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Separation and characterization of human microbiomes by metaproteomics

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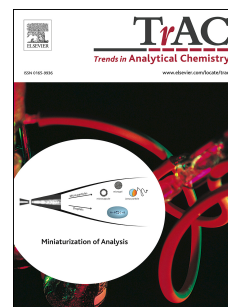
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1 Separation and characterization of human 2 microbiomes by metaproteomics

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10 bioinformatics

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12 ABSTRACT

13 The surface of the human body, including the gastrointestinal tract, is occupied by trillions of microbial
14 cells with diverse metabolic functions, constituting the human microbiome. The composition of the
15 microbiome varies with body region and among individuals, and the majority of the microbiomes, their
16 genes and protein products are poorly characterized. Recent studies have highlighted the importance of
17 mass spectrometry-based omics approaches, and in particular metaproteomics, for deep functional
18 characterization of the human microbiome. However, major analytical and bioinformatics challenges
19 remain due to the enormous complexity, high dynamic range and large intra- and inter-individual
20 variations in the human microbiome. Herein, we review the analytical approaches that have been
21 implemented for metaproteomic studies of the microbiome and discuss the challenges in sample
22 separation and instrument measurements. As well, we review the bioinformatics tools available for
23 metaproteomic data processing, their challenges and their applications for deep characterizations of
24 human microbiomes.

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