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REVIEW

Proteomics
Proteomics and Systems Biology

Mass spectrometry-based proteomic platforms for better understanding of SARS-CoV-2 induced pathogenesis and potential diagnostic approaches

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Abstract

While protein–protein interaction is the first step of the SARS-CoV-2 infection, recent comparative proteomic profiling enabled the identification of over 11,000 protein dynamics, thus providing a comprehensive reflection of the molecular mechanisms underlying the cellular system in response to viral infection. Here we summarize and rationalize the results obtained by various mass spectrometry (MS)-based proteomic approaches applied to the functional characterization of proteins and pathways associated with SARS-CoV-2-mediated infections in humans. Comparative analysis of cell-lines versus tissue samples indicates that our knowledge in proteome profile alternation in response to SARS-CoV-2 infection is still incomplete and the tissue-specific response to SARS-CoV-2 infection can probably not be recapitulated efficiently by in vitro experiments. However, regardless of the viral infection period, sample types, and experimental strategies, a thorough cross-comparison of the recently published proteome, phosphoproteome, and interactome datasets led to the identification of a com-

Abbreviations: PI3K-Akt, phosphatidylinositol 3-kinase- protein kinase B; EGFR, epidermal growth factor receptor; MAPK, mitogen-activated protein kinase; Rap1, ras-related protein 1; AMPK, AMP-activated protein kinase; BioID, proximitydependent biotin identification; DDA, data-dependent acquisition; MEK, mitogen-activated protein kinase kinase' SRC; protooncogene tyrosine-protein kinase Src