

## TRANSBIO training sessions

### "Study Metabolomic"

Toulouse, 13-14<sup>th</sup> of February 2014

These training sessions will provide practical courses. 4 sessions will be proposed on different sites of MetaToul : the Toulouse Metabolomic Core Facility.

Each session will be planned for 4 persons during 1 day and half: 13th (1pm)-14th (5pm) of February 2014

#### PROGRAMME:

##### INTRODUCTION-CONCLUSION : Jean Charles PORTAIS

##### 1. QUANTITATIVE METABOLOMIC (Lindsay PEYRIGA, Hanna KULYK and Fabien LETISSE)

For this session, we will study absolute quantification of intracellular metabolites using MS-based metabolomic approach. The different steps of the analysis will be presented and practiced :

- a. Culture of *E. Coli*
- b. Sampling (differential method and fast filtration)
- c. Sample preparation (Isotopic Dilution Mass Spectrometry method)
- d. Ion Chromatography/MS-MS analysis
- e. Data processing and absolute quantification

##### 2. GLOBAL METABOLOMIC with 1H-NMR APPROACH (Cécile CANLET, Marie TREMBLAY-FRANCO)

For this session, we will study plasma samples using NMR-based metabolomic approach. The different steps of the analysis will be presented and practiced:

- a. Sample preparation
- b. 1H NMR spectroscopy of plasma samples
- c. Pre-treatment of NMR data
- d. Multivariate statistical Analysis of NMR data ( Principal Component Analysis, Hierarchical Cluster Analysis, Partial Least Squares Regression)
- e. Identification of discriminant metabolites

**3. GLOBAL METABOLOMICS using High Resolution MS** (Emilien JAMIN, Marie TREMBLAY-FRANCO, Laurent DEBRAUWER)

In this session, HRMS based global metabolomic approach will be illustrated. The different steps of the analysis will be presented and practiced:

- a. Sample preparation
- b. Data generation using LC coupled to Orbitrap HRMS
- c. Filtering and pre-treatment of MS data (XCMS, Camera...)
- d. Multivariate statistical Analyses ( Principal Component Analysis, Hierarchical Cluster Analysis, Partial Least Squares Regression)
- e. Metabolite identification

**4. LIPIDOMIC** (Pauline LE FAOUDER, Aude DUPUY, Justine BERTRAND-MICHEL) :

Studying lipids on biological samples is quite complicated because of the very large diversity of lipid molecules. We have to choose which family of lipids we want to quantify. For this session the targeted lipids to study in the course will be decided on the basis of the participant requirements: fatty acids, phospholipids, sphingolipids, eicosanoids, sterols...The different steps of the analysis will be presented and practiced

- a. Extraction
- b. Pre-purification
- c. Derivation
- d. Chromatographic analysis
- e. Quantification

**REGISTRATION to be done before the 31<sup>st</sup> of January 2014!**

Participants have to register directly to the person in charge of each session:

For **QUANTITATIVE METABOLOMIC** session: [lindsay.peyriga@insa-toulouse.fr](mailto:lindsay.peyriga@insa-toulouse.fr)

For **GLOBAL METABOLOMIC with 1H-NMR APPROACH** session: [cscanlet@toulouse.inra.fr](mailto:cscanlet@toulouse.inra.fr)

For **GLOBAL METABOLOMICS using High Resolution MS** session: [jamin@toulouse.inra.fr](mailto:jamin@toulouse.inra.fr)

For **LIPIDOMIC** session: [justine.bertrand-michel@inserm.fr](mailto:justine.bertrand-michel@inserm.fr)

For all registrations: please, put in copy: [amoca@adm.ups-tlse.fr](mailto:amoca@adm.ups-tlse.fr)