



The dawn of the omics era in human precision-cut lung slices

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New techniques permit the use of multiple omics and advanced imaging technologies with human precision-cut lung slices (PCLS) to allow for more objective and comprehensive molecular analysis to bring PCLS closer to the era of precision medicine <https://bit.ly/3deBjx2>

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Precision-cut lung slices (PCLS) have been used in biomedical research for over 50 years (30 years for human PCLS), but the majority of initial work focused on toxicology, tissue mechanics, and modelling airway responses for asthma [1–3]. In recent years, PCLS have been increasingly used for studying acute and chronic lung diseases at the molecular level, as well as for evaluating therapeutics [3, 4]. In particular, there is high interest in using PCLS derived from human lungs, due to the ability to directly study species-specific effects in human tissue and because they better capture clinical heterogeneity (*e.g.* age, broader spectrum of disease status, or the presence of other co-morbidities). However, one of the major difficulties hampering the further use of this model system has been due to difficulties in directly applying new and emerging state-of-the-art analysis methods to PCLS, including for example mass spectrometry, next-generation sequencing, and advanced microscopy. The study by KHAN *et al.* [5] in this issue of the *European Respiratory Journal* details multiple technical advances and makes a significant leap forward in our ability to perform advanced and detailed molecular analysis of human PCLS-based disease models.