What is claimed:

1. A method for purifying a protein, from a solution containing at least one contaminant by superantigen chromatography comprising: a) adsorbing the protein to the superantigen immobilized on a solid support; b) removing the at least one contaminant by contacting the immobilized superantigen containing the adsorbed protein with a first wash buffer comprising an aliphatic carboxylate, wherein said aliphatic carboxylate comprises a 6-12 carbon backbone; and c) eluting the protein from the superantigen immobilized on the solid support.

2. The method according to claim 1 wherein the superantigen is selected from the group consisting of Protein A, Protein G, and Protein L.

3. The method according to any preceding claim wherein the aliphatic carboxylate is selected from the group consisting of caproate, heptanoate, caprylate, decanoate, and dodecanoate and wherein the source of the aliphatic carboxylate is selected from the group consisting of an aliphatic carboxylic acid, a sodium salt of an aliphatic carboxylic acid, and a potassium salt of an aliphatic carboxylic acid.

4. The method according to any preceding claim wherein the wash buffer comprises 10 mM to 125 mM sodium caprylate, 1 mM to 30 mM sodium decanoate, or 1 mM to 30 mM sodium dodecanoate.

5. The method according to any preceding claim wherein the wash buffer further comprises 100 mM to 400 mM sodium acetate, such as 300 mM sodium acetate.

6. The method according to any preceding claim wherein the at least one contaminant is a host cell protein or host cell DNA.

7. The method according to claim 6 wherein the host cell is selected from the group consisting of CHO cells, NS0 cells, Sp2/0 cells, COS cells, K562 cells, BHK cells, PER.C6 cells, HEK cells, *E.coli* cells, fungal cells or yeast cells.

8. The method according to any preceding claim wherein the protein is selected from the group consisting of soluble receptor, antibody, antibody fragment, immunoglobulin single variable domain, Fab, F(ab')2, Fv, disulphide linked Fv, scFv, closed conformation multispecific antibody, disulphide-linked scFv, or diabody.

9. The method of any preceding claim wherein the wash buffer further comprises an organic acid, an alkaline metal or ammonium salt of the conjugate base of the organic acid, and an organic base and wherein the wash buffer is made without the addition of NaCl.

10. The method of claim 9 wherein the organic acid is selected from the group consisting of formic acid, acetic acid, lactic acid, citric acid, malic acid, maleic acid, glycine, glycylclycine, succinic acid, TES (2-{[tris(hydroxymethyl)methyl]amino}ethanesulfonic acid), MOPS (3-(N-morpholino)propanesulfonic acid), PIPES (piperazine-N,N′-bis(2-ethanesulfonic acid)), and MES (2-(N-morpholino)ethanesulfonic acid) and wherein the organic base is selected from the group consisting of tris base, Bis-tris, Bis-tris-Propane, Bicine (N,N-bis(2-hydroxyethyl)glycine), HEPES (4-2-hydroxyethyl-1-piperazineethanesulfonic acid), TAPS (3-{[tris(hydroxymethyl)methyl]amino}propanesulfonic acid), and Tricine (N-tris(hydroxymethyl)methylglycine).

11. The method claim 9 or claim 10 wherein the conjugate base of the organic acid is the sodium, potassium, or ammonium salt of the conjugate base of the organic acid.

12. A method for purifying a protein from a contaminated solution thereof by Protein A or Protein L chromatography comprising:

(a) equilibrating a Protein A immobilized on a solid phase with a Protein A equilibration buffer or a Protein L immobilized on a solid phase with a Protein L equilibration buffer;

(b) adsorbing the protein from the contaminated solution to the Protein A or Protein L immobilized on the solid phase;

(c) removing at least one contaminant by washing the solid phase with a first Protein A or Protein L wash buffer comprising 50 mM to 55 mM tris base, 45 mM to 50

mM acetic acid, at least one aliphatic carboxylate, at pH 7.2, wherein the aliphatic carboxylate is selected from the group consisting of 100 mM sodium caprylate, 20 mM sodium decanoate, and 20 mM sodium dodecanoate; and

(d) recovering the protein from the solid phase with a Protein A or Protein L elution buffer, wherein all the buffers are made without the addition of NaCl.

13. The method of claim 12, further comprising the following step after step (c) and before step (d): removing contaminants by washing the solid phase with a second Protein A wash buffer comprising 55 mM tris base, 45 mM acetic acid, at pH 7.2, wherein the second Protein A wash buffer is made without the addition of NaCl.

14. The method of claim 12 or claim 13, further comprising the following steps after step (d): (e) titrating the solution containing the recovered protein to pH 3.0 with 30 mM acetic acid, 100 mM HCl; (f) allowing the solution of step (e) to remain at pH 3.0 for 30 to 60 minutes; and (g) adjusting the pH of the solution of step (f) to pH 7.5 with 1 M tris and optionally filtering the solution produced by step (g).

15. The method of claim 12 or 14, wherein the Protein A or Protein L wash buffer further comprises 1 mM to 500 mM sodium acetate, such as 300 mM sodium acetate.

What is claimed:

1. A method for purifying a protein, from a solution containing at least one contaminant by superantigen chromatography comprising: a) adsorbing the protein to the superantigen immobilized on a solid support; b) removing the at least one contaminant by contacting the immobilized superantigen containing the adsorbed protein with a first wash buffer comprising an aliphatic carboxylate, wherein said aliphatic carboxylate comprises a 6-12 carbon backbone; and c) eluting the protein from the superantigen immobilized on the solid support.

2. The method according to claim 1 wherein the superantigen is selected from the group consisting of Protein A, Protein G, and Protein L.

3. The method according to any preceding claim wherein the aliphatic carboxylate is selected from the group consisting of caproate, heptanoate, caprylate, decanoate, and dodecanoate.

4. The method according to any preceding claim wherein the source of the aliphatic carboxylate is selected from the group consisting of an aliphatic carboxylic acid, a sodium salt of an aliphatic carboxylic acid, and a potassium salt of an aliphatic carboxylic acid.

5. The method according to any preceding claim wherein the wash buffer comprises sodium caprylate, sodium decanoate, or sodium dodecanoate.

6. The method according to any preceding claim wherein the wash buffer comprises about 10 mM to about 125 mM sodium caprylate, about 1 mM to about 30 mM sodium decanoate, or about 1 mM to about 30 mM sodium dodecanoate.

7. The method according to any preceding claim wherein the wash buffer comprises about 100 mM sodium caprylate, about 20 mM sodium decanoate, or about 20 mM sodium dodecanoate.

8. The method according to any preceding claim wherein the wash buffer further comprises about 100 mM to about 400 mM sodium acetate.

9. The method according to any preceding claim wherein the wash buffer comprises about 300 mM sodium acetate.

10. The method according to any preceding claim wherein the at least one contaminant is a host cell protein or host cell DNA.

11. The method according to claim 10 wherein the host cell is a mammalian cell selected from the group consisting of CHO cells, NS0 cells, Sp2/0 cells, COS cells, K562 cells, BHK cells, PER.C6 cells, and HEK cells,

12. The method according to claim 10 wherein the host cell is selected from the group consisting of *E.coli*, fungal cells or yeast cells.

13. The method according to any preceding claim wherein the solid support is selected from the group consisting of agarose, polymethacrylate, cross-linked poly(styrene-divinylbenzene), and agarose with dextran surface extender.

14. The method according to any preceding claim wherein the protein is selected from the group consisting of soluble receptor, antibody, antibody fragment, immunoglobulin single variable domain, Fab, F(ab')2, Fv, disulphide linked Fv, scFv, closed conformation multispecific antibody, disulphide-linked scFv, or diabody.

15. The method according to any preceding claim wherein the solution is a cell culture filtrate.

16. The method according to any preceding claim wherein after step c) the relative fold reduction of host cell proteins is about 2 to about 10 fold.

17. The method according to claim 16 wherein after step c) the relative fold reduction of host cell proteins is about 5 fold.

18. The method according to any preceding claim wherein after step c) the relative fold reduction of DNA is about 2 to about 150 fold.

19. The method according to claim 18 wherein after step c) the relative fold reduction of DNA is about 100 fold.

20. The method of any preceding claim wherein after step c) the amount of host cell protein or DNA is less than about 5000 ppm, 4000 ppm, 3000 ppm, 2,500 ppm, 2000 ppm, 1500 ppm, 1000 ppm, about 900 ppm, about 800 ppm, about 700 ppm, about 600 ppm, about 500 ppm, about 400 ppm, about 300 ppm, about 200 ppm, about 100 ppm, about 90 ppm, about 80 ppm, about 70 ppm, about 60 ppm, or about 50 ppm.

21..The method of any preceding claim wherein after step c) the protein is not subjected to any further affinity chromatography.

22. The method of any preceding claim wherein the wash buffer further comprises an organic acid, an alkaline metal or ammonium salt of the conjugate base of the organic acid, and an organic base and wherein the wash buffer is made without the addition of NaCl.

23. The method of claim 22 wherein the organic acid is selected from the group consisting of formic acid, acetic acid, lactic acid, citric acid, malic acid, maleic acid, glycine, glycylclycine, succinic acid, TES (2-{[tris(hydroxymethyl)methyl]amino}ethanesulfonic acid), MOPS (3-(N-morpholino)propanesulfonic acid), PIPES (piperazine-N,N′-bis(2-ethanesulfonic acid)), and MES (2-(N-morpholino)ethanesulfonic acid).

24. The method of claim 22 wherein the organic base is selected from the group consisting of tris base, Bis-tris, Bis-tris-Propane, Bicine (N,N-bis(2-hydroxyethyl)glycine), HEPES (4-2-hydroxyethyl-1-piperazineethanesulfonic acid), TAPS (3-{[tris(hydroxymethyl)methyl]amino}propanesulfonic acid), and Tricine (N-tris(hydroxymethyl)methylglycine).

25. The method of any one of claims 22-24 wherein the conjugate base of the organic acid is the sodium, potassium, or ammonium salt of the conjugate base of the organic acid.

26. The method of any one of claims 22-25 wherein the organic acid is acetic acid.

27. The method of any one of claims 22-26 wherein the organic base is tris base.

28. The method of any one of claims 22-27 wherein the organic acid is acetic acid and the conjugate base of acetic acid is the sodium salt.

29. A method for purifying a protein from a contaminated solution thereof by Protein A chromatography comprising:

(a) equilibrating a Protein A immobilized on a solid phase with a Protein A equilibration buffer;

(b) adsorbing the protein from the contaminated solution to the Protein A immobilized on the solid phase;

(c) removing at least one contaminant by washing the solid phase with a first Protein A wash buffer comprising about 50 mM to about 55 mM tris base, about 45 mM to about 55 mM acetic acid, at least one aliphatic carboxylate, at about pH 7.2 to about 8.0, wherein the aliphatic carboxylate is selected from the group consisting of about 100 mM sodium caprylate, about 20 mM sodium decanoate, and about 20 mM sodium dodecanoate; and

(d) recovering the protein from the solid phase with a Protein A elution buffer, wherein all the buffers are made without the addition of NaCl.

30. The method of claim 29, wherein the equilibration buffer comprises about 50 mM to about 55 mM tris base, about 45 mM to about 50 mM acetic acid, at about pH 7.2; and the elution buffer comprises 1.8 mM sodium acetate and about 28.2 mM to about 300 mM acetic acid, at about pH 2.4 to about pH 3.6.

31. The method of claim 29 or 30, further comprising the following step after step (c) and before step (d): removing contaminants by washing the solid phase with a second Protein A wash buffer comprising about 50-55 mM tris base, about 45-50 mM acetic acid, at about pH 7.2, wherein the second Protein A wash buffer is made without the addition of NaCl.

32. The method of any one of claims 29-31, further comprising the following steps after step (d): (e) titrating the solution containing the recovered protein to about pH 3.0 with 30 mM acetic acid, 100 mM HCl; (f) allowing the solution of step (e) to remain at about pH 3.0 for about 30 to about 60 minutes; and (g) adjusting the pH of the solution of step (f) to about pH 7.5 with 1 M tris.

33. The method of claim 32 further comprising filtering the solution produced by step (g).

34. A method for purifying a protein from a contaminated solution thereof by Protein L chromatography comprising:

(a) equilibrating a Protein L immobilized on a solid phase with a Protein L equilibration buffer;

(b) adsorbing the protein from the contaminated solution to the Protein L immobilized on the solid phase;

(c) removing at least one contaminant by washing the solid phase with a first Protein L wash buffer comprising about 50 mM to about 55 mM tris base, about 45 mM to about 50 mM acetic acid, at least one aliphatic carboxylate, at about pH 7.), wherein the aliphatic carboxylate is selected from the group consisting of about 100 mM sodium caprylate, about 20 mM sodium decanoate, and about 20 mM sodium dodecanoate; and

(d) recovering the protein from the solid phase with a Protein L elution buffer, wherein all the buffers are made without the addition of NaCl.

35. The method of claim 34, wherein the equilibration buffer comprises about 50 mM to about 55 mM tris base, about 45 mM to about 50 mM acetic acid, at about pH 7.2; and the elution buffer comprises about 1.8 mM sodium acetate and about 28.2 mM to about 300 mM acetic acid, at about pH 2.4 to about pH 3.6.

36. The method of claim 34 or 35, further comprising the following step after step (c) and before step (d): removing contaminants by washing the solid phase with a second Protein L wash buffer comprising 55 mM tris base, 45 mM acetic acid, at about pH 7.2, wherein the second Protein L wash buffer is made without the addition of NaCl.

37. The method of any one of claims 34-36, further comprising the following steps after step (d): (e) titrating the solution containing the recovered protein to about pH 3.0 with 30 mM acetic acid, 100 mM HCl; (f) allowing the solution of step (e) to remain at about pH 3.0 for about 30 to about 60 minutes; and (g) adjusting the pH of the solution of step (f) to about pH 7.5 with 1 M tris.

38. The method of claim 37 further comprising filtering the solution produced by step (g).

39. The method of claim 29 or 34, wherein the Protein A or Protein L wash buffer further comprises about 1 mM to about 500 mM sodium acetate.

40. The method of claim 39, wherein the Protein A or Protein L wash buffer comprises about 300 mM sodium acetate.