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(57) Abstract

The present invention relates to the field of compounds which are substrates or inhibitors of proteolytic enzymes and to apparatus and methods for identifying substrates or inhibitors for proteolytic enzymes. We have devised a combinatorial method for the rapid identification of binding motifs which will greatly expedite the synthesis of inhibitors of a variety of proteolytic enzymes such as aspartyl proteases, serine proteases, metallo proteases and cysteinyl proteases.



Substrates And Inhibitors of Proteolytic Enzymes

The present invention relates to the field of compounds which are substrates or inhibitors of proteolytic enzymes 5 and to apparatus and methods for identifying substrates or inhibitors for proteolytic enzymes.

Many therapeutically useful drugs act as enzyme inhibitors. In particular, proteolytic enzyme inhibitors have been the focus of much attention in the 10 pharmaceutical industry, because they play a variety of roles in a multitude of biological systems. Their proteolytic activities are related to processes ranging from cell invasion associated with metastatic cancer to evasion of an immune response, as seen in certain 15 parasitic organisms; from nutrition to intracellular signalling to the site-specific proteolysis of viral proteases and eukaryotic hormone-processing enzymes. However, the traditional random screening methods for the 20 identification of lead molecules as inhibitors of proteolytic enzymes are often laborious and time-consuming. Therefore new and efficient methods which can accelerate the drug discovery process are greatly in demand.

We consider that proteases contain an active catalytic 25 site which tends to become increasingly activated as the recognition pockets¹ (S₁ and S₂ etc) and (S₁' and S₂' etc) become better occupied. Therefore, it is important that those parts (P₁ and P₂ etc) (P₁' and P₂' etc) of the 30 inhibitor that best fit into these pockets are identified as quickly as possible in order to design novel protease

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inhibitors. Therefore, we have devised a combinatorial method for the rapid identification of these binding motifs which will greatly expedite the synthesis of inhibitors of a variety of proteolytic enzymes such as 5 aspartyl proteases, serine proteases, metallo proteases and cysteinyl proteases.

Proteases of interest include (but are not limited to):

1. Aspartyl proteases, such as renin, HIV, cathepsin D and cathepsin E etc.
- 10 2. Metalloproteases, such as ECE, gelatinase A and B, collagenases, stromolysins etc.
3. Cysteinyl proteases, such as apopain, ICI, DerPI, cathepsin B, cathepsin K etc.
- 15 4. Serine proteases, such as thrombin, factor VIIa, factor Xa, elastase, trypsin.
5. Threonyl proteases, such as proteasome S.

The use of a fluorescence resonance energy transfer (FRET) substrate for the analysis of proteolytic enzyme specificity was first published by Carmel.² Since then 20 many different quenched fluorogenic substrates for measuring enzyme inhibition have been described in the literature.⁴⁻¹¹ These substrates contain a fluorophore, F, in a P position (*vide supra*), which is quenched by another group, Q, present in a P' position (*vide supra*) and separated from F by the scissile bond. The advantage of 25

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the positioning of these residues, F and Q, is that cleavage of a peptide bond occurs between the two natural residues and, therefore, represents a more natural hydrolytic event rather than the cleavage and release of a C-terminal chromophore.

For example, Bratovanova and Petkov¹² have synthesised fluorogenic substrates from peptide 4-nitroanilides. N-acylation of peptide 4-nitroanilides with the aminobenzoyl (ABz) group yielded substrates that are internally quenched by the presence of the 4-nitroanilide moiety. Upon hydrolysis of the aminoacyl-4-nitroanilide bond, the highly fluorescent N-ABz group is released attached either to an amino acid or peptide.

Immobilised libraries, where substrates are attached to a polymer or biopolymer support, have also been used for mapping protease binding sites.¹³ Singh et al. reported recently that enzymatic substrate activity of 38 selected octapeptides attached via a linker to controlled pore glass is predictive of the same activity of similar peptides in solution. However, these results are preliminary and only for a specific example. Therefore, it is not clear whether immobilised substrates attached to polymers can reliably replace soluble substrates in mapping the hindered protease binding sites, especially since the hydrophilic or lipophilic nature of the polymer and the size of the interstices within the polymer are bound to influence the reaction between the enzyme and its substrates.

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Mixtures of internally quenched, fluorogenic substrates have also recently been described in which the quencher group, Q, is 2,4-dinitrophenyl (Dnp) and is attached to the P side of the scissile bond, while the fluorogenic group, is N-methyl anthranilic acid (Nma) and is attached to the P' side.¹⁴

Examples of other Donor-Acceptor Chromophore Pairs that have been applied to Biological Systems are shown in Table 1.

Table 1 : Donor-Acceptor Chromophore Pairs That Have Been Applied To Biological Samples

Donor	Acceptor	Donor	Acceptor
Naphthalene	Dansyl	LAEDANS	TNP-ATP
IANBD	DDPM	ε-A	IANBD
15 IAEDANS	DDPM	NBD	SRH
DNSM	LY	ISA	TNP
IAEDANS	IANBD	Dansyl	ODR
E-A	F ₂ DNB	DANZ	IAF
Pyrene	Bimane	FNAI	EITC
20 ANAI	IPM	NBD	LRH
IAANS	IAF	IAF	EIA
ε-A	F ₂ DPS	FITC	ENAI
ε-A	DDPM	Proflavin	ETSC
IAEDANS	TNP	CPM	TNP-ATP
25 MNA	DACM	IAEDANS	IAF
PM	NBD	CPM	Fluorescein
FITC	TNP-ATP	IAEDANS	FITC
DANZ	DABM	FITC	TMR
NCP	CPM	IAF	TMR
30 NAA	DNP	CF	TR
LY	TNP-ATP	CPM	FTS
IAF	dil-C ₁₈	ε-A	TNP-ATP
IAF	TMR	CPM	FM
FMA	FMA	LY	EM
35 PM	DMAMS	FITC	EITC
mBBR	FITC	IAEDANS	DiO-C ₁₄
mBBR	DABM	IAF	ErITC
ε-A	NBD	FITC	EM
Pyrene	Coumarin	FITC	ETSC
40 IPM	FNAI	FITC	ErITC
IAEDANS	DABM	BPE	CY5

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ANAI, 2-anthracene N-acetylimidazole; BPE, B-phycoerythrin; CF, carboxyfluorescein succinimidyl ester; CPM, 7-doethylamino-3-(4'maleimidylphenyl)-4-methylcoumarin; CY5, carboxymethylindocyanine-N-hydroxysuccinimidyl ester; diI-C₁₈, 1,1'-dioctadecyl-3,3,3'-tetramethyl-indocarbocyanine; DiO-C₁₄, 3,3'-ditetradecyloxacarbocyanine; DABM, 4-dimethylaniniphenylazo-phenyl-4'-maleimide; DACM, (7-(dimethylamino)coumarin-4-yl)-acetyl; DANZ, dansylaziridine; DDPM, N-(4-dimethylamino-3-5-dinitrophenyl)maleimide; DACM, di-methylamino-4-maleimidostilbene; DMSM, N-(2,5-dimethoxystiben-4-yl)-maleimide; DNP, 2,4-dinitrophenyl; ε-A, 1,N⁶-ethenoadenosine; EIA, 5-(iodoacetetamido)eosin; EITC, eosin-5-isothiocyanate; ENAI, eosin N-acetylimidazole; EM, eosin maleimide; ErITC, erythrosin-5'-isothiocyanate; ETSC, eosin thiosemicarbazide; F₂DPB, 1,5-difluoro-2,4'dinitrobenzene; F₂DPS, 4,4'-difluoro-3,3'dinitropheylsulphone; FITC, fluorescein N-acetylimidazole; FTS, fluorescein thiosemicarbazide; IAANS, 2-((4'-iodoacetamido)anilino)naphthalene-6-sulphonic acid; IAEDANS, 5-(2-((iodoacetyl)amino)ethylamino)-naphthlene-1-sulphonic acid; IAF, 5-iodoacetamidofluorescein; IANBD, N-((2-(iodoacetoxy)ethyl)-N-methyl)amino-7-nitrobenz-2-oxa1,3,diazole; IPM, 3(4-isothiocyanatophenyl)7-diethyl-4-methylcoumarin; ISA, 4-(iodoacetamido)salicylic acid; LRH, lissaminerho-2,1,3-benzoxadiazol-4-yl; NCP, N-cyclohexyl-N'-(1-pyrenyl)carbodiimide; ODR, octadecylrhodamine; PM, N-(1-pyrene)-maleimide; SRHsulphurhodamine; TMR, tetramethylrhodamine; TNP, trinitrophenyl; TR, Texas red.

from: Wu, P. and Brand, L. 1994. Anal. Biochem. 218, 1-13.

The specificity of soluble peptide libraries have been determined.^{15,16} Berman et al. described¹⁶ an HPLC mass spectrometry technique in which 6 mixtures of 128 peptides were synthesised which were N-terminally labelled with the Dnp group in order to allow UV monitoring on the HPLC. The disadvantage of this approach is that each assay mixture has to be individually analysed, because no fluorogenic substrate is revealed, and that the effective concentration of each separate component is limited by the size of the mixture because of overall solubility factors.

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Drevin et al.¹⁷ have suggested the use of individually synthesised fluorogenic substrates for the determination of enzyme activity using a chromophore which chelates lanthanide ions. Garmann and Phillips have suggested the use of FRET substrates in which the fluorogenic and quencher moieties are attached via thiol or amino functional groups after the peptide has been synthesised, but this has the disadvantage that they are not in library form and that these functional amino and thiol groups need to be selectively revealed after the peptide has been synthesised. Wang et al. have suggested the use of the EDANS and DABCYL fluorescor and quencher pairing for the individual synthesis of substrates for proteolytic enzymes.

The above methods which have used FRET techniques for the mapping of the active site around a specific protease suffer from one or more of the following disadvantages:

- i. because of general aqueous insolubility they do not produce mixtures of compounds in a form suitable for high throughput screening in aqueous solution.
- ii. the derivatised compounds cannot be prepared in combinatorial library form using solid phase techniques.
- iii. the mixtures which have been used^{8,9} were not self-decoding, and needed time-consuming deconvolutive resynthesis for identification of the active molecules.

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Description of the Drawings

Figures 1 to 14 inclusive exemplify component distributions in the plates of a library matrix;

Figure 15 illustrates a reaction scheme for production of
5 compound number 4: Boc-Val-Ala-Leu-H wherein
i. isobutylchloroformate, N-methylmorpholine, then N,O-dimethylhydroxylamine HCl, THF.
ii. HCl, dioxan. iii. isobutylchloroformate, N-methylmorpholine, then Boc-Ala-OH, THF.
10 iv. HCl, dioxan. V. Boc-Val-Osuc, N-methylmorpholine, DMF. Vi. LAH;

Figure 16 illustrates a reaction scheme for production of active inhibitors of *Der PI*.

Brief Description of the Invention

15 The present invention relates to the field of:
i. Compounds which are substrates or inhibitors of proteolytic enzymes.
ii. Apparatus and methods which provide the rapid generation of structure-activity relationships
20 using auto-deconvoluting combinatorial libraries, which facilitate the invention of novel inhibitors of proteolytic enzymes.
iii. Apparatus and methods which provide the detection and measurement of proteolytic enzyme activity using combinatorial FRET (fluorescence resonance energy transfer) libraries of molecules.
25

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iv. Apparatus and methods which provide the establishment of biological assays for proteolytic enzymes through the rapid discovery of highly active substrates for proteolytic enzymes.

We describe herein apparatus and methods which can be used for the rapid generation of structure-activity relationship (SAR) data and, therefore, the characterisation of the binding motif of any protease, and which will, therefore, facilitate:

- i. the development of a sensitive enzyme inhibition assay by using the best compound in the library as the fluorogenic substrate for the proteolytic enzyme under scrutiny.
- ii. the invention of novel compounds which are proteolytic enzyme inhibitors by rapid characterisation of the best binding motif.
- iii. computer aided drug design to design potent inhibitors using known methodology, and also in prioritising which pre-synthesised compounds in the in-house and commercially available databases to assay.

In a first aspect the invention provides novel compounds represented by the formula A-B-C-D-nE-F [I] in which; A represents a fluorescor internally quenched by F; B, C, D, and E represent groups such that the scissile bond between any two of these groups is a suitable bond; F represents a quencher capable of internally quenching the fluorescor A; and

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n represents an integer between 1 and 4 inclusive.

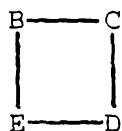
In some embodiments the suitable bond is an unsubstituted amide bond (see Example 1); in other embodiments the suitable bond is an ester bond (see Example 2).

5 In preferred embodiments B, C, D, E are amino acids or hydroxy acids. That is a molecule with an amine or hydroxy terminus and a carboxylic acid terminus. The amine/hydroxy group may be positioned on the same carbon atom or separated by a number of atoms and atom types.

10 The molecules may be cyclic or alicyclic. They may be linear or cyclic on the same structure

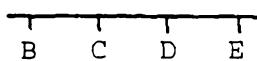
B-C-D-E

or

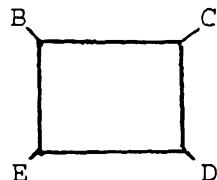


or BCDE can be on a central scaffold (linear or cyclic)

15

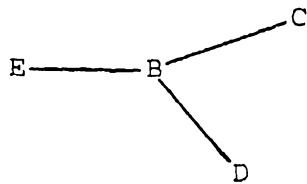


or



or one of the residues can be the backbone

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Where the symbol -B-C-D-E- or -B-C-D-nE- is used herein,
5 it is to be understood to include all of these linear and
cyclic variants within its definition.

At least one but not all the bonds between B, C, D, E need
to be scissile. Non scissile bonds may include
sulphonamide, urea, aminomethylene.

10 Several non-limiting examples of "scaffold" molecules are
shown in Table 2, in which substituents R₁-R₄ correspond to
possible variable groups B, C, D and E.

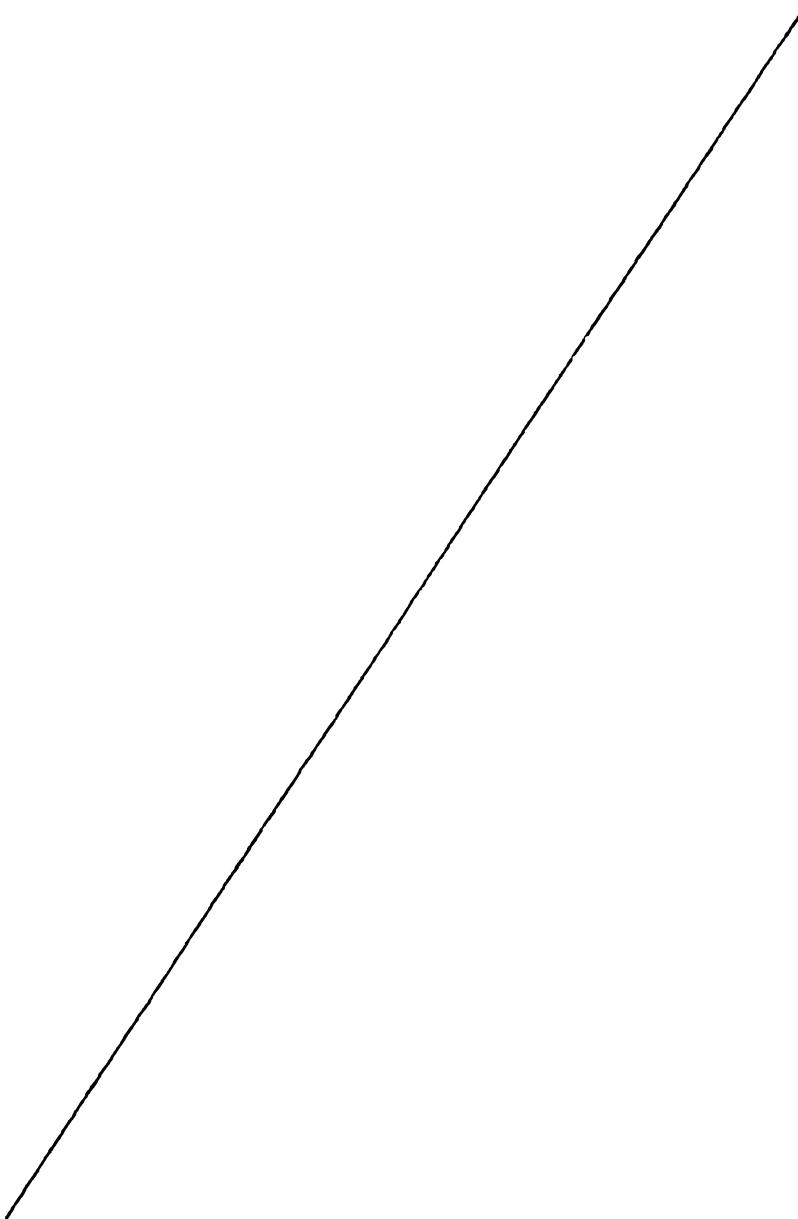
15 In a second aspect the invention provides a combinatorial
library of FRET compounds comprising a mixture of
compounds of formula [I].

20 In a third aspect the invention provides for the use of
such a combinatorial FRET library in a method which
provides rapid generation of structure-activity
relationships (SAR) which comprises detection and
measurement of proteolytic enzyme activity by carrying out
an assay with a library of combinatorial FRET
25 (fluorescence resonance energy transfer) molecules to find
a substrate or substrates for the enzyme. According to
this method an identified substrate can be synthesised and
used in biological assay for proteolytic enzymes. Novel
substrates are included in the scope of the invention.

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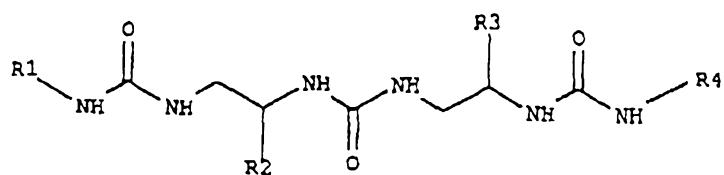
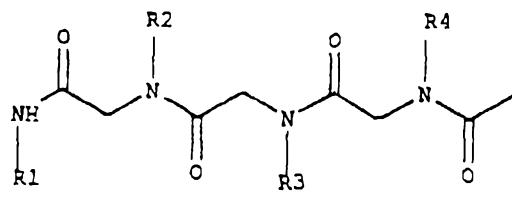
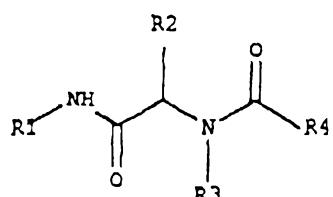
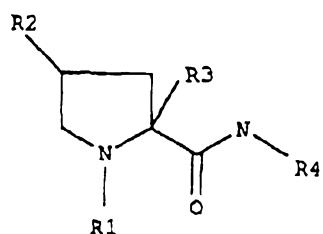
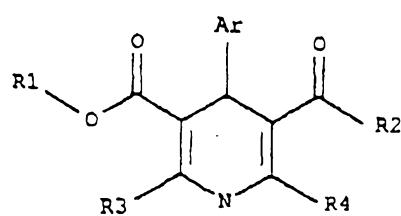
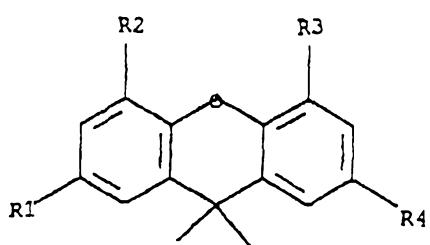
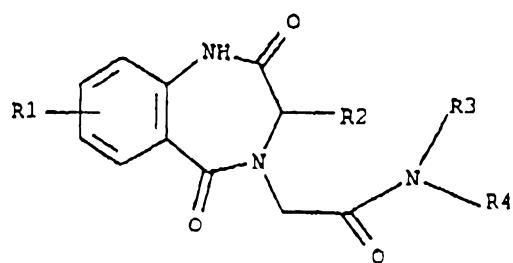
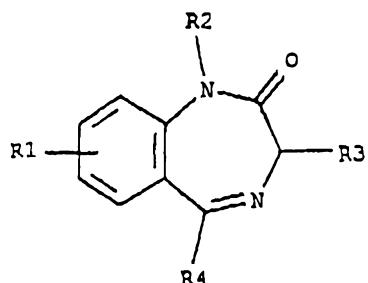
In a forth aspect the invention provides for the use of such a combinatorial FRET library in a method for detection and measurement of proteolytic enzyme activity against compounds of the library.

5 In a fifth aspect the invention provides a method which comprises the identification of an enzyme inhibitor or inhibitors wherein a FRET compound which has been



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TABLE 2



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identified as a substrate is used in an inhibition assay with the enzyme separately against a panel of possible inhibitors.

In a sixth aspect the invention provides a set of 5 compounds which comprises two complementary FRET compound libraries. Such a set will be referred to hereafter as "apparatus" because it allows for the screening or assay method for identifying substrates or inhibitors of proteolytic enzymes. This set of compounds constituting an 10 apparatus is capable of providing an auto-deconvoluting combinatorial library as will be described below.

In a seventh aspect the invention provides a method of identifying and synthesising an inhibitor of a proteolytic enzyme which comprises detection and measurement of 15 proteolytic enzyme activity by carrying out an assay with a library of combinatorial FRET (fluorescence resonance energy transfer) molecules, deconvoluting the library to find a substrate or substrates for the enzyme and synthesis of an inhibitor based on the substrate or 20 substrates. The direct product of this method is one or more novel proteolytic enzyme inhibitors.

In an eighth aspect the invention provides an inhibition assay which uses a FRET molecule, which has been identified as a substrate for the enzyme, wherein the 25 molecule is assayed with the enzyme separately against a panel of possible inhibitors.

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In a ninth aspect the invention provides a complementary pair of compound libraries L1 and L2 which constitute a set containing compounds of formula:

Aa-Bb-Cc-Dd-n(Ee)-Ff-Gg

5 giving $a \times b \times c \times d \times e \times f \times g = M_n$ compounds in each library, there being a predetermined number (P1, P2) of mixtures each consisting of a predetermined number (Q1, Q2) of individual identifiable compounds in each library, wherein both L1 and L2 contain the same M_n compounds, but 10 wherein any two compounds which are found together in one mixture of Q1 compounds of L1 are not found together in any one of the P2 mixtures of L2.

In a tenth aspect the invention provides a method of screening for enzymic activity using the libraries L1, L2 15 described above in which the P1 mixtures of L1 and the P2 mixtures of L2 are each placed separately into individual wells of well plates, the well plates having wells arranged in a format adapted to allow deduction of a unique active compound formula from the presence of 20 activity in one well of L1 and one well of L2.

The apparatus of the invention preferably comprises two complementary compound libraries, L1 and L2, each containing $n \times 1600$ compounds of the invention, of the type A-B₁₋₁₀-C₁₋₁₀-D₁₋₈-n(E₁₋₂)-F-G [II], in which:

25 A = a fluorescor internally quenched by F, preferably an unsubstituted or substituted anthranilic acid derivative, connected by an amide bond to B

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B, C, D, E, are natural or unnatural amino acid residues connected together by suitable bonds, although B, C, D and E can be any set of groups, provided that the scissile bond between D-E is an unsubstituted bond.

5 F = a quencher capable of internally quenching the fluorescor A, preferably an unsubstituted or substituted 3-nitrotyrosine derivative.

10 G = optionally present and is a hydrophilic moiety, preferably an aspartyl amide moiety. If present, G advantageously ensures that all compounds in the library are imparted with aqueous solubility. Also, G should not be a substrate for any type of enzyme.

n = any integer between 1 and 4 inclusive.

15 In an alternative, the scissile bond could be between B-C or C-D.

(Note that A and F herein correspond generally and respectively to moieties F and Q of the prior art referred to above).

20 The numbers represented in subscript following residues B, C, D and E refer to the number of possibilities from which those residues are selected. Thus, by way of illustrative example, A-B_{1.5}-C-D-E_{1.2}-F-G represents a mixture of the following ten compounds:

25 A-B₁-C-D-E₁-F-G
A-B₂-C-D-E₁-F-G
A-B₃-C-D-E₁-F-G
A-B₄-C-D-E₁-F-G
A-B₅-C-D-E₁-F-G
A-B₁-C-D-E₂-F-G

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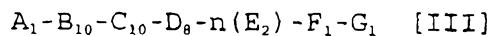
A-B₁-C-D-E₂-F-G

A-B₁-C-D-E₂-F-G

A-B₄-C-D-E₂-F-G

A-B₅-C-D-E₂-F-G

5 The general combinatorial formula for each library can be expressed as:



providing $1 \times 10 \times 10 \times 8 \times n \times 2 \times 1 \times 1 = 1600n$ compounds.

10 Both compound libraries, L1 and L2, of the above type are synthesized using solid phase techniques using the Multipin approach²⁴ such that each library contains 1600n compounds as 80n mixtures of 20 distinct, identifiable compounds. These 20 component mixtures are then placed
15 separately into each of 80 wells of a 96 well plate (the other two lanes are used for control experiments) and then screened against a known quantity of the protease.

Thus it is an important part of the invention that regardless of the number of compounds contained in the two
20 libraries L1 and L2 (e.g. in the preferred embodiment: 1600n, where n = any integer between 1 and 4) the libraries themselves are complementary and amenable to deconvolution without recourse to resynthesis. It is also an important part of the invention that the library matrix
25 has been especially formatted so that the most important site pairings P₂ and P₁ for proteolytic enzymes can be identified immediately without recourse to resynthesis.

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Those compounds of the type A-B-C-D-E-F-G that are the better substrates for the protease will be cleaved, and can be readily identified because the fluorescor, A, will be cleaved from its nearby quencher F, in a time dependent manner which can be easily quantified. The fluorescent quenching by F of A only occurs when the two are in nearby proximity, normally within 30 angstrom units. Hence cleavage of a scissile bond (e.g. the scissile bond D-E) allows F to move further away from A and thus allow A to fluoresce when excited by light of the correct wavelength.

1. In this manner the most active compound can be rapidly identified without the need for further resynthesis and deconvolution. Moreover, the wells that show the most rapid development of fluorescence can also be analysed by mass spectrometry, since by comparison with the original mixture, the identity of the most efficient substrate can be found by its disappearance into its two component parts, e.g A-B-C-D and E-F-G.

Hence the problem of library deconvolution can be overcome and the most active substrate for the enzyme can be rapidly identified.

In addition, after the initial treatment of the proteolytic enzyme with the library mixtures, L1 and L2, the residual enzymatic activity in each well can be quantified by the addition of the most potent fluorogenic substrate for the enzyme, S1, which is found in the 16xn compound library. Because of the nature of the library

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design this can be quickly prepared and purified. If there is no appearance of increased fluorescence with the known substrate, S1, then the presence of an enzyme inhibitor can be inferred, which again can be quickly identified without the need for resynthesis.

The general description of the library layout will now be described with reference to figures 1 to 14.

For example, when $n=1$ and the library contains 1600 compounds, in the first column of the first row (A1) (Fig.1) in the first plate (P1) of the library L1, (hereinafter designated as location A1,P1,L1) there will be one C component, C₁, one D component, D₁, the ten B components and the two E components (E₁ and E₂) (Fig. 2). In the tenth column of the first row (A10) in the first plate (P1) of the library L1, (hereinafter designated as location A10,P1,L1) there will be one C component, C₁₀, one D component, D₁, the ten B components and the two E components (E₁ and E₂). In the tenth column of the eighth row (H10) in the first plate (P1) of the library L1, (hereinafter designated as location H10,P1,L1) there will be one C component, C₁₀, one D component, D₈, the ten B components and the two E components (E₁ and E₂). Hence all 1600 components are present in the one plate, because the 80 wells each contain 20 components.

A second complementary library is synthesised as follows (Fig. 3). In the first column of the first row (A1) of the first plate (P1) of the library, L2, (hereinafter designated as location A1,P1,L2), there will be ten C components, two D components (D₁ and D₂), one B component,

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B₁, and one E component, E₁. In the tenth column of the first row (A10) of the first plate (P1) of the library, L2, (hereinafter designated as location A10,P1,L2), there will be ten C components, two D components (D₁ and D₂), one B component, B₁₀, and one E component, E₁. In the first column of the second row (B1) of the first plate (P1) of the library, L2, (hereinafter designated as location B1,P1,L2), there will be ten C components, two D components (D₁ and D₂), one B component, B₁, and one E component, E₂. In the tenth column of the second row (B10) of the first plate (P1) of the library, L2, (B10,P1,L2) there will be ten C components, two D components (D₁ and D₂), one B component, B₁₀, and one E component, E₂. Hence only the first two rows are used to accommodate 400 compounds in total.

In the first column of the first row (A1) of the second plate (P2) of the library, L2, (hereinafter designated as location A1,P2,L2), there will be ten C components, two D components (D₃ and D₄), one B component, B₁, and one E component, E₁ (Fig. 4). In the tenth column of the first row (A10) of the second plate (P2) of the library, L2, (hereinafter designated as location A10,P2,L2), there will be ten C components, two D components (D₃ and D₄), one B component, B₁₀, and one E component, E₁. In the first column of the second row (B1) of the second plate (P2) of the library, L2, (hereinafter designated as location B1,P2,L2), there will be ten C components, two D components (D₃ and D₄), one B component, B₁, and one E component, E₂. In the tenth column of the second row (B10) of the second plate (P2) of the library, L2, (B10,P2,L2), there will be ten C components, two D components (D₃ and

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D_4), one B component, B_{10} , and one E component, E_2 . Hence only the first two rows are used to accommodate 400 compounds in total.

In the first column of the first row (A1) of the third plate (P3) of the library, L2, (hereinafter designated as location A1,P3,L2), there will be ten C components, two D components (D_5 and D_6), one B component, B_1 , and one E component, E_1 (Fig 5). In the tenth column of the first row (A10) of the third plate (P3) of the library, L2, (hereinafter designated as location A10,P3,L2), there will be ten C components, two D components (D_5 and D_6), one B component, B_{10} , and one E component, E_1 . In the first column of the second row (B1) of the third plate (P3) of the library, L2, (hereinafter designated as location B1,P3,L2), there will be ten C components, two D components (D_5 and D_6), one B component, B_1 , and one E component, E_2 . In the tenth column of the second row (B10) of the third plate (P3) of the library, L2, (B10,P3,L2), there will be ten C components, two D components (D_5 and D_6), one B component, B_{10} , and one E component, E_2 . Hence only the first two rows are used to accommodate 400 compounds in total.

In the first column of the first row (A1) of the fourth plate (P4) of the library, L2, (hereinafter designated as location A1,P4,L2), there will be ten C components, two D components (D_7 and D_8), one B component, B_1 , and one E component, E_1 (Fig. 6). In the tenth column of the first row (A10) of the fourth plate (P4) of the library, L2, (hereinafter designated as location A10,P4,L2), there will be ten C components, two D components (D_7 and D_8), one B

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component, B_{10} , and one E component, E_1 . In the first column of the second row (B1) of the fourth plate (P4) of the library, L2, (hereinafter designated as location B1, P4, L2), there will be ten C components, two D components (D, and D_8), one B component, B_1 , and one E component, E_2 . In the tenth column of the second row (B10) of the fourth plate (P4) of the library, L2, (B10, P4, L2), there will be ten C components, two D components (D, and D_8), one B component, B_{10} , and one E component, E_2 . Hence only the first two rows are used to accommodate 400 compounds in total.

In this fashion two complementary libraries, L1 and L2 are prepared. In library, L1, each of the 80 of wells contains a mixture of 20 components providing 1600 compounds for screening. In library, L2, four plates are used in which only the first two rows are employed, providing 20 wells of 20 components per well per plate, and furnishing the same 1600 compounds as are present in library L1, but in a format in which no two compounds found together in library, L1, will be found together in library, L2.

Thus it is an important part of the invention that the compounds contained in the two libraries L1 and L2 are themselves complementary, in that any two compounds which are found together in a 20 component mixture in the same location (e.g. A1P1L1) in library L1, are not found together in any of the 20 component mixtures in any location of the library L2.

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Thus, for example, with reference to the primary library P1 L1 of figure 2 and the secondary libraries P1 L2, P2 L2, P3 L2 and P4 L2 of figures 3-6 it is possible to deconvolute an exemplary sequence:

5

-B₂-C₃-D₄-E₁-

If this sequence is a substrate fluorescence will occur in P1 L1 at C₃D₄. This gives the information that the substrate is

-?-C₃-D₄-?-

10

If fluorescence occurs in P2 L2 at B₂E₁ it indicates a substrate

-B₂-?-?-E₁-

The confirmation of the substrate as

-B₂-C₃-D₄-E₁-

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should be provided by non-fluorescence of P1 L2, P3 L2 and P4 L2 which all contain -B₂-C₃-X-E₁- where X is not D₄.

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In practice it is likely that more than one sequence will result in a substrate. Information as to which positions B-C-D-E- are sensitive to change (i.e. require a specific group) and which are insensitive (i.e. can tolerate more than one choice of group) in the context of the whole sequence gives valuable SAR data which can be used to model and/or synthesise related compounds.

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In analogous examples, where separately $n=2$, 3 or 4 , extra plates are constructed in library L1 format to accommodate the component pairs E_3 and E_4 ($n = 2$), E_5 and E_6 ($n = 3$), and E_7 and E_8 ($n = 4$), respectively. For the respective 5 deconvolution libraries of the type, L2, the respective rows in the plates P1, P2, P3, and P4, are increasingly filled with the paired components D_1 and D_2 , D_3 and D_4 , and D_5 and D_6 , and D_7 and D_8 , respectively.

For example, when $n = 3$, and the library contains 4800 10 compounds, in the first column of the first row (A1) in the first plate (P1) of the library L1, (hereinafter designated as location A1,P1,L1) there will be one C component, C_1 , one D component, D_1 , the ten B components and the two E components (E_1 and E_2). In the tenth column 15 of the first row (A10) in the first plate (P1) of the library L1, (hereinafter designated as location A10,P1,L1) there will be one C component, C_{10} , one D component, D_1 , the ten B components and the two E components (E_1 and E_2). In the tenth column of the eighth row (H10) in the first 20 plate (P1) of the library L1, (hereinafter designated as location H10,P1,L1) there will be one C component, C_{10} , one D component, D_8 , the ten B components and the two E components (E_1 and E_2). Hence 1600 components are present 25 in the one plate, because the 80 wells each contain 20 components.

In the first column of the first row (A1) in the second plate (P2) of the library L1, (hereinafter designated as location A1,P2,L1) there will be one C component, C_1 , one D component, D_1 , the ten B components and the two E components (E_3 and E_4). In the tenth column of the first 30

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row (A10) in the second plate (P2) of the library L1, (hereinafter designated as location A10,P2,L1) there will be one C component, C₁₀, one D component, D₁, the ten B components and the two E components (E₃ and E₄). In the 5 tenth column of the eighth row (H10) in the second plate (P2) of the library L1, (hereinafter designated as location H10,P1,L1) there will be one C component, C₁₀, one D component, D₈, the ten B components and the two E components (E₃ and E₄). Hence 1600 components are present 10 in the one plate, because the 80 wells each contain 20 components.

In the first column of the first row (A1) in the third plate (P3) of the library L1, (hereinafter designated as location A1,P3,L1) there will be one C component, C₁, one D component, D₁, the ten B components and the two E 15 components (E₅ and E₆). In the tenth column of the first row (A10) in the third plate (P3) of the library L1, (hereinafter designated as location A10,P3,L1) there will be one C component, C₁₀, one D component, D₁, the ten B components and the two E components (E₅ and E₆). In the 20 tenth column of the eighth row (H10) in the third plate (P3) of the library L1, (hereinafter designated as location H10,P3,L1) there will be one C component, C₁₀, one C component, C₈, the ten B components and the two E components (E₅ and E₆). Hence 1600 components are present 25 in the one plate, because the 80 wells each contain 20 components. In total the three plate, P1, P2 and P3, contain 1600 compounds/plate 4800 compounds in total.

For example, when n = 4, and the library contains 6400 30 compounds, in the first column of the first row (A1) in

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the first plate (P1) of the library L1, (hereinafter designated as location A1,P1,L1) there will be one C component, C₁, one D component, D₁, the ten B components and the two E components (E₁ and E₂) (Fig. 7). In the tenth column of the first row (A10) in the first plate (P1) of the library L1, (hereinafter designated as location A10,P1,L1) there will be one C component, C₁₀, one D component, D₁, the ten B components and the two E components (E₁ and E₂). In the tenth column of the eighth row (H10) in the first plate (P1) of the library L1, (hereinafter designated as location H10,P1,L1) there will be one C component, C₁₀, one D component, D₈, the ten B components and the two E components (E₁ and E₂). Hence all 1600 components are present in the one plate, because the 15 80 wells each contain 20 components.

In the first column of the first row (A1) in the second plate (P2) of the library L1, (hereinafter designated as location A1,P2,L1) there will be one C component, C₁, one D component, D₁, the ten B components and the two E components (E₃ and E₄) (Fig. 8). In the tenth column of the first row (A10) in the second plate (P2) of the library L1, (hereinafter designated as location A10,P2,L1) there will be one C component, C₁₀, one D component, D₁, the ten B components and the two E components (E₃ and E₄). In the tenth column of the eighth row (H10) in the second plate (P2) of the library L1, (hereinafter designated as location H10,P2,L1) there will be one C component, C₁₀, one D component, D₈, the ten B components and the two E components (E₃ and E₄). 20 25

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In the first column of the first row (A1) in the third plate (P3) of the library L1, (hereinafter designated as location A1,P3,L1) there will be one C component, C₁, one D component, D₁, the ten B components and the two E components (E₅ and E₆) (Fig. 9). In the tenth column of the first row (A10) in the third plate (P3) of the library L1, (hereinafter designated as location A10,P3,L1) there will be one C component, C₁₀, one D component, D₁, the ten B components and the two E components (E₅ and E₆). In the tenth column of the eighth row (H10) in the third plate (P3) of the library L1, (hereinafter designated as location H10,P3,L1) there will be one C component, C₁₀, one D component, D₈, the ten B components and the two E components (E₅ and E₆).

In the first column of the first row (A1) in the fourth plate (P4) of the library L1, (hereinafter designated as location A1,P4,L1) there will be one C component, C₁, one D component, D₁, the ten B components and the two E components (E₇ and E₈) (Fig. 10). Likewise, in the tenth column of the first row (A10) in the fourth plate (P4) of the library L1, (hereinafter designated as location A10,P4,L1) there will be one C component, C₁₀, one D component, D₁, the ten B components and the two E components (E₇ and E₈). In the tenth column of the eighth row (H10) in the fourth plate (P4) of the library L1, (hereinafter designated as location H10,P4,L1) there will be one C component, C₁₀, one D component, D₈, the ten B components and the two E components (E₇ and E₈).

A second complementary library is synthesised as follows.

In the first column of the first row (A1) of the first

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plate (P1) of the library, L2, (hereinafter designated as location A1,P1,L2), there will be ten C components, two D components (D₁ and D₂), one B component, B₁, and one E component, E₁ (Fig. 11). In the tenth column of the first 5 row (A10) of the first plate (P1) of the library, L2, (hereinafter designated as location A10,P1,L2), there will be the ten C components, two D components (D₁ and D₂), one B component, B₁₀, and one E component, E₁. In the first column of the eighth row (H1) of the first plate (P1) of 10 the library, L2, (hereinafter designated as location H1,P1,L2), there will be the ten C components, two D components (D₁ and D₂), one B component, B₁, and one E component, E₈. In the tenth column of the eighth row (H10) of the first plate (P1) of the library, L2, (H10,P1,L2) 15 there will be the ten C components, two D components (D₁ and D₂), one B component, B₁₀, and one E component, E₈. Hence the matrix containing all ten columns and all eight rows are used to accommodate 1600 compounds in total.

In the first column of the first row (A1) of the second 20 plate (P2) of the library, L2, (hereinafter designated as location A1,P2,L2), there will be ten C components, two D components (D₃ and D₄), one B component, B₁, and one E component, E₁ (Fig. 12). In the tenth column of the first row (A10) of the second plate (P2) of the library, L2, 25 (hereinafter designated as location A10,P2,L2), there will be ten C components, two D components (D₃ and D₄), one B component, B₁₀, and one E component, E₁. In the first column of the second row (B1) of the second plate (P2) of the library, L2, (hereinafter designated as location B1,P2,L2), 30 there will be ten C components, two D components (D₃ and D₄), one B component, B₁, and one E

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component, E₂. In the tenth column of the eighth row (H10) of the second plate (P2) of the library, L2, (H10,P2,L2), there will be ten C components, two D components (D₅ and D₆), one B component, B₁₀, and one E component, E₈.

5 In the first column of the first row (A1) of the third plate (P3) of the library, L2, (hereinafter designated as location A1,P3,L2), there will be ten C components, two D components (D₅ and D₆), one B component, B₁, and one E component, E₁ (Fig. 13). In the tenth column of the first row (A10) of the third plate (P3) of the library, L2, (hereinafter designated as location A10,P3,L2), there will be ten C components, two D components (D₅ and D₆), one B component, B₁₀, and one E component, E₁. In the first column of the second row (B1) of the third plate (P3) of the library, L2, (hereinafter designated as location B1,P3,L2), there will be ten C components, two D components (D₅ and D₆), one B component, B₁, and one E component, E₂. In the tenth column of the eighth row (H10) of the third plate (P3) of the library, L2, (H10,P3,L2), there will be ten C components, two D components (D₅ and D₆), one B component, B₁₀, and one E component, E₈.

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In the first column of the first row (A1) of the fourth plate (P4) of the library, L2, (hereinafter designated as location A1,P4,L2), there will be ten C components, two D components (D₅ and D₆), one B component, B₁, and one E component, E₁ (Fig.14). In the tenth column of the first row (A10) of the fourth plate (P4) of the library, L2, (hereinafter designated as location A10,P4,L2), there will be ten C components, two D components (D₅ and D₆), one B component, B₁₀, and one E component, E₁. In the first

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column of the second row (B1) of the fourth plate (P4) of the library, L2, (hereinafter designated as location B1,P4,L2), there will be ten C components, two D components (D, and D₈), one B component, B₁, and one E component, E₂. In the tenth column of the eighth row (H10) of the fourth plate (P4) of the library, L2, (H10,P4,L2), there will be ten C components, two D components (D, and D₈), one B component, B₁₀, and one E component, E₈.

It will be apparent to those skilled in the art that the synthesis of two orthogonal sets of mixtures in solution providing two complementary FRET libraries indexed in two dimensions for autodeconvolution does not require the currently preferred arrangement -B₁₋₁₀-C₁₋₁₀-D₁₋₈-E₁₋₈-.

The general concept of two orthogonal sets of mixtures indexed in two dimensions can be applied to various permutations of numbers of wells, plate layout, number of permutations per mixture etc.

A numerical interrelationship can be defined as follows:

General Deconvolution Formulae

-Bb-Cc-Dd-n(Ee) - (I)

- 1) Primary and Secondary plates preferably have the same number of compounds per well [X]: otherwise there are two values, having X_p and X_s respectively.
- 2) The primary library comprises [np] plates.

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If $Rp.Cp=Rs.Cs$, then the number of plates in the secondary library is also [np]. If not, the number of plates in the secondary library [ns] is:

$$ns = \frac{Rp.Cp}{Rs.Cs} \cdot np$$

5

eg. A primary library of $np=4$, $Rp=8$, $Cp=10$ can be set out in an $Rs=4$, $Cs=5$ secondary library with the number of plates equal to:

$$ns = \frac{8 \times 10}{4 \times 5} \cdot np$$

10

$$= 16 \text{ plates.}$$

Number of compounds per well

$$-Bb-Cc-Dd-np(Ee)- \quad (1)$$

Number of possible combinations [k] is given by:

$$15 \quad k = b.c.d.np.e \quad (2)$$

When number of wells on a plate = [N], number of compounds per well = [X] and number of plates = [np] :

$$k = X.N.np \quad (3)$$

However, number of wells [N] is also defined by the number of rows [Rp] and number of columns [Cp] :

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$$N = Rp \cdot Cp \quad (4)$$

Combining (3) and (4) :

$$k = X \cdot Rp \cdot Cp \cdot np \quad (5)$$

Combining (2) and (5) :

5 $b \cdot c \cdot d \cdot np \cdot e = X \cdot Rp \cdot Cp \cdot np \quad (6)$

Cancelling [np] from both sides of the equation:

$$b \cdot c \cdot d \cdot e = X \cdot Rp \cdot Cp \quad (7)$$

Two of the variables (e.g. b.c) on the left side of the
equation must each be equal in number to the number of
10 columns [Cp], whilst a remaining variable (e.g. d) on the
left side must be equal in number to the number of rows
[Rp]. So:

$$[Cp]^2 \cdot Rp \cdot e = X \cdot Rp \cdot Cp \quad (8)$$

Cancelling [Cp] and [Rp] from both sides of the equation:

15 $Cp \cdot e = X \quad (9)$

where [e] is the number of variants along a fixed row; and

if $Rp=Cp$, then $Rp \cdot e = X$.

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Example

for a 10 x 10 x 8 x 8 format over 4 plates:

$$np.e = 8 \Rightarrow e = 2$$

$$10 \times 2 = X$$

5 X = 20.

From an understanding of the general deconvolution formulae shown above, those skilled in the art will readily appreciate that the advantageous results of self-deconvolution according to the invention are obtainable 10 utilising a number of different arrangements of wells, plate layouts, mixtures etc and that such variants on the preferred embodiment illustrated herein are intended to be within the scope of the present invention.

The FRET strategy is based on the synthesis of two 15 orthogonal sets of mixtures in solution. These solutions are each indexed in two dimensions. Thus the data from, for example, a protease scan identifies the most active compounds without the need for decoding or resynthesis. The positional preferences of sub-units (in this case 20 amino acids) are optimised with respect to all other variant positions simultaneously. The synergistic relationship between all four positions is realised and both positive, beneficial and negative, deactivating data are generated. This leads to families (sub-populations) 25 of substrates and their sub-unit preferences. The data can be fed into molecular modelling programs to generate

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pharmacophoric descriptors that encompass both the desirable features (from the positive data) and indicate undesirable interactions (from the negative data sets). Note that a one dimensional scan only indicates one position at a time as 'most active' and does not explore the synergistic relationship between positions.

The invention will now be described by reference to the following examples.

Example 1:

10 In this Example the proteolytic enzyme of interest is Der p1, which is found in house dust mite faeces. The example illustrates the synthesis of a number of FRET compounds in which the suitable bond is an unsubstituted amide bond, their use as a library for screening for potential 15 substrates of Der p1, and subsequent identification and synthesis of active inhibitors of the enzyme.

Purification of Der p1.

Crude mite extract (~100mg, SmithKline-Beecham, U.K) was dissolved in 5mL Phosphate Buffered Saline (PBS; 50 mM potassium phosphate; pH 7.4 containing 150 mM NaCl Der p1 was purified by affinity column chromatography using 4C1 antibody (indoor Biotechnology, Deeside, U.K.) The crude preparation was mixed with ~2 mL of affinity resin for 2 h at 4°C and then washed with 2-3 volumes of PBS. Elution of 25 bound protein was carried out using 5mM glycine containing 50% (v/v) ethylene glycol. Fractions (2.2 mL) were collected and neutralised with 0.8 mL of 0.2 M sodium phosphate

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buffer, pH 7.0. The fractions were pooled and dialysed overnight against 4 L PBS followed by a second dialysis against 2 L PBS for 2-3h. The total protein was concentrated as required by ultrafiltration (MacroSep, 5 Flowgen, U.K.)

Synthesis of compounds

The compounds were synthesised using the Multipin approach^{25,26} using Fmoc-Rink amide Macro crowns (Chiron Mimotypes Pty., Ltd., 11 Duerdin Street, Clayton Victoria 10 3168, Australia) with a loading of 7 μ Moles.

The amino acid residues of each of the compounds were linked using amide bonds in a suitable form. The coupling chemistry employed is similar to that reported in the literature²⁷ for fluorenylmethoxycarbonyl protected amino acids and activated pentafluorophenyl esters, in which the 15 side-chains are protected using acid labile protecting groups known to those skilled in the art, such as Boc- (for the -NH₂ of Lysine, -NH₂ of anthranilic acid and guanidino of arginine), tBu- (for the -OH groups of 20 serine, threonine and tyrosine), t-Bu for the -COOH group of Aspartic acid and Glutamic acid, Trityl- (for the Amide of Asparagine and Glutamine, and the amine functionality of the Histidine ring).

The N- α -fluorenylmethoxycarbonyl protecting group of the 25 coupled residues were cleaved using 20% piperidine in dimethylformamide (DMF) for 30 minutes at 20° C. The coupling reactions for the free acids such as Boc-ABz-OH (Boc-2-aminobenzoic acid), and Fmoc-(3-nitro)tyrosine-OH

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were accomplished using 10 equivalents of a mixture of the free acid (1 eq.) :TBTU (0.98 eq.): HOBT (0.98 eq.) : N-methylmorpholine (1.96 eq.) in dimethylformamide (500 μ L) as solvent for 5 hours at 20° C. The other amino acids were 5 coupled as their pentafluorophenyl esters²⁶ for 2-6 hours.

Hence, in order to couple approximately equal ratios of each component in the mixture of the derivatised amino acids as their pentafluorophenyl esters, a solution of a total of 0.98 equivalents (relative to the amino group 10 loading on the crown) of the mixture of amino acid pentafluorophenyl esters : HOBT (1 eq.) in DMF (500 μ L) were coupled for 16 hours at 20° C. The pins were then washed well with DMF and then recoupled using the same mixture under the same conditions. A third coupling of 10 15 equivalents (relative to the amino group loading of the crown) for 2 hours in DMF was performed using this coupling protocol with equimolar mixtures of the derivatised pentafluorophenyl esters of the amino acids in slightly less than 1 equivalent, it is possible to obtain 20 approximately equal amounts of the coupled products to the crown. In this fashion the libraries are constructed with 20 compounds present on each crown. The compounds were cleaved from the crowns directly into the 80 designated wells of the desired 96 well plate. In the cleavage 25 protocol each crown was treated with a mixture (600 μ L) containing trifluoroacetic acid (95%), triethylsilane (5%) for 2 hours at 20° C. The crowns were then washed with trifluoroacetic acid (500 μ L) and this was then combined with the cleavage solution.

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The Fmoc-Rink amide Macro crowns (Chiron Mimotypes Pty., Ltd., 11 Duerdin Street, Clayton Victoria 3168, Australia) at 7 μ Mol loading per crown, were coupled with a 10 fold excess of a mixture containing L-Fmoc-Asp(O-t-Bu)-OH (1eq) 5 using TBTU (0.98 eq) and N-methylmorpholine (1.96 eq.) in the presence of HOBt (0.98 eq.) in DMF at 0.14M concentration. After deblocking of the Fmoc group with 20% piperidine in DMF for 30 minutes and subsequent washing with DMF and then methanol, coupling of the Fmoc-(3-nitro)tyrosine-OH was accomplished using 10 equivalents of 10 a mixture of the Fmoc-(3-nitro)tyrosine-OH (1 eq.) :TBTU (0.98 eq.) : HOBt (0.98 eq.) : N-methylmorpholine (1.96 eq.) in dimethylformamide as solvent at 0.14 M 15 concentration for 5 hours at 20° C. Removal of the Fmoc group (vide infra) was followed by coupling of the mixtures of amino acids in the ratios outlined and under the conditions described (vide infra).

In a particular example the amino acids comprising group B include Ala, Val, Leu, Ser, Asn, Gln, Glu, Lys, Phe, Pro. 20 The amino acids comprising group C include Ala, Val, Leu, Ser, Asn, Gln, Glu, Lys, Phe, Pro. The amino acids comprising group D include Ala, Val, Ile, Leu, Nle, Ser, Glu, Phe. For n=4, the amino acids comprising group E include Ala, Val, Ile, Leu, Nle, Ser, Glu, Phe. Otherwise 25 any selection from the amino acids can be made for n=1, 2, or 3.

The plates containing the combined cleavage solutions and were then evaporated to dryness to yield the component mixtures using a rotary centrifuge ("SPEEDVAC", Savant 30 Instruments Inc., Farmingdale, NY) at 800 rpm for 1 hour

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at 20° C under a reduced pressure of 10⁻² mmHg. Each component was then transferred to the final mother plate using a (50%: 45%: 5%) mixture of acetonitrile: water: acetic acid. The plates were then lyophilised to dryness using at 20° C under a reduced pressure of 10⁻² mmHg, and then stored at -20° C. In this fashion libraries of the type shown in Figures 2-14 were prepared.

In further detail, the Multipin approach which was employed is described below:

10 **Multipin Synthesis Of Potential Substrates of *Der pI***

The 'Chiron' multipin kit consists of a standard 8 x 12 pin holder containing 96 'pin stems' to which are reversibly attached 'crowns'. The 'crowns' provide a reactive polymer surface upon which a growing peptide is anchored during solid phase peptide synthesis. Each crown (the equivalent of the peptide-resin in standard solid phase synthesis) can be considered to be an independent reactor by performing simultaneous synthesis in individual 1mL wells of industry standard 96 well plates. Each well, and thus each crown, can be charged with a unique set of reagents providing unique sequences to each crown. Common steps such as washing or removal of N_α protection can be performed concomitantly.

25 Synthesis is based upon the use of N_α-fluorenylmethyloxycarbonyl (Fmoc) protected amino acids. Side-chains of tri-functional amino acids are protected with acid labile groups such as trityl or tert-butyl. The addition of amino-acid residues to the growing peptide

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chain, a process termed 'coupling' proceeds through the utilisation of pre-formed pentafluorophenyl (pfp) esters or activation of the free acid, using the reagents HBTU or BOP in the presence of tertiary base (NMM) and HOBr as catalyst.

5 The experimental techniques used are fully documented (Maeji, N. J. Bray, A. M. Valerio, R. M. and Wang, W., *Peptide Research*, 8(1), 33-38, 1995 and Valerio, R. M. Bray, A. M. and Maeji, N. J. *Int. J. Pept. Prot. Res.*, 44, 10 158-165, 1994) and the main steps are briefly as follows.

General Methods

Preparation of Multipin Assembly

Whilst wearing standard plastic gloves, Fmoc-Rink Amide derivitized macrocrowns are assembled (simply clipped) 15 onto stems and slotted into the 8 x 12 stem holder in the desired pattern for synthesis.

Removal of N_α-Fmoc Protection

A 250mL solvent resistant bath is charged with 200 ml of a 20% piperidine/DMF solution. The multipin assembly is added and deprotection allowed to proceed for 30 minutes. The assembly is then removed and excess solvent removed by brief shaking. The assembly is then washed consecutively with (200mL each), DMF (5mins) and MeOH (5mins, 2mins, 2mins) and left to air dry for 15mins.

25 Quantitative UV Measurement of Fmoc Chromophore Release

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A 1cm path length UV cell is charged with 1.2mL of a 20% piperidine/DMF solution and used to zero the absorbance of the UV spectrometer at a wavelength of 290nm. A UV standard is then prepared consisting of 5.0mg Fmoc-
5 Asp(OBut)-Pepsyn KA (0.08mmol/g) in 3.2mL of a 20% piperidine/DMF solution. This standard gives $\text{Abs}_{290} = 0.55 - 0.65$ (at RT). An aliquot of the multipin deprotection solution is then diluted as appropriate to give a theoretical $\text{Abs}_{290} = 0.6$, and this value compared with the
10 actual experimentally measured absorbance showing the efficiency of previous coupling reaction.

Coupling of amino-acid residues

Whilst the multipin assembly is drying, the appropriate Na^+ -Fmoc amino acid pfp esters (10 equivalents calculated
15 from the loading of each crown) and HOBt (10 equivalents) required for the particular round of coupling are accurately weighed into suitable containers.

Alternatively, the appropriate Na^+ -Fmoc amino acids (10 equivalents calculated from the loading of each crown),
20 desired coupling agent e.g. HBTU (9.9 equivalents calculated from the loading of each crown) and activation eg HOBt (9.9 equivalents calculated from the loading of each crown), NMM (19.9 equivalents calculated from the loading of each crown) are accurately weighed into
25 suitable containers.

The protected and activated Fmoc amino acid derivatives are then dissolved in DMF (500 μ l for each macrocrown, e.g. for 20 macrocrowns, $20 \times 10\text{eq} \times 7\text{mmoles}$ of derivative would be dissolved in 10 000 μ L DMF). The appropriate

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derivatives are then dispensed to the appropriate wells ready for commencement of the 'coupling cycle'. As a standard, coupling reactions are allowed to proceed for 2-6 hours (depending upon nature of coupling e.g. Ala to Ala 5 2 hours Val to Leu 6 hours.

When coupling Fmoc amino-acid pentafluorophenyl esters, 10eq of derivative in DMF (400 μ l) with bromophenol blue stock solution (100 μ l) is used for each macrocrown. This allows monitoring of the progress of the acylation 10 reaction through the disappearance of the deep blue coloration of bromophenol blue in the presence of unreacted amine to a pale yellow upon completion of acylation.

Preparation of Bromophenol Blue Stock Solution

15 Bromophenol blue (20mg) is dissolved in DMF (50mL) and HOBr (10mg) added.

Washing Following Coupling

If a 20% piperidine/DMF deprotection is to immediately 20 follow the coupling cycle, then the multipin assembly is briefly shaken to remove excess solvent washed consecutively with (200mL each), MeOH (5mins) and DMF (5mins) and deprotected (see above). If the multipin assembly is to be stored, then a full washing cycle consisting brief shaking then consecutive washes with 25 (200mL each), DMF (5mins) and MeOH (5mins, 2mins, 2mins) is performed.

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Acidolytic Mediated Cleavage of Peptide-Pin Assembly

Acid mediated cleavage protocols are strictly performed in a fume hood. A polystyrene 96 well plate (1mL / well) is labelled, then the tare weight measured to the nearest mg.

5 Appropriate wells are then charged with a trifluoroacetic acid / triethylsilane (95:5, v/v, 600 μ l) cleavage solution, in a pattern corresponding to that of the multipin assembly to be cleaved.

10 The multipin assembly is added, the entire construct covered in tin foil and left for 2hrs. The multipin assembly is then added to another polystyrene 96 well plate (1mL /well) containing trifluoroacetic acid / triethylsilane (95:5, v/v, 600 μ l) (as above) for 5 mins.

15 The cleaved assembly is washed with DMF (200 μ L, 5mins), MeOH (200 μ L, 5mins), the spent crowns removed and discarded, the stems removed and washed by sonication in methanol (1hr, RT).

Work up of Cleaved Peptides

20 The primary polystyrene cleavage plate (2hr cleavage) and the secondary polystyrene plate (5min wash) (see above) are then placed in the SpeedVac and the solvents removed (minimum drying rate) for 90mins.

25 The contents of the secondary polystyrene plate (see above) are transferred to their corresponding wells on the primary plate using an acetonitrile / water / acetic acid

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(50:45:5, v/v/v) solution (3 x 150 μ l) and the spent secondary plate discarded.

Analysis of Products

1.0 μ l of each well (see above) is diluted to 400 μ l with 5 0.1%aq TFA and analysed by HPLC-MS. Column Vydac C4 (214TP52, narrowbore, 21 x 250mm). Eluents :- Solvent A = 0.1%aq trifluoroacetic acid, Solvent B = acetonitrile / 10 10%A. Gradient :- 10-90% B in A over 27mins, 250ml / min, 215nm UV detection. The individual substrates described below were prepared by the above methods and shown by HPLC-MS to be >95% with the correct mass.

Final Lyophilisation of Peptides

The primary polystyrene plate (plus the washings from the secondary plate) is covered with tin foil, held to the 15 plate with an elastic band. A pin prick is placed in the foil directly above each well and the plate placed at -80°C for 30mins. The plate is then lyophilised on the 'Heto freeze drier' overnight. Where appropriate individual peptides were then weighed and dissolved to 20 10mM stock solutions in DMSO prior to biological screening. Alternatively the 20 component mixture is weighed and the peptide/20 component ratio is calculated.

Further coupling of amino acid residues was carried out according to the multipin approach described above. Whilst 25 the multipin assembly was drying, the appropriate $\text{N}\alpha$ -Fmoc amino acids (10 equivalents calculated from the loading of each crown), HATU coupling agent (9.9 equivalents

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calculated from the loading of each crown), HOAt catalyst (9.9 equivalents calculated from the loading of each crown) and DIPEA (19.9 equivalents calculated from the loading of each crown) were accurately weighed into 5 suitable containers.

The protected N^{α} -Fmoc amino acids and coupling agents were then dissolved in DMF (500 μl for each macrocrown) and activated by the addition of DIPEA. The appropriate derivatives were then dispensed to their appropriate wells 10 and as standard coupling to each macro crown was allowed to proceed for 2 hours.

When coupling particularly hindered amino acid residues such as N-Methyl, C^{α} -Methyl or unusual amino acids (whose coupling efficiency is unknown) the coupling reaction was 15 repeated, as standard, for a further 2 hours.

Substrates for Der pI

Using the general techniques described above, the following compounds were prepared and assayed as potential substrates against Der pI purified as described above.

20	Peptide [SEQ ID Nos. 1-76]	Measured K_m (μM)
	Abz-Val-Ala-Nle-Ser-Tyr(NO_2) -Asp-NH ₂	12
	H-Val-Ala-Nle-Ser-TyrNO ₂ -Asp-NH ₂	NS
	H-Ala-Nle-Ser-Tyr(NO_2) -Asp-NH ₂	NS
	Ac-Val-Ala-Nle-Ser-Tyr(NO_2) -Asp-NH ₂	NS
25	H-Val-Ala-Nle-Ser-Tyr(NO_2) -NH ₂	NS
	H-Ala-Nle-Ser-Tyr(NO_2) -Asp-NH ₂	NS

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	Ac-Val-Ala-Nle-Ser-Tyr (NO ₂) -NH ₂	NS
	Abz-Val-Ala-Nle-Ser-Tyr (NO ₂) -NH ₂	NM
	Abz-Val-Ala-Nle-Ser-NH ₂	NM
	Abz-Val-Ala-Nle-Ser-Phe-Asp-NH ₂	NM
5	Abz-Val-Ala-Nle-Ser-Tyr-Asp-NH ₂	NM
	Abz-Val-Ala-Nle-Ser-Ala-Asp-NH ₂	NM
	Abz-Val-Ala-Nle-Ser-Lys-Asp-NH ₂	NM
	Abz-Val-Ala-Nle-Ser-eAHA-Asp-NH ₂	NM
	Abz-Ala-Nle-Ser-Tyr (NO ₂) -Asp-NH ₂	NM
10	Abz-Nle-Ser-Tyr (NO ₂) -Asp-NH ₂	NS
	Bz-Val-Ala-Nle-Ser-Tyr (NO ₂) -NH ₂	NM ^a
	Bz (2-carboxy)-Val-Ala-Nle-Ser-Tyr (NO ₂) -NH ₂	NM ^a
	Chex-Val-Ala-Nle-Ser-Tyr (NO ₂) -NH ₂	NM ^a
	n-Bu-Val-Ala-Nle-Ser-Tyr (NO ₂) -NH ₂	NM ^a
15	Piv-Val-Ala-Nle-Ser-Tyr (NO ₂) -NH ₂	NM ^a
	Bz-Val-Ala-Nle-Ser-Tyr (NO ₂) -NH ₂	NM ^a
	Abz-Val-Ala-Lys-Ser-Tyr (NO ₂) -Asp-NH ₂	14
	Abz-Val-Ala-Gln-Ser-Tyr (NO ₂) -Asp-NH ₂	6
	Abz-Val-Ala-Thr-Ser-Tyr (NO ₂) -Asp-NH ₂	6
20	Abz-Val-Ala-hLeu-Ser-Tyr (NO ₂) -Asp-NH ₂	4
	Abz-Val-Ala-Cha-Ser-Tyr (NO ₂) -Asp-NH ₂	5
	Abz-Val-Ala-His-Ser-Tyr (NO ₂) -Asp-NH ₂	> 20
	Abz-Val-Ala-ACH-Ser-Tyr (NO ₂) -Asp-NH ₂	NS
	Abz-Val-Ala- <u>D</u> Nle-Ser-Tyr (NO ₂) -Asp-NH ₂	NS
25	Abz-Val-Ala-3pyr-Ser-Tyr (NO ₂) -Asp-NH ₂	10
	Abz-Val-Ala-Hyp-Ser-Tyr (NO ₂) -Asp-NH ₂	NS
	Abz-Val-Ala-ACP-Ser-Tyr (NO ₂) -Asp-NH ₂	NS
	Abz-Val-Lys-hLeu-Ser-Tyr (NO ₂) -Asp-NH ₂	35
	Abz-Val- <u>D</u> Ala-hLeu-Ser-Tyr (NO ₂) -Asp-NH ₂	NS
30	Abz-Val-Tic-hLeu-Ser-Tyr (NO ₂) -Asp-NH ₂	NS
	Abz-Val-ACH-hLeu-Ser-Tyr (NO ₂) -Asp-NH ₂	NS
	Abz-Val-Met (O) -hLeu-Ser-Tyr (NO ₂) -Asp-NH ₂	35

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	Abz-Val-2Nal-hLeu-Ser-Tyr(NO ₂)-Asp-NH ₂	NS
	Abz-Val-ACP-hLeu-Ser-Tyr(NO ₂)-Asp-NH ₂	NS
	Abz-Val-DLys-hLeu-Ser-Tyr(NO ₂)-Asp-NH ₂	NS
	Abz-Val-DGln-hLeu-Ser-Tyr(NO ₂)-Asp-NH ₂	NS
5	Abz-Val-3pyr-hLeu-Ser-Tyr(NO ₂)-Asp-NH ₂	NS
	Abz-Val-Cha-hLeu-Ser-Tyr(NO ₂)-Asp-NH ₂	NS
	Abz-DVal-Ala-hLeu-Ser-Tyr(NO ₂)-Asp-NH ₂	NS
	Abz-Gln-Ala-hLeu-Ser-Tyr(NO ₂)-Asp-NH ₂	12
	Abz-Lys-Ala-hLeu-Ser-Tyr(NO ₂)-Asp-NH ₂	>15
10	Abz-Tic-Ala-hLeu-Ser-Tyr(NO ₂)-Asp-NH ₂	NS
	Abz-ACH-Ala-hLeu-Ser-Tyr(NO ₂)-Asp-NH ₂	NS
	Abz-Met(O)-Ala-hLeu-Ser-Tyr(NO ₂)-Asp-NH ₂	20
	Abz-3pyr-Ala-hLeu-Ser-Tyr(NO ₂)-Asp-NH ₂	>10
	Abz-2Nal-Ala-hLeu-Ser-Tyr(NO ₂)-Asp-NH ₂	15
15	Abz-Leu-Ala-hLeu-Ser-Tyr(NO ₂)-Asp-NH ₂	18
	Abz-Cha-Ala-hLeu-Ser-Tyr(NO ₂)-Asp-NH ₂	9
	Abz-Bip-Ala-hLeu-Ser-Tyr(NO ₂)-Asp-NH ₂	2.5
	Abz-Bip-Ala-hLeu-Tyr-Tyr(NO ₂)-Asp-NH ₂	3
	Abz-Bip-Ala-hLeu-Leu-Tyr(NO ₂)-Asp-NH ₂	3.7
20	Abz-Bip-Ala-hLeu-Lys-Tyr(NO ₂)-Asp-NH ₂	2
	Abz-Bip-Ala-hLeu-Asp-Tyr(NO ₂)-Asp-NH ₂	5.0
	Abz-Bip-Ala-hLeu-Abu-Tyr(NO ₂)-Asp-NH ₂	1.7
	Abz-Bip-Ala-hLeu-Cha-Tyr(NO ₂)-Asp-NH ₂	2.5
	Abz-Bip-Ala-hLeu-Met(O)-Tyr(NO ₂)-Asp-NH ₂	5
25	Abz-Bip-Ala-hLeu-Thr-Tyr(NO ₂)-Asp-NH ₂	2.5
	Abz-Bip-Ala-hLeu-3pyr-Tyr(NO ₂)-Asp-NH ₂	4
	Abz-Bip-Ala-hLeu-Bu ^t Gly-Tyr(NO ₂)-Asp-NH ₂	4
	Abz-Bip-Ala-hLeu-Hyp-Tyr(NO ₂)-Asp-NH ₂	4
	Abz-Phe-Val-Ala-Nle-Ser-Tyr(NO ₂)-Asp-NH ₂	NM
30	Abz-3.Pyr-Val-Ala-Nle-Ser-Tyr(NO ₂)-Asp-NH ₂	NM
	Abz-1.Naph-Val-Ala-Nle-Ser-Tyr(NO ₂)-Asp-NH ₂	17
	Abz-2.Naph-Val-Ala-Nle-Ser-Tyr(NO ₂)-Asp-NH ₂	NM

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Abz-Tyr-Val-Ala-Nle-Ser-Tyr(NO ₂) -Asp-NH ₂	NM
Abz-Bip-Val-Ala-Nle-Ser-Tyr(NO ₂) -Asp-NH ₂	10
Abz-Lys-Val-Ala-Nle-Ser-Tyr(NO ₂) -Asp-NH ₂	15
Abz-Glu-Val-Ala-Nle-Ser-Tyr(NO ₂) -Asp-NH ₂	20
5 Abz-Leu-Val-Ala-Nle-Ser-Tyr(NO ₂) -Asp-NH ₂	NM
Abz-Hyp-Val-Ala-Nle-Ser-Tyr(NO ₂) -Asp-NH ₂	NS

NS indicates that the peptide was not hydrolysed by *Der pI*.

10 NM indicates that the peptide was a substrate for *Der pI*, but the *K_m* was not measured.

NM^a indicates that the peptide was a substrate for *Der pI*, and its cleavage was followed by HPLC-MS showing hydrolysis to occur between-Nle-Ser-.

15 Ranked in order of cleavage rate :-Bz > n-But > Piv > Bz(2-carboxy) > Abz.

20 Coupling of amino acid residues was carried out according to the multipin approach described above. Whilst the multipin assembly was drying, the appropriate Na-Fmoc amino acids (10 equivalents calculated from the loading of each crown), HATU coupling agent (9.9 equivalents calculated from the loading of each crown), HOAt catalyst (9.9 equivalents calculated from the loading of each crown) and DIPEA (19.9 equivalents calculated from the loading of each crown) were accurately weighed into 25 suitable containers.

The protected Na-Fmoc amino acids and coupling agents were then dissolved in DMF (500 μl for each macrocrown) and activated by the addition of DIPEA. The appropriate

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derivatives were then dispensed to their appropriate wells and standard coupling to each macrocrown was allowed to proceed for 2 hours.

When coupling particularly hindered amino acid residues such as N-Methyl, C α -Methyl or unusual amino acids (whose coupling efficiency is unknown) the coupling reaction was 5 repeated, as standard, for a further 2 hours.

The following sequences were synthesised in this way:

	Peptide Sequence [SEQ ID Nos. 77-85]	Measured Km (μ M)
10	Abz-Val-Ala-(NMe)Nle-Ser-Tyr(NO ₂)-Asp-NH ₂	NS
	Abz-Val-(NMe)Ala-Nle-Ser-Tyr(NO ₂)-Asp-NH ₂	NS
	Abz-Val-Ala-Aib-Ser-Tyr(NO ₂)-Asp-NH ₂	NS
	Abz-Val-Aib-Nle-Ser-Tyr(NO ₂)-Asp-NH ₂	NS
	Abz-Deg-Ala-Nle-Ser-Tyr(NO ₂)-Asp-NH ₂	NS
15	nBu-D.Ser-D.Nle-D.Ala-D.Val-p.Aba-NH ₂	NS
	Bz-Val-Ala-Statine-Ser-eAha-NH ₂	NS
	Abz-p.Aba-Nle-Ser-Tyr(NO ₂)-Asp-NH ₂	NS
	Abz-Cmpi-Nle-Ser-Tyr(NO ₂)-Asp-NH ₂	NS

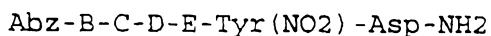
NS-Not Substrate: Not hydrolysed by *Der pI*
20 NM-Substrate but not measured: Substrate for *Der pI* but not measured.

Assay procedure

Each mixture of 20 compounds in the libraries of the apparatus described herein was screened at a concentration 25 of 1.0 μ M per compound in an assay against the cysteinyl

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protease *Der pI*. The most active wells were identified by the rate of emission of fluorescence at 420 nm when the samples were irradiated at 320 nm. An analysis of the two complementary libraries showed that the best substrates 5 for the enzyme were:



Where

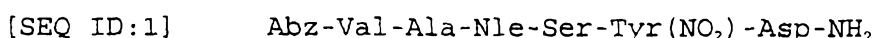
B= Valine>Alanine, Glutamine, Leucine, Phenylalanine

C= Alanine>>Glutamine, or Lysine.

10 D= Leucine, Norleucine or Alanine>Serine

E=Serine

The best substrate was:



This compound was then resynthesised as a single component 15 using the peptide synthesis methodology described herein. The k_{cat}/K_m value for the pure substrate in the *Der pI* assay was measured as $3.5 \times 10^4 \text{M}^{-1}\text{s}^{-1}$, and was considered to be suitably high for use in a high throughput assay for the general screening of inhibitors of *Der pI*.

20 **High throughput assay development**

Plate assays were carried out in 96 well plate format, using 0.1 ug of *Der pI* per 100 μL assay volume in each well and using 20 μM of the substrate. All assays were performed in Assay Buffer (AB; 50 mM potassium phosphate, 25 pH 8.25 containing 1mM ethylenediaminetetraacetic acid (EDTA) and 1mM dithiothreitol (DTT). The *Der pI* enzyme is

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pre-activated by addition of DTT and this is incubated at room temperature for 5 min. prior to initiation of the assay. As an example for the screening methodology, each well contains a 5 μ L of a 20 μ M solution of the test compound in DMSO, 10 μ L of a 200 μ M aqueous solution of the substrate, 2, and 85 μ L of *Der pI* in AB is added to initiate the reaction. Enzyme activity is monitored by fluorescence using 320 nm for excitation and 420nm for the emission wavelengths using a Labsystems Fluroskan Ascent machine. Kinetic measurements were carried out using a Hitachi F-4500 Fluorescence Spectrophotometer.

Synthesis of inhibitors of *Der pI*

The best substrate described above was shown by HPLC-mass spectroscopic analysis of the enzyme/ assay solution, to be cleaved between the Norleucine-Serine amide bond. Replacement of the terminal Abz group by a series of derivatives (e.g. Boc-, Pivaloyl, Benzoyl, and 2- carboxy- Benzoyl) affected substrate activity and specificity for the *Der pI* enzyme. With this knowledge of the $P_1 - P_1'$ cleavage site and for the $P_4 - P_3 - P_2 - P_1$ motif, the compound Boc-Val-Ala-Leu-H, 4, was synthesised as shown in Scheme 1a, figure 15.

Attachment of a suitable Michael acceptor such as CH=CH-CO₂Et, and -CH=CH-SO₂ Ph to the motif (Scheme 2, figure 16), provided active inhibitors of the enzyme with apparent IC₅₀ values of 50nM, 1000 nM and 100nM respectively.

Preparation of an Acyloxymethylketone Series

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A series of acyloxymethylketone compounds having active Der PI inhibitor activity was prepared by the following procedures:

N-Benzoyl-L-valyl-L-alanyl-L-norleucine

5 N-Benzoyl-L-valyl-L-alanyl-L-norleucine was prepared by solid phase benzoylated peptide synthesis as follows:

Resin loading (step 1)

10 2-Chlorotriptylchloride resin (4.9g, 1.05mmol/g, Novabiochem) was swelled in dichloromethane (40ml) and a suspension of Fmoc-L-norleucine added and stirred for 5 minutes. A solution of diisopropylethylamine in DCM (10ml, 57mmol in 30ml) was added over 5minutes and the resulting mixture stirred at room temperature for 2 hours. Methanol (5ml) added and reaction mixture stirred for a further 15 10minutes before resin filtered and washed with 3x DCM, 2x DMF, 2x 2-propanol, 2x DMF, 2x 2-propanol, methanol, 2x ether and dried under vacuum for 24 hours.

Amino acid deprotection (step 2)

20 Fmoc-L-norleucine loaded resin was deprotected by treatment with 20% piperidine in DMF over 4 hours. The swollen resin was filtered, washed with 5x DMF, 2x ether and dried under vacuum for 24 hours.

Peptide chain extension (step 3)

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L-Norleucine loaded resin (5mmol) was added to a solution of Fmoc-L-alanine (6.23g, 20mmol), hydroxybenzotriazole (3.0g, 20mmol), 2-(1-H-benzotriazole-1-yl)-1,1,3,3-tetramethyluronium hexafluorophosphate (7.59g, 20mmol) and diisopropylethylamine (6.97ml, 40mmol) in DMF (20ml) and allowed to swell over 4 hours with mild agitation. Resin was filtered and washed with 4x DMF, 2x ether and dried under vacuum overnight.

5 Steps (2) and (3) were carried out repetitively with Fmoc-L-alanine and Fmoc-L-valine to afford resin bound 10 tripeptide H-L-valyl-L-alanyl-L-norleucine.

Peptide chain benzylation (step 4)

15 L-Valyl-L-alanyl-L-norleucine loaded resin (1g, approx. 1mmol) was added to a solution of benzoic acid (0.488g, 4mmol), hydroxybenzotriazole (0.6g, 4mmol), 2-(1-H-benzotriazole-1-yl)-1,1,3,3-tetramethyluronium 20 hexafluorophosphate (1.52g, 4mmol) and diisopropylethylamine (1.40ml, 8mmol) in DMF (5ml) and allowed to swell over 6 hours with mild agitation. Resin was filtered and washed with 4x DMF, 2x ether and dried under vacuum overnight.

Resin cleavage (step 5)

25 N-Benzoyl-L-valyl-L-alanyl-L-norleucine loaded resin (1.0g, approx. 1mmol) was treated with a 1% solution of trifluoroacetic acid in dichloromethane (20ml) containing triethylsilane (320ml, 2mmol) for 1 hour. Resin was removed by filtration and washed with dichloromethane

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(3x10ml). Organic layer was collected, evaporated and titrated with ether to afford N-benzoyl-L-valyl-L-alanyl-L-norleucine. (285mg). Electrospray-MS m/z 407 [MH⁺].

Bromomethylketone formation (step 6)

5 **N-Benzoyl-L-valyl-L-alanyl-L-norleucine bromomethyl ketone**
N-Benzoyl-L-valyl-L-alanyl-L-norleucine (140mg, 0.34mmol) was suspended in dry THF (3ml) and dry DMF was added dropwise to afford homogeneity. The reaction mixture was cooled to -10°C and isobutylchloroformate (129ml, 1.0mmol) and N-methylmorpholine (109ml, 1.0mmol) added with stirring under Argon. The mixture was stirred for 30 minutes before a solution of diazomethane in ether (5ml, approx. 2mmol) was added. The reaction mixture was allowed to warm to room temperature over 1 hour before a 1:1 solution of acetic acid and 50% HBr (1ml, 3.0mmol HBr) was added 10 dropwise and stirred for 15 minutes. The organic phase was diluted with ethylacetate (40ml), washed with water (10ml), brine (10ml) and sodium bicarbonate (2x10ml), dried over MgSO₄, solvent removed under vacuum. This 15 afforded an off white solid (152mg) which could be further purified as required by prep. HPLC. Electrospray-MS m/z 482 [MH⁺] and 484 [MH⁺].

Acyloxymethylketone formation (step 7)

20 **N-Benzoyl-L-valyl-L-alanyl-L-norleucine 2, 6-bis(trifluoromethyl) benzyloxymethyl ketone**
A mixture of potassium fluoride (0.1mmol, 6mg) and 2,6-bis(trifluoromethyl)benzoic acid (0.066mmol, 17mg) in dry DMF (500ml) was stirred over molecular sieves at room

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temperature for 5 minutes. A solution of N-benzoyl-L-valyl-L-alanyl-L-norleucine bromomethyl ketone (0.033mmol, 16mg) in dry DMF (500ml) was added and the reaction mixture stirred for 1 hour. The reaction mixture was 5 passed through a short silica plug and washed with 5% methanol in dichloromethane. Solvent was removed under vacuum and the residue purified using prep. HPLC. Freeze drying afforded (6.4mg) as a white lyophilisate.
Electrospray-MS m/z 660 [MH⁺].

10 Similarly the following compounds were prepared:

N-Benzoyl-L-valyl-L-alanyl-L-norleucine 2, 6-dimethylbenzoyloxymethyl ketone (Electrospray-MS m/z 552 [MH⁺]) from of N-benzoyl-L-valyl-L-alanyl-L-norleucine bromomethyl ketone and 2,6-dimethylbenzoic acid.

15 **N-Benzoyl-L-valyl-L-alanyl-L-norleucine 2-hydroxybenzoyloxymethyl ketone** (Electrospray-MS m/z 540 [MH⁺]) from of N-benzoyl-L-valyl-L-alanyl-L-norleucine bromomethyl ketone and 2-hydroxybenzoic acid.

20 **N-Benzoyl-L-valyl-L-alanyl-L-norleucine 2,6-dichlorobenzoyloxymethyl ketone** (Electrospray-MS m/z 592 [MH⁺] and 594 [MH⁺]) from of N-benzoyl-L-valyl-L-alanyl-L-norleucine bromomethyl ketone and 2,6-dichlorobenzoic acid.

25 **N-Benzoyl-L-valyl-L-alanyl-L-norleucine benzoyloxymethyl ketone** (Electrospray-MS m/z 524 [MH⁺]) from of N-benzoyl-L-valyl-L-alanyl-L-norleucine bromomethyl ketone and benzoic acid.

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N-Benzoyl-L-valyl-L-alanyl-L-norleucine 2,3,4,5,6-
pentafluorobenzoyloxymethyl ketone (Electrospray-MS m/z
614 [MH⁺]) from of N-benzoyl-L-valyl-L-alanyl-L-norleucine
bromomethyl ketone and 2,3,4,5,6-pentafluorobenzoic acid.

5 **N-Benzoyl-L-valyl-L-alanyl-L-norleucine 1,1-**
dimethylpropyloxymethyl ketone (Electrospray-MS m/z 504
[MH⁺]) from of N-benzoyl-L-valyl-L-alanyl-L-norleucine
bromomethyl ketone and 1,1-dimethylpropanoic acid.

10 **N-Benzoyl-L-valyl-L-alanyl-L-norleucine N(-**
benzyloxycarbonyl)-D-serinyl-(O-tert-butyl)oxymethyl
ketone (Electrospray-MS m/z 697 [MH⁺]) from of N-benzoyl-L-
valyl-L-alanyl-L-norleucine bromomethyl ketone and N-
benzyloxycarbonyl-D-serine-O-tert-butylether.

15 **N-Benzoyl-L-valyl-L-alanyl-L-norleucine N(-**
benzyloxycarbonyl)-D-serineoxy methyl ketone
(Electrospray-MS m/z 641 [MH⁺]) from of N-benzoyl-L-valyl-
L-alanyl-L-norleucine bromomethyl ketone and N-
benzyloxycarbonyl-D-serine.

20 **N-Benzoyl-L-valyl-L-alanyl-L-norleucine 2-furanoxy methyl**
ketone (Electrospray-MS m/z 514 [MH⁺]) from of N-benzoyl-L-
valyl-L-alanyl-L-norleucine bromomethyl ketone and 2-furan
carboxylic acid.

25 **N-Benzoyl-L-valyl-L-alanyl-L-norleucine 2,6-**
dichlorophenylacyloxy methyl ketone (Electrospray-MS m/z
606 [MH⁺], 608 [MH⁺]) from of N-benzoyl-L-valyl-L-alanyl-L-
norleucine bromomethyl ketone and 2,6-dichlorophenylacetic
acid.

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Standard Prep. HPLC conditions were as follows: C4 preparative HPLC system (Vydac, 22x 250mm) eluting at 10ml per minute a.gradient of 5-95% (90% acetonitrile (0.1% TFA)) over 30 minutes.

5 The following compounds were prepared by the techniques and procedures described beneath each named compound.

Preparation of Ethyl-(S)-(E)-3-((tert-butoxy carbonyl amino valyl alanyl) amino-6-methyl-hept-2-enoate

10 To a suspension of sodium hydride (46mg, 1.9mmol) in anhydrous THF (4ml) cooled to 0°C was added a solution of triethylphosphonoacetate (420mg, 1.9 mmol) in THF (2 ml) dropwise over 5 minutes and the mixture stirred until gas evolution ceased. The solution was added dropwise to a solution of BocVAL-CHO (600mg, 1.56mmol) in dry THF cooled 15 to-10°C. The reaction mixture was stirred for 1 hour and saturated ammonium chloride (10ml) was added. A white solid precipitated which was removed by filtration and the filtrate was partitioned between ethyl acetate and water. The organic layer was dried with magnesium sulphate and 20 evaporated to give an oil which was crystallised from acetonitrile water to yield the title compound, 640mg, 91%.

MS (EI +ve) required $(M^+(C_{23}H_{41}N_3O_6) + 1) = 456$: found $(M^++H) = 456$, $((M^+-t\text{BOC}) + 1) = 356$ (100%).

25 **Preparation of (S)-(E)-3-((tert-butoxy carbonyl amino valyl alanyl) amino-6-methyl-hept-2-enoic acid**

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The ethyl ester (455mg, 1mmol) was dissolved in dioxane (10ml) and water added followed by lithium hydroxide (126mg, 3mmol). The solution was stirred for 3 hours and 1M HCl aq was added until the pH reached neutrality. The dioxane was removed by rotary evaporation and the pH adjusted to 4 with 1M HCl aq. The title compound precipitated, filtered and washed with water to yield 420mg, 98%.

MS (EI +ve) required ($M^+(C_{21}H_{37}N_3O_6) + 1$) = 428: found (M^++H) = 428 (100%).

Preparation of 1,1,1-Trifluoroethyl-(S)-(E)-3-((tert-butoxy carbonyl amino valyl alanyl) amino-6-methyl-hept-2-enoate

The acid (BocVAL-CO₂H) (50mg, 0.117mmol) and 15 dimethylaminopyridine (29mg, 0.24mmol) was dissolved in dry dichloromethane (1ml) and cooled to 0°C. Water soluble carbodiimide hydrochloride salt (26mg, 0.13mmol) in 0.5ml dichloromethane was added and the solution stirred for 5 minutes. 1,1,1-Trifluoroethanol (0.017ml, 0.23mmol) in 0.5ml dichloromethane was added and the reaction was allowed to warm to room temperature after 1 hour and the reaction mixture stirred overnight. The reaction mixture was washed 2x2ml 0.5M citric acid solution, 1x2ml water, 1x2ml saturated sodium bicarbonate solution, 1x2ml water, 25 dried with magnesium sulphate and evaporated to dryness to give the title compound.

MS (EI +ve) required ($M^+(C_{23}H_{38}N_3O_6F_3) + 1$) = 510: found (M^++H) = 510, ((M^+-t BOC) + 1) = 410, ((M^+-t Bu) + 1) = 454 (100%).

Preparation of Ethyl-(S)-(E)-3-(N-benzoyl valyl alanyl) amino-6-methyl-hept-2-enoate

The tert-butoxy carbonyl protected ethyl ester (16.6mg, 0.036mmol) was dissolved in 4.0M HCl in dioxane (2ml) 5 stirred at room temperature for 30 minutes and evaporated to dryness. The residue was dissolved in DMF (0.5ml) and N-methylmorpholine (7.36mg, 0.073mmol) added followed by benzoyl chloride (5.4mg, 0.038mmol) in DMF 0.5ml. The reaction stirred for 2 hours, diluted with 0.1% 10 trifluoroacetic acid solution (4ml) and acetonitrile (2ml) and injected onto a C4 preparative HPLC system (22x250mm) eluting at 10ml per minute, monitoring at 215nm and a gradient of 10-90% system B over 25 minutes and holding at 90% for 15 minutes. System A = 0.1% TFA in water, system B 15 = 90% acetonitrile, 10% system A. The peak eluting at 26-28 minutes was collected and lyophilised to a white solid, yield 4.5mg, 27%.

Analysis by MS (EI +ve) required $(M^+(C_{25}H_{37}N_3O_5) + 1) = 460$: found $(M^++H) = 460$.

20 **Preparation of Diethyl Phenylsulfonylmethylphosphonate**

The Diethyl Phenyl sulfonylmethylphosphonate was prepared using a method adapted from I. Shahak, and J. Almog. (Synthesis, 145, 1970).

25 The commercially available diethyl phenylthiomethylphosphonate (1.0 ml, 4.1 mmol) was dissolved in dichloromethane (10 ml). Sulphuric acid (10 ml, 25 %) was added and the mixture cooled on ice. Solid

potassium permanganate was then added in three aliquots of 0.5g with stirring. After the additions the reaction appeared to be complete. Solid sodium metabisulfite was added slowly until the mixture turned colourless. This was 5 then extracted with ethyl acetate (x3) and the combined organic washings washed with saturated sodium bicarbonate solution followed by brine before drying over sodium sulphate. The volatiles were removed *in vacuo*. The residue was purified by flash chromatography on silica eluting 10 initially with ethyl acetate/hexane 8/2 followed by pure ethyl acetate.

In this way the desired product, diethyl phenylsulfonylmethylphosphonate (1.0 g, quant) was obtained as a colourless solid.

15 The product was analysed by mass spectrometry (MS) (MALDI-TOF): required (M^+ ($C_{11}H_{11}O_5PS$) +1) = 292; obtained (M^++1) = 292

20 **Preparation of (S)-(E)-3-((tert-butoxycarbonylamino-
valyl)alanyl)amino-1-phenylsulfonyl-5-methyl-1-hexene**

Diethyl phenylsulfonylmethylphosphonate (38 mg, 129 mmol) was dissolved in dry THF (10 ml) and then cooled to 0°C under an atmosphere of nitrogen. Sodium hydride (8 mg of 60% dispersion in oil, 200 mmol) was added and the mixture 25 stirred for 15 mins (effervescence). The aldehyde ^tBoc-Val-Ala-Leu-CHO (50 mg, 129 mmol) was then added to the resulting solution and the mixture was stirred for 60 mins. The reaction was quenched by the addition of dilute hydrochloric acid (0.1 M), followed by extraction with

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ethyl acetate (x3). The separated organic phase was sequentially washed with saturated sodium bicarbonate solution and brine before drying over sodium sulphate. The volatiles were removed *in vacuo*. The residue was purified 5 by flash chromatography on silica eluting with ethyl acetate/hexane 4/6. An unidentified by-product was eluted first (12 mg) followed by the desired product (S)-(E)-3-((tert-butoxycarbonylamino-valyl)alanyl)amino-phenylsulfonyl-5-methyl-1-hexene (22 mg, 32%) as a solid.

10 MS (electrospray) required ($M^+(C_{26}H_{41}O_6N_3S)+1$) =523: found (M^++Na) =546, ((M^- Boc)+1) =424 (100%).

Preparation of Diethyl methylsulfonylmethylphosphonate

The commercially available Diethyl 15 methylthiomethylphosphonate was converted to the title compound using the method of I. Shahak and J. Almog (*Synthesis*, 171, 1969).

Preparation of (S)-(E)-3-((tert-butoxycarbonylamino-valyl)alanyl)amino-1-methylsulfonyl-5-methyl-1-hexene

Diethyl methylsulfonylmethylphosphonate (30 mg, 130 mmol) 20 was dissolved in dry THF (5 ml) and then cooled to 0°C under an atmosphere of nitrogen. Sodium hydride (7 mg of 60% dispersion in oil, 175 mmol) was added and the mixture stirred for 15 mins (effervescence). The aldehyde ^tBoc-Val-Ala-Leu-CHO (50 mg, 129 mmol) was then added to the 25 resulting solution and the mixture then stirred for 60 mins. The reaction was quenched by addition of dilute hydrochloric acid (0.1 M), followed by extraction with

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ethyl acetate(x3). The separated organic phase was sequentially washed with saturated sodium bicarbonate solution and brine before drying over sodium sulphate. The volatiles were then removed *in vacuo*. The residue was purified by flash chromatography on silica eluting with ethyl acetate/hexane 8/2. An unidentified by-product was eluted first (4 mg), followed by the desired product (S)-(E)-3-((tert-butoxycarbonylamino-valyl)alanyl)amino-methylsulfonyl-5-methyl-1-hexene (24 mg, 40%) as a solid.

MS (electrospray) required ($M^+(C_{21}H_{39}O_6N_3S)+1$) = 462: found (M^++Na) = 484, ($(M^- Boc)+1$) = 362 (100%).

Preparation of Ethyl diethylphosphorylmethylsulfonate

Prepared in accordance with procedure B described in L. Ghosez et. al. (*Tetrahedron*, 43, 5125, 1987).

The product was analysed on MS (electrospray) required ($M^+(C_7H_{17}O_6PS)+1$) = 261: Found (M^++H) = 261, (M^++Na) = 283.

Preparation of Diethyl(S)-(E)-3-((tert-butoxycarbonylamino-valyl)alanyl)amino-5-methylhexenylsulfonate.

Ethyl diethylphosphorylmethanesulfonate (36 ml, ~138mmol) was dissolved in dry THF (5 ml) and then cooled to 0°C under an atmosphere of nitrogen. Sodium hydride (8 mg of 60% dispersion in oil, 200 mmol) was added and the mixture stirred for 15 mins (effervescence). The aldehyde *t*Boc-Val-Ala-Leu-CHO (50 mg, 129 mmol) was added to the resulting solution and the mixture stirred for 30 mins.

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The reaction was quenched by addition of dilute hydrochloric acid (0.1 M), followed by extraction with ethyl acetate (x3). The separated organic phase was sequentially washed with sodium bicarbonate solution and 5 brine before drying over sodium sulphate. The volatiles were then removed in vacuo. The residue was purified by flash chromatography on silica eluting with ethyl acetate/hexane 1/1. The desired product Diethyl(S)-(E)-3-((tert-butoxycarbonylamino-valyl)alanyl)amino-5- 10 methylhexenylsulfonate, (22 mg, 35%) was obtained as a solid.

MS (electrospray) required ($M^+ (C_{22}H_{41}O_7N_3S) + 1$) = 492: found ($M^+ + 1$) = 492, (($M^+ - t$ Boc) + 1) = 392 (100%)

Example 2:

15 **Design of Depsipeptides**

Another suitable bond in a compound of general formula (I), (II) or (III) according to the invention is an ester bond to form a depsipeptide. The incorporation of depsipeptide substrates aided the identification of 20 substrates for low reactivity viral proteases, such as viral serine proteases.

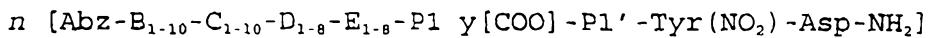
For example, substrates of the general formula



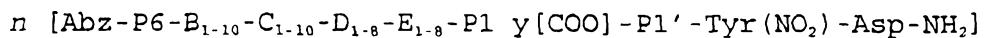
were produced.

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However, a significant proportion of viral proteases only recognise substrate sequences larger than those represented by the general structure above. It is well acknowledged that by the very nature of action of a viral protease (function is to cleave immature viral proteins into the mature viral package) one automatically receives data concerning the natural substrate sites. Thus, the general structure above can be extended by introducing extra fixed amino-acids at appropriate sites. A logical extension would be to introduce the known P1-P1' cleavage site as the depsipeptide bond, then subsequently introduce the four variant positions following the standard format thus;



Furthermore, if these substrates again proved to be too small, one may use the known substrate sequences to introduce additional fixed positions. For instance, with Hepatitis NS3 protease it is known that the natural P6 position is a conserved acidic residue (aspartic or glutamic acid). Thus one could extend the above structure as detailed below.



The novel methodology described herein greatly facilitates the invention of therapeutically useful proteolytic enzyme inhibitors and is commercially exploitable. This is because the best substrate motif for the proteolytic enzyme can be rapidly identified, and, since there exist in the literature a variety of ways for attaching motifs

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which react with the active site of a proteolytic enzyme, especially for aspartyl, metallo, serine and cysteinyl proteases, an enzyme inhibitor can be readily synthesised. Moreover, amide bond replacements or transition state mimetics can be incorporated into the molecule, which would be especially useful for the inhibition of aspartyl or metallo proteases.

5 The method described also facilitates the rapid development of a screening assay for novel protease 10 inhibitors. The most potent fluorogenic substrate discovered by library screening can subsequently be used for the detection of inhibitors of the particular proteolytic enzyme under scrutiny.

15 The presence of an inhibitor within the compound libraries described is readily detected by retreatment of the assay mixture with the most active fluorogenic substrate, which will allow the immediate measurement of the remaining proteolytic enzyme activity.

20 The invention provides self-decoding, combinatorial fluorogenic libraries, and it will greatly facilitate the design and invention of novel protease inhibitors because:

- 25 i. The peptides of the library may have increased aqueous solubility in comparison to peptides containing similar and other fluorogenic and quencher groups.
- ii. The peptides are stable to contaminating exopeptidases.

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iii. The self deconvolution method described, coupled with the continuous analysis of the rate of substrate cleavage data, allows the immediate identification of the most active binding motif contained within the substrate library.

5 iv. The method allows for the rapid assessment of the enzyme assay mixture for any compounds in the library that are acting as enzyme inhibitors.

10

Abbreviations

Abbreviations used herein are as follows:

Abbreviations for amino acids and nomenclature of peptide structures follow the recommendations given in: IUPAC-IUB
5 Commission on Biochemical Nomenclature, (*J. Biol. Chem.*,
247, 997, 1971). All chiral amino acids are of the L
configuration unless otherwise stated. Other abbreviations
used are :

-Abu , b-amino butyric acid, : Abz, 2-amino benzoyl : ACH,
10 1-amino-1-carboxy-cyclohexane : ACP, 1-amino-1-carboxy-
cyclopropane : Bip, Biphenylalanine : n-Bu, n-
butoxycarbonyl : Bz, Benzoyl : Bz(2-carboxy), 2-
carboxybenzoyl : Bu^tGly, tert-Butylglycyl : BOP,
benzotriazoyl-oxy-tris-(dimethylamino)-phosphonium
15 hexafluorophosphate: Cha, cyclohexylalanine : Chex, 1-
carboxycyclohexyl : eAHA, gamma aminohexanoyl : HBTU, O-
benzotriazoyl-N,N,N',N'-tetramethyluronium
hexafluorophosphate : HOBt, 1-hydroxybenzotriazole : Hyp,
trans-4-hydroxyprolinyl : hLeu, homoleucyl : 2Nal, 2-
20 naphtylalanine : NMM, N-methylmorpholine : Piv, pivoyl :
3pyr, 3-pyridylalanine : Tic, 2-carboxytetrahydroquinolyl
: Tyr(NO₂), 3-nitrotyrosine.

25 DMF, dimethylformamide; Fmoc, fluorenylmethoxycarbonyl;
HPLC, high performance liquid chromatography; Pfp,
pentafluorophenyl, tBoc, tert-butoxycarbonyl; tBu, tert-
butyl; TFA, trifluoroacetic acid; Pmc, pentamethyl
chroman, Pbf, pentamethylbenzofuran, TBTU, 2-(1H-

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Benzotriazole-1-yl)-1,1,1,3,3-tetramethyluronium
tetrafluoroborate; Trt, Trityl.

p.Aba, 4-aminobenzoyl; Aib, Aminoisobutyric acid; Bip,
Biphenylalanine; nBu, n-Butyl; Bz, Benzoyl; Cmpi,
5 Carboxymethylpiperazine; Deg, Diethylglycine; DIPEA, N,N-
Diisopropyl-ethylamine; HATU, O-(7-azabenzotriazol-1-yl)-
1,1,3,3-tetramethyluronium hexafluorophosphate; HOAT, 1-
hydroxy-7-azabenzotriazole; Naph, Naphthylalanine; 3.Pyr,
3-pyridylalanine; Tyr(NO₂), 3-nitro-tyrosine.

10

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SEQUENCE LISTING

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(ii) TITLE OF INVENTION: Substrates and Inhibitors of Proteolitic Enzymes

(iii) NUMBER OF SEQUENCES: 52

(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: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "X at position 1 is Abz"

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION:4
- (D) OTHER INFORMATION:/note= "X at position 4 is Nle"

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "X at position 6 is Tyr(NO₂)"



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

Xaa Val Ala Xaa Ser Xaa Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION:/note= "Xaa at position 6 is Tyr(NO₂)"

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

Xaa Val Ala Lys Ser Xaa Asp
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(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION:/note= "Xaa at position 6 is Tyr(NO₂)"



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

Xaa Val Ala Gln Ser Xaa Asp
1 5

(2) INFORMATION FOR SEQ. ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "Xaa at position 6 is Tyr(NO2)"

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

Xaa Val Ala Thr Ser Xaa Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:4
- (D) OTHER INFORMATION:/note= "Xaa at position 4 is hLeu"

(ix) FEATURE:



- (A) NAME/KEY: Modified-site
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "Xaa at position 6 is Tyr(NO2)"

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

Xaa Val Ala Xaa Ser Xaa Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:4
- (D) OTHER INFORMATION:/note= "Xaa at position 4 is Cha"

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "Xaa at position 6 is Tyr(NO2)"

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

Xaa Val Ala Xaa Ser Xaa Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide



(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "Xaa at position 6 is Tyr(NO2)"

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

Xaa Val Ala His Ser Xaa Asp
 1 5

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:4
- (D) OTHER INFORMATION:/note= "Xaa at position 4 is 3pyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "Xaa at position 6 is Tyr(NO2)"

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

Xaa Val Ala Xaa Ser Xaa Asp
 1 5

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid



- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:4
- (D) OTHER INFORMATION:/note= "Xaa at position 4 is hLeu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "Xaa at position 6 is Tyr(NO₂)"

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

Xaa Val Lys Xaa Ser Xaa Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

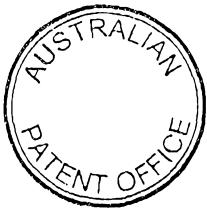
- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:3
- (D) OTHER INFORMATION:/note= "Xaa at position 3 is Met(O)"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:4
- (D) OTHER INFORMATION:/note= "Xaa at position 4 is hLeu"



(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "Xaa at position 6 is
Tyr(NO₂)"

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

Xaa Val Xaa Xaa Ser Xaa Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION:1
(D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 4
(D) OTHER INFORMATION:/note= "Xaa at position 4 is hLeu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "Xaa at position 6 is
Tyr(NO₂)"

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

Xaa Gln Ala Xaa Ser Xaa Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide



(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION:1
 (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION:4
 (D) OTHER INFORMATION:/note= "Xaa at position 4 is hLeu"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION:6
 (D) OTHER INFORMATION:/note= "Xaa at position 6 is
 Tyr(NO2)"

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

Xaa Lys Ala Xaa Ser Xaa Asp
 1 5

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION:1
 (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION:2
 (D) OTHER INFORMATION:/note= "Xaa at position 2 is
 Met(O)"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION:4
 (D) OTHER INFORMATION:/note= "Xaa at position 4 is hLeu"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION:6
 (D) OTHER INFORMATION:/note= "Xaa at position 6 is
 Tyr(NO2)"



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

Xaa Xaa Ala Xaa Ser Xaa Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION:/note= "Xaa at position 2 is 3pyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION:/note= "Xaa at position 4 is hLeu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION:/note= "Xaa at position 6 is Tyr(NO2)"

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

Xaa Xaa Ala Xaa Ser Xaa Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:



(A) NAME/KEY: Modified-site
 (B) LOCATION:2
 (D) OTHER INFORMATION:/note= "Xaa at position 2 is 2Nal"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION:4
 (D) OTHER INFORMATION:/note= "Xaa at position 4 is hLeu"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION:6
 (D) OTHER INFORMATION:/note= "Xaa at position 6 is
 Tyr(NO2)"

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

Xaa Xaa Ala Xaa Ser Xaa Asp
 1 5

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION:1
 (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION:4
 (D) OTHER INFORMATION:/note= "Xaa at position 4 is hLeu"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION:6
 (D) OTHER INFORMATION:/note= "Xaa at position 6 is
 Tyr(NO2)"

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

Xaa Leu Ala Xaa Ser Xaa Asp
 1 5

(2) INFORMATION FOR SEQ ID NO: 17:



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:2
- (D) OTHER INFORMATION:/note= "Xaa at position 2 is Cha"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:4
- (D) OTHER INFORMATION:/note= "Xaa at position 4 is hLeu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "Xaa at position 6 is Tyr(NO2)"

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

Xaa Xaa Ala Xaa Ser Xaa Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

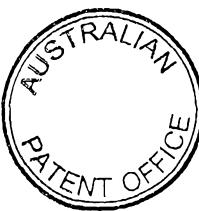
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:2



(D) OTHER INFORMATION:/note= "Xaa at position 2 is Bip"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:4
- (D) OTHER INFORMATION:/note= "Xaa at position 4 is hLeu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "Xaa at position 6 is Tyr(NO2)"

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

Xaa Xaa Ala Xaa Ser Xaa Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:2
- (D) OTHER INFORMATION:/note= "Xaa at position 2 is Bip"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:4
- (D) OTHER INFORMATION:/note= "Xaa at position 4 is hLeu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "Xaa at position 6 is Tyr(NO2)"

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

Xaa Xaa Ala Xaa Tyr Xaa Asp



1

5

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:2
- (D) OTHER INFORMATION:/note= "Xaa at position 2 is Bip"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:4
- (D) OTHER INFORMATION:/note= "Xaa at position 4 is hLeu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "Xaa at position 6 is Tyr(NO2)"

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

Xaa Xaa Ala Xaa Leu Xaa Asp

1

5

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"



(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:2
(D) OTHER INFORMATION:/note= "Xaa at position 2 is Bip"

(ix) FEATURE: .
(A) NAME/KEY: Modified-site
(B) LOCATION: 4
(D) OTHER INFORMATION:/note= "xaa at position 4 is hLeu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:6
(D) OTHER INFORMATION:/note= "Xaa at position 6 is
Tyr(NO₂)"

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

Xaa Xaa Ala Xaa Lys Xaa Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:2
(D) OTHER INFORMATION:/note= "Xaa at position 2 is Bip"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 4
(D) OTHER INFORMATION:/note= "Xaa at position 4 is hLeu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:6
(D) OTHER INFORMATION:/note= "Xaa at position 6 is
Tyr(NO₂)"



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

Xaa Xaa Ala Xaa Xaa Xaa Asp
1 5

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

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION:/note= "Xaa at position 2 is Bip"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION:/note= "Xaa at position 4 is hLeu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION:/note= "Xaa at position 5 is Abu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION:/note= "Xaa at position 6 is
Tyr(NO₂)"

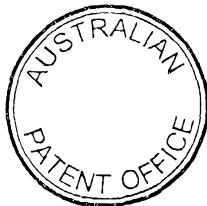
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Xaa Xaa Ala Xaa Xaa Xaa Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown



(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:2
- (D) OTHER INFORMATION:/note= "Xaa at position 2 is Bip"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:4
- (D) OTHER INFORMATION:/product= "X"
/note= "Xaa at position 4 is hLeu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:5
- (D) OTHER INFORMATION:/note= "Xaa at position 5 is Cha"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "Xaa at position 6 is
Tyr(NO2)"

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

Xaa Xaa Ala Xaa Xaa Xaa Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:2



(D) OTHER INFORMATION:/note= "Xaa at position 2 is Bip"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION:4

(D) OTHER INFORMATION:/note= "Xaa at position 4 is hLeu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION:5

(D) OTHER INFORMATION:/note= "Xaa at position 5 is Met(O)"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION:6

(D) OTHER INFORMATION:/note= "Xaa at position 6 is Tyr(NO2)"

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

Xaa Xaa Ala Xaa Xaa Xaa Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION:1

(D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION:2

(D) OTHER INFORMATION:/note= "Xaa at position 2 is Bip"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION:4

(D) OTHER INFORMATION:/note= "Xaa at position 4 is hLeu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION:6

(D) OTHER INFORMATION:/note= "Xaa at position 6 is



Tyr(NO₂) "

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

Xaa Xaa Ala Xaa Thr Xaa Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION:/note= "Xaa at position 2 is BIP"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION:/note= "Xaa at position 4 is hLeu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION:/note= "Xaa at position 5 is 3pyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION:/note= "Xaa at position 6 is Tyr(NO₂) "

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

Xaa Xaa Ala Xaa Xaa Xaa Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids



- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa at position1 is Abz"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:2
- (D) OTHER INFORMATION:/note= "Xaa at position 2 is Bip"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:4
- (D) OTHER INFORMATION:/note= "Xaa at position 4 is hLeu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:5
- (D) OTHER INFORMATION:/note= "Xaa at position 5 is BuGly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "Xaa at position 6 is Tyr(NO2) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Xaa Xaa Ala Xaa Xaa Xaa Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 29:

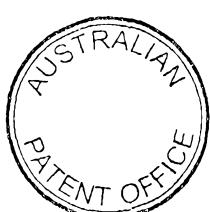
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"



(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:2
- (D) OTHER INFORMATION:/note= "Xaa at position2 is Bip"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:4
- (D) OTHER INFORMATION:/note= "Xaa at position 4 is hLeu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:5
- (D) OTHER INFORMATION:/note= "Xaa at position 5 is Hyp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "Xaa at position 6 is
Tyr(NO2)"

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

Xaa Xaa Ala Xaa Xaa Xaa Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:2
- (D) OTHER INFORMATION:/note= "Xaa at position 2 is 1
Naph"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:5
- (D) OTHER INFORMATION:/note= "Xaa at position 5 is Nle"

(ix) FEATURE:



- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION:/note= "Xaa at position 7 is Tyr(NO₂)"

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

Xaa Xaa Val Ala Xaa Ser Xaa Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION:/note= "Xaa at position 2 is Bip"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION:/note= "Xaa at position 5 is Nle"

(ix) FEATURE:

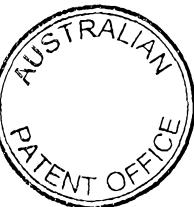
- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION:/note= "Xaa at position 7 is Tyr(NO₂)"

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

Xaa Xaa Val Ala Xaa Ser Xaa Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single



(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:5
- (D) OTHER INFORMATION:/note= "Xaa at position 5 is Nle"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:7
- (D) OTHER INFORMATION:/note= "Xaa at position 7 is Tyr(NO2)"

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

Xaa Lys Val Ala Xaa Ser Xaa Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa at position 1 is Abz"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:5
- (D) OTHER INFORMATION:/note= "Xaa at position 5 is Nle"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:7
- (D) OTHER INFORMATION:/note= "Xaa at position 7 is Tyr(NO2)"



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

Xaa Glu Val Ala Xaa Ser Xaa Asp
1 5

(2) INFORMATION FOR SEQ. ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa in position 1 is n-benzoyl"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:4
- (D) OTHER INFORMATION:/note= "Xaa ain position 4 is 1-norleucine bromomethyl ketone"

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

Xaa Val Ala Xaa
1

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa in position 1 is N-benzoyl"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:4
- (D) OTHER INFORMATION:/note= "Xaa ainm position 4 is



L-norleucine 2,6-bis(trifluoromethyl)benzoyloxomethyl ketone"

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

Xaa Val Ala Xaa
1

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION:/note= "Xaa in position 4 is
L-norleucine 2,6-bimethylbenzoyloxomethyl ketone"

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

Xaa Val Ala Xaa
1

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION:/note= "Xaa in position is
L-norleucine 2-hydroxybenzoyloxomethyl ketone"

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

Xaa Val Ala Xaa
1

(2) INFORMATION FOR SEQ ID NO: 38:



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa in position 1 is N-benzoyl"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:4
- (D) OTHER INFORMATION:/note= "Xaa in position 4 is L-norleucine 2,6-dichlorobenzoyloxomethyl ket..."

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

Xaa Val Ala Xaa
1

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa in position 1 is N-benzoyl"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:4
- (D) OTHER INFORMATION:/note= "Xaa in position 4 is L-norleucine benzoyloxomethyl ketone"

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

Xaa Val Ala Xaa
1



(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note= "Xaa in position 1 is N-benzoyl"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION:/note= "Xaa in position 4 is L-norleucine 2,3,4,5,6-pentafluorobenzoyloxymethyl ketone"

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

Xaa Val Ala Xaa
1

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note= "Xaa in position 1 is Benzoyl"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION:/note= "Xaa in position 4 is L-norleucine 1,1-dimethylpropyloxymethyl ketone"

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



Xaa Val Ala Xaa

1

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note= "Xaa in position 1 is N-benzoyl"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION:/note= "Xaa in position 4 is L-norleucine"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION:/note= "Xaa in position 5 is N(benzyloxycarbonyl)-D-serinyl-(O-tert-butyl)oxymethyl ketone"

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

Xaa Val Ala Xaa Xaa

1

5

(2) INFORMATION FOR SEQ ID NO: 43:

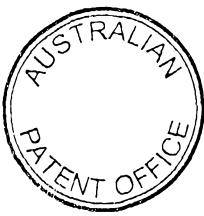
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION:/note= "Xaa in position 4 is L-norleucine"



(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION:/note= "Xaa in position 5 is N(-benzyloxycarbonyl)-D-serineoxy methyl ketone"

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

Xaa	Val	Ala	Xaa
1			5

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note= "Xaa in position 1 is N-benzoyl"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION:/note= "Xaa in position 4 is L-norleucine"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION:/note= "Xaa in position 5 is 2-furanoxy methyl ketone"

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

Xaa	Val	Ala	Xaa
1			5

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown



(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa in position 1 is N-benzoyl"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:4
- (D) OTHER INFORMATION:/note= "Xaa in position 4 is L-norleucine 2,6-dichlorophenylacyloxy methyl ketone"

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

Xaa Val Ala Xaa
1

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa in the 1 position is Ethyl-(s)-(e)-3-TERT BUTOXY CARBONYL"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:4
- (D) OTHER INFORMATION:/note= "XAA IN THE 4 POSITION is amino-6-methyl-hept-2-enoate"

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

Xaa Val Ala Xaa
1

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid



- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note= "Xaa in the 1 position is (S)-(E)-3-(tertbutoxycarbonyl)"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION:/note= "Xaa in the 4 position is amino-6-methyl-hept-2-enoic acid"

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

Xaa Val Ala Xaa
1

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note= "Xaa in the 1 position is 1,1,1-trifluoroethyl-(S)-(E)-3-(tertbutoxycarbonyl)"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION:/note= "Xaa in the 4 position is amino-6-methyl-hept-2-enoate"

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

Xaa Val Ala Xaa
1

(2) INFORMATION FOR SEQ ID NO: 49:



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa in the 1 position is Ethyl-(S)-(E)-3-(N-benzoyl)"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:4
- (D) OTHER INFORMATION:/note= "Xaa in the 4 position is amino-6-methyl-hept-2-enoate"

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

Xaa Val Ala Xaa

1

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa in the 1 position is (S)-(E)-3(tertbutoxycarbonyl)"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:4
- (D) OTHER INFORMATION:/note= "Xaa in the 4 position is amino-1-phenylsulfonyl-5-methyl-1-hexene"

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

Xaa Val Ala Xaa

1



(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note= "Xaa in the 1 position is (S) - (E) - 3-tertbutoxycarbonyl"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION:/note= "Xaa in the 4 position is amino-1-methylsulfonyl-5-methyl-1-hexene"

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

Xaa Val Ala Xaa
1

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note= "Xaa in the 1 position is Diehtyl(S) - (E) - 3 ((tert-butoxycarbonyl))"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION:/note= "Xaa in the 4 position is 5-methylhexenylsulfonate"

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



101

Xaa Val Ala Xaa
1



THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. A complementary pair of compound libraries L1 and L2 which constitute a set containing combinatorial FRET compounds of formula:

5 Aa-Bb-Cc-Dd-n(Ee)-Ff-Gg

in which;

A represents a fluorescor internally quenched by F;

B, C, D, and E represent groups such that the scissile bond between any two of these groups is a suitable bond;

10 F represents a quencher capable of internally quenching the fluorescor A; and wherein all compounds are in aqueous solution; and

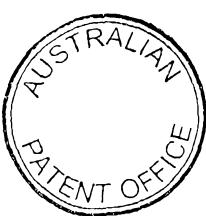
n represents an integer between 1 and 4 inclusive;

giving $a \times b \times c \times d \times e \times f \times g = M^n$ compounds in each

15 library, there being a predetermined number (P1, P2) of mixtures each consisting of a predetermined number (Q1, Q2) of individual identifiable compounds in each library, wherein both L1 and L2 contain the same Mⁿ compounds, but wherein any two compounds which are found together in one 20 mixture of Q1 compounds of L1 are not found together in any one of the P2 mixtures of L2.

2. A method of screening for enzymic activity, wherein the activity is the interaction of proteolytic enzyme applied to a well with one or more compounds of a mixture

25 in the well, using the libraries L1, L2 according to claim 1, in which the P1 mixtures of L1 and the P2 mixtures of L2 are each placed separately into individual wells of well plates, the well plates having wells arranged in a format adapted to allow deduction of a unique active 30 compound formula from the presence of activity in one well of L1 and one well of L2.



3. A method according to claim 2 wherein the format complies with general deconvolution formulae in which:

$$(i) \quad ns = \frac{Rp \cdot Cp}{Rs \cdot Cs} \cdot Np$$

5 (ii) $k = b \cdot c \cdot d \cdot np \cdot e$

(iii) $k = x \cdot N \cdot np$

(iv) $N = Rp \cdot Cp$

(v) $K = X \cdot Rp \cdot Cp \cdot np$

(vi) $b \cdot c \cdot d \cdot e = X \cdot Rp \cdot Cp$

10 (vii) $Cp \cdot e = X$

(viii) $Rp \cdot e = X, \text{ if } Rp = Cp$

and wherein

15 np = number of primary plates

ns = number of secondary plates

Rp = number of primary rows

Rs = number of secondary rows

Cp = number of primary columns

Cs = number of secondary columns

20 K = number of combinations of compounds

N = number of wells on a plate, and

X = number of compounds per well.

4. A method according to claim 3 wherein

np = 4



ns	=	16
Rp	=	8
Rs	=	4
Cp	=	10
5 Cs	=	5
K	=	6400
N	=	80
X	=	20

5. A library pair according to claim 1 wherein the
10 scissile bond is between D and E.

6. A library pair according to claim 1 wherein A
represents an unsubstituted or substituted anthranilic
acid derivative.

7. A library pair according to claim 1 wherein B, C, D
15 and E independently represent natural or unnatural amino
acid residues.

8. A library pair according to claim 1 wherein F
represents an unsubstituted or substituted 3-nitrotyrosine
derivative.

20 9. A library pair according to claim 1 wherein the
scissile bond is a suitable bond selected from the group
consisting of an unsubstituted amide bond, and an ester
bond.

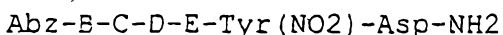
25 10. A library pair according to claim 1 wherein the
formula further comprises G which ensures the compound is
imparted with aqueous solubility.

11. A library pair according to claim 10 which is
represented by the formula A-B-C-D-n(E)-F-G in which



A, B, C, D, E, F and n are as defined in claim 1; and G represents a hydrophilic moiety which is not an enzyme substrate.

12. A library pair according to claim 10 or 11 of general formula:



Where

B= Valine>Alanine, Glutamine, Leucine, Phenylalanine

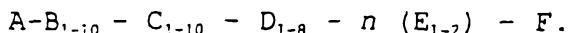
C= Alanine>>Glutamine, or Lysine.

10 D= Leucine, Norleucine or Alanine>Serine

E=Serine

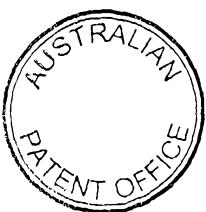
13. Apparatus which comprises an auto-deconvoluting set of compounds according to claim 1 that facilitates the invention of novel inhibitors of proteolytic enzymes and 15 the rapid generation of structure-activity relationships (SAR) by the detection and measurement of proteolytic enzyme activity.

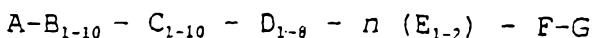
14. Apparatus according to claims 13 wherein each library comprises a mixture of compounds represented by the 20 formula:



15. Apparatus according to claim 14 wherein the formula further comprises G which ensures that compounds in the library are imparted with aqueous solubility.

25 16. Apparatus according to claim 15 wherein each library comprises a mixture of compounds represented by the formula:





in which;

G represents a hydrophilic moiety which is not an enzyme substrate.

5 17. Apparatus according to claim 15 or 16 in which G represents an aspartyl amide moiety.

18. Apparatus according to any one of claims 13 to 17 wherein the library comprises $1600n$ compounds as $80n$ mixtures of 20 distinct, identifiable compounds.

10 19. Apparatus according to claim 18 wherein the mixtures of 20 distinct, identifiable compounds are placed separately into each of 80 wells of an microtitre plate.

15 20. Use of a combinatorial FRET library pair according to claim 1 in a method which provides rapid generation of structure-activity relationships (SAR) which comprises detection and measurement of proteolytic enzyme activity by carrying out an assay with a library pair of combinatorial FRET (fluorescence resonance energy transfer) molecules to find a substrate or substrates for the enzyme.

20 21. Use of a combinatorial FRET library pair according to claim 1 in a method for detection and measurement of proteolytic enzyme activity against compounds of the library.

25 22. A method of identifying and synthesising an inhibitor of a proteolytic enzyme which comprises detection and measurement of proteolytic enzyme activity by carrying out an assay with a library pair of combinatorial FRET

(fluorescence resonance energy transfer) molecules according to claim 1, deconvoluting the library to find a substrate or substrates for the enzyme and synthesis of an inhibitor based on the substrate or substrates.

- 5 23. An inhibition assay which uses a FRET molecule, which has been identified as a substrate for the enzyme by the method of claim 2, wherein the molecule is assayed with the enzyme separately against a panel of possible inhibitors.
- 10 24. A method which provides the rapid generation of structure-activity relationships (SAR) which comprises detection and measurement of proteolytic enzyme activity by carrying out an assay with a library pair of combinatorial FRET (fluorescence resonance energy transfer) molecules according to claim 1 to find a substrate or substrates for the enzyme.
- 15 25. A method which comprises the identification of an enzyme inhibitor or inhibitors wherein a FRET compound which has been identified as a substrate by the method of claim 2 is used in an inhibition assay with the enzyme separately against a panel of possible inhibitors.
- 20 26. A method according to claim 25 wherein the assay is performed by using the apparatus according to any of claims 13 to 19.
- 25 27. A method according to any proceeding method claim wherein the compounds of the library pair are synthesized using a solid phase technique.



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28. A library pair, apparatus, method or assay substantially as described herein with reference to example 1.

DATED this 15th day of April 1999

PEPTIDE THERAPEUTICS LIMITED

By Its Patent Attorneys

DAVIES COLLISON CAVE



SEARCHED INDEXED

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	1	2	3	4	5	6	7	8	9	10	11	12
A	A1	A2	A3	A4	A5	A6	A7	A8	A9	A10		
B	B1	B2	B3	B4	B5	B6	B7	B8	B9	B10		
C	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10		
D	D1	D2	D3	D4	D5	D6	D7	D8	D9	D10		
E	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10		
F	F1	F2	F3	F4	F5	F6	F7	F8	F9	F10		
G	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10		
H	H1	H2	H3	H4	H5	H6	H7	H8	H9	H10		

10 Figure 1

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First Example of Library Matrix where n=1

Component Distribution in Plate 1, Library 1 (n=1)

	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10
D1	B ₁₋₁₀									
	E ₁₋₂									
D2	B ₁₋₁₀									
	E ₁₋₂									
D3	B ₁₋₁₀									
	E ₁₋₂									
D4	B ₁₋₁₀									
	E ₁₋₂									
D5	B ₁₋₁₀									
	E ₁₋₂									
D6	B ₁₋₁₀									
	E ₁₋₂									
D7	B ₁₋₁₀									
	E ₁₋₂									
D8	B ₁₋₁₀									
	E ₁₋₂									

Figure 2

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Component Location in Plate 1, Library 2 (n=1).

	B1	B2	B3	B4	B5	B6	B7	B8	B9	B10
E1	C ₁₋₁₀									
	D ₁₋₂									
E2	C ₁₋₁₀									
	D ₁₋₂									

5 **Figure 3**

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Component Location in Plate 2, Library 2 (n=1).

	B1	B2	B3	B4	B5	B6	B7	B8	B9	B10
E1	C ₁₋₁₀									
	D ₃₋₄									
E2	C ₁₋₁₀									
	D ₃₋₄									

5 Figure 4

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Component Location in Plate 3, Library 2 (n=1).

	B1	B2	B3	B4	B5	B6	B7	B8	B9	B10
E1	C ₁₋₁₀									
	D ₅₋₆									
E2	C ₁₋₁₀									
	D ₅₋₆									

5 Figure 5

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Component Location in Plate 4, Library 2 (n=1).

	B1	B2	B3	B4	B5	B6	B7	B8	B9	B10
E1	C ₁₋₁₀									
	D ₇₋₈									
E2	C ₁₋₁₀									
	D ₇₋₈									

5

Figure 6

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Example Library where n=4

Component Distribution in Plate 1, Library 1 (n=4)

	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10
D1	B ₁₋₁₀									
	E ₁₋₂									
D2	B ₁₋₁₀									
	E ₁₋₂									
D3	B ₁₋₁₀									
	E ₁₋₂									
D4	B ₁₋₁₀									
	E ₁₋₂									
D5	B ₁₋₁₀									
	E ₁₋₂									
D6	B ₁₋₁₀									
	E ₁₋₂									
D7	B ₁₋₁₀									
	E ₁₋₂									
D8	B ₁₋₁₀									
	E ₁₋₂									

Figure 7

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Component Location in Plate 2, Library 1 (n=4)

	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10
D1	B ₁₋₁₀ E ₃₋₄									
D2	B ₁₋₁₀ E ₃₋₄									
D3	B ₁₋₁₀ E ₃₋₄									
D4	B ₁₋₁₀ E ₃₋₄									
D5	B ₁₋₁₀ E ₃₋₄									
D6	B ₁₋₁₀ E ₃₋₄									
D7	B ₁₋₁₀ E ₃₋₄									
D8	B ₁₋₁₀ E ₃₋₄									

Figure 8

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Component Location in Plate 3, Library 1 (n=4)

	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10
D1	B ₁₋₁₀									
	E ₅₋₆									
D2	B ₁₋₁₀									
	E ₅₋₆									
5	D3	B ₁₋₁₀								
	E ₅₋₆									
D4	B ₁₋₁₀									
	E ₅₋₆									
D5	B ₁₋₁₀									
	E ₅₋₆									
D6	B ₁₋₁₀									
	E ₅₋₆									
10	D7	B ₁₋₁₀								
	E ₅₋₆									
D8	B ₁₋₁₀									
	E ₅₋₆									

Figure 9

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Component Location in Plate 4, Library 1 (n=4).

	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10
D1	B ₁₋₁₀									
	E ₇₋₈									
D2	B ₁₋₁₀									
	E ₇₋₈									
D3	B ₁₋₁₀									
	E ₇₋₈									
D4	B ₁₋₁₀									
	E ₇₋₈									
D5	B ₁₋₁₀									
	E ₇₋₈									
D6	B ₁₋₁₀									
	E ₇₋₈									
D7	B ₁₋₁₀									
	E ₇₋₈									
D8	B ₁₋₁₀									
	E ₇₋₈									

Figure 10

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Component Location in Plate 1, Library 2 (n=4).

	B1	B2	B3	B4	B5	B6	B7	B8	B9	B10
E1	C ₁₋₁₀									
	D ₁₋₂									
E2	C ₁₋₁₀									
	D ₁₋₂									
E3	C ₁₋₁₀									
	D ₁₋₂									
E4	C ₁₋₁₀									
	D ₁₋₂									
E5	C ₁₋₁₀									
	D ₁₋₂									
E6	C ₁₋₁₀									
	D ₁₋₂									
E7	C ₁₋₁₀									
	D ₁₋₂									
E8	C ₁₋₁₀									
	D ₁₋₂									

Figure 11.

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Component Location in Plate 2, Library 2 (n=4).

	B1	B2	B3	B4	B5	B6	B7	B8	B9	B10
E1	C ₁₋₁₀ D ₃₋₄									
E2	C ₁₋₁₀ D ₃₋₄									
E3	C ₁₋₁₀ D ₃₋₄									
E4	C ₁₋₁₀ D ₃₋₄									
E5	C ₁₋₁₀ D ₃₋₄									
E6	C ₁₋₁₀ D ₃₋₄									
E7	C ₁₋₁₀ D ₃₋₄									
E8	C ₁₋₁₀ D ₃₋₄									

Figure 12

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Component Location in Plate 3, Library 2 (n=4).

	B1	B2	B3	B4	B5	B6	B7	B8	B9	B10
E1	C ₁₋₁₀									
	D ₅₋₆									
E2	C ₁₋₁₀									
	D ₅₋₆									
E3	C ₁₋₁₀									
	D ₅₋₆									
E4	C ₁₋₁₀									
	D ₅₋₆									
E5	C ₁₋₁₀									
	D ₅₋₆									
E6	C ₁₋₁₀									
	D ₅₋₆									
E7	C ₁₋₁₀									
	D ₅₋₆									
E8	C ₁₋₁₀									
	D ₅₋₆									

Figure 13

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Component Location in Plate 4, Library 2 (n=4).

	B1	B2	B3	B4	B5	B6	B7	B8	B9	B10
E1	C ₁₋₁₀									
	D ₇₋₈									
E2	C ₁₋₁₀									
	D ₇₋₈									
E3	C ₁₋₁₀									
	D ₇₋₈									
E4	C ₁₋₁₀									
	D ₇₋₈									
E5	C ₁₋₁₀									
	D ₇₋₈									
E6	C ₁₋₁₀									
	D ₇₋₈									
E7	C ₁₋₁₀									
	D ₇₋₈									
E8	C ₁₋₁₀									
	D ₇₋₈									

Figure 14.

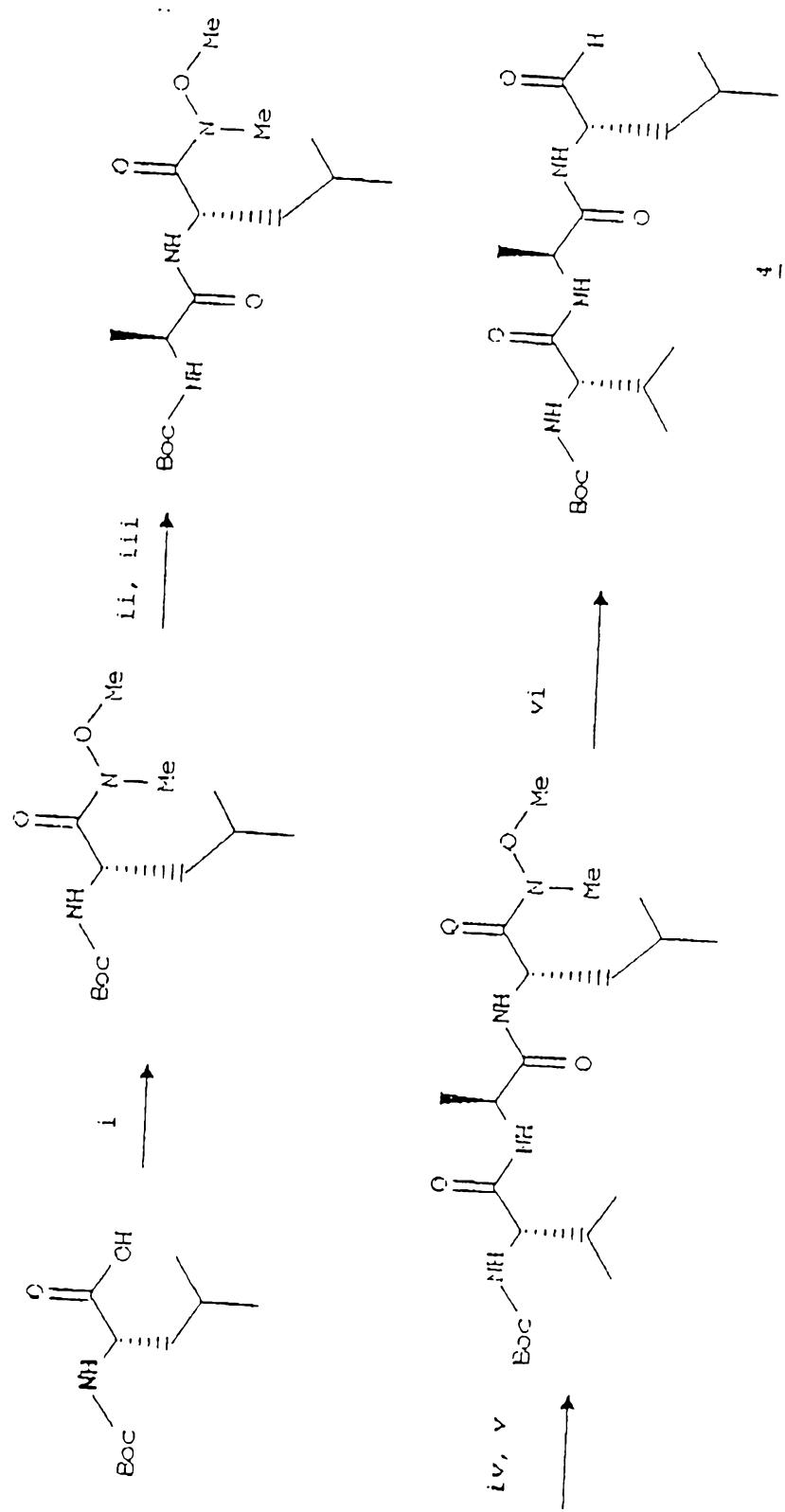


Figure 15

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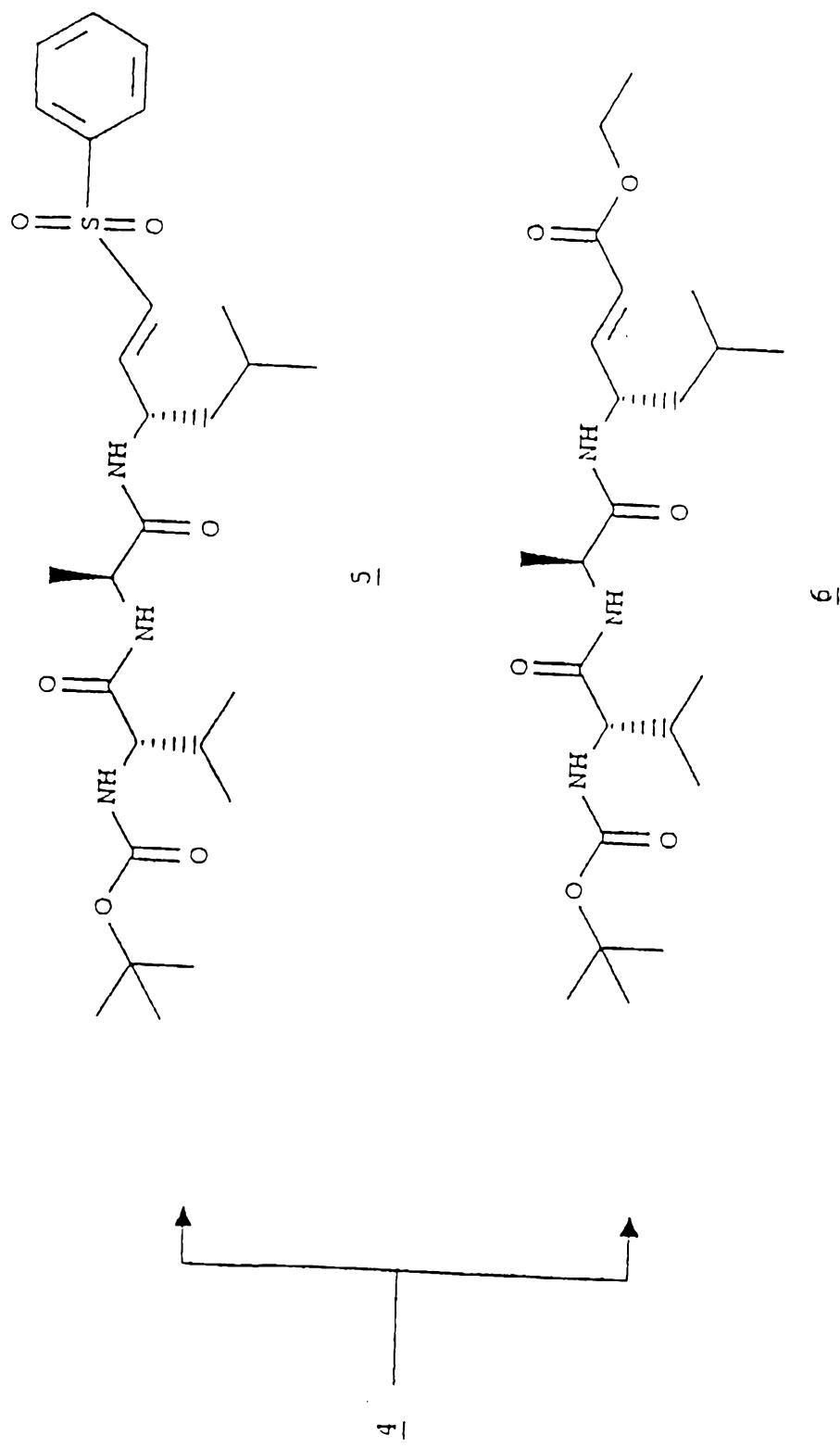


Figure 16