CLAIMS

1. A method comprising the steps of:

(a) providing a repertoire of polypeptides;

(b) conjugating the polypeptides to a molecular scaffold which binds to the polypeptides at two or more amino acid residues to form a repertoire of polypeptide conjugates;

(c) treating the repertoire with a protease; and

(d) screening the protease treated repertoire for binding against a target, and selecting members of the repertoire which bind to the target.

2. A method according to Claim 1, in which step (c) comprises screening the repertoire for binding against a target and selecting members of the repertoire which bind to the target and step (d) comprises treating the repertoire with a protease.

3. A method comprising the steps of:

(a) providing a repertoire of polypeptides;

(b) conjugating the polypeptides to a molecular scaffold which binds to the polypeptides at two or more amino acid residues to form a repertoire of polypeptide conjugates;

(c) screening the repertoire for binding against a target, and selecting the members of the repertoire which bind to a target;

(c) treating the selected members with a protease; and

(d) further screening the protease treated selected members for binding to the target.

4. A method according to any preceding claim, in which the repertoire of polypeptides is a genetic display system.

5. A method according to Claim 4, in which the genetic display system is phage display.

6. A repertoire of peptide ligands, each comprising a polypeptide comprising two or more reactive groups, covalently linked to a molecular scaffold, and at least one loop which comprises a sequence of amino acids subtended between two of the reactive groups, which repertoire is protease resistant, in which the sequence of amino acids is modified by

(a) amino acid side chain modification or substitution; or

(b) polypeptide backbone modification.

7. A repertoire according to Claim 6, in which each polypeptide comprises three or more reactive groups covalently linked to a molecular scaffold.

8. A repertoire according to Claim 6, in which the backbone modification is selected from the group consisting of introducing, near the site of protease cleavage, a D-amino acid, a reduced peptide bond, and N-methylation.