/T0' WI) in light grey
 log₂(T30' CI/T0' CI) in dark grey

General considerations

All the samples of your dataset should be treated in the same way.

For new type of samples: make your own SOPs for specific types of samples and/or metabolites you are interested to characterize. Simulate and validate all the procedures to identify possible “critical” points

.

Collect data on patient treatment, if possible

Collect the sample before patient treatment, if possible (i.e. anesthesia)

Perform the processing procedures as soon as possible from sample collection

Keep the samples at 4° C before the processing

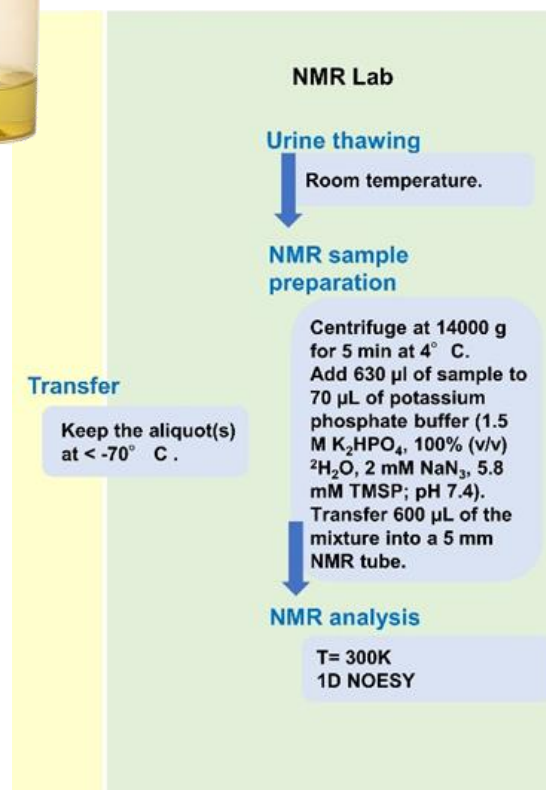
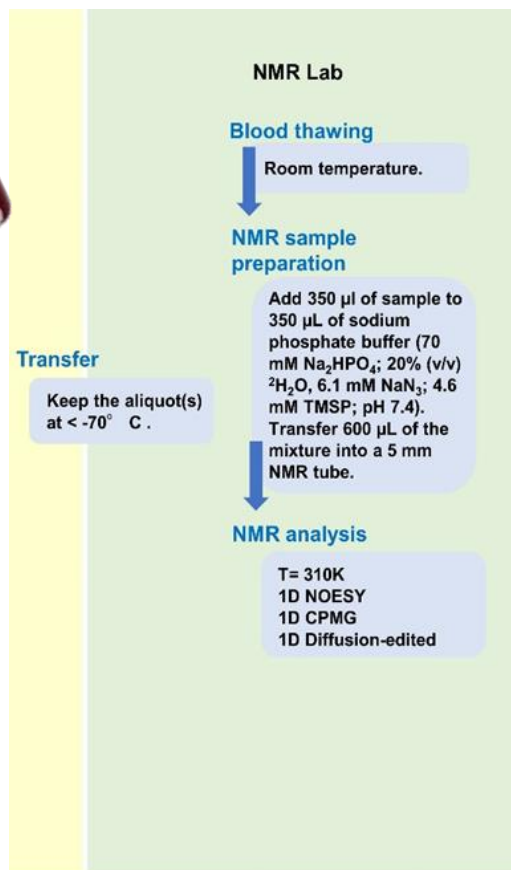
Store at -80°C the processed samples as soon as possible

Use a refrigerate sample changer for automatic acquisition

Reduce the oxygen exposure

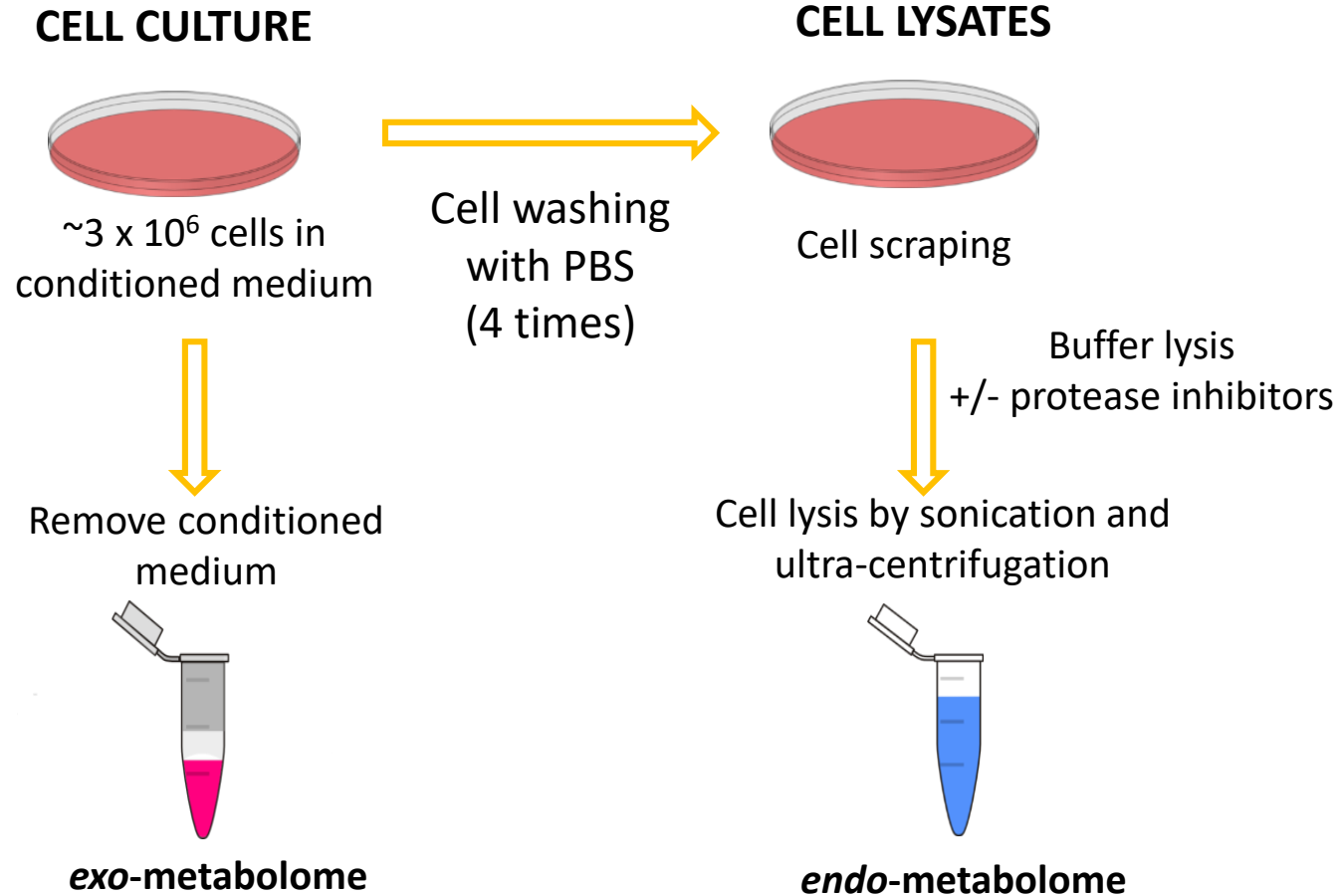
Avoid freezing/thawing cycle (divide the samples into different small volume aliquots)

NMR-Sample preparation



Cell lysates and growing media

Cell culture procedure suitable for NMR analysis



Minimal sample handling

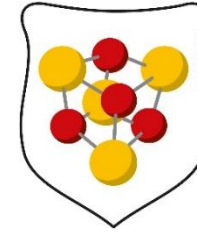
Type of sample	Experimental procedure	NMR analysis
Urine	<ul style="list-style-type: none"> • Thawing at room temperature and shaking • Centrifugation at 14 000g for 5 min • Dilution 1:9 with potassium phosphate buffer (1.5 M K_2HPO_4, 100% (v/v) 2H_2O, 10 mM sodium TMSP; pH 7.4) • 600 μL of each mixture was transferred into a 5 mm NMR tube for the analysis. 	<ul style="list-style-type: none"> • NOESY experiment • J-resolved experiment
Serum/Plasma	<ul style="list-style-type: none"> • Thawing at room temperature and shaking • Dilution 1:1 with sodium phosphate buffer (10.05 g $Na_2HPO_4 \cdot 7H_2O$; 0.2 g NaN_3; 0.4 g sodium TMSP in 500 mL of H_2O with 20% (v/v) 2H_2O; pH 7.4) • 600 μL of each mixture was transferred into a 5 mm NMR tube for the analysis. 	<ul style="list-style-type: none"> • NOESY experiment • CPMG experiment • Diffusion-edited experiment • J-resolved experiment
Saliva	<ul style="list-style-type: none"> • Thawing at room temperature and shaking • Centrifugation at 14 000g for 5 min • Dilution 1:9 with potassium phosphate buffer (1.5 M K_2HPO_4, 100% (v/v) 2H_2O, 10 mM sodium TMSP pH 7.4). • 600 μL of each mixture was transferred into a 5 mm NMR tube for the analysis. 	<ul style="list-style-type: none"> • NOESY experiment • J-resolved experiment

Minimal sample handling

Type of sample	Experimental procedure	NMR analysis
Cerebrospinal fluid	<ul style="list-style-type: none"> Thawing at room temperature and shaking Dilution 1:1 with sodium phosphate buffer (10.05 g $\text{Na}_2\text{HPO}_4 \cdot 7\text{H}_2\text{O}$; 0.2 g NaN_3; 0.4 g sodium TMSP in 500 mL of H_2O with 20% (v/v) $^2\text{H}_2\text{O}$; pH 7.4). 600 μL of each mixture was transferred into a 5 mm NMR tube for the analysis. 	<ul style="list-style-type: none"> NOESY experiment CPMG experiment
Cell lysates	<ul style="list-style-type: none"> Cells were plated in 100 mm dishes and were grown until they reached 70% confluence. Dishes were placed onto ice and cells were rinsed twice with Phosphate-Buffered Saline (DPBS). Cells were scraped and collected with DPBS supplemented with 1% Protease Inhibitor Cocktail and 1% Phosphatase Inhibitor Cocktail. Cellular lysates were sonicated on ice and centrifuged. Supernatants were collected and stored at -80°C. Thawing in ice and shaking Adding 10% in volume of $^2\text{H}_2\text{O}$ 600 μL of each mixture was transferred into a 5 mm NMR tube for the analysis. 	<ul style="list-style-type: none"> NOESY experiment CPMG experiment J-resolved experiment
Tissues	<ul style="list-style-type: none"> Frozen tissue samples were trimmed (10–15 mg) to fit rotor insert capacity The insert was filled with a solution of TMSP in $^2\text{H}_2\text{O}$. Rotor inserts were covered with plug and plug-restraining screw and inserted into the 4 mm rotor for HR-MAS. 	<ul style="list-style-type: none"> NOESY experiment CPMG experiment

**HR-MAS
NMR**

Thanks to... and all of you for your attention!



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Regione Toscana

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