NEWS

Process understanding is becoming increasingly easy. In this study(1) label free quantitative LC-MS/MS and biostatistics analysis were used to follow-up the liver cells proteome during infection by dengue virus. The quantitative information regarding protein expression in the early stages of infection was very useful in understanding viral infectious processes.

(1) Quantitative proteomic analysis of Huh-7 cells infected with Dengue virus by label-free LC–MS. <u>Pando-Robles</u> and all.
2014 <u>http://www.sciencedirect.com/science/article/pii/S1874391914003443</u>

High-resolution nano LC-MS/MS quantitative proteomics and CORAVALID[™] data processing: The efficient tool

PHYLOGENE

62, Route Nationale 113 30620 BERNIS Tel : +33 4 66 04 77 99 Fax : +33 4 66 04 77 97 e-mail : <u>gskorski@phylogene.com</u> web : <u>www.phylogene.com</u> <u>http://ms.phylogene.com</u>