Metabolomics Service

We offer a comprehensive metabolomics service covering cell cultivation, sample preparation, analysis of intracellular metabolites and data analysis.

Background
Intracellular metabolite analysis has become an essential tool increasingly used in human- and bio-sciences for phenotyping as well as to identify health-associated biomarkers and process-limiting metabolic bottlenecks, respectively. Hundreds of intracellular metabolites can be addressed today by state-of-the-art mass spectrometry-based analytics in one sample run. However, preparation of phenotype-representative metabolite extract samples is still a critical issue. Dictated by the diversity of cellular systems a one hit sample preparation procedure does not exist. Moreover selection of inadequate sampling affects the metabolic state of the cells. Metabolite-specific degradation during the sample preparation process heavily distorts the metabolite composition and ion suppression a result of the sample matrix falsifies mass-spec signals of metabolites. Hence both sample preparation and data acquisition are extremely error-prone and necessitate sophisticated and typically complex working routines. The development of suitable protocols is a demanding and very time-consuming process and therefore out of question for many companies and research institutes.

acib-Technology
acib and TU Graz have comprehensive expertise in metabolomics of different cell systems. The service covers all steps from cultivation design over cell sampling and metabolite extract preparation to mass spectrometry-based compound and MS data analysis and is outlined in the following in more detail. Standard routines permit qualitative (n >100) and quantitative (n ≤50) analysis of water-soluble intracellular metabolite pools (Trausinger et al. 2015, Biotechnol. Biofuels, 8:157). A distinctive feature of our service is the analysis of time-resolved metabolite dynamics induced by exogenous stimuli. All works are carried out in conformity with the respective quality standards (Goodacre, et al. 2007, Metabolomics, 3:231).

acib-Offer
- Cultivation
  ✓ Scale: Shake flask, stirred bioreactor (< 2L), filter, adherent systems
  ✓ Aeration: Aerobic, anaerobic
  ✓ Substrate: Unlabeled substrates, isotopically labeled substrates
  ✓ Monitoring
- Sampling and metabolite extraction
  ✓ Single time point
  ✓ Multiple time points to study metabolite dynamics
  ✓ Metabolite extraction: Quenching/extraction, metabolite-specific internal standardization

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acib-Offer continued

- **Mass spectrometry**
  - LC-MS (Exactive Orbitrap, Thermo Fisher Scientific, USA)
- **Data analysis**
  - Compound identification, signal integration, calculation of $^{12}\text{C}/^{13}\text{C}$ compound ratios for qualitative analysis
  - External standardization for absolute quantitative analysis
  - Isotopologue-specific analysis

**Extras**
- We are highly interested in expanding our repertoire of addressable cell systems and intracellular compounds. We therefore offer support in the development of (i) sample preparation routines of cell types currently not accessible by our protocols and (ii) analytical tools to address special compounds or other compound classes.