Claims

1. A library of polypeptides, wherein each member of the library comprises a helix-turn-helix scaffold structure of the formula Helix-1 – Li – Helix-2 , wherein

   Helix-1 and Helix-2 comprise a first and second α-helical peptide, wherein each of said α-helical peptides comprises the amino acid sequence

   X1 – X2 – Hy – Var1 –X3 – Hy –Var1 – Var2 – X4 – Hy – Var1 – X5 – Hy – Var1 – Var3 (SEQ ID NO: 1),

   wherein

   X1 is D, T, N, S or P,
   X2 is E, P, Q, W or D,
   X3 is M, A, I, Q or R,
   X4 is A, L, R, M, K or E,
   X5 is M, L, A, W, F or K,
   Hy is any amino-acid residue having a side chain exhibiting a hydrophobicity of greater than 0.62, and
   Var1, Var2 and Var3 are mixtures of the natural occurring amino acids, excluding G, P and C,

   Li is a linker, and

   said first and said second α-helical peptide form an anti-parallel, coiled-coil structure.

2. A library according to claim 1, wherein the linker Li comprises 1 to 30 amino acid residues (SEQ ID NO: 2).

3. A library according to any one of the preceding claims (SEQ ID NO: 3), wherein

   X1 is D,
   X2 is E,
   X3 is Q in Helix-1 and A in Helix-2,
   X4 is E in Helix-1 and K in Helix-2, and
   X5 is K in Helix-1 and M in Helix-2.

4. A library according to any one of the preceding claims, wherein Hy is L, V or I (SEQ ID NO: 4).

5. A library according to any one of the preceding claims (SEQ ID NO: 5), wherein

   Var2 is a mixture of R, Q and E, and
   Var3 is a mixture of R, Q and H.

6. A library according to any one of the preceding claims, wherein the polypeptides of said library are displayed on bacteriophage.

7. A library according to any one of the preceding claims, wherein said library comprises at least $1x10^6$ polypeptide members.

8. The library according to any one of the preceding claims, wherein each member of said library is linked to at least one additional moiety.

9. The library according to claim 8, wherein said additional moiety is an antibody or antibody fragment thereof, a toxin, a cytokine, a reporter enzyme, a moiety being capable of binding a metal ion, a tag suitable for detection and/or purification, a homo- or hetero-association domain, a moiety which increases solubility of a protein, or a moiety which comprises an enzymatic cleavage site.

10. A collection of nucleic acid molecules encoding the library members of any one of the preceding claims.

11. A vector comprising the collection of nucleic acid molecules of claim 10.

12. A recombinant host cell comprising the collection of nucleic acid molecules according to claim 10 or the vector according to claim 11.

13. A method to isolate a polypeptide specific for an antigen, said method comprising the steps of:

    a. contacting the library according to any one of the claims 1-9 with an antigen;
    b. removing those members of the library which do not bind to the antigen; and

c. recovering those members of the library which did bind to the antigen.

14. A polypeptide identified using the method of claim 13.

15. A helix-turn-helix scaffold structure of the formula Helix-1 – Li – Helix-2 linked to an antibody or an antibody fragment, wherein Helix-1 and Helix-2 comprise a first and a second α-helical peptide that form an anti-parallel, coiled-coil structure wherein each of said α-helical peptides comprises the amino acid sequence

X1 – X2 – Hy – Var1 –X3 – Hy –Var1 – Var2 – X4 – Hy – Var1 – X5 – Hy – Var1 – Var3 (SEQ ID NO: 1),

wherein

X1 is D, T, N, S or P,
X2 is E, P, Q, W or D,
X3 is M, A, I, Q or R,
X4 is A, L, R, M, K or E,
X5 is M, L, A, W, F or K,
Hy is any amino-acid residue having a side chain exhibiting a hydrophobicity of greater than 0.62, and
Var1, Var2 and Var3 are mixtures of the natural occurring amino acids, excluding G, P and C, and

Li is a linker.