EUROPEAN RESPIRATORY JOURNAL
ERJ METHODS
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Metabolomics in pulmonary medicine: extracting the most from your data

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The metabolome enables unprecedented insight into biochemistry, providing an integrated signature of the genome, transcriptome, proteome and exposome. Measurement requires rigorous protocols combined with specialised data analysis to achieve its promise. https://bit.ly/3yPiYkQ

Cite this article as: Reinke SN, Chaleckis R, Wheelock CE. Metabolomics in pulmonary medicine: extracting the most from your data. *Eur Respir J* 2022; 60: 2200102 [DOI: 10.1183/13993003.00102-2022].

This single-page version can be shared freely online.

Received: 14 Jan 2022
Accepted: 14 May 2022

Obstructive lung diseases including asthma and COPD are heterogenous syndromes for which the molecular determinants of individual subtypes of pathogenesis remain unclear. This is a major barrier in understanding disease aetiology and in stratifying patients for treatment as well as in identifying actionable therapeutic targets. There is an unmet need to understand the dysregulated biochemical processes driven by the interaction between genetic and environmental factors [1]. While challenging to study, this complex intersection can be captured *via* the metabolome. Metabolic phenotyping (metabotyping) has demonstrated sufficient molecular resolution to identify phenotypes and endotypes of respiratory disease, including asthma [2–4], COPD [5, 6], respiratory syncytial virus bronchiolitis [7] and cystic fibrosis [8–10].