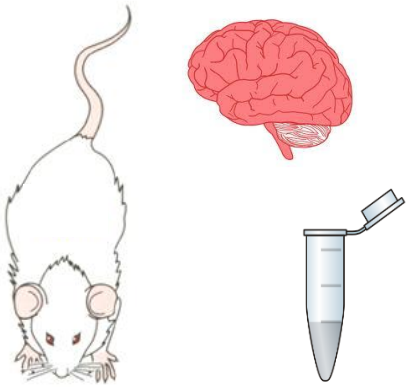
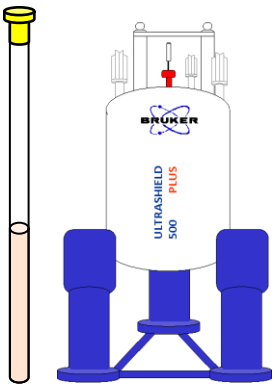
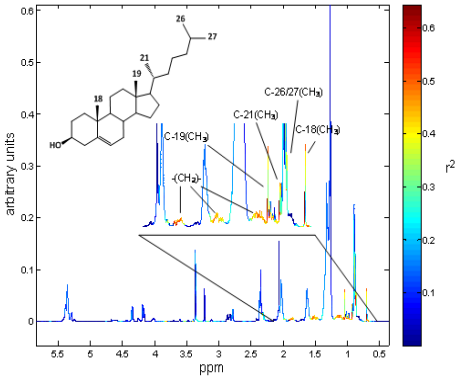
***Brain metabolite profiling** in animal models is highly relevant since it allows simultaneous monitoring of up to several tens of metabolites in the same analysis. Thus, it represents a superb opportunity in the global assessment of the metabolic status of the brain.*







Principle

Simultaneous identification and relative quantization of up to several tens metabolites in mouse/rat brain tissue extracts using ^{1}H-NMR spectroscopy. **Proton nuclear magnetic resonance** may detect metabolites which are present at high concentrations (greater than **10 µM**).

Easy and Fast Sample Treatment/ High-throughput Analysis

75-100 mg of fresh brain tissue are submitted to dual (lypophilic ($CHCl_3$/MeOH) and hydrophilic (CH_3CN/H_2O)) extraction and ^{1}H-NMR spectra are recorded on each one of the extracts.

Wide range of metabolites covered

Brain (aqueous extract)			Brain (lipidic extract)	
2-Hydroxybutyrate	Glutamate	Nicotinurate	ARA+EPA	Sphyngomyelin
4-Aminobutyrate	Glutamine	O-Phosphocholine	DHA	Total Cholesterol
ATP	Glutathione	O-Phosphoethanolamine	Diglycerides	Total Phospholipids
Acetate	Glycerol	Oxypurinol	Linoleic acid	Triglycerides
Adenosine	Glycine	Phenylalanine	Lysophosphatidylcholine	w-3 fatty acids
Alanine	Inosine	Sn-Glycero-3-phosphocholine	Monoglycerides	
Ascorbate	Isocaproate	Taurine	MUFA	
Aspartate	Isoleucine	Tyrosine	Oleic acid	
Caprylate	Lactate	UDP-glucose	Phosphatidylcholine	
Choline	Leucine	Uridine	Phosphatidylethanolamine	
Creatine	Methanol	Valine	Phosphatidylinositol	
Ethanol	Myo-Inositol		Phosphatidylserine	
Ethanol amine	N-Acetyl aspartate		Plasmalogen	
Fumarate	NAD+		PUFA	
GTP	NADP+		PUFA/MUFA	

** The identification of the above list of metabolites will depend on the metabolic or pathologic status of the study samples as well as the quality of the extraction.*

Data Analysis: Move

^{1}H-NMR spectra identification and interpretation. Semi-quantization of metabolites identified. Basic univariate statistical test. Use of advanced statistical, chemometric, multivariate and artificial intelligence algorithms to handle high-troughput metabolomics data sets and turn them into useful clinical information (PCA, PLS-DA, ANNs). Identify metabolic relationships, mechanism, functions and pathways in the experimental data and mapping of relevant pathways.

Advantages:

Semi-quantitative results, low cost per sample, high-throughput analysis.

Wide range of applications:

Phenotyping of genetically modified animals; Toxicology (drug toxicity and pre-clinical drug candidate safety assessment); Biomarker Discovery; Clinical studies (Diagnose and therapeutic efficacy); Monitoring of diet-related health phenotyping.

References:

Vinaixa, M. et al., J. Proteome Research. 2010; 9(5):2527-2538.

Samino, S. et al., Biochimie. 2013; 95(4):808-816.

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