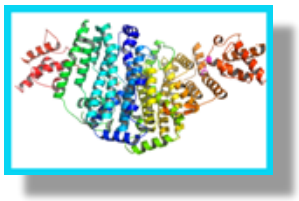
NEWS:



Complete characterization of Host Cell Proteins with label-free nanoLC-MS/MS

Host cell protein (HCP) impurities are generated by the host organism during the production of therapeutic recombinant proteins, and are difficult to remove completely. Commonly present in small quantities, if levels are not controlled, HCPs can potentially reduce drug efficacy and cause adverse patient reactions.

Mass spectrometry is a useful tool for HCP analysis. MS-based label free methods are capable of identifying and quantifying individual proteins down to single digit ppm (ng/mg) when compared to a reference. Also, quantitation of individual HCPs can be performed using normalized spectral counting as the number of peptide spectrum matches (PSMs) per protein is proportional to protein abundance
ELISA is the routine tool to compare HCP clearance before and after the change, but as different processes may result in different HCPs, mass spec is the method of choice to first qualify an HCP-ELISA for a specific process.
In this article (1), after removing of the antibody, 700 proteins could be identified. HCP profiles enabled high resolution differentiation of commercial grade monoclonal antibody samples generated from different cell lines, cell culture, and purification processes.

(1) Toward the complete characterization of host cell proteins in biotherapeutics via affinity depletions, LC-MS/MS, and multivariate analysis. MadsenJA, and all.2015 https://www.ncbi.nlm.nih.gov/pubmed/26291024

With MS-Phylogene, you can also characterize your antibody productions HCP:

- ***High-resolution nano LC-MS/MS quantitative proteomics and data processing: The efficient tool.***
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