487c Enabling Cell Factory Design through High-Throughput and Quantitative Metabolome Analysis

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In the context of designing cell factories, it is desirable to obtain quantitative data for a large number of state variables within the cell. Metabolome analysis is an important, yet relatively unexploited tool for this purpose. The use of high-throughput metabolome analysis in metabolic engineering has been limited by the lack of global approaches to quantitatively identify large families of intracellular and extracellular metabolites. Specifically, sample preparation is still considered to be a limiting step. The diverse chemical and physical nature of metabolite structures gives rise to considerable experimental challenges in extracting diverse molecular families. We have explored six different strategies for their ability to extract a significant number of metabolite families from the yeast *Saccharomyces cerevisiae*. We will report a rapid, robust, and consistent method that can be applied to the identification of a large number of intracellular metabolites from this yeast. In addition, we will comment on the use of this method in a more general framework for the integration of quantitative metabolome analysis with transcriptome studies for identification of regulatory networks in yeast.