Transcriptomic Monitoring of 
*Escherichia coli* Growth

Nadine Wappler, Eric Zuchantke, Tina Giersch, Lucy Stark, 
Röbbe Wünschiers

**GOAL**
Analysis of the transcriptome is a powerful tool for understanding genetic regulatory processes. Prerequisite to any transcriptomic analysis is biological sampling and statistical data analysis. Exemplified by transcriptomic monitoring of bacterial growth we established a data processing pipeline for the analysis of RNASeq data. The goal was to find strongly regulated genes during growth phases of *Escherichia coli*. The ultimate goal is the generation of time-line expression vectors for metabolic modeling (FIGURE 1).

**METHOD**
Strain K12 (DSM-No 498) was grown as batch culture and sampled at four different time-points (45 min, 3 h, 5 h, 7 h) covering major growth states (FIGURE 2). mRNA was separated from total RNA and sequenced. Sequences were quality filtered, trimmed and clipped and finally aligned to the *Escherichia coli* K-12 MG1655 genome (GI 545778205). After annotation significant differentially expressed transcripts (p<0.05) were extracted (FIGURE 3). Three biological replicates have been analyzed.

**RESULTS**
For a first insight into gene regulatory processes with focussed our analysis on expressed enzymes. 204/257 individual enzymes were found to be significantly up/down-regulated between time-point 45 min and 5 h (FIGURE 4). These could be allocated to 97 pathway categories (see TABLE 1 for examples).