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Mapping Metabolic Pathways by Targeted Metabolomics Solutions

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Metabolomics is a very powerful technology that is successfully applied in various research fields. The metabolome incorporates the information of all upstream endogenous cellular events, such as regulation on the genomic, transcriptomic and proteomic level, as well as of exogenous effects from nutrition, drugs and microbiome activity. Therefore it provides a highly integrated, very sensitive and – among all 'omics' technologies – the most comprehensive readout of the biological phenotype.

Targeted metabolomics aims at the accurate quantification of specific metabolites in a biological system. It holds the potential to deliver new diagnostic markers for the sensitive and specific detection and prognosis of diseases, to monitor the response to therapeutic interventions and additionally provides insights into the underlying mechanisms.

In classical biomarker research, e.g. in the genomics or proteomics field, it is common and also appropriate to consider single, separate markers. In most cases, this is still also the predominant approach in metabolomics research. However, in contrast to genes or proteins, metabolites are interconnected by metabolic network reactions. Data analysis in metabolomics can be enriched by taking into account connections between metabolites in the form of specific metabolic sums and ratios. Moving the level of interpretation and understanding from a classical single biomarker concept to a way of thinking that takes into account the network-structure of metabolism will help to obtain a comprehensive picture and result in more robust and reliable predictions.

Short Biography
Dr Judith Wahrheit

A. **Judith Wahrheit** joined Biocrates Life Sciences AG in 08/2014 – Contract Research Department.

B. Judith is responsible for:

1. Metabolomics data analysis, interpretation and reporting for various customer projects from academic institutions and from pharmaceutical and biotechnology industry as well as for funding projects.
2. Project management of contract research and funding projects.
3. Scientific support of research and development, sales and quality management.

C. Studied Human and Molecular Biology at Saarland University (Germany) and Biochemistry and Molecular Biology at Université Louis Pasteur (Strasbourg, France).

D. Graduated 2009 with a degree in Human and Molecular Biology from Saarland University.

E. Promotion (Dr. rer. nat., summa cum laude) at the Institute of Biochemical Engineering (Saarland University) on “Metabolic dynamics and compartmentation in the central metabolism of Chinese hamster ovary cells”.

F. Received Dissertation awards of the Elisabeth and Prof. Dr. Horst-Dietrich Hardt foundation in 2015 and “Dr. Eduard-Martin Preis” in 2016.

G. Several years of experience on metabolic studies using metabolomics and fluxomics (metabolic flux analysis) techniques in various contexts (Basic Research, Biotechnology, Toxicology, Cancer, Neurological Disorders, Nutrition, …)

Recent relevant publications:

1. Leuthold P, Schaeffeler E, Winter S, Büttner F, Hofmann U, Mürdter TE, Rausch S, Sonntag D, Wahrheit J, Fend F, Hennenlotter J, Bedke J, Schwab M, Haag M, (2017) Comprehensive Metabolomic and Lipidomic Profiling of Human Kidney Tissue: A Platform Comparison. J Proteome Res. 2017 Jan 12. doi: 10.1021/acs.jproteome.6b00875.

2. Casanova R, Varma S, Simpson B, Kim M, An Y, Saldana S, Riveros C, Moscato P, Griswold M, Sonntag D, Wahrheit J, Klavins K, Jonsson PV, Eiriksdottir G, Aspelund T, Launer LJ, Gudnason V, Quigley CL, Thambisetty M, (2016). Blood metabolite markers of preclinical Alzheimer's disease in two longitudinally followed cohorts of older individuals. Alzheimer's & Dementia 2016 Jul; 12(7): 815-22.

3. Nicolae A, Wahrheit J, Nonnenmacher Y, Weyler C, Heinzle E, (2015) Identification of active elementary flux modes in mitochondria using selectively permeabilized CHO cells, Metabolic Engineering 2015 Nov; 32: 95-105.

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5. Nicolae A, Wahrheit J, Bahnemann J, Zeng A-P, Heinzle E, (2014) Non-stationary 13C metabolic flux analysis of Chinese hamster ovary cells in batch culture using extracellular labeling highlights metabolic reversibility and compartmentation, BMC Systems Biology, Apr 28; 8(1): 50.

6. Wahrheit J, Niklas J, Heinzle E, (2014) Metabolic control at the cytosol-mitochondria interface in different growth phases of CHO cells, Metabolic Engineering, May; 23: 9-21.

7. Wahrheit J, Nicolae A, Heinzle E, (2014) Dynamics of growth and metabolism controlled by glutamine availability in Chinese hamster ovary cells, Applied Microbiology and Biotechnology. 98, 1771-1783.

8. Wahrheit J, Heinzle E, (2014) Quenching Methods for the Analysis of Intracellular Metabolites, In: Pörtner, R., (Ed.), Animal Cell Biotechnology. vol. 1104. Humana Press, pp. 211-221 (book chapter).

9. Wahrheit J, Heinzle E (2013) Sampling and quenching of CHO suspension cells for the analysis of intracellular metabolites, BMC Proceedings 7(Suppl 6):P42, DOI: 10.1186/1753-6561-7-S6-P42.

10. Wahrheit J, Nicolae A, Heinzle E (2013) 13C labeling dynamics of intra- and extracellular metabolites in CHO suspension cells, BMC Proceedings 7(Suppl 6):P43, DOI: 10.1186/1753-6561-7-S6-P43.

11. Wahrheit J, Nicolae A, Heinzle E (2013) Investigation of glutamine metabolism in CHO cells by dynamic metabolic flux analysis, BMC Proceedings 7(Suppl 6):P44, DOI:10.1186/1753-6561-7-S6-P44.

12. Bahnemann J, Kayo S, Wahrheit J, Heinzle E, Pörtner R, Zeng A-P (2013), In search of an effective cell disruption method to isolate intact mitochondria from CHO cells, Engineering in Life Sciences, March 2014; 14(2): 161–169.

13. Wahrheit J, Nicolae A, Heinzle E (2011), Eukaryotic metabolism: Measuring compartment fluxes. Biotechnol J. 2011 Sep; 6(9): 1071-85 (review article).

14. Wahrheit J, Niklas J, Heinzle E (2011) Evaluation of sampling and quenching procedures for the analysis of intracellular metabolites in CHO suspension cells, BMC Proceedings 5 (Suppl 8): P82.

15. Strigun A*, Wahrheit J*, Niklas J, Heinzle E, Noor F (2011) Doxorubicin increases oxidative metabolism in HL-1 cardiomyocytes as shown by 13C- metabolic flux analysis Toxicol Sci. 2012 Feb;125(2): 595-606. *contributed equally.

16. Strigun A, Wahrheit J, Beckers S, Heinzle E, Noor F (2011), Metabolic profiling using HPLC allows classification of drugs according to their mechanisms of action in HL-1 cardiomyocytes, Toxicol Appl Pharmacol. 2011 Apr 15;252(2): 183-91.