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(21) International Application Number: PCT/GB98/02630 (22) International Filing Date: 2 September 1998 (02.09.98) (30) Priority Data: 9718455.0 2 September 1997 (02.09.97) GB (71) Applicant (for all designated States except US): ROWETT RESEARCH SERVICES LIMITED [GB/GB]; Greenburn Road, Bucksburn, Aberdeen AB21 9SB (GB). (72) Inventor; and (75) Inventor/Applicant (for US only): MCGREGOR, Duncan [GB/GB]; 6 Balcairn Cottages, Oldmeldrum, Aberdeenshire AB51 0EU (GB). (74) Agent: MURGITROYD & COMPANY; 373 Scotland Street, Glasgow G5 8QA (GB).		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>
(54) Title: CHIMERIC BINDING PEPTIDE LIBRARY SCREENING METHOD (57) Abstract There is described a method of isolating nucleotide sequences encoding target peptides from DNA libraries using DNA binding proteins to link the peptide to the sequence which encodes it. DNA libraries are prepared from cells encoding the protein of interest, or from synthetic DNA, and inserted into, or adjacent to, a DNA binding protein in an expression vector to create a chimeric fusion protein. Incorporation of the vector DNA into a carrier package, during expression of the chimeric fusion protein, results in the production of a peptide display carrier package (PDCP) displaying the DNA-bound fusion protein on the external surface of the carrier package. Employment of affinity purification techniques results in the PDCP particles containing sequences encoding the desired peptide to be selected and the desired nucleotide sequences obtained therefrom.		

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1 **Chimeric binding peptide library screening method**

2
3 The present invention relates generally to methods for
4 screening nucleotide libraries for sequences that
5 encode peptides of interest.

6
7 Isolating an unknown gene which encodes a desired
8 peptide from a recombinant DNA library can be a
9 difficult task. The use of hybridisation probes may
10 facilitate the process, but their use is generally
11 dependent on knowing at least a portion of the sequence
12 of the gene which encodes the protein. When the
13 sequence is not known, DNA libraries can be expressed
14 in an expression vector, and antibodies have been used
15 to screen for plaques or colonies displaying the
16 desired protein antigen. This procedure has been useful
17 in screening small libraries, but rarely occurring
18 sequences which are represented in less than about 1 in
19 10^5 clones (as is the case with rarely occurring cDNA
20 molecules or synthetic peptides) can be easily missed,
21 making screening libraries larger than 10^6 clones at
22 best laborious and difficult. Methods designed to
23 address the isolation of rarely occurring sequences by
24 screening libraries of 10^6 clones have been developed
25 and include phage display methods and LacI fusion phage

1 display, discussed in more detail below.

2

3 Phage display methods. Members of DNA libraries which
4 are fused to the N-terminal end of filamentous
5 bacteriophage pIII and pVIII coat proteins have been
6 expressed from an expression vector resulting in the
7 display of foreign peptides on the surface of the phage
8 particle with the DNA encoding the fusion protein
9 packaged in the phage particle (Smith G. P., 1985,
10 Science 228: 1315-1317). The expression vector can be
11 the bacteriophage genome itself, or a phagemid vector,
12 into which a bacteriophage coat protein has been
13 cloned. In the latter case, the host bacterium,
14 containing the phagemid vector, must be co-infected
15 with autonomously replicating bacteriophage, termed
16 helper phage, to provide the full complement of
17 proteins necessary to produce mature phage particles.
18 The helper phage normally has a genetic defect in the
19 origin of replication which results in the preferential
20 packaging of the phagemid genome. Expression of the
21 fusion protein following helper phage infection, allows
22 incorporation of both fusion protein and wild type coat
23 protein into the phage particle during assembly.
24 Libraries of fusion proteins incorporated into phage,
25 can then be selected for binding members against
26 targets of interest (ligands). Bound phage can then be
27 allowed to reinfect *Escherichia coli* (*E. coli*) bacteria
28 and then amplified and the selection repeated,
29 resulting in the enrichment of binding members
30 (Parmley, S. F., & Smith, G. P. 1988., Gene 73: 305-
31 318; Barrett R. W. et al., 1992, Analytical
32 Biochemistry 204: 357-364 Williamson et al., Proc.
33 Natl. Acad. Sci. USA, 90: 4141-4145; Marks et al.,
34 1991, J. Mol. Biol. 222: 581-597).

35

36 Several publications describe this method. For example,

1 US Patent No 5,403,484 describes production of a
2 chimeric protein formed from the viral coat protein and
3 the peptide of interest. In this method at least a
4 functional portion of a viral coat protein is required
5 to cause display of the chimeric protein or a processed
6 form thereof on the outer surface of the virus. In
7 addition, US Patent No 5,571,698 describes a method for
8 obtaining a nucleic acid encoding a binding protein, a
9 key component of which comprises preparing a population
10 of amplifiable genetic packages which have a
11 genetically determined outer surface protein, to cause
12 the display of the potential binding domain on the
13 outer surface of the genetic package. The genetic
14 packages are selected from the group consisting of
15 cells, spores and viruses. For example when the
16 genetic package is a bacterial cell, the outer surface
17 transport signal is derived from a bacterial outer
18 surface protein, and when the genetic package is a
19 filamentous bacteriophage, the outer surface transport
20 signal is provided by the gene pIII (minor coat
21 protein) or pVIII (major coat protein) of the
22 filamentous phage.

23
24 WO-A-92/01047 and WO-A-92/20791 describe methods for
25 producing multimeric specific binding pairs, by
26 expressing a first polypeptide chain fused to a viral
27 coat protein, such as the gene pIII protein, of a
28 secreted replicable genetic display package (RGDP)
29 which displays a polypeptide at the surface of the
30 package, and expressing a second polypeptide chain of
31 the multimer, and allowing the two chains to come
32 together as part of the RGDP.

33
34 LacI fusion plasmid display. This method is based on
35 the DNA binding ability of the lac repressor. Libraries
36 of random peptides are fused to the lacI repressor

1 protein, normally to the C-terminal end, through
2 expression from a plasmid vector carrying the fusion
3 gene. Linkage of the LacI-peptide fusion to its
4 encoding DNA occurs via the lacO sequences on the
5 plasmid, forming a stable peptide-LacI-peptide complex.
6 These complexes are released from their host bacteria
7 by cell lysis, and peptides of interest isolated by
8 affinity purification on an immobilised target. The
9 plasmids thus isolated can then be reintroduced into *E.*
10 *coli* by electroporation to amplify the selected
11 population for additional rounds of screening (Cull, M.
12 G. et al. 1992. Proc. Natl. Acad. Sci. U.S.A. 89:1865-
13 1869).

14
15 US Patent No 5498530 describes a method for
16 constructing a library of random peptides fused to a
17 DNA binding protein in appropriate host cells and
18 culturing the host cells under conditions suitable for
19 expression of the fusion proteins intra-cellularly, in
20 the cytoplasm of the host cells. This method also
21 teaches that the random peptide is located at the
22 carboxy terminus of the fusion protein and that the
23 fusion protein-DNA complex is released from the host
24 cell by cell lysis. No method is described for the
25 protection of the DNA from degradation once released
26 from the lysed cell. Several DNA binding proteins are
27 claimed but no examples are shown except lacI.

28
29 There remains a need for methods of constructing
30 peptide libraries in addition to the methods described
31 above. For instance, the above methods do not permit
32 production of secreted peptides with a free carboxy
33 terminus. The present invention describes an
34 alternative method for isolating peptides of interest
35 from libraries and has significant advantages over the
36 prior art methods.

1 In general terms, the present invention provides a
2 method for screening a nucleotide library (usually a
3 DNA library) for a nucleotide sequence which encodes a
4 target peptide of interest. The method involves
5 physically linking each peptide to a polynucleotide
6 including the specific nucleotide sequence encoding
7 that peptide. Linkage of a peptide to its encoding
8 nucleotide sequence is achieved via linkage of the
9 peptide to a nucleotide binding domain. A bifunctional
10 chimeric protein with a nucleotide binding domain and a
11 library member or target peptide (preferably with a
12 function of interest) is thus obtained. The peptide of
13 interest is bound to the polynucleotide encoding that
14 peptide via the nucleotide binding domain of the
15 chimeric protein.

16

17 The polynucleotide-chimeric protein complex is then
18 incorporated within a peptide display carrier package
19 (PDCP), protecting the polynucleotide from subsequent
20 degradation, while displaying the target peptide
21 portion on the outer surface of the peptide display
22 carrier package (PDCP).

23

24 Thus, in one aspect, the present invention provides a
25 peptide display carrier package (PDCP), said package
26 comprising a polynucleotide-chimeric protein complex
27 wherein the chimeric protein has a nucleotide binding
28 portion and a target peptide portion, wherein said
29 polynucleotide comprises a nucleotide sequence motif
30 which is specifically bound by said nucleotide binding
31 portion, and wherein at least the chimeric protein
32 encoding portion of the polynucleotide not bound by the
33 nucleotide binding portion of the chimeric protein is
34 protected.

35

36 In one embodiment the polynucleotide is protected by a

1 protein which binds non-specifically to naked
2 polynucleotide. Examples include viral coat proteins,
3 many of which are well-known in the art. Where the
4 chosen viral coat protein requires an initiation
5 sequence to commence general binding to the
6 polynucleotide, this will be provided on the
7 polynucleotide at appropriate location(s). A preferred
8 coat protein is coat protein from a bacteriophage,
9 especially M13.

10
11 Generally, the nucleic binding portion of the chimeric
12 protein is selected for its specificity for the
13 nucleotide sequence motif present in the recombinant
14 polynucleotide encoding the chimeric protein.

15
16 Optionally, the nucleotide sequence motif may be an
17 integral part of the protein encoding region of the
18 polynucleotide. Alternatively, and more usually, the
19 motif may be present in a non-coding region of the
20 polynucleotide. For the purposes of this invention,
21 all that is required is for the motif to be located on
22 the polynucleotide such that the nucleotide binding
23 portion of the chimeric protein is able to recognise
24 and bind to it. Desirably the polynucleotide-chimeric
25 protein complex has a dissociation constant of at least
26 one hour.

27
28 Optionally, the recombinant polynucleotide may comprise
29 two or more nucleotide sequence motifs, each of which
30 will be bound by a chimeric protein molecule.
31 Preferably, the motifs are positioned along the length
32 of the polynucleotide to avoid steric hindrance between
33 the bound chimeric proteins.

34
35 Preferably, the nucleotide sequence motif is not
36 affected by the presence of additional nucleotide

1 sequence (e.g. encoding sequence) at its 5' and/or 3'
2 ends. Thus the chimeric fusion protein may include a
3 target peptide portion at its N terminal end, at its C
4 terminal end or may include two target peptide portions
5 (which may be the same or different) at each end of the
6 nucleotide binding portion, ie at both the N and C
7 terminal ends of the chimeric protein. For example one
8 target peptide may be an antibody of known specificity
9 and the other peptide may be a peptide of potential
10 interest.

11

12 Desirably the target peptide portion of the chimeric
13 protein is displayed externally on the peptide display
14 carrier package, and is thus available for detection,
15 reaction and/or binding.

16

17 In more detail the PDCP may be composed two distinct
18 elements:

19 a. A polynucleotide-chimeric protein complex. This
20 links the displayed target peptide portion to the
21 polynucleotide encoding that peptide portion
22 through a specific polynucleotide binding portion.
23 The nucleotide sequence encoding the chimeric
24 protein, and the specific nucleotide sequence
25 motif recognised by the nucleotide binding portion
26 of the chimeric protein must be present on a
27 segment of polynucleotide which can be
28 incorporated into the PDCP; and

29 b. A protective coat. This may be supplied by a
30 replicable carrier or helper package capable of
31 independent existence. Alternatively, a coat
32 protein could be encoded by the recombinant
33 polynucleotide of the invention. The protective
34 coat for the polynucleotide-chimeric protein
35 complex may be composed of a biological material
36 such as protein or lipid, but the protective coat

1 is not required for linking the target peptide to
2 the polynucleotide encoding that peptide. The
3 protective coat must allow the display of the
4 target peptide portion of the chimeric protein on
5 its outer surface. The carrier or helper package
6 may also provide the mechanism for releasing the
7 intact PDCP from host cells when so required. By
8 way of example, when a bacteriophage is the
9 replicable carrier package, a protein coat of the
10 bacteriophage surrounds the polynucleotide-
11 chimeric protein complex to form the PDCP, which
12 is then extruded from the host bacterial cell.

13

14 The invention described herein demonstrates that
15 peptides fused to a nucleotide binding domain can be
16 displayed externally, even through a bacteriophage
17 carrier package protein coat, while still bound to the
18 polynucleotide encoding the displayed peptide.

19

20 The present invention also provides a recombinant
21 polynucleotide comprising a nucleotide sequence
22 encoding a chimeric protein having a nucleotide binding
23 portion operably linked to a target peptide portion,
24 wherein said polynucleotide includes a specific
25 nucleotide sequence motif which is bound by the
26 nucleotide binding portion of said chimeric protein and
27 further encoding a non-sequence-specific nucleotide
28 binding protein.

29

30 Desirably, the recombinant polynucleotide is a
31 recombinant expression system, able to express the
32 chimeric protein when placed in a suitable environment,
33 for example a compatible host cell. After its
34 expression, the chimeric protein binds to the specific
35 nucleotide sequence (motif) present in the
36 polynucleotide comprising the nucleotide sequence

1 encoding the chimeric protein.

2

3 Optionally there may be a linker sequence located
4 between the nucleotide sequence encoding the nucleotide
5 binding portion and the polynucleotide inserted into
6 the restriction enzyme site of the construct.

7

8 Desirably the nucleotide binding portion is a DNA
9 binding domain of an oestrogen or progesterone
10 receptor, or a functional equivalent thereof. Examples
11 of sequences encoding such nucleotide binding portions
12 are set out in SEQ ID Nos 11 and 13.

13

14 The term "expression system" is used herein to refer to
15 a genetic sequence which includes a protein-encoding
16 region and is operably linked to all of the genetic
17 signals necessary to achieve expression of that region.
18 Optionally, the expression system may also include
19 regulatory elements, such as a promoter or enhancer to
20 increase transcription and/or translation of the
21 protein encoding region or to provide control over
22 expression. The regulatory elements may be located
23 upstream or downstream of the protein encoding region
24 or within the protein encoding region itself. Where
25 two or more distinct protein encoding regions are
26 present these may use common regulatory element(s) or
27 have separate regulatory element(s).

28

29 Generally, the recombinant polynucleotide described
30 above will be DNA. Where the expression system is
31 based upon an M13 vector, usually the polynucleotide
32 binding portion of the expressed chimeric portion will
33 be single-stranded DNA. However, other vector systems
34 may be used and the nucleotide binding portion may be
35 selected to bind preferentially to double-stranded DNA
36 or to double or single-stranded RNA, as convenient.

1 Additionally the present invention provides a vector
2 containing such a recombinant expression system and
3 host cells transformed with such a recombinant
4 expression system (optionally in the form of a vector).
5

6 Whilst the recombinant polynucleotide described above
7 forms an important part of the present invention, we
8 are also concerned with the ability to screen large
9 (e.g. of at least 10^5 members, for example 10^6 or even
10 10^7 members) libraries of genetic material. One of the
11 prime considerations therefore is the provision of a
12 recombinant genetic construct into which each member of
13 said library can individually be incorporated to form
14 the recombinant polynucleotide described above and to
15 express the chimeric protein thereby encoded (the
16 target peptide of which is encoded by the nucleotide
17 library member incorporated into the construct).
18

19 Thus viewed in a further aspect the present invention
20 provides a genetic construct or set of genetic
21 constructs comprising a polynucleotide having a
22 sequence which includes:
23

- 24 i) a sequence encoding a nucleotide binding portion
25 able to recognise and bind to a specific sequence
26 motif;
- 27 ii) the sequence motif recognised and bound by the
28 nucleotide binding portion encoded by (i);
- 29 iii) a restriction enzyme site which permits insertion
30 of a polynucleotide, said site being designed to
31 operably link said polynucleotide to the sequence
32 encoding the nucleotide binding portion so that
33 expression of the operably linked polynucleotide
34 sequences yields a chimeric protein; and
- 35 iv) a sequence encoding a nucleotide binding protein
36 which binds non-specifically to naked

1 polynucleotide.

2

3 Optionally there may be a linker sequence located
4 between the nucleotide sequence encoding the nucleotide
5 binding portion and the sequence of the polynucleotide
6 from the library inserted into the restriction enzyme
7 site of the construct.

8

9 Desirably the nucleotide binding portion is a DNA
10 binding domain of an oestrogen or progesterone
11 receptor, or a functional equivalent thereof. Examples
12 of sequences encoding such nucleotide binding portions
13 are set out in SEQ ID Nos 11 and 13.

14

15 Suitable genetic constructs according to the invention
16 include pDM12, pDM14 and pDM16, deposited at NCIMB on
17 28 August 1998 under Nos NCIMB 40970, NCIMB 40971 and
18 NCIMB 40972 respectively.

19

20 It is envisaged that a conventionally produced genetic
21 library may be exposed to the genetic construct(s)
22 described above. Thus, each individual member of the
23 genetic library will be separately incorporated into
24 the genetic construct and the library will be present
25 in the form of a library of recombinant polynucleotides
26 (as described above), usually in the form of vectors,
27 each recombinant polynucleotide including as library
28 member.

29

30 Thus, in a further aspect, the present invention
31 provides a library of recombinant polynucleotides (as
32 defined above) wherein each polynucleotide includes a
33 polynucleotide obtained from a genetic library and
34 which encodes the target peptide portion of the
35 chimeric protein expressed by the recombinant
36 polynucleotide.

1 Optionally, the chimeric protein may further include a
2 linker sequence located between the nucleotide binding
3 portion and the target peptide portion. The linker
4 sequence will reduce steric interference between the
5 two portions of the protein. Desirably the linker
6 sequence exhibits a degree of flexibility.

7
8 Also disclosed are methods for constructing and
9 screening libraries of PDCP particles, displaying many
10 different peptides, allowing the isolation and
11 identification of particular peptides by means of
12 affinity techniques relying on the binding activity of
13 the peptide of interest. The resulting polynucleotide
14 sequences can therefore be more readily identified, re-
15 cloned and expressed.

16
17 A method of constructing a genetic library, said method
18 comprising:

- 19
20 a) constructing multiple copies of a recombinant
21 vector comprising a polynucleotide sequence which
22 encodes a nucleotide binding portion able to
23 recognise and bind to a specific sequence motif
24 (and optionally also including the specific
25 sequence motif);
26
27 b) operably linking each said vector to a
28 polynucleotide encoding a target polypeptide, such
29 that expression of said operably linked vector
30 results in expression of a chimeric protein
31 comprising said target peptide and said nucleotide
32 binding portions; wherein said multiple copies of
33 said operably linked vectors collectively express
34 a library of target peptide portions;
35
36 c) transforming host cells with the vectors of step

1 b) ;

2

3 d) culturing the host cells of step c) under
4 conditions suitable for expression of said
5 chimeric protein;

6

7 e) providing a recombinant polynucleotide comprising
8 the nucleotide sequence motif specifically
9 recognised by the nucleotide binding portion and
10 exposing this polynucleotide to the chimeric
11 protein of step d) to yield a polynucleotide-
12 chimeric protein complex; and

13

14 f) causing production of a non-sequence-specific
15 moiety able to bind to the non-protected portion
16 of the polynucleotide encoding the chimeric
17 protein to form a peptide display carrier package.

18

19 The present invention further provides a method of
20 screening a genetic library, said method comprising:

21

22 a) exposing the polynucleotide members of said
23 library to multiple copies of a genetic construct
24 comprising a nucleotide sequence encoding a
25 nucleotide binding portion able to recognise and
26 bind to a specific sequence motif, under
27 conditions suitable for the polynucleotides of
28 said library each to be individually ligated into
29 one copy of said genetic construct, to create a
30 library of recombinant polynucleotides;

31

32 b) exposing said recombinant polynucleotides to a
33 population of host cells, under conditions
34 suitable for transformation of said host cells by
35 said recombinant polynucleotides;

36

- 1 c) selecting for transformed host cells;
2
3 d) exposing said transformed host cells to conditions
4 suitable for expression of said recombinant
5 polynucleotide to yield a chimeric protein; and
6
7 e) providing a recombinant polynucleotide comprising
8 the nucleotide sequence motif specifically
9 recognised by the nucleotide binding portion and
10 exposing this polynucleotide to the chimeric
11 protein of step d) to yield a polynucleotide-
12 chimeric protein complex;
13
14 f) protecting any exposed portions of the
15 polynucleotide in the complex of step e) to form a
16 peptide display carrier package; and
17
18 g) screening said peptide display carrier package to
19 select only those packages displaying a target
20 peptide portion having the characteristics
21 required.

22
23 Desirably in step a) the genetic construct is pDM12,
24 pDM14 or pDM16.

25
26 Desirably in step f) the peptide display package
27 carrier is extruded from the transformed host cell
28 without lysis of the host cell.

29
30 Generally the transformed host cells will be plated out
31 or otherwise divided into single colonies following
32 transformation and prior to expression of the chimeric
33 protein.

34
35 The screening step g) described above may look for a
36 particular target peptide either on the basis of

1 function (e.g. enzymic activity) or structure (e.g.
2 binding to a specific antibody). Once the peptide
3 display carrier package is observed to include a target
4 peptide with the desired characteristics, the
5 polynucleotide portion thereof (which of course encodes
6 the chimeric protein itself) can be amplified, cloned
7 and otherwise manipulated using standard genetic
8 engineering techniques.

9
10 The current invention differs from the prior art
11 teaching of the previous disclosures US Patent No
12 5,403,484 and US Patent No 5,571,698, as the invention
13 does not require outer surface transport signals, or
14 functional portions of viral coat proteins, to enable
15 the display of chimeric binding proteins on the outer
16 surface of the viral particle or genetic package.

17
18 The current invention also differs from the teaching of
19 WO-A-92/01047 and WO-A-92/20791, as no component of a
20 secreted replicable genetic display package, or viral
21 coat protein is required, to enable display of the
22 target peptide on the outer surface of the viral
23 particle.

24
25 The current invention differs from the teaching of US
26 Patent No 5498530, as it enables the display of
27 chimeric proteins, linked to the polynucleotide
28 encoding the chimeric protein, extra-cellularly, not in
29 the cytoplasm of a host cell. In the current invention
30 the chimeric proteins are presented on the outer
31 surface of a peptide display carrier package (PDCP)
32 which protects the DNA encoding the chimeric protein,
33 and does not require cell lysis to obtain access to the
34 chimeric protein-DNA complex. Finally, the current
35 invention does not rely upon the lacI DNA binding
36 protein to form the chimeric protein-DNA complex.

1 In one embodiment of the invention, the nucleotide
2 binding portion of the chimeric protein comprises a DNA
3 binding domain from one or more of the nuclear steroid
4 receptor family of proteins, or a functional equivalent
5 of such a domain. Particular examples include (but are
6 not limited to) a DNA binding domain of the oestrogen
7 receptor or the progesterone receptor, or functional
8 equivalents thereof. These domains can recognise
9 specific DNA sequences, termed hormone response
10 elements (HRE), which can be bound as both double and
11 single-stranded DNA. The DNA binding domain of such
12 nuclear steroid receptor proteins is preferred.

13
14 The oestrogen receptor is especially referred to below
15 by way of example, for convenience since:

16 (a) The oestrogen receptor is a large multifunctional
17 polypeptide of 595 amino acids which functions in the
18 cytoplasm and nucleus of eukaryotic cells (Green et
19 al., 1986, Science 231: 1150-1154). A minimal high
20 affinity DNA binding domain (DBD) has been defined
21 between amino acids 176 and 282 (Mader et al., 1993,
22 Nucleic Acids Res. 21: 1125-1132). The functioning of
23 this domain (i.e. DNA binding) is not inhibited by the
24 presence of non-DNA binding domains at both the N and C
25 terminal ends of this domain, in the full length
26 protein.

27
28 (b) The oestrogen receptor DNA binding domain fragment
29 (amino acids 176-282) has been expressed in *E. coli* and
30 shown to bind to the specific double stranded DNA
31 oestrogen receptor target HRE nucleotide sequence, as a
32 dimer with a similar affinity (0.5nM) to the parent
33 molecule (Murdoch et al. 1990, Biochemistry 29: 8377-
34 8385; Mader et al., 1993, Nucleic Acids Research 21:
35 1125-1132). DBD dimerization on the surface of the PDCP
36 should result in two peptides displayed per particle.

1 This bivalent display can aid in the isolation of low
2 affinity peptides and peptides that are required to
3 form a bivalent conformation in order to bind to a
4 particular target, or activate a target receptor. The
5 oestrogen receptor is capable of binding to its 38 base
6 pair target HRE sequence, consensus sequence:

7
8 1) 5'-TCAGGTCAGAGTGACCTGAGCTAAAATAACACATTCAG-3'
9 ("minus strand") SEQ ID No 1, and

10

11 2) 3'-AGTCCAGTCTCACTGGACTCGATTTTATTGTGTAAGTC-5'
12 ("plus strand") SEQ ID No 2,

13

14 with high affinity and specificity, under the salt and
15 pH conditions normally required for selection of
16 binding peptides. Moreover, binding affinity is
17 increased 60-fold for the single-stranded coding, or
18 "plus", strand (i.e. SEQ ID No 2) of the HRE nucleotide
19 sequence over the double stranded form of the specific
20 target nucleotide sequence (Peale et al. 1988, Proc.
21 Natl. Acad. Sci. USA 85: 1038-1042; Lannigan & Notides,
22 1989, Proc. Natl. Acad. Sci. USA 86: 863-867).

23

24 In an embodiment of the invention where the DNA binding
25 component of the peptide display carrier package is the
26 oestrogen receptor, the nucleotide (DNA) binding
27 portion contains a minimum sequence of amino acids 176-
28 282 of the oestrogen receptor protein. In addition, the
29 consensus oestrogen receptor target HRE sequence is
30 cloned in such a way that if single stranded DNA can be
31 produced then the coding, or "plus", strand of the
32 oestrogen receptor HRE nucleotide sequence is
33 incorporated into single-stranded DNA. An example of a
34 vector suitable for this purpose is pUC119 (see Viera
35 et al., Methods in Enzymology, Vol 153, pages 3-11,
36 1987).

1 In a preferred embodiment of the invention a peptide
2 display carrier package (PDCP) can be assembled when a
3 bacterial host cell is transformed with a bacteriophage
4 vector, which vector comprises a recombinant
5 polynucleotide as described above. The expression
6 vector will also comprise the specific nucleotide motif
7 that can be bound by the nucleotide binding portion of
8 the chimeric protein. Expression of recombinant
9 polynucleotide results in the production of the
10 chimeric protein which comprises the target peptide and
11 the nucleotide binding portion. The host cell is grown
12 under conditions suitable for chimeric protein
13 expression and assembly of the bacteriophage particles,
14 and the association of the chimeric protein with the
15 specific nucleotide sequence in the expression vector.

16
17 In this embodiment, since the vector is a
18 bacteriophage, which replicates to produce a single-
19 stranded DNA, the nucleotide binding portion preferably
20 has an affinity for single-stranded DNA. Incorporation
21 of the vector single-stranded DNA-chimeric protein
22 complex into bacteriophage particles results in the
23 assembly of the peptide display carrier package (PDCP),
24 and display of the target peptide on the outer surface
25 of the PDCP.

26
27 In this embodiment both of the required elements for
28 producing peptide display carrier packages are
29 contained on the same vector. Incorporation of the DNA-
30 chimeric protein complex into a peptide display carrier
31 package (PDCP) is preferred as DNA degradation is
32 prevented, large numbers of PDCPs are produced per host
33 cell, and the PDCPs are easily separated from the host
34 cell without recourse to cell lysis.

35
36 In a more preferred embodiment, the vector of the is a

1 phagemid vector (for example pUC119) where expression
2 of the chimeric protein is controlled by an inducible
3 promoter. In this embodiment the PDCP can only be
4 assembled following infection of the host cell with
5 both phagemid vector and helper phage. The transfected
6 host cell is then cultivated under conditions suitable
7 for chimeric protein expression and assembly of the
8 bacteriophage particles.

9
10 In this embodiment the elements of the PDCP are
11 provided by two separate vectors. The phagemid derived
12 PDCP is superior to phagemid derived display packages
13 disclosed in WO-A-92/01047 where a proportion of
14 packages displaying bacteriophage coat protein fusion
15 proteins will contain the helper phage DNA, not the
16 fusion protein DNA sequence. In the current invention,
17 a PDCP can display the chimeric fusion protein only
18 when the package contains the specific nucleotide motif
19 recognised by the nucleotide binding portion. In most
20 embodiments this sequence will be present on the same
21 DNA segment that encodes the fusion protein. In
22 addition, the prior art acknowledges that when mutant
23 and wild type proteins are co-expressed in the same
24 bacterial cell, the wild type protein is produced
25 preferentially. Thus, when the wild type helper phage,
26 phage display system of WO-A-92/01047 is used, both
27 wild type gene pIII and target peptide-gene pIII
28 chimeric proteins are produced in the same cell. The
29 result of this is that the wild type gene pIII protein
30 is preferentially packaged into bacteriophage
31 particles, over the chimeric protein. In the current
32 invention, there is no competition with wild type
33 bacteriophage coat proteins for packaging.

34
35 Desirably the target peptide is displayed in a location
36 exposed to the external environment of the PDCP, after

1 the PDCP particle has been released from the host cell
2 without recourse to cell lysis. The target peptide is
3 then accessible for binding to its ligand. Thus, the
4 target peptide may be located at or near the N-terminus
5 or the C-terminus of a nucleotide binding domain, for
6 example the DNA binding domain of the oestrogen
7 receptor.

8
9 The present invention also provides a method for
10 screening a DNA library expressing one or more
11 polypeptide chains that are processed, folded and
12 assembled in the periplasmic space to achieve
13 biological activity. The PDCP may be assembled by the
14 following steps:

15
16 (a) Construction of N- or C-terminal DBD chimeric
17 protein fusions in a phagemid vector.

18 (i) When the target peptide is located at the N-
19 terminus of the nucleotide binding portion, a library
20 of DNA sequences each encoding a potential target
21 peptide is cloned into an appropriate location of an
22 expression vector (i.e. behind an appropriate promoter
23 and translation sequences and a sequence encoding a
24 signal peptide leader directing transport of the
25 downstream fusion protein to the periplasmic space) and
26 upstream of the sequence encoding the nucleotide
27 binding portion. In a preferred embodiment the DNA
28 sequence(s) of interest may be joined, by a region of
29 DNA encoding a flexible amino acid linker, to the 5'-
30 end of an oestrogen receptor DBD.

31 (ii) Alternatively, when the target peptide is
32 located at the C-terminus of the nucleotide binding
33 domain, a library of DNA sequences each encoding a
34 potential target peptide is cloned into the expression
35 vector so that the nucleotide sequence coding for the
36 nucleotide binding portion is upstream of the cloned

1 DNA target peptide encoding sequences, said nucleotide
2 binding portion being positioned behind an appropriate
3 promoter and translation sequences and a sequence
4 encoding a signal peptide leader directing transport of
5 the downstream fusion protein to the periplasmic space.
6 In a preferred embodiment, DNA sequence(s) of interest
7 may be joined, by a region of DNA encoding a flexible
8 amino acid linker oestrogen receptor DBD DNA sequence.

9
10 Located on the expression vector is the specific HRE
11 nucleotide sequence recognised, and bound, by the
12 oestrogen receptor DBD. In order to vary the number of
13 chimeric proteins displayed on each PDCP particle, this
14 sequence can be present as one or more copies in the
15 vector.

16
17 (b) Incorporation into the PDCP. Non-lytic helper
18 bacteriophage infects host cells containing the
19 expression vector. Preferred types of bacteriophage
20 include the filamentous phage fd, fl and M13. In a
21 more preferred embodiment the bacteriophage may be
22 M13K07.

23
24 The protein(s) of interest are expressed and
25 transported to the periplasmic space, and the properly
26 assembled proteins are incorporated into the PDCP
27 particle by virtue of the high affinity interaction of
28 the DBD with the specific target nucleotide sequence
29 present on the phagemid vector DNA which is naturally
30 packaged into phage particles in a single-stranded
31 form. The high affinity interaction between the DBD
32 protein and its specific target nucleotide sequence
33 prevents displacement by bacteriophage coat proteins
34 resulting in the incorporation of the protein(s) of
35 interest onto the surface of the PDCP as it is extruded
36 from the cell.

1 (c) Selection of the peptide of interest. Particles
2 which display the peptide of interest are then selected
3 from the culture by affinity enrichment techniques.
4 This is accomplished by means of a ligand specific for
5 the protein of interest, such as an antigen if the
6 protein of interest is an antibody. The ligand may be
7 presented on a solid surface such as the surface of an
8 ELISA plate, or in solution. Repeating the affinity
9 selection procedure provides an enrichment of clones
10 encoding the desired sequences, which may then be
11 isolated for sequencing, further cloning and/or
12 expression.

13

14 Numerous types of libraries of peptides fused to the
15 DBD can be screened under this embodiment including:

16

17 (i) Random peptide sequences encoded by synthetic
18 DNA of variable length.

19

20 (ii) Single-chain Fv antibody fragments. These
21 consist of the antibody heavy and light chain
22 variable region domains joined by a flexible
23 linker peptide to create a single-chain antigen
24 binding molecule.

25

26 (iii) Random fragments of naturally occurring
27 proteins isolated from a cell population
28 containing an activity of interest.

29

30 In another embodiment the invention concerns methods
31 for screening a DNA library whose members require more
32 than one chain for activity, as required by, for
33 example, antibody Fab fragments for ligand binding. In
34 this embodiment heavy or light chain antibody DNA is
35 joined to a nucleotide sequence encoding a DNA binding
36 domain of, for example, the oestrogen receptor in a

1 phagemid vector. Typically the antibody DNA library
2 sequences for either the heavy (VH and CH1) or light
3 chain (VL and CL) genes are inserted in the 5' region
4 of the oestrogen receptor DBD DNA, behind an
5 appropriate promoter and translation sequences and a
6 sequence encoding a signal peptide leader directing
7 transport of the downstream fusion protein to the
8 periplasmic space.

9
10 Thus, a DBD fused to a DNA library member-encoded
11 protein is produced and assembled in to the viral
12 particle after infection with bacteriophage. The second
13 and any subsequent chain(s) are expressed separately
14 either:

15

16 (a) from the same phagemid vector containing the DBD
17 and the first polypeptide fusion protein,
18 or

19

20 (b) from a separate region of DNA which may be present
21 in the host cell nucleus, or on a plasmid, phagemid or
22 bacteriophage expression vector that can co-exist, in
23 the same host cell, with the first expression vector,
24 so as to be transported to the periplasm where they
25 assemble with the first chain that is fused to the DBD
26 protein as it exits the cell. Peptide display carrier
27 packages (PDCP) which encode the protein of interest
28 can then be selected by means of a ligand specific for
29 the protein.

30

31 In yet another embodiment, the invention concerns
32 screening libraries of bi-functional peptide display
33 carrier packages where two or more activities of
34 interest are displayed on each PDCP. In this
35 embodiment, a first DNA library sequence(s) is inserted
36 next to a first DNA binding domain (DBD) DNA sequence,

1 for example the oestrogen receptor DBD, in an
2 appropriate vector, behind an appropriate promoter and
3 translation sequences and a sequence encoding a signal
4 peptide leader directing transport of this first
5 chimeric protein to the periplasmic space. A second
6 chimeric protein is also produced from the same, or
7 separate, vector by inserting a second DNA library
8 sequence(s) next to a second DBD DNA sequence which is
9 different from the first DBD DNA sequence, for example
10 the progesterone receptor DBD, behind an appropriate
11 promoter and translation sequences and a sequence
12 encoding a signal peptide leader. The first, or only,
13 vector contains the specific HRE nucleotide sequences
14 for both oestrogen and progesterone receptors.
15 Expression of the two chimeric proteins, results in a
16 PDCP with two different chimeric proteins displayed. As
17 an example, one chimeric protein could possess a
18 binding activity for a particular ligand of interest,
19 while the second chimeric protein could possess an
20 enzymatic activity. Binding by the PDCP to the ligand
21 of the first chimeric protein could then be detected by
22 subsequent incubation with an appropriate substrate for
23 the second chimeric protein. In an alternative
24 embodiment a bi-functional PDCP may be created using a
25 single DBD, by cloning one peptide at the 5'-end of the
26 DBD, and a second peptide at the 3'-end of the DBD.
27 Expression of this single bi-functional chimeric
28 protein results in a PDCP with two different
29 activities.
30
31 We have investigated the possibility of screening
32 libraries of peptides, fused to a DNA binding domain
33 and displayed on the surface of a display package, for
34 particular peptides with a biological activity of
35 interest and recovering the DNA encoding that activity.
36 Surprisingly, by manipulating the oestrogen receptor

DNA binding domain in conjunction with M13 bacteriophage we have been able to construct novel particles which display large biologically functional molecules, that allows enrichment of particles with the desired specificity.

The invention described herein provides a significant breakthrough in DNA library screening technology.

The invention will now be further described by reference to the non-limiting examples and figures below.

Description of Figures

Figure 1 shows the pDM12 N-terminal fusion oestrogen receptor DNA binding domain expression vector nucleotide sequence (SEQ ID No 3), between the HindIII and EcoRI restriction sites, comprising a pelB leader secretion sequence (in italics), multiple cloning site containing SfiI and NotI sites, flexible (glycine)₄-serine linker sequence (boxed), a fragment of the oestrogen receptor gene comprising amino acids 176-282 (SEQ ID No 4) of the full length molecule, and the 38 base pair consensus oestrogen receptor DNA binding domain HRE sequence.

Figure 2 shows the OD_{450nm} ELISA data for negative control M13K07 phage, and single-clone PDCP display culture supernatants (#1-4, see Example 3) isolated by selection of the lymphocyte cDNA-pDM12 library against anti-human immunoglobulin kappa antibody.

Figure 3 shows partial DNA (SEQ ID No 5) and amino acid (SEQ ID No 6) sequence for the human immunoglobulin kappa constant region (Kabat, E. A. et al., Sequences

1 of Proteins of Immunological Interest. 4th edition. U.S.
2 Department of Health and Human Services. 1987), and
3 ELISA positive clones #2 (SEQ ID Nos 7 and 8) and #3
4 (SEQ ID Nos 9 and 10) from Figure 2 which confirms the
5 presence of human kappa constant region DNA in-frame
6 with the pelB leader sequence (pelB leader sequence is
7 underlined, the leader sequence cleavage site is
8 indicated by an arrow). The differences in the 5'-end
9 sequence demonstrates that these two clones were
10 selected independently from the library stock. The PCR
11 primer sequence is indicated in bold, clone #2 was
12 originally amplified with CDNAPCRBAK1 and clone #3 was
13 amplified with CDNAPCRBAK2.

14
15 Figure 4 shows the pDM14 N-terminal fusion oestrogen
16 receptor DNA binding domain expression vector
17 nucleotide sequence (SEQ ID No 11), between the HindIII
18 and EcoRI restriction sites, comprising a pelB leader
19 secretion sequence (in italics), multiple cloning site
20 containing SfiI and NotI sites, flexible (glycine)₄-
21 serine linker sequence (boxed), a fragment of the
22 oestrogen receptor gene comprising amino acids 176-282
23 (SEQ ID No 12) of the full length molecule, and the two
24 38 base pair oestrogen receptor DNA binding domain HRE
25 sequences (HRE 1 and HRE 2).

26
27 Figure 5 shows the pDM16 C-terminal fusion oestrogen
28 receptor DNA binding domain expression vector
29 nucleotide sequence (SEQ ID No 13), between the HindIII
30 and EcoRI restriction sites, comprising a pelB leader
31 secretion sequence (in italics), a fragment of the
32 oestrogen receptor gene comprising amino acids 176-282
33 (SEQ ID No 14) of the full length molecule, flexible
34 (glycine)₄-serine linker sequence (boxed), multiple
35 cloning site containing SfiI and NotI sites and the 38
36 base pair oestrogen receptor DNA binding domain HRE

1 sequence.

2

3 Figure 6 shows the OD_{450nm} ELISA data for N-cadherin-
4 pDM16 C-terminal display PDCP binding to anti-pan-
5 cadherin monoclonal antibody in serial dilution ELISA
6 as ampicillin resistance units (a.r.u.). Background
7 binding of negative control M13K07 helper phage is also
8 shown.

9

10 Figure 7 shows the OD_{450nm} ELISA data for *in vivo*
11 biotinylated PCC-pDM16 C-terminal display PDCP binding
12 to streptavidin in serial dilution ELISA as ampicillin
13 resistance units (a.r.u.). Background binding of
14 negative control M13K07 helper phage is also shown.

15

16 Figure 8 shows the OD_{450nm} ELISA data for a human scFv
17 PDCP isolated from a human scFv PDCP display library
18 selected against substance P. The PDCP was tested
19 against streptavidin (1), streptavidin-biotinylated
20 substance P (2), and streptavidin-biotinylated CGRP
21 (3), in the presence (B) or absence (A) of free
22 substance P.

23

24 Figure 9 shows the DNA (SEQ ID Nos 15 and 17) and amino
25 acid (SEQ ID No 16 and 18) sequence of the substance P
26 binding scFv isolated from a human scFv PDCP display
27 library selected against substance P. Heavy chain (SEQ
28 ID Nos 15 and 16) and light chain (SEQ ID Nos 17 and
29 18) variable region sequence is shown with the CDRs
30 underlined and highlighted in bold.

31

32 **Materials and Methods**

33 The following procedures used by the present applicant
34 are described in Sambrook, J., et al., 1989 supra.:
35 restriction enzyme digestion, ligation, preparation of
36 electrocompetent cells, electroporation, analysis of

1 restriction enzyme digestion products on agarose gels,
2 DNA purification using phenol/chloroform, preparation
3 of 2xTY medium and plates, preparation of ampicillin,
4 kanamycin, IPTG (Isopropyl β -D-Thiogalactopyranoside)
5 stock solutions, and preparation of phosphate buffered
6 saline.

7
8 Restriction enzymes, T4 DNA ligase and cDNA synthesis
9 reagents (Superscript plasmid cDNA synthesis kit) were
10 purchased from Life Technologies Ltd (Paisley,
11 Scotland, U.K.). Oligonucleotides were obtained from
12 Cruachem Ltd (Glasgow, Scotland, U.K.), or Genosys
13 Biotechnologies Ltd (Cambridge, U.K.). Taq DNA
14 polymerase, Wizard SV plasmid DNA isolation kits,
15 streptavidin coated magnetic beads and mRNA isolation
16 reagents (PolyAtract 1000) were obtained from Promega
17 Ltd (Southampton, Hampshire, U.K.). Taqplus DNA
18 polymerase was obtained from Stratagene Ltd (Cambridge,
19 U.K.). PBS, BSA, streptavidin, substance P and anti-pan
20 cadherin antibody were obtained from SIGMA Ltd (Poole,
21 Dorset, U.K.). Anti-M13-HRP conjugated antibody,
22 Kanamycin resistant M13K07 helper bacteriophage and
23 RNAGuard were obtained from Pharmacia Ltd (St. Albans,
24 Herts, U.K.) and anti-human Ig κ antibody from Harlan-
25 Seralab (Loughborough, Leicestershire, U.K.)
26 Biotinylated substance P and biotinylated calcitonin
27 gene related peptide (CGRP) were obtained from
28 Peninsula Laboratories (St. Helens, Merseyside, U.K.).

29
30 Specific embodiments of the invention are given below
31 in Examples 1 to 9.

32

Example 1. Construction of a N-terminal PDCP display phagemid vector pDM12.

The pDM12 vector was constructed by inserting an oestrogen receptor DNA binding domain, modified by appropriate PCR primers, into a phagemid vector pDM6. The pDM6 vector is based on the pUC119 derived phage display vector pHEN1 (Hoogenboom et al., 1991, Nucleic Acids Res. 19: 4133-4137). It contains (Gly)₄Ser linker, Factor Xa cleavage site, a full length gene III, and streptavidin tag peptide sequence (Schmidt, T.G. and Skerra, A., 1993, Protein Engineering 6: 109-122), all of which can be removed by NotI-EcoRI digestion and agarose gel electrophoresis, leaving a pelB leader sequence, SfiI, NcoI and PstI restriction sites upstream of the digested NotI site. The cloned DNA binding domain is under the control of the lac promoter found in pUC119.

Preparation of pDM6

The pDM12 vector was constructed by inserting an oestrogen receptor DNA binding domain, modified by appropriate PCR primers, into a phagemid vector pDM6. The pDM6 vector is based on the gene pIII phage display vector pHEN1 (Hoogenboom et al., 1991, Nucleic Acids Res. 19: 4133-4137), itself derived from pUC119 (Viera, J. and Messing, J., 1987, Methods in Enzymol. 153: 3-11). It was constructed by amplifying the pIII gene in pHEN1 with two oligonucleotides:

PDM6BAK: 5 -TTT TCT GCA GTA ATA GGC GGC CGC AGG GGG AGG
AGG GTC CAT CGA AGG TCG CGA AGC AGA GAC TGT TGA AAG T-3
(SEQ ID No 19) and

PDM6FOR: 5 - TTT TGA ATT CTT ATT AAC CAC CGA ACT GCG

1 GGT GAC GCC AAG CGC TTG CGG CCG TTA AGA CTC CTT ATT ACG
2 CAG-3 (SEQ ID No 20).

3
4 and cloning the PstI-EcoRI digested PCR product back
5 into similarly digested pHEN1, thereby removing the
6 c-myc tag sequence and supE TAG codon from pHEN1. The
7 pDM6 vector contains a (Gly)₄Ser linker, Factor Xa
8 cleavage site, a full length gene III, and streptavidin
9 tag peptide sequence (Schmidt, T.G. and Skerra, A.,
10 1993, Protein Engineering 6: 109-122), all of which can
11 be removed by NotI-EcoRI digestion and agarose gel
12 electrophoresis, leaving a pelB leader sequence, SfiI,
13 NcoI and PstI restriction sites upstream of the
14 digested NotI site. The cloned DNA binding domain is
15 under the control of the lac promoter found in pUC119.

16
17 The oestrogen receptor DNA binding domain was isolated
18 from cDNA prepared from human bone marrow (Clontech,
19 Palo Alto, California, U.S.A.). cDNA can be prepared by
20 many procedures well known to those skilled in the art.
21 As an example, the following method using a Superscript
22 plasmid cDNA synthesis kit can be used:

23
24 (a) First strand synthesis.

25
26 5µg of bone marrow mRNA, in 5µl DEPC-treated water was
27 thawed on ice and 2µl (50pmol) of cDNA synthesis primer
28 (5'-AAAAGCGGCCGCACTGGCCTGAGAGA(N)₆-3') (SEQ ID No 21)
29 was added to the mRNA and the mixture heated to 70°C
30 for 10 minutes, then snap-chilled on ice and spun
31 briefly to collect the contents to the bottom of the
32 tube. The following were then added to the tube:

33	1000u/ml RNAGuard	1µl
34	5x first strand buffer	4µl
35	0.1M DTT	2µl
36	10mM dNTPs	1µl

1 200u/ μ l SuperScript II reverse transcriptase 5 μ l
2 The mixture was mixed by pipetting gently and incubated
3 at 37°C for 1 hour, then placed on ice.

4
5 **(b) Second strand synthesis.**

6
7 The following reagents were added to the first strand
8 reaction:

9	DEPC-treated water	93 μ l
10	5x second strand buffer	30 μ l
11	10mM dNTPs	3 μ l
12	10u/ μ l <i>E. coli</i> DNA ligase	1 μ l
13	10u/ μ l <i>E. coli</i> DNA polymerase	4 μ l
14	2u/ μ l <i>E. coli</i> RNase H	1 μ l

15 The reaction was vortex mixed and incubated at 16°C for
16 2 hours. 2 μ l (10u) of T4 DNA polymerase was added and
17 incubation continued at 16°C for 5 minutes. The
18 reaction was placed on ice and 10 μ l 0.5M EDTA added,
19 then phenol-chloroform extracted, precipitated and
20 vacuum dried.

21

22 **(c) Sal I adaptor ligation.**

23

24 The cDNA pellet was resuspended in 25 μ l DEPC-treated
25 water, and ligation set up as follows.

26	cDNA	25 μ l
27	5x T4 DNA ligase buffer	10 μ l
28	1 μ g/ μ l Sal I adapters*	10 μ l
29	1u/ μ l T4 DNA ligase	5 μ l

30 *Sal I adapters: TCGACCCACGCGTCCG-3' (SEQ ID No 22)

31 GGGTGCCGAGGC-5' (SEQ ID No 23)

32 The ligation was mixed gently and incubated for 16
33 hours at 16°C, then phenol-chloroform extracted,
34 precipitated and vacuum dried. The cDNA/adaptor pellet
35 was resuspended in 41 μ l of DEPC-treated water and
36 digested with 60 units of NotI at 37°C for 2 hours,

1 then phenol-chloroform extracted, precipitated and
2 vacuum dried. The cDNA pellet was re-dissolved in 100 μ l
3 TEN buffer (10mM Tris pH 7.5, 0.1mM EDTA, 25mM NaCl)
4 and size fractionated using a Sephacryl S-500 HR column
5 to remove unligated adapters and small cDNA fragments
6 (<400bp) according to the manufacturers instructions.
7 Fractions were checked by agarose gel electrophoresis
8 and fractions containing cDNA less than 400 base pairs
9 discarded, while the remaining fractions were pooled.

10

11 (d) PCR amplification of oestrogen receptor DNA binding
12 domain.

13

14 The oestrogen receptor was PCR amplified from 5 μ l (150-
15 250ng) of bone marrow cDNA using 25pmol of each of the
16 primers pDM12FOR (SEQ ID No 24) (5'-
17 AAAAGAATTCTGAATGTGTTATTTTAGCTCAGGTCCTGACCTGATTATCAAG
18 ACCCCACTTCACCCCT) and pDM12BAK (SEQ ID No 25) (5'-
19 AAAAGCGGCCGCAGGGGAGGAGGGTCCATGGAATCTGCCAAGGAG-3') in
20 two 50 μ l reactions containing 0.1mM dNTPs, 2.5 units
21 Taq DNA polymerase, and 1x PCR reaction buffer (10mM
22 Tris-HCl pH 9.0, 5mM KCl, 0.01% Triton X[®]-100, 1.5mM
23 MgCl₂) (Promega Ltd, Southampton, U.K.). The pDM12FOR
24 primer anneals to the 3'-end of the DNA binding domain
25 of the oestrogen receptor and incorporates two stop
26 codons, the 38 base pair consensus oestrogen receptor
27 HRE sequence, and an EcoRI restriction site. The
28 pDM12BAK primer anneals to the 5'-end of the DNA
29 binding domain of the oestrogen receptor and
30 incorporates the (Gly)₄Ser linker and the NotI
31 restriction site.

32

33 Reactions were overlaid with mineral oil and PCR
34 carried out on a Techne PHC-3 thermal cycler for 30
35 cycles of 94°C, 1 minute; 65°C, 1 minute; 72°C, 1
36 minute. Reaction products were electrophoresed on an

1 agarose gel, excised and products purified from the gel
2 using a Geneclean II kit according to the manufacturers
3 instructions (Bio101, La Jolla, California, U.S.A.).
4

5 **(e) Restriction digestion and ligation.**
6

7 The PCR reaction appended NotI and EcoRI restriction
8 sites, the (Gly)₄Ser linker, stop codons and the 38 base
9 pair oestrogen receptor target HRE nucleotide sequence
10 to the oestrogen receptor DNA binding domain sequence
11 (see Figure 1). The DNA PCR fragment and the target
12 pDM6 vector (approximately 500ng) were NotI and EcoRI
13 digested for 1 hour at 37°C, and DNA purified by
14 agarose gel electrophoresis and extraction with
15 Geneclean II kit (Bio101, La Jolla, California,
16 U.S.A.). The oestrogen receptor DNA binding domain
17 cassette was ligated into the NotI-EcoRI digested pDM6
18 vector overnight at 16°C, phenol/chloroform extracted
19 and precipitated then electroporated into TG1 *E. coli*
20 (genotype: K12, (Δ lac-pro), supE, thi, hsd5/F' traD36,
21 proA⁺B⁺, LacI^q, LacZ Δ 15) and plated onto 2xTY agar
22 plates supplemented with 1% glucose and 100 μ g/ml
23 ampicillin. Colonies were allowed to grow overnight at
24 37°C. Individual colonies were picked into 5ml 2xTY
25 supplemented with 1% glucose and 100 μ g/ml ampicillin
26 and grown overnight at 37°C. Double stranded phagemid
27 DNA was isolated with a Wizard SV plasmid DNA isolation
28 kit and the sequence confirmed with a Prism dyedeoxy
29 cycle sequencing kit (Perkin-Elmer, Warrington,
30 Lancashire, U.K.) using M13FOR (SEQ ID No 26) (5'-
31 GTAAAACGACGGCCAGT) and M13REV (SEQ ID No 27) (5'-
32 GGATAACAATTTTCACACAGG) oligonucleotides. The pDM12 PDCP
33 display vector DNA sequence between the HindIII and
34 EcoRI restriction sites is shown in Figure 1.
35

36 **Example 2. Insertion of a random-primed human**

1 lymphocyte cDNA into pDM12 and preparation of a master
2 PDCP stock.

3

4 Libraries of peptides can be constructed by many
5 methods known to those skilled in the art. The example
6 given describes a method for constructing a peptide
7 library from randomly primed cDNA, prepared from mRNA
8 isolated from a partially purified cell population.

9

10 mRNA was isolated from approximately 10^9 human
11 peripheral blood lymphocytes using a polyAtract 1000
12 mRNA isolation kit (Promega, Southampton, UK). The cell
13 pellet was resuspended in 4ml extraction buffer (4M
14 guanidine thiocyanate, 25mM sodium citrate pH 7.1, 2%
15 β -mercaptoethanol). 8ml of pre-heated (70°C) dilution
16 buffer (6xSSC, 10mM Tris pH 7.4, 1mM EDTA, 0.25% SDS,
17 1% β -mercaptoethanol) was added to the homogenate and
18 mixed thoroughly by inversion. 10 μ l of biotinylated
19 oligo-dT (50 pmol/ μ l) was added, mixed and the mixture
20 incubated at 70°C for 5 minutes. The lymphocyte cell
21 lysate was transferred to 6x 2ml sterile tubes and spun
22 at 13,000 rpm in a microcentrifuge for ten minutes at
23 ambient temperature to produce a cleared lysate. During
24 this centrifugation, streptavidin coated magnetic beads
25 were resuspended and 6ml transferred to a sterile 50ml
26 Falcon tube, then placed in the magnetic stand in a
27 horizontal position until all the beads were captured.
28 The supernatant was carefully poured off and beads
29 resuspended in 6ml 0.5xSSC, then the capture repeated.
30 This wash was repeated 3 times, and beads resuspended
31 in a final volume of 6ml 0.5xSSC. The cleared lysate
32 was added to the washed beads, mixed by inversion and
33 incubated at ambient temperature for 2 minutes, then
34 beads captured in the magnetic stand in a horizontal
35 position. The beads were resuspended gently in 2ml
36 0.5xSSC and transferred to a sterile 2ml screwtop tube,

1 then captured again in the vertical position, and the
2 wash solution discarded. This wash was repeated twice
3 more. 1ml of DEPC-treated water was added to the beads
4 and mixed gently. The beads were again captured and the
5 eluted mRNA transferred to a sterile tube. 50 μ l was
6 electrophoresed to check the quality and quantity of
7 mRNA, while the remainder was precipitated with 0.1
8 volumes 3M sodium acetate and three volumes absolute
9 ethanol at -80°C overnight in 4 aliquots in sterile
10 1.5ml screwtop tubes.

11

12 Double stranded cDNA was synthesised as described in
13 Example 1 using 5 μ g of lymphocyte mRNA as template.
14 The cDNA was PCR amplified using oligonucleotides
15 CDNAPCRFOR (SEQ ID No 28) (5'-
16 AAAGCGGCCGCACTGGCCTGAGAGA), which anneals to the cDNA
17 synthesis oligonucleotide described in Example 1 which
18 is present at the 3'-end of all synthesised cDNA
19 molecules incorporates a NotI restriction site, and an
20 equimolar mixture of CDNAPCRBAK1, CDNAPCRBAK2 and
21 CDNAPCRBAK3.

22 CDNAPCRBAK1: (SEQ ID No 29) 5'-

23 AAAAGGCCCAGCCGGCCATGGCCCAGCCCACCACGCGTCCG,

24 CDNAPCRBAK2: (SEQ ID No 30) 5'-

25 AAAAGGCCCAGCCGGCCATGGCCCAGTCCCACCACGCGTCCG,

26 CDNAPCRBAK3: (SEQ ID No 31) 5'-

27 AAAAGGCCCAGCCGGCCATGGCCCAGTACCCACCACGCGTCCG),

28 all three of which anneal to the SalI adaptor sequence
29 found at the 5'-end of the cDNA and incorporate a SfiI
30 restriction site at the cDNA 5'-end. Ten PCR reactions
31 were carried out using 2 μ l of cDNA (50ng) per reaction
32 as described in Example 1 using 25 cycles of 94°C, 1
33 minute; 60°C, 1 minute; 72°C, 2 minutes. The reactions
34 were pooled and a 20 μ l aliquot checked by agarose gel
35 electrophoresis, the remainder was phenol/chloroform
36 extracted and ethanol precipitated and resuspended in

1 100 μ l sterile water. 5 μ g of pDM12 vector DNA and
2 lymphocyte cDNA PCR product were SfiI-NotI digested
3 phenol/chloroform extracted and small DNA fragments
4 removed by size selection on Chromaspin 1000 spin
5 columns (Clontech, Palo Alto, California, U.S.A.) by
6 centrifugation at 700g for 2 minutes at room
7 temperature. Digested pDM12 and lymphocyte cDNA were
8 ethanol precipitated and ligated together for 16 hours
9 at 16°C. The ligated DNA was precipitated and
10 electroporated in to TG1 *E. coli*. Cells were grown in
11 1ml SOC medium per cuvette used for 1 hour at 37°C, and
12 plated onto 2xTY agar plates supplemented with 1%
13 glucose and 100 μ g/ml ampicillin. 10⁻⁴, 10⁻⁵ and 10⁻⁶
14 dilutions of the electroporated bacteria were also
15 plated to assess library size. Colonies were allowed to
16 grow overnight at 30°C. 2x10⁸ ampicillin resistant
17 colonies were recovered on the agar plates.
18 The bacteria were then scraped off the plates into 40ml
19 2xTY broth supplemented with 20% glycerol, 1% glucose
20 and 100 μ g/ml ampicillin. 5ml was added to a 20ml 2xTY
21 culture broth supplemented with 1% glucose and 100 μ g/ml
22 ampicillin and infected with 10¹¹ kanamycin resistance
23 units (kru) M13K07 helper phage at 37°C for 30 minutes
24 without shaking, then for 30 minutes with shaking at
25 200rpm. Infected bacteria were transferred to 200ml
26 2xTY broth supplemented with 25 μ g/ml kanamycin,
27 100 μ g/ml ampicillin, and 20 μ M IPTG, then incubated
28 overnight at 37°C, shaking at 200rpm. Bacteria were
29 pelleted at 4000rpm for 20 minutes in 50ml Falcon
30 tubes, and 40ml 2.5M NaCl/20% PEG 6000 was added to
31 200ml of particle supernatant, mixed vigorously and
32 incubated on ice for 1 hour to precipitate PDCP
33 particles. Particles were pelleted at 11000rpm for 30
34 minutes in 250ml Oakridge tubes at 4°C in a Sorvall
35 RC5B centrifuge, then resuspended in 2ml PBS buffer
36 after removing all traces of PEG/NaCl with a pipette,

1 then bacterial debris removed by a 5 minute 13500rpm
2 spin in a microcentrifuge. The supernatant was filtered
3 through a 0.45µm polysulfone syringe filter and stored
4 at -20°C.

5
6 **Example 3. Isolation of human immunoglobulin kappa**
7 **light chains by repeated rounds of selection against**
8 **anti-human kappa antibody.**

9
10 For the first round of library selection a 70x11mm NUNC
11 Maxisorp Immuntube (Life Technologies, Paisley,
12 Scotland U.K.) was coated with 2.5ml of 10µg/ml of
13 anti-human kappa antibody (Seralab, Crawley Down,
14 Sussex, U.K.) in PBS for 2 hours at 37°C. The tube was
15 rinsed three times with PBS (fill & empty) and blocked
16 with 3ml PBS/2% BSA for 2 hours at 37°C and washed as
17 before. 4×10^{12} a.r.u. of pDM12-lymphocyte cDNA PDGP
18 stock was added in 2ml 2% BSA/PBS/0.05% Tween 20, and
19 incubated for 30 minutes on a blood mixer, then for 90
20 minutes standing at ambient temperature. The tube was
21 washed ten times with PBS/0.1% Tween 20, then a further
22 ten times with PBS only. Bound particles were eluted in
23 1ml of freshly prepared 0.1M triethylamine for 10
24 minutes at ambient temperature on a blood mixer. Eluted
25 particles were transferred to 0.5ml 1M Tris pH 7.4,
26 vortex mixed briefly and transferred to ice.

27
28 Neutralised particles were added to 10ml log phase TG1
29 E coli bacteria (optical density: OD_{600nm} 0.3-0.5) and
30 incubated at 37°C without shaking for 30 minutes, then
31 with shaking at 200rpm for 30 minutes. 10^{-3} , 10^{-4} & 10^{-5}
32 dilutions of the infected culture were prepared to
33 estimate the number of particles recovered, and the
34 remainder was spun at 4000 rpm for 10 minutes, and the
35 pellet resuspended in 300µl 2xTY medium by vortex
36 mixing. Bacteria were plated onto 2xTY agar plates

1 supplemented with 1% glucose and 100 μ g/ml ampicillin.
2 Colonies were allowed to grow overnight at 30°C.

3
4 A PDCP stock was prepared from the bacteria recovered
5 from the first round of selection, as described in
6 Example 2 from a 100ml overnight culture. 250 μ l of the
7 round 1 amplified PDCP stock was then selected against
8 anti-human kappa antibody as described above with the
9 tube was washed twelve times with PBS/0.1% Tween 20,
10 then a further twelve times with PBS only.

11
12 To identify selected clones, eighty-eight individual
13 clones recovered from the second round of selection
14 were then tested by ELISA for binding to anti-human
15 kappa antibody. Individual colonies were picked into
16 100 μ l 2xTY supplemented with 100 μ g/ml ampicillin and 1%
17 glucose in 96-well plates (Costar) and incubated at
18 37°C and shaken at 200rpm for 4 hours. 25 μ l of each
19 culture was transferred to a fresh 96-well plate,
20 containing 25 μ l/well of the same medium plus 10⁷ k.r.u.
21 M13K07 kanamycin resistant helper phage and incubated
22 at 37°C for 30 minutes without shaking, then incubated
23 at 37°C and shaken at 200rpm for a further 30 minutes.
24 160 μ l of 2xTY supplemented with 100 μ g/ml ampicillin,
25 25 μ g/ml kanamycin, and 20 μ M IPTG was added to each well
26 and particle amplification continued for 16 hours at
27 37°C while shaking at 200rpm. Bacterial cultures were
28 spun in microtitre plate carriers at 2000g for 10
29 minutes at 4°C in a benchtop centrifuge to pellet
30 bacteria and culture supernatant used for ELISA.

31
32 A Dynatech Immulon 4 ELISA plate was coated with
33 200ng/well anti-human kappa antibody in 100 μ l /well PBS
34 for one hour at 37°C. The plate was washed 2x200 μ l/well
35 PBS and blocked for 1 hour at 37°C with 200 μ l/well 2%
36 BSA/PBS and then washed 2x200 μ l/well PBS. 50 μ l PDCP

1 culture supernatant was added to each well containing
2 50 μ l/well 4% BSA/PBS/0.1%Tween 20, and allowed to bind
3 for 1 hour at ambient temperature. The plate was washed
4 three times with 200 μ l/well PBS/0.1% Tween 20, then
5 three times with 200 μ l/well PBS. Bound PDCPs were
6 detected with 100 μ l/well, 1:5000 diluted anti-M13-HRP
7 conjugate (Pharmacia) in 2% BSA/PBS/0.05% Tween 20 for
8 1 hour at ambient temperature and the plate washed six
9 times as above. The plate was developed for 5 minutes
10 at ambient temperature with 100 μ l/well freshly prepared
11 TMB (3,3',5,5'-Tetramethylbenzidine) substrate buffer
12 (0.005% H₂O₂, 0.1mg/ml TMB in 24mM citric acid/52mM
13 sodium phosphate buffer pH 5.2). The reaction was
14 stopped with 100 μ l/well 12.5% H₂SO₄ and read at 450nm.
15 (ELISA data for binding clones is shown in Figure 2).

16

17 These clones were then sequenced with M13REV primer
18 (SEQ ID No 27) as in Example 1. The sequence of two of
19 the clones isolated is shown in Figure 3 (see SEQ ID
20 Nos 7 to 10).

21

22 **Example 4. Construction of the pDM14 N-terminal display** 23 **vector**

24

25 It would be useful to design vectors that contain a
26 second DBD binding sequence, such as a second oestrogen
27 receptor HRE sequence, thus allowing the display of
28 increased numbers of peptides per PDCP. Peale et al.
29 (1988, Proc. Natl. Acad. Sci. USA 85: 1038-1042)
30 describe a number of oestrogen receptor HRE sequences.
31 These sequences were used to define an HRE sequence,
32 which differs from that cloned in pDM12, which we used
33 to create a second N-terminal display vector (pDM14).
34 The oligonucleotide: 5'-AAAAGAATTCGAGGTTACATTAACCTTGT
35 CCGGTCAGACTGACCCAAGTCGACCTGAATGTGTTATTTTAG-3' (SEQ ID
36 No 32) was synthesised and used to mutagenise pDM12 by

1 PCR with pDM12BAK oligonucleotide as described in
2 Example 1 using 100ng pDM12 vector DNA as template. The
3 resulting DNA fragment, which contained the oestrogen
4 receptor DBD and two HRE sequences separated by a SalI
5 restriction enzyme site, was NotI-EcoRI restriction
6 enzyme digested and cloned into NotI-EcoRI digested
7 pDM12 vector DNA as described in Example 1 to create
8 pDM14. The sequence of pDM14 between the HindIII and
9 EcoRI restriction enzyme sites was checked by DNA
10 sequencing. The final vector sequence between these two
11 sites is shown in Figure 4 (see SEQ ID Nos 11 and 12).

12

13 **Example 5. Construction of the pDM16 C-terminal display**
14 **vector**

15

16 In order to demonstrate the display of peptides fused
17 to the C-terminus of a DBD on a PDCP a suitable vector,
18 pDM16, was created.

19

20 In pDM16 the pelB leader DNA sequence is fused directly
21 to the oestrogen receptor DBD sequence removing the
22 multiple cloning sites and the Gly₄Ser linker DNA
23 sequence found in pDM12 and pDM14, which are appended
24 to the C-terminal end of the DBD sequence upstream of
25 the HRE DNA sequence.

26

27 To create this vector two separate PCR reactions were
28 carried out on a Techne Progene thermal cycler for 30
29 cycles of 94°C, 1 minute; 60°C, 1 minute; 72°C, 1
30 minute. Reaction products were electrophoresed on an
31 agarose gel, excised and products purified from the gel
32 using a Mermaid or Geneclean II kit, respectively,
33 according to the manufacturers instructions (Bio101, La
34 Jolla, California, U.S.A.).

35

36 In the first, the 5'-untranslated region and pelB

1 leader DNA sequence was amplified from 100ng of pDM12
2 vector DNA using 50pmol of each of the oligonucleotides
3 pelBFOR (SEQ ID No 33) (5'-CCTTGGCAGATTCCATCT
4 CGGCCATTGCCGGC-3') and M13REV (SEQ ID NO 27) (see
5 above) in a 100 μ l reaction containing 0.1mM dNTPs, 2.5
6 units Taqplus DNA polymerase, and 1x High Salt PCR
7 reaction buffer (20mM Tris-HCl pH 9.2, 60mM KCl, 2mM
8 MgCl₂) (Stratagene Ltd, Cambridge, U.K.).

9
10 In the second, the 3'-end of the pelB leader sequence
11 and the oestrogen receptor DBD was amplified from 100ng
12 of pDM12 vector DNA using 50pmol of each of the
13 oligonucleotides pelBBAK (SEQ ID No 34) (5'-CCGGCAA
14 TGGCCGAGATGGAATCTGCCAAGG-3') and pDM16FOR (SEQ ID No
15 35) (5'-TTTGTGCGACTCAATCAGTTATGCGGCCGCCAGCTGCAGG
16 AGGGCCGGCTGGGCCGACCCTCCTCCCCCAGACCCCACTTCACCCC-3') in a
17 100 μ l reaction containing 0.1mM dNTPs, 2.5 units
18 Taqplus DNA polymerase, and 1x High Salt PCR reaction
19 buffer (Stratagene Ltd, Cambridge, U.K.). Following gel
20 purification both products were mixed together and a
21 final round of PCR amplification carried out to link
22 the two products together as described above, in a
23 100 μ l reaction containing 0.1mM dNTPs, 2.5 units Taq
24 DNA polymerase, and 1x PCR reaction buffer (10mM Tris-
25 HCl pH 9.0, 5mM KCl, 0.01% Triton X[®]-100, 1.5mM MgCl₂)
26 (Promega Ltd, Southampton, U.K.).

27
28 The resulting DNA fragment, was HindIII-SalI
29 restriction enzyme digested and cloned into HindIII-
30 SalI digested pDM14 vector DNA as described in Example
31 1 to create pDM16. The sequence of pDM16 between the
32 HindIII and EcoRI restriction enzyme sites was checked
33 by DNA sequencing. The final vector sequence between
34 these two sites is shown in Figure 5 (see SEQ ID Nos 13
35 and 14).

36

Example 6. Display of the C-terminal fragment of human N-cadherin on the surface of a PDCP

cDNA libraries of peptides can be constructed by many methods known to those skilled in the art. One commonly used method for constructing a peptide library uses oligo dT primed cDNA, prepared from polyA⁺ mRNA. In this method the first-strand synthesis is carried out using an oligonucleotide which anneals to the 3'-end polyA tail of the mRNA composed of T_n (where n is normally between 10 and 20 bases) and a restriction enzyme site such as NotI to facilitate cloning of cDNA. The cDNA cloned by this method is normally composed of the polyA tail, the 3'- end untranslated region and the C-terminal coding region of the protein. As an example of the C-terminal display of peptides on a PDCP, a human cDNA isolated from a library constructed by the above method was chosen.

The protein N-cadherin is a cell surface molecule involved in cell-cell adhesion. The C-terminal cytoplasmic domain of the human protein (Genbank database accession number: M34064) is recognised by a commercially available monoclonal antibody which was raised against the C-terminal 23 amino acids of chicken N-cadherin (SIGMA catalogue number: C-1821). The 1.4kb human cDNA fragment encoding the C-terminal 99 amino acids, 3'- untranslated region and polyA tail (NotI site present at the 3'-end of the polyA tail) was amplified from approximately 20ng pDM7-NCAD#C with 25pmol of each oligonucleotide M13FOR (SEQ ID No 26) and CDNPCRBAK1 (SEQ ID No 29) (see above) in a 50μl reaction containing 0.1mM dNTPs, 2.5 units Taqplus DNA polymerase, and 1x High Salt PCR reaction buffer (20mM Tris-HCl pH 9.2, 60mM KCl, 2mM MgCl₂) (Stratagene Ltd, Cambridge, U.K.) on a Techne Progene thermal cycler for

1 30 cycles of 94°C, 1 minute; 60°C, 1 minute; 72°C, 1
2 minute. Following gel purification and digestion with
3 SfiI and NotI restriction enzymes, the PCR product was
4 cloned into pDM16 using an analogous protocol as
5 described in Example 1.

6
7 Clones containing inserts were identified by ELISA of
8 96 individual PDCP cultures prepared as described in
9 Example 3. A Dynatech Immulon 4 ELISA plate was coated
10 with 1:250 diluted anti-pan cadherin monoclonal
11 antibody in 100µl /well PBS overnight at 4°C. The plate
12 was washed 3x200µl/well PBS and blocked for 1 hour at
13 37°C with 200µl/well 2% Marvel non-fat milk powder/PBS
14 and then washed 2x200µl/well PBS. 50µl PDCP culture
15 supernatant was added to each well containing 50µl/well
16 4% Marvel/PBS, and allowed to bind for 1 hour at
17 ambient temperature. The plate was washed three times
18 with 200µl/well PBS/0.1% Tween 20, then three times
19 with 200µl/well PBS. Bound PDCPs were detected with
20 100µl/well, 1:5000 diluted anti-M13-HRP conjugate
21 (Pharmacia) in 2% Marvel/PBS for 1 hour at ambient
22 temperature and the plate washed six times as above.
23 The plate was developed for 15 minutes at ambient
24 temperature with 100µl/well freshly prepared TMB
25 (3,3',5,5'-Tetramethylbenzidine) substrate buffer
26 (0.005% H₂O₂, 0.1mg/ml TMB in 24mM citric acid/52mM
27 sodium phosphate buffer pH 5.2). The reaction was
28 stopped with 100µl/well 12.5% H₂SO₄ and read at 450nm.
29 The nucleotide sequence of an ELISA positive clone
30 insert and DBD junction was checked by DNA sequencing
31 using oligonucleotides M13FOR (SEQ ID No 26) (see
32 Example 1) and ORSEQBAK (SEQ ID No 36) (5'-
33 TGTGAAACACAAGCGCCAG-3').

34
35 A fifty-fold concentrated stock of C-terminal N-
36 cadherin PDCP particles was prepared by growing the un-

1 infected TG1 clone in 1ml 2xTY culture broth
2 supplemented with 1% glucose and 100µg/ml ampicillin
3 for five hours at 37°C, shaking at 200rpm and infecting
4 with 10⁸ kanamycin resistance units (kru) M13K07 helper
5 phage at 37°C for 30 minutes without shaking, then for
6 30 minutes with shaking at 200rpm. Infected bacteria
7 were transferred to 20ml 2xTY broth supplemented with
8 25µg/ml kanamycin, 100µg/ml ampicillin, and 20µM IPTG,
9 then incubated overnight at 30°C, shaking at 200rpm.
10 Bacteria were pelleted at 4000rpm for 20 minutes in
11 50ml Falcon tubes, and 4ml 2.5M NaCl/20% PEG 6000 was
12 added to 20ml of PDCP supernatant, mixed vigorously and
13 incubated on ice for 1 hour to precipitate particles.

14
15 The particles were pelleted at 11000rpm for 30 minutes
16 in 50ml Oakridge tubes at 4°C in a Sorvall RC5B
17 centrifuge, then resuspended in PBS buffer after
18 removing all traces of PEG/NaCl with a pipette, then
19 bacterial debris removed by a 5 minute 13500rpm spin in
20 a microcentrifuge. The supernatant was filtered through
21 a 0.45µm polysulfone syringe filter. The concentrated
22 stock was two-fold serially diluted and used in ELISA
23 against plates coated with anti-pan-cadherin antibody
24 as described above (see Figure 6).

25
26 This example demonstrates the principle of C-terminal
27 display using PDCPs, that C-terminal DBD-peptide fusion
28 PDCPs can be made which can be detected in ELISA, and
29 the possibility that oligo dT primed cDNA libraries may
30 be displayed using this method.

31

32 **Example 7. Display of *in vivo* biotinylated C-terminal**
33 **domain of human propionyl CoA carboxylase on the**
34 **surface of a PDCP**

35

36 Example 6 shows that the C-terminal domain of human N-

1 cadherin can be expressed on the surface of a PDCP as a
2 C-terminal fusion with the DBD. Here it is shown that
3 the C-terminal domain of another human protein
4 propionyl CoA carboxylase alpha chain (Genbank
5 accession number: X14608) can similarly be displayed,
6 suggesting that this methodology may be general.

7
8 The alpha sub-unit of propionyl CoA carboxylase alpha
9 chain (PCC) contains 703 amino acids and is normally
10 biotinylated at position 669. It is demonstrated that
11 the PCC peptide displayed on the PDCP is biotinylated,
12 as has been shown to occur when the protein is
13 expressed in bacterial cells (Leon-Del-Rio & Gravel;
14 1994, J. Biol. Chem. 37, 22964-22968).

15
16 The 0.8kb human cDNA fragment of PCC alpha encoding the
17 C-terminal 95 amino acids, 3'- untranslated region and
18 polyA tail (NotI site present at the 3'-end of the
19 polyA tail) was amplified and cloned into pDM16 from
20 approximately 20ng pDM7-PCC#C with 25pmol of each
21 oligonucleotide M13FOR (SEQ ID No 26) and CDNPCRBAK1
22 (SEQ ID No 29) as described in Example 6.

23
24 Clones containing inserts were identified by ELISA as
25 described in Example 6, except that streptavidin was
26 coated onto the ELISA plate at 250ng/well, in place of
27 the anti-cadherin antibody. The nucleotide sequence of
28 an ELISA positive clone insert and DBD junction was
29 checked by DNA sequencing using oligonucleotides M13FOR
30 (SEQ ID No 26) and ORSEQBAK (SEQ ID No 36) (see above).
31 A fifty-fold concentrated stock of C-terminal PCC PDCP
32 particles was prepared and tested in ELISA against
33 streptavidin as described in Example 6 (see Figure 7).

34
35 This example shows not only that the peptide can be
36 displayed as a C-terminal fusion on a PDCP, but also

1 that *in vivo* modified peptides can be displayed.

2

3 **Example 8. Construction of a human scFv PDCP display**
4 **library**

5

6 This example describes the generation of a human
7 antibody library of scFvs made from an un-immunised
8 human. The overall strategy for the PCR assembly of
9 scFv fragments is similar to that employed by Marks, J.
10 D. et al. 1991, J. Mol. Biol. 222: 581-597. The
11 antibody gene oligonucleotides used to construct the
12 library are derived from the Marke et al., paper and
13 from sequence data extracted from the Kabat database
14 (Kabat, E. A. et al., Sequences of Proteins of
15 Immunological Interest. 4th edition. U.S. Department of
16 Health and Human Services. 1987). The three linker
17 oligonucleotides are described by Zhou et al. (1994,
18 Nucleic Acids Res., 22: 888-889), all oligonucleotides
19 used are detailed in Table 1.

20

21 First, mRNA was isolated from peripheral blood
22 lymphocytes and cDNA prepared for four repertoires of
23 antibody genes IgD, IgM, Ig κ and Ig λ , using four
24 separate cDNA synthesis primers. VH genes were
25 amplified from IgD and IgM primed cDNA, and VL genes
26 were amplified from Ig κ and Ig λ primed cDNA. A portion
27 of each set of amplified heavy chain or light chain DNA
28 was then spliced with a separate piece of linker DNA
29 encoding the 15 amino acids (Gly₄ Ser)₃ (Huston, J. S.
30 et al. 1989, Gene, 77: 61). The 3'-end of the VH PCR
31 products and the 5'-end of the VL PCR products overlap
32 the linker sequence as a result of incorporating linker
33 sequence in the JH, V κ and V λ family primer sets (Table
34 1). Each VH-linker or linker-VL DNA product was then
35 spliced with either VH or VL DNA to produce the primary
36 scFv product in a VH-linker-VL configuration. This scFv

1 product was then amplified and cloned into pDM12 as a
2 SfiI-NotI fragment, electroporated into TG1 and a
3 concentrated PDCP stock prepared.

4
5 **mRNA isolation and cDNA synthesis.**

6 Human lymphocyte mRNA was purified as described in
7 Example 2. Separate cDNA reactions were performed with
8 IGDCDNAFOR (SEQ ID No 37), IGMCDNAFOR (SEQ ID No 38),
9 IGKCDNAFOR (SEQ ID No 39) and IGLCDNAFOR (SEQ ID No 40)
10 oligonucleotides. 50pmol of each primer was added to
11 approximately 5µg of mRNA in 20µl of nuclease free
12 water and heated to 70°C for 5 minutes and cooled
13 rapidly on ice, then made up to a final reaction volume
14 of 100µl containing 50mM Tris pH 8.3, 75mM KCl, 3mM
15 MgCl₂, 10mM DTT, 0.5mM dNTPs, and 2000 units of
16 Superscript II reverse transcriptase (Life
17 Technologies, Paisley, Scotland, U.K.). The reactions
18 were incubated at 37°C for two hours, then heated to
19 95°C for 5 minutes.

20
21 **Primary PCRs.**

22 For the primary PCR amplifications separate
23 amplifications were set up for each family specific
24 primer with either an equimolar mixture of the JHFOR
25 primer set (SEQ ID Nos 41 to 44) for IgM and IgD cDNA,
26 or with SCFVκFOR (SEQ ID No 51) or SCFVλFOR (SEQ ID No
27 52) for IgK or Igλ cDNA respectively e.g. VH1BAK and
28 JHFOR set; Vκ2BAK (SEQ ID No 54) and SCFVκFOR (SEQ ID
29 No 51); Vλ3aBAK (SEQ ID No 66) and SCFVλFOR (SEQ ID No
30 52) etc. Thus, for IgM, IgD and Igκ cDNA six separate
31 reactions were set up, and seven for Igλ cDNA. A 50µl
32 reaction mixture was prepared containing 2µl cDNA,
33 25pmol of the appropriate FOR and BAK primers, 0.1mM
34 dNTPs, 2.5 units Taqplus DNA polymerase, and 1x High
35 Salt PCR reaction buffer (20mM Tris-HCl pH 9.2, 60mM
36 KCl, 2mM MgCl₂) (Stratagene Ltd, Cambridge, U.K.).

1 Reactions were amplified on a Techne Progene thermal
2 cyclor for 30 cycles of 94°C, 1 minute; 60°C, 1 minute;
3 72°C, 2 minutes, followed by 10 minutes at 72°C. Fifty
4 microlitres of all 25 reaction products were
5 electrophoresed on an agarose gel, excised and products
6 purified from the gel using a Geneclean II kit
7 according to the manufacturers instructions (Bio101, La
8 Jolla, California, U.S.A.). All sets of IgD, IgM, IgK
9 or Igλ reaction products were pooled to produce VH or
10 VL DNA sets for each of the four repertoires. These
11 were then adjusted to approximately 20ng/μl.
12

13 **Preparation of linker.**

14 Linker product was prepared from eight 100μl reactions
15 containing 5ng LINKAMP3T (SEQ ID No 76) template
16 oligonucleotide, 50pmol of LINKAMP3 (SEQ ID No 74) and
17 LINKAMP5 (SEQ ID No 75) primers, 0.1mM dNTPs, 2.5 units
18 Taqplus DNA polymerase, and 1x High Salt PCR reaction
19 buffer (20mM Tris-HCl pH 9.2, 60mM KCl, 2mM MgCl₂)
20 (Stratagene Ltd, Cambridge, U.K.). Reactions were
21 amplified on a Techne Progene thermal cyclor for 30
22 cycles of 94°C, 1 minute; 60°C, 1 minute; 72°C, 1
23 minute, followed by 10 minutes at 72°C. All reaction
24 product was electrophoresed on a 2% low melting point
25 agarose gel, excised and products purified from the gel
26 using a Mermaid kit according to the manufacturers
27 instructions (Bio101, La Jolla, California, U.S.A.) and
28 adjusted to 5ng/μl.
29

30 **First stage linking.**

31 Four linking reactions were prepared for each
32 repertoire using 20ng of VH or VL DNA with 5ng of
33 Linker DNA in 100μl reactions containing (for IgM or
34 IgD VH) 50pmol of LINKAMPFOR and VH1-6BAK set, or,
35 50pmol LINKAMPBAK and either SCFVκFOR (Igκ) or SCFVλFOR
36 (Igλ), 0.1mM dNTPs, 2.5 units Taq DNA polymerase, and

1 1x PCR reaction buffer (10mM Tris-HCl pH 9.0, 5mM KCl,
2 0.01% Triton X^{*}-100, 1.5mM MgCl₂) (Promega Ltd,
3 Southampton, U.K.). Reactions were amplified on a
4 Techne Progene thermal cycler for 30 cycles of 94°C, 1
5 minute; 60°C, 1 minute; 72°C, 2 minutes, followed by 10
6 minutes at 72°C. Reaction products were electrophoresed
7 on an agarose gel, excised and products purified from
8 the gel using a Geneclean II kit according to the
9 manufacturers instructions (Bio101, La Jolla,
10 California, U.S.A.) and adjusted to 20ng/μl.

11

12 **Final linking and reamplification.**

13 To prepare the final scFv DNA products, five 100μl
14 reactions were performed for VH-LINKER plus VL DNA,
15 and, five 100μl reactions were performed for VH plus
16 LINKER-VL DNA for each of the four final repertoires
17 (IgM VH-VK, VH-Vλ; IgD VH-VK, VH-Vλ) as described in
18 step (d) above using 20ng of each component DNA as
19 template. Reaction products were electrophoresed on an
20 agarose gel, excised and products purified from the gel
21 using a Geneclean II kit according to the manufacturers
22 instructions (Bio101, La Jolla, California, U.S.A.) and
23 adjusted to 20ng/μl. Each of the four repertoires was
24 then re-amplified in a 100μl reaction volume containing
25 2ng of each linked product, with 50pmol VHBK1-6 (SEQ
26 ID Nos 53 to 58) and either the JKFOR (SEQ ID Nos 66 to
27 70) or JλFOR (SEQ ID Nos 71 to 73) primer sets, in the
28 presence of 0.1mM dNTPs, 2.5 units Taq DNA polymerase,
29 and 1x PCR reaction buffer (10mM Tris-HCl pH 9.0, 5mM
30 KCl, 0.01% Triton X^{*}-100, 1.5mM MgCl₂) (Promega Ltd,
31 Southampton, U.K.). Thirty reactions were performed per
32 repertoire to generate enough DNA for cloning.
33 Reactions were amplified on a Techne Progene thermal
34 cycler for 25 cycles of 94°C, 1 minute; 65°C, 1 minute;
35 72°C, 2 minutes, followed by 10 minutes at 72°C.
36 Reaction products were phenol-chloroform extracted,

1 ethanol precipitated, vacuum dried and re-suspended in
2 80 μ l nuclease free water.

3
4 **Cloning into pDM12.**

5 Each of the four repertoires was SfiI-NotI digested,
6 and electrophoresed on an agarose gel, excised and
7 products purified from the gel using a Geneclean II kit
8 according to the manufacturers instructions (Bio101, La
9 Jolla, California, U.S.A.). Each of the four
10 repertoires was ligated overnight at 16°C in 140 μ l with
11 10 μ g of SfiI-NotI cut pDM12 prepared as in Example 2,
12 and 12 units of T4 DNA ligase (Life Technologies,
13 Paisley, Scotland, U.K.). After incubation the
14 ligations were adjusted to 200 μ l with nuclease free
15 water, and DNA precipitated with 1 μ l 20mg/ml glycogen,
16 100 μ l 7.5M ammonium acetate and 900 μ l ice-cold (-20°C)
17 absolute ethanol, vortex mixed and spun at 13,000rpm
18 for 20 minutes in a microfuge to pellet DNA. The
19 pellets were washed with 500 μ l ice-cold 70% ethanol by
20 centrifugation at 13,000rpm for 2 minutes, then vacuum
21 dried and re-suspended in 10 μ l DEPC-treated water. 1 μ l
22 aliquots of each repertoire was electroporated into
23 80 μ l *E. coli* (TG1). Cells were grown in 1ml SOC medium
24 per cuvette used for 1 hour at 37°C, and plated onto
25 2xTY agar plates supplemented with 1% glucose and
26 100 μ g/ml ampicillin. 10⁻⁴, 10⁻⁵ and 10⁻⁶ dilutions of the
27 electroporated bacteria were also plated to assess
28 library size. Colonies were allowed to grow overnight
29 at 30°C. Cloning into SfiI-NotI digested pDM12 yielded
30 an IgM- κ/λ repertoire of 1.16x10⁹ clones, and an IgD- κ/λ
31 repertoire of 1.21x10⁹ clones.

32
33 **Preparation of PDCP stock.**

34 Separate PDCP stocks were prepared for each repertoire
35 library. The bacteria were then scraped off the plates
36 into 30ml 2xTY broth supplemented with 20% glycerol, 1%

1 glucose and 100 μ g/ml ampicillin. 3ml was added to a
2 50ml 2xTY culture broth supplemented with 1% glucose
3 and 100 μ g/ml ampicillin and infected with 10¹¹ kanamycin
4 resistance units (kru) M13K07 helper phage at 37°C for
5 30 minutes without shaking, then for 30 minutes with
6 shaking at 200rpm. Infected bacteria were transferred
7 to 500ml 2xTY broth supplemented with 25 μ g/ml
8 kanamycin, 100 μ g/ml ampicillin, and 20 μ M IPTG, then
9 incubated overnight at 30°C, shaking at 200rpm.
10 Bacteria were pelleted at 4000rpm for 20 minutes in
11 50ml Falcon tubes, and 80ml 2.5M NaCl/20% PEG 6000 was
12 added to 400ml of particle supernatant, mixed
13 vigorously and incubated on ice for 1 hour to
14 precipitate PDCP particles. Particles were pelleted at
15 11000rpm for 30 minutes in 250ml Oakridge tubes at 4°C
16 in a Sorvall RC5B centrifuge, then resuspended in 40ml
17 water and 8ml 2.5M NaCl/20% PEG 6000 added to
18 reprecipitate particles, then incubated on ice for 20
19 minutes. Particles were again pelleted at 11000rpm for
20 30 minutes in 50ml Oakridge tubes at 4°C in a Sorvall
21 RC5B centrifuge, then resuspended in 5ml PBS buffer,
22 after removing all traces of PEG/NaCl with a pipette.
23 Bacterial debris was removed by a 5 minute 13500rpm
24 spin in a microcentrifuge. The supernatant was filtered
25 through a 0.45 μ m polysulfone syringe filter, adjusted
26 to 20% glycerol and stored at -70°C.

27

28 **Example 9. Isolation of binding activity from a N-**
29 **terminal display PDCP library of human scFvs**

30

31 The ability to select binding activities to a target of
32 interest from a human antibody library is important due
33 to the possibility of generating therapeutic human
34 antibodies. In addition, such libraries allow the
35 isolation of antibodies to targets which cannot be used
36 for traditional methods of antibody generation due to

1 toxicity, low immunogenicity or ethical considerations.
2 In this example we demonstrate the isolation of
3 specific binding activities against a peptide antigen
4 from a PDCP library of scFvs from an un-immunised
5 human.

6
7 The generation of the library, used for the isolation
8 of binding activities in this example, is described in
9 Example 8.

10
11 Substance P is an eleven amino acid neuropeptide
12 involved in inflammatory and pain responses *in vivo*. It
13 has also been implicated in a variety of disorders such
14 as psoriasis and asthma amongst others (Misery, L.
15 1997, Br. J. Dermatol., 137: 843-850; Maggi, C. A.
16 1997, Regul. Pept. 70: 75-90; Choi, D. C. & Kwon, O.J.,
17 1998, Curr. Opin. Pulm. Med., 4: 16-24). Human
18 antibodies which neutralise this peptide may therefore
19 have some therapeutic potential. As this peptide is too
20 small to coat efficiently on a tube, as described in
21 Example 3, selection of binding activities was
22 performed in-solution, using N-terminal biotinylated
23 substance P and capturing bound PDCP particles on
24 streptavidin-coated magnetic beads.

25
26 **Enrichment for substance P binding PDCP particles.**

27 An aliquot of approximately 10^{13} a.r.u. IgM and IgD scFv
28 library stock was mixed with $1\mu\text{g}$ biotinylated substance
29 P in $800\mu\text{l}$ 4% BSA/0.1% Tween 20/PBS, and allowed to
30 bind for two hours at ambient temperature. Bound PDCPs
31 were then captured onto 1ml of BSA blocked streptavidin
32 coated magnetic beads for 10 minutes at ambient
33 temperature. The beads were captured to the side of the
34 tube with a magnet (Promega), and unbound material
35 discarded. The beads were washed eight times with 1ml
36 PBS/0.1% Tween 20/ $10\mu\text{g/ml}$ streptavidin, then two times

1 with 1ml of PBS by magnetic capture and removal of wash
2 buffer. After the final wash bound PDCPs were eluted
3 with 1ml of freshly prepared 0.1M triethylamine for 10
4 minutes, the beads were captured, and eluted particles
5 transferred to 0.5ml 1M Tris-HCl pH 7.4. Neutralised
6 particles were added to 10ml log phase TG1 *E. coli*
7 bacteria and incubated at 37°C without shaking for 30
8 minutes, then with shaking at 200rpm for 30 minutes.
9 10^{-3} , 10^{-4} & 10^{-5} dilutions of the infected culture were
10 prepared to estimate the number of particles recovered,
11 and the remainder was spun at 4000 rpm for 10 minutes,
12 and the pellet resuspended in 300 μ l 2xTY medium by
13 vortex mixing. Bacteria were plated onto 2xTY agar
14 plates supplemented with 1% glucose and 100 μ g/ml
15 ampicillin. Colonies were allowed to grow overnight at
16 30°C. A 100-fold concentrated PDCP stock was prepared
17 from a 200ml amplified culture of these bacteria as
18 described above, and 0.5ml used in as second round of
19 selection with 500ng biotinylated substance P. For this
20 round 100 μ g/ml streptavidin was included in the wash
21 buffer.

22

23 ELISA identification of binding clones.

24 Binding clones were identified by ELISA of 96
25 individual PDCP cultures prepared as described in
26 Example 3 from colonies recovered after the second
27 round of selection. A Dynatech Immulon 4 ELISA plate
28 was coated with 200ng/well streptavidin in 100 μ l /well
29 PBS for 1 hour at 37°C. The plate was washed
30 3x200 μ l/well PBS and incubated with 10ng/well
31 biotinylated substance P in 100 μ l /well PBS for 30
32 minutes at 37°C The plate was washed 3x200 μ l/well PBS
33 and blocked for 1 hour at 37°C with 200 μ l/well 2%
34 Marvel non-fat milk powder/PBS and then washed
35 2x200 μ l/well PBS. 50 μ l PDCP culture supernatant was
36 added to each well containing 50 μ l/well 4% Marvel/PBS,

1 and allowed to bind for 1 hour at ambient temperature.
2 The plate was washed three times with 200 μ l/well
3 PBS/0.1% Tween 20, then three times with 200 μ l/well
4 PBS. Bound PDCPs were detected with 100 μ l/well, 1:5000
5 diluted anti-M13-HRP conjugate (Pharmacia) in 2%
6 Marvel/PBS for 1 hour at ambient temperature and the
7 plate washed six times as above. The plate was
8 developed for 10 minutes at ambient temperature with
9 100 μ l/well freshly prepared TMB (3,3',5,5'-
10 Tetramethylbenzidine) substrate buffer (0.005% H₂O₂,
11 0.1mg/ml TMB in 24mM citric acid/52mM sodium phosphate
12 buffer pH 5.2). The reaction was stopped with
13 100 μ l/well 12.5% H₂SO₄ and read at 450nm. Out of 96
14 clones tested, 10 gave signals greater than twice
15 background (background = 0.05).
16

17 **Characterization of a binding clone.**

18 A 50-fold concentrated PDCP stock was prepared from a
19 100ml amplified culture of a single ELISA positive
20 clone as described above. 10 μ l per well of this stock
21 was tested in ELISA as described above for binding to
22 streptavidin, streptavidin-biotinylated-substance P and
23 streptavidin-biotinylated-CGRP (N-terminal
24 biotinylated). Binding was only observed in
25 streptavidin-biotinylated-substance P coated wells
26 indicating that binding was specific. In addition,
27 binding to streptavidin-biotinylated substance P was
28 completely inhibited by incubating the PDCP with 1 μ g/ml
29 free substance P (see Figure 8). The scFv VH (SEQ ID
30 Nos 15 and 16) and VL (SEQ ID Nos 17 and 18) DNA and
31 amino acid sequence was determined by DNA sequencing
32 with oligonucleotides M13REV (SEQ ID No27) and ORSEQFOR
33 (SEQ ID No 36) and is shown in Figure 9.
34

35 The results indicate that target binding activities can
36 be isolated from PDCP display libraries of human scFv

1 fragments.

2

3 **Example 10**

4 In another example the invention provides methods for
5 screening a DNA library whose members require more than
6 one chain for activity, as required by, for example,
7 antibody Fab fragments for ligand binding. To increase
8 the affinity of an antibody of known heavy and light
9 chain sequence, libraries of unknown light chains
10 co-expressed with a known heavy chain are screened for
11 higher affinity antibodies. The known heavy chain
12 antibody DNA sequence is joined to a nucleotide
13 sequence encoding a oestrogen receptor DNA binding
14 domain in a phage vector which does not contain the
15 oestrogen receptor HRE sequence. The antibody DNA
16 sequence for the known heavy chain (VH and CH1) gene is
17 inserted in the 5' region of the oestrogen receptor DBD
18 DNA, behind an appropriate promoter and translation
19 sequences and a sequence encoding a signal peptide
20 leader directing transport of the downstream fusion
21 protein to the periplasmic space. The library of
22 unknown light chains (VL and CL) is expressed
23 separately from a phagemid expression vector which also
24 contains the oestrogen receptor HRE sequence. Thus when
25 both heavy and light chains are expressed in the same
26 host cell, following infection with the phage
27 containing the heavy chain-DBD fusion, the light chain
28 phagemid vector is preferentially packaged into mature
29 phage particles as single stranded DNA, which is bound
30 by the heavy chain-DBD fusion protein during the
31 packaging process. The light chain proteins are
32 transported to the periplasm where they assemble with
33 the heavy chain that is fused to the DBD protein as it
34 exits the cell on the PDCP. In this example the DBD
35 fusion protein and the HRE DNA sequences are not
36 encoded on the same vector, the unknown peptide

1 sequences are present on the same vector as the HRE
2 sequence. Peptide display carrier packages (PDCP) which
3 encode the protein of interest can then be selected by
4 means of a ligand specific for the antibody.

Table 1 (i) Oligonucleotide primers used for human scFv library construction

cDNA synthesis primers

IgMCDNAFOR	TGGAAGAGGCACGTTCTTTTCTTT
IgDCDNAFOR	CTCCTTCTTACTCTTGCTGGCGGT
IgKCDNAFOR	AGACTCTCCCCTGTTGAAGCTCTT
IgλCDNAFOR	TGAAGATTCTGTAGGGGCCACTGTCTT

JHFOR primers

JH1-2FOR	TGAACCGCCTCCACCTGAGGAGACGGTGACCAGGGTGCC
JH3FOR	TGAACCGCCTCCACCTGAAGAGACGGTGACCATTGTCCC
JH4-5FOR	TGAACCGCCTCCACCTGAGGAGACGGTGACCAGGGTTCC
JH6FOR	TGAACCGCCTCCACCTGAGGAGACGGTGACCGTGGTCCC

VH familyBAKprimers

VH1BAK	TTTTTGGCCCAGCCGGCCATGGCCCAGGTGCAGCTGGTGCAGTCTGG
VH2BAK	TTTTTGGCCCAGCCGGCCATGGCCCAGGTCAACTTAAGGGAGTCTGG
VH3BAK	TTTTTGGCCCAGCCGGCCATGGCCGAGGTGCAGCTGGTGGAGTCTGG
VH4BAK	TTTTTGGCCCAGCCGGCCATGGCCCAGGTGCAGCTGCAGGAGTCGGG
VH5BAK	TTTTTGGCCCAGCCGGCCATGGCCGAGGTGCAGCTGTTGCAGTCTGC
VH6BAK	TTTTTGGCCCAGCCGGCCATGGCCCAGGTACAGCTGCAGCAGTCAGG

Light chain FOR primers

SCFVKFOR	TTATTCGCGGCCCGCCTAAACAGAGGCAGTTCAGATTTT
SCFVλFOR	GTCACTTGCGGCCCGCCTACAGTGTGGCCTTGTTGGCTTG

VK family BAK primers

VK1BAK	TCTGGCGGTGGCGGATCGGACATCCAGATGACCCAGTCTCC
VK2BAK	TCTGGCGGTGGCGGATCGGATGTTGTGATGACTCAGTCTCC
VK3BAK	TCTGGCGGTGGCGGATCGGAAATTGTGTTGACGCAGTCTCC
VK4BAK	TCTGGCGGTGGCGGATCGGACATCGTGATGACCCAGTCTCC
VK5BAK	TCTGGCGGTGGCGGATCGGAAACGACACTCACGCAGTCTCC
VK6BAK	TCTGGCGGTGGCGGATCGGAAATTGTGCTGACTCAGTCTCC

JK FOR primers

JK1FOR	TTCTCGTGCGGCCGCCTAACGTTTGATTTCCACCTTGGTCCC
JK2FOR	TTCTCGTGCGGCCGCCTAACGTTTGATCTCCAGCTTGGTCCC
JK3FOR	TTCTCGTGCGGCCGCCTAACGTTTGATATCCACTTTGGTCCC
JK4FOR	TTCTCGTGCGGCCGCCTAACGTTTGATCTCCACCTTGGTCCC
JK5FOR	TTCTCGTGCGGCCGCCTAACGTTTAATCTCCAGTCGTGTCCC

Vλ family BAK primers

Vλ1BAK	TCTGGCGGTGGCGGATCGCAGTCTGTGTTGACGCAGCCGCC
Vλ2BAK	TCTGGCGGTGGCGGATCGCAGTCTGCCCTGACTCAGCCTGC

Table 1 (ii) Oligonucleotide primers used for human scFv library construction

Vλ3aBAK	TCTGGCGGTGGCGGATCGTCCTATGTGCTGACTCAGCCACC
Vλ3bBAK	TCTGGCGGTGGCGGATCGTCTTCTGAGCTGACTCAGGACCC
Vλ4BAK	TCTGGCGGTGGCGGATCGCACGTTATACTGACTCAACCGCC
Vλ5BAK	TCTGGCGGTGGCGGATCGCAGGCTGTGCTCACTCAGCCGTC
Vλ6BAK	TCTGGCGGTGGCGGATCGAATTTTATGCTGACTCAGCCCCA

Jλ primers

Jλ1FOR	TTCTCGTGCGGCCGCCTAACCTAGGACGGTGACCTTGGTCCC
Jλ2-3FOR	TTCTCGTGCGGCCGCCTAACCTAGGACGGTCAGCTTGGTCCC
Jλ4-5FOR	TTCTCGTGCGGCCGCCTAACCTAAACGGTGAGCTGGGTCCC

Linker primers

LINKAMP3	CGATCCGCCACCGCCAGA
LINKAMP5	GTCTCCTCAGGTGGAGGC
LINKAMP3T	CGATCCGCCACCGCCAGAGCCACCTCCGCCTGAACCGCCTCCACCTGAGGAGAC

1 Claims

2

- 3 1. A peptide display carrier package (PDCP), said
4 package comprising a recombinant polynucleotide-
5 chimeric protein complex wherein the chimeric
6 protein has a nucleotide binding portion and a
7 target peptide portion, wherein said recombinant
8 polynucleotide comprises a nucleotide sequence
9 motif which is specifically bound by said
10 nucleotide binding portion, and wherein at least
11 the chimeric protein-encoding portion of the
12 recombinant polynucleotide not bound by the
13 chimeric protein nucleotide binding portion is
14 protected by a binding moiety.
15
- 16 2. A peptide display carrier package (PDCP) as claimed
17 in Claim 1, wherein said chimeric protein-encoding
18 portion of the recombinant polynucleotide not bound
19 by the chimeric protein nucleotide binding portion
20 is protected by a non-sequence-specific protein.
21
- 22 3. A peptide display carrier package (PDCP) as claimed
23 in Claim 2, wherein said non-sequence-specific
24 protein is a viral coat protein.
25
- 26 4. A peptide display carrier package (PDCP) as claimed
27 in any one of Claims 1 to 3, wherein said target
28 peptide portion is displayed externally on the
29 package.
30
- 31 5. A peptide display carrier package (PDCP) as claimed
32 in any one of Claims 1 to 4 wherein said
33 recombinant polynucleotide includes a linker
34 sequence between the nucleotide sequence encoding
35 the nucleotide binding portion and the nucleotide
36 sequence encoding the target peptide portion.

- 1 6. A peptide display carrier package (PDCP) as claimed
2 in any one of Claims 1 to 5 wherein said
3 recombinant polynucleotide has two or more
4 nucleotide sequence motifs each of which can be
5 bound by the nucleotide binding portion of the
6 chimeric protein.
7
- 8 7. A peptide display carrier package (PDCP) as claimed
9 in any one of Claims 1 to 6 wherein said nucleotide
10 binding portion is a DNA binding domain of an
11 oestrogen or progesterone receptor.
12
- 13 8. A peptide display carrier package (PDCP) as claimed
14 in any one of Claims 1 to 7 wherein said
15 recombinant polynucleotide is bound to said
16 chimeric protein as single stranded DNA.
17
- 18 9. A peptide display carrier package (PDCP) as claimed
19 in any one of Claims 1 to 8 wherein said target
20 peptide portion is located at the N and/or C
21 terminal of the chimeric protein.
22
- 23 10. A peptide display carrier package (PDCP) as claimed
24 in any one of Claims 1 to 9 which is produced in a
25 host cell transformed with said recombinant
26 polynucleotide and extruded therefrom without lysis
27 of the host cell.
28
- 29 11. A recombinant polynucleotide comprising a
30 nucleotide sequence encoding a chimeric protein
31 having a nucleotide binding portion operably linked
32 to a target peptide portion, wherein said
33 polynucleotide includes a specific nucleotide
34 sequence motif which is bound by the nucleotide
35 binding portion of said chimeric protein and
36 further encoding a non-sequence-specific nucleotide

1 binding protein.

2

3 12. A recombinant polynucleotide as claimed in Claim 11
4 wherein said non-sequence-specific nucleotide
5 binding protein is a viral coat protein.

6

7 13. A recombinant polynucleotide as claimed in either
8 one of Claims 11 and 12 which includes a linker
9 sequence between the nucleotide sequence encoding
10 the nucleotide binding portion and the nucleotide
11 sequence encoding the target peptide portion.

12

13 14. A recombinant polynucleotide as claimed in any one
14 of Claims 11 to 13 which has two or more nucleotide
15 sequence motifs each of which can be bound by the
16 nucleotide binding portion of the chimeric protein.

17

18 15. A recombinant polynucleotide as claimed in any one
19 of Claims 11 to 14 wherein said nucleotide binding
20 portion is a DNA binding domain of an oestrogen or
21 progesterone receptor.

22

23 16. A recombinant polynucleotide as claimed in any one
24 of Claims 11 to 15 wherein said recombinant
25 polynucleotide is bound to said chimeric protein as
26 single stranded DNA.

27

28 17. A genetic construct or set of genetic constructs
29 which collectively comprises a polynucleotide
30 having a sequence which includes:

- 31 i) a sequence encoding a nucleotide binding
32 portion able to recognise and bind to a
33 specific sequence motif;
34 ii) the sequence motif recognised and bound by the
35 nucleotide binding portion encoded by (i);
36 iii) a restriction enzyme site which permits

1 insertion of a polynucleotide, said site being
2 designed to operably link said polynucleotide
3 to the sequence encoding the nucleotide
4 binding portion so that expression of the
5 operably linked polynucleotide sequences
6 yields a chimeric protein; and
7 iv) a sequence encoding a nucleotide binding
8 protein which binds non-specifically to naked
9 polynucleotide.

10

11 18. A genetic construct or set of genetic constructs as
12 claimed in Claim 17 wherein a linker sequence is
13 located between the nucleotide sequence encoding
14 the nucleotide binding portion and the site for
15 insertion of the polynucleotide.

16

17 19. A genetic construct or set of genetic constructs as
18 claimed in either one of Claims 17 and 18 which
19 includes a vector pDM12, pDM14 or pDM16, deposited
20 at NCIMB under Nos 40970, 40971 and 40972
21 respectively.

22

23 20. A method of constructing a genetic library, said
24 method comprising:

25

26 a) constructing multiple copies of a recombinant
27 vector comprising a polynucleotide sequence
28 which encodes a nucleotide binding portion
29 able to recognise and bind to a specific
30 sequence motif;

31

32 b) operably linking each said vector to a
33 polynucleotide encoding a target polypeptide,
34 such that expression of said operably linked
35 vector results in expression of a chimeric
36 protein comprising said target peptide and

- 1 said nucleotide binding portions; wherein said
2 multiple copies of said operably linked
3 vectors collectively express a library of
4 target peptide portions;
5
6 c) transforming host cells with the vectors of
7 step b);
8
9 d) culturing the host cells of step c) under
10 conditions suitable for expression of said
11 chimeric protein;
12
13 e) providing a recombinant polynucleotide
14 comprising the nucleotide sequence motif
15 specifically recognised by the nucleotide
16 binding portion and exposing this
17 polynucleotide to the chimeric protein of step
18 d) to yield a polynucleotide-chimeric protein
19 complex; and
20
21 f) causing production of a non-sequence-specific
22 moiety able to bind to the non-protected
23 portion of the polynucleotide encoding the
24 chimeric protein to form a peptide display
25 carrier package.
26
27 21. A method of screening a genetic library, said
28 method comprising:
29
30 a) exposing the polynucleotide members of said
31 library to multiple copies of a genetic
32 construct comprising a nucleotide sequence
33 encoding a nucleotide binding portion able to
34 recognise and bind to a specific sequence
35 motif, under conditions suitable for the
36 polynucleotides of said library each to be

- 1 individually ligated into one copy of said
2 genetic construct, to create a library of
3 recombinant polynucleotides;
4
- 5 b) exposing said recombinant polynucleotides to a
6 population of host cells, under conditions
7 suitable for transformation of said host cells
8 by said recombinant polynucleotides;
9
- 10 c) selecting for transformed host cells;
11
- 12 d) exposing said transformed host cells to
13 conditions suitable for expression of said
14 recombinant polynucleotide to yield a chimeric
15 protein; and
16
- 17 e) providing a recombinant polynucleotide
18 comprising the nucleotide sequence motif
19 specifically recognised by the nucleotide
20 binding portion and exposing this
21 polynucleotide to the chimeric protein of step
22 d) to yield a polynucleotide-chimeric protein
23 complex;
24
- 25 f) protecting any exposed portions of the
26 polynucleotide in the complex of step e) to
27 form a peptide display carrier package; and
28
- 29 g) screening said peptide display carrier package
30 to select only those packages displaying a
31 target peptide portion having the
32 characteristics required.
33
- 34 22. A method as claimed in Claim 21 wherein the peptide
35 display package carrier is extruded from the host
36 cell without lysis thereof.

- 1 23. A polynucleotide comprising a nucleotide sequence
- 2 substantially as set out in SEQ ID No. 15 or SEQ ID
- 3 No. 17.

Figure 1

1/9

1

pel B

MET LYS TYR LEU LEU PRO THR ALA ALA ALA GLY LEU

AAGCTTGCATGCCAAATTCATTTCAAGGACAGTCATAA ATG AAA TAC CTA TTG OCT ACG GCA GCC GCT GGA TTG
 TTCGAACGTACGTTTAAGATAAAGTTCCTCTGTCACTATT TAC TTT ATG GAT AAC GGA TGC CGT CGG CGA CCT AAC
Hin dIII

77

*Sfi*I*Pst*I*Not*I

LEU LEU LEU ALA ALA GLN PRO ALA MET ALA GLU VAL GLN LEU GLN *** ** ALA ALA ALA
 TTA TTA CTC GCG GCC CAG CCG GCC ATG GCC GAG GTG CAA CTG CAG TAA TAG GCG GCC GCA
 AAT AAT GAG CGC CGG GTC GGC CGG TAC CGG GTC CAC GTC GAC GTC ATT ATC CGC CGG CGT

137

GLY GLY GLY GLY SER MET GLU SER ALA LYS GLU THR ARG TYR CYS ALA VAL CYS ASN ASP
 GGG GGA GGA GGG TCC ATG GAA TCT GCC AAG GAG ACT CGC TAC TGT GCA GTG TGC AAT GAC
 CCC CCT OCT CCC AGG TAC CTT AGA CGG TTC CTC TGA GCG ATG ACA CGT CAC ACG TTA CTG

197

TYR ALA SER GLY TYR HIS TYR GLY VAL TRP SER CYS GLU GLY CYS LYS ALA PHE PHE LYS
 TAT GCT TCA GGC TAC CAT TAT GGA GTC TGG TCC TGT GAG GGC TGC AAG GCC TTC TTC AAG
 ATA CGA AGT CCG ATG GTA ATA CCT CAG ACC AGG ACA CTC CCG ACG TTC CGG AAG AAG TTC

257

ARG SER ILE GLN GLY HIS ASN ASP TYR MET CYS PRO ALA THR ASN GLN CYS THR ILE ASP
 AGA AGT ATT CAA GGA CAT AAC GAC TAT ATG TGT CCA GCC ACC AAC CAG TGC ACC ATT GAT
 TCT TCA TAA GTT CCT GTA TTG CTG ATA TAC ACA GGT CGG TGG TTG GTC ACG TGG TAA CTA

317

Oestrogen receptor DBD

LYS ASN ARG ARG LYS SER CYS GLN ALA CYS ARG LEU ARG LYS CYS TYR GLU VAL GLY MET
 AAA AAC AGG AGG AAG AGC TGC CAG GCC TGC CGG CTC CGT AAA TGC TAC GAA GTG GGA ATG
 TTT TTG TCC TCC TTC TCG ACG GTC CGG ACG GCC GAG GCA TTT ACG ATG CTT CAC CCT TAC

377

MET LYS GLY GLY ILE ARG LYS ASP ARG ARG GLY GLY ARG MET LEU LYS HIS LYS ARG GLN
 ATG AAA GGT GGG ATA CGA AAA GAC CGA AGA GGA GGG AGA ATG TTG AAA CAC AAG CGC CAG
 TAC TTT CCA CCC TAT GCT TTT CTG GCT TCT CCT CCC TCT TAC AAC TTT GTG TTC GCG GTC

437

ARG ASP ASP GLY GLU GLY ARG GLY GLU VAL GLY SER *** **

HRE

Eco RI

AGA GAT GAT GGG GAG GGC AGG GGT GAA GTG GGG TCT TGA TAA TCAGGTCAGACTGACCTGAGCTAAAATAACACATTTCAG AATTC
 TCT CTA CTA CCC CTC CCG TCC CCA CTT CAC CCC AGA ACT ATT AGTCCAGTCTCACTGGACTCGATTTTATGTGTAAAGTC TTAAG

2/9

Figure 2

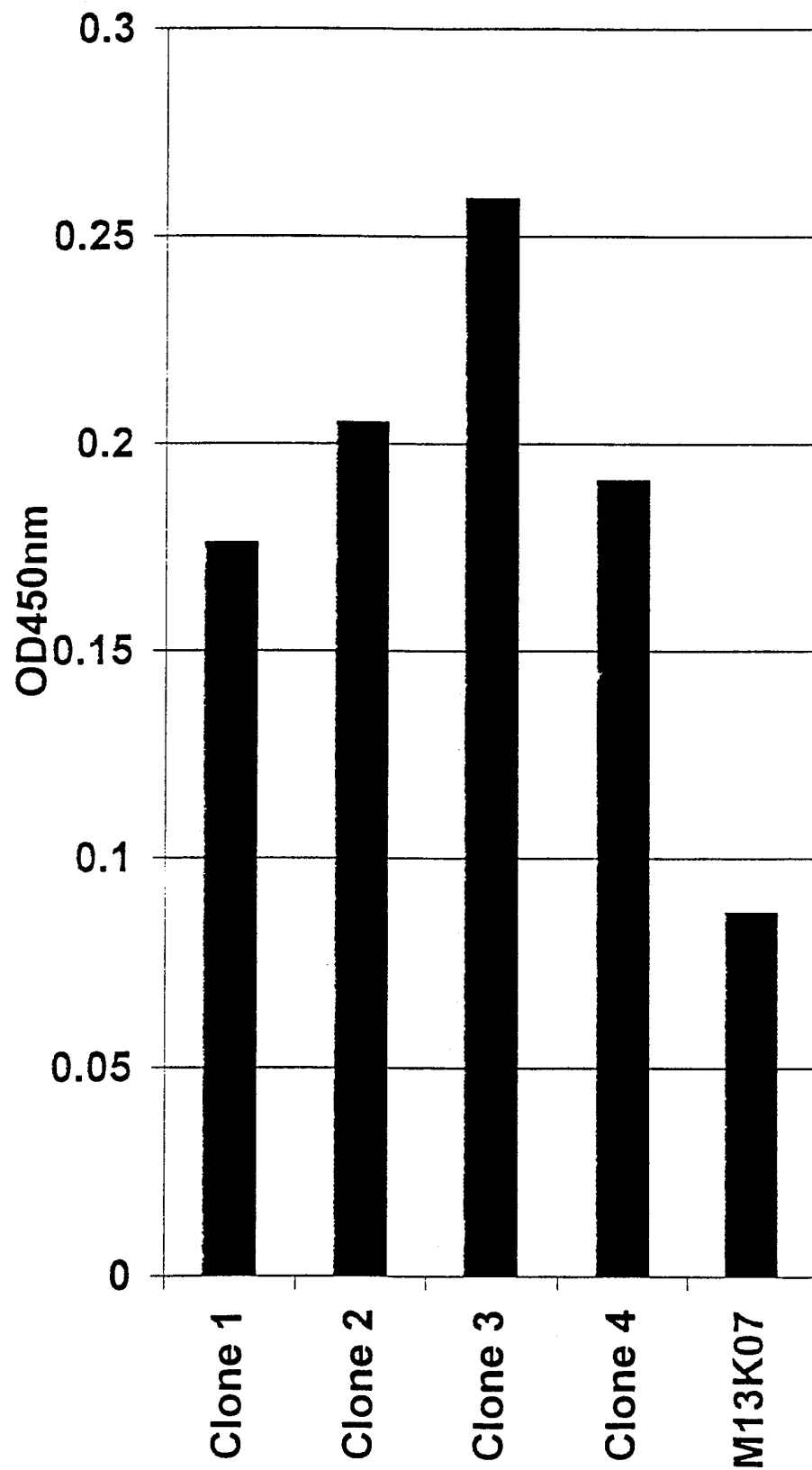


Figure 3

3/9

Human Igk constant region

K R T V A A P S V
AAACGAACTGTGGCTGCACCATCTGTC

Clone #2

M A↓Q P T T R P G Q G T R L D I K R T V A A P S V
ATGGCCCAGCCCACCACGCGTCCGGGCCAAGGGACACGACTGGACATTAAACGAACTGTGGCTGCACCATCTGTC

Clone #3

M A↓Q S H H A S G G G T K V E I K R T V A A P S V
ATGGCCCAGTCCCACCACGCGTCCGGCGGAGGGACCAAGGTGGAGATCAAACGAACTGTGGCTGCACCATCTGTC

Human Igk constant region

F I F P P S D E Q L K S G T A S V V C L L N N F Y
TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTAT

Clone #2

F I F P P S D E Q L K S G T A S V V C L L N N F Y
TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTAT

Clone #3

F I F P P S D E Q L K S G T A S V V C L L N N F Y
TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTAT

Figure 4

4/9 pel B

1Hin dIII

MET LYS TYR LEU LEU PRO THR ALA ALA

AAGCTTGCAT GCAAATTCTA TTTCAAGGAG ACAGTCATAA ATG AAA TAC CTA TTG CCT ACG GCA GCC

TTCGAACGTA CGTTTAAGAT AAAGTTCCTC TGTCAGTATT TAC TTT ATG GAT AAC GGA TGC CGT CGG

68

Sfi I

Pst I

ALA GLY LEU LEU LEU LEU ALA ALA GLN PRO ALA MET ALA GLU VAL GLN LEU GLN *** **

GCT GGA TTG TTA TTA CTC GCG GCC CAG CCG GCC ATG GCC GAG GTG CAA CTG CAG TAA TAG

CGA CCT AAC AAT AAT GAG CGC CGG GTC GGC CGG TAC CGG CTC CAC GTT GAC GTC ATT ATC

128 Not I

ALA ALA ALA GLY GLY GLY GLY SER MET GLU SER ALA LYS GLU THR ARG TYR CYS ALA VAL

GCG GCC GCA GGG GGA GGA GGG TCC ATG GAA TCT GCC AAG GAG ACT CGC TAC TGT GCA GTG

CGC CGG CGT CCC CCT CCT CCC AGG TAC CTT AGA CGG TTC CTC TGA GCG ATG ACA CGT CAC

188

CYS ASN ASP TYR ALA SER GLY TYR HIS TYR GLY VAL TRP SER CYS GLU GLY CYS LYS ALA

TGC AAT GAC TAT GCT TCA GGC TAC CAT TAT GGA GTC TGG TCC TGT GAG GGC TGC AAG GCC

ACG TTA CTG ATA CGA AGT CCG ATG GTA ATA CCT CAG ACC AGG ACA CTC CCG ACG TTC CGG

248

PHE PHE LYS ARG SER ILE GLN GLY HIS ASN ASP TYR MET CYS PRO ALA THR ASN GLN CYS

TTC TTC AAG AGA AGT ATT CAA GGA CAT AAC GAC TAT ATG TGT CCA GCC ACC AAC CAG TGC

AAG AAG TTC TCT TCA TAA GTT CCT GTA TTG CTG ATA TAC ACA GGT CGG TGG TTG GTC ACG

308

THR ILE ASP LYS ASN ARG ARG LYS SER CYS GLN ALA CYS ARG LEU ARG LYS CYS TYR GLU

ACC ATT GAT AAA AAC AGG AGG AAG AGC TGC CAG GCC TGC CGG CTC CGT AAA TGC TAC GAA

TGG TAA CTA TTT TTG TCC TCC TTC TCG ACG GTC CGG ACG GCC GAG GCA TTT ACG ATG CTT

368

VAL GLY MET MET LYS GLY GLY ILE ARG LYS ASP ARG ARG GLY GLY ARG MET LEU LYS HIS

GTG GGA ATG ATG AAA GGT GGG ATA CGA AAA GAC CGA AGA GGA GGG AGA ATG TTG AAA CAC

CAC CCT TAC TAC TTT CCA CCC TAT GCT TTT CTG GCT TCT CCT CCC TCT TAC AAC TTT GTG

428

LYS ARG GLN ARG ASP ASP GLY GLU GLY ARG GLY GLU VAL GLY SER Ter Ter HRE 1

AAG CGC CAG AGA GAT GAT GGG GAG GGC AGG GGT GAA GTG GGG TCT TGA TAA TCAGGTCAGAGT

TTC GCG GTC TCT CTA CTA CCC CTC CCG TCC CCA CTT CAC CCC AGA ACT ATT AGTCCAGTCTCA

491

HRE 1

Sal I

HRE 2

Eco RI

GACCTGAGCTAAAATAACACATTTCAG GTCGAC TTGGGTCAGTCTGACCGGGACAAAGTTAATGTAACCTC GAATTC

CTGGACTCGATTTTATTGTGTAAGTC CAGCTG AACCCAGTCAGACTGGCCCTGTTTCAATTACATTGGAG CTTAAG

Figure 5

5/9

pel B

¹ *Hin*DIII

AAGCTTGCAT GCAAATTCTA TTTCAAGGAG ACAGTCATAA ATG AAA TAC CTA TTG CCT ACG GCA GCC
 TTCGAACGTA CGTTTAAGAT AAAGTTCCTC TGTCAGTATT TAC TTT ATG GAT AAC GGA TGC CGT CGG
 68

ALA GLY LEU LEU LEU LEU ALA ALA GLN PRO ALA MET ALA GLU MET GLU SER ALA LYS GLU
 GCT GGA TTG TTA TTA CTC GCG GCC CAG CCG GCA ATG GCC GAG ATG GAA TCT GCC AAG GAG
 CGA CCT AAC AAT AAT GAG CGC CGG GTC GGC CGT TAC CGG CTC TAC CTT AGA CGG TTC CTC
 128

THR ARG TYR CYS ALA VAL CYS ASN ASP TYR ALA SER GLY TYR HIS TYR GLY VAL TRP SER
 ACT CGC TAC TGT GCA GTG TGC AAT GAC TAT GCT TCA GGC TAC CAT TAT GGA GTC TGG TCC
 TGA GCG ATG ACA CGT CAC ACG TTA CTG ATA CGA AGT CCG ATG GTA ATA CCT CAG ACC AGG
 188

CYS GLU GLY CYS LYS ALA PHE PHE LYS ARG SER ILE GLN GLY HIS ASN ASP TYR MET CYS
 TGT GAG GGC TGC AAG GCC TTC TTC AAG AGA AGT ATT CAA GGA CAT AAC GAC TAT ATG TGT
 ACA CTC CCG ACG TTC CGG AAG AAG TTC TCT TCA TAA GTT CCT GTA TTG CTG ATA TAC ACA
 248

PRO ALA THR ASN GLN CYS THR ILE ASP LYS ASN ARG ARG LYS SER CYS GLN ALA CYS ARG
 CCA GCC ACC AAC CAG TGC ACC ATT GAT AAA AAC AGG AGG AAG AGC TGC CAG GCC TGC CGG
 GGT CGG TGG TTG GTC ACG TGG TAA CTA TTT TTG TCC TCC TTC TCG ACG GTC CGG ACG GCC
 308

LEU ARG LYS CYS TYR GLU VAL GLY MET MET LYS GLY GLY ILE ARG LYS ASP ARG ARG GLY
 CTC CGT AAA TGC TAC GAA GTG GGA ATG ATG AAA GGT GGG ATA CGA AAA GAC CGA AGA GGA
 GAG GCA TTT ACG ATG CTT CAC CCT TAC TAC TTT CCA CCC TAT GCT TTT CTG GCT TCT CCT
 368

GLY ARG MET LEU LYS HIS LYS ARG GLN ARG ASP ASP GLY GLU GLY ARG GLY GLU VAL GLY
 GGG AGA ATG TTG AAA CAC AAG CGC CAG AGA GAT GAT GGG GAG GGC AGG GGT GAA GTG GGG
 CCC TCT TAC AAC TTT GTG TTC GCG GTC TCT CTA CTA CCC CTC CCG TCC CCA CTT CAC CCC
 428

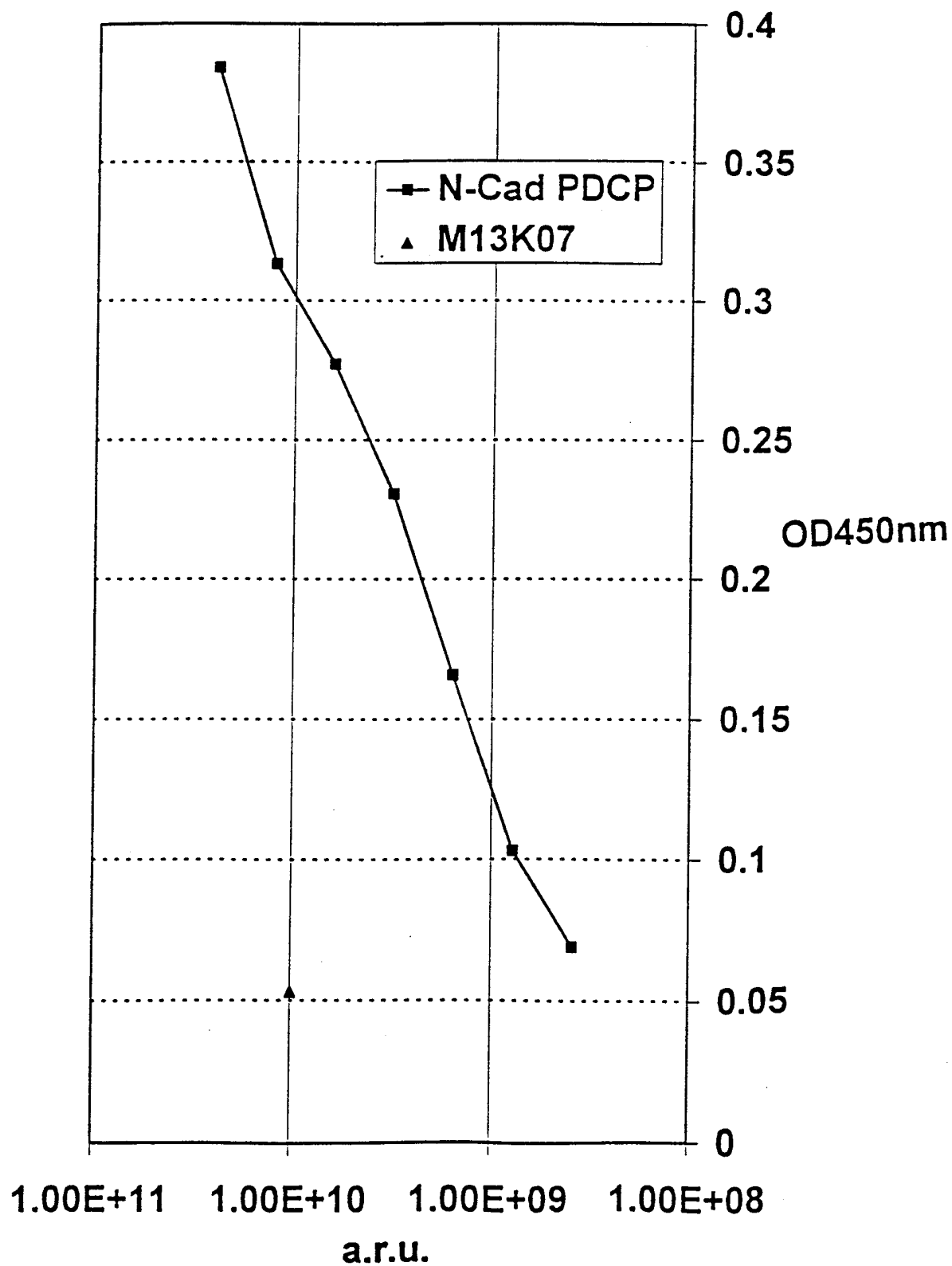
		<i>Sfi</i> I		<i>Pst</i> I		<i>Not</i> I	
SER	GLY GLY GLY GLY SER	ALA GLN PRO ALA LEU	LEU GLN LEU	ALA ALA ALA	TER		
TCT	GGG GGA GGA GGG TCG	GCC CAG CCG GCC CTC	CTG CAG CTG	GCG GCC GCA	TAAGTATTG		
AGA	CCC CCT CCT CCC AGC	CGG GTC GGC CGG GAG	GAC GTC GAC	CGC CGG CGT	ATTGACTAAC		

⁴⁸⁹ <i>Sal</i> I		<i>Eco</i> RI
AGTCGAC	TTG GGTCACTCTG ACCGGGACAA AGTTAATGTA ACCTC	GAATTC
TCAGCTGAAC	CCAGTCAGAC TGGCCCTGTT TCAATTACAT TGGAG	CTTAAG

HRE

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Figure 6



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Figure 7

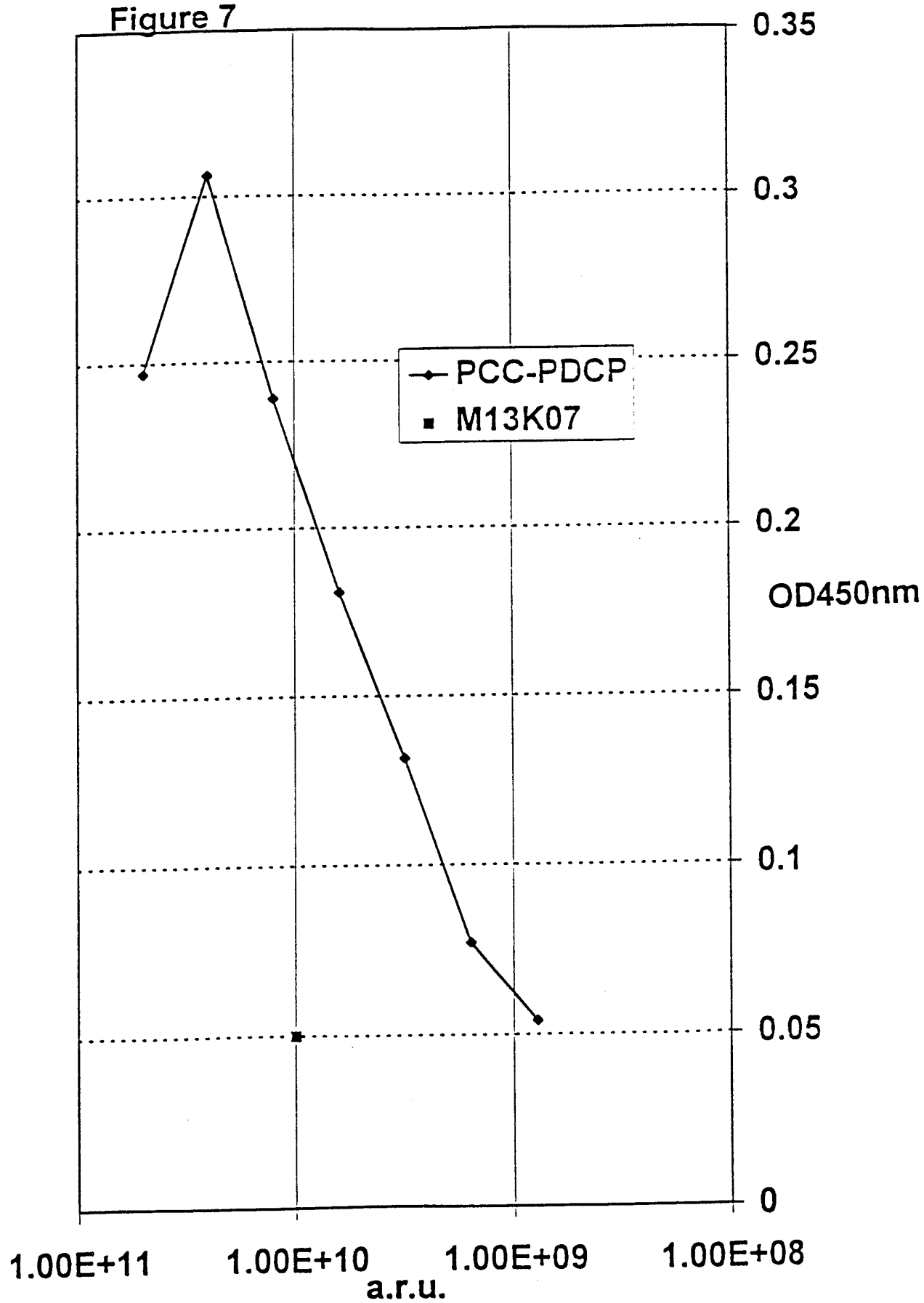
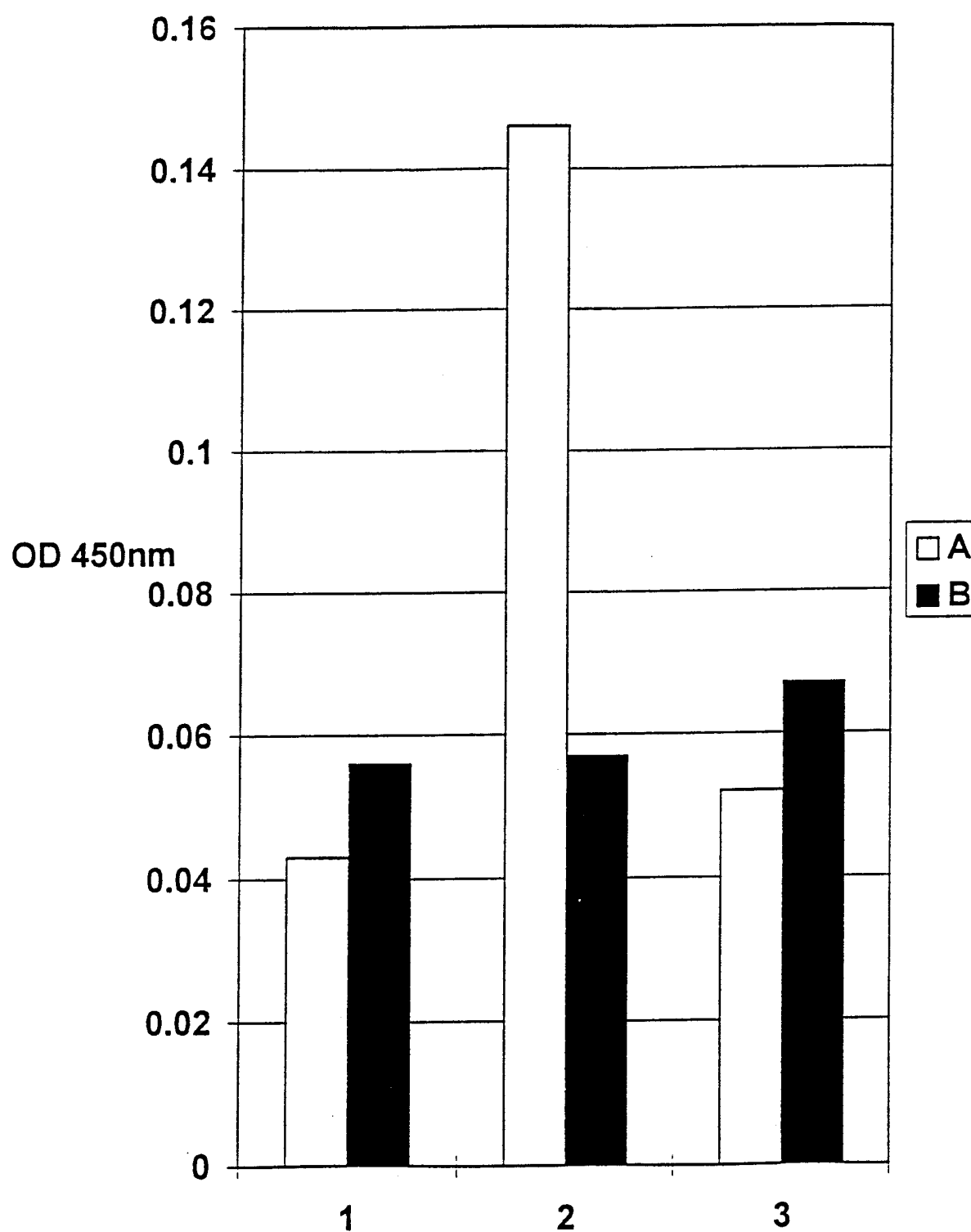


Figure 8

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HEAVY CHAIN**9/9****Figure 9**

Q V Q L Q Q S G G G V V Q P G R S L
 CAGGTACAGCTGCAGCAGTCAGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTG
 GTCCATGTCGACGTCGTCAGTCCCCCTCCGCACCAGGTTCGGACCCTCCAGGGAC
 R L S C A A S G F P F S T Y G M H W
 AGACTCTCCTGTGCAGCCTCGGGATTCCCCTTTAGTACTTATGGCATGCACTGG
 TCTGAGAGGACACGTTCGGAGCCCTAAGGGGAAATCATGAATACCGTACGTGACC
 R Q A V P G K G L E W V A V I S Y D
 CGCCAGGCTGTCCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGAT
 GCGGTCCGACAGGGTCCGTTCCCCGACCTCACCCACCGTCAATATAGTATACTA
G S N K Y Y A D S V K G R F T I S R
 GGAAGTAATAAATACTACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGA
 CCTTCATTATTTATGATGCGTCTGAGGCACTTCCCCGGCTAAGTGGTAGAGGTCT
 D N S K N T L Y L Q M N S L R A E D
 GACAATTCCAAGAACACGTTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGAC
 CTGTTAAGGTTCTTGTGCAACATAGACGTTTACTTGTTCGGACTCTCGACTCCTG
 T A V Y Y C A R D L D P T R Y S S G
 ACGGCTGTGTATTACTGTGCGAGAGATTTAGACCCACCAGGTATAGCAGTGGC
 TGCCGACACATAATGACACGCTCTCTAAATCTGGGGTGGTCCATATCGTCACCG
 W D T D Y W G Q G H L V T V S S
 TGGGACACTGACTACTGGGGCCAGGGGCACCTGGTCACTGTCTCCTCA
 ACCCTGTGACTGATGACCCCGGTCCCCGTGGACCAGTGACAGAGGAGT

LIGHT CHAIN

E T T L T Q S P G T L S L S P G E R
 GAAACGACACTCACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCGGGGGAAAGA
 CTTTGCTGTGAGTGCCTCAGAGGTCCGTGGGACAGAAACAGAGGCCCCCTTTCT
 A T L S C R A S Q N I G S S S L A W
 GCCACCCTCTCCTGCAGGGCCAGTCAGAATATTGGCAGCAGCTCCTTAGCCTGG
 CGGTGGGAGAGGACGTCCCCGTGAGTCTTATAACCGTCGTCGAGGAATCGGACC
 Y Q Q K P G Q A P R L L I Y G A S T
 TACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACC
 ATGGTTGTCTTTGGACCGGTCCGAGGGTCCGAGGAGTAGATAACCACGTAGGTGG
 R A T G F S G S G S G T Q F T L T I
 AGGGCCACTGGTTTCAGTGGCAGTGGGTGAGGGACACAATTCACTCTCACCATC
 TCCCCGTGACCAAAGTCACCGTCACCCAGTCCCTGTGTTAAGTGAGAGTGGTAG
 I P A R S S L Q S E D F A V Y Y C Q
 ATCCCAGCCAGGAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTGAG
 TAGGGTTCGGTCCCTCGTTCGGACGTCAGACTTCTAAAACGTCAAATAATGACAGTC
 Q Y N F W P F T F G P G T K L E I K
 CAGTATAATTTCTGGCCATTCACCTTTTGGCCCTGGGACCAAGCTGGAGATCAAA
 GTCATATTAAAGACCGGTAAGTGAAAACCGGGACCCTGGTTCGACCTCTAGTTT

R
 CGT
 GCA

1
SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Rowett Research Services Limited
- (B) STREET: Greenburn
- (C) CITY: Buckburn ABERDEEN
- (E) COUNTRY: United Kingdom
- (F) POSTAL CODE (ZIP): AB21 9SB

(ii) TITLE OF INVENTION: Chimeric binding peptide library screening method

(iii) NUMBER OF SEQUENCES: 76

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TCAGGTCAGA GTGACCTGAG CTAAAATAAC ACATTCAG

39

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

AGTCCAGTCT CACTGGACTC GATTTTATTG TGTAAGTC

38

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 521 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:41..475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AAGCTTGCAT GCAAATTCTA TTTCAAGGAG ACAGTCATAA ATG AAA TAC CTA TTG	55
Met Lys Tyr Leu Leu	
1 5	
CCT ACG GCA GCC GCT GGA TTG TTA TTA CTC GCG GCC CAG CCG GCC ATG	103
Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met	
10 15 20	
GCC CAA GTG CAG CTG CAG TAA TAG GCG GCC GCA GGG GGA GGA GGG TCC	151
Ala Gln Val Gln Leu Gln * * Ala Ala Ala Gly Gly Gly Gly Ser	
25 30 35	
ATG GAA TCT GCC AAG GAG ACT CGC TAC TGT GCA GTG TGC AAT GAC TAT	199
Met Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr	
40 45 50	
GCT TCA GGC TAC CAT TAT GGA GTC TGG TCC TGT GAG GGC TGC AAG GCC	247
Ala Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala	
55 60 65	
TTC TTC AAG AGA AGT ATT CAA GGA CAT AAC GAC TAT ATG TGT CCA GCC	295
Phe Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala	
70 75 80 85	
ACC AAC CAG TGC ACC ATT GAT AAA AAC AGG AGG AAG AGC TGC CAG GCC	343
Thr Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala	
90 95 100	
TGC CGG CTC CGT AAA TGC TAC GAA GTG GGA ATG ATG AAA GGT GGG ATA	391
Cys Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly Gly Ile	
105 110 115	
CGA AAA GAC CGA AGA GGA GGG AGA ATG TTG AAA CAC AAG CGC CAG AGA	439
Arg Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg	

3

	120		125		130								
GAT	GAT	GGG	GAG	GGC	AGG	GGT	GAA	GTG	GGG	TCT	TGA	TAATCAGGTC	485
Asp	Asp	Gly	Glu	Gly	Arg	Gly	Glu	Val	Gly	Ser	*		
	135					140					145		
AGAGTGACCT GAGCTAAAAT AACACATTCA GAATTC												521	

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

[illegible]

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

4

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AAA CGA ACT GTG GCT GCA CCA TCT GTC TTC ATC TTC CCG CCA TCT GAT	48
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp	
150 155 160	
GAG CAG TTG AAA TCT GGA ACT GCC TCT GTT GTG TGC CTG CTG AAT AAC	96
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn	
165 170 175	
TTC TAT	102
Phe Tyr	

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
1 5 10 15
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
20 25 30
Phe Tyr

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

(2) INFORMATION FOR SEQ ID NO: 8:

(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

(2) INFORMATION FOR SEQ ID NO: 9:

(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

																6	
ATG	GCC	CAG	TCC	CAC	CAC	GCG	TCC	GGC	GGA	GGG	ACC	AAG	GTG	GAG	ATC	48	
Met	Ala	Gln	Ser	His	His	Ala	Ser	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile		
				55					60					65			
AAA	CGA	ACT	GTG	GCT	GCA	CCA	TCT	GTC	TTC	ATC	TTC	CCG	CCA	TCT	GAT	96	
Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp		
				70					75					80			
GAG	CAG	TTG	AAA	TCT	GGA	ACT	GCC	TCT	GTT	GTG	TGC	CTG	CTG	AAT	AAC	144	
Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn		
				85					90					95			
TTC	TAT															150	
Phe	Tyr																
100																	

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```

Met Ala Gln Ser His His Ala Ser Gly Gly Gly Thr Lys Val Glu Ile
 1          5          10          15
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
          20          25          30
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
          35          40          45
Phe Tyr
 50

```

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 41..475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

AAGCTTGCAT GCAAATTCTA TTTCAAGGAG ACAGTCATAA ATG AAA TAC CTA TTG 55

																7	Met Lys Tyr Leu Leu					55		
CCT	ACG	GCA	GCC	GCT	GGA	TTG	TTA	TTA	CTC	GCG	GCC	CAG	CCG	GCC	ATG	103								
Pro	Thr	Ala	Ala	Ala	Gly	Leu	Leu	Leu	Leu	Ala	Ala	Gln	Pro	Ala	Met									
				60					65					70										
GCC	GAG	GTG	CAA	CTG	CAG	TAA	TAG	GCG	GCC	GCA	GGG	GGA	GGA	GGG	TCC	151								
Ala	Glu	Val	Gln	Leu	Gln	*	*	Ala	Ala	Ala	Gly	Gly	Gly	Gly	Ser									
				75					80					85										
ATG	GAA	TCT	GCC	AAG	GAG	ACT	CGC	TAC	TGT	GCA	GTG	TGC	AAT	GAC	TAT	199								
Met	Glu	Ser	Ala	Lys	Glu	Thr	Arg	Tyr	Cys	Ala	Val	Cys	Asn	Asp	Tyr									
				90					95					100										
GCT	TCA	GGC	TAC	CAT	TAT	GGA	GTC	TGG	TCC	TGT	GAG	GGC	TGC	AAG	GCC	247								
Ala	Ser	Gly	Tyr	His	Tyr	Gly	Val	Trp	Ser	Cys	Glu	Gly	Cys	Lys	Ala									
				105					110					115										
TTC	TTC	AAG	AGA	AGT	ATT	CAA	GGA	CAT	AAC	GAC	TAT	ATG	TGT	CCA	GCC	295								
Phe	Phe	Lys	Arg	Ser	Ile	Gln	Gly	His	Asn	Asp	Tyr	Met	Cys	Pro	Ala									
				120					125					130			135							
ACC	AAC	CAG	TGC	ACC	ATT	GAT	AAA	AAC	AGG	AGG	AAG	AGC	TGC	CAG	GCC	343								
Thr	Asn	Gln	Cys	Thr	Ile	Asp	Lys	Asn	Arg	Arg	Lys	Ser	Cys	Gln	Ala									
				140					145					150										
TGC	CGG	CTC	CGT	AAA	TGC	TAC	GAA	GTG	GGA	ATG	ATG	AAA	GGT	GGG	ATA	391								
Cys	Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Val	Gly	Met	Met	Lys	Gly	Gly	Ile									
				155					160					165										
CGA	AAA	GAC	CGA	AGA	GGA	GGG	AGA	ATG	TTG	AAA	CAC	AAG	CGC	CAG	AGA	439								
Arg	Lys	Asp	Arg	Arg	Gly	Gly	Arg	Met	Leu	Lys	His	Lys	Arg	Gln	Arg									
				170					175					180										
GAT	GAT	GGG	GAG	GGC	AGG	GGT	GAA	GTG	GGG	TCT	TGA	TAATCAGGTC				485								
Asp	Asp	Gly	Glu	Gly	Arg	Gly	Glu	Val	Gly	Ser	*					195								
				185					190					195										
AGAGTGACCT GAGCTAAAAT AACACATTCA GGTCGACTTG GGTCAGTCTG ACCGGGACAA																545								
AGTTAATGTA ACCTCGAATT C																566								

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1 5 10 15

Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gln * * Ala Ala Ala
 20 25 30

Gly Gly Gly Gly Ser Met Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala
 35 40 45

8

Val Cys Asn Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp Ser Cys
 50 55 60

Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His Asn Asp
 65 70 75 80

Tyr Met Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg
 85 90 95

Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val Gly Met
 100 105 110

Met Lys Gly Gly Ile Arg Lys Asp Arg Arg Gly Gly Arg Met Leu Lys
 115 120 125

His Lys Arg Gln Arg Asp Asp Gly Glu Gly Arg Gly Glu Val Gly Ser
 130 135 140

*

145

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 539 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 41..481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

AAGCTTGCAT GCAAATTCTA TTTCAAGGAG ACAGTCATAA ATG AAA TAC CTA TTG	55
Met Lys Tyr Leu Leu	150
CCT ACG GCA GCC GCT GGA TTG TTA TTA CTC GCG GCC CAG CCG GCA ATG	103
Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met	165
155 160	
GCC GAG ATG GAA TCT GCC AAG GAG ACT CGC TAC TGT GCA GTG TGC AAT	151
Ala Glu Met Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys Asn	130
170 175	
GAC TAT GCT TCA GGC TAC CAT TAT GGA GTC TGG TCC TGT GAG GGC TGC	199
Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys	195
185 190	
AAG GCC TTC TTC AAG AGA AGT ATT CAA GGA CAT AAC GAC TAT ATG TGT	247
Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys	

200	205	210	
CCA GCC ACC AAC CAG TGC ACC ATT GAT AAA AAC AGG AGG AAG AGC TGC			295
Pro Ala Thr Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys			
215	220	225	230
CAG GCC TGC CGG CTC CGT AAA TGC TAC GAA GTG GGA ATG ATG AAA GGT			343
Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly			
	235	240	245
GGG ATA CGA AAA GAC CGA AGA GGA GGG AGA ATG TTG AAA CAC AAG CGC			391
Gly Ile Arg Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg			
	250	255	260
CAG AGA GAT GAT GGG GAG GGC AGG GGT GAA GTG GGG TCT GGG GGA GGA			439
Gln Arg Asp Asp Gly Glu Gly Arg Gly Glu Val Gly Ser Gly Gly Gly			
	265	270	275
GGG TCG GCC CAG CCG GCC CTC CTG CAG CTG GCG GCC GCA TAA			481
Gly Ser Ala Gln Pro Ala Leu Leu Gln Leu Ala Ala *			
280	285	290	
CTGATTGAGT CGACTTGGGT CAGTCTGACC GGGACAAAGT TAATGTAACC TCGAATTC			539

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala	
1 5 10 15	
Ala Gln Pro Ala Met Ala Glu Met Glu Ser Ala Lys Glu Thr Arg Tyr	
20 25 30	
Cys Ala Val Cys Asn Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp	
35 40 45	
Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His	
50 55 60	
Asn Asp Tyr Met Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Lys Asn	
65 70 75 80	
Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val	
85 90 95	
Gly Met Met Lys Gly Gly Ile Arg Lys Asp Arg Arg Gly Gly Arg Met	
100 105 110	
Leu Lys His Lys Arg Gln Arg Asp Asp Gly Glu Gly Arg Gly Glu Val	
115 120 125	
Gly Ser Gly Gly Gly Gly Ser Ala Gln Pro Ala Leu Leu Gln Leu Ala	
130 135 140	

Ala Ala 10
145

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 372 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CAG GTA CAG CTG CAG CAG TCA GGG GGA GGC GTG GTC CAG CCT GGG AGG	49
Gln Val Gln Leu Gln Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg	
150 155 160	
TCC CTG AGA CTC TCC TGT GCA GCC TCG GGA TTC CCC TTT AGT ACT TAT	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Thr Tyr	
165 170 175	
GGC ATG CAC TGG CGC CAG GCT GTC CCA GGC AAG GGG CTG GAG TGG GTG	144
Gly Met His Trp Arg Gln Ala Val Pro Gly Lys Gly Leu Glu Trp Val	
180 185 190 195	
GCA GTT ATA TCA TAT GAT GGA AGT AAT AAA TAC TAC GCA GAC TCC GTG	192
Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val	
200 205 210	
AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG TTG TAT	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
215 220 225	
CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC ACG GCT GTG TAT TAC TGT	288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
230 235 240	
GCG AGA GAT TTA GAC CCC ACC AGG TAT AGC AGT GGC TGG GAC ACT GAC	336
Ala Arg Asp Leu Asp Pro Thr Arg Tyr Ser Ser Gly Trp Asp Thr Asp	
245 250 255	
TAC TGG GGC CAG GGG CAC CTG GTC ACT GTC TCC TCA	372
Tyr Trp Gly Gln Gly His Leu Val Thr Val Ser Ser	
260 265 270	

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 amino acids

11

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

```

Gln Val Gln Leu Gln Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Thr Tyr
          20           25           30
Gly Met His Trp Arg Gln Ala Val Pro Gly Lys Gly Leu Glu Trp Val
          35           40           45
Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
          50           55           60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
          65           70           75           80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
          85           90           95
Ala Arg Asp Leu Asp Pro Thr Arg Tyr Ser Ser Gly Trp Asp Thr Asp
          100          105          110
Tyr Trp Gly Gln Gly His Leu Val Thr Val Ser Ser
          115          120

```

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```

GAA ACG ACA CTC ACG CAG TCT CCA GGC ACC CTG TCT TTG TCT CCG GGG      48
Glu Thr Thr Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
125          130          135          140

GAA AGA GCC ACC CTC TCC TGC AGG GCC AGT CAG AAT ATT GGC AGC AGC      96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asn Ile Gly Ser Ser
          145          150          155

TCC TTA GCC TGG TAC CAA CAG AAA CCT GGC CAG GCT CCC AGG CTC CTC      144
Ser Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

```

		12		
	160	165	170	
ATC TAT GGT GCA TCC ACC AGG GCC ACT GGT ATC CCA GCC AGG TTC AGT				192
Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser				
175	180	185		
GGC AGT GGG TCA GGG ACA CAA TTC ACT CTC ACC ATC AGC AGC CTG CAG				240
Gly Ser Gly Ser Gly Thr Gln Phe Thr Leu Thr Ile Ser Ser Leu Gln				
190	195	200		
TCT GAA GAT TTT GCA GTT TAT TAC TGT CAG CAG TAT AAT TTC TGG CCA				288
Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Phe Trp Pro				
205	210	215	220	
TTC ACT TTT GGC CCT GGG ACC AAG CTG GAG ATC AAA CGT				327
Phe Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys Arg				
225	230			

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Glu Thr Thr Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly	
1 5 10 15	
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asn Ile Gly Ser Ser	
20 25 30	
Ser Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	
35 40 45	
Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser	
50 55 60	
Gly Ser Gly Ser Gly Thr Gln Phe Thr Leu Thr Ile Ser Ser Leu Gln	
65 70 75 80	
Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Phe Trp Pro	
85 90 95	
Phe Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys Arg	
100 105	

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

13

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TTTTCTGCAG TAATAGGCGG CCGCAGGGGG AGGAGGGTCC ATCGAAGGTC GCGAAGCAGA 60
GACTGTTGAA AG 72

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TTTTGAATTC TTATTAACCA CCGAACTGCG GGTGACGCCA AGCGCTTGCG GCCGTTAAGA 60
CTCCTTATTA CGCAG 75

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

AAAAGCGGCC GCACTGGCCT GAGAGANNNN NN 32

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs

14

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TCGACCCACG CGTCCG

16

- (2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GGGTGCCGAG GC

12

- (2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

AAAAGAATTC TGAATGTGTT ATTTTAGCTC AGGTCACCTCT GACCTGATTA TCAAGACCCC

60

ACTTCACCCC CT

72

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

AAAAGCGGCC GCAGGGGGAG GAGGGTCCAT GGAATCTGCC AAGGAG

46

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GTAAAACGAC GGCCAGT

17

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GGATAACAAT TTCACACAGG

20

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

AAAGCGGCCG CACTGGCCTG AGAGA

25

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

AAAAGGCCCA GCCGGCCATG GCCCAGCCCA CCACGCGTCC G

41

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

17

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

AAAAGGCCCA GCCGGCCATG GCCCAGTCCC ACCACGCGTC CG

42

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AAAAGGCCCA GCCGGCCATG GCCCAGTACC CACCACGCGT CCG

43

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

AAAAGAATTC GAGGTTACAT TAACTTTGTT CCGGTCAGAC TGACCCAAGT CGACCTGAAT

60

GTGTTATTTT AG

72

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

18

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CCTTGGCAGA TTCCATCTCG GCCATTGCCG GC

32

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CCGGCAATGG CCGAGATGGA ATCTGCCAAG G

31

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

TTTTGTGCGAC TCAATCAGTT ATGCGGCCGC CAGCTGCAGG AGGGCCGGCT GGGCCGACCC

60

TCCTCCCCCA GACCCCACTT CACCCC

86

19

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

TGTTGAAACA CAAGCGCCAG

20

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

TGGAAGAGGC ACGTTCCTTT CTTT

24

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

20

CTCCTTCTTA CTCTTGCTGG CGGT

24

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

AGACTCTCCC CTGTTGAAGC TCTT

24

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

TGAAGATTCT GTAGGGGCCA CTGTCTT

27

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

TGAACCGCCT CCACCTGAGG AGACGGTGAC CAGGGTGCC

39

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

TGAACCGCCT CCACCTGAAG AGACGGTGAC CATTGTCCC

39

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

TGAACCGCCT CCACCTGAGG AGACGGTGAC CAGGGTTCC

39

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

22

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

TGAACCGCCT CCACCTGAGG AGACGGTGAC CGTGGTCCC

39

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

TTTTTGGCCC AGCCGGCCAT GGCCAGGTG CAGCTGGTGC AGTCTGG

47

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

TTTTTGGCCC AGCCGGCCAT GGCCAGGTC AACTTAAGGG AGTCTGG

47

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

23

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

TTTTTGGCCC AGCCGGCCAT GGCCGAGGTG CAGCTGGTGG AGTCTGG

47

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

TTTTTGGCCC AGCCGGCCAT GGCCGAGGTG CAGCTGCAGG AGTCGGG

47

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

TTTTTGGCCC AGCCGGCCAT GGCCGAGGTG CAGCTGTTGC AGTCTGC

47

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

TTTTTGGCCC AGCCGGCCAT GGCCCAGGTA CAGCTGCAGC AGTCAGG

47

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

TTATTCGCGG CCGCCTAAAC AGAGGCAGTT CCAGATTTC

39

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

GTCACCTTGCG GCCGCCTACA GTGTGGCCTT GTTGGCTTG

39

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

25

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

TCTGGCGGTG GCGGATCGGA CATCCAGATG ACCCAGTCTC C

41

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

TCTGGCGGTG GCGGATCGGA TGTGTGATG ACTCAGTCTC C

41

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TCTGGCGGTG GCGGATCGGA AATTGTGTTG ACGCAGTCTC C

41

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

26

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

TCTGGCGGTG GCGGATCGGA CATCGTGATG ACCCAGTCTC C

41

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

TCTGGCGGTG GCGGATCGGA AACGACACTC ACGCAGTCTC C

41

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

TCTGGCGGTG GCGGATCGGA AATTGTGCTG ACTCAGTCTC C

41

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid

27

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

TTCTCGTGCG GCCGCCTAAC GTTTGATTTC CACCTTGGTC CC

42

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

TTCTCGTGCG GCCGCCTAAC GTTTGATCTC CAGCTTGGTC CC

42

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

TTCTCGTGCG GCCGCCTAAC GTTTGATATC CACTTTGGTC CC

42

(2) INFORMATION FOR SEQ ID NO: 62:

28

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

TTCTCGTGCG GCCGCCTAAC GTTTGATCTC CACCTTGGTC CC

42

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

TTCTCGTGCG GCCGCCTAAC GTTTAATCTC CAGTCGTGTC CC

42

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

29

TCTGGCGGTG GCGGATCGCA GTCTGTGTTG ACGCAGCCGC C
41

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TCTGGCGGTG GCGGATCGCA GTCTGCCCTG ACTCAGCCTG C
41

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthesis DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

TCTGGCGGTG GCGGATCGTC CTATGTGCTG ACTCAGCCAC C
41

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthesis DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

TCTGGCGGTG GCGGATCGTC TTCTGAGCTG ACTCAGGACC C

41

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthesis DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

TCTGGCGGTG GCGGATCGCA CGTTATACTG ACTCAACCGC C

41

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthesis DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

TCTGGCGGTG GCGGATCGCA GGCTGTGCTC ACTCAGCCGT C

41

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthesis DNA"

31

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

TCTGGCGGTG GCGGATCGAA TTTTATGCTG ACTCAGCCCC A

41

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

TTCTCGTGCG GCCGCCTAAC CTAGGACGGT GACCTTGGTC CC

42

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

TTCTCGTGCG GCCGCCTAAC CTAGGACGGT CAGCTTGGTC CC

42

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

32

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

TTCTCGTGCG GCCGCCTAAC CTAAACGGT GAGCTGGGTC CC

42

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

CGATCCGCCA CCGCCAGA

18

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

GTCTCCTCAG GTGGAGGC

18

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

33

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CGATCCGCCA CCGCCAGAGC CACCTCCGCC TGAACCGCCT CCACCTGAGG AGAC

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/GB 98/02630

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C12N15/10 C12N15/62 C07K14/72 C07K16/00
C12Q1/68 G01N33/577

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K C12Q G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 93 08278 A (AFFYMAX TECH NV) 29 April 1993 see page 9, line 32 - line 37 ---	1-23
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A	M. BROWN AND P.A. SHARP: "Human estrogen receptor forms multiple protein-DNA complexes" J. BIOL. CHEM., vol. 265, no. 19, 5 July 1990, pages 11238-11243, XP002092292 AM. SOC. BIOCHEM. MOL.BIOL., INC., BALTIMORE, US see the whole document --- -/-	1-23

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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"&" document member of the same patent family

Date of the actual completion of the international search

4 February 1999

Date of mailing of the international search report

18/02/1999

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/GB 98/02630

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

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Information on patent family members

International Application No

PCT/GB 98/02630

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