Claims

1. A method of determining a binding interaction between a binding agent and a target comprising

a. contacting a binding agent library with a target to allow formation of binding agent/target complex, wherein each member of said binding agent library is associated with a unique nucleotide sequence and wherein said target is associated with a unique nucleotide sequence;

b. isolating said complexes into compartments so that there is a single complex in one compartment;

c. linking the unique nucleotide sequence(s) associated with the binding agent and target in the complex to form a linked nucleotide sequence, wherein isolation of the isolated complexes is maintained during the linking step;

d. identifying the binding agent(s) present in the complex from the linked nucleotide sequence; and

e. using the linked nucleotide sequence correlating the unique nucleotide sequence of each member of said binding agent library with the binding characteristics of said member.

2. The method as claimed in claim 1 wherein said binding agent library comprises an antibody library.

3. The method of claim 2 wherein said antibody library comprises an antibody display library or a library of antibodies wherein each antibody is labelled with said unique nucleotide sequence.

4. The method of any preceding claim wherein said target comprises a protein.

5. The method of any preceding claim wherein said target comprises a protein display library, wherein each member of said library is associated with a unique nucleotide sequence.

6. The method of claim 54 wherein said protein display library is a cDNA phage display library.

7. The method of claim 4, wherein said protein is within a protein mixture.

8. The method of claim 7, wherein said protein mixture is an enriched protein mixture.

9. The method of claim 7 or claim 8, wherein said protein mixture is enriched for phosphoproteins, membrane proteins, and/or naturally or artificially modified proteins.

10. The method of any preceding claim wherein binding agents which bind to other binding agents are removed from the binding agent library prior to use.

11. The method of any preceding claim wherein the binding agent library is enriched prior to use.

12. The method of claim 1 wherein said compartment is on a solid surface.

13. The method of claim 1 wherein said compartment is an emulsion droplet, diffusion limited or separated compartment.

14. The method of any preceding claim wherein the nucleotide sequence associated with binding agent in the complex is linked to another nucleotide sequence associated with a binding agent in the complex.

15. The method of any one of claims 4 to 13 wherein the nucleotide sequence associated with a binding agent in the complex is linked to the nucleotide sequence associated with the target within the binding agent/target complex.

16 The method of any one of any preceding claim, wherein the binding agent and/or target present within the complex are identified from the linked nucleotide sequence.

17. The method of any preceding claim wherein the (i) binding agent or (ii) binding agent and target present within the complex are identified by sequencing said linked nucleotide sequence.

18. The method of any preceding claim wherein said binding agent/target complex is immobilised following separation.

19. The method of any preceding claim wherein linked nucleotide sequences from more than one complex are combined prior to identifying the binding agent and/or target present. ~~The method of any preceding claim wherein the (i) binding agent or (ii) binding agent and target present within the complex are identified by sequencing said linked nucleotide sequence.~~

20. The method of any preceding claim wherein step (a) of contacting the binding agent library with a target is carried out in the presence and/ or absence of a compound.

21. The method of claims 4-20 wherein said protein is cross-linked to other proteins within a protein mixture.

~~22. The method of any preceding claim wherein separation of the separated complexes is maintained during the linking step.~~

~~23~~22. The method of any preceding claim wherein the separation is carried out by dilution, specific binding, or separation by physical and/or chemical properties of the complexes.

~~24~~23. The method of claims 3-~~23~~ 22 wherein the unique nucleotide sequence associated with each member of the antibody phage library is the nucleotide sequence within the phage encoding the CDR of said antibody.

~~25~~24. The method of claims 6 to ~~23~~ 22 wherein the unique nucleotide sequence associated with each member of the cDNA phage display library is the sequence within the phage encoding the displayed protein.

~~26~~25. The method of any preceding claim wherein linking the nucleotide sequences comprises:

i. Amplifying the nucleotide sequence associated with the binding agent or binding agent and target using at least two pairs of PCR primers to produce at least two sets of amplicons, wherein the primers are designed so that the amplicons generated by a first set of primers comprise a sequence which is complementary to a sequence in the amplicons generated by the second set of primers;

ii. Annealing the sets of amplicons;

iii. Carrying out an amplification reaction to produce a linked nucleotide sequence.

~~27~~26. The method of claim ~~26~~ 25 wherein said amplification is carried out using emulsion PCR amplification.

~~28~~27. The method of claim ~~26~~ 25 or claim ~~27~~ 26 wherein steps i-iii are carried out concurrently.

~~29~~28. The method of any preceding claim wherein the method is repeated and the concentration of the target or binding agent library is varied.

~~30~~29. A kit for carrying out the method of any preceding claim comprising

a) A binding agent library wherein each member of said binding agent library is associated with a unique nucleotide sequence;

b) a set of at least two pairs of primers for linking the nucleotide sequences associated with the binding agent; and optionally instructions for use; and

c) a protein display library wherein each member of said library is associated with a unique nucleotide sequence.