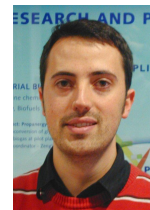


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Description

The turnover of metabolites in microbial metabolism can be in a subsecond scale. Thus fast sampling and proper sample processing are critical steps in metabolomics studies. Besides the need to quench all metabolic activities as fast as possible, the sampling is followed by several processing steps that can cause large errors in metabolite concentrations as well. Another challenge is the fast and efficient separation of the exo- and endometabolome without cell leakage. In this project, new technologies and methods are developed to address these problems and to access the true intracellular metabolic dynamics.

Rapid Sampling Unit

A new and fully automated rapid sampling unit has been developed in our institute. Due to the modular design, the system satisfies the needs in accuracy as well as in terms of flexibility. A special valve system assures defined sample volumes and efficient mixing of sample and quenching solution. The system can handle up to five hundred samples with a frequency of up to ten samples per second. All parts with contact to the fermentation broth are in-situ sterilizable to allow working with pathogens. The flexibility of the system allows different experimental setups such as the parallel application of different quenching protocols in one experiment.

To address the challenge of leakage-free separation of endo- and exometabolome, we are developing a system for the fast filtration of fermentation broth with subsequent quenching of the filter-cake. This filtration system should be embedded to the Rapid-Sampling-Unit for fully automated fast sampling and sample filtration.

System characterisation and application

The Rapid-Sampling-Unit is characterised in terms of speed, accuracy, back-mixing behaviour and reproducibility. In the first experiments, the system showed excellent results. Now the system will be used to investigate two model processes, which are the suppression based incorporation of non-canonical amino acids into target proteins in *E. coli* and the investigation of the metabolic behaviour of *P. polymyxa* in the process for the production of pure R,R-2,3-butanediol.

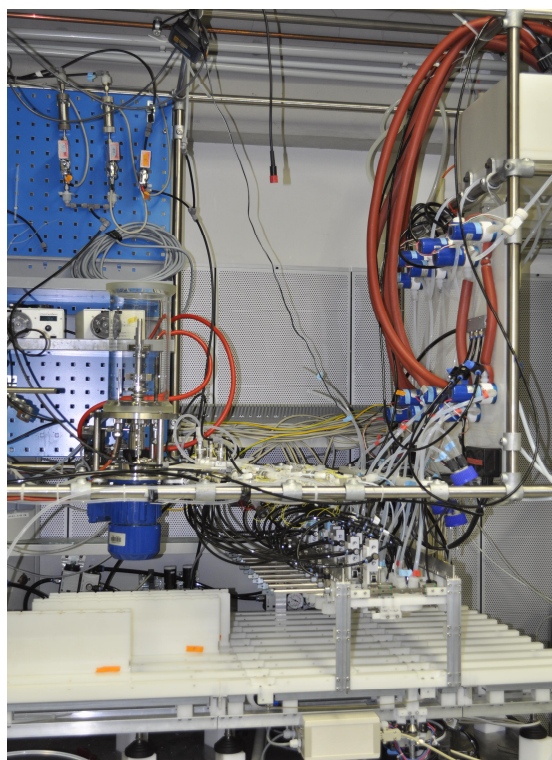


Fig. 1. Rapid-Sampling-Unit with 3,7 L Bioreactor

References:

- Bo Yu, Jibin Sun, Rajesh Reddy Bommareddy, Lifu Song, An-Ping Zeng (2011) **A novel (2R,3R)-2,3-Butanediol Dehydrogenase from an Industrially Potential Strain *Paenibacillus polymyxa* ATCC12321**. Appl. Environ. Microbiol. In pring.
- Budisa, N. (2004) **Prolegomena to future experimental efforts on genetic code engineering by expanding its amino acid repertoire**. Angew. Chem. Int. Ed., 43, 6426 – 6463
- Xiu Z-L, Zeng, A-P (2008) **Present state and perspective of downstream processing of biologically produced 1,3-propanediol and 2,3-butanediol**. Appl Microbiol Biotechnol 78:917-926.

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