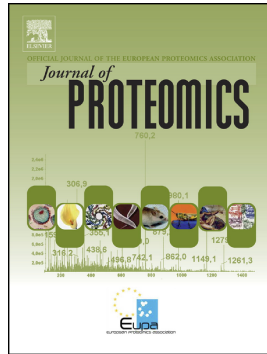


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Proteomics in infectious diseases



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PROTEOMICS IN INFECTIOUS DISEASES

With the increasing prevalence of microorganisms with multiple resistance to antibiotics or other agents, the relapse threatens the pre-antibiotic era. The search for new options for effective control of infectious diseases is becoming increasingly important. Recently, the World Health Organization (WHO) published a list of the ten most dangerous microorganisms, including members of the genera *Acinetobacter*, *Pseudomonas*, *Streptococcus*, *Staphylococcus* or *Enterobacter*. Besides, the WHO has developed a tool for determining which diseases and pathogens should be prioritized for research and development in public health emergency contexts. There are also many viral diseases including Ebola and Marburg virus, Zika and Middle East respiratory syndrome coronavirus (MERS-CoV) and Severe Acute Respiratory Syndrome (SARS), among others. Interestingly disease X is in the list and it exemplifies how an important epidemic could be caused by a microorganism that by now was not known to be an etiologic agent of human disease, and thus the R&D Blueprint seeks to enable cross-cutting R&D preparation that is also relevant for an unknown disease.

With the help of proteomics, the function of pathogens and hosts can now be considered globally with the genome sequences as the basis for the monitoring of proteins, their modifications and interactions. While considerable progress has been made in mass spectrometry in the identification and quantification of proteins, the analysis of host-pathogen interactions has analytical limits due to the numerically unfavorable relationship between host and pathogen proteins. However, the new technical achievements mean that it is increasingly possible to characterize complex mixtures and thus open up new possibilities.

In order to promote the collaboration between scientists working on proteomic studies related to infectious diseases caused by virus, bacteria, fungi and parasites, the Human Infectious Diseases initiative in the context of the Human Proteome Project (HID-HPP) was established in 2014. New diagnostic tests, therapeutic agents and vaccines are required to control these infectious diseases. International collaboration of scientists working in infectious diseases

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