6-12-2022

# Acceleration of vaccine development by improvement of process understanding - Analysis of the host cell proteome

Roxana Disela

Daphne Keulen

Geoffroy Geldhof

Olivier Le Bussy

Martin Pabst

*See next page for additional authors*

## Authors

Roxana Disela, Daphne Keulen, Geoffroy Geldhof, Olivier Le Bussy, Martin Pabst, and Marcel Ottens

# ACCELERATION OF VACCINE DEVELOPMENT BY IMPROVEMENT OF PROCESS UNDERSTANDING – ANALYSIS OF THE HOST CELL PROTEOME

Roxana Disela, Delft University of Technology, The Netherlands; GSK Vaccines, Technical Research & Development – Microbial Drug Substance, Belgium
r.c.disela@tudelft.nl
Daphne Keulen, Delft University of Technology, The Netherlands; GSK Vaccines, Technical Research & Development – Microbial Drug Substance, Belgium
Geoffroy Geldhof, GSK Vaccines, Technical Research & Development – Microbial Drug Substance, Belgium
Olivier Le Bussy, GSK Vaccines, Technical Research & Development – Microbial Drug Substance, Belgium
Martin Pabst, Delft University of Technology, The Netherlands
Marcel Ottens, Delft University of Technology, The Netherlands

Key Words: Downstream processing, chromatography, High Throughput experimentation, recombinant subunit vaccine, host cell proteome

While regulatory agencies require stringent product quality and safety to be upheld in biopharmaceutical products, today's competitive biopharmaceutical market requires short process development times. The demand to accelerate especially the development of vaccines became obvious with the COVID-19 pandemic. By expanding process understanding with the use of process design tools the development time of the purification could be significantly shortened.

High throughput experimentation (HTE) provides an automated experimentation platform, which minimizes the amount of used samples and saves experimental time. In this approach, HTE is used to acquire experimental data to regress parameters used as inputs for a chromatographic mechanistic model with the objective to establish an *E. coli* vaccine purification process development platform for a recombinant subunit vaccine. To provide a generic process development strategy that can be applied to novel antigens, the focus lies on the description of the adsorption behavior of the impurities such as host cell proteins (HCPs) during the capture step. Therefore our approach focuses on the present impurities, in specific the HCPs (Figure 1). When using the same *E.coli* strain the knowledge regarding the host cell proteins could be transferred to a new product. The first step is the identification of HCPs. Over a thousand HCPs are identified in the *E.coli* harvest sample investigated by means of mass spectrometry based proteomics. A database containing the properties of these proteins can provide assistance in the decision on chromatography resins suited for the purification process of a new developed antigen.

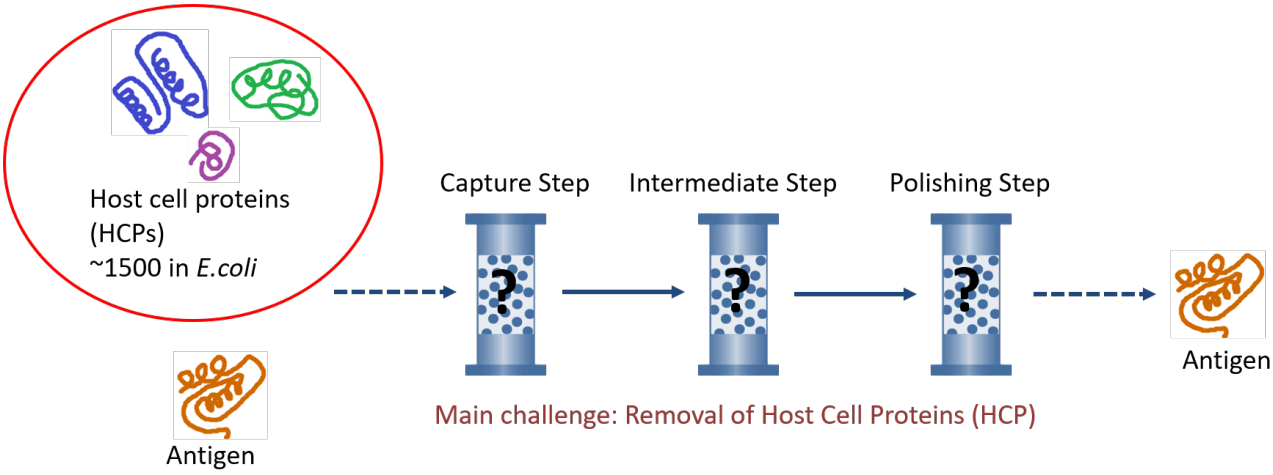


*Figure 1 – Development of purification process for new antigen*