What is claimed is:

1. A method of purifying an antibody from a sample comprising one or more impurities including viral particles, the method comprising the steps of:

providing the sample comprising the antibody produced in a host-cell,

adding a sodium citrate buffer to the sample to produce a loading sample, wherein a concentration of the sodium citrate buffer is from 10 mM to 200 mM, and wherein adding the sodium citrate buffer adjusts a hydrophobicity of the viral particles in the loading sample,

adjusting a pH of the loading sample to a range of from 4.2 to 8.0,

loading the loading sample to a hydrophobic interaction chromatography (HIC) column to produce an HIC treated sample, wherein a concentration of the antibody in the loading sample is from 40 g/L to 200 g/L, and

collecting the HIC treated sample.

2. The method of claim 1, wherein a resin of the HIC column is phenyl resin.

3. The method of claim 1, wherein a resin of the HIC column is capto phenyl resin.

4. The method of claim 1, wherein a hydrophobic strength of the HIC column is within a range having a lower bound corresponding to a hydrophobic strength of phenyl resin and an upper bound corresponding to a hydrophobic strength of capto phenyl resin.

5. The method of claim 1, wherein the antibody is a monoclonal antibody or a bispecific antibody.

6. The method of claim 1, wherein the antibody has an IgG1 isotype or an IgG4 isotype.

7. The method of claim 1, wherein a flow rate through the HIC column has a linear velocity of 100 cm/hr to 300 cm/hr.

8. The method of claim 1 further comprising measuring the presence of viral genomic copies.

9. The method of claim 1 further comprising measuring the presence of viral particles.

10. The method of claim 1 further comprising measuring the presence of both viral genomic copies and viral particles.

11. A method of purifying an antibody from a sample comprising one or more impurities including viral particles, the method comprising the steps of:

providing the sample comprising the antibody produced in a host-cell,

adding a citrate buffer to the sample to produce a loading sample, wherein adding the citrate buffer to the sample modulates adsorption of the viral particles to a hydrophobic interaction chromatography (HIC) column,

adjusting a pH of the sample to a range of from 4.2 to 8.0,

loading the loading sample to a hydrophobic interaction chromatography (HIC) column to produce an HIC treated sample, wherein a concentration of the antibody in the loading sample is from 40 g/L to 200 g/L,

collecting the HIC treated sample,

measuring the presence of viral genomic copies and/or viral particles in the collected HIC treated sample, and

identifying, using a D-Optimal design of experiment generated by a computer algorithm, a significant development factor from a plurality of factors, wherein the D-optimal design of experiment is optimized for removal of viral genomic copies or viral particles.

12. The method of claim 11, wherein the plurality of factors comprises:

the pH of the loading sample,

a type of HIC column,

the concentration of the antibody in the loading sample,

a linear velocity of a flow rate through the HIC column, and

a hydrophobic strength of the HIC column within a range having a lower bound corresponding to a hydrophobic strength of phenyl resin and an upper bound corresponding to a hydrophobic strength of capto phenyl resin.

13. The method of claim 12, wherein the D-Optimal design of experiment further evaluates an isotype of the antibody.

14. The method of claim 11, wherein the antibody is a monoclonal antibody or a bispecific antibody.

15. A method of purifying an antibody from a sample comprising one or more impurities including viral particles, the method comprising the steps of:

providing the sample comprising the antibody produced in a host-cell,

adding a citrate buffer to the sample to produce a buffered sample, wherein a concentration of the citrate buffer is from 10 mM to 200 mM, and wherein adding the citrate buffer to the sample modulates adsorption of the viral particles to a hydrophobic interaction chromatography (HIC) column,

adjusting a pH of the buffered sample to a range of from 4.2 to 8.0 by adjusting an amount of citrate buffer in the buffered sample to produce a loading sample,

loading the loading sample to a hydrophobic interaction chromatography (HIC) column to produce an HIC treated sample, wherein a concentration of the sample is from 40 g/L to 200 g/L,

collecting the HIC treated sample,

measuring the presence of viral genomic copies and/or viral particles in the collected HIC treated sample, and

identifying, using a D-Optimal design of experiment generated by a computer algorithm, a significant development factor from a plurality of factors, wherein the D-optimal design of experiment is optimized for removal of viral genomic copies or viral particles.

16. The method of claim 15, wherein the D-Optimal design of experiment evaluates the following factors:

the pH of the loading sample,

a concentration of the citrate buffer in the buffered sample,

a type of HIC column,

the concentration of the antibody in the loading sample,

a linear velocity of a flow rate through the HIC column, and

a hydrophobic strength of the HIC column within a range having a lower bound corresponding to a hydrophobic strength of phenyl resin and an upper bound corresponding to a hydrophobic strength of capto phenyl resin.

17. The method of claim 15, wherein the antibody is a monoclonal antibody or a bispecific antibody.

18. The method of claim 16, wherein the D-Optimal design of experiment further evaluates:

an isotype of the antibody.

19. The method of claim 11, wherein the HIC column comprises phenyl resin or capto phenyl resin.

20. The method of claim 15, wherein the HIC column comprises phenyl resin or capto phenyl resin.

21. The method of claim 1, wherein measuring a presence of viral genomic copies or viral particles in the collected HIC treated sample comprises an infectivity assay, a quantitative PCR assay, or a combination thereof.

22. The method of claim 11, wherein measuring a presence of viral genomic copies or viral particles in the collected HIC treated sample comprises an infectivity assay, a quantitative PCR assay, or a combination thereof.

23. The method of claim 15, wherein measuring a presence of viral genomic copies or viral particles in the collected HIC treated sample comprises an infectivity assay, a quantitative PCR assay, or a combination thereof.

24. The method of claim 11, wherein a flow rate through the HIC column has a linear velocity of 100 cm/hr to 300 cm/hr.