separate sets of polypeptides, 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 as confirmed by sequencing or other technique; assaying each set for at least one and preferably two predetermined properties, characteristics or activities; (b) for each member identifying any change in said property, characteristic or activity relative to the template polypeptide; and (c) creating a functional map reflecting such changes. The number of different member polypeptides generated is equivalent to n x X.

[0007] In the alternative, the method comprises generating a single population comprising the sets of mutated polypeptides. In this example, the entire population is sequenced, tested for expression and screened for a function, the individual members identified, and, preferably, the functional map generated.

[0008] Typically, where each naturally occurring amino acid is used, X will be 19 (representing the 20 naturally occurring amino acid residues and excluding the particular residue present in a given position of the template polypeptide). However, any subset of amino acids may be used throughout, and each set of polypeptides may be substituted with all or a subset of the total X used for the entire population.

[0009] Any mutational or synthetic means may be used to generate the set of mutants. In one example, the generation of polypeptides comprises (i) subjecting a codon-containing polynucleotide encoding for the template polypeptide to polymerase-based amplification using a 63-fold degenerate oligonucleotide for each codon to be mutagenized, wherein each of the 63-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 the set of progeny polynucleotides to clonal amplification such that polypeptides encoded by the progeny polynucleotides are cloned, sequenced, expressed and screened.

[0010] In one example, the entire polypeptide is subjected to comprehensive mutagenesis. In another example, one or more regions are selected for comprehensive mutagenesis. In such case, n represents a subset or region of the template polypeptide. For example, where the polypeptide is an antibody, the entire antibody or one or more complementarity determining regions (CDRs) of the antibody are subjected to comprehensive mutagenesis.

[0011] The disclosure thus includes methods of mapping a set of mutant antibodies formed from a template antibody having at least one, and preferably six, complementarity determining regions (CDRs), the CDRs together comprising n amino acid residues, the method comprising (a) generating 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 n x X; (b) confirming by sequencing or other method that each member antibody has been made; (c) expressing each member antibody; (d) assaying each set for at least one predetermined property, characteristic or activity; (e) for each member identifying any change in a property, characteristic or activity relative to the template polypeptide; and (f) creating a structural positional map of such changes. For antibodies, the predetermined property, characteristic or property may be binding affinity and/or immunogenicity. As set forth above, in the alternative a single population comprising all sets of mutated antibodies may be generated.

[0012] In addition, provided are methods of producing a set of mutant antibodies formed from a template antibody having at least one complementarity determining region (CDR), the CDR comprising n amino acid residues, the method comprising: (a) generating 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 n x X. In another example, antibody comprises six CDRs, and together the CDRs comprise n amino acid residues.

[0012a] In one aspect, there is provided a method of identifying a cross-species mutant antibody from a template antibody of a species, wherein the template antibody shows an activity on a first target from the species and the template antibody has six complementarity determining regions together comprising n amino acid residues, the method comprising the steps of: i. generating a library of n separate sets mutant antibodies from the template antibody, each set comprising mutant antibodies having X number of different predetermined amino acid residues of a single predetermined position in one of the six complementarity determining regions; wherein each set of mutant antibodies differs in the single predetermined position; and the number of different mutant antibodies generated is equivalent to n x X; ii. selecting mutant antibodies that show the activity on an ortholog of the first target in another species; and iii. screening the selected mutant antibodies for a cross-species mutant antibody that shows the activity on the first target.

[0013] One example of the disclosure includes a functional positional map (EvoMap^{TM}) made by the methods described herein.

[0014] In an additional example, certain residues particularly sensitive to change may be so indicated on the EvoMap^{TM}. Further optimization may be implemented by making additional mutational changes at positions outside of these sensitive positions.

[0015] In a specific example, the mutations generated in the comprehensive evolution techniques of the disclosure are confirmed by sequencing, or some other method.

[0016] Methods of the present disclosure are useful for generating polypeptides as drugs that are safe and effective in humans and also function in animal model systems, such as rat, mouse, rabbit, hamster, guinea pig, monkey, dog, cat, non-human primates and other non-humans, for evaluation.

BRIEF DESCRIPTION OF THE DRAWINGS

[0017] Figure 1 illustrates how comprehensive positional evolution (CPE^{TM}) is used to generate a molecule specific database (EvoMap^{TM}).

[0018] Figure 2 shows an example of a EvoMap^{TM} and how additional optimization may be implemented by Synergy evolution.

CLAIMS

1. A method of identifying a cross-species mutant antibody from a template antibody of a species, wherein the template antibody shows an activity on a first target from the species and the template antibody has six complementarity determining regions together comprising n amino acid residues, the method comprising the steps of:
    i. generating a library of n separate sets mutant antibodies from the template antibody, each set comprising mutant antibodies having X number of different predetermined amino acid residues at a single predetermined position of one of the six complementarity determining regions; wherein each set of mutant antibodies differs in the single predetermined position; and the number of different mutant antibodies generated is equivalent to n x X;
    ii. selecting mutant antibodies that show the activity on an ortholog of the first target in another species; and
    iii. screening the selected mutant antibodies for a cross-species mutant antibody that shows the activity on the first target.

2. The method of claim 1, wherein X is 19 amino acid residues.

3. The method of claim 1, wherein each set of the mutant antibodies is generated by incorporating N,N,N at the predetermined codon position in a polynucleotide that encodes the template antibody.

4. The method of claim 1, wherein the species is human.

5. The method of claim 4, wherein the another species is selected from rat, mouse, rabbit, hamster, guinea pig, monkey, dog, cat and non-human primates.

6. The method of claim 1, wherein the species is a non-human species selected from rat, mouse, rabbit, hamster, guinea pig, monkey, dog, cat and non-human primates.

7. The method of claim 1, wherein the another species is a non-human species selected from rat, mouse, rabbit, hamster, guinea pig, monkey, dog, cat and non-human primates.

8. The method of claim 1, wherein the species and the another species are different and independently selected from rat, mouse, rabbit, hamster, guinea pig, monkey, dog, cat and non-human primates.

9. The method of claim 1, wherein the library of n separate sets of mutant antibodies is expressed in a eukaryotic cell production host.

10. The method of claim 9, wherein the eukaryotic cell production host is a mammalian cell production host.

11. The method of claim 10, 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 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.

12. The method of claim 10, wherein the mammalian cell production host is a GS-NS0 cell or a GS-CHOK1 cell.

13. The method of claim 9, wherein the library of n separate sets of mutant antibodies is expressed using cell surface display in the eukaryotic cell production host.

14. The method of claim 13, wherein the cell surface display is a yeast cell surface display.

15. The method of claim 13, wherein the cell surface display is a mammalian cell surface display.

16. The method of claim 9, further comprising a step of producing the mutant antibody in the same eukaryotic cell production host as was used in the expressing step.

17. The method of claim 3, wherein the predetermined codon position is in a complementarity determining region.