# Next-generation proteomics in the fight against pathogens: a guide tour

Jean Armengaud

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**Abstract**

**Invited KEYNOTE**

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# Title: Next-generation proteomics in the fight against pathogens: a guide tour

**Authors: Armengaud J.**[1]

**Affiliations:** [1]CEA, ProGénoMix platform, Bagnols-sur-Cèze, France

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**Text:**

Since proteins are the workhorses of biological systems, their global study by proteomics provides a wealth of information. Next-generation proteomics is based on high-resolution tandem mass spectrometry which can record spectra on hundreds of thousands of different molecules, allowing the identification and quantitation of thousands of proteins. Highly complementary to genomics and transcriptomics, proteomics better explain the resulting phenotype and can be performed in a timely manner. Interestingly, it can be applied to any pathogen, delivering a better understanding of its specific characteristics as well as new insights into the host response to infection. Remarkably, the identification of virulence and antibiotic-resistance factors, as well as other key molecular players, became ultimately straightforward thanks to comparative proteomics. Pathogen detection by proteotyping is also a promising methodology that takes into account taxon-specific information that can be rapidly recorded by mass spectrometry and interpreted for rapid diagnosis. Indeed, tandem mass spectrometry is able to quickly distinguish closely related strains and helps in their taxonomical study. Finally, pathogens are often part of more complex microbial communities. Recent advances in metaproteomics make it possible to address pathogens in such a complex environment. Challenging questions in metaproteomics benefit from recent advances in bioinformatics and this methodology has gained maturity for envisioning now its large scale application in clinical settings. The different facets of proteomics and metaproteomics, including sample preparation, data acquisition, database construction, search strategy and data interpretation, will be presented and discussed in light of several studies carried out on a variety of pathogens and biological questions.