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## Metabolic inventory of *Streptococcus pneumoniae* growing in a chemical defined environment.

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### Abstract

The Gram-positive bacterium *Streptococcus pneumoniae* can cause a broad range of severe diseases including pneumonia and septicemia. The pneumococcal pathophysiology is highly dependent on host nutrients such as purines, pyrimidines, amino acids and carbon sources. Therefore, we aimed to decipher the metabolome with a metabolomics approach that allows for the investigation of the basic metabolic characteristics during growth in a chemical defined medium composed of typical host metabolites. By using a combination of <sup>1</sup>H-NMR, HPLC-MS and GC-MS methods we monitored extracellular uptake and secretion of metabolites as well as the intracellular metabolic composition. Employing our validated protocol for the pneumococcal intracellular metabolome analysis, a time resolved snapshot of the primary metabolism of pneumococci was obtained. The intracellular metabolic profile indicates a high glycolytic flux and displays high concentrated precursors of peptidoglycan synthesis probably to fuel cell-wall-metabolism in growing cells. Furthermore, our data reflect the biochemical dependency for *S. pneumoniae* on external host derived nutrients such as nucleosides. These essential pathways may serve as new targets in the drug development against *S. pneumoniae*.

Keywords: *Streptococcus pneumoniae*; metabolism; glycolysis; energy metabolism

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