# Cell Proteins in Biologics Using In Silico and In Vitro Methods National National Comprehensive Assessment of Immunogenicity Risk of Host

M1030-01-04

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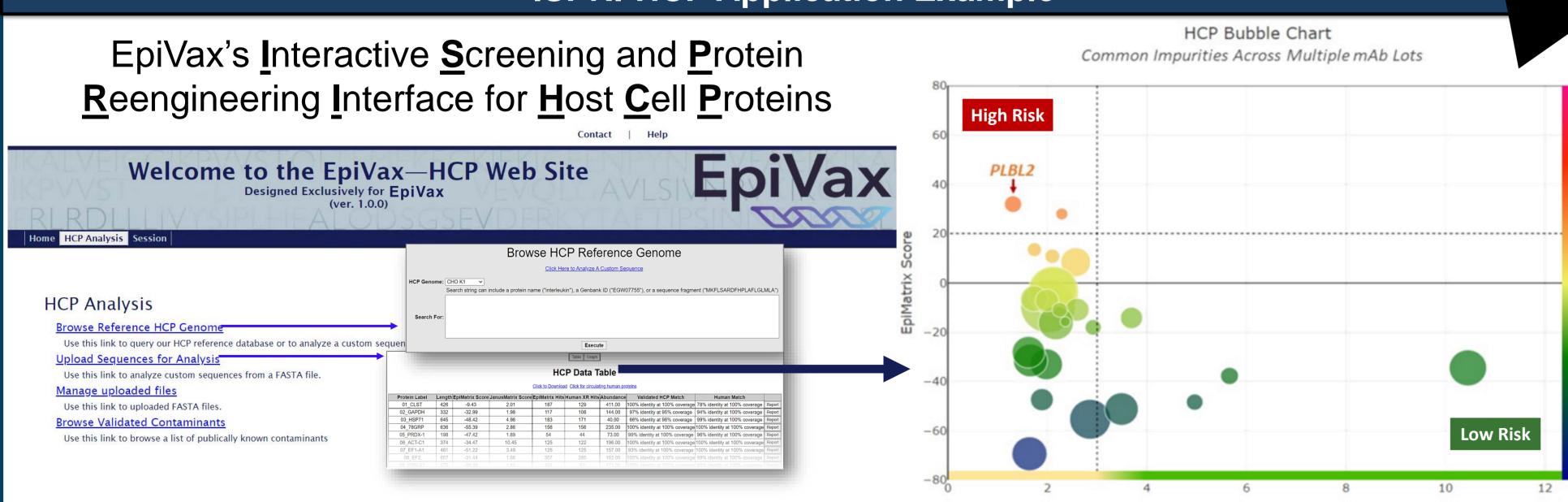
## **PURPOSE**

Host cell protein (HCP) impurities are a critical quality attribute (CQA) because they may trigger undesired immune responses with the potential to compromise the safety and efficacy of biologics. The presence of immune responses to Chinese hamster ovary (CHO)-derived HCPs has contributed to the suspension of clinical trials in the past. EpiVax has developed a web-based tool to evaluate the immunogenicity of HCP impurities. This tool, the Interactive Screening and Protein Re-engineering Interface for Host Cell Proteins (ISPRI-HCP) has been in use by industry clients and collaborators since 2003. ISPRI-HCP evaluates the immunogenic potential of proteins based on T cell epitope content and their similarity to the human proteome. We used ISPRI-HCP, to perform an in-silico immunogenicity risk assessment of 140 HCPs identified by a consortium of monoclonal antibody producers. EpiVax will further evaluate and validate the ISPRI-HCP platform by performing in-vitro T cell assays for this set of commonly found HCP impurities.

#### **OBJECTIVE**

To offer therapeutic developers the ability to determine which host cell protein impurities may be of highest risk for immunogenicity through a quick and easy web based tool.

#### HCP and other process related impurities in biotherapeutics can potentially generate **METHODS** immune responses. ISPRI\_HCP tool assesses the immunogenicity risk posed by HCPs. EpiMatrix™ will parse each HCP JanusMatrix searches for potentiall Predicted ligands from an protein into overlapping 9-mer HCP that share the same cross-reactive sequences based on frames and assess 9-mer frames for the preservation of the TCR-facing HLA restriction and TCR-HLA binding potential with respect facing contour as epitopes residues and established HLA to nine Class II HLA supertype derived from self (human) binding preferences of given 9-me are presumed to be **ISPRI-HCP Application Example**



HCP Bubble Chart (right). Each circle represents an HCP impurity found in two or more monoclonal antibody lots. The diameter of the circle indicates relative abundance in ppm (highest observed abundance across lots plotted). EpiMatrix Score indicates putative epitope density across the whole protein (0 is random, >10 is higher than random, >20 is considered elevated). JanusMatrix Score indicates average humanness of all predicted epitopes within each protein (≥3 is considered elevated). Data extracted from Jawa et al., AAPS J 2016.

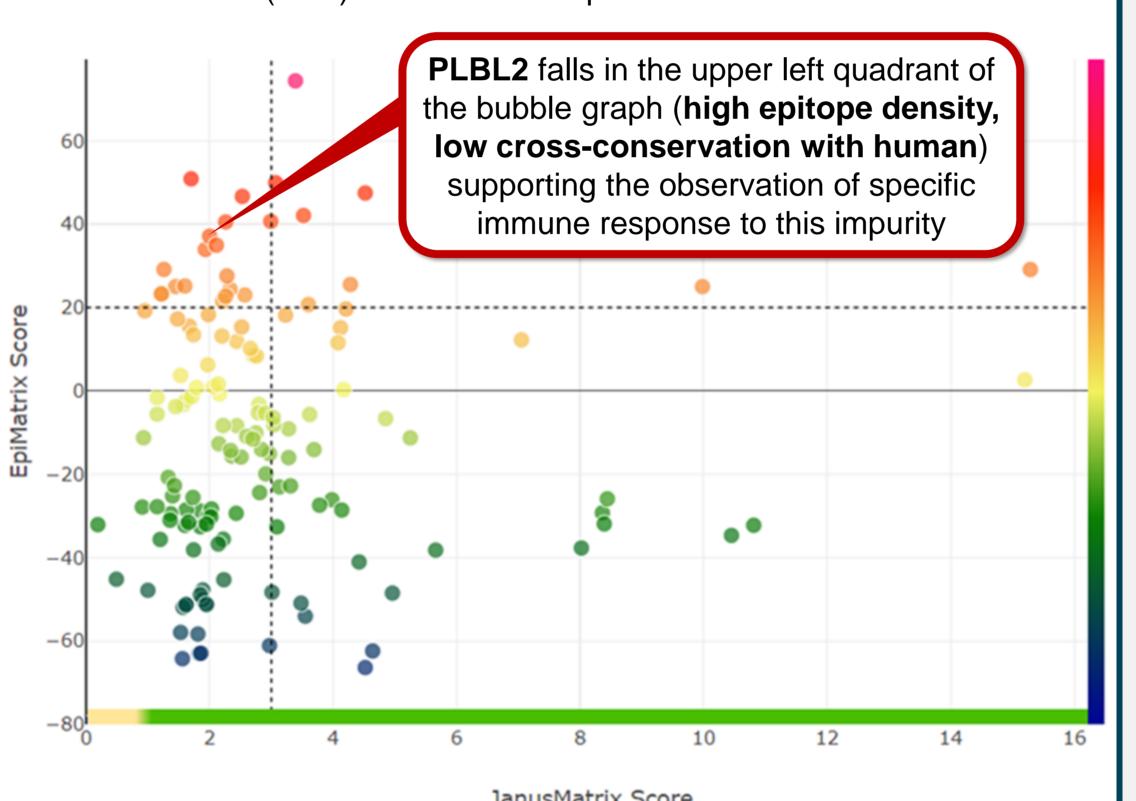
#### **RESULTS**

#### Common "high risk" copurifying HCP

The BioPhorum Development Group (BPDG) compiled a list of frequently seen high-risk HCPs based on information gathered through literature searches, company experiences, and surveys.

"High-risk" host cell proteins (HCPs): A multicompany collaborative view

Using ISPRI-HCP, we assessed the immunogenicity of 140 commonly found CHO HCP impurities. Shown is a subset of the calculated EpiMatrix (EMX) and JanusMatrix (JMX) scores for each protein.



The immunogenicity of HCPs can vary dramatically.

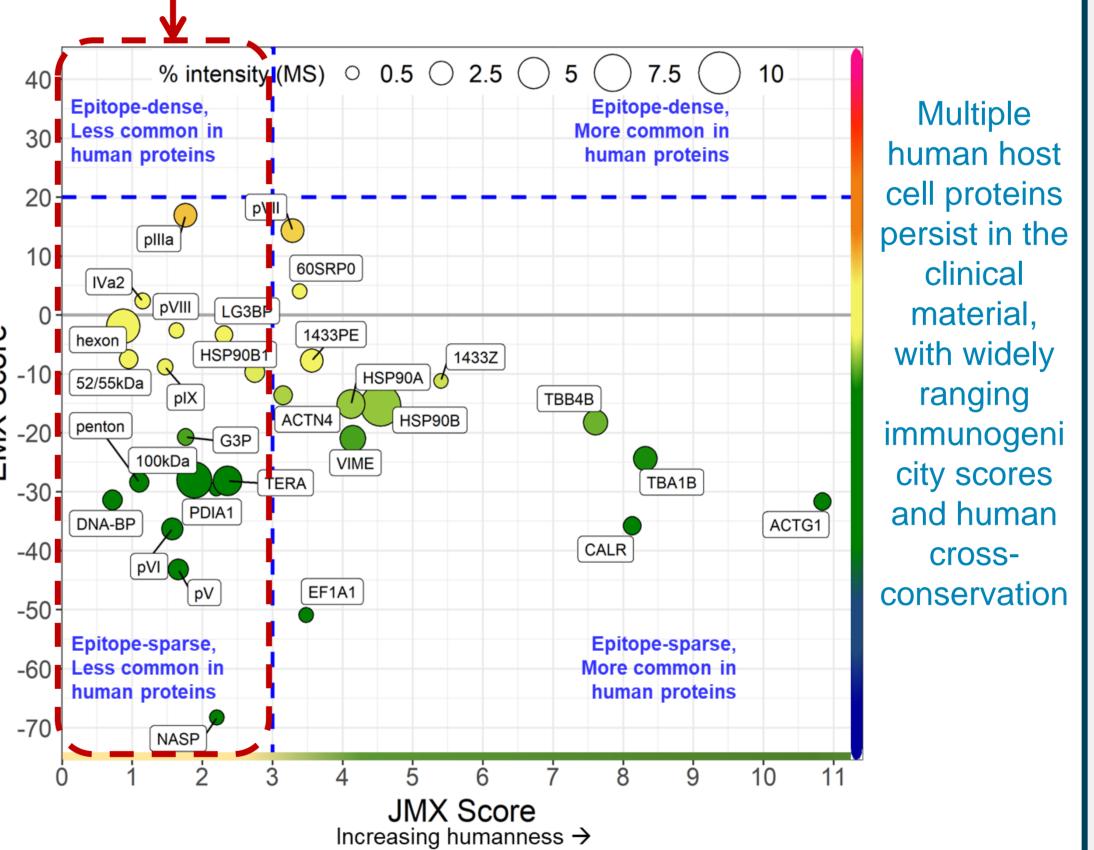
- Phospholipase B-Like 2 Protein (PLBL2) is an example of a CHO protein found with high frequency in monoclonal antibody lots
- PLBL2 was later observed to generate a specific immune response in patients treated with Lebrikizumab, whose clinical material contained the CHO HCP impurity [Fischer et al.].

#### COVID Vaccine HCP and vector proteins: Krutzke et al.

Process-related impurities in ChAdOx1 nCov-19 vaccine

Krutzke et al. analyzed the ChAdOx1 nCov-19 vaccine using biochemical and proteomic methods. They found that in addition to the adenovirus vector, the vaccine contains substantial amounts of both human and nonstructural viral proteins.

Using ISPRI\_HCP, we found that several viral vector proteins have elevated immunogenicity scores and low human cross-conservation, indicating considerable risk for impurity-driven immune response.



Best case scenario, highly cross-conserved human epitopes are well tolerated in this material. Worst case scenario, however, it is possible that immune responses against the copurifying human host cell proteins or other human epitopes with which they are cross-conserved, might be capable of stimulating auto-immunity, particularly if response against residual viral vector proteins provides an adjuvanting effect.

# Hexon, an Adenovirus protein reported to be found in COVID-19 vaccine formulations: Pitkänen et al.

Thromb Res. 2021 Dec; 208:129-137. doi: 10.1016/j.thromres.2021.10.027. Epub 2021 Nov 6

COVID-19 adenovirus vaccine triggers antibodies against PF4 complexes to activate complement and platelets

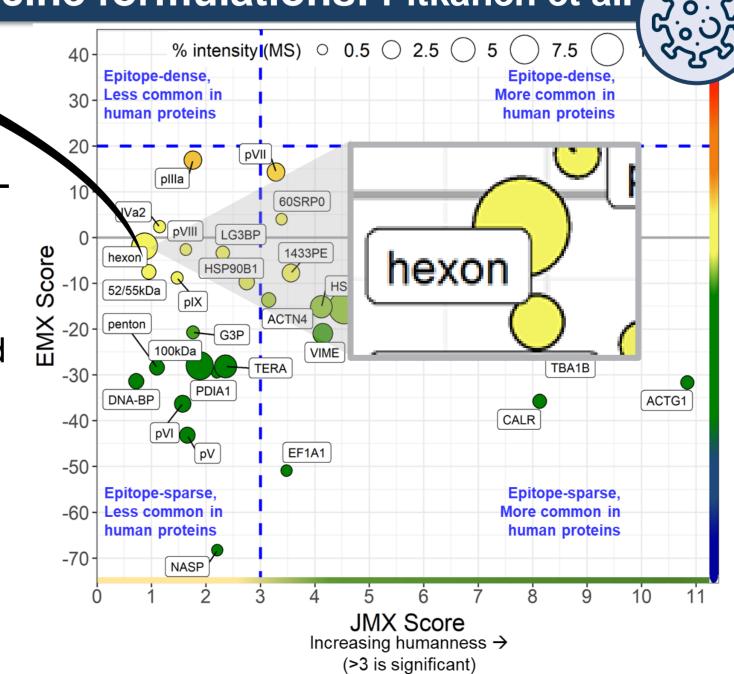
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- Hexon protein complexes with platelet factor 4 (PF4) and induces ADA in vaccine-induced thrombotic thrombocytopenia (VITT) subjects.
- This immunological stimulus co-activates the complement system and triggers spontaneous aggregation of healthy platelets [Pitkänen et al.].

Adenoviral **hexon** protein present in the ChAdOx1 nCoV-19 and Ad26.COV2.S SARS-CoV-2 vector vaccines

# **ISPRI-HCP** Results:

Hexon falls in the elevated immunogenicity scores and low human crossconservation quadrant of our HCP bubble graphs, indicating considerable risk for impurity-driven immune response.



## **CONCLUSION**

Further development of the ISPRI\_HCP tool, in collaboration with biologics industry partners, will enable exploration of immune responses in vitro, enhancing the prediction of immunogenic and tolerated T cell epitopes from HCPs, as well as evaluate the correlations with resultant ADA when patient data are available.

#### REFERENCE

- Bailey-Kellogg C, Gutierrez AH, Moise L, Terry F, Martin WD, De Groot AS, et al. CHOPPI: a web tool for the analysis of immunogenicity risk from host cell proteins in CHO-based protein production. Biotechnology and Bioengineering. United States; 2014 Nov 2; :2170-82. PMID: 24888712
- 2. Koren E, De Groot a. S, Jawa V, Beck KD, Boone T, Rivera D, et al. Clinical validation of the "in silico" prediction of immunogenicity of a human recombinant therapeutic protein. Clin Immunol. 2007; 124:26-32. PMID: 17490912
- 3. De Groot AS, Martin W. Reducing risk, improving outcomes: Bioengineering less immunogenic protein therapeutics. Clin Immunol. United States: Elsevier Inc.; 2009 May; 131(2):189-201.
- 4. Moise L, Gutierrez AH, Bailey-Kellogg C, Terry F, Leng Q, Abdel Hady KM, et al. The two-faced T cell epitope: Examining the hostmicrobe interface with JanusMatrix. Human Vaccines and Immunotherapeutics. 2013. p. 1577-86. PMID: 235842515.
- 5. Fischer SK, Cheu M, Peng K, Lowe J, Araujo J, Murray E, McClintock D, Matthews J, Siguenza P, Song A. Specific Immune Response to Phospholipase B-Like 2 Protein, a Host Cell Impurity in Lebrikizumab Clinical Material. AAPS J. 2017 Jan;19(1):254-263. doi: 10.1208/s12248-016-9998-7. Epub 2016 Oct 13. PMID:
- 6. Jones M, Palackal N, Wang F, Gaza-Bulseco G, Hurkmans K, Zhao Y, Chitikila C, Clavier S, Liu S, Menesale E, Schonenbach NS, Sharma S, Valax P, Waerner T, Zhang L, Connolly T. "Highrisk" host cell proteins (HCPs): A multi-company collaborative view. Biotechnol Bioeng. 2021 Aug;118(8):2870-2885. doi: 10.1002/bit.27808. Epub 2021 May 31. PMID: 33930190.
- 7. Krutzke, L., Rösler, R., Wiese, S., & Kochanek, S. Research Square 2021. Process-related impurities in the ChAdOx1 nCov-19 8. Pitkänen HH, Jouppila A, Helin T, Dulipati V, Kotimaa J, Meri S,
- Kantele A, Jalkanen P, Julkunen I, Lassila R. COVID-19 adenovirus vaccine triggers antibodies against PF4 complexes to activate complement and platelets. Thromb Res. 2021 Dec;208:129-137. doi: 10.1016/j.thromres.2021.10.027. Epub 2021 Nov 6. PMID: 34768097; PMCID: PMC8571998

