WE CLAIM:

1. A method of selection, evolution and expression of an antibody, or antibody fragment, in a eukaryotic cell production host; the method comprising:
    a. generating an anti-antigen antibody library in a eukaryotic cell production host with antibody cell surface display;
    b. screening the library for at least one predetermined property, characteristic or activity;
    c. selecting a template antibody from the library;
    d. evolving the template antibody to produce a set of mutant antibodies in the eukaryotic cell production host with antibody cell surface display;
    e. screening the mutant antibodies for the at least one predetermined property, characteristic or activity;
    f. selecting an up-mutant antibody from the set of mutant antibodies based upon optimization of the at least one predetermined property, characteristic or activity when compared to the template antibody; and
    g. expressing the up-mutant antibody in the same eukaryotic cell production host as in the generating step.

2. The method of claim 1 wherein the eukaryotic cell production host is selected from a member of the group consisting of 3T3 mouse fibroblast cells; BHK21 Syrian hamster fibroblast cells; MDCK, dog epithelial cells; Hela human epithelial cells; PtK1 rat kangaroo epithelial cells; SP2/0 mouse plasma cells; and NS0 mouse mouse plasma cells; HEK 293 human embryonic kidney cells; COS monkey kidney cells; CHO, CHO-S Chinese hamster ovary cells; R1 mouse embryonic cells; E14.1 mouse embryonic cells; H1 human embryonic cells; H9 human embryonic cells; PER C.6, human embryonic cells; S. cerevisiae yeast cells; and picchia yeast cells.

3. The method of claim 2 wherein the mammalian system is CHO-S or HEK293.

4. The method of claim 1 wherein the screening steps comprise fluorescence-activated cell sorting (FACS).

5. The method of claim 1 wherein the evolving step comprises producing a set of mutant antibodies formed from the template antibody having m complementary determining regions (CDR), wherein m is an integer 1 to 6, each said CDR comprising n amino acid residues, the method comprising:

   a. generating m x n separate sets of antibodies, each set comprising member antibodies having X number of different predetermined amino acid residues at a single predetermined position of the CDR; wherein each set of antibodies differs in the single predetermined position; and the number of different member antibodies generated is equivalent to m x n x X.

6. The method of claim 5 wherein m is 6.

7. The method of claim 1 wherein the antibody fragment is selected from a heavy chain, light chain, variable domain, constant domain, hypervariable region, complementarity determining region 1 (CDR1), complementarity determining region 2 (CDR2), and complementarity determining region 3 (CDR3).

8. The method of claim 1 wherein the evolving step (d) comprises

   h. generating n-1 separate sets of mutant polypeptides from the template antibody, each set comprising member polypeptides having X number of different predetermined amino acid residues at a single predetermined position of the polypeptide; wherein each set of polypeptides differs in the single predetermined position; and the number of different member polypeptides generated is equivalent to [n-1] x X;

and wherein the screening step (e) comprises

   i. assaying each member polypeptide for at least one predetermined property, characteristic or activity;

j. identifying any change in said property, characteristic or activity of the member polypeptide relative to the template polypeptide;

k. creating a functional map wherein the functional map is used to identify positions and mutations in the mutant polypeptide which result in an up-mutant and/or a silent mutation compared to the template polypeptide.

9. The method of claim 8 wherein 1 wherein X represents the 19 naturally occurring amino acid residues not present in a given position of the template polypeptide.

10. The method of claim 9 wherein said generating step comprises:

i. subjecting a codon-containing polynucleotide encoding for said template polypeptide to polymerase-based amplification using a 64-fold degenerate oligonucleotide for each codon to be mutagenized, wherein each of said 64-fold degenerate oligonucleotides is comprised of a first homologous sequence and a degenerate N,N,N triplet sequence, so as to generate a set of progeny polynucleotides; and

ii. subjecting said set of progeny polynucleotides to clonal amplification such that polypeptides encoded by the progeny polynucleotides are expressed.

11. The method of claim 8 wherein the functional map is used to identify one or more of the group consisting of (a) positions and mutations which do not affect the activity of the mutant polypeptide compared to the template polypeptide; (b) fully mutable sites compared to the template polypeptide; and (c) positions and mutations which result in an up-mutant compared to the template polypeptide.

12. The method of claim 1 wherein the predetermined property, characteristic or activity is selected from reduction of protein-protein aggregation, enhancement of protein stability, increased protein solubility, introduction of glycosylation sites, introduction of conjugation sites, reduction of immunogenicity, enhancement of protein expression, increase in antigen

affinity, decrease in antigen affinity, change in binding affinity, change in immunogenicity, or enhancement of specificity.

13. A method of evolution and expression of an antibody in a mammalian cell production host; the method comprising:
    a. selecting a template antibody;
    b. evolving the template antibody to produce a set of mutant antibodies in a mammalian cell production host with antibody cell surface display;
    c. screening the mutant antibodies for the at least one predetermined property, characteristic or activity;
    d. selecting an up-mutant antibody from the set of mutant antibodies based upon optimization of the at least one predetermined property, characteristic or activity compared to the template antibody; and
    e. expressing the up-mutant antibody in the same mammalian cell production host as in step b.

14. The method of claim 13 wherein the mammalian cell production host is selected from a member of the group consisting of 3T3 mouse fibroblast cells; BHK21 Syrian hamster fibroblast cells; MDCK, dog epithelial cells; Hela human epithelial cells; PtK1 rat kangaroo epithelial cells; SP2/0 mouse plasma cells; and NS0 mouse mouse plasma cells; HEK 293 human embryonic kidney cells; COS monkey kidney cells; CHO, CHO-S Chinese hamster ovary cells; R1 mouse embryonic cells; E14.1 mouse embryonic cells; H1 human embryonic cells; H9 human embryonic cells; and PER C.6, human embryonic cells.

15. The method of claim 14 wherein the mammalian system is CHO-S or HEK293.

16. The method of claim 1 wherein the screening steps comprise fluorescence-activated cell sorting (FACS).

17. The method of claim 1, wherein step (a) is preceded by a step comprising:
selecting an antigen.

18. The method of claim 1, wherein the anti-antigen antibody library is a humanized anti-antigen antibody library.

19. A method of evolution and expression of a protein in a eukaryotic cell production host; the method comprising:
a. selecting a template antibody;
b. evolving the template antibody to produce a set of mutant antibodies in a eukaryotic cell production host;
c. screening the mutant antibodies for at least one predetermined property, characteristic or activity;
d. selecting an up-mutant antibody from the set of mutant antibodies based upon optimization of the at least one predetermined property, characteristic or activity compared to the template antibody; and
e. expressing the up-mutant antibody in the same eukaryotic cell production host as in step b for any commercial scale.

20. The method of claim 1 wherein the mammalian cell production host is selected from CHOK1SV or NSO host cell lines.

21. The method of claim 13 wherein the screening step comprises
creating a functional map wherein the functional map is used to identify positions and mutations in the mutant polypeptide which result in an up-mutant and/or a silent mutation compared to the template polypeptide.

22. A method of evolution and manufacturing of a human protein in a cell production host; the method comprising:
a. generating a human protein library in a cell production host selected from one of the group consisting of a bacterial or eukaryotic production host;

b. screening the library for at least one predetermined property, characteristic or activity;
c. selecting a template human protein from the library based upon the at least one predetermined property, characteristic or activity;
d. evolving the template human protein to produce a set of mutant human proteins in the cell production host;
e. screening the set of mutant human proteins for the at least one predetermined property, characteristic or activity and screening for modified expression;
f. selecting an up-mutant human protein from the set of mutant human proteins based upon (1) optimization of the at least one predetermined property, characteristic or activity and (2) modified expression when compared to the template human protein; and
g. manufacturing the human protein comprising expressing the up-mutant human protein in the same production host as in the generating step (a).

23. The method of claim 22 wherein the modified expression is improved expression.

24. The method of claim 23 wherein the evolving step comprises one of comprehensive positional evolution (CPE); comprehensive positional insertion evolution (CPI); comprehensive positional deletion evolution (CPD); comprehensive positional evolution (CPE) followed by combinatorial protein synthesis (CPS); comprehensive positional deletion evolution (CPD) followed by combinatorial protein synthesis (CPS); or comprehensive positional deletion evolution (CPD) followed by combinatorial protein synthesis (CPS).

25. The method of claim 23 wherein the human protein is an antibody.

26. The method of claim 25 wherein the antibody is a full length antibody.

27. The method of claim 26 wherein the at least one predetermined property, characteristic or activity in screening step (e) comprises one or more of (1) screening for a silent mutation and (2) screening for a missense mutation; compared to the template antibody.

28. The method of claim 26 wherein one or more of the group selected from Fc and Fv; framework; and one or more CDRs are modified in the up-mutant human antibody compared to the template human antibody.

29. The method of claim 22 wherein the screening step (e) comprises screening the set of mutant human proteins for the at least one predetermined property, characteristic or activity and screening for modified expression simultaneously.

30. The method of claim 22 wherein the human protein is selected from an enzyme cytokine, receptor, DNA binding protein, chelating agent or hormone.

31. The method of claim 22 wherein the cell production host is a eukaryotic production host and the evolving step comprises evolving the template human protein to produce a set of mutant human proteins in the eukaryotic cell production host with cell surface display.

32. The method of claim 26 wherein the cell production host is a eukaryotic production host and the evolving step comprises evolving the template human protein to produce a set of mutant human proteins in the eukaryotic cell production host with cell surface display.

33. A method of evolution for enhanced expression and manufacturing of a human protein in a eukaryotic cell production host; the method comprising:

a. selecting a template human protein for evolution;
b. evolving the template human protein comprising generation of mutant codons encoding the template human protein to produce a set of mutant human proteins in the production host;

c. screening the set of mutant human proteins for at least one predetermined property, characteristic or activity and screening for enhanced expression when compared to the template human protein;

d. selecting an up-mutant human protein from the set of mutant human proteins based upon (1) retention or optimization of the at least one predetermined property, characteristic or activity and (2) enhanced expression when compared to the template human protein; and

e. manufacturing the up-mutant human protein comprising expressing the up-mutant human protein in the same production host as in the evolving step.

34. The method of claim 33 wherein the mutant codons of the up-mutant human protein result in at least one silent mutation and/or missense mutation.

35. The method of claim 34 wherein the mutant codons of the up-mutant human protein result in at least one silent mutation.

36. The method of claim 35 wherein the template human protein is an approved ethical protein therapeutic drug, and the up-mutant human protein is a biosimilar.

37. The method of claim 33, wherein the selecting step (d) comprises selecting an up-mutant human protein from the set of mutant human proteins based upon (1) optimization of the at least one predetermined property, characteristic or activity and (2) enhanced expression when compared to the template human protein.

38. A method of identifying and producing a target human protein, the method comprising:

a. generating an human protein library in a eukaryotic cell production host with protein cell surface display;

b. screening the library for at least one predetermined property, characteristic or activity;

c. identifying a target human protein from the library based upon the at least one predetermined property, characteristic or activity; and

d. expressing the target human protein in the same eukaryotic cell production host as in the generating step to produce a target human protein.

39. The method of claim 38 wherein the target human protein is an antibody.

40. The method of claim 39 wherein the antibody is a full length antibody.

41. A method of evolution of a human protein in a manufacturing host, the method comprising:

a. mutating a template human protein to produce a set of mutant human proteins in a manufacturing host; and

b. screening the set of mutant progeny proteins for at least one predetermined property, characteristic or activity.

42. The method of claim 41 further comprising:

c. selecting an up-mutant human protein from the set of mutant human proteins based upon the at least one predetermined property, characteristic or activity.

43. The method of claim 42, the method further comprising:

d. manufacturing the up-mutant human protein comprising expressing the up-mutant human protein in the same production host as in the mutating step (a).

44. The method of claim 42 wherein the selecting step (c) further comprises selecting an up-mutant human protein from the set of mutant human proteins based upon (1) optimization of the at least one predetermined property, characteristic or activity when compared to the template human

protein, and (2) modified expression when compared to the template human protein.

45. The method of claim 44 wherein the modified expression is enhanced expression.

46. A method of evolution and manufacturing of a human protein in a cell manufacturing host; the method comprising:

a. mutating a template human protein to produce a set of mutant human proteins in a manufacturing host;

b. screening the set of mutant human proteins for at least one predetermined property, characteristic or activity and screening for modified expression;

c. selecting an up-mutant human protein from the set of mutant human proteins based upon (1) optimization of the at least one predetermined property, characteristic or activity, and (2) modified expression when compared to the template human protein; and

d. manufacturing the human protein comprising expressing the up-mutant human protein in the same manufacturing host as in step a.

47. A method of evolution for enhanced expression and manufacturing of a human protein in a eukaryotic cell production host; the method comprising:

a. mutating a template human protein comprising generation of mutant codons encoding the template human protein to produce a set of mutant human proteins in a manufacturing host;

b. screening the set of mutant human proteins for at least one predetermined property, characteristic or activity and screening for enhanced expression when compared to the template human protein;

c. selecting an up-mutant human protein from the set of mutant human proteins based upon (1) retention or optimization of the at least one predetermined property, characteristic or activity and (2) enhanced expression when compared to the template human protein; and

d. manufacturing the up-mutant human protein in the same manufacturing host as in step (a).

48. The method of claim 47 wherein the screening step (b) comprises screening the set of mutant human proteins for the at least one predetermined property, characteristic or activity and screening for enhanced expression simultaneously.

WE CLAIM:

1. A method of evolution and expression of an antibody in an eukaryotic cell production host, the method comprising:
    a. selecting a template antibody;
    b. evolving the template antibody to enable production of a set of mutant antibodies in the host using eukaryotic cell surface display of the mutant antibodies;
    c. screening the mutant antibodies for at least one predetermined property, characteristic or activity;
    d. selecting an up-mutant antibody from the set of mutant antibodies based upon optimization of the at least one predetermined property, characteristic or activity as compared to a same property, characteristic or activity of the template antibody; and
    e. expressing the up-mutant antibody in the same host as in step b.

2. The method of claim 1, wherein step a is preceded by steps comprising:
    a1. generating an anti-antigen antibody library in the eukaryotic cell production host using eukaryotic cell surface display of antibodies; and
    a2. screening the library for the at least one predetermined property, characteristic or activity; and
    wherein the template antibody is selected from the library.

3. The method of claim 1 wherein the eukaryotic cell production host is selected from 3T3 mouse fibroblast cells; BHK21 Syrian hamster fibroblast cells; MDCK, dog epithelial cells; Hela human epithelial cells; PtK1 rat kangaroo epithelial cells; SP2/0 mouse plasma cells; and NS0 mouse mouse plasma cells; HEK 293 human embryonic kidney cells; COS monkey kidney cells; CHO, CHO-S Chinese hamster ovary cells; R1 mouse embryonic cells; E14.1 mouse embryonic cells; H1 human embryonic cells; H9 human embryonic cells; PER C.6, human embryonic cells; S. cerevisiae yeast cells; and picchia yeast cells.

4. The method of claim 2, wherein the screening steps comprise fluorescence-activated cell sorting.

5. The method of claim 1 wherein the evolving step comprises enabling production of a set of mutant antibodies formed from the template antibody having m

complementarity determining regions, wherein m is an integer 1 to 6, each said complementarity determining region comprising n amino acid residues, the method comprising:

a. generating m x n separate sets of antibodies, each set comprising member antibodies having X number of different predetermined amino acid residues at a single predetermined position of the complementarity determining regions; wherein each set of antibodies differs in the single predetermined position; and the number of different member antibodies generated is equivalent to m x n x X.

6. The method of claim 5 wherein m is 6.

7. The method of claim 1 wherein the antibody is an antibody fragment selected from a heavy chain, light chain, variable domain, constant domain, hypervariable region, complementarity determining region 1, complementarity determining region 2, and complementarity determining region 3.

8. The method of claim 1 wherein the evolving step b comprises

h. generating n-1 separate sets of mutant polypeptides from the template antibody, each set comprising member polypeptides having X number of different predetermined amino acid residues at a single predetermined position of the polypeptide; wherein each set of polypeptides differs in the single predetermined position; and the number of different member polypeptides generated is equivalent to [n-1] x X;

and wherein the screening step c comprises

i. assaying each member polypeptide for the at least one predetermined property, characteristic or activity;

j. identifying any change in said property, characteristic or activity of the member polypeptide relative to the template polypeptide; and

k. creating a functional map wherein the functional map is used to identify positions and mutations in the mutant polypeptide which result in an up-mutant and/or a silent mutation compared to the template polypeptide.

9. The method of claim 8 wherein X represents the 19 naturally occurring amino acid residues not present in a given position of the template polypeptide.

10. The method of claim 9 wherein said generating step comprises:

i. subjecting a codon-containing polynucleotide encoding for said template polypeptide to polymerase-based amplification using a 64-fold degenerate oligonucleotide for each codon to be mutagenized, wherein each of said 64-fold degenerate oligonucleotides is comprised of a first homologous sequence and a degenerate N,N,N triplet sequence, so as to generate a set of progeny polynucleotides; and

ii. subjecting said set of progeny polynucleotides to clonal amplification such that polypeptides encoded by the progeny polynucleotides are expressed.

11. The method of claim 8 wherein the functional map is used to identify one or more of (a) positions and mutations which do not affect the activity of the mutant polypeptide compared to the template polypeptide; (b) fully mutable sites compared to the template polypeptide; and (c) positions and mutations which result in an up-mutant compared to the template polypeptide.

12. The method of claim 1 wherein the predetermined property, characteristic or activity is selected from reduction of protein-protein aggregation, enhancement of protein stability, increased protein solubility, introduction of glycosylation sites, introduction of conjugation sites, reduction of immunogenicity, enhancement of protein expression, increase in antigen affinity, decrease in antigen affinity, change in binding affinity, change in immunogenicity, and enhancement of specificity.

13. The method of claim 1, wherein the eukaryotic cell production host is a mammalian cell production host.

14. The method of claim 13 wherein the mammalian cell production host is selected from 3T3 mouse fibroblast cells; BHK21 Syrian hamster fibroblast cells; MDCK, dog epithelial cells; Hela human epithelial cells; PtK1 rat kangaroo epithelial cells; SP2/0 mouse plasma cells; and NS0 mouse mouse plasma cells; HEK 293 human embryonic kidney cells; COS monkey kidney cells; CHO, CHO-S Chinese hamster ovary cells; R1 mouse embryonic cells; E14.1 mouse embryonic cells; H1 human embryonic cells; H9 human embryonic cells; and PER C.6, human embryonic cells, CHOK1SV and NSO host cell lines.

15. The method of any one of claims 3 and 14, wherein the mammalian cell production host or the eukaryotic cell production host is selected from CHO-S or HEK293.

16. The method of claim 2, wherein step a1 is preceded by a step comprising:

selecting an antigen.

17. The method of claim 2, wherein the anti-antigen antibody library is a humanized anti-antigen antibody library.

18. The method of claim 1, wherein the eukaryotic cell production host for both of the evolving and expression steps is CHO.

19. The method of claim 1, wherein the antibody is a full-length antibody.

20. The method of claim 1, wherein the expressing step comprises manufacturing the up-mutant antibody.

21. The method of claim 13 wherein the screening step comprises

creating a functional map wherein the functional map is used to identify positions and mutations in the mutant polypeptide which result in an up-mutant and/or a silent mutation compared to the template polypeptide.