

(12) STANDARD PATENT APPLICATION (11) Application No. AU 2022283467 A9
(19) AUSTRALIAN PATENT OFFICE

(54) Title
ANTHRACYCLINE ANTIBODY CONJUGATES

(51) International Patent Classification(s)
A61K 47/68 (2017.01) **C07K 16/30** (2006.01)
A61P 35/00 (2006.01)

(21) Application No: **2022283467** (22) Date of Filing: **2022.05.25**

(87) WIPO No: **WO22/251850**

(30) Priority Data

(31) Number	(32) Date	(33) Country
63/194,606	2021.05.28	US

(43) Publication Date: **2022.12.01**

(48) Corrigenda Journal Date: **2023.12.21**

(71) Applicant(s)
SEAGEN INC.

(72) Inventor(s)
BURKE, Patrick J; HAMILTON, Joseph Z.

(74) Agent / Attorney
Davies Collison Cave Pty Ltd, Level 15 1 Nicholson Street, MELBOURNE, VIC, 3000, AU

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property

Organization

International Bureau

(43) International Publication Date

01 December 2022 (01.12.2022)



(10) International Publication Number

WO 2022/251850 A1

(51) International Patent Classification:

A61K 47/68 (2017.01) C07K 16/30 (2006.01)

A61P 35/00 (2006.01)

Published:

- with international search report (Art. 21(3))
- before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))
- with sequence listing part of description (Rule 5.2(a))

(21) International Application Number:

PCT/US2022/072570

(22) International Filing Date:

25 May 2022 (25.05.2022)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

63/194,606 28 May 2021 (28.05.2021) US

(71) Applicant: SEAGEN INC. [US/US]; 21823-30th Drive S.E., Bothell, Washington 98021 (US).

(72) Inventors: BURKE, Patrick J; 21823-30th Drive S.E., Bothell, Washington 98021 (US). HAMILTON, Joseph Z.; 21823-30th Drive S.E., Bothell, Washington 98021 (US).

(74) Agent: ALTMAN, Daniel, E; KNOBBE, MARTENS, OLSON & BEAR, LLP, 2040 Main Street, 14th Floor, Irvine, California 92614 (US).

(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IQ, IR, IS, IT, JM, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, WS, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Declarations under Rule 4.17:

- as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))
- as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii))

(54) Title: ANTHRACYCLINE ANTIBODY CONJUGATES

(57) Abstract: The present disclosure provides, *inter alia*, antibody drug conjugates that are useful in treating various diseases such as cancer.



WO 2022/251850 A1

ANTHRACYCLINE ANTIBODY CONJUGATES

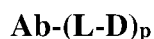
BACKGROUND

[0001] Anthracyclines are cytotoxic compounds that have been used in anticancer therapy for more than 40 years. *See* Mattarollo, et al., *Cancer Res.* 2011; Vol. 71, pp. 4809-20. Anthracyclines primarily exert their cytotoxic activity through interfering with DNA topoisomerase II, which is also the mechanism of anthracycline-induced cardiotoxicity. *See* Dal Ben, et al., *Curr. Pharm. Des.* 2007; Vol. 13, No. 27, pp. 2766-80. While these compounds may be useful in the treatment of cancer and other diseases, their therapeutic utility is often limited by their dose-dependent toxicity. Anthracycline chemotherapy causes dose-related cardiomyocyte injury and death leading to left ventricular dysfunction. Clinical heart failure may ensue in up to 5% of high-risk patients. *See* Henriksen, *Heart*, 2018; Vol. 104, No. 12, pp. 971-77. These off target effects are particularly problematic for more recently developed, highly cytotoxic anthracyclines such as nemorubicin.

[0002] The use of antibody-drug conjugates (ADCs) for the local delivery of cytotoxic compounds provides targeted delivery of these drugs directly into tumor cells, or in proximity to tumor cells, whereas systemic administration of these drugs may result in unacceptable levels of toxicity to normal cells. *See, e.g.,* Lambert, *Curr. Opin. Pharmacol.* 2005; Vol. 5, pp. 543-49 and Doronina, et al., *Bioconj. Chem.* 2006; Vol. 17, pp. 114-24. Anthracycline ADCs, such as conjugates of doxorubicin and daunorubicin have been studied, but none have been approved for clinical use. *See, e.g.,* Nagy, et al., *Proc. Natl. Acad. Sci.* 2000; Vol. 97, pp. 829-34 and Dubowchik, et al., *Bioorg. Med. Chem. Lett.* 2002; Vol 12, pp. 1529-32. Thus, there remains a need for targeted delivery of highly-potent anthracycline compounds to localize the cytotoxic effect to the desired cells while minimizing off-target effects.

SUMMARY

[0003] Some embodiments provide an antibody drug conjugate (ADC) having the structure:



or a salt thereof;

wherein:

Ab is an antibody;

wherein each L is covalently attached to Ab via a sulfur atom of a cysteine residue or an ϵ -amino group of a lysine residue in Ab;

subscript p is an integer from 1 to 16;

each D is an anthracycline;

each L is a linker that has the formula $-M-(A)_a-(W)_w-(Y)_y-(X)-$, wherein:

M is a succinimide, a hydrolyzed succinimide, an amide, or a triazole, wherein M is covalently attached to Ab;

subscript a is 0 or 1;

subscript y is 0 or 1;

subscript w is 0 or 1;

A is a C_{2-10} alkylene optionally substituted with 1-3 R^{a1} ; or a 3 to 20 membered heteroalkylene optionally substituted with 1-3 R^{b1} ;

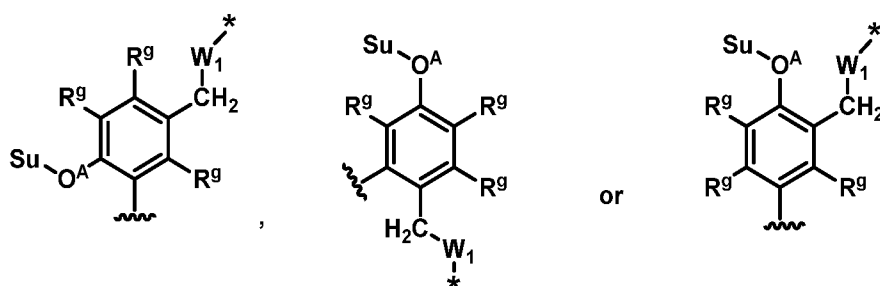
each R^{a1} is independently selected from the group consisting of: C_{1-6} alkyl, C_{1-6} haloalkyl, C_{1-6} alkoxy, C_{1-6} haloalkoxy, halogen, $-OH$, $=O$, $-NR^{d1}R^{e1}$, $-(C_{1-6} \text{ alkylene})-NR^{d1}R^{e1}$, $-C(=O)NR^{d1}R^{e1}$, $-C(=O)(C_{1-6} \text{ alkyl})$, and $-C(=O)O(C_{1-6} \text{ alkyl})$;

each R^{b1} is independently selected from the group consisting of: C_{1-6} alkyl, C_{1-6} haloalkyl, C_{1-6} alkoxy, C_{1-6} haloalkoxy, halogen, $-OH$, $-NR^{d1}R^{e1}$, $-(C_{1-6} \text{ alkylene})-NR^{d1}R^{e1}$, $-C(=O)NR^{d1}R^{e1}$, $-C(=O)(C_{1-6} \text{ alkyl})$, and $-C(=O)O(C_{1-6} \text{ alkyl})$;

each R^{d1} and R^{e1} are independently hydrogen or C_{1-3} alkyl;

W is from 1-6 amino acids; or

W has the structure:



wherein Su is a Sugar moiety;

$-O^A-$ represents the oxygen atom of a glycosidic bond;

each R^g is independently hydrogen, halogen, C_1 - C_6 alkoxy, $-N(C_1-C_6 \text{ alkyl})_2$, $-NHC(=O)(C_1-C_6 \text{ alkyl})$, $-CN$, $-CF_3$, acyl, carboxamido, C_1 - C_6 alkyl, or $-NO_2$;

W^1 is absent, $*-C(=O)-O-$, or $*-O-C(=O)-$;

 represents covalent attachment to A or M;

* represents covalent attachment to Y or X;

Y is a self-immolative moiety, a non-self-immolative releasable moiety, or a non-cleavable moiety;

X is from 1-10 amino acids; or

X is a 4-16 membered heteroalkylene, wherein X is optionally substituted with 1-3 independently selected R^X ;

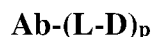
each R^X is independently a C_2 - C_6 alkynyl group, $-NR^{X1}R^{X2}$, or a C_1 - C_6 alkyl group optionally substituted with hydroxyl, $-NR^{X1}R^{X2}$, guanidino, 1 or 2 $-CO_2H$ groups, $-C(=O)NR^{X1}R^{X2}$, urea, phenyl, naphthyl, indolyl, imidazolyl, $-SH$, $-SCH_3$, $-SeCH_3$, or 4-hydroxyphenyl optionally substituted with C_2 - C_6 alkenyl; or

two R^X attached to the same or adjacent carbon atom(s) of X, together with the carbon atom(s) to which they are attached form an unsubstituted 5-6 membered heterocyclyl;

each R^{X1} and R^{X2} are independently hydrogen or C_{1-6} alkyl; and

L is optionally substituted with a PEG Unit from PEG1 to PEG72.

[0004] Some embodiments provide an antibody drug conjugate (ADC) having the structure:



or a salt thereof;

wherein:

Ab is an antibody;

wherein each L is covalently attached to Ab via a sulfur atom of a cysteine residue or an ϵ -amino group of a lysine residue in Ab;

subscript p is an integer from 1 to 16;

each D is an anthracycline;

each L is a linker that has the formula $-M-(A)_a-(W)_w-(Y)_y-(X)-$, wherein:

M is a succinimide, a hydrolyzed succinimide, an amide, or a triazole, wherein M is covalently attached to Ab;

subscript a is 0 or 1;

subscript y is 0 or 1;

subscript w is 0 or 1;

A is a C₂₋₁₀ alkylene optionally substituted with 1-3 R^{al}; or a 3 to 20 membered heteroalkylene optionally substituted with 1-3 R^{bl};

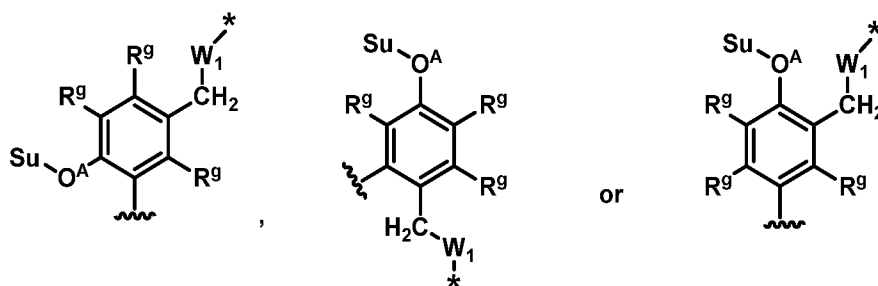
each R^{al} is independently selected from the group consisting of: C₁₋₆ alkyl, C₁₋₆ haloalkyl, C₁₋₆ alkoxy, C₁₋₆ haloalkoxy, halogen, -OH, =O, -NR^{dl}R^{el}, -(C₁₋₆ alkylene)-NR^{dl}R^{el}, -C(=O)NR^{dl}R^{el}, -C(=O)(C₁₋₆ alkyl), and -C(=O)O(C₁₋₆ alkyl);

each R^{bl} is independently selected from the group consisting of: C₁₋₆ alkyl, C₁₋₆ haloalkyl, C₁₋₆ alkoxy, C₁₋₆ haloalkoxy, halogen, -OH, -NR^{dl}R^{el}, -(C₁₋₆ alkylene)-NR^{dl}R^{el}, -C(=O)NR^{dl}R^{el}, -C(=O)(C₁₋₆ alkyl), and -C(=O)O(C₁₋₆ alkyl);

each R^{dl} and R^{el} are independently hydrogen or C₁₋₃ alkyl;

W is from 1-6 amino acids; or

W has the structure:



wherein Su is a Sugar moiety;

-O^A- represents the oxygen atom of a glycosidic bond;

each R^g is independently hydrogen, halogen, C₁₋₆ alkoxy, -N(C₁₋₆ alkyl)₂, -NHC(=O)(C₁₋₆ alkyl), -CN, -CF₃, acyl, carboxamido, C₁₋₆ alkyl, or -NO₂;

W¹ is absent, *-C(=O)-O-, or *-O-C(=O)-;

~~~~~ represents covalent attachment to A or M;

\* represents covalent attachment to Y or X;

Y is a self-immolative moiety, a non-self-immolative releasable moiety, or a non-cleavable moiety;

X is a 4-16 membered heteroalkylene, wherein X is optionally substituted with 1-3 independently selected  $R^X$ ;

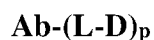
each  $R^X$  is independently a  $C_2$ - $C_6$  alkynyl group,  $-NR^{X1}R^{X2}$ , or a  $C_1$ - $C_6$  alkyl group optionally substituted with hydroxyl,  $-NR^{X1}R^{X2}$ , guanidino, 1 or 2  $-CO_2H$  groups,  $-C(=O)NR^{X1}R^{X2}$ , urea, phenyl, naphthyl, indolyl, imidazolyl,  $-SH$ ,  $-SCH_3$ ,  $-SeCH_3$ , or 4-hydroxyphenyl optionally substituted with  $C_2$ - $C_6$  alkenyl; or

two  $R^X$  attached to the same or adjacent carbon atom(s) of X, together with the carbon atom(s) to which they are attached form an unsubstituted 5-6 membered heterocyclyl;

each  $R^{X1}$  and  $R^{X2}$  are independently hydrogen or  $C_{1-6}$  alkyl; and

L is optionally substituted with a PEG Unit from PEG1 to PEG72.

**[0005]** Some embodiments provide an antibody drug conjugate (ADC) having the structure:



or a salt thereof;

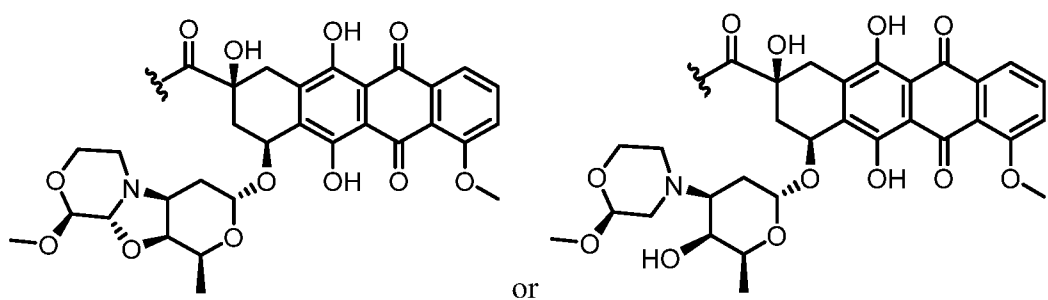
wherein:

Ab is an antibody;

wherein each L is covalently attached to Ab via a sulfur atom of a cysteine residue or an  $\epsilon$ -amino group of a lysine residue in Ab;

subscript p is an integer from 1 to 16;

each D is:



wherein  represents covalent attachment to L;

each L is a linker that has the formula  $-M-(A)_a-(W)_w-(Y)_y-(X)-$ , wherein:

M is a succinimide, a hydrolyzed succinimide, an amide, or a triazole, wherein M is covalently attached to Ab;

subscript a is 0 or 1;

subscript y is 0 or 1;

subscript w is 0 or 1;

A is a C<sub>2-10</sub> alkylene optionally substituted with 1-3 R<sup>al</sup>; or a 3 to 20 membered heteroalkylene optionally substituted with 1-3 R<sup>bl</sup>;

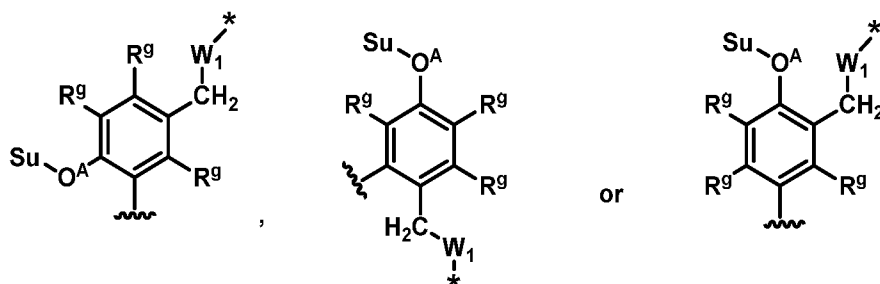
each R<sup>al</sup> is independently selected from the group consisting of: C<sub>1-6</sub> alkyl, C<sub>1-6</sub> haloalkyl, C<sub>1-6</sub> alkoxy, C<sub>1-6</sub> haloalkoxy, halogen, -OH, =O, -NR<sup>dl</sup>R<sup>el</sup>, -(C<sub>1-6</sub> alkylene)-NR<sup>dl</sup>R<sup>el</sup>, -C(=O)NR<sup>dl</sup>R<sup>el</sup>, -C(=O)(C<sub>1-6</sub> alkyl), and -C(=O)O(C<sub>1-6</sub> alkyl);

each R<sup>bl</sup> is independently selected from the group consisting of: C<sub>1-6</sub> alkyl, C<sub>1-6</sub> haloalkyl, C<sub>1-6</sub> alkoxy, C<sub>1-6</sub> haloalkoxy, halogen, -OH, -NR<sup>dl</sup>R<sup>el</sup>, -(C<sub>1-6</sub> alkylene)-NR<sup>dl</sup>R<sup>el</sup>, -C(=O)NR<sup>dl</sup>R<sup>el</sup>, -C(=O)(C<sub>1-6</sub> alkyl), and -C(=O)O(C<sub>1-6</sub> alkyl);

each R<sup>dl</sup> and R<sup>el</sup> are independently hydrogen or C<sub>1-3</sub> alkyl;

W is from 1-6 amino acids; or

W has the structure:



wherein Su is a Sugar moiety;

-O<sup>A</sup>- represents the oxygen atom of a glycosidic bond;

each R<sup>g</sup> is independently hydrogen, halogen, C<sub>1-6</sub> alkoxy, -N(C<sub>1-6</sub> alkyl)<sub>2</sub>, -NHC(=O)(C<sub>1-6</sub> alkyl), -CN, -CF<sub>3</sub>, acyl, carboxamido, C<sub>1-6</sub> alkyl, or -NO<sub>2</sub>;

W<sup>1</sup> is absent, \*-C(=O)-O-, or \*-O-C(=O)-;

~~~~~ represents covalent attachment to A or M;

* represents covalent attachment to Y or X;

Y is a self-immolative moiety, a non-self-immolative releasable moiety, or a non-cleavable moiety;

X is from 1-10 amino acids; or

subscript a is 0 or 1;

subscript y is 0 or 1;

subscript w is 0 or 1;

A is a C₂₋₁₀ alkylene optionally substituted with 1-3 R^{al}; or a 3 to 20 membered heteroalkylene optionally substituted with 1-3 R^{bl};

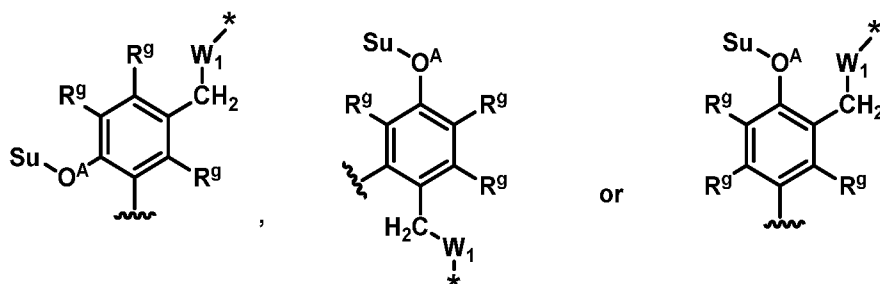
each R^{al} is independently selected from the group consisting of: C₁₋₆ alkyl, C₁₋₆ haloalkyl, C₁₋₆ alkoxy, C₁₋₆ haloalkoxy, halogen, -OH, =O, -NR^{dl}R^{el}, -(C₁₋₆ alkylene)-NR^{dl}R^{el}, -C(=O)NR^{dl}R^{el}, -C(=O)(C₁₋₆ alkyl), and -C(=O)O(C₁₋₆ alkyl);

each R^{bl} is independently selected from the group consisting of: C₁₋₆ alkyl, C₁₋₆ haloalkyl, C₁₋₆ alkoxy, C₁₋₆ haloalkoxy, halogen, -OH, -NR^{dl}R^{el}, -(C₁₋₆ alkylene)-NR^{dl}R^{el}, -C(=O)NR^{dl}R^{el}, -C(=O)(C₁₋₆ alkyl), and -C(=O)O(C₁₋₆ alkyl);

each R^{dl} and R^{el} are independently hydrogen or C₁₋₃ alkyl;

W is from 1-6 amino acids; or

W has the structure:



wherein Su is a Sugar moiety;

-O^A- represents the oxygen atom of a glycosidic bond;

each R^s is independently hydrogen, halogen, C_{1-C6} alkoxy, -N(C_{1-C6} alkyl)₂, -NHC(=O)(C_{1-C6} alkyl), -CN, -CF₃, acyl, carboxamido, C_{1-C6} alkyl, or -NO₂;

W¹ is absent, *-C(=O)-O-, or *-O-C(=O)-;

~~~~~ represents covalent attachment to A or M;

\* represents covalent attachment to Y or X;

Y is a self-immolative moiety, a non-self-immolative releasable moiety, or a non-cleavable moiety;

X is a 4-16 membered heteroalkylene, wherein X is optionally substituted with 1-3 independently selected R<sup>X</sup>;

each  $R^X$  is independently a C<sub>2</sub>-C<sub>6</sub> alkynyl group,  $-NR^{X1}R^{X2}$ , or a C<sub>1</sub>-C<sub>6</sub> alkyl group optionally substituted with hydroxyl,  $-NR^{X1}R^{X2}$ , guanidino, 1 or 2 -CO<sub>2</sub>H groups,  $-C(=O)NR^{X1}R^{X2}$ , urea, phenyl, naphthyl, indolyl, imidazolyl, -SH, -SCH<sub>3</sub>, -SeCH<sub>3</sub>, or 4-hydroxyphenyl optionally substituted with C<sub>2</sub>-C<sub>6</sub> alkenyl; or

two  $R^X$  attached to the same or adjacent carbon atom(s) of X, together with the carbon atom(s) to which they are attached form an unsubstituted 5-6 membered heterocyclyl;

each  $R^{X1}$  and  $R^{X2}$  are independently hydrogen or C<sub>1-6</sub> alkyl; and

L is optionally substituted with a PEG Unit from PEG1 to PEG72.

**[0007]** Some embodiments provide an ADC composition comprising a distribution of ADCs, as described herein. In some embodiments, the composition further comprises at least one pharmaceutically acceptable carrier.

**[0008]** Some embodiments provide a method of treating cancer in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of an ADC, as described herein.

**[0009]** Some embodiments provide a method of treating cancer in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of an ADC composition, as described herein.

**[0010]** Some embodiments provide a method of treating an autoimmune disorder in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of an ADC, as described herein.

**[0011]** Some embodiments provide a method of treating an autoimmune disorder in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of an ADC composition, as described herein.

## BRIEF DESCRIPTION OF THE FIGURES

**[0012]** Figure 1 illustrates the activity of cAC10-PNU antibody-drug conjugates in a SCID mouse xenograft model with L540cy CD30+ Hodgkin lymphoma.

**[0013]** Figure 2 illustrates the activity of cAC10-PNU antibody-drug conjugates in a SCID mouse xenograft model with DEL/BVR MDR+, CD30+ anaplastic large cell lymphoma.

## DETAILED DESCRIPTION

**[0014]** Provided herein are antibody anthracycline-drug conjugates (ADCs) that can elicit a localized cytotoxic response to target cells, and hence, improved activity and reduced off-target toxicity. For example, the ADCs provided herein can elicit reduced off-target toxicity, such as neutropenia, alopecia, and cardiotoxicity, as compared to the toxicity often observed with systemic administration of anthracyclines. See, e.g., Plosker, *Adis Drug Eval.* 2008; Vol. 68, pp. 2535-51. Indeed, since their introduction in the 1960s, anthracycline-induced cardiotoxicity has been a primary limiting factor in the use of these compounds in the clinic. See Cardinale, et al., *Front. Cardiovasc. Med.* 2020; Vol. 7, No. 26, pp. 1-14. The present disclosure provides targeted delivery of anthracyclines to maximize damage to target cells, while avoiding systemic administration of these compounds and their concomitant adverse effects.

### Definitions

**[0015]** Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure belongs. Methods and materials are described herein for use in the present application; other, suitable methods and materials known in the art in some aspects of this disclosure are also used. The materials, methods, and examples are illustrative only and not intended to be limiting. All publications, patent applications, patents, sequences, database entries, and other references mentioned herein are incorporated by reference in their entireties. In case of conflict, the present specification, including definitions, will control. When trade names are used herein, the trade name includes the product formulation, the generic drug, and the active pharmaceutical ingredient(s) of the trade name product, unless otherwise indicated by context.

**[0016]** The terms “a,” “an,” or “the” as used herein not only include aspects with one member, but also include aspects with more than one member. For instance, the singular forms “a,” “an,” and “the” include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to “a linker” includes reference to one or more such linkers, and reference to “the cell” includes reference to a plurality of such cells.

**[0017]** The term “about” when referring to a number or a numerical range means that the number or numerical range referred to is an approximation, for example, within experimental variability and/or statistical experimental error, and thus the number or numerical range may vary



up to  $\pm 10\%$  of the stated number or numerical range. In reference to an ADC composition comprising a distribution of ADCs as described herein, the average number of conjugated anthracycline compounds to an antibody in the composition can be an integer or a non-integer, particularly when the antibody is to be partially loaded. Thus, the term “about” recited prior to an average drug loading value is intended to capture the expected variations in drug loading within an ADC composition.

**[0018]** The term “antibody” as used herein covers intact monoclonal antibodies, polyclonal antibodies, monospecific antibodies, multispecific antibodies (*e.g.*, bispecific antibodies), including intact antibodies and antigen binding antibody fragments, and reduced forms thereof in which one or more of the interchain disulfide bonds are disrupted, that exhibit the desired biological activity and provided that the antigen binding antibody fragments have the requisite number of attachment sites for the desired number of attached groups, such as a linker (L), as described herein. In some embodiments, the linkers are attached via a succinimide or hydrolyzed succinimide to the sulfur atoms of cysteine residues of reduced interchain disulfide bonds and/or cysteine residues introduced by genetic engineering. The native form of an antibody is a tetramer and consists of two identical pairs of immunoglobulin chains, each pair having one light chain and one heavy chain. In each pair, the light and heavy chain variable domains (VL and VH) are together primarily responsible for binding to an antigen. The light chain and heavy chain variable domains consist of a framework region interrupted by three hypervariable regions, also called “complementarity determining regions” or “CDRs.” The light chain and heavy chains also contain constant regions that may be recognized by and interact with the immune system. (*see, e.g.*, Janeway *et al.*, 2001, *Immuno. Biology*, 5th Ed., Garland Publishing, New York). An antibody includes any isotype (*e.g.*, IgG, IgE, IgM, IgD, and IgA) or subclass (*e.g.*, IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) thereof. The antibody is derivable from any suitable species. In some embodiments, the antibody is of human or murine origin, and in some embodiments the antibody is a human, humanized or chimeric antibody. Antibodies can be fucosylated to varying extents or afucosylated.

**[0019]** The term “monoclonal antibody” as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, *i.e.*, the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a

single antigenic site. The modifier “monoclonal” indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies and is not to be construed as requiring production of the antibody by any particular method.

**[0020]** An “intact antibody” is one which comprises an antigen-binding variable region as well as light chain constant domains ( $C_L$ ) and heavy chain constant domains,  $C_{H1}$ ,  $C_{H2}$ ,  $C_{H3}$  and  $C_{H4}$ , as appropriate for the antibody class. The constant domains are either native sequence constant domains (*e.g.*, human native sequence constant domains) or amino acid sequence variants thereof.

**[0021]** An “antibody fragment” comprises a portion of an intact antibody, comprising the antigen-binding or variable region thereof. Antibody fragments of the present disclosure include at least one cysteine residue (natural or engineered) that provides a site for attachment of a linker and/or linker-drug compound. In some embodiments, an antibody fragment includes Fab, Fab', or F(ab')<sub>2</sub>.

**[0022]** An “antigen” is an entity to which an antibody specifically binds.

**[0023]** As used herein the term “engineered cysteine residue” or “eCys residue” refers to a cysteine amino acid or a derivative thereof that is incorporated into an antibody. In those embodiments one or more eCys residues can be incorporated into an antibody, and typically, the eCys residues are incorporated into either the heavy chain or the light chain of an antibody. Generally, incorporation of an eCys residue into an antibody is performed by mutagenizing a nucleic acid sequence of a parent antibody to encode for one or more amino acid residues with a cysteine or a derivative thereof. Suitable mutations include replacement of a desired residue in the light or heavy chain of an antibody with a cysteine or a derivative thereof, incorporation of an additional cysteine or a derivative thereof at a desired location in the light or heavy chain of an antibody, as well as adding an additional cysteine or a derivative thereof to the N- and/or C-terminus of a desired heavy or light chain of an amino acid. Further information can be found in U.S. Pat. No. 9,000,130, the contents of which are incorporated herein in its entirety. Derivatives of cysteine (Cys) include but are not limited to beta-2-Cys, beta-3-Cys, homocysteine, and N-methyl cysteine.

**[0024]** In some embodiments, the antibodies of the present disclosure include those having one or more engineered cysteine (eCys) residues. In some embodiments, derivatives of

cysteine (Cys) include, but are not limited to beta-2-Cys, beta-3-Cys, homocysteine, and N-methyl cysteine.

**[0025]** In some embodiments, the antibodies of the present disclosure include those having one or more engineered lysine (eLys) residues. In some embodiments, one or more native lysine and/or eLys residues are activated prior to conjugation with a drug-linker intermediate (to form an ADC, as described herein). In some embodiments, the activation comprises contacting the antibody with a compound comprising a succinimydyl ester and a functional group selected from the group consisting of: maleimido, pyridyldisulfide and iodoacetamido.

**[0026]** The terms “specific binding” and “specifically binds” mean that the antibody or antibody fragment thereof will bind, in a selective manner, with its corresponding target antigen and not with a multitude of other antigens. Typically, the antibody or antibody fragment binds with an affinity of at least about  $1 \times 10^{-7}$  M, for example,  $10^{-8}$  M to  $10^{-9}$  M,  $10^{-10}$  M,  $10^{-11}$  M, or  $10^{-12}$  M and binds to the predetermined antigen with an affinity that is at least two-fold greater than its affinity for binding to a non-specific antigen (*e.g.*, BSA, casein) other than the predetermined antigen or a closely-related antigen.

**[0027]** The term “amino acid” as used herein, refers to natural, non-natural, non-classical, and proteogenic amino acids. Exemplary amino acids include, but are not limited to alanine, arginine, aspartic acid, asparagine, histidine, glycine, glutamic acid, glutamine, phenylalanine, lysine, leucine, serine, tyrosine, threonine, isoleucine, proline, tryptophan, valine, cysteine, methionine, ornithine,  $\beta$ -alanine, citrulline, ornithine, serine methyl ether, aspartate methyl ester, glutamate methyl ester, homoserine methyl ether, N,N-dimethyl lysine, methionine sulfoxide,  $\gamma$ -carboxy-glutamic acid,  $\alpha$ -aminobutyric acid,  $\alpha$ -aminoisobutyric acid, norvaline, naphthylalanine, *O*-allyl tyrosine, propargylglycine, 2-aminobut-3-ynoic acid, and selenomethionine.

**[0028]** “Natural amino acid” as used herein refers to a naturally occurring amino acid, namely, arginine, glutamine, phenylalanine, tyrosine, tryptophan, lysine, glycine, alanine, histidine, serine, proline, glutamic acid, aspartic acid, threonine, cysteine, methionine, leucine, asparagine, isoleucine, and valine or a residue thereof, in the L or D-configuration.

**[0029]** “Non-natural amino acid” as used herein refers to an alpha-amino-containing acid or residue thereof, which has the backbone structure of a natural amino acid, but has a side chain group attached to the alpha carbon that is not present in natural amino acids.

**[0030]** “Non-classical amino acid” as used herein refers to an amine-containing acid compound that does not have its amine substituent bonded to the carbon alpha to the carboxylic acid and therefore is not an alpha-amino acid. Non-classical amino acids include  $\beta$ -amino acids in which a methylene is inserted between the carboxylic acid and amino functional groups in a natural amino acid or a non-natural amino acid.

**[0031]** “Peptide” as used herein refers to a polymer of two or more amino acids wherein the carboxylic acid group of one amino acid forms an amide bond with the alpha-amino group of the next amino acid in the peptide sequence. Peptides may be comprised of naturally occurring amino acids in the L- or D-configuration and/or non-natural and/or non-classical amino acids.

**[0032]** Peptides may be comprised of naturally occurring amino acids in the L- or D-configuration or unnatural or non-classical amino acids, which include, but are not limited to, ornithine, citrulline, diaminobutyric acid, norleucine, pyrolysine, thienylalanine, naphthylalanine and phenylglycine. Other examples of non-natural and non-classical amino acids are alpha and alpha-disubstituted amino acids, N-alkyl amino acids, lactic acid, halide derivatives of natural amino acids such as trifluorotyrosine, p-Cl-phenylalanine, p-Br-phenylalanine, p-F-phenylalanine, L-allyl-glycine, beta-alanine, L-alpha-amino butyric acid, L-gamma-amino butyric acid, L-alpha-amino isobutyric acid, L-epsilon-amino caproic acid, 7-amino heptanoic acid, L-methionine sulfone, L-norleucine, L-norvaline, p-nitro- L-phenylalanine, L-hydroxyproline, L-thioproline, methyl derivatives of phenylalanine (Phe) such as 4-methyl-Phe, pentamethyl-Phe, L-Phe (4-amino), L-Tyr (methyl), L-Phe (4-isopropyl), L-Tic (1,2,3,4-tetrahydroisoquinoline-3-carboxyl acid), L-diaminopropionic acid, L-Phe (4-benzyl), 2,4-diaminobutyric acid, 4-aminobutyric acid (gamma-Abu), 2-amino butyric acid (alpha-Abu), 6-amino hexanoic acid (epsilon-Ahx), 2-amino isobutyric acid (Aib), 3-amino propionic acid, ornithine, norleucine, norvaline, hydroxyproline, sarcosine, citrulline, homocitrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, fluoroamino acids, beta-methyl amino acids, alpha-methyl amino acids, N-methyl amino acids, naphthyl alanine, and the like.

**[0033]** A “sortase enzyme recognition motif” as used herein, refers to a sequence of natural amino acids recognized by one or more sortase enzymes as a site for transpeptidation. In some embodiments, the recognition motif includes the sequence LPXTG, wherein “X” refers to any natural amino acid. In some embodiments, the recognition motif is as described in any of

Puorger, et al., Biochemistry, 2017; Vol. 56, No. 21, pp. 2641-50; Antos, et al., Curr. Protoc. Prot. Sci. 2009; Ch. 15, Unit 15-3; Guimares, et al., Nat. Protoc. 2013; Vol. 8, pp. 1787-99; or U.S. Patent No. 10,960,083, each of which is incorporated by reference herein solely for purposes of disclosing sortase recognition motifs.

**[0034]** A “sugar moiety” as used herein, refers to a monovalent monosaccharide group, for example, a pyranose or a furanose. A sugar moiety may comprise a hemiacetal or a carboxylic acid (from oxidation of the pendant  $-\text{CH}_2\text{OH}$  group). In some embodiments, the sugar moiety is in the  $\beta$ -D conformation. In some embodiments, the sugar moiety is a glucose, glucuronic acid, or mannose group.

**[0035]** The term “inhibit” or “inhibition of” means to reduce by a measurable amount, or to prevent entirely (e.g., 100% inhibition).

**[0036]** The term “therapeutically effective amount” refers to an amount of an ADC, or a salt thereof (as described herein), that is effective to treat a disease or disorder in a mammal. In the case of cancer, the therapeutically effective amount of the ADC or the compound provides one or more of the following biological effects: reduction of the number of cancer cells; reduction of tumor size; inhibition of cancer cell infiltration into peripheral organs; inhibition of tumor metastasis; inhibition, to some extent, of tumor growth; and/or relief, to some extent, of one or more of the symptoms associated with the cancer. For cancer therapy, efficacy, in some aspects, is measured by assessing the time to disease progression (TTP) and/or determining the response rate (RR).

**[0037]** The term “substantial” or “substantially” refers to a majority, *i.e.* >50% of a population, of a mixture, or a sample, typically more than 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97 %, 98%, or 99%.

**[0038]** The terms “intracellularly cleaved” and “intracellular cleavage” refer to a metabolic process or reaction occurring inside a cell, in which the cellular machinery acts on the ADC or a fragment thereof, to intracellularly release free drug from the ADC, or other degradant products thereof. The moieties resulting from that metabolic process or reaction are thus intracellular metabolites.

**[0039]** The terms “cancer” and “cancerous” refer to or describe the physiological condition or disorder in mammals that is typically characterized by unregulated cell growth. A “tumor” comprises multiple cancerous cells.

**[0040]** An “autoimmune disorder” as used herein refers to a disease or disorder arising from and directed against an individual’s own tissues or proteins.

**[0041]** “Subject” as used herein refers to an individual to which an ADC or ADC composition, as described herein, is administered. Examples of a “subject” include, but are not limited to, a mammal such as a human, rat, mouse, guinea pig, non-human primate, pig, goat, cow, horse, dog, cat, bird and fowl. Typically, a subject is a rat, mouse, dog, non-human primate, or human. In some embodiments, the subject is a human.

**[0042]** The terms “treat” or “treatment,” refer to therapeutic treatment and prophylactic measures to prevent relapse, wherein the object is to inhibit an undesired physiological change or disorder, such as, for example, the development or spread of cancer. For purposes of the present disclosure, beneficial or desired clinical results include, but are not limited to, alleviation of symptoms, diminishment of extent of disease, stabilized (*i.e.*, not worsening) state of disease, delay or slowing of disease progression, amelioration or palliation of the disease state, and remission (whether partial or total), whether detectable or undetectable. “Treatment” in some aspects also means prolonging survival as compared to expected survival if not receiving treatment.

**[0043]** In the context of cancer, the term “treating” includes any or all of: inhibiting growth of cancer cells or of a tumor; inhibiting replication of cancer cells, lessening of overall tumor burden or decreasing the number of cancer cells, and ameliorating one or more symptoms associated with the disease.

**[0044]** In the context of an autoimmune disorder, the term “treating” includes any or all of: inhibiting replication of cells associated with an autoimmune disorder state including, but not limited to, cells that produce an autoimmune antibody, lessening the autoimmune-antibody burden and ameliorating one or more symptoms of an autoimmune disorder.

**[0045]** The term “salt,” as used herein, refers to organic or inorganic salts of a compound, such as a Drug Unit (D) (e.g., an anthracycline), a linker, a drug-linker intermediate, or an ADC, such as those described herein. In some embodiments, the compound contains at least one amino group, and accordingly acid addition salts can be formed with the amino group. Exemplary salts include, but are not limited to, sulfate, trifluoroacetate, citrate, acetate, oxalate, chloride, bromide, iodide, nitrate, bisulfate, phosphate, acid phosphate, isonicotinate, lactate, salicylate, acid citrate, tartrate, oleate, tannate, pantothenate, bitartrate, ascorbate, succinate, maleate, gentisinate, fumarate, gluconate, glucuronate, saccharate, formate, benzoate, glutamate,

methanesulfonate, ethanesulfonate, benzenesulfonate, *p*-toluenesulfonate, and pamoate (*i.e.*, 1,1'-methylene-bis-(2-hydroxy-3-naphthoate)) salts. A salt may involve the inclusion of another molecule such as an acetate ion, a succinate ion, or other counterion. The counterion may be any organic or inorganic moiety that stabilizes the charge on the parent compound. Furthermore, a salt has one or more than one charged atom in its structure. In instances where there are multiple charged atoms as part of the salt, multiple counter ions can be present. Hence, a salt can have one or more charged atoms and/or one or more counterions. A "pharmaceutically acceptable salt" is one that is suitable for administration to a subject as described herein and in some aspects includes salts as described by P. H. Stahl and C. G. Wermuth, editors, *Handbook of Pharmaceutical Salts: Properties, Selection and Use*, Weinheim/Zürich:Wiley-VCH/VHCA, 2002, the list for which is specifically incorporated by reference in its entirety. In some embodiments, the ADCs described herein are present in the form of a pharmaceutically acceptable salt. In some embodiments, the compounds described herein are present in the form of a pharmaceutically acceptable salt.

**[0046]** The term "anthracycline," as used herein refers to a class of compounds that contain a fused tetracyclic ring system and are isolated from certain types of *Streptomyces* bacteria, such as *S. peucetius*. This term also includes derivatives (e.g., semisynthetic derivatives) and metabolites of isolated anthracyclines. Anthracyclines include, but are not limited to doxorubicin, daunorubicin, nemorubicin, idrarubicin, epirubicin, aclarubicin, amrubicin, pirarubicin, valrubicin, doxazolidine, carubicin, mitoxantrone, and PNU-159682.

**[0047]** The term "tautomer," as used herein refers to compounds whose structures differ markedly in arrangement of atoms, but which exist in easy and rapid equilibrium, and it is to be understood that compounds provided herein may be depicted as different tautomers, and when compounds have tautomeric forms, all tautomeric forms are intended to be within the scope of the disclosure, and the naming of the compounds does not exclude any tautomer.

**[0048]** The term "optionally substituted," refers to an indicated group being either substituted or unsubstituted.

**[0049]** The term "alkyl" refers to an unsubstituted straight chain or branched, saturated hydrocarbon having the indicated number of carbon atoms (e.g., "C<sub>1</sub>-C<sub>4</sub> alkyl," "C<sub>1</sub>-C<sub>6</sub> alkyl," "C<sub>1</sub>-C<sub>8</sub> alkyl," or "C<sub>1</sub>-C<sub>10</sub>" alkyl have from 1 to 4, to 6, 1 to 8, or 1 to 10 carbon atoms, respectively) and is derived by the removal of one hydrogen atom from the parent alkane. Representative straight chain "C<sub>1</sub>-C<sub>8</sub> alkyl" groups include, but are not limited to, methyl, ethyl, n-propyl, n-butyl,

n-pentyl, n-hexyl, n-heptyl and n-octyl; while branched C<sub>1</sub>-C<sub>8</sub> alkyls include, but are not limited to, isopropyl, *sec*-butyl, isobutyl, *tert*-butyl, isopentyl, and 2-methylbutyl.

**[0050]** The term “alkylene” refers to a bivalent unsubstituted saturated branched or straight chain hydrocarbon of the stated number of carbon atoms (e.g., a C<sub>1</sub>-C<sub>6</sub> alkylene has from 1 to 6 carbon atoms) and having two monovalent centers derived by the removal of two hydrogen atoms from the same or two different carbon atoms of the parent alkane. Alkylene groups can be substituted with 1-6 fluoro groups, for example, on the carbon backbone (as -CHF- or -CF<sub>2</sub>-) or on terminal carbons of straight chain or branched alkyls (such as -CHF<sub>2</sub> or -CF<sub>3</sub>). Alkylene groups include but are not limited to: methylene (-CH<sub>2</sub>-), ethylene (-CH<sub>2</sub>CH<sub>2</sub>-), n-propylene (-CH<sub>2</sub>CH<sub>2</sub>CH<sub>2</sub>-), n-propylene (-CH<sub>2</sub>CH<sub>2</sub>CH<sub>2</sub>-), n-butylene (-CH<sub>2</sub>CH<sub>2</sub>CH<sub>2</sub>CH<sub>2</sub>-), difluoromethylene (-CF<sub>2</sub>-), tetrafluoroethylene (-CF<sub>2</sub>CF<sub>2</sub>-), and the like.

**[0051]** The term “alkynyl” refers to an unsubstituted straight chain or branched, hydrocarbon having at least one carbon-carbon triple bond and the indicated number of carbon atoms (e.g., “C<sub>2</sub>-C<sub>8</sub> alkynyl” or “C<sub>2</sub>-C<sub>10</sub>” alkynyl have from 2 to 8 or 2 to 10 carbon atoms, respectively). When the number of carbon atoms is not indicated, the alkynyl group has from 2 to 6 carbon atoms.

**[0052]** The term “heteroalkyl” refers to a stable straight or branched chain saturated hydrocarbon having the stated number of total atoms and at least one (e.g., 1 to 15) heteroatom selected from the group consisting of O, N, Si and S. The carbon and heteroatoms of the heteroalkyl group can be oxidized (e.g., to form ketones, N-oxides, sulfones, and the like) and the nitrogen atoms can be quaternized. The heteroatom(s) can be placed at any interior position of the heteroalkyl group and/or at any terminus of the heteroalkyl group, including termini of branched heteroalkyl groups), and/or at the position at which the heteroalkyl group is attached to the remainder of the molecule. Heteroalkyl groups can be substituted with 1-6 fluoro groups, for example, on the carbon backbone (as -CHF- or -CF<sub>2</sub>-) or on terminal carbons of straight chain or branched heteroalkyls (such as -CHF<sub>2</sub> or -CF<sub>3</sub>). Examples of heteroalkyl groups include, but are not limited to, -CH<sub>2</sub>-CH<sub>2</sub>-O-CH<sub>3</sub>, -CH<sub>2</sub>-CH<sub>2</sub>-NH-CH<sub>3</sub>, -CH<sub>2</sub>-CH<sub>2</sub>-N(CH<sub>3</sub>)<sub>2</sub>, -C(=O)-NH-CH<sub>2</sub>-CH<sub>2</sub>-NH-CH<sub>3</sub>, -C(=O)-N(CH<sub>3</sub>)-CH<sub>2</sub>-CH<sub>2</sub>-N(CH<sub>3</sub>)<sub>2</sub>, -C(=O)-NH-CH<sub>2</sub>-CH<sub>2</sub>-NH-C(=O)-CH<sub>2</sub>-CH<sub>3</sub>, -C(=O)-N(CH<sub>3</sub>)-CH<sub>2</sub>-CH<sub>2</sub>-N(CH<sub>3</sub>)-C(=O)-CH<sub>2</sub>-CH<sub>3</sub>, -O-CH<sub>2</sub>-CH<sub>2</sub>-CH<sub>2</sub>-NH(CH<sub>3</sub>), -O-CH<sub>2</sub>-CH<sub>2</sub>-CH<sub>2</sub>-N(CH<sub>3</sub>)<sub>2</sub>, -O-CH<sub>2</sub>-CH<sub>2</sub>-CH<sub>2</sub>-NH-C(=O)-CH<sub>2</sub>-CH<sub>3</sub>, -O-CH<sub>2</sub>-CH<sub>2</sub>-CH<sub>2</sub>-N(CH<sub>3</sub>)-C(=O)-CH<sub>2</sub>-CH<sub>3</sub>, -CH<sub>2</sub>-CH<sub>2</sub>-CH<sub>2</sub>-NH(CH<sub>3</sub>), -O-CH<sub>2</sub>-CH<sub>2</sub>-CH<sub>2</sub>-N(CH<sub>3</sub>)<sub>2</sub>, -CH<sub>2</sub>-CH<sub>2</sub>-CH<sub>2</sub>-NH-C(=O)-CH<sub>2</sub>-



CH<sub>3</sub>, -CH<sub>2</sub>-CH<sub>2</sub>-CH<sub>2</sub>-N(CH<sub>3</sub>)-C(=O)-CH<sub>2</sub>-CH<sub>3</sub>, -CH<sub>2</sub>-S-CH<sub>2</sub>-CH<sub>3</sub>, -CH<sub>2</sub>-CH<sub>2</sub>-S(O)-CH<sub>3</sub>, -NH-CH<sub>2</sub>-CH<sub>2</sub>-NH-C(=O)-CH<sub>2</sub>-CH<sub>3</sub>, -CH<sub>2</sub>-CH<sub>2</sub>-S(O)<sub>2</sub>-CH<sub>3</sub>, -CH<sub>2</sub>-CH<sub>2</sub>-O-CF<sub>3</sub>, and -Si(CH<sub>3</sub>)<sub>3</sub>. Up to two heteroatoms may be consecutive, such as, for example, -CH<sub>2</sub>-NH-OCH<sub>3</sub> and -CH<sub>2</sub>-O-Si(CH<sub>3</sub>)<sub>3</sub>. A terminal polyethylene glycol (PEG) moiety is a type of heteroalkyl group.

**[0053]** The term "heteroalkylene" refers to a bivalent unsubstituted straight or branched group derived from heteroalkyl (as defined herein). Examples of heteroalkylene groups include, but are not limited to, -NH-CH<sub>2</sub>-CH<sub>2</sub>-NH-, -NH-CH<sub>2</sub>-CH<sub>2</sub>-CH<sub>2</sub>-NH-, -NH-CH<sub>2</sub>-CH<sub>2</sub>-CH<sub>2</sub>-CH<sub>2</sub>-NH-, -CH<sub>2</sub>-CH<sub>2</sub>-O-CH<sub>2</sub>-, -CH<sub>2</sub>-CH<sub>2</sub>-O-CF<sub>2</sub>-, -CH<sub>2</sub>-CH<sub>2</sub>-NH-CH<sub>2</sub>-, -C(=O)-NH-CH<sub>2</sub>-CH<sub>2</sub>-NH-CH<sub>2</sub>-, -C(=O)-N(CH<sub>3</sub>)-CH<sub>2</sub>-CH<sub>2</sub>-N(CH<sub>3</sub>)-CH<sub>2</sub>-, -C(=O)-NH-CH<sub>2</sub>-CH<sub>2</sub>-NH-C(=O)-CH<sub>2</sub>-CH<sub>2</sub>-, -C(=O)-N(CH<sub>3</sub>)-CH<sub>2</sub>-CH<sub>2</sub>-N(CH<sub>3</sub>)-C(=O)-CH<sub>2</sub>-CH<sub>2</sub>-, -O-CH<sub>2</sub>-CH<sub>2</sub>-CH<sub>2</sub>-NH-CH<sub>2</sub>-, -O-CH<sub>2</sub>-CH<sub>2</sub>-CH<sub>2</sub>-N(CH<sub>3</sub>)-CH<sub>2</sub>-, -O-CH<sub>2</sub>-CH<sub>2</sub>-CH<sub>2</sub>-NH-C(=O)-CH<sub>2</sub>-CH<sub>2</sub>-, -O-CH<sub>2</sub>-CH<sub>2</sub>-CH<sub>2</sub>-N(CH<sub>3</sub>)-C(=O)-CH<sub>2</sub>-CH<sub>2</sub>-, -CH<sub>2</sub>-CH<sub>2</sub>-CH<sub>2</sub>-NH-CH<sub>2</sub>-, -CH<sub>2</sub>-CH<sub>2</sub>-CH<sub>2</sub>-N(CH<sub>3</sub>)-CH<sub>2</sub>-, -CH<sub>2</sub>-CH<sub>2</sub>-CH<sub>2</sub>-NH-C(=O)-CH<sub>2</sub>-CH<sub>2</sub>-, -CH<sub>2</sub>-CH<sub>2</sub>-CH<sub>2</sub>-N(CH<sub>3</sub>)-C(=O)-CH<sub>2</sub>-CH<sub>2</sub>-, -CH<sub>2</sub>-CH<sub>2</sub>-NH-C(=O)-, -CH<sub>2</sub>-CH<sub>2</sub>-N(CH<sub>3</sub>)-CH<sub>2</sub>-, -CH<sub>2</sub>-CH<sub>2</sub>-N<sup>+</sup>(CH<sub>3</sub>)<sub>2</sub>-, -NH-CH<sub>2</sub>-CH<sub>2</sub>(NH<sub>2</sub>)-CH<sub>2</sub>-, and -NH-CH<sub>2</sub>-CH<sub>2</sub>(NHCH<sub>3</sub>)-CH<sub>2</sub>-. A bivalent polyethylene glycol (PEG) moiety is a type of heteroalkylene group. In some embodiments, heteroalkylene groups do not include poly-glycine chains, such as di-glycine, tri-glycine, tetra-glycine, and higher order polyglycine peptides. In some embodiments, heteroalkylene groups are straight chain groups derived from heteroalkyl (as defined herein), and do not include branched groups derived from heteroalkyl (as defined herein).

**[0054]** The term "alkoxy" refers to an alkyl group, as defined herein, which is attached to a molecule via an oxygen atom. For example, alkoxy groups include, but are not limited to methoxy, ethoxy, n-propoxy, iso-propoxy, n-butoxy, sec-butoxy, tert-butoxy, n-pentoxy and n-hexoxy.

**[0055]** The term "haloalkyl" refers to an unsubstituted straight chain or branched, saturated hydrocarbon having the indicated number of carbon atoms (*e.g.*, "C<sub>1</sub>-C<sub>4</sub> alkyl," "C<sub>1</sub>-C<sub>6</sub> alkyl," "C<sub>1</sub>-C<sub>8</sub> alkyl," or "C<sub>1</sub>-C<sub>10</sub>" alkyl have from 1 to 4, to 6, 1 to 8, or 1 to 10 carbon atoms, respectively) wherein at least one hydrogen atom of the alkyl group is replaced by a halogen (*e.g.*, fluoro, chloro, bromo, or iodo). When the number of carbon atoms is not indicated, the haloalkyl group has from 1 to 6 carbon atoms. Representative C<sub>1-6</sub> haloalkyl groups include, but are not limited to, trifluoromethyl, 2,2,2-trifluoroethyl, and 1-chloroisopropyl.

**[0056]** The term "cycloalkyl" refers to a cyclic, saturated or partially unsaturated hydrocarbon having the indicated number of carbon atoms (e.g., "C<sub>3-8</sub> cycloalkyl" or "C<sub>3-6</sub>" cycloalkyl have from 3 to 8 or 3 to 6 carbon atoms, respectively). When the number of carbon atoms is not indicated, the cycloalkyl group has from 3 to 6 carbon atoms. Cycloalkyl groups include bridged, fused, and spiro ring systems, and bridged bicyclic systems where one ring is aromatic and the other is unsaturated. Representative "C<sub>3-6</sub> cycloalkyl" groups include, cyclopropyl, cyclobutyl, cyclopentyl, and cyclohexyl. Cycloalkenyl and cycloalkynyl are types of cycloalkyl groups having at least one double bond, or at least one triple bond, respectively.

**[0057]** The term "aryl" refers to an unsubstituted monovalent carbocyclic aromatic hydrocarbon group of 6-10 carbon atoms derived by the removal of one hydrogen atom from a single carbon atom of a parent aromatic ring system. Aryl groups include, but are not limited to, phenyl, naphthyl, anthracenyl, biphenyl, and the like.

**[0058]** The terms "heterocycle" and "heterocyclyl" are used interchangeably herein and refer to a saturated or partially unsaturated ring or a multiple condensed ring system, including bridged, fused, and spiro ring systems, in which one or more ring atoms is a heteroatom (e.g., oxygen, nitrogen, and sulfur). Heterocycles can be described by the total number of atoms in the ring system, for example a 3-10 membered heterocycle has 3 to 10 total ring atoms. The term includes single saturated or partially unsaturated rings (e.g., 3, 4, 5, 6 or 7-membered rings) from about 1 to 6 carbon atoms and from about 1 to 3 heteroatoms selected from the group consisting of oxygen, nitrogen and sulfur in the ring. The ring may be substituted with one or more (e.g., 1, 2 or 3) oxo groups and the sulfur and nitrogen atoms may also be present in their oxidized forms. Such rings include but are not limited to azetidiny, tetrahydrofuranyl and piperidiny. The terms "heterocycle" and "heterocyclyl" also include multiple condensed ring systems (e.g., ring systems comprising 2, 3 or 4 rings) wherein a single heterocycle ring (as defined above) can be condensed with one or more heterocycles (e.g., decahydronaphthyridiny), carbocycles (e.g., decahydroquinoly) or aryls. The rings of a multiple condensed ring system can be connected to each other via fused, spiro and bridged bonds when allowed by valency requirements. It is to be understood that the point of attachment of a multiple condensed ring system (as defined above for a heterocycle) can be at any position of the multiple condensed ring system including a heterocycle, aryl and carbocycle portion of the ring. It is also to be understood that the point of attachment for a heterocycle or heterocycle multiple condensed ring system can be at any suitable atom of the

heterocycle or heterocycle multiple condensed ring system including a carbon atom and a heteroatom (e.g., a nitrogen). Exemplary heterocycles include, but are not limited to aziridinyl, azetidiny, pyrrolidinyl, piperidinyl, homopiperidinyl, morpholinyl, thiomorpholinyl, piperazinyl, tetrahydrofuranyl, dihydrooxazolyl, tetrahydropyranyl, tetrahydrothiopyranyl, 1,2,3,4-tetrahydroquinolyl, benzoxazinyl, dihydrooxazolyl, chromanyl, 1,2-dihydropyridinyl, 2,3-dihydrobenzofuranyl, 1,3-benzodioxolyl, and 1,4-benzodioxanyl.

**[0059]** The term “heteroaryl” refers to an aromatic hydrocarbon ring system with at least one heteroatom within a single ring or within a fused ring system, selected from the group consisting of O, N and S. The ring or ring system has  $4n + 2$  electrons in a conjugated  $\pi$  system where all atoms contributing to the conjugated  $\pi$  system are in the same plane. In some embodiments, heteroaryl groups have 5-10 total ring atoms and 1, 2, or 3 heteroatoms (referred to as a “5-10 membered heteroaryl”). Heteroaryl groups include, but are not limited to, imidazole, triazole, thiophene, furan, pyrrole, benzimidazole, pyrazole, pyrazine, pyridine, pyrimidine, and indole.

**[0060]** The term “hydroxyl” refers to an –OH group.

**[0061]** The term “cyano” refers to a –CN group.

**[0062]** The term “oxo” refers to a =O group.

**[0063]** The term “acyl” refers to an alkyl, haloalkyl, alkenyl, alkynyl, aryl cycloalkyl, heteroaryl, or heterocyclyl group, as defined herein, connected to the remainder of the compound by a C=O (carbonyl) group.

**[0064]** The term “carboxamido” refers to a –C(=O)NRR' group, wherein R and R' are independently selected from the group consisting of hydrogen, alkyl, alkenyl, alkynyl, aryl cycloalkyl, heteroaryl, and heterocyclyl, as defined herein.

**[0065]** It will be appreciated by those skilled in the art that compounds described herein having a chiral center may exist in and be isolated in optically active and racemic forms.

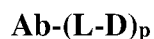
**[0066]** As used herein, the term “free drug” refers to a biologically active species that is not covalently attached to an antibody. Accordingly, free drug refers to a compound as it exists immediately upon cleavage from the ADC. The release mechanism can be via a cleavable linker in the ADC, or via intracellular conversion or metabolism of the ADC. The free drug is a pharmacologically active species which is capable of exerting the desired biological effect. In some embodiments, the pharmacologically active species is the parent drug alone. In some

embodiments, the pharmacologically active species is the parent drug bonded to a component or vestige of the ADC (e.g., a component of the linker, succinimide, hydrolyzed succinimide, and/or antibody that has not undergone subsequent intracellular metabolism). In some embodiments, free drug refers to an anthracycline compound, or a salt thereof, as described herein, for example, wherein one or more of X, Y, W, A, and M are absent. In some embodiments, free drug refers to PNU-159682, or a salt thereof.

**[0067]** As used herein, the term “Drug Unit” refers to the free drug that is conjugated to an antibody in an ADC, as described herein.

#### Antibody Drug Conjugates (ADCs)

**[0068]** Some embodiments provide an antibody drug conjugate (ADC) having the structure:



or a salt thereof;

wherein:

Ab is an antibody;

wherein each L is covalently attached to Ab via a sulfur atom of a cysteine residue or an  $\epsilon$ -amino group of a lysine residue in Ab;

subscript p is an integer from 1 to 16;

each D is an anthracycline;

each L is a linker that has the formula  $-\text{M}-(\text{A})_a-(\text{W})_w-(\text{Y})_y-(\text{X})-$ , wherein:

M is a succinimide, a hydrolyzed succinimide, an amide, or a triazole, wherein M is covalently attached to Ab;

subscript a is 0 or 1;

subscript y is 0 or 1;

subscript w is 0 or 1;

A is a  $\text{C}_{2-10}$  alkylene optionally substituted with 1-3  $\text{R}^{\text{al}}$ ; or a 3 to 20 membered heteroalkylene optionally substituted with 1-3  $\text{R}^{\text{bl}}$ ;

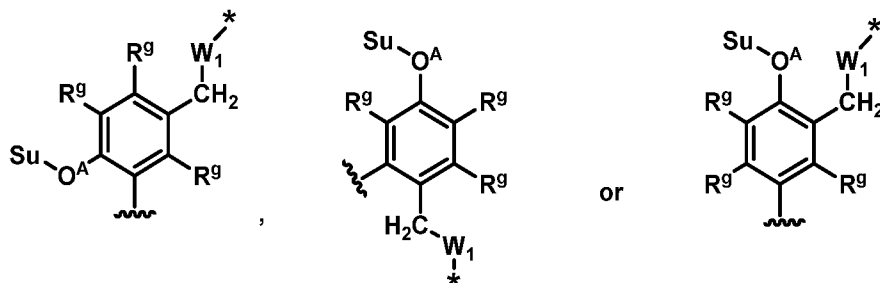
each  $\text{R}^{\text{al}}$  is independently selected from the group consisting of:  $\text{C}_{1-6}$  alkyl,  $\text{C}_{1-6}$  haloalkyl,  $\text{C}_{1-6}$  alkoxy,  $\text{C}_{1-6}$  haloalkoxy, halogen,  $-\text{OH}$ ,  $=\text{O}$ ,  $-\text{NR}^{\text{dl}}\text{R}^{\text{el}}$ ,  $-(\text{C}_{1-6} \text{ alkylene})-\text{NR}^{\text{dl}}\text{R}^{\text{el}}$ ,  $-\text{C}(=\text{O})\text{NR}^{\text{dl}}\text{R}^{\text{el}}$ ,  $-\text{C}(=\text{O})(\text{C}_{1-6} \text{ alkyl})$ , and  $-\text{C}(=\text{O})\text{O}(\text{C}_{1-6} \text{ alkyl})$ ;

each  $R^{b1}$  is independently selected from the group consisting of:  $C_{1-6}$  alkyl,  $C_{1-6}$  haloalkyl,  $C_{1-6}$  alkoxy,  $C_{1-6}$  haloalkoxy, halogen,  $-OH$ ,  $-NR^{d1}R^{e1}$ ,  $-(C_{1-6} \text{ alkylene})-NR^{d1}R^{e1}$ ,  $-C(=O)NR^{d1}R^{e1}$ ,  $-C(=O)(C_{1-6} \text{ alkyl})$ , and  $-C(=O)O(C_{1-6} \text{ alkyl})$ ;

each  $R^{d1}$  and  $R^{e1}$  are independently hydrogen or  $C_{1-3}$  alkyl;

W is from 1-6 amino acids; or

W has the structure:



wherein Su is a Sugar moiety;

$-O^A-$  represents the oxygen atom of a glycosidic bond;

each  $R^g$  is independently hydrogen, halogen,  $C_1-C_6$  alkoxy,  $-N(C_1-C_6 \text{ alkyl})_2$ ,  $-NHC(=O)(C_1-C_6 \text{ alkyl})$ ,  $-CN$ ,  $-CF_3$ , acyl, carboxamido,  $C_1-C_6$  alkyl, or  $-NO_2$ ;

$W^1$  is absent,  $^*-C(=O)-O-$ , or  $^*-O-C(=O)-$ ;

~~~~~ represents covalent attachment to A or M;

* represents covalent attachment to Y or X;

Y is a self-immolative moiety, a non-self-immolative releasable moiety, or a non-cleavable moiety;

X is from 1-10 amino acids; or

X is a 4-16 membered heteroalkylene, wherein X is optionally substituted with 1-3 independently selected R^X ;

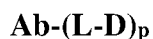
each R^X is independently a C_2-C_6 alkynyl group, $-NR^{X1}R^{X2}$, or a C_1-C_6 alkyl group optionally substituted with hydroxyl, $-NR^{X1}R^{X2}$, guanidino, 1 or 2 $-CO_2H$ groups, $-C(=O)NR^{X1}R^{X2}$, urea, phenyl, naphthyl, indolyl, imidazolyl, $-SH$, $-SCH_3$, $-SeCH_3$, or 4-hydroxyphenyl optionally substituted with C_2-C_6 alkenyl; or

two R^X attached to the same or adjacent carbon atom(s) of X, together with the carbon atom(s) to which they are attached form an unsubstituted 5-6 membered heterocyclyl;

each R^{X1} and R^{X2} are independently hydrogen or C_{1-6} alkyl; and

L is optionally substituted with a PEG Unit from PEG1 to PEG72.

[0069] Some embodiments provide an antibody drug conjugate (ADC) having the structure:



or a salt thereof;

wherein:

Ab is an antibody;

wherein each L is covalently attached to Ab via a sulfur atom of a cysteine residue or an ϵ -amino group of a lysine residue in Ab;

subscript p is an integer from 1 to 16;

each D is an anthracycline;

each L is a linker that has the formula $-\text{M}-(\text{A})_a-(\text{W})_w-(\text{Y})_y-(\text{X})-$, wherein:

M is a succinimide, a hydrolyzed succinimide, an amide, or a triazole, wherein M is covalently attached to Ab;

subscript a is 0 or 1;

subscript y is 0 or 1;

subscript w is 0 or 1;

A is a C_{2-10} alkylene optionally substituted with 1-3 R^{a1} ; or a 3 to 20 membered heteroalkylene optionally substituted with 1-3 R^{b1} ;

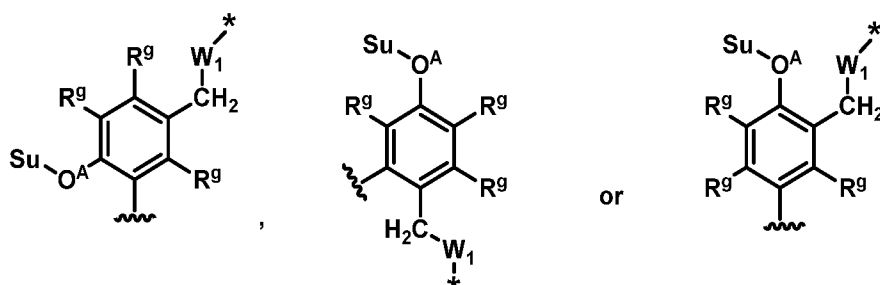
each R^{a1} is independently selected from the group consisting of: C_{1-6} alkyl, C_{1-6} haloalkyl, C_{1-6} alkoxy, C_{1-6} haloalkoxy, halogen, -OH, =O, $-\text{NR}^{d1}\text{R}^{e1}$, $-(C_{1-6} \text{ alkylene})-\text{NR}^{d1}\text{R}^{e1}$, $-\text{C}(=\text{O})\text{NR}^{d1}\text{R}^{e1}$, $-\text{C}(=\text{O})(C_{1-6} \text{ alkyl})$, and $-\text{C}(=\text{O})\text{O}(C_{1-6} \text{ alkyl})$;

each R^{b1} is independently selected from the group consisting of: C_{1-6} alkyl, C_{1-6} haloalkyl, C_{1-6} alkoxy, C_{1-6} haloalkoxy, halogen, -OH, $-\text{NR}^{d1}\text{R}^{e1}$, $-(C_{1-6} \text{ alkylene})-\text{NR}^{d1}\text{R}^{e1}$, $-\text{C}(=\text{O})\text{NR}^{d1}\text{R}^{e1}$, $-\text{C}(=\text{O})(C_{1-6} \text{ alkyl})$, and $-\text{C}(=\text{O})\text{O}(C_{1-6} \text{ alkyl})$;

each R^{d1} and R^{e1} are independently hydrogen or C_{1-3} alkyl;

W is from 1-6 amino acids; or

W has the structure:



wherein Su is a Sugar moiety;

$-O^A$ represents the oxygen atom of a glycosidic bond;

each R^g is independently hydrogen, halogen, C_1 - C_6 alkoxy, $-N(C_1$ - C_6 alkyl) $_2$, $-NHC(=O)(C_1$ - C_6 alkyl), $-CN$, $-CF_3$, acyl, carboxamido, C_1 - C_6 alkyl, or $-NO_2$;

W^1 is absent, $^*-C(=O)-O-$, or $^*-O-C(=O)-$;

represents covalent attachment to A or M;

* represents covalent attachment to Y or X;

Y is a self-immolative moiety, a non-self-immolative releasable moiety, or a non-cleavable moiety;

X is a 4-16 membered heteroalkylene, wherein X is optionally substituted with 1-3 independently selected R^X ;

each R^X is independently a C_2 - C_6 alkynyl group, $-NR^{X1}R^{X2}$, or a C_1 - C_6 alkyl group optionally substituted with hydroxyl, $-NR^{X1}R^{X2}$, guanidino, 1 or 2 $-CO_2H$ groups, $-C(=O)NR^{X1}R^{X2}$, urea, phenyl, naphthyl, indolyl, imidazolyl, $-SH$, $-SCH_3$, $-SeCH_3$, or 4-hydroxyphenyl optionally substituted with C_2 - C_6 alkenyl; or

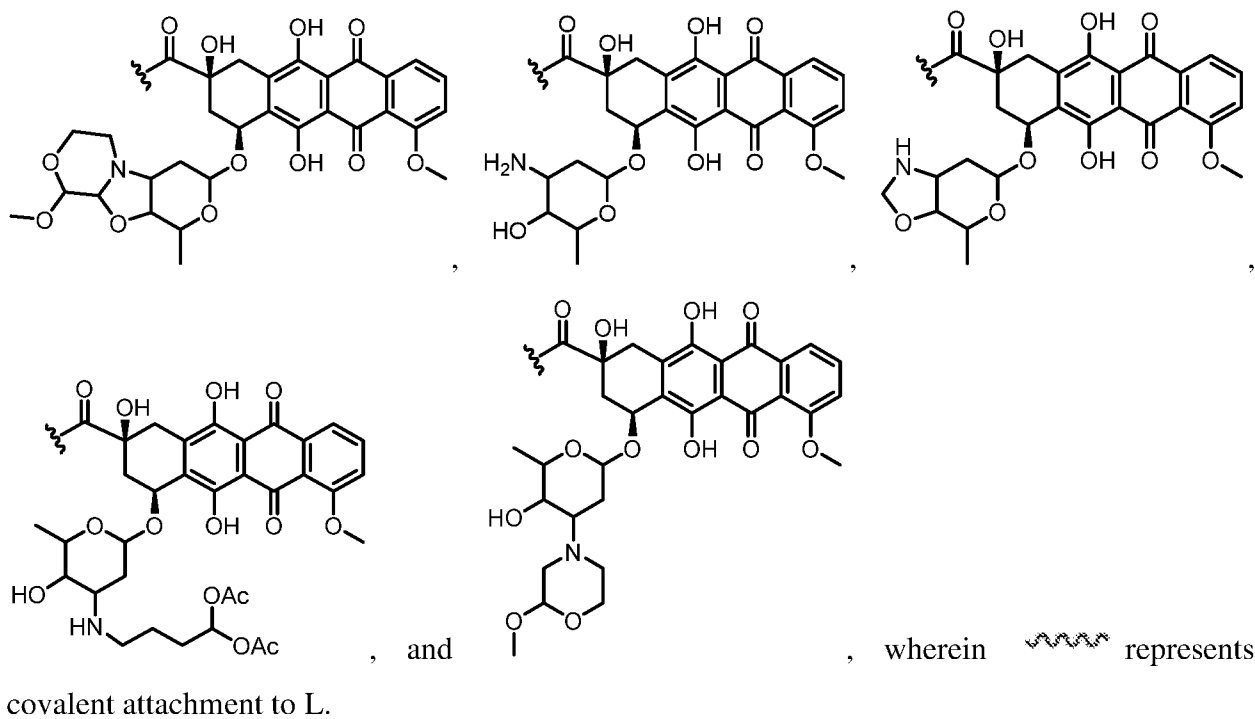
two R^X attached to the same or adjacent carbon atom(s) of X, together with the carbon atom(s) to which they are attached form an unsubstituted 5-6 membered heterocyclyl;

each R^{X1} and R^{X2} are independently hydrogen or C_{1-6} alkyl; and

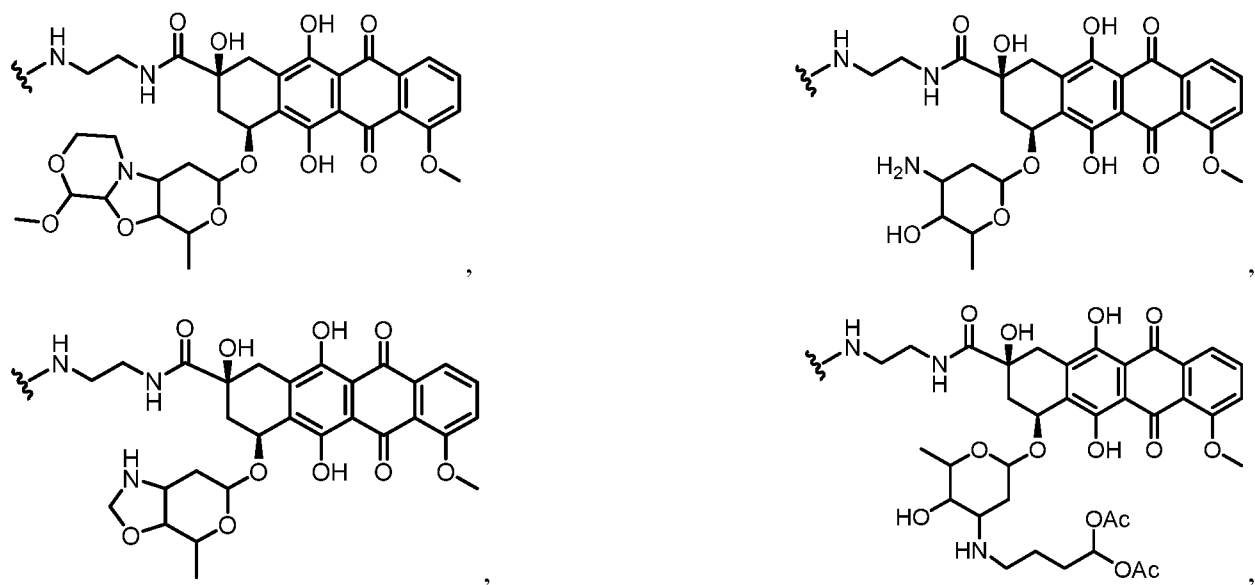
L is optionally substituted with a PEG Unit from PEG1 to PEG72.

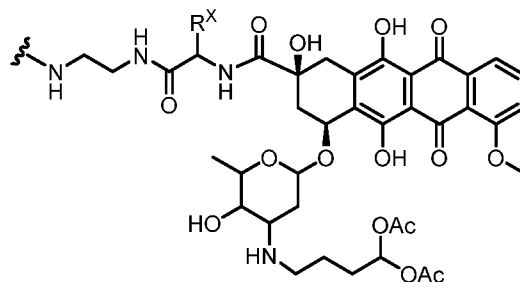
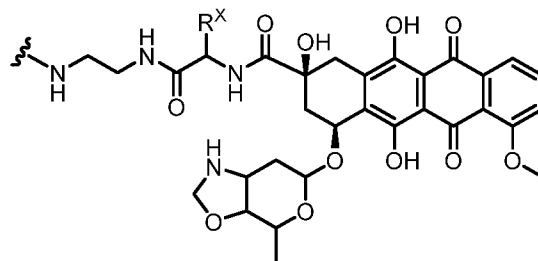
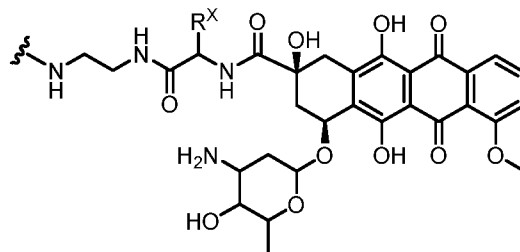
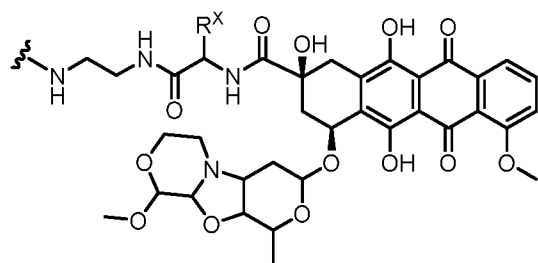
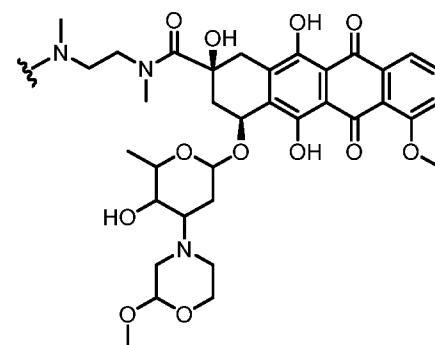
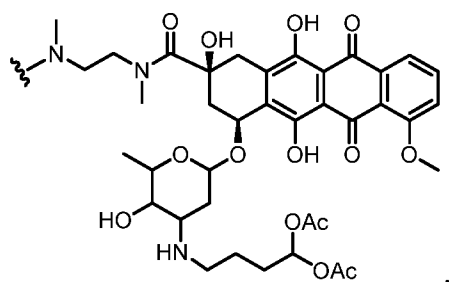
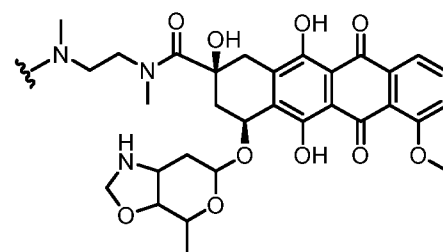
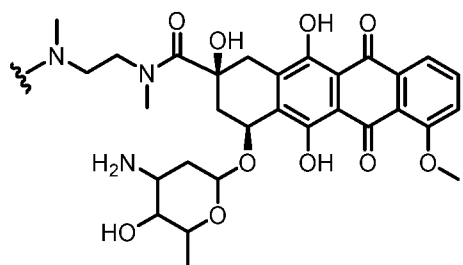
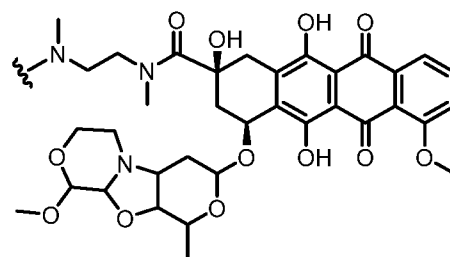
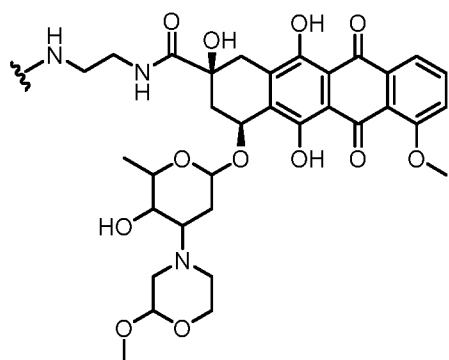
[0070] In some embodiments, the anthracycline is selected from the group consisting of doxorubicin, daunorubicin, nemorubicin, idrubicin, epirubicin, aclarubicin, amrubicin, pirarubicin, valrubicin, doxazolidine, carubicin, mitoxantrone, and PNU-159682.

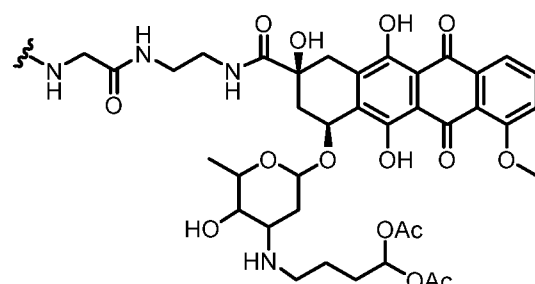
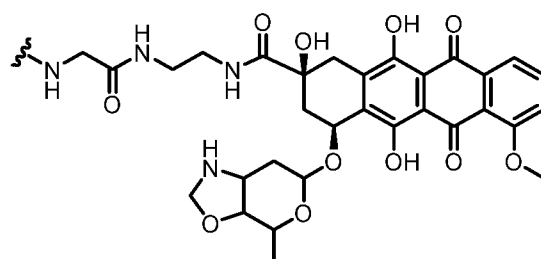
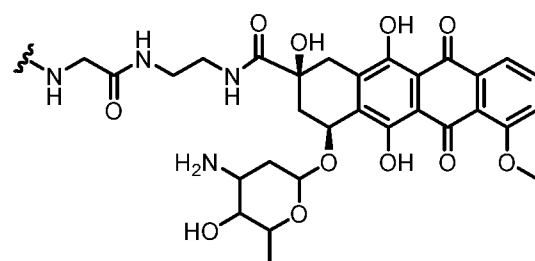
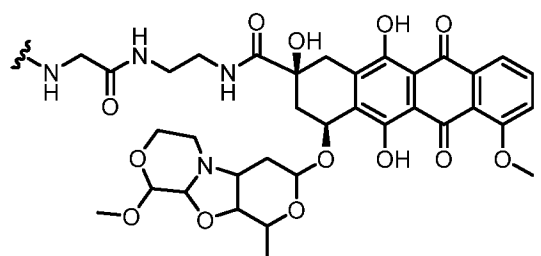
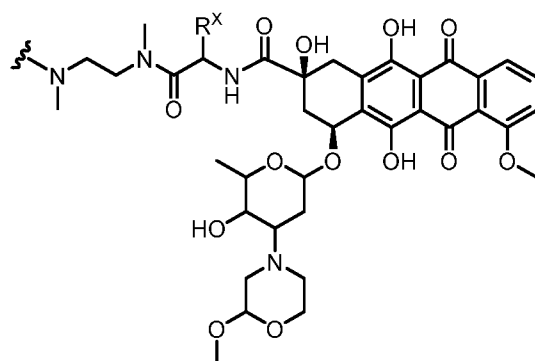
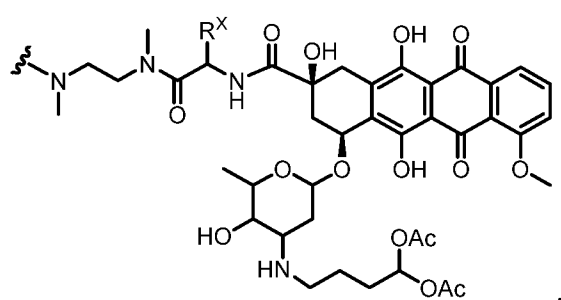
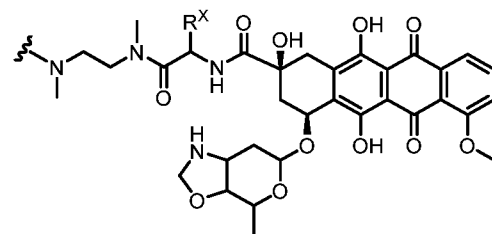
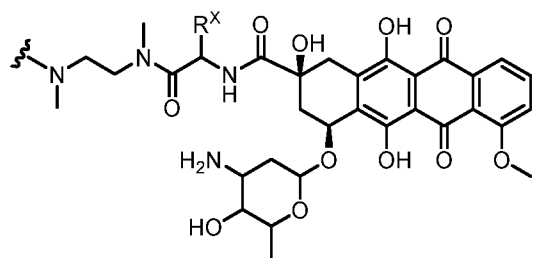
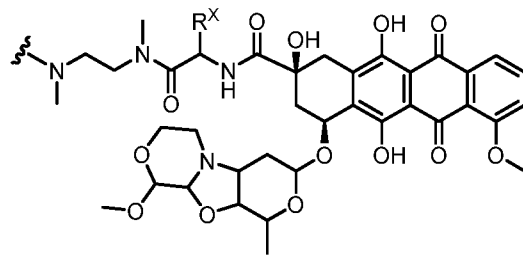
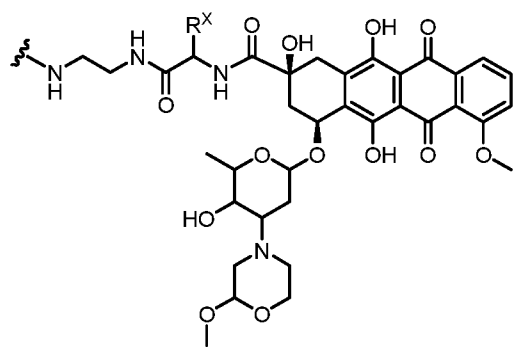
[0071] In some embodiments, each D is selected from the group consisting of:

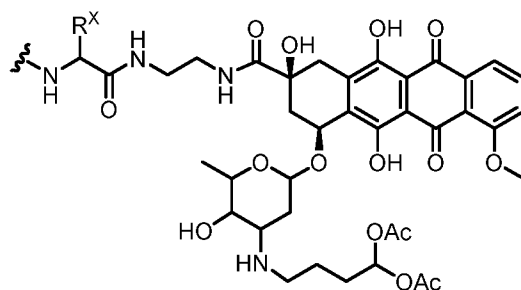
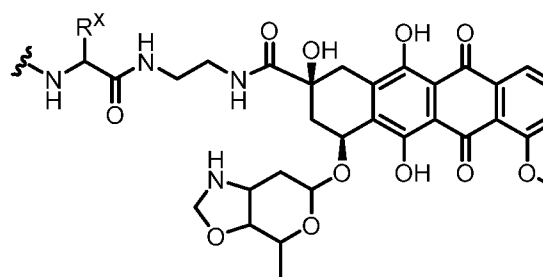
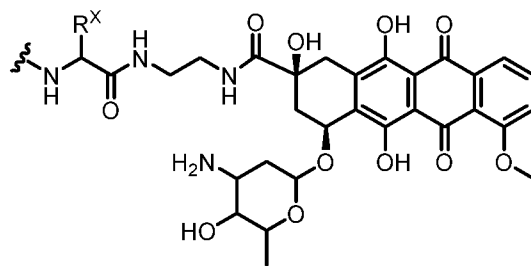
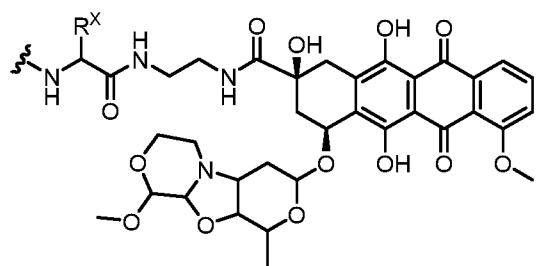
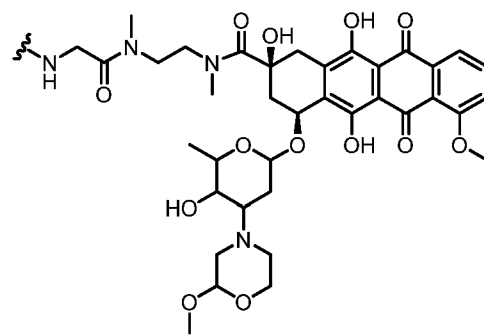
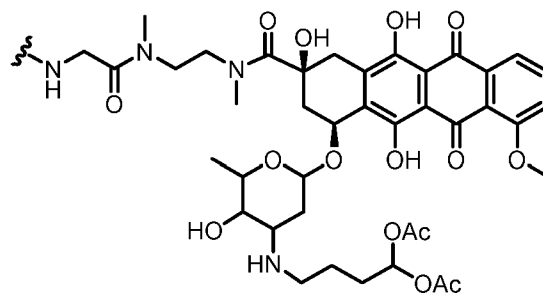
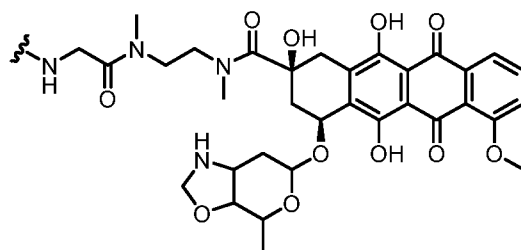
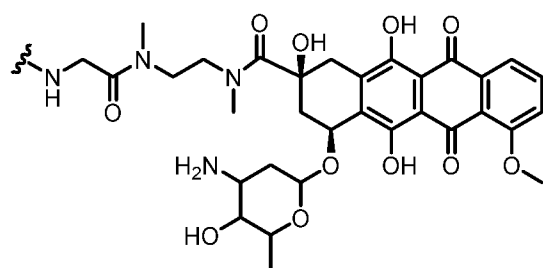
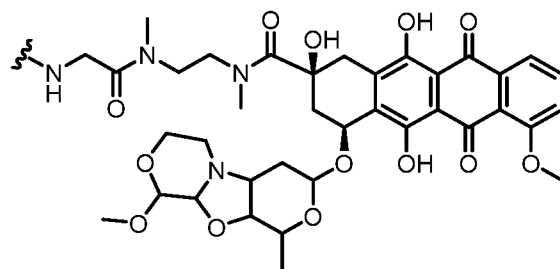
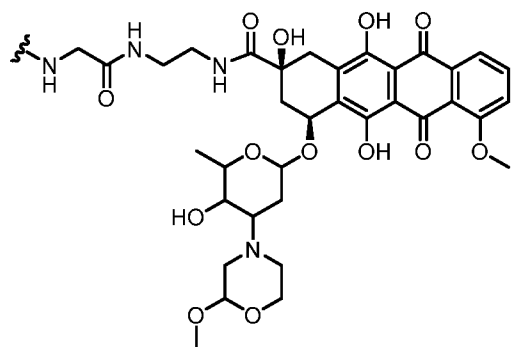


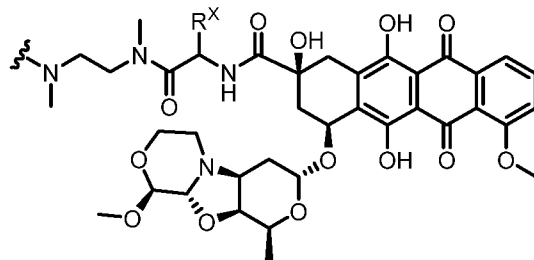
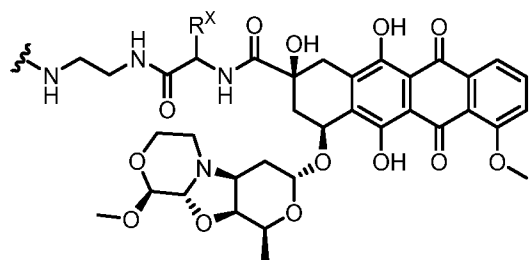
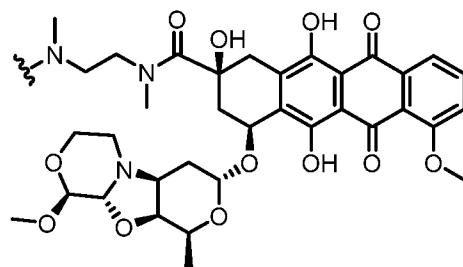
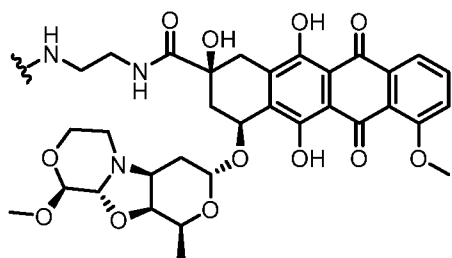
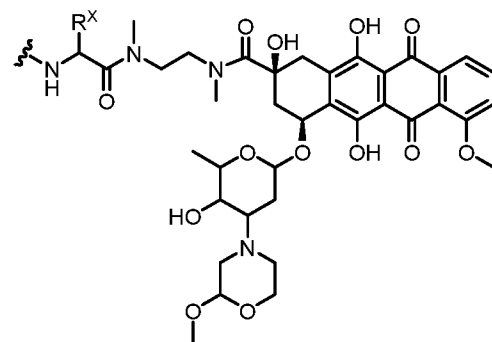
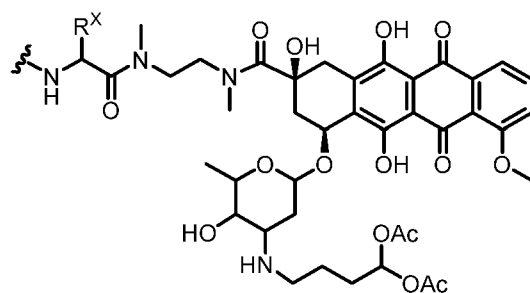
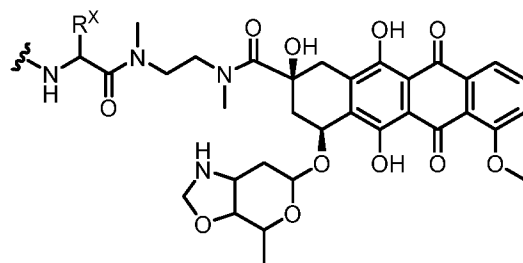
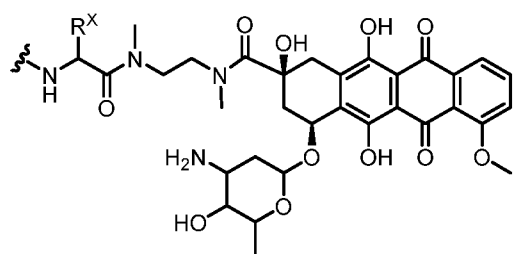
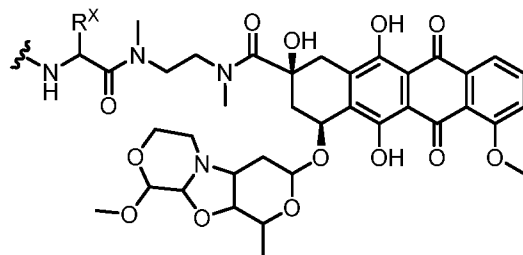
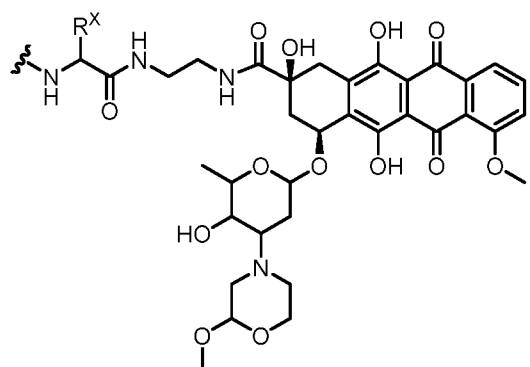
[0072] In some embodiments, each D-X is selected from the group consisting of:

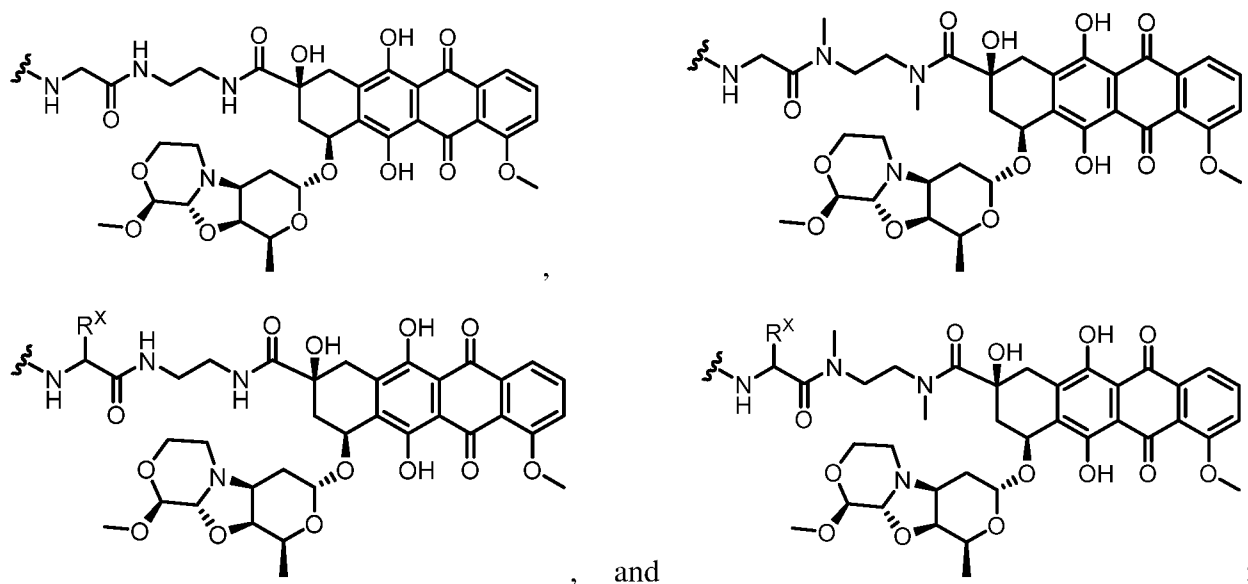






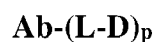






wherein R^X is as described herein, and wherein  represents covalent attachment to Y, W, A, or M.

[0073] Some embodiments provide an antibody drug conjugate (ADC) having the structure:



or a salt thereof;

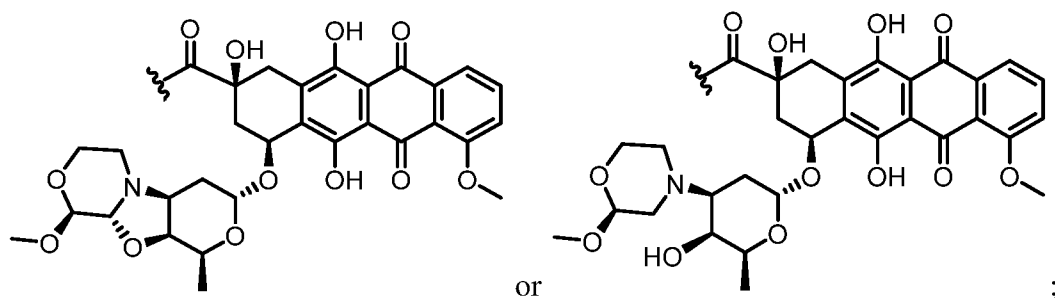
wherein:

Ab is an antibody;

wherein each L is covalently attached to Ab via a sulfur atom of a cysteine residue or an ϵ -amino group of a lysine residue in Ab;

subscript p is an integer from 1 to 16;

each D is:



wherein  represents covalent attachment to L;

each L is a linker that has the formula $-\text{M}-(\text{A})_a-(\text{W})_w-(\text{Y})_y-(\text{X})-$, wherein:

M is a succinimide, a hydrolyzed succinimide, an amide, or a triazole, wherein M is covalently attached to Ab;

subscript a is 0 or 1;

subscript y is 0 or 1;

subscript w is 0 or 1;

A is a C₂₋₁₀ alkylene optionally substituted with 1-3 R^{al}; or a 3 to 20 membered heteroalkylene optionally substituted with 1-3 R^{bl};

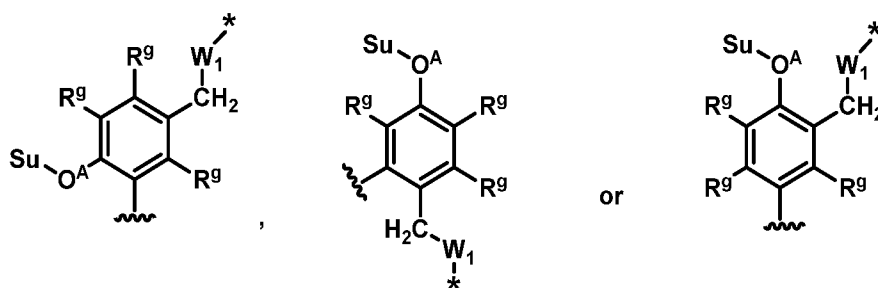
each R^{al} is independently selected from the group consisting of: C₁₋₆ alkyl, C₁₋₆ haloalkyl, C₁₋₆ alkoxy, C₁₋₆ haloalkoxy, halogen, -OH, =O, -NR^{dl}R^{el}, -(C₁₋₆ alkylene)-NR^{dl}R^{el}, -C(=O)NR^{dl}R^{el}, -C(=O)(C₁₋₆ alkyl), and -C(=O)O(C₁₋₆ alkyl);

each R^{bl} is independently selected from the group consisting of: C₁₋₆ alkyl, C₁₋₆ haloalkyl, C₁₋₆ alkoxy, C₁₋₆ haloalkoxy, halogen, -OH, -NR^{dl}R^{el}, -(C₁₋₆ alkylene)-NR^{dl}R^{el}, -C(=O)NR^{dl}R^{el}, -C(=O)(C₁₋₆ alkyl), and -C(=O)O(C₁₋₆ alkyl);

each R^{dl} and R^{el} are independently hydrogen or C₁₋₃ alkyl;

W is from 1-6 amino acids; or

W has the structure:



wherein Su is a Sugar moiety;

-O^A- represents the oxygen atom of a glycosidic bond;

each R^g is independently hydrogen, halogen, C₁₋₆ alkoxy, -N(C₁₋₆ alkyl)₂, -NHC(=O)(C₁₋₆ alkyl), -CN, -CF₃, acyl, carboxamido, C₁₋₆ alkyl, or -NO₂;

W¹ is absent, *-C(=O)-O-, or *-O-C(=O)-;

~~~~~ represents covalent attachment to A or M;

\* represents covalent attachment to Y or X;

Y is a self-immolative moiety, a non-self-immolative releasable moiety, or a non-cleavable moiety;

X is from 1-10 amino acids; or

X is a 4-16 membered heteroalkylene, wherein X is optionally substituted with 1-3 independently selected  $R^X$ ;

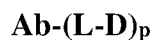
each  $R^X$  is independently a  $C_2$ - $C_6$  alkynyl group,  $-NR^{X1}R^{X2}$ , or a  $C_1$ - $C_6$  alkyl group optionally substituted with hydroxyl,  $-NR^{X1}R^{X2}$ , guanidino, 1 or 2  $-CO_2H$  groups,  $-C(=O)NR^{X1}R^{X2}$ , urea, phenyl, naphthyl, indolyl, imidazolyl,  $-SH$ ,  $-SCH_3$ ,  $-SeCH_3$ , or 4-hydroxyphenyl optionally substituted with  $C_2$ - $C_6$  alkenyl; or

two  $R^X$  attached to the same or adjacent carbon atom(s) of X, together with the carbon atom(s) to which they are attached form an unsubstituted 5-6 membered heterocyclyl;

each  $R^{X1}$  and  $R^{X2}$  are independently hydrogen or  $C_{1-6}$  alkyl; and

L is optionally substituted with a PEG Unit from PEG1 to PEG72.

**[0074]** Some embodiments provide an antibody drug conjugate (ADC) having the structure:



or a salt thereof;

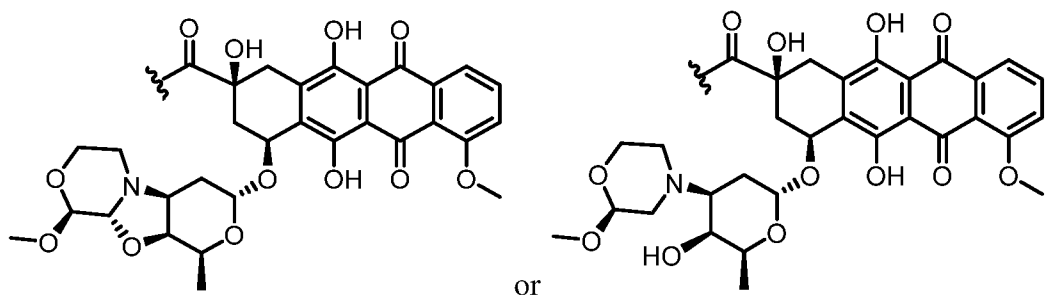
wherein:

Ab is an antibody;

wherein each L is covalently attached to Ab via a sulfur atom of a cysteine residue or an  $\epsilon$ -amino group of a lysine residue in Ab;

subscript p is an integer from 1 to 16;

each D is:



wherein  represents covalent attachment to L;

each L is a linker that has the formula  $-M-(A)_a-(W)_w-(Y)_y-(X)-$ , wherein:

M is a succinimide, a hydrolyzed succinimide, an amide, or a triazole, wherein M is covalently attached to Ab;

subscript a is 0 or 1;

subscript y is 0 or 1;

subscript w is 0 or 1;

A is a C<sub>2-10</sub> alkylene optionally substituted with 1-3 R<sup>al</sup>; or a 3 to 20 membered heteroalkylene optionally substituted with 1-3 R<sup>bl</sup>;

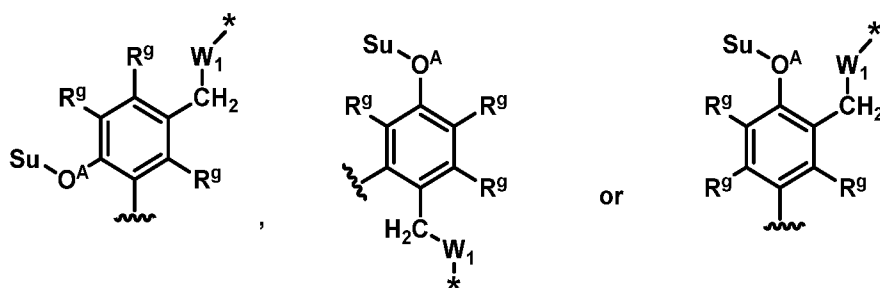
each R<sup>al</sup> is independently selected from the group consisting of: C<sub>1-6</sub> alkyl, C<sub>1-6</sub> haloalkyl, C<sub>1-6</sub> alkoxy, C<sub>1-6</sub> haloalkoxy, halogen, -OH, =O, -NR<sup>dl</sup>R<sup>el</sup>, -(C<sub>1-6</sub> alkylene)-NR<sup>dl</sup>R<sup>el</sup>, -C(=O)NR<sup>dl</sup>R<sup>el</sup>, -C(=O)(C<sub>1-6</sub> alkyl), and -C(=O)O(C<sub>1-6</sub> alkyl);

each R<sup>bl</sup> is independently selected from the group consisting of: C<sub>1-6</sub> alkyl, C<sub>1-6</sub> haloalkyl, C<sub>1-6</sub> alkoxy, C<sub>1-6</sub> haloalkoxy, halogen, -OH, -NR<sup>dl</sup>R<sup>el</sup>, -(C<sub>1-6</sub> alkylene)-NR<sup>dl</sup>R<sup>el</sup>, -C(=O)NR<sup>dl</sup>R<sup>el</sup>, -C(=O)(C<sub>1-6</sub> alkyl), and -C(=O)O(C<sub>1-6</sub> alkyl);

each R<sup>dl</sup> and R<sup>el</sup> are independently hydrogen or C<sub>1-3</sub> alkyl;

W is from 1-6 amino acids; or

W has the structure:



wherein Su is a Sugar moiety;

-O<sup>A</sup>- represents the oxygen atom of a glycosidic bond;

each R<sup>g</sup> is independently hydrogen, halogen, C<sub>1-6</sub> alkoxy, -N(C<sub>1-6</sub> alkyl)<sub>2</sub>, -NHC(=O)(C<sub>1-6</sub> alkyl), -CN, -CF<sub>3</sub>, acyl, carboxamido, C<sub>1-6</sub> alkyl, or -NO<sub>2</sub>;

W<sup>1</sup> is absent, \*-C(=O)-O-, or \*-O-C(=O)-;

~~~~~ represents covalent attachment to A or M;

* represents covalent attachment to Y or X;

Y is a self-immolative moiety, a non-self-immolative releasable moiety, or a non-cleavable moiety;

X is a 4-16 membered heteroalkylene, wherein X is optionally substituted with 1-3 independently selected R^X ;

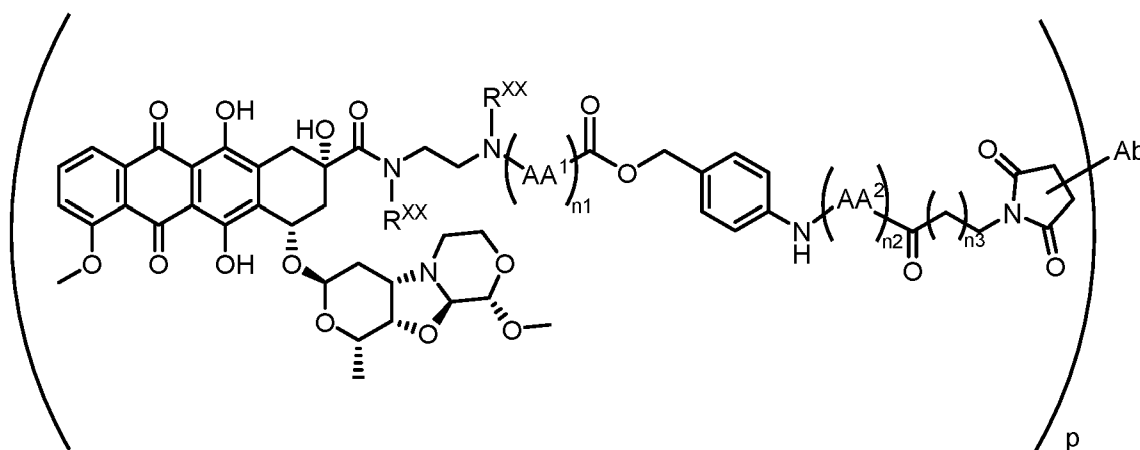
each R^X is independently a C_2 - C_6 alkynyl group, $-NR^{X1}R^{X2}$, or a C_1 - C_6 alkyl group optionally substituted with hydroxyl, $-NR^{X1}R^{X2}$, guanidino, 1 or 2 $-CO_2H$ groups, $-C(=O)NR^{X1}R^{X2}$, urea, phenyl, naphthyl, indolyl, imidazolyl, $-SH$, $-SCH_3$, $-SeCH_3$, or 4-hydroxyphenyl optionally substituted with C_2 - C_6 alkenyl; or

two R^X attached to the same or adjacent carbon atom(s) of X, together with the carbon atom(s) to which they are attached form an unsubstituted 5-6 membered heterocyclyl;

each R^{X1} and R^{X2} are independently hydrogen or C_{1-6} alkyl; and

L is optionally substituted with a PEG Unit from PEG1 to PEG72.

[0075] In some embodiments, the ADC has the structure:



wherein:

each R^{XX} is independently hydrogen or C_{1-3} alkyl;

$n1$ is an integer from 0 to 4;

$n2$ is an integer from 1 to 4;

$n3$ is an integer from 1 to 4;

each AA^1 is independently selected from the group consisting of alanine, glycine, lysine, serine, aspartic acid, aspartate methyl ester, N,N-dimethyl-lysine, phenylalanine, citrulline, valine, asparagine, homoserine methyl ether, isoleucine, leucine, glutamic acid, histidine, arginine, threonine, O-methylserine, O-methylaspartic acid, O-methylglutamic acid, N-methyllysine, O-methyltyrosine, O-methylhistidine, and O-methylthreonine;

each AA² is independently selected from the group consisting of alanine, glycine, lysine, serine, aspartic acid, aspartate methyl ester, N,N-dimethyl-lysine, phenylalanine, citrulline, valine, asparagine, homoserine methyl ether, isoleucine, leucine, glutamic acid, histidine, arginine, threonine, O-methylserine, O-methylaspartic acid, O-methylglutamic acid, N-methyllysine, O-methyltyrosine, O-methylhistidine, and O-methylthreonine;

Ab is an antibody; and

p is an integer from 1 to 16.

[0076] In some embodiments, each AA¹ is independently selected from the group consisting of alanine, glycine, valine, and serine.

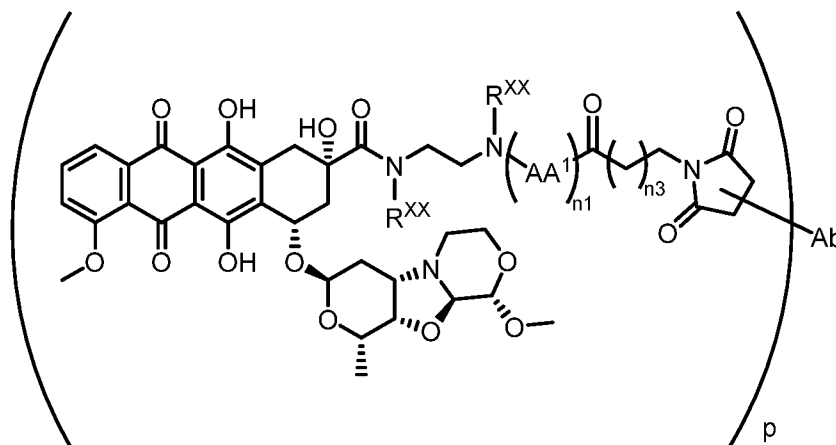
[0077] In some embodiments, n1 is 0. In some embodiments, n1 is 1. In some embodiments, n1 is 2. In some embodiments, n1 is 3.

[0078] In some embodiments, each AA² is independently selected from the group consisting of alanine, glycine, valine, serine, leucine, and aspartic acid. In some embodiments, each AA² is independently selected from the group consisting of alanine and valine.

[0079] In some embodiments, n2 is 2. In some embodiments, (AA²)_{n2} is -Ala-Val-.

[0080] In some embodiments, n3 is 1.

[0081] In some embodiments, the ADC has the structure:



wherein:

each R^{XX} is independently hydrogen or C₁₋₃ alkyl;

n1 is an integer from 0 to 4;

each AA¹ is independently selected from the group consisting of alanine, glycine, lysine, serine, aspartic acid, aspartate methyl ester, N,N-dimethyl-lysine, phenylalanine, citrulline, valine, asparagine, homoserine methyl ether, isoleucine, leucine, glutamic acid, histidine, arginine, threonine, O-methylserine, O-methylaspartic acid, O-methylglutamic acid, N-methyllysine, O-methyltyrosine, O-methylhistidine, and O-methylthreonine;

n₃ is an integer from 1 to 4;

Ab is an antibody; and

p is an integer from 1 to 16.

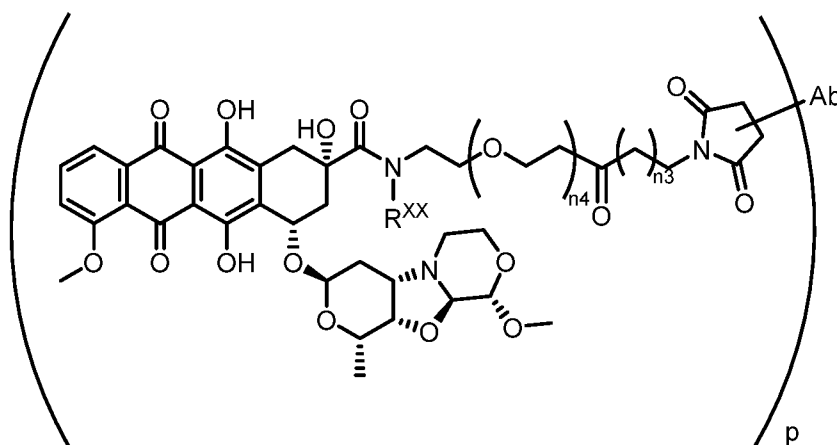
[0082] In some embodiments, n₁ is 0. In some embodiments, n₁ is 1. In some embodiments, n₁ is 2. In some embodiments, n₁ is 3. In some embodiments, when n₁ is 3, at least one AA¹ is not glycine.

[0083] In some embodiments, each AA¹ is independently selected from the group consisting of alanine, glycine, valine, serine, leucine, arginine, and aspartic acid. In some embodiments, each AA¹ is independently selected from the group consisting of alanine, glycine, valine, and serine.

[0084] In some embodiments, n₁ is 3; each AA¹ is independently selected from the group consisting of alanine, glycine, valine, serine, leucine, arginine, and aspartic acid; and wherein at least one AA¹ is not glycine.

[0085] In some embodiments, n₃ is 1.

[0086] In some embodiments, the ADC has the structure:



wherein:

R^{xx} is hydrogen or C₁₋₃ alkyl;

n4 is an integer from 2 to 8;

n3 is an integer from 1 to 4;

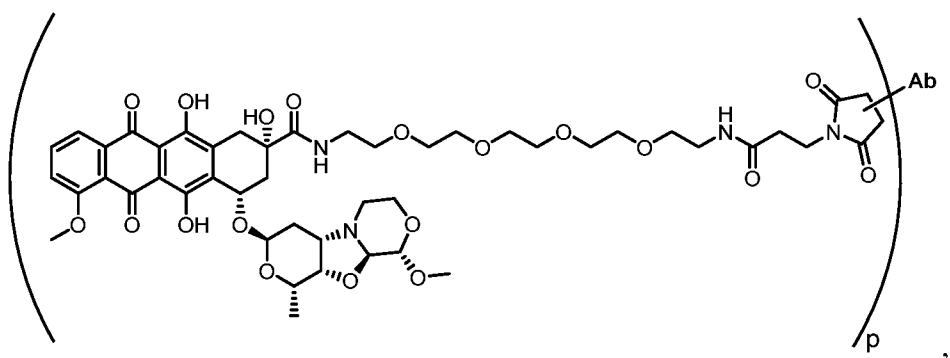
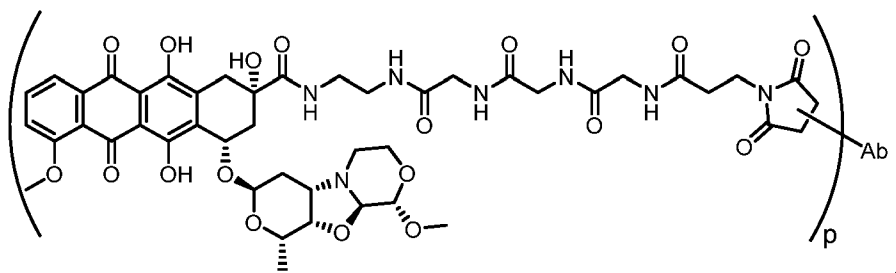
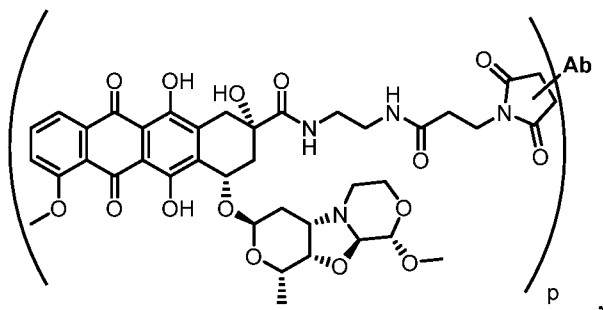
Ab is an antibody; and

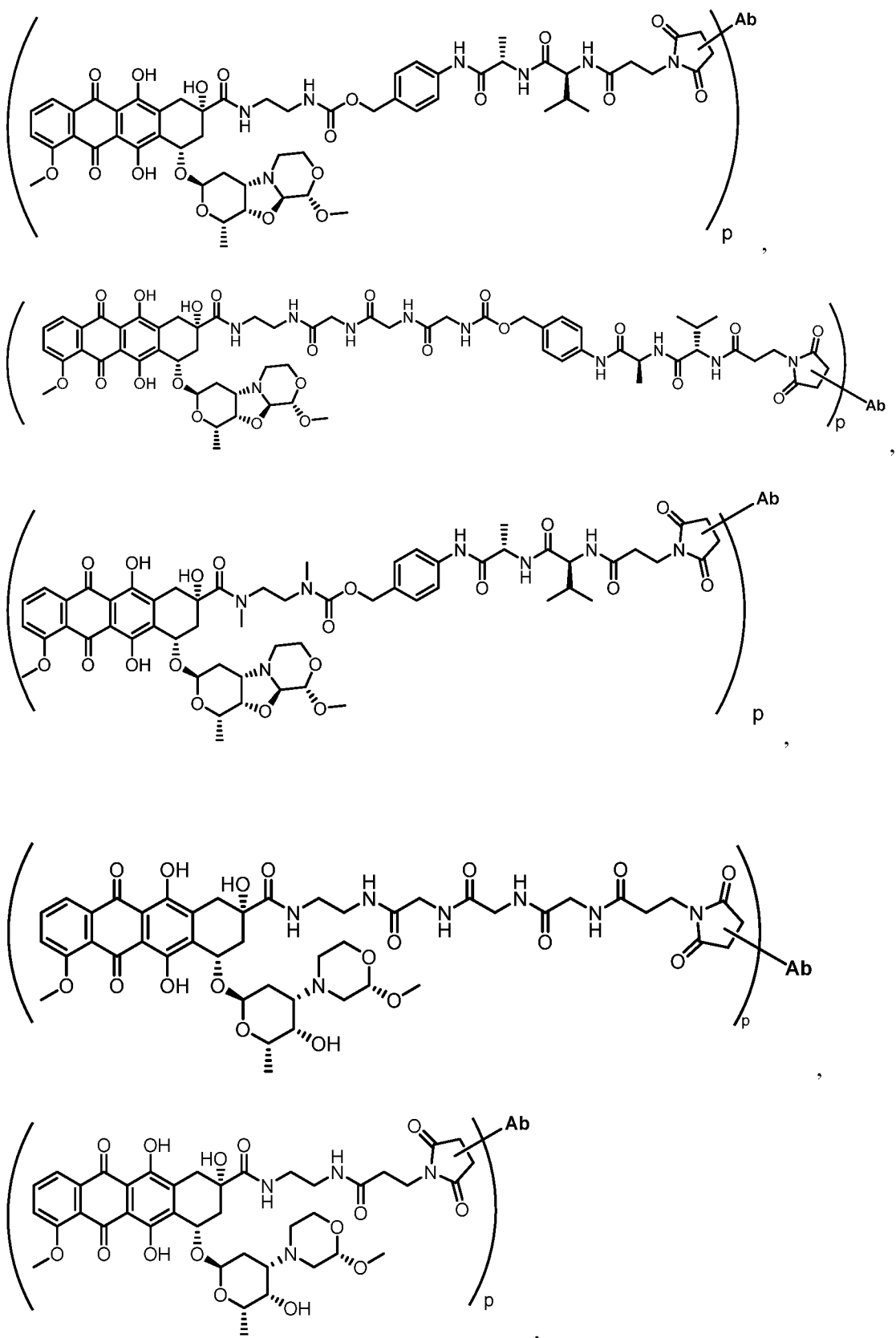
p is an integer from 1 to 16.

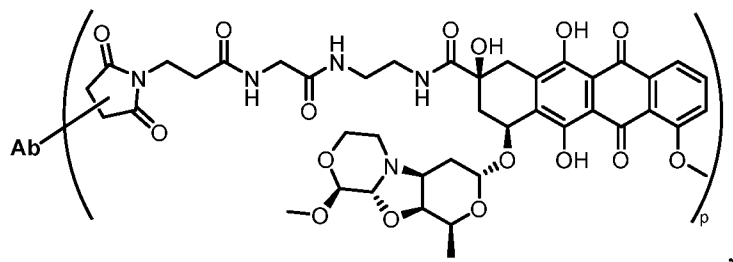
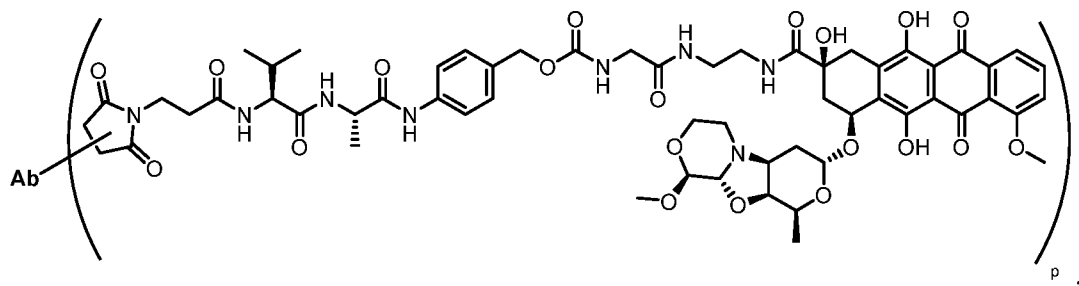
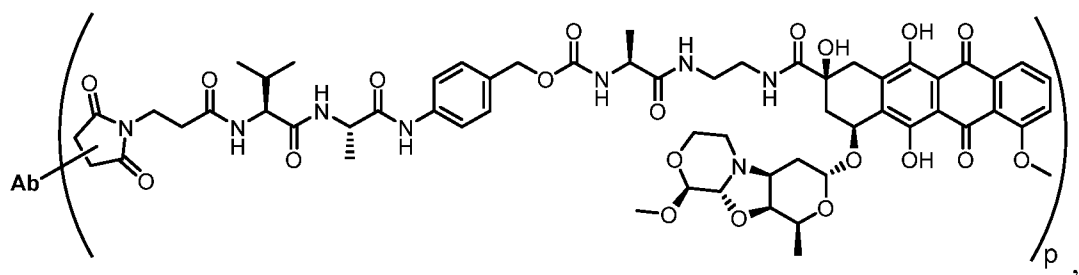
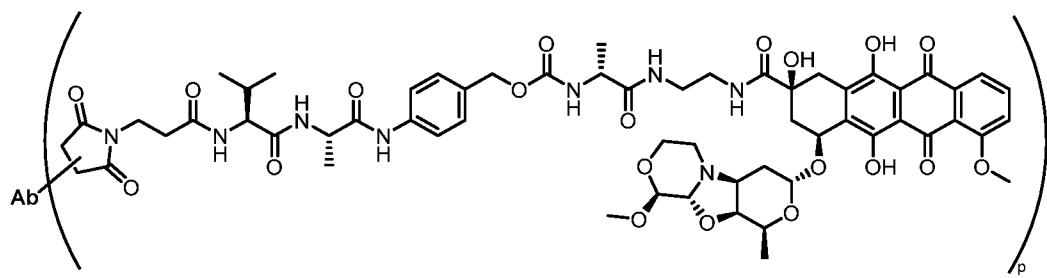
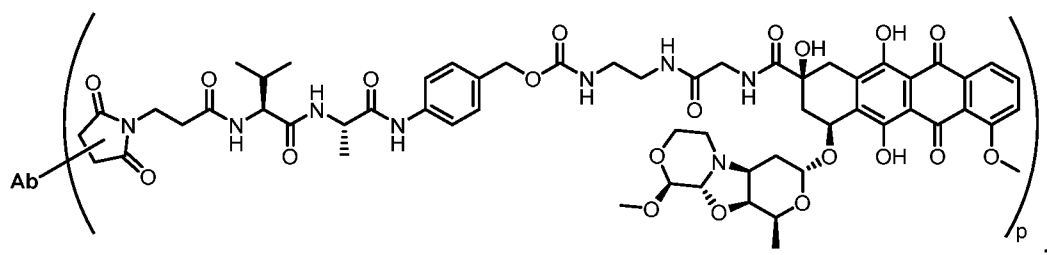
[0087] In some embodiments, n4 is an integer from 3 to 6.

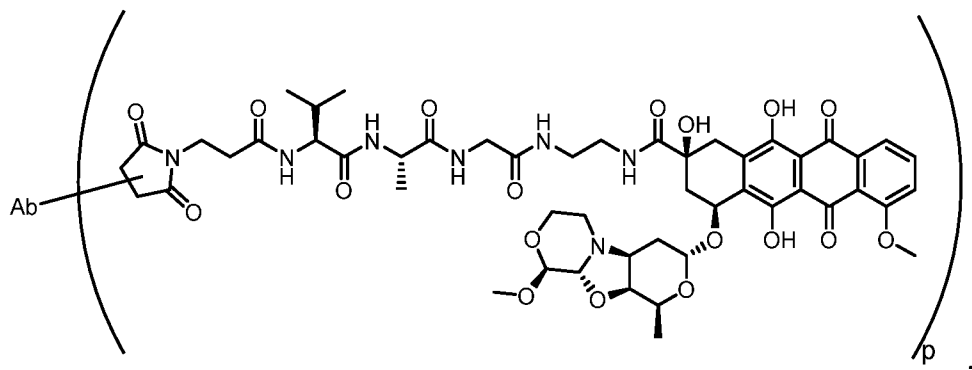
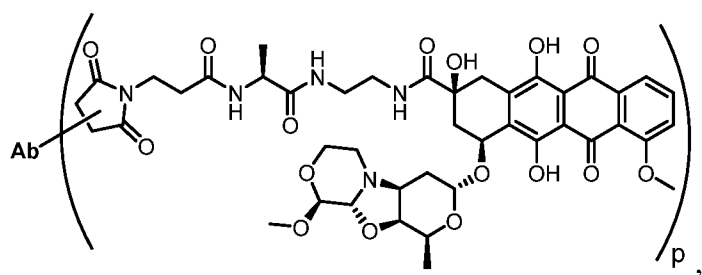
[0088] In some embodiments, n3 is 1.

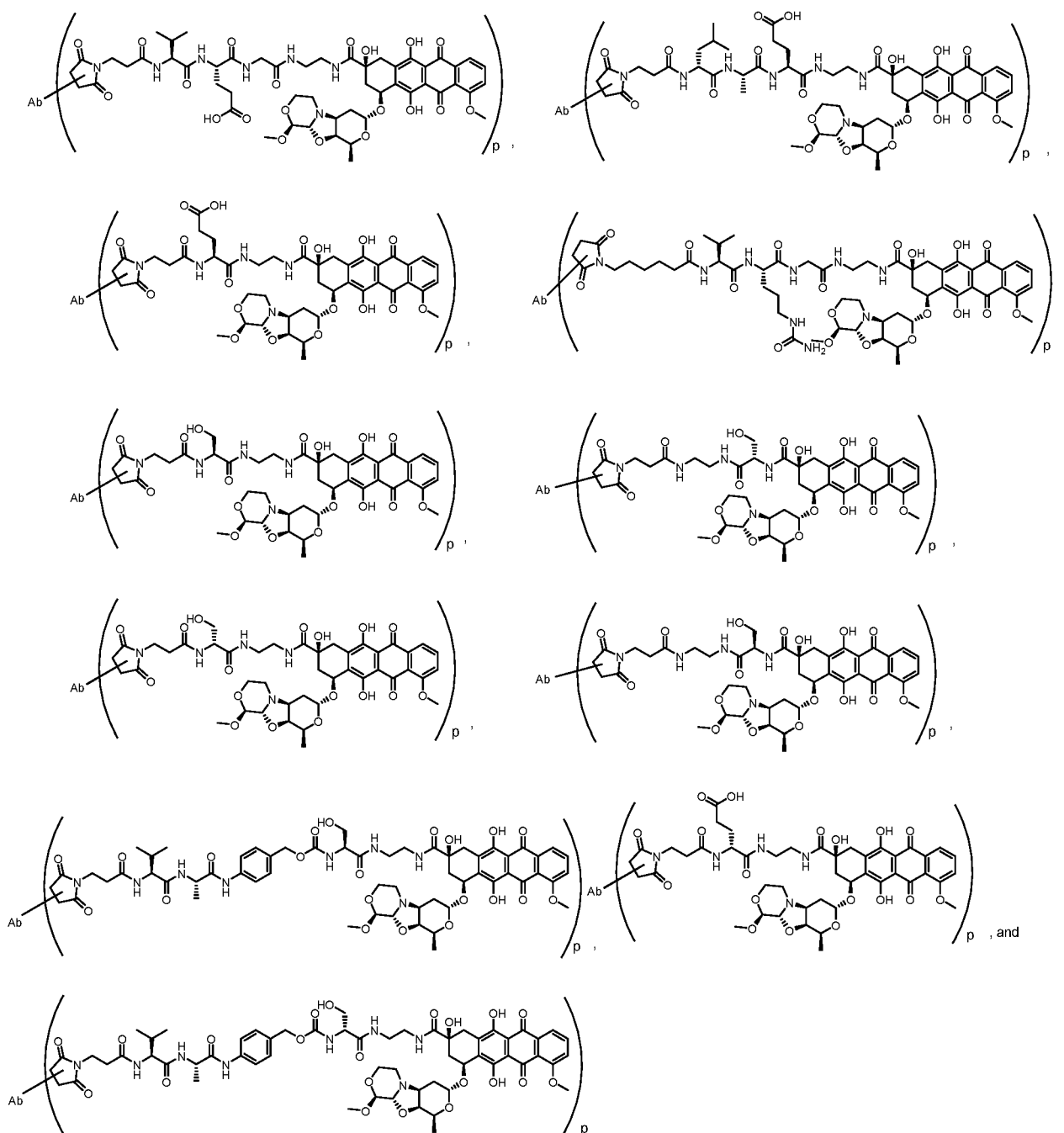
[0089] In some embodiments, the ADC has a structure selected from the group consisting of:











or a pharmaceutically acceptable salts of any of the foregoing.

[0090] In some embodiments, the ADCs described herein are present in the form of a salt. In some embodiments, the salt is a pharmaceutically acceptable salt.

[0091] In some embodiments subscript p is an integer from 1 to 8; from 4 to 12; or from 8 to 16. In some embodiments, subscript p is an even number. In some embodiments, subscript p is 2, 4, 6, 8, 10, 12, 14, or 16. In some embodiments, subscript p is 2, 4, 6, or 8.

[0092] In some embodiments, each L is covalently attached to Ab via a sulfur atom of a cysteine residue. In some embodiments, one or more of the cysteine residues is an engineered cysteine residue. In some embodiments, each cysteine residue is an engineered cysteine residue. In some embodiments, one or more of the cysteine residues is a native cysteine residue. In some embodiments, each cysteine residue is a native cysteine residue. In some embodiments, each sulfur atom is from a cysteine residue from a reduced interchain disulfide bond.

[0093] In some embodiments, each L is covalently attached to Ab via an ϵ -amino group of a lysine residue.

[0094] In some embodiments, the ADC is capable of releasing (i) a component of the linker bound to D; (ii) a component of antibody that has not undergone subsequent intracellular metabolism bound to L-D; and/or (iii) the parent compound D, as the free drug (as defined herein). In some embodiments, the free drug is released at the intended site of action targeted by the antibody. In some embodiments, the free drug is released within the intended site of action targeted by the antibody.

Antibodies

[0095] In some embodiments, an antibody is a polyclonal antibody. In some embodiments, an antibody is a monoclonal antibody. In some embodiments, an antibody is chimeric. In some embodiments, an antibody is humanized. In some embodiments, an antibody is an antigen binding fragment.

[0096] Useful polyclonal antibodies are heterogeneous populations of antibody molecules derived from the sera of immunized animals. Useful monoclonal antibodies are homogeneous populations of antibodies to a particular antigenic determinant (*e.g.*, a cancer or immune cell antigen, a protein, a peptide, a carbohydrate, a chemical, nucleic acid, or fragments thereof). A monoclonal antibody (mAb) to an antigen-of-interest can be prepared by using any technique known in the art which provides for the production of antibody molecules by continuous cell lines in culture.

[0097] Useful monoclonal antibodies include, but are not limited to, human monoclonal antibodies, humanized monoclonal antibodies, or chimeric human-mouse (or other species) monoclonal antibodies. The antibodies include full-length antibodies and antigen binding fragments thereof. Human monoclonal antibodies may be made by any of numerous techniques

known in the art (e.g., Teng *et al.*, 1983, *Proc. Natl. Acad. Sci. USA*. 80:7308-7312; Kozbor *et al.*, 1983, *Immunology Today* 4:72-79; and Olsson *et al.*, 1982, *Meth. Enzymol.* 92:3-16).

[0098] In some embodiments, an antibody includes a functionally active fragment, derivative or analog of an antibody that binds specifically to target cells (e.g., cancer cell antigens) or other antibodies bound to cancer cells or matrix. In this regard, “functionally active” means that the fragment, derivative or analog is able to bind specifically to target cells. To determine which CDR sequences bind the antigen, synthetic peptides containing the CDR sequences are typically used in binding assays with the antigen by any binding assay method known in the art (e.g., the Biacore assay) (See, e.g., Kabat *et al.*, 1991, *Sequences of Proteins of Immunological Interest*, Fifth Edition, National Institute of Health, Bethesda, Md; Kabat E *et al.*, 1980, *J. Immunology* 125(3):961-969).

[0099] Additionally, recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which are typically obtained using standard recombinant DNA techniques, are useful antibodies. A chimeric antibody is a molecule in which different portions are derived from different animal species, such as for example, those having a variable region derived from a murine monoclonal and a constant region derived from a human immunoglobulin. See, e.g., U.S. Patent No. 4,816,567; and U.S. Patent No. 4,816,397, which are incorporated herein by reference in their entireties. Humanized antibodies are antibody molecules from non-human species having one or more CDRs from the non-human species and a framework region from a human immunoglobulin molecule. See, e.g., U.S. Patent No. 5,585,089, which is incorporated herein by reference in its entirety. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in International Publication No. WO 87/02671; European Patent Publication No. 0 184 187; European Patent Publication No. 0 171 496; European Patent Publication No. 0 173 494; International Publication No. WO 86/01533; U.S. Patent No. 4,816,567; European Patent Publication No. 012 023; Berter *et al.*, 1988, *Science* 240:1041-1043; Liu *et al.*, 1987, *Proc. Natl. Acad. Sci. USA* 84:3439-3443; Liu *et al.*, 1987, *J. Immunol.* 139:3521-3526; Sun *et al.*, 1987, *Proc. Natl. Acad. Sci. USA* 84:214-218; Nishimura *et al.*, 1987, *Cancer Res.* 47:999-1005; Wood *et al.*, 1985, *Nature* 314:446-449; and Shaw *et al.*, 1988, *J. Natl. Cancer Inst.* 80:1553-1559; Morrison, 1985, *Science* 229:1202-1207; Oi *et al.*, 1986, *BioTechniques* 4:214; U.S. Patent No. 5,225,539; Jones *et al.*, 1986, *Nature* 321: 522-525; Verhoeyan *et al.*, 1988,

Science 239:1534; and Beidler *et al.*, 1988, *J. Immunol.* 141:4053-4060; each of which is incorporated herein by reference in its entirety.

[0100] In some embodiments, an antibody is a completely human antibody. In some embodiments, an antibody is produced using transgenic mice that are incapable of expressing endogenous immunoglobulin heavy and light chain genes, but which are capable of expressing human heavy and light chain genes.

[0101] In some embodiments, an antibody is an intact or fully-reduced antibody. The term ‘fully-reduced’ is meant to refer to an antibody in which all four inter-chain disulfide linkages have been reduced to provide eight thiols that can be attached to a linker (L).

[0102] Attachment to an antibody can be via thioether linkages from native and/or engineered cysteine residues, or from an amino acid residue engineered to participate in a cycloaddition reaction (such as a click reaction) with the corresponding linker intermediate. *See, e.g.*, Maerle, et al., *PLOS One* 2019: 14(1); e0209860. In some embodiments, an antibody is an intact or fully-reduced antibody, or is an antibody bearing engineered an cysteine group that is modified with a functional group that can participate in, for example, click chemistry or other cycloaddition reactions for attachment of other components of the ADC as described herein (e.g., Diels-Alder reactions or other [3+2] or [4+2] cycloadditions). *See, e.g.*, Agard, et al., *J. Am. Chem. Soc.* Vol. 126, pp. 15046-15047 (2004); Laughlin, et al., *Science*, Vol. 320, pp. 664-667 (2008); Beatty, et al., *ChemBioChem*, Vol. 11, pp. 2092-2095 (2010); and Van Geel, et al., *Bioconjug. Chem.* Vol. 26, pp.2233-2242 (2015).

[0103] Antibodies that bind specifically to a cancer or immune cell antigen are available commercially or produced by any method known to one of skill in the art such as, *e.g.*, chemical synthesis or recombinant expression techniques. The nucleotide sequences encoding antibodies that bind specifically to a cancer or immune cell antigen are obtainable, *e.g.*, from the GenBank database or similar database, literature publications, or by routine cloning and sequencing.

[0104] In some embodiments, the antibody can be used for the treatment of a cancer (e.g., an antibody approved by the FDA and/or EMA). In some embodiments, the antibody described herein is selected from the group consisting of avelumab, durvalumab, daratumumab, elotuzumab, necitumumab, atezolizumab, nivolumab, dinutuximab, bevacizumab, pembrolizumab, ramucirumab, alemtuzumab, pertuzumab, obinutuzumab, ipilimumab,

denosumab, ofatumumab, catumaxomab, panitumumab, bevacizumab, cetuximab, tositumomab, alemtuzumab, trastuzumab, rituximab, sintilimab, tislelizumab, camrelizumab, huJ591, JS001, hu3S193, TRC093, TRC105, AGEN1181, AGEN2034, MEDI4736, NEO-102, MK-0646, ZKAB001, TB-403, GLS-010, CT-011, INCMGA00012, AGEN1884, MK-3475, GC1118, DS-8201a, CC-95251, Sym004, CS1001, and REGN2810. In some embodiments, the antibody described herein is selected from the group consisting of rituximab, obinutuzumab, ofatumumab, trastuzumab, alemtuzumab, mogamulizumab, cetuximab, and dinutuximab. In some embodiments, the antibody described herein is rituximab. In some embodiments, the antibody described herein is obinutuzumab. In some embodiments, the antibody described herein is ofatumumab. In some embodiments, the antibody described herein is trastuzumab. In some embodiments, the antibody described herein is alemtuzumab. In some embodiments, the antibody described herein is mogamulizumab. In some embodiments, the antibody described herein is cetuximab. In some embodiments, the antibody described herein is dinutuximab.

[0105] Antibodies that bind specifically to a cancer or immune cell antigen are available commercially or produced by any method known to one of skill in the art such as, *e.g.*, recombinant expression techniques. The nucleotide sequences encoding antibodies that bind specifically to a cancer or immune cell antigen are obtainable, *e.g.*, from the GenBank database or similar database, literature publications, or by routine cloning and sequencing.

[0106] In some embodiments, an antibody can bind specifically to a receptor or a receptor complex expressed on lymphocytes. The receptor or receptor complex can comprise an immunoglobulin gene superfamily member, a TNF receptor superfamily member, an integrin, a cytokine receptor, a chemokine receptor, a major histocompatibility protein, a lectin, or a complement control protein or other immune cell expressed surface receptor.

In some embodiments, an antibody can bind specifically to a cancer cell antigen. In some embodiments, an antibody can bind specifically to an immune cell antigen. It will be understood that the antibody component in an ADC is an antibody in residue form such that “Ab” in the ADC structures described herein incorporates the structure of the antibody.

[0107] Non-limiting examples of antibodies that can be used for treatment of cancer and antibodies that bind specifically to tumor associated antigens are disclosed in Franke, A. E., Sievers, E. L., and Scheinberg, D. A., “Cell surface receptor-targeted therapy of acute myeloid leukemia: a review” *Cancer Biother Radiopharm.* 2000,15, 459-76; Murray, J. L., “Monoclonal

antibody treatment of solid tumors: a coming of age” *Semin Oncol.* 2000, 27, 64-70; Breitling, F., and Dubel, S., *Recombinant Antibodies*, John Wiley, and Sons, New York, 1998, each of which is hereby incorporated by reference in its entirety.

[0108] Exemplary antigens are provided below. Exemplary antibodies that bind the indicated antigen are shown in parentheses.

[0109] In some embodiments, the antigen is a tumor-associated antigen. In some embodiments, the tumor-associated antigen is a transmembrane protein. For example, the following antigens are transmembrane proteins: ANTXR1, BAFF-R, CA9 (exemplary antibodies include girentuximab), CD147 (exemplary antibodies include gavilimomab and metuzumab), CD19, CD20 (exemplary antibodies include divozilimab and ibritumomab tiuxetan), CD274 also known as PD-L1 (exemplary antibodies include adebrelimab, atezolizumab, garivulimab, durvalumab, and avelumab), CD30 (exemplary antibodies include iratumumab and brentuximab), CD33 (exemplary antibodies include lintuzumab), CD352, CD45 (exemplary antibodies include apamistamab), CD47 (exemplary antibodies include letaplimab and magrolimab), CLPTM1L, DPP4, EGFR, ERVMER34-1, FASL, FSHR, FZD5, FZD8, GUCY2C (exemplary antibodies include indusatumab), IFNAR1 (exemplary antibodies include faralimomab), IFNAR2, LMP2, MLANA, SIT1, TLR2/4/1 (exemplary antibodies include tomaralimab), TM4SF5, TMEM132A, TMEM40, UPK1B, VEGF, and VEGFR2 (exemplary antibodies include gentuximab).

[0110] In some embodiments, the tumor-associated antigen is a transmembrane transport protein. For example, the following antigens are transmembrane transport proteins: ASCT2 (exemplary antibodies include idactamab), MFSD13A, Mincle, NOX1, SLC10A2, SLC12A2, SLC17A2, SLC38A1, SLC39A5, SLC39A6 also known as LIV1 (exemplary antibodies include ladiratuzumab), SLC44A4, SLC6A15, SLC6A6, SLC7A11, and SLC7A5.

[0111] In some embodiments, the tumor-associated antigen is a transmembrane or membrane-associated glycoprotein. For example, the following antigens are transmembrane or membrane-associated glycoproteins: CA-125, CA19-9, CAMPATH-1 (exemplary antibodies include alemtuzumab), carcinoembryonic antigen (exemplary antibodies include arcitumomab, cergutuzumab, amunaleukin, and labetuzumab), CD112, CD155, CD24, CD247, CD37 (exemplary antibodies include lilotomab), CD38 (exemplary antibodies include felzartamab), CD3D, CD3E (exemplary antibodies include foralumab and teplizumab), CD3G, CD96, CDCP1, CDH17, CDH3, CDH6, CEACAM1, CEACAM6, CLDN1, CLDN16, CLDN18.1 (exemplary

antibodies include zolbetuximab), CLDN18.2 (exemplary antibodies include zolbetuximab), CLDN19, CLDN2, CLEC12A (exemplary antibodies include tepoditamab), DPEP1, DPEP3, DSG2, endosialin (exemplary antibodies include ontuxizumab), ENPP1, EPCAM (exemplary antibodies include adecatumumab), FN, FN1, Gp100, GPA33, gpNMB (exemplary antibodies include glembatumumab), ICAM1, L1CAM, LAMP1, MELTF also known as CD228, NCAM1, Nectin-4 (exemplary antibodies include enfortumab), PDPN, PMSA, PROM1, PSCA, PSMA, Siglecs 1-16, SIRPa, SIRPg, TACSTD2, TAG-72, Tenascin, Tissue Factor also known as TF (exemplary antibodies include tisotumab), and ULBP1/2/3/4/5/6.

[0112] In some embodiments, the tumor-associated antigen is a transmembrane or membrane-associated receptor kinase. For example, the following antigens are transmembrane or membrane-associated receptor kinases: ALK, Axl (exemplary antibodies include tilvestamab), BMPR2, DCLK1, DDR1, EPHA receptors, EPHA2, ERBB2 also known as HER2 (exemplary antibodies include trastuzumab, bevacizumab, pertuzumab, and margetuximab), ERBB3, FLT3, PDGFR-B (exemplary antibodies include rinucumab), PTK7 (exemplary antibodies include cofetuzumab), RET, ROR1 (exemplary antibodies include cirmtuzumab), ROR2, ROS1, and Tie3.

[0113] In some embodiments, the tumor-associated antigen is a membrane-associated or membrane-localized protein. For example, the following antigens are membrane-associated or membrane-localized proteins: ALPP, ALPPL2, ANXA1, FOLR1 (exemplary antibodies include farletuzumab), IL13Ra2, IL1RAP (exemplary antibodies include nidanilimab), NT5E, OX40, Ras mutant, RGS5, RhoC, SLAMF7 (exemplary antibodies include elotuzumab), and VSIR.

[0114] In some embodiments, the tumor-associated antigen is a transmembrane G-protein coupled receptor (GPCR). For example, the following antigens are GPCRs: CALCR, CD97, GPR87, and KISS1R.

[0115] In some embodiments, the tumor-associated antigen is cell-surface-associated or a cell-surface receptor. For example, the following antigens are cell-surface-associated and/or cell-surface receptors: B7-DC, BCMA, CD137, CD 244, CD3 (exemplary antibodies include oteixizumab and visilizumab), CD48, CD5 (exemplary antibodies include zolimomab aritox), CD70 (exemplary antibodies include cusatuzumab and vorsetuzumab), CD74 (exemplary antibodies include milatuzumab), CD79A, CD-262 (exemplary antibodies include tigatuzumab), DR4 (exemplary antibodies include mapatumumab), FAS, FGFR1, FGFR2 (exemplary antibodies include aprutumab), FGFR3 (exemplary antibodies include vofatamab), FGFR4, GTR

(exemplary antibodies include ragifilimab), Gpc3 (exemplary antibodies include ragifilimab), HAVCR2, HLA-E, HLA-F, HLA-G, LAG-3 (exemplary antibodies include encelimumab), LY6G6D, LY9, MICA, MICB, MSLN, MUC1, MUC5AC, NY-ESO-1, OY-TES1, PVRIG, Sialyl-Thomsen-Nouveau Antigen, Sperm protein 17, TNFRSF12, and uPAR.

[0116] In some embodiments, the tumor-associated antigen is a chemokine receptor or cytokine receptor. For example, the following antigens are chemokine receptors or cytokine receptors: CD115 (exemplary antibodies include axatilimab, cabiralizumab, and emactuzumab), CD123, CXCR 4 (exemplary antibodies include ulocuplumab), IL-21R, and IL-5R (exemplary antibodies include benralizumab).

[0117] In some embodiments, the tumor-associated antigen is a co-stimulatory, surface-expressed protein. For example, the following antigens are co-stimulatory, surface-expressed proteins: B7-H3 (exemplary antibodies include enoblituzumab and omburtamab), B7-H4, B7-H6, and B7-H7.

[0118] In some embodiments, the tumor-associated antigen is a transcription factor or a DNA-binding protein. For example, the following antigens are transcription factors: ETV6-AML, MYCN, PAX3, PAX5, and WT1. The following protein is a DNA-binding protein: BORIS.

[0119] In some embodiments, the tumor-associated antigen is an integral membrane protein. For example, the following antigens are integral membrane proteins: SLITRK6 (exemplary antibodies include sirtratumab), UPK2, and UPK3B.

[0120] In some embodiments, the tumor-associated antigen is an integrin. For example, the following antigens are integrin antigens: alpha v beta 6, ITGAV (exemplary antibodies include abituzumab), ITGB6, and ITGB8.

[0121] In some embodiments, the tumor-associated antigen is a glycolipid. For example, the following are glycolipid antigens: FucGM1, GD2 (exemplary antibodies include dinutuximab), GD3 (exemplary antibodies include mitumomab), GloboH, GM2, and GM3 (exemplary antibodies include racotumomab).

[0122] In some embodiments, the tumor-associated antigen is a cell-surface hormone receptor. For example, the following antigens are cell-surface hormone receptors: AMHR2 and androgen receptor.

[0123] In some embodiments, the tumor-associated antigen is a transmembrane or membrane-associated protease. For example, the following antigens are transmembrane or membrane-associated proteases: ADAM12, ADAM9, TMPRSS11D, and metalloproteinase.

[0124] In some embodiments, the tumor-associated antigen is aberrantly expressed in individuals with cancer. For example, the following antigens may be aberrantly expressed in individuals with cancer: AFP, AGR2, AKAP-4, ARTN, BCR-ABL, C5 complement, CCNB1, CSPG4, CYP1B1, De2-7 EGFR, EGF, Fas-related antigen 1, FBP, G250, GAGE, HAS3, HPV E6 E7, hTERT, IDO1, LCK, Legumain, LYPD1, MAD-CT-1, MAD-CT-2, MAGEA3, MAGEA4, MAGEC2, MerTk, ML-IAP, NA17, NY-BR-1, p53, p53 mutant, PAP, PLAVI, polysialic acid, PR1, PSA, Sarcoma translocation breakpoints, SART3, sLe, SSX2, Survivin, Tn, TRAIL, TRAIL1, TRP-2, and XAGE1.

[0125] In some embodiments, the antigen is an immune-cell-associated antigen. In some embodiments, the immune-cell-associated antigen is a transmembrane protein. For example, the following antigens are transmembrane proteins: BAFF-R, CD163, CD19, CD20 (exemplary antibodies include rituximab, ocrelizumab, divozilimab; ibritumomab tiuxetan), CD25 (exemplary antibodies include basiliximab), CD274 also known as PD-L1 (exemplary antibodies include adebrelimab, atezolizumab, garivulimab, durvalumab, and avelumab), CD30 (exemplary antibodies include iratumumab and brentuximab), CD33 (exemplary antibodies include lintuzumab), CD352, CD45 (exemplary antibodies include apamistamab), CD47 (exemplary antibodies include letaplimab and magrolimab), CTLA4 (exemplary antibodies include ipilimumab), FASL, IFNAR1 (exemplary antibodies include faralimomab), IFNAR2, LAYN, LILRB2, LILRB4, PD-1 (exemplary antibodies include ipilimumab, nivolumab, pembrolizumab, balstilimab, budigalimab, geptanolimab, toripalimab, and pidilizumabsf), SIT1, and TLR2/4/1 (exemplary antibodies include tomaralimab).

[0126] In some embodiments, the immune-cell-associated antigen is a transmembrane transport protein. For example, Mincle is a transmembrane transport protein.

[0127] In some embodiments, the immune-cell-associated antigen is a transmembrane or membrane-associated glycoprotein. For example, the following antigens are transmembrane or membrane-associated glycoproteins: CD112, CD155, CD24, CD247, CD28, CD30L, CD37 (exemplary antibodies include lilotomab), CD38 (exemplary antibodies include felzartamab), CD3D, CD3E (exemplary antibodies include foralumab and teplizumab), CD3G, CD44,

CLEC12A (exemplary antibodies include tepoditamab), DCIR, DCSIGN, Dectin 1, Dectin 2, ICAM1, LAMP1, Siglecs 1-16, SIRPa, SIRPg, and ULBP1/2/3/4/5/6.

[0128] In some embodiments, the immune-cell-associated antigen is a transmembrane or membrane-associated receptor kinase. For example, the following antigens are transmembrane or membrane-associated receptor kinases: Axl (exemplary antibodies include tilvestamab) and FLT3.

[0129] In some embodiments, the immune-cell-associated antigen is a membrane-associated or membrane-localized protein. For example, the following antigens are membrane-associated or membrane-localized proteins: CD83, IL1RAP (exemplary antibodies include nidanilimab), OX40, SLAMF7 (exemplary antibodies include elotuzumab), and VSIR.

[0130] In some embodiments, the immune-cell-associated antigen is a transmembrane G-protein coupled receptor (GPCR). For example, the following antigens are GPCRs: CCR4 (exemplary antibodies include mogamulizumab-kpkc), CCR8, and CD97.

[0131] In some embodiments, the immune-cell-associated antigen is cell-surface-associated or a cell-surface receptor. For example, the following antigens are cell-surface-associated and/or cell-surface receptors: B7-DC, BCMA, CD137, CD2 (exemplary antibodies include sipilizumab), CD 244, CD27 (exemplary antibodies include varlilumab), CD278 (exemplary antibodies include feladilimab and vopratelimab), CD3 (exemplary antibodies include otelixizumab and visilizumab), CD40 (exemplary antibodies include dacetuzumab and lucatumumab), CD48, CD5 (exemplary antibodies include zolimomab aritox), CD70 (exemplary antibodies include cusatuzumab and vorsetuzumab), CD74 (exemplary antibodies include milatuzumab), CD79A, CD-262 (exemplary antibodies include tigatuzumab), DR4 (exemplary antibodies include mapatumumab), GITR (exemplary antibodies include ragifilimab), HAVCR2, HLA-DR, HLA-E, HLA-F, HLA-G, LAG-3 (exemplary antibodies include encelimumab), MICA, MICB, MRC1, PVRIG, Sialyl-Thomsen-Nouveau Antigen, TIGIT (exemplary antibodies include etigilimab), Trem2, and uPAR.

[0132] In some embodiments, the immune-cell-associated antigen is a chemokine receptor or cytokine receptor. For example, the following antigens are chemokine receptors or cytokine receptors: CD115 (exemplary antibodies include axatilimab, cabiralizumab, and emactuzumab), CD123, CXCR4 (exemplary antibodies include ulocuplumab), IL-21R, and IL-5R (exemplary antibodies include benralizumab).

[0133] In some embodiments, the immune-cell-associated antigen is a co-stimulatory, surface-expressed protein. For example, the following antigens are co-stimulatory, surface-expressed proteins: B7-H 3 (exemplary antibodies include enoblituzumab and omburtamab), B7-H4, B7-H6, and B7-H7.

[0134] In some embodiments, the immune-cell-associated antigen is a peripheral membrane protein. For example, the following antigens are peripheral membrane proteins: B7-1 (exemplary antibodies include galiximab) and B7-2.

[0135] In some embodiments, the immune-cell-associated antigen is aberrantly expressed in individuals with cancer. For example, the following antigens may be aberrantly expressed in individuals with cancer: C5 complement, IDO1, LCK, MerTk, and Tyrol.

[0136] In some embodiments, the antigen is a stromal-cell-associated antigen. In some embodiments, the stromal-cell-associated antigens is a transmembrane or membrane-associated protein. For example, the following antigens are transmembrane or membrane-associated proteins: FAP (exemplary antibodies include sibrotuzumab), IFNAR1 (exemplary antibodies include faralimomab), and IFNAR2.

[0137] In some embodiments, the antigen is CD30. In some embodiments, the antibody is an antibody or antigen-binding fragment that binds to CD30, such as described in International Patent Publication No. WO 02/43661. In some embodiments, the anti-CD30 antibody is cAC10, which is described in International Patent Publication No. WO 02/43661. cAC10 is also known as brentuximab. In some embodiments, the anti-CD30 antibody comprises the CDRs of cAC10. In some embodiments, the CDRs are as defined by the Kabat numbering scheme. In some embodiments, the CDRs are as defined by the Chothia numbering scheme. In some embodiments, the CDRs are as defined by the IMGT numbering scheme. In some embodiments, the CDRs are as defined by the AbM numbering scheme. In some embodiments, the anti-CD30 antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 1, 2, 3, 4, 5, and 6, respectively. In some embodiments, the anti-CD30 antibody comprises a heavy chain variable region comprising an amino acid sequence that is at least 95%, at least 96%, at least 97%, at last 98%, at least 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 7 and a light chain variable region comprising an amino acid sequence that is at least 95% at least 96%, at least 97%, at last 98%, at least 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 8. In some embodiments, the anti-CD30 antibody

comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 9 or SEQ ID NO: 10 and a light chain comprising the amino acid sequence of SEQ ID NO: 11.

[0138] In some embodiments, the antigen is CD70. In some embodiments, the antibody is an antibody or antigen-binding fragment that binds to CD70, such as described in International Patent Publication No. WO 2006/113909. In some embodiments, the antibody is a h1F6 anti-CD70 antibody, which is described in International Patent Publication No. WO 2006/113909. h1F6 is also known as vorsetuzumab. In some embodiments, the anti-CD70 antibody comprises a heavy chain variable region comprising the three CDRs of SEQ ID NO:12 and a light chain variable region comprising the three CDRs of SEQ ID NO:13. In some embodiments, the CDRs are as defined by the Kabat numbering scheme. In some embodiments, the CDRs are as defined by the Chothia numbering scheme. In some embodiments, the CDRs are as defined by the IMGT numbering scheme. In some embodiments, the CDRs are as defined by the AbM numbering scheme. In some embodiments, the anti-CD70 antibody comprises a heavy chain variable region comprising an amino acid sequence that is at least 95%, at least 96%, at least 97%, at last 98%, at least 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 12 and a light chain variable region comprising an amino acid sequence that is at least 95% at least 96%, at least 97%, at last 98%, at least 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 13. In some embodiments, the anti-CD30 antibody comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 14 and a light chain comprising the amino acid sequence of SEQ ID NO: 15.

[0139] In some embodiments, the antigen is interleukin-1 receptor accessory protein (IL1RAP). IL1RAP is a co-receptor of the IL1 receptor (IL1R1) and is required for interleukin-1 (IL1) signaling. IL1 has been implicated in the resistance to certain chemotherapy regimens. IL1RAP is overexpressed in various solid tumors, both on cancer cells and in the tumor microenvironment, but has low expression on normal cells. IL1RAP is also overexpressed in hematopoietic stem and progenitor cells, making it a candidate to target for chronic myeloid leukemia (CML). IL1RAP has also been shown to be overexpressed in acute myeloid leukemia (AML). Antibody binding to IL1RAP could block signal transduction from IL-1 and IL-33 into cells and allow NK-cells to recognize tumor cells and subsequent killing by antibody dependent cellular cytotoxicity (ADCC).

[0140] In some embodiments, the antigen is ASCT2. ASCT2 is also known as SLC1A5. ASCT2 is a ubiquitously expressed, broad-specificity, sodium-dependent neutral amino acid exchanger. ASCT2 is involved in glutamine transport. ASCT2 is overexpressed in different cancers and is closely related to poor prognosis. Downregulating ASCT2 has been shown to suppress intracellular glutamine levels and downstream glutamine metabolism, including glutathione production. Due to its high expression in many cancers, ASCT2 is a potential therapeutic target. These effects attenuated growth and proliferation, increased apoptosis and autophagy, and increased oxidative stress and mTORC1 pathway suppression in head and neck squamous cell carcinoma (HNSCC). Additionally, silencing ASCT2 improved the response to cetuximab in HNSCC.

[0141] In some embodiments, an antibody provided herein binds to TROP2. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 16, 17, 18, 19, 20, and 21, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 22 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 23. In some embodiments, the antibody is sacituzumab. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 24, 25, 26, 27, 28, and 29, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 30 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 31. In some embodiments, the antibody is datopotamab.

[0142] In some embodiments, an antibody provided herein binds to MICA. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 32, 33, 34, 35, 36, and 37, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 38 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 39. In some embodiments, the antibody is h1D5v11 hIgG1K. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 40, 41, 42, 43, 44, and 45, respectively. In some embodiments, the antibody comprises a heavy chain

variable region comprising the amino acid sequence of SEQ ID NO: 46 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 47. In some embodiments, the antibody is MICA.36 hIgG1K G236A. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 48, 49, 50, 51, 52, and 53, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 54 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 55. In some embodiments, the antibody is h3F9 H1L3 hIgG1K. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 56, 57, 58, 59, 60, and 61, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 62 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 63. In some embodiments, the antibody is CM33322 Ab28 hIgG1K.

[0143] In some embodiments, an antibody provided herein binds to CD24. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 64, 65, 66, 67, 68, and 69, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 70 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 71. In some embodiments, the antibody is SWA11.

[0144] In some embodiments, an antibody provided herein binds to ITGav. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 72, 73, 74, 75, 76, and 77, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 78 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 79. In some embodiments, the antibody is intetumumab. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 80, 81, 82, 83, 84, and 85, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 86 and a light chain variable region

comprising the amino acid sequence of SEQ ID NO: 87. In some embodiments, the antibody is abituzumab.

[0145] In some embodiments, an antibody provided herein binds to gpA33. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 88, 89, 90, 91, 92, and 93, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 94 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 95.

[0146] In some embodiments, an antibody provided herein binds to IL1Rap. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 96, 97, 98, 99, 100, and 101, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 102 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 103. In some embodiments, the antibody is nidanilimab.

[0147] In some embodiments, an antibody provided herein binds to EpCAM. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 104, 105, 106, 107, 108, and 109, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 110 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 111. In some embodiments, the antibody is adecatumumab. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 112, 113, 114, 115, 116, and 117, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 118 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 119. In some embodiments, the antibody is Ep157305. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 120, 121, 122, 123, 124, and 125, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 126 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 127. In some embodiments,

the antibody is Ep3-171. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 128, 129, 130, 131, 132, and 133, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 134 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 135. In some embodiments, the antibody is Ep3622w94. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 136, 137, 138, 139, 140, and 141, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 142 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 143. In some embodiments, the antibody is EpING1. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 144, 145, 146, 147, 148, and 149, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 150 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 151. In some embodiments, the antibody is EpAb2-6.

[0148] In some embodiments, an antibody provided herein binds to CD352. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 152, 153, 154, 155, 156, and 157, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 158 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 159. In some embodiments, the antibody is h20F3.

[0149] In some embodiments, an antibody provided herein binds to CS1. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 160, 161, 162, 163, 164, and 165, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 166 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 167. In some embodiments, the antibody is elotuzumab.

[0150] In some embodiments, an antibody provided herein binds to CD38. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 168, 169, 170, 171, 172, and 173, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 174 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 175. In some embodiments, the antibody is daratumumab.

[0151] In some embodiments, an antibody provided herein binds to CD25. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 176, 177, 178, 179, 180, and 181, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 182 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 183. In some embodiments, the antibody is daclizumab.

[0152] In some embodiments, an antibody provided herein binds to ADAM9. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 184, 185, 186, 187, 188, and 189, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 190 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 191. In some embodiments, the antibody is chMAbA9-A. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 192, 193, 194, 195, 196, and 197, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 198 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 199. In some embodiments, the antibody is hMAbA9-A.

[0153] In some embodiments, an antibody provided herein binds to CD59. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 200, 201, 202, 203, 204, and 205, respectively. In some embodiments, the antibody comprises a heavy chain variable region

comprising the amino acid sequence of SEQ ID NO: 206 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 207.

[0154] In some embodiments, an antibody provided herein binds to CD25. In some embodiments, the antibody is Clone123.

[0155] In some embodiments, an antibody provided herein binds to CD229. In some embodiments, the antibody is h8A10.

[0156] In some embodiments, an antibody provided herein binds to CD19. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 208, 209, 210, 211, 212, and 213, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 214 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 215. In some embodiments, the antibody is denintuzumab, which is also known as hBU12. See WO2009052431.

[0157] In some embodiments, an antibody provided herein binds to CD70. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 216, 217, 218, 219, 220, and 221, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 222 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 223. In some embodiments, the antibody is vorsetuzumab.

[0158] In some embodiments, an antibody provided herein binds to B7H4. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 224, 225, 226, 227, 228, and 229, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 230 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 231. In some embodiments, the antibody is mirzotamab.

[0159] In some embodiments, an antibody provided herein binds to CD138. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 232, 233, 234, 235, 236, and 237, respectively. In some embodiments, the antibody comprises a heavy chain variable region

comprising the amino acid sequence of SEQ ID NO: 238 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 239. In some embodiments, the antibody is indatuxumab.

[0160] In some embodiments, an antibody provided herein binds to CD166. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 240, 241, 242, 243, 244, and 245, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 246 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 247. In some embodiments, the antibody is praluzatamab.

[0161] In some embodiments, an antibody provided herein binds to CD51. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 248, 249, 250, 251, 252, and 253, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 254 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 255. In some embodiments, the antibody is intetumumab.

[0162] In some embodiments, an antibody provided herein binds to CD56. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 256, 257, 258, 259, 260, and 261, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 262 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 263. In some embodiments, the antibody is lorvotuzumab.

[0163] In some embodiments, an antibody provided herein binds to CD74. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 264, 265, 266, 267, 268, and 269, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 270 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 271. In some embodiments, the antibody is milatuzumab.

[0164] In some embodiments, an antibody provided herein binds to CEACAM5. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 272, 273, 274, 275, 276, and 277, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 278 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 279. In some embodiments, the antibody is labetuzumab.

[0165] In some embodiments, an antibody provided herein binds to CanAg. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 280, 281, 282, 283, 284, and 285, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 286 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 287. In some embodiments, the antibody is cantuzumab.

[0166] In some embodiments, an antibody provided herein binds to DLL-3. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 288, 289, 290, 291, 292, and 293, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 294 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 295. In some embodiments, the antibody is rovalpituzumab.

[0167] In some embodiments, an antibody provided herein binds to DPEP-3. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 296, 297, 298, 299, 300, and 301, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 302 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 303. In some embodiments, the antibody is tamrintamab.

[0168] In some embodiments, an antibody provided herein binds to EGFR. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 304, 305, 306, 307, 308, and 309,

respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 310 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 311. In some embodiments, the antibody is laprituximab. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOS: 312, 313, 314, 315, 316, and 317, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 318 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 319. In some embodiments, the antibody is losatuxizumab. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOS: 320, 321, 322, 323, 324, and 325, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 326 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 327. In some embodiments, the antibody is serclutamab. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOS: 328, 329, 330, 331, 332, and 333, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 334 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 335. In some embodiments, the antibody is cetuximab.

[0169] In some embodiments, an antibody provided herein binds to FRa. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOS: 336, 337, 338, 339, 340, and 341, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 342 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 343. In some embodiments, the antibody is mirvetuximab. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOS: 344, 345, 346, 347, 348, and 349, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 350 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 351. In some embodiments, the antibody is farletuzumab.

[0170] In some embodiments, an antibody provided herein binds to MUC-1. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 352, 353, 354, 355, 356, and 357, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 358 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 359. In some embodiments, the antibody is gatipotuzumab.

[0171] In some embodiments, an antibody provided herein binds to mesothelin. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 360, 361, 362, 363, 364, and 365, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 366 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 367. In some embodiments, the antibody is anetumab.

[0172] In some embodiments, an antibody provided herein binds to ROR-1. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 368, 369, 370, 371, 372, and 373, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 374 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 375. In some embodiments, the antibody is zilovertamab.

[0173] In some embodiments, an antibody provided herein binds to ASCT2. In some embodiments, an antibody provided herein binds to B7H4. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 376, 377, 378, 379, 380, and 381, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 382 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 383. In some embodiments, the antibody is 20502. See WO2019040780.

[0174] In some embodiments, an antibody provided herein binds to B7-H3. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 384, 385, 386, 387, 388, and 389,

respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 390 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 391. In some embodiments, the antibody is chAb-A (BRCA84D). In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 392, 393, 394, 395, 396, and 397, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 398 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 399. In some embodiments, the antibody is hAb-B. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 400, 401, 402, 403, 404, and 405, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 406 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 407. In some embodiments, the antibody is hAb-C. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 408, 409, 410, 411, 412, and 413, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 414 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 415. In some embodiments, the antibody is hAb-D. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 416, 417, 418, 419, 420, and 421, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 422 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 423. In some embodiments, the antibody is chM30. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 424, 425, 426, 427, 428, and 429, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 430 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 431. In some embodiments, the antibody is hM30-H1-L4. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 432, 433, 434, 435, 436, and 437, respectively. In some embodiments, the antibody comprises a

heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 438 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 439. In some embodiments, the antibody is AbV_huAb18-v4. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 440, 441, 442, 443, 444, and 445, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 446 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 447. In some embodiments, the antibody is AbV_huAb3-v6. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 448, 449, 450, 451, 452, and 453, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 454 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 455. In some embodiments, the antibody is AbV_huAb3-v2.6. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 456, 457, 458, 459, 460, and 461, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 462 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 463. In some embodiments, the antibody is AbV_huAb13-v1-CR. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 464, 465, 466, 467, 468, and 469, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 470 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 471. In some embodiments, the antibody is 8H9-6m. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 472 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 473. In some embodiments, the antibody is m8517. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 474, 475, 476, 477, 478, and 479, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 480 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 481. In some embodiments, the antibody is

TPP-5706. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 482 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 483. In some embodiments, the antibody is TPP-6642. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 484 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 485. In some embodiments, the antibody is TPP-6850.

[0175] In some embodiments, an antibody provided herein binds to CDCP1. In some embodiments, the antibody is 10D7.

[0176] In some embodiments, an antibody provided herein binds to HER3. In some embodiments, the antibody comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 486 and a light chain comprising the amino acid sequence of SEQ ID NO: 487. In some embodiments, the antibody is patritumab. In some embodiments, the antibody comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 488 and a light chain comprising the amino acid sequence of SEQ ID NO: 489. In some embodiments, the antibody is scribantumab. In some embodiments, the antibody comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 490 and a light chain comprising the amino acid sequence of SEQ ID NO: 491. In some embodiments, the antibody is elgemtumab. In some embodiments, the antibody comprises a heavy chain the amino acid sequence of SEQ ID NO: 492 and a light chain comprising the amino acid sequence of SEQ ID NO: 493. In some embodiments, the antibody is lumretuzumab.

[0177] In some embodiments, an antibody provided herein binds to RON. In some embodiments, the antibody is Zt/g4.

[0178] In some embodiments, an antibody provided herein binds to claudin-2.

[0179] In some embodiments, an antibody provided herein binds to HLA-G.

[0180] In some embodiments, an antibody provided herein binds to PTK7. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 494, 495, 496, 497, 498, and 499, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 500 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 501. In some embodiments, the antibody is PTK7 mab 1. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-

L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 502, 503, 504, 505, 506, and 507, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 508 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 509. In some embodiments, the antibody is PTK7 mab 2. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 510, 511, 512, 513, 514, and 515, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 516 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 517. In some embodiments, the antibody is PTK7 mab 3.

[0181] In some embodiments, an antibody provided herein binds to LIV1. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 518, 519, 520, 521, 522, and 523, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 524 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 525. In some embodiments, the antibody is ladiratuzumab, which is also known as hLIV22 and hglg. See WO2012078668.

[0182] In some embodiments, an antibody provided herein binds to avb6. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 526, 527, 528, 529, 530, and 531, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 532 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 533. In some embodiments, the antibody is h2A2. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 534, 535, 536, 537, 538, and 539, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 540 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 541. In some embodiments, the antibody is h15H3.

[0183] In some embodiments, an antibody provided herein binds to CD48. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and

CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 542, 543, 544, 545, 546, and 547, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 548 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 549. In some embodiments, the antibody is hMEM102. See WO2016149535.

[0184] In some embodiments, an antibody provided herein binds to PD-L1. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 550, 551, 552, 553, 554, and 555, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 556 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 557. In some embodiments, the antibody is SG-559-01 LALA mAb.

[0185] In some embodiments, an antibody provided herein binds to IGF-1R. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 558, 559, 560, 561, 562, and 563, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 564 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 565. In some embodiments, the antibody is cixutumumab.

[0186] In some embodiments, an antibody provided herein binds to claudin-18.2. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 566, 567, 568, 569, 570, and 571, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 572 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 573. In some embodiments, the antibody is zolbetuximab (175D10). In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 574, 575, 576, 577, 578, and 579, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 580 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 581. In some embodiments, the antibody is 163E12.

[0187] In some embodiments, an antibody provided herein binds to Nectin-4. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 582, 583, 584, 585, 586, and 587, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 588 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 589. In some embodiments, the antibody is enfortumab. See WO 2012047724.

[0188] In some embodiments, an antibody provided herein binds to SLTRK6. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 590, 591, 592, 593, 594, and 595, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 596 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 597. In some embodiments, the antibody is sirtratumab.

[0189] In some embodiments, an antibody provided herein binds to CD228. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 598, 599, 600, 601, 602, and 603, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 604 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 605. In some embodiments, the antibody is hL49. See WO 2020/163225.

[0190] In some embodiments, an antibody provided herein binds to CD142 (tissue factor; TF). In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 606, 607, 608, 609, 610, and 611, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 612 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 613. In some embodiments, the antibody is tisotumab. See WO 2010/066803.

[0191] In some embodiments, an antibody provided herein binds to STn. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 614, 615, 616, 617, 618, and 619,

respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 620 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 621. In some embodiments, the antibody is h2G12.

[0192] In some embodiments, an antibody provided herein binds to CD20. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 622, 623, 624, 625, 626, and 627, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 628 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 629. In some embodiments, the antibody is rituximab.

[0193] In some embodiments, an antibody provided herein binds to HER2. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 630, 631, 632, 633, 634, and 635, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 636 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 637. In some embodiments, the antibody is trastuzumab.

[0194] In some embodiments, an antibody provided herein binds to FLT3.

[0195] In some embodiments, an antibody provided herein binds to CD46.

[0196] In some embodiments, an antibody provided herein binds to GloboH.

[0197] In some embodiments, an antibody provided herein binds to AG7.

[0198] In some embodiments, an antibody provided herein binds to mesothelin.

[0199] In some embodiments, an antibody provided herein binds to FCRH5.

[0200] In some embodiments, an antibody provided herein binds to ETBR.

[0201] In some embodiments, an antibody provided herein binds to Tim-1.

[0202] In some embodiments, an antibody provided herein binds to SLC44A4.

[0203] In some embodiments, an antibody provided herein binds to ENPP3.

[0204] In some embodiments, an antibody provided herein binds to CD37.

[0205] In some embodiments, an antibody provided herein binds to CA9.

[0206] In some embodiments, an antibody provided herein binds to Notch3.

[0207] In some embodiments, an antibody provided herein binds to EphA2.

[0208] In some embodiments, an antibody provided herein binds to TRFC.

[0209] In some embodiments, an antibody provided herein binds to PSMA.

[0210] In some embodiments, an antibody provided herein binds to LRRC15.

[0211] In some embodiments, an antibody provided herein binds to 5T4.

[0212] In some embodiments, an antibody provided herein binds to CD79b. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 638, 639, 640, 641, 642, and 643, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 644 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 645. In some embodiments, the antibody is polatuzumab.

[0213] In some embodiments, an antibody provided herein binds to NaPi2B. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 646, 647, 648, 649, 650, and 651, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 652 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 653. In some embodiments, the antibody is lifastuzumab.

[0214] In some embodiments, an antibody provided herein binds to Muc16. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 654, 655, 656, 657, 658, and 659, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 660 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 661. In some embodiments, the antibody is sofituzumab.

[0215] In some embodiments, an antibody provided herein binds to STEAP1. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 662, 663, 664, 665, 666, and 667, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 668 and a light chain variable region

comprising the amino acid sequence of SEQ ID NO: 669. In some embodiments, the antibody is vandortuzumab.

[0216] In some embodiments, an antibody provided herein binds to BCMA. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 670, 671, 672, 673, 674, and 675, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 676 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 677. In some embodiments, the antibody is belantamab.

[0217] In some embodiments, an antibody provided herein binds to c-Met. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 678, 679, 680, 681, 682, and 683, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 684 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 685. In some embodiments, the antibody is telisotuzumab.

[0218] In some embodiments, an antibody provided herein binds to EGFR. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 686, 687, 688, 689, 690, and 691, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 692 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 693. In some embodiments, the antibody is depatuxizumab.

[0219] In some embodiments, an antibody provided herein binds to SLAMF7. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 694, 695, 696, 697, 698, and 699, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 700 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 701. In some embodiments, the antibody is azintuxizumab.

[0220] In some embodiments, an antibody provided herein binds to SLITRK6. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 702, 703, 704, 705, 706, and 707, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 708 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 709. In some embodiments, the antibody is sirtratumab.

[0221] In some embodiments, an antibody provided herein binds to C4.4a. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 710, 711, 712, 713, 714, and 715, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 716 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 717. In some embodiments, the antibody is lupartumab.

[0222] In some embodiments, an antibody provided herein binds to GCC. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 718, 719, 720, 721, 722, and 723, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 724 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 725. In some embodiments, the antibody is indusatumab.

[0223] In some embodiments, an antibody provided herein binds to Axl. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 726, 727, 728, 729, 730, and 731, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 732 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 733. In some embodiments, the antibody is enapotamab.

[0224] In some embodiments, an antibody provided herein binds to gpNMB. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 734, 735, 736, 737, 738, and 739,

respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 740 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 741. In some embodiments, the antibody is glembatumumab.

[0225] In some embodiments, an antibody provided herein binds to Prolactin receptor. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 742, 743, 744, 745, 746, and 747, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 748 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 749. In some embodiments, the antibody is rolinsatamab.

[0226] In some embodiments, an antibody provided herein binds to FGFR2. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 750, 751, 752, 753, 754, and 755, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 756 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 757. In some embodiments, the antibody is aprutumab.

[0227] In some embodiments, an antibody provided herein binds to CDCP1. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 758, 759, 760, 761, 762, and 763, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 764 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 765. In some embodiments, the antibody is Humanized CUB4 #135 HC4-H. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 766, 767, 768, 769, 770, and 771, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 772 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 773. In some embodiments, the antibody is CUB4. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of

SEQ ID NOs: 774, 775, 776, 777, 778, 779, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 780 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 781. In some embodiments, the antibody is CP13E10-WT. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 782, 783, 784, 785, 786, and 787, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 788 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 789. In some embodiments, the antibody is CP13E10-54HCv13-89LCv1.

[0228] In some embodiments, an antibody provided herein binds to ASCT2. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 790 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 791. In some embodiments, the antibody is KM8094a. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 792 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 793. In some embodiments, the antibody is KM8094b. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 794, 795, 796, 797, 798, and 799, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 800 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 801. In some embodiments, the antibody is KM4018.

[0229] In some embodiments, an antibody provided herein binds to CD123. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 802, 803, 804, 805, 806, and 807, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 808 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 809. In some embodiments, the antibody is h7G3. See WO 2016201065.

[0230] In some embodiments, an antibody provided herein binds to GPC3. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 810, 811, 812, 813, 814, and 815,

respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 816 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 817. In some embodiments, the antibody is hGPC3-1. See WO 2019161174.

[0231] In some embodiments, an antibody provided herein binds to B6A. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 818, 819, 820, 821, 822, and 823, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 824 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 825. In some embodiments, the antibody is h2A2. See PCT/US20/63390. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 826, 827, 828, 829, 830, and 831, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 832 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 833. In some embodiments, the antibody is h15H3. See WO 2013/123152.

[0232] In some embodiments, an antibody provided herein binds to PD-L1. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 834, 835, 836, 837, 838, and 839, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 840 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 841. In some embodiments, the antibody is SG-559-01. See PCT/US2020/054037.

[0233] In some embodiments, an antibody provided herein binds to TIGIT. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 842, 843, 844, 845, 846, and 847, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 848 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 849. In some embodiments, the antibody is Clone 13 (also known as ADI-23674 or mAb13). See WO 2020041541.

[0234] In some embodiments, an antibody provided herein binds to STN. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 850, 851, 852, 853, 854, and 855, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 856 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 857. In some embodiments, the antibody is 2G12-2B2. See WO 2017083582.

[0235] In some embodiments, an antibody provided herein binds to CD33. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 858, 859, 860, 861, 862, and 863, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 864 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 865. In some embodiments, the antibody is h2H12. See WO2013173496.

[0236] In some embodiments, an antibody provided herein binds to NTBA (also known as CD352). In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 866, 867, 868, 869, 870, and 871, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 872 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 873. In some embodiments, the antibody is h20F3 HDLD. See WO 2017004330.

[0237] In some embodiments, an antibody provided herein binds to BCMA. In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 874, 875, 876, 877, 878, and 879, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 880 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 881. In some embodiments, the antibody is SEA-BCMA (also known as hSG16.17). See WO 2017/143069.

[0238] In some embodiments, an antibody provided herein binds to Tissue Factor (also known as TF). In some embodiments, the antibody comprises CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 comprising the amino acid sequences of SEQ ID NOs: 882, 883, 884,

885, 886, and 887, respectively. In some embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 888 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 889. In some embodiments, the antibody is tisotumab. See WO 2010/066803 and US 9,150,658.

TABLE OF SEQUENCES

| SEQ ID NO | Description | Sequence |
|-----------|--------------|---|
| 1 | cAC10 CDR-H1 | DYYIT |
| 2 | cAC10 CDR-H2 | WIYPGSGNTKYNEKFKG |
| 3 | cAC10 CDR-H3 | YGNWYFAY |
| 4 | cAC10 CDR-L1 | KASQSVDFDGD SYMN |
| 5 | cAC10 CDR-L2 | AASNLES |
| 6 | cAC10 CDR-L3 | QQSNEDPWT |
| 7 | cAC10 VH | QIQLQQSGPEVVKPGASVKISCKASGYTFTDYYITWVKQKPGQG LEWIGWIYPGSGNTKY
NEKFKGKATLTVDTSSTAFMQLSSLTSED TAVYFCANYGNYWFAYWGQGTQVTVSA |
| 8 | cAC10 VL | DIVLTQSPASLAVSLGQRATISCKASQSVDFDGD SYMNWYQQKPGQPPKVLIIYAASNLES
GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPWTFGGGTKLEIK |
| 9 | cAC10 HC | QIQLQQSGPEVVKPGASVKISCKASGYTFTDYYITWVKQKPGQG LEWIGWIYPGSGNTKY
NEKFKGKATLTVDTSSTAFMQLSSLTSED TAVYFCANYGNYWFAYWGQGTQVTVSAAS
T KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSS
GLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK |
| 10 | cAC10 HC v2 | QIQLQQSGPEVVKPGASVKISCKASGYTFTDYYITWVKQKPGQG LEWIGWIYPGSGNTKY
NEKFKGKATLTVDTSSTAFMQLSSLTSED TAVYFCANYGNYWFAYWGQGTQVTVSAAS
T KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSS
GLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPG |
| 11 | cAC10 LC | DIVLTQSPASLAVSLGQRATISCKASQSVDFDGD SYMNWYQQKPGQPPKVLIIYAASNLES
GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPWTFGGGTKLEIKR
TVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS
KDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC |
| 12 | h1F6 VH | QVQLVQSGAEVKKPGASVKVSKASGYTFTNYGMNWVRQAPGQGLKWMGWINTYTGE
PTY
ADAFKGRVTMTTRDTSISTAYMELSRRLRSDDTAVYYCARDYGDYGM DYWGQGT TVTVSS |
| 13 | h1F6 VL | DIVMTQSPDSLAVSLGERATINCRASKSVSTSGYSFMHWYQQKPGQPPKLLIYLAASNLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQHSREVPWTFGQGTKEIK |
| 14 | h1F6 HC | QVQLVQSGAEVKKPGASVKVSKASGYTFTNYGMNWVRQAPGQGLKWMGWINTYTGE
PTY
ADAFKGRVTMTTRDTSISTAYMELSRRLRSDDTAVYYCARDYGDYGM DYWGQGT TVTVSSA
S
TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGL
YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS
VFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST
YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL T
KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
Q
GNVFSCSVMHEALHNHYTQKSLSLSPGK |

| SEQ ID NO | Description | Sequence |
|-----------|--------------|--|
| 15 | h1F6 LC | DIVMTQSPDSLAVSLGERATINCRASKSVSTSGYSFMHWYQQKPGQPPKLLIYLASNLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQHSREVPWTFGGGTKVEIKRTVAAPSVF
IFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSL
STLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC |
| 16 | TROP2 CDR-H1 | NYGMN |
| 17 | TROP2 CDR-H2 | WINTYTGEPTYTDDFKG |
| 18 | TROP2 CDR-H3 | GGFGSSYWYFDV |
| 19 | TROP2 CDR-L1 | KASQDVSIABA |
| 20 | TROP2 CDR-L2 | SASYRYT |
| 21 | TROP2 CDR-L3 | QQHYITPLT |
| 22 | TROP2 VH | QVQLQQSGSELKKPGASVKVSCASGYTFTNYGMNWVKAPGQGLKWMGWINTYTGE
PT
YTDDFKGRFAFSLDTSVSTAYLQISSLKADDTAVYFCARGGGFGSSYWYFDVWGGGSLVT
VSS |
| 23 | TROP2 VL | DIQLTQSPSSLSASVGDRTITCKASQDVSIABAWYQQKPGKAPKLLIYSASYRYTGVP
DRFSGSGSGTDFTLTISSLQPEDFAVYYCQQHYITPLTFGAGTKVEIK |
| 24 | TROP2 CDR-H1 | TAGMQ |
| 25 | TROP2 CDR-H2 | WINTHSGVPKYAEDFKG |
| 26 | TROP2 CDR-H3 | SGFGSSYWYFDV |
| 27 | TROP2 CDR-L1 | KASQDVSTABA |
| 28 | TROP2 CDR-L2 | SASYRYT |
| 29 | TROP2 CDR-L3 | QQHYITPLT |
| 30 | TROP2 VH | QVQLVQSGAEVKKPGASVKVSCASGYTFTTAGMQWVRQAPGQGLEWMGWINTHSGV
PKYAEDFKGRVTISADTSTSTAYLQLSSLKSEDTAVYYCARSGFGSSYWYFDVWGGGTLV
TVSS |
| 31 | TROP2 VL | DIQMTQSPSSLSASVGDRTITCKASQDVSTABAWYQQKPGKAPKLLIYSASYRYTGVP
RFSGSGSGTDFTLTISSLQPEDFAVYYCQQHYITPLTFGQGTKLEIK |
| 32 | MICA CDR-H1 | SQNIY |
| 33 | MICA CDR-H2 | YIEPYNVPMYNPKFKG |
| 34 | MICA CDR-H3 | SGSSNFDY |
| 35 | MICA CDR-L1 | SASSISSHYLH |
| 36 | MICA CDR-L2 | RTSNLAS |
| 37 | MICA CDR-L3 | QQGSSLPLT |
| 38 | MICA VH | EIQLVQSGAEVKKPGASVKVSCASGYAFTSQNIYWVRQAPGQGLEWIGYIEPYNVPMY
NPKFKGRATLTVDKSTSTAYLELSSLRSEDVAVYYCARSGSSNFDYWGGGTLTVSS |
| 39 | MICA VL | DIQLTQSPSSLSASVGDRTITCSASSISSHYLHWYQQKPGKSPKLLIYRTSNLASGVPSR
FSGSGSGTDYTLTISSLQPEDFATYYCQQGSSLPLTFGQGTKVEIK |
| 40 | MICA CDR-H1 | NYAMH |
| 41 | MICA CDR-H2 | LIWYDGSNKFYGDVKG |
| 42 | MICA CDR-H3 | EGSGHY |
| 43 | MICA CDR-L1 | RASQGISSALA |
| 44 | MICA CDR-L2 | DASSLES |
| 45 | MICA CDR-L3 | QQFNSYPIT |
| 46 | MICA VH | QVQLVESGGGVVQPGSRSLRSCAASGFTFSNYAMHWVRQAPGEGLEWVALIWYDGSNK
FYGDSVKGRFTISRDNKNTLYLQMNSLSAEDTAVYYCAREGSGHYWGQGTLLTVSS |

| SEQ ID NO | Description | Sequence |
|-----------|--------------|---|
| 47 | MICA VL | AIQLTQSPSSLSASVGDRVITITCRASQGISSALAWYQQKPGKVPKSLIYDASSLESGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCQQFNSYPITFGQGTRLEIK |
| 48 | MICA CDR-H1 | NYAMS |
| 49 | MICA CDR-H2 | YISPGGDYIYYADSVKG |
| 50 | MICA CDR-H3 | DRRHYSYAMDY |
| 51 | MICA CDR-L1 | RSSKSLHLSNLNTLY |
| 52 | MICA CDR-L2 | RMSNLAS |
| 53 | MICA CDR-L3 | MQHLEYPFT |
| 54 | MICA VH | QVQLVESGGGLVKPGGSLRLSCAASGFTFSNYAMSWIRQAPGKGLEWVSYSISPGGDYIY
YADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCTTDRRHYSYAMDYWGQGTQVTVSS |
| 55 | MICA VL | DIVMTQSPLSLPVTPGEPASISCRSSKSLHLSNLNTLYWFLQKPGQSPQILYRMSNLASG
VPDRFSGSGSGTAFTLKISRVEAEDVGVYYCMQHLEYPFTFGPGTKLEIK |
| 56 | MICA CDR-H1 | TYAFH |
| 57 | MICA CDR-H2 | GIVPIFGTLKYAQKFQD |
| 58 | MICA CDR-H3 | AIQLEGRPFDH |
| 59 | MICA CDR-L1 | RASQGITSYLA |
| 60 | MICA CDR-L2 | AASALQS |
| 61 | MICA CDR-L3 | QQVNRGAAT |
| 62 | MICA VH | QVQLVQSGAEVKKPGSSVRVSCRASGGSSTTYAFHWVRQAPGQGLEWMGGIVPIFGTL
KYAQKFQDRVTLTADKSTGTAYMELNSLRLLDDTAVYYCARAIQLEGRPFDHWGQGTQVTVSA |
| 63 | MICA VL | DIQLTQSPSFLSASVGDRVITITCRASQGITSYLAWYQQKPGKAPKLLIYAASALQSGVPSR
FSGRSGTEFTLTISLQPEDFATYYCQQVNRGAATFGHGTRLDIK |
| 64 | CD24 CDR-H1 | TYAFH |
| 65 | CD24 CDR-H2 | GIVPIFGTLKYAQKFQD |
| 66 | CD24 CDR-H3 | AIQLEGRPFDH |
| 67 | CD24 CDR-L1 | RASQGITSYLA |
| 68 | CD24 CDR-L2 | AASALQS |
| 69 | CD24 CDR-L3 | QQVNRGAAT |
| 70 | CD24 VH | QVQLVQSGAEVKKPGSSVRVSCRASGGSSTTYAFHWVRQAPGQGLEWMGGIVPIFGTL
KYAQKFQDRVTLTADKSTGTAYMELNSLRLLDDTAVYYCARAIQLEGRPFDHWGQGTQVTVSA |
| 71 | CD24 VL | DIQLTQSPSFLSASVGDRVITITCRASQGITSYLAWYQQKPGKAPKLLIYAASALQSGVPS
RFSGRSGTEFTLTISLQPEDFATYYCQQVNRGAATFGHGTRLDIK |
| 72 | ITGav CDR-H1 | RYTMH |
| 73 | ITGav CDR-H2 | VISFDGSNKKYYVDSVKG |
| 74 | ITGav CDR-H3 | EARGSYAFDI |
| 75 | ITGav CDR-L1 | RASQSVSSYLA |
| 76 | ITGav CDR-L2 | DASNRAT |
| 77 | ITGav CDR-L3 | QQRSNWPPFT |
| 78 | ITGav VH | QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTMHWVRQAPGKGLEWVAVISFDGSNK
YYVDSVKGRFTISRDNSENTLYLQVNLRAEDTAVYYCAREARGSYAFDIWGQGTMTVSS |

| SEQ ID NO | Description | Sequence |
|-----------|---------------|---|
| 79 | ITGav VL | EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSELPEDFAVYYCQQRSNWPPFTFGPGTKVDIK |
| 80 | ITGav CDR-H1 | SFWMH |
| 81 | ITGav CDR-H2 | YINPRSGYTEYNEIFRD |
| 82 | ITGav CDR-H3 | FLGRGAMDY |
| 83 | ITGav CDR-L1 | RASQDISNYLA |
| 84 | ITGav CDR-L2 | YTSKIHS |
| 85 | ITGav CDR-L3 | QQGNTFPYT |
| 86 | ITGav VH | QVQLQQSGGELAKPGASVKVSCASGYTFSSFWMHVWRQAPGQGLEWIGYINPRSGYTEYNEIFRDKATMTTDTSTSTAYMELSSLRSEDAVYYCASFLGRGAMDYWGQGTITVTVSS |
| 87 | ITGav VL | DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYYTSKIHSGVPSRFSGSGSGTDYFTISLQPEDATYYCQQGNTFPYTFGQGTKVEIK |
| 88 | gpA33 CDR-H1 | TSSYYWG |
| 89 | gpA33 CDR-H2 | TIYYNGSTYYSPSLKS |
| 90 | gpA33 CDR-H3 | QGYDIKINIDV |
| 91 | gpA33 CDR-L1 | RASQSVSSYLA |
| 92 | gpA33 CDR-L2 | VASNRAT |
| 93 | gpA33 CDR-L3 | QQRSNWPLT |
| 94 | gpA33 VH | QLQLQESGPGLVKPSSETLSLTCTVSGGSISTSSYYWGWIRQPPGKGLEWIGTIYYNGSTYYSPSLKSRVSVSDTSKNQFSLKLSSVTAADTSVYYCARQGQYDIKINIDVWGQGTITVTVSS |
| 95 | gpA33 VL | EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYVASNRATGIPARFSGSGSGTDFTLTISSELPEDFAVYYCQQRSNWPLTFGGGTKVEIK |
| 96 | IL1Rap CDR-H1 | SSWMN |
| 97 | IL1Rap CDR-H2 | RIYPGDGNTHYAQKFQG |
| 98 | IL1Rap CDR-H3 | GYLDPM DY |
| 99 | IL1Rap CDR-L1 | QASQGINNYLN |
| 100 | IL1Rap CDR-L2 | YTSGLHA |
| 101 | IL1Rap CDR-L3 | QQYSILPWT |
| 102 | IL1Rap VH | QVQLVQSGAEVKKPGSSVKVSCASGYAFTSSWMNVWRQAPGQGLEWMGRIYPGDGNTHYAKKFQGRVTLTADKSTSTAYMELSSLRSEDAVYYCGEGYLDPM DYWGQGTITVTVSS |
| 103 | IL1Rap VL | DIQMTQSPSSLSASVGDRVTITCQASQGINNYLNWYQQKPGKAPKLLIHYTSGLHAGVPSRFSGSGSGTDYTLTISSELPEDVATYYCQQYSILPWTFGGGTKVEIK |
| 104 | EpCAM CDR-H1 | SYGMH |
| 105 | EpCAM CDR-H2 | VISYDGSNKYYADSVKG |
| 106 | EpCAM CDR-H3 | DMG |
| 107 | EpCAM CDR-L1 | RTSQSISSYLN |
| 108 | EpCAM CDR-L2 | WASTRES |
| 109 | EpCAM CDR-L3 | QQSYDIPYT |
| 110 | EpCAM VH | EVQLLESGGGVWQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLR AEDAVYYCAKDMGWGSGWRPYYYYGMDVWGQGTITVTVSS |
| 111 | EpCAM VL | ELQMTQSPSSLSASVGDRVTITCRTSQSISSYLNWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISLQPEDSATYYCQQSYDIPYTFGQGTKLEIK |
| 112 | EpCAM CDR-H1 | NYWMS |
| 113 | EpCAM CDR-H2 | NIKQDGSEKFYADSVKG |
| 114 | EpCAM CDR-H3 | VGPSWEQDY |

| SEQ ID NO | Description | Sequence |
|-----------|--------------|---|
| 115 | EpCAM CDR-L1 | TGSSSNIGSYYG VH |
| 116 | EpCAM CDR-L2 | SDTNRPS |
| 117 | EpCAM CDR-L3 | QSYDKGFGHRV |
| 118 | EpCAM VH | EVQLVESGGGLVQP GGS LRLSCAASGFTFSNYWMSWVRQAPGKGLEWVANIKQDGSEK
FYADSVKGRFTISRDN AKNSLYLQMNSLRAEDTAVYYCARVGPSWEQDYWGQGLTVTVS
A |
| 119 | EpCAM VL | QSVLTQPPSVSGAPGQRVTISCTGSSSNIGSYYG VHWHYQQLPGTAPKLLIYSDTNRPSGV
PDRFSGSKSGTSASLAITGLQAED EADYYCQSYD |
| 120 | EpCAM CDR-H1 | SYAIS |
| 121 | EpCAM CDR-H2 | GIPIFGTANYAQKFQG |
| 122 | EpCAM CDR-H3 | GLLWNY |
| 123 | EpCAM CDR-L1 | RASQSVSSNLA |
| 124 | EpCAM CDR-L2 | GASTTAS |
| 125 | EpCAM CDR-L3 | QQYNNWPPAYT |
| 126 | EpCAM VH | QVQLVQSGAEVKKPGSSVKV SCKASGGTFS SYAISWVRQAPGQGLEWMGGIPIFGTANY
AQKFQGRVTITADESTSTAYMELSSLRSED TAVYYCARGLLWNYWGQGLTVTVSS |
| 127 | EpCAM VL | EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLIYGASTTASGIPAR
FSASGSGDTFTLTISSLQSEDFAVYYCQQYNNWPPAYTFGQGTKLEIK |
| 128 | EpCAM CDR-H1 | NYGMN |
| 129 | EpCAM CDR-H2 | WINTYTGEPTYGEDFKG |
| 130 | EpCAM CDR-H3 | FGNYVDY |
| 131 | EpCAM CDR-L1 | RSSKNLLHSNGITYLY |
| 132 | EpCAM CDR-L2 | QMSNLAS |
| 133 | EpCAM CDR-L3 | AQNLEIPRT |
| 134 | EpCAM VH | QVQLVQSGPEVKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMGWINTYTGE
PTYGEDFKGRFAFSLDTSASTAYMELSSLRSED TAVYFCARFGNYVDYWGQGS LTVTVSS |
| 135 | EpCAM VL | DIVMTQSPLSLPVTGPGEPAISCRSSKNLLHSNGITYLYWYLQKPGQSPQLLIYQMSNLAS
GVPDRFSSSGSGDTFTLKISRVEAEDVGVYYCAQNLEIPRTFGQGTKVEIK |
| 136 | EpCAM CDR-H1 | KYGMN |
| 137 | EpCAM CDR-H2 | WINTYTEPTYGDDFKG |
| 138 | EpCAM CDR-H3 | FGSAVDY |
| 139 | EpCAM CDR-L1 | RSSKSLLHSNGITYLY |
| 140 | EpCAM CDR-L2 | QMSNRAS |
| 141 | EpCAM CDR-L3 | AQNLELPRT |
| 142 | EpCAM VH | QIQLVQSGPEVKKPGESVKISCKASGYTFTKYGMNWVKQAPGQGLKWMGWINTYTEPT
YGDDFKGRFTFTLDTSTSTAYLEISSLRSED TATYFCARFGSAVDYWGQGLTVTVSS |
| 143 | EpCAM VL | DIVMTQSALSNPVTLGESGSISCRSSKSLLSNGITYLYWYLQKPGQSPQLLIYQMSNRAS
GVPDRFSSSGSGDTFTLKISRVEAEDVGVYYCAQNLELPRTFGQGTKLEMKR |
| 144 | EpCAM CDR-H1 | DYSMH |
| 145 | EpCAM CDR-H2 | WINTETGEPTYADDFKG |
| 146 | EpCAM CDR-H3 | TAVY |
| 147 | EpCAM CDR-L1 | RASQEISVSL |
| 148 | EpCAM CDR-L2 | ATSTLDS |
| 149 | EpCAM CDR-L3 | LQYASYPWT |
| 150 | EpCAM VH | QVKLQESGP ELKKPGETVKISCKASGYTFTDYSMHWWVKQAPGKGLKWMGWINTETGEPT
YADDFKGRFAFSL ETSASTAYLQINN LKNEDTATYFCARTAVYWGQGT TVTVSS |

| SEQ ID NO | Description | Sequence |
|-----------|--------------|---|
| 151 | EpCAM VL | DIQMTQSPSSLSASLGERVSLTCRASQEISVSLSWLQQEPDGTIKRLIYATSTLD SGVPKRF
SGSRSGSDYSLTISSLESEDFVDYYCLQYASYPWTFGGG TKLEIKR |
| 152 | CD352 CDR-H1 | NYGMN |
| 153 | CD352 CDR-H2 | WINTYSGEPRYADDFKG |
| 154 | CD352 CDR-H3 | DYGRWYFDV |
| 155 | CD352 CDR-L1 | RASSSVSHMH |
| 156 | CD352 CDR-L2 | ATSNLAS |
| 157 | CD352 CDR-L3 | QQWSSTPRT |
| 158 | CD352 VH | QIQLVQSGSELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQDLKWMGWINTYSGEP
RYADDFKGRFVFSLDKSVNTAYLQISSLKAEDTAVYYCARDYGRWYFDVWGQGTTVTVS
S |
| 159 | CD352 VL | QIVLSQSPATLSLSPGERATMSCRASSSVSHMHWYQQKPGQAPRPWIYATSNLASGVPA
RFSGSGSGTDYTLTISSLEPEDFAVYYCQQWSSTPRTFGG GTKVEIKR |
| 160 | CS1 CDR-H1 | RYWMS |
| 161 | CS1 CDR-H2 | EINPDSSTINYAPSLKD |
| 162 | CS1 CDR-H3 | PDGNYWYFDV |
| 163 | CS1 CDR-L1 | KASQDVGIABA |
| 164 | CS1 CDR-L2 | WASTRHT |
| 165 | CS1 CDR-L3 | QQYSSYPYT |
| 166 | CS1 VH | EVQLVESGGGLVQP GGSRLS CAASGFD FSR YWMSWVRQAPGKGLEWIGEINPDSSTIN
YAPSLKDKFIISRDNAKNSLYLQMNSLRAEDTAVYYCARPDGNYWYFDVWGQGTLTVSS |
| 167 | CS1 VL | DIQMTQSPSSLSASVGDRTITCKASQDVGIABAWYQQKPGKVPKLLIYWASTRHTGVPD
RFSGSGSGTDFTLTISLQPEDVATYYCQQYSSYPYTFGQGT KVEIKR |
| 168 | CD38 CDR-H1 | SFAMS |
| 169 | CD38 CDR-H2 | AISGSGGGTYADSVKG |
| 170 | CD38 CDR-H3 | DKILWFGEPVFDY |
| 171 | CD38 CDR-L1 | RASQSVSSYLA |
| 172 | CD38 CDR-L2 | DASNRAT |
| 173 | CD38 CDR-L3 | QQRSNWPPT |
| 174 | CD38 VH | EVQLLES GGGGLVQP GGSRLS CAVSGFTFNSFAMSWVRQAPGKGLEWVSAISGSGGGT
YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYFCAKDILWFGEPVFDYWGQGTLV
TVSS |
| 175 | CD38 VL | EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASNRATGIPAR
FSGSGSGTDFTLTISLQPEDFAVYYCQQRSNWPPTFGQGT KVEIKR |
| 176 | CD25 CDR-H1 | SYRMH |
| 177 | CD25 CDR-H2 | YINPSTGYTEYNQKFKD |
| 178 | CD25 CDR-H3 | GGGVFDY |
| 179 | CD25 CDR-L1 | SASSSISYMH |
| 180 | CD25 CDR-L2 | TTSNLAS |
| 181 | CD25 CDR-L3 | HQRSTYPLT |
| 182 | CD25 VH | QVQLVQSGAEVKKPGSSVKVSCASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGYTE
YNQKFKDKATITADESTNTAYMELSSLRSED TAVYYCARGGGVFDYWGQGTLTVSS |
| 183 | CD25 VL | DIQMTQSPSTLSASVGDRTITCSASSSISYMHWYQQKPGKAPKLLIYTTSNLASGVPARF
SGSGSGTEFTLTISLQPD D FAYYYCHQRSTYPLTFGQGT KVEVK |
| 184 | ADAM9 CDR-H1 | SYWM |

| SEQ ID NO | Description | Sequence |
|-----------|--------------|---|
| 185 | ADAM9 CDR-H2 | EIIPINGHTNYNEKFKS |
| 186 | ADAM9 CDR-H3 | GGYYYYGSRDYFDY |
| 187 | ADAM9 CDR-L1 | KASQSVDDYDGDSYMN |
| 188 | ADAM9 CDR-L2 | AASDLES |
| 189 | ADAM9 CDR-L3 | QQSHEDPFT |
| 190 | ADAM9 VH | QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKRPGQGLEWIGEIIIPINGHTN
YNEKFKSKATLTLDKSSSTAYMQLSSLASEDSAVYYCARGGYYYYGSRDYFDYWGGQTT
LTVSS |
| 191 | ADAM9 VL | DIVLTQSPASLAVSLGQRATISCKASQSVDDYDGDSYMNWYQQIPGQPPKLLIYAASDLESG
IPARFSGSGSGTDFTLNHPVEEEDAATYYCQQSHEDPFTFGGGTKLEIK |
| 192 | ADAM9 CDR-H1 | SYWM |
| 193 | ADAM9 CDR-H2 | EIPIFGHTNYNEKFKS |
| 194 | ADAM9 CDR-H3 | GGYYYYPRQGFLDY |
| 195 | ADAM9 CDR-L1 | KASQSVDDYDSGDSYMN |
| 196 | ADAM9 CDR-L2 | AASDLES |
| 197 | ADAM9 CDR-L3 | QQSHEDPFT |
| 198 | ADAM9 VH | EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYWMHWVRQAPGKGLEWVGEIPIFGHTN
YNEKFKSRFTISLDNSKNTLYLQMGSRAEDTAVYYCARGGYYYYPRQGFLDYWGQGT
VTVSS |
| 199 | ADAM9 VL | DIVMTQSPDSLAVSLGERATISCKASQSVDDYSGDSYMNWYQQKPGQPPKLLIYAASDLES
GIPARFSGSGSGTDFTLTISLEPEDFATYYCQQSHEDPFTFGGGTKLEIK |
| 200 | CD59 CDR-H1 | YGMN |
| 201 | CD59 CDR-H2 | YISSSSSTIYADSVKG |
| 202 | CD59 CDR-H3 | GPGMDV |
| 203 | CD59 CDR-L1 | KSSQSVLYSSNNKNYLA |
| 204 | CD59 CDR-L2 | WASTRES |
| 205 | CD59 CDR-L3 | QQYYSTPQLT |
| 206 | CD59 VH | QVQLQQSGGGVVPGRSLGLSCAASFTFSSYGMNWVRQAPGKGLEWVSYISSSSSTIYA
DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGPGMDVWGQGTTVTVS |
| 207 | CD59 VL | DIVLTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRE
SGVPDRFSGSGSGTDFTPAISLQAEDVAVYYCQQYYSTPQLTFGGGTVKDIK |
| 208 | CD19 CDR-H1 | TSGMGVG |
| 209 | CD19 CDR-H2 | HIWWDDDKRYNPALKS |
| 210 | CD19 CDR-H3 | MELWSYFDY |
| 211 | CD19 CDR-L1 | SASSSVSYMH |
| 212 | CD19 CDR-L2 | DTSKLAS |
| 213 | CD19 CDR-L3 | FQGSVYPFT |
| 214 | CD19 VH | QVQLQESGPGLVKPSQTLSTCTVSGGSISTSGMGVGWIRQHPGKGLEWIGHIWWDDDK
RYNPALKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARMELWSYFDYWGGGTLTVS
S |
| 215 | CD19 VL | EIVLTQSPATLSLSPGERATLSCSASSSVSYMHWYQQKPGQAPRLIYDTSKLASGIPARF
SGSGSGTDFTLTISLEPEDVAVYYCFQGSVYPFTFGGGTKLEIKR |
| 216 | CD70 CDR-H1 | NYGMN |
| 217 | CD70 CDR-H2 | WINTYTGEPTYADAFKG |
| 218 | CD70 CDR-H3 | DYGDYGM DY |
| 219 | CD70 CDR-L1 | RASKSVSTSGYSFMH |

| SEQ ID NO | Description | Sequence |
|-----------|--------------|---|
| 220 | CD70 CDR-L2 | LASNLES |
| 221 | CD70 CDR-L3 | QHSREVPWT |
| 222 | CD70 VH | QVQLVQSGAEVKKPGASVKVSKASGYTFTNYGMNWVRQAPGQGLKWMGWINTYTGE
PTYADAFKGRVTMTRDTSISTAYMELSRRLSDDTAVYYCARDYGDYGM DYWGQGT TVT
SS |
| 223 | CD70 VL | DIVMTQSPDSLAVSLGERATINCRASKSVSTSGYSFMHWYQQKPGQPPKLLIYLASNLES
GVPDRFSGSGSGTDFTLTISLQAEDVAVYYCQHSREVPWTFGQGTKVEIK |
| 224 | B7H4 CDR-H1 | SGYSWH |
| 225 | B7H4 CDR-H2 | YIHSSGSTNYPNLSKS |
| 226 | B7H4 CDR-H3 | YDDYFEY |
| 227 | B7H4 CDR-L1 | KASQNVGFNVA |
| 228 | B7H4 CDR-L2 | SASYRYS |
| 229 | B7H4 CDR-L3 | QQYNWYPFT |
| 230 | B7H4 VH | EVQLQESGPGLVKPSSETLSLTCAVTGYSITSGYSWHWIRQFPGNGLEWMGYIHSSGSTN
YNPSLKSRLISRTSKNQFFLKLSSVTAADTAVYYCAGYDDYFEYWGQGT TVT
VSS |
| 231 | B7H4 VL | DIQMTQSPSSLSASVGDRTITCKASQNVGFNVAWYQQKPGKSPKALIYSASYRYS
GVP
RFSGSGSGTDFTLTISLQPEDFAEYFCQQYNWYPFTFGQGTKLEIK |
| 232 | CD138 CDR-H1 | NYWIE |
| 233 | CD138 CDR-H2 | EILPGTGRTIYNEKFKG |
| 234 | CD138 CDR-H3 | RDYYGNFYAMDY |
| 235 | CD138 CDR-L1 | SASQGINNYLN |
| 236 | CD138 CDR-L2 | YTSTLQS |
| 237 | CD138 CDR-L3 | QQYSKLPRT |
| 238 | CD138 VH | QVQLQQSGSELMMPGASVKISKATGYTFSNYWIEWVKQRPGHGLEWIGEILPGTGRTIY
NEKFKGKATFTADISSNTVQMLSSLTSEDSAVYYCARRDYGNFYAMDYWGQGT
SVT
VSS |
| 239 | CD138 VL | DIQMTQSTSSLSASLGDRVTISCSASQGINNYLNWYQQKPDGTVELLIYYTSTLQSGVP
SRFSGSGSGTDYSLTISNLEPEDIGTYCQQYSKLPRTFGGGTKLEIK |
| 240 | CD166 CDR-H1 | TYGMGVG |
| 241 | CD166 CDR-H2 | NIWWSEDKHYSPSLKS |
| 242 | CD166 CDR-H3 | IDYGNDYAFTY |
| 243 | CD166 CDR-L1 | RSSKSLHSHNGITYLY |
| 244 | CD166 CDR-L2 | QMSNLAS |
| 245 | CD166 CDR-L3 | AQNLELPYT |
| 246 | CD166 VH | QITLKESGPTLVKPTQTLTLCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWSEDKH
YSPSLKSRLTITKDTSKNQVLTITNVDPVDTATYYCVQIDYGNDYAFTYWGQGT
LTV
VSS |
| 247 | CD166 VL | DIVMTQSPLSLPVTGPGEPAISCRSSKSLHSHNGITYLYWYLQKPGQSPQLLIYQMSNLAS
GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCAQNLELPYTFGQGTKLEIK |
| 248 | CD51 CDR-H1 | RYTMH |
| 249 | CD51 CDR-H2 | VISFDGSNKYYVDSVKG |
| 250 | CD51 CDR-H3 | EARGSYAFDI |
| 251 | CD51 CDR-L1 | RASQSVSSYLA |
| 252 | CD51 CDR-L2 | DASNRAT |
| 253 | CD51 CDR-L3 | QQRSNWPPFT |
| 254 | CD51 VH | QVQLVESGGGVVQPGRSRRLSCAASGFTFSRYTMHWVRQAPGKGLEWVAVISFDGSNK
YYVDSVKGRFTISRDNSENTLYLQVNILRAEDTAVYYCAREARGSYAFDIWGQGT
MT
V
S |

| SEQ ID NO | Description | Sequence |
|-----------|----------------|---|
| 255 | CD51 VL | EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK |
| 256 | CD56 CDR-H1 | SFGMH |
| 257 | CD56 CDR-H2 | YISSGSFTIYYADSVKG |
| 258 | CD56 CDR-H3 | MRKGYAMDY |
| 259 | CD56 CDR-L1 | RSSQIIHSDGNTYLE |
| 260 | CD56 CDR-L2 | KVSNRFS |
| 261 | CD56 CDR-L3 | FQGSHVPHT |
| 262 | CD56 VH | QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEWVAYISSGSFTIYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARMRKGYAMDYWGQGTLVTVSS |
| 263 | CD56 VL | DVVMTQSPLSLPVTLGQPASISCRSSQIIHSDGNTYLEWFQQRPGQSPRRLIYKVSNRFS GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPHTFGQGTKVEIK |
| 264 | CD74 CDR-H1 | NYGVN |
| 265 | CD74 CDR-H2 | WINPNTGEPTFDDDFKG |
| 266 | CD74 CDR-H3 | SRGKNEAWFAY |
| 267 | CD74 CDR-L1 | RSSQSLVHRNGNTYLH |
| 268 | CD74 CDR-L2 | TVSNRFS |
| 269 | CD74 CDR-L3 | SQSSHVPPT |
| 270 | CD74 VH | QVQLQQSGSELKKPGASVKVSKASGYTFTNYGVNWIKQAPGQGLQWMGWINPNTGEP TFDDDFKGRFAFLDTSVSTAYLQISSLKADDTAVYFCRSRGRKNEAWFAYWGQGTLVTVSS |
| 271 | CD74 VL | DIQLTQSPSLPVTLGQPASISCRSSQSLVHRNGNTYLHWFQQRPGQSPRLLIYTVSNRFS GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFCSQSSHVPPTFGAGTRLEIK |
| 272 | CEACAM5 CDR-H1 | TYWMS |
| 273 | CEACAM5 CDR-H2 | EIHPDSSTINYAPSLKD |
| 274 | CEACAM5 CDR-H3 | LYFGFPWFAY |
| 275 | CEACAM5 CDR-L1 | KASQDVGTSVA |
| 276 | CEACAM5 CDR-L2 | WTSTRHT |
| 277 | CEACAM5 CDR-L3 | QQYSLYRS |
| 278 | CEACAM5 VH | EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPSSTIN YAPSLKDRFTISRDNKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGPVTVSS |
| 279 | CEACAM5 VL | DIQLTQSPSSLSASVGDRTITCKASQDVGTSVAWYQQKPGKAPKLLIYWTSTRHTGVPS RFSGSGSGTDFTFTISLQPEDATYYCQQYSLYRSFGQGTKVEIK |
| 280 | CanAg CDR-H1 | YYGMN |
| 281 | CanAg CDR-H2 | WIDTTTGEPTYAQKFQG |
| 282 | CanAg CDR-H3 | RGPNWYFDV |
| 283 | CanAg CDR-L1 | RSSKSLHNSGNTYLY |
| 284 | CanAg CDR-L2 | RMSNLVS |
| 285 | CanAg CDR-L3 | LQHLEYPFT |

| SEQ ID NO | Description | Sequence |
|-----------|---------------|---|
| 286 | CanAg VH | QVQLVQSGAEVKKPGETVKISCKASDYFTFTYYGMNWVKQAPGQGLKWMGWIDTTTGEP
TYAQKFQGRIAFSLETSASTAYLQIKSLKSEDATYFCARRGPYNWYFDVWGQGT TVTS
S |
| 287 | CanAg VL | DIVMTQSPLSVPVTPGEPVSISCRSSKSLLSHNGNTYLYWFLQRPQGSPQLLIYRMSNLVS
GVPDRFSGSGSGTAFTLRISRVEAEDVGVYYCLQHLEYPFTFGPGTKLELK |
| 288 | DLL-3 CDR-H1 | NYGMN |
| 289 | DLL-3 CDR-H2 | WINTYTGEPTYADDFKG |
| 290 | DLL-3 CDR-H3 | IGDSSPSDY |
| 291 | DLL-3 CDR-L1 | KASQSVSNDVW |
| 292 | DLL-3 CDR-L2 | YASNRYT |
| 293 | DLL-3 CDR-L3 | QQDYTSPWT |
| 294 | DLL-3 VH | QVQLVQSGAEVKKPGASVKVSKASGYFTFTNYGMNWVRQAPGQGLEWMGWINTYTGE
PTY
ADDFKGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARIGDSSPSDYWGQGLTVTVSS |
| 295 | DLL-3 VL | EIVMTQSPATLSVSPGERATLSCKASQSVSNDVWVYQQKPGQAPRLLIYYASNRYTGIPA
RFSGSGSGTEFTLTISLQSEDFAVYYCQQDYTSPWTFGQGT KLEIK |
| 296 | DPEP-3 CDR-H1 | SYWIE |
| 297 | DPEP-3 CDR-H2 | EILPGSGNTYYNERFKD |
| 298 | DPEP-3 CDR-H3 | RAAAYYSNPEWFAY |
| 299 | DPEP-3 CDR-L1 | TASSSVNSFY LH |
| 300 | DPEP-3 CDR-L2 | STSNLAS |
| 301 | DPEP-3 CDR-L3 | HQYHRSPYT |
| 302 | DPEP-3 VH | QVQLVQSGAEVKKPGSSVKVSKASGGTFSSYWIEWVRQAPGQGLEWMGEILPGSGNT
YYNERFKDRVTITADESTSTAYMELSSLRSEDATVYYCARRAAAYYSNPEWFAYWGQGT
LTVSS |
| 303 | DPEP-3 VL | EIVLTQSPATLSLSPGERATLSCTASSSVNSFY LHWYQQKPLAPRLIYSTSNLASGIPDR
FSGSGSGTDFLTISRLEPEDFAVYYCHQYHRSPYTFGQGT KLEIK |
| 304 | EGFR CDR-H1 | SYWMQ |
| 305 | EGFR CDR-H2 | TIYPGDGDTTYTQKFQG |
| 306 | EGFR CDR-H3 | YDAPGYAMDY |
| 307 | EGFR CDR-L1 | RASQDINNYLA |
| 308 | EGFR CDR-L2 | YTSTLHP |
| 309 | EGFR CDR-L3 | LQYDNLLYT |
| 310 | EGFR VH | QVQLVQSGAEVAKPGASVKLSCKASGYFTFTSYWMQWVKQRPQGQGLEICGTIYPGDGDTT
YTQKFQ GKATLTADKSSSTAYMQLSSLRSEDSAVYYCARYDAPGYAMDYWGQGLTVTS
S |
| 311 | EGFR VL | DIQMTQSPSSLSASVGDRVTITCRASQDINNYLA WYQHKGPGKPKLLIHYTSTLHPGIPSR
FSGSGSGRDYSFSSISLEPEDIATYYCLQYDNLLYTFGQGT KLEIK |
| 312 | EGFR CDR-H1 | RDFAWN |
| 313 | EGFR CDR-H2 | YISYNGNTRYQPSLKS |
| 314 | EGFR CDR-H3 | ASRGFPY |
| 315 | EGFR CDR-L1 | HSSQDINSNIG |
| 316 | EGFR CDR-L2 | HGTNLDD |
| 317 | EGFR CDR-L3 | VQYAQFPWT |

| SEQ ID NO | Description | Sequence |
|-----------|-------------|--|
| 318 | EGFR VH | EVQLQESGPGLVKPSQTLSTCTVSGYSISRDFAWNWRQPPGKGLEWMGYISYNGNTRYQPSLKSRTISRDTSKNQFFLKLNSVTAADTATYYCVTASRGFPYWGQGLTVTVSS |
| 319 | EGFR VL | DIQMTQSPSSMSVSVGDRVTITCHSSQDINSNIGWLQQKPGKSFKGLIYHGTNLDDGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCVQYAQFPWTFGGGKLEIK |
| 320 | EGFR CDR-H1 | RDFAWN |
| 321 | EGFR CDR-H2 | YISYNGNTRYQPSLKS |
| 322 | EGFR CDR-H3 | ASRGFPY |
| 323 | EGFR CDR-L1 | HSSQDINSNIG |
| 324 | EGFR CDR-L2 | HGTNLDD |
| 325 | EGFR CDR-L3 | VQYAQFPWT |
| 326 | EGFR VH | EVQLQESGPGLVKPSQTLSTCTVSGYSISRDFAWNWRQPPGKGLEWMGYISYNGNTRYQPSLKSRTISRDTSKNQFFLKLNSVTAADTATYYCVTASRGFPYWGQGLTVTVSS |
| 327 | EGFR VL | DIQMTQSPSSMSVSVGDRVTITCHSSQDINSNIGWLQQKPGKSFKGLIYHGTNLDDGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCVQYAQFPWTFGGGKLEIK |
| 328 | EGFR CDR-H1 | NYGVH |
| 329 | EGFR CDR-H2 | VIWGGNTDYNTPTFS |
| 330 | EGFR CDR-H3 | ALTYDYEFAY |
| 331 | EGFR CDR-L1 | RASQSIGTNIH |
| 332 | EGFR CDR-L2 | YASESIS |
| 333 | EGFR CDR-L3 | QQNNNWPTT |
| 334 | EGFR VH | QVQLKQSGPGLVQPSQSLITCTVSGFSLTNYGVHWRQSPGKGLEWLGVIWGGNTDYNTPTFSRLSINKDNSKSQVFFKMNSLQSNDAIYYCARALTYDYEFAYWGQGLTVTVSA |
| 335 | EGFR VL | DILLTQSPVILSVSPGERVSFSCRASQSIGTNIHWYQQRNTGSPRLLIKYASESISGIPSRFSGSGSGTDFTLSINSVESEDIADYYCQQNNNWPTTFGAGTKLELK |
| 336 | FRa CDR-H1 | GYFMN |
| 337 | FRa CDR-H2 | RIHPYDGDTFYNQKFQG |
| 338 | FRa CDR-H3 | YDGSRAMDY |
| 339 | FRa CDR-L1 | KASQSVSFAGTSLMH |
| 340 | FRa CDR-L2 | RASNLEA |
| 341 | FRa CDR-L3 | QQSREYPYT |
| 342 | FRa VH | QVQLVQSGAEVVKPGASVKISCKASGYTFTGYFMNWVKQSPGQSLEWIGRIHPYDGDTFY
NQKFQGKATLTVDKSSNTAHMELLSTSEDAVYYCTRYDGSRAMDYWGQGTTVTVSS |
| 343 | FRa VL | DIVLTQSPLSLAVSLGQPAIISCKASQSVSFAGTSLMHWHYHQPQGPRLLIYRASNLEAGVPDRFSGSGSKTDFTLTISPVEAEDAATYYCQQSREYPYTFGGGKLEIK |
| 344 | FRa CDR-H1 | GYGLS |
| 345 | FRa CDR-H2 | MISSGGSYTYADSVKG |
| 346 | FRa CDR-H3 | HGDDPAWFAY |
| 347 | FRa CDR-L1 | SVSSSISSNNLH |
| 348 | FRa CDR-L2 | GTSNLAS |
| 349 | FRa CDR-L3 | QQWSSYPYMYT |
| 350 | FRa VH | EVQLVESGGGVWQPGRSLRLSCSASGFTFSGYGLSWVRQAPGKGLEWVAMISSGGSYTY
ADSVKGRFAISRDNKNTLFLQMDSLRPEDTGVIYFCARHGDDPAWFAYWGQGTPVTVSS |
| 351 | FRa VL | DIQLTQSPSSLSASVGDRTITCSVSSSISSNNLHWYQQKPGKAPKRWIYGTSNLASGVPSRFSGSGSGTDYTFITISLQPEDATYYCQQWSSYPYMYTFGQGTKEIK |

| SEQ ID NO | Description | Sequence |
|-----------|-------------------|--|
| 352 | MUC-1 CDR-H1 | NYWMN |
| 353 | MUC-1 CDR-H2 | EIRLKSNNYTHYAESVKG |
| 354 | MUC-1 CDR-H3 | HYYFDY |
| 355 | MUC-1 CDR-L1 | RSSKSLHNSNGITYFF |
| 356 | MUC-1 CDR-L2 | QMSNLAS |
| 357 | MUC-1 CDR-L3 | AQNLELPPT |
| 358 | MUC-1 VH | EVQLVESGGGLVQPGGSMRLSCVASGFPSNYWMNWVRQAPGKGLEWVGEIRLKSNN
YTHYAESVKGRFTISRDDSKNSLYLQMNSLKTEDAVYYCTRHYFFDYWGQGTLTVSS |
| 359 | MUC-1 VL | DIVMTQSPLSNPVTGPGEASISCRSSKSLHNSNGITYFFWYLQKPGQSPQLLIYQMSNLAS
GVPDRFSGSGSGTDFTLRISRVEADVGVYYCAQNLELPPTFGGQGTKVEIK |
| 360 | Mesothelin CDR-H1 | SYWIG |
| 361 | Mesothelin CDR-H2 | IIDPGDSRTRYSPSFQG |
| 362 | Mesothelin CDR-H3 | GQLYGGTYMDG |
| 363 | Mesothelin CDR-L1 | TGTSSDIGGYNSVS |
| 364 | Mesothelin CDR-L2 | GVNNRPS |
| 365 | Mesothelin CDR-L3 | SSYDIESATPV |
| 366 | Mesothelin VH | QVELVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQAPGKGLEWMGIIDPGDSRTR
YSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARGQLYGGTYMDGWGQGTTLTV
SS |
| 367 | Mesothelin VL | DIALTPASVSGSPGQSITISCTGTSSDIGGYNSVSWYQQHPGKAPKLMYGVNNRPSGV
SNRFSGSKSGNTASLTISGLQAEDEADYYCSSYDIESATPVFGGGTKLTVL |
| 368 | ROR-1 CDR-H1 | AYNIH |
| 369 | ROR-1 CDR-H2 | SFDPYDGGSSYNQKFKD |
| 370 | ROR-1 CDR-H3 | GWYYFDY |
| 371 | ROR-1 CDR-L1 | RASKSISKYLA |
| 372 | ROR-1 CDR-L2 | SGSTLQS |
| 373 | ROR-1 CDR-L3 | QQHDESPYT |
| 374 | ROR-1 VH | QVQLQESGPGLVKPSQTLSTCTVSGYAFTAYNIHWVRQAPGQGLEWMGSFDPYDGG
SYNQKFKDRLTISKDTSKNQVLTMTNMDPVDATYYCARGWYYFDYWGHTLTVSS |
| 375 | ROR-1 VL | DIVMTQTPLSLPVTGPGEASISCRASKSISKYLAWYQQKPGQAPRLLIYSGSTLQSGIPPRF
SGSGYGTDFLTINNIESEDAAYYFCQQHDESPYTFGEGTKVEIK |
| 376 | B7H4 CDR-H1 | GSIKSGSYYWG |
| 377 | B7H4 CDR-H2 | NIYYSGSTYYNPSLRS |
| 378 | B7H4 CDR-H3 | AREGSYPNQFDP |
| 379 | B7H4 CDR-L1 | RASQSVSSNLA |
| 380 | B7H4 CDR-L2 | GASTRAT |
| 381 | B7H4 CDR-L3 | QQYHSFPFT |
| 382 | B7H4 VH | QLQLQESGPGLVKPSSETLSLTCTVSGSGSIKSGSYYWGWIRQPPGKGLEWIGNIYYSGSTY
YNPSLRSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGSYPNQFDPWGQGTTLTVSS |
| 383 | B7H4 VL | EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA
RFSGSGSGTEFTLTISLQSEDAVYYCQQYHSFPFTFGGGTKVEIK |

| SEQ ID NO | Description | Sequence |
|-----------|--------------|--|
| 384 | B7-H3 CDR-H1 | SFGMH |
| 385 | B7-H3 CDR-H2 | YISSDSSAIYY |
| 386 | B7-H3 CDR-H3 | GRENIYYGSRLD |
| 387 | B7-H3 CDR-L1 | KASQNV |
| 388 | B7-H3 CDR-L2 | SASYRYSQVPS |
| 389 | B7-H3 CDR-L3 | QQYNNYPFTFGS |
| 390 | B7-H3 VH | DVQLVESGGGLVQPGGSRKLSAASGFTFSSFGMHWVRQAPEKGLEWVAYISSDSSAIY
Y
ADTVKGRFTISRDNPKNTLFLQMTSLRSEDAMYYCGRGRENIYYGSRLDYWGQGTTLTV
SS |
| 391 | B7-H3 VL | DIAMTQSQKFMSTSVGDRVSVTCKASQNVDTNVAWYQQKPGQSPKALIYSASYRYSQVPS
D
RFTGSGSGTDFTLTINNVSQEDLAIEYFCQQYNNYPFTFGSGTKLEIK |
| 392 | B7-H3 CDR-H1 | SYWMQWVRQA |
| 393 | B7-H3 CDR-H2 | TIYPGDGDTRY |
| 394 | B7-H3 CDR-H3 | RGIPRLWYFDVM |
| 395 | B7-H3 CDR-L1 | ITCRASQDIS |
| 396 | B7-H3 CDR-L2 | YTSRLHSGVPS |
| 397 | B7-H3 CDR-L3 | QQGNTLPPFTGG |
| 398 | B7-H3 VH | DVQLVESGGGLVQPGGSRKLSAASGFTFSSFGMHWVRQAPEKGLEWVAYISSDSSAIY
Y
ADTVKGRFTISRDNPKNTLFLQMTSLRSEDAMYYCGRGRENIYYGSRLDYWGQGTTLTV
SS |
| 399 | B7-H3 VL | DIAMTQSQKFMSTSVGDRVSVTCKASQNVDTNVAWYQQKPGQSPKALIYSASYRYSQVPS
D
RFTGSGSGTDFTLTINNVSQEDLAIEYFCQQYNNYPFTFGSGTKLEIK |
| 400 | B7-H3 CDR-H1 | SYGMSWVRQA |
| 401 | B7-H3 CDR-H2 | INSGGSNTYY |
| 402 | B7-H3 CDR-H3 | HDGGAMDYW |
| 403 | B7-H3 CDR-L1 | ITCRASESIYSYLA |
| 404 | B7-H3 CDR-L2 | NTKTLPE |
| 405 | B7-H3 CDR-L3 | HHYGTTPWTFG |
| 406 | B7-H3 VH | EVQLVESGGGLVQPGGSLRLSASGFTFSSYGMHWVRQAPGKGLEWVATINSGGSNT
YY
PDSLKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCARHDGGAMDYWGQGTTLTVSS |
| 407 | B7-H3 VL | DIQMTQSPSSLSASVGRVTITCRASESIYSYLAWYQQKPGKAPKLLVYNTKTLPEGVPSR
FSGSGSGTDFTLTISSLQPEDFATYYCQHHYGTTPWTFGQGTLEIK |
| 408 | B7-H3 CDR-H1 | SFGMHWVRQA |
| 409 | B7-H3 CDR-H2 | ISSGSGTIYYADTVKGRFTI |
| 410 | B7-H3 CDR-H3 | HGYRYEGFDYWG |
| 411 | B7-H3 CDR-L1 | ITCKASQNVDTNVA |
| 412 | B7-H3 CDR-L2 | SASYRYSQVPS |
| 413 | B7-H3 CDR-L3 | QQYNNYPFTFGQ |
| 414 | B7-H3 VH | EVQLVESGGGLVQPGGSLRLSASGFTFSSFGMHWVRQAPGKGLEWVAYISSGSGTIY
YADTVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCARHGYRYEGFDYWGQGTTLTVS
S |

| SEQ ID NO | Description | Sequence |
|-----------|--------------|---|
| 415 | B7-H3 VL | DIQMTQSPSFLSASVGDRVTITCKASQNVDTNVAWYQQKPGKAPKALIYSASYRYSGVPS
RFGSGSGTDFLTITSSLPEDFAEYFCQQYNNYPFTFGQGTKLEIK |
| 416 | B7-H3 CDR-H1 | NYVMH |
| 417 | B7-H3 CDR-H2 | YINPYNDDVKYNEKFKG |
| 418 | B7-H3 CDR-H3 | WGYGSPLYYFDY |
| 419 | B7-H3 CDR-L1 | RASSRLIYMH |
| 420 | B7-H3 CDR-L2 | ATSNLAS |
| 421 | B7-H3 CDR-L3 | QQWNSNPPT |
| 422 | B7-H3 VH | EVQLQQSGPELVKPGASVKMSCKASGYTFTNYVMHWVKQKPGQGLEWIGYINPYNDDV
KYNEKFKGKATQTSKSSSTAYMELSSLTSEDSAVYYCARWGYGSPLYYFDYWGQGT
LTVSS |
| 423 | B7-H3 VL | QIVLSQSPTILSASPGEKVTMTCRASSRLIYMHWYQQKPGSSPKWIYATSNLASGVPAR
FSGSGSGTSYSLTISRVEAEDAATYYCQQWNSNPPTFGTGTKLEIK |
| 424 | B7-H3 CDR-H1 | NYVMH |
| 425 | B7-H3 CDR-H2 | YINPYNDDVKYNEKFKG |
| 426 | B7-H3 CDR-H3 | WGYGSPLYYFDY |
| 427 | B7-H3 CDR-L1 | RASSRLIYMH |
| 428 | B7-H3 CDR-L2 | ATSNLAS |
| 429 | B7-H3 CDR-L3 | QQWNSNPPT |
| 430 | B7-H3 VH | QVQLVQSGAEVKKPGSSVKVSKASGYTFTNYVMHWVRQAPGQGLEWMGYINPYNDDV
KYNE
KFKGRVTITADESTSTAYMELSSLRSEDTAVYYCARWGYGSPLYYFDYWGQGT
LTVSS |
| 431 | B7-H3 VL | EIVLTQSPATLSLSPGERATLSCRASSRLIYMHWYQQKPGQAPRPLIYATSNLASGIPARFS
GSGSGTDFLTITSSLEPEDFAVYYCQQWNSNPPTFGQGTKVEIK |
| 432 | B7-H3 CDR-H1 | GYSFTSYTIH |
| 433 | B7-H3 CDR-H2 | YINPNSRNTDYAQKFQG |
| 434 | B7-H3 CDR-H3 | YSGSTPYWYFDV |
| 435 | B7-H3 CDR-L1 | RASSSVSYMN |
| 436 | B7-H3 CDR-L2 | ATSNLAS |
| 437 | B7-H3 CDR-L3 | QQWSSNPLT |
| 438 | B7-H3 VH | EVQLVQSGAEVKKPGSSVKVSKASGYSTSYTIHWVRQAPGQGLEWMGYINPNSRNTD
YAKFKQGRVTLTADKSTSTAYMELSSLRSEDTAVYYCARYSGSTPYWYFDVWGQGT
TVSS |
| 439 | B7-H3 VL | DIQMTQSPSSLSASVGDRVTITCKASQNVGFNVAWYQQKPGKSPKALIYSASYRYSGVPS
RFGSGSGTDFLTITSSLPEDFAEYFCQQYNWYPFTFGQGTKLEIK |
| 440 | B7-H3 CDR-H1 | GYTFSSYWMH |
| 441 | B7-H3 CDR-H2 | LIHPDSGSTNYNEMFKN |
| 442 | B7-H3 CDR-H3 | GGRLYFD |
| 443 | B7-H3 CDR-L1 | RSSQSLVHSNGDTYLR |
| 444 | B7-H3 CDR-L2 | KVSNRFS |
| 445 | B7-H3 CDR-L3 | SQSTHVPYT |
| 446 | B7-H3 VH | EVQLVQSGAEVKKPGSSVKVSKASGYTFSSYWMHWVRQAPGQGLEWIGLIHPDSGST
NYNEMFKNRATLTVDRTSTAYVELSSLRSEDTAVYFCAGGGRLYFDYWGQGT
TVSS |
| 447 | B7-H3 VL | DVVMTQSPLSLPVTGPGEASISCRSSQSLVHSNGDTYLRWYLQKPGQSPQLLIYKVS
NRFSGVPDRFSGSGSGTDFLTISRVEAEDVGVYYCSQSTHVPYTFGGGTKVEIK |
| 448 | B7-H3 CDR-H1 | GYTFSSYWMH |
| 449 | B7-H3 CDR-H2 | LIHPESGSTNYNEMFKN |

| SEQ ID NO | Description | Sequence |
|-----------|--------------|---|
| 450 | B7-H3 CDR-H3 | GGRLYFDY |
| 451 | B7-H3 CDR-L1 | RSSQSLVHSNQDTYLR |
| 452 | B7-H3 CDR-L2 | KVSNRFS |
| 453 | B7-H3 CDR-L3 | SQSTHVPYT |
| 454 | B7-H3 VH | EVQLVQSGAEVKKPGSSVKVSCASGYTFSSYWMHWVRQAPGQGLEWIGLIHPESGST
NY
NEMFKNRATLTVDRTSTAYMELSSLRSED TAVYYCAGGGRLYFDYWGQGTTTVTVSS |
| 455 | B7-H3 VL | DIVMTQSPSLPVP TPGEPASISCRSSQSLVHSNQDTYLRWYLQKPGQSPQLLIYKVS NRF
SGVPDRFSGSGSGTDFTLTKISRVEAEDVGVYYCSQSTHVPYTFGGGTKVEIK |
| 456 | B7-H3 CDR-H1 | TGYSITSGYSWH |
| 457 | B7-H3 CDR-H2 | YIHSSGSTNYPNPSLKS |
| 458 | B7-H3 CDR-H3 | YDDYFEY |
| 459 | B7-H3 CDR-L1 | KASQNVGFNVAW |
| 460 | B7-H3 CDR-L2 | SASYRYS |
| 461 | B7-H3 CDR-L3 | QQYNWYPFT |
| 462 | B7-H3 VH | EVQLQESGPGLVKPS ETLTCAVTGYSITSGYSWHWIRQFPNGLEWMGYIHSSGSTN
Y
NPSLKSRISSRDTSKNQFFLKLSSVTAAD TAVYYCAGYDDYFEYWGQGTTTVTVSS |
| 463 | B7-H3 VL | DIQMTQSPSSLSASV GDRVITITCKASQNVGGFNVAWYQQKPGKSPKALIYSASYRSGV
PSRFSGSGSGTDFTLTISLQPEDFAEYFCQQYNWYPFTFGQGTKLEIK |
| 464 | B7-H3 CDR-H1 | NYDIN |
| 465 | B7-H3 CDR-H2 | WIGWIFPGDDSTQYNEKFKG |
| 466 | B7-H3 CDR-H3 | QTTGTWFAY |
| 467 | B7-H3 CDR-L1 | RASQSISDYLY |
| 468 | B7-H3 CDR-L2 | YASQSI |
| 469 | B7-H3 CDR-L3 | CQNGHSFPL |
| 470 | B7-H3 VH | QVQLVQSGAEVVKPGASVKLSCKTSGYFTNYDINWVRQRPQGLEWIGWIFPGDDSTQ
Y
NEKFKGKATLT TDTSTAYMELSSLRSED TAVYFCARQTTGTWFAYWGQGLTVTVSS |
| 471 | B7-H3 VL | EIVMTQSPATLSVSP GERVTLS CRASQSISDYLYWYQQKSHESPRLLIKYASQSISGIPA
RFSGSGSGSEFTLTINSVEPEDVGVYYCQNGHSFPLTFGQGTKLEIK |
| 472 | B7-H3 VH | QVQLQQSGAEVKKPGSSVKVSCASGGTFSSY AISWVRQAPGQGLEWMGGIIPILGIAN
YAQKFQGRVTITADESTAYMELSSLRSED TAVYYCARGGSGSYHMDVWGKGT TVTS
S |
| 473 | B7-H3 VL | EIVLTQSPATLSLSP GERATLS CRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATGIP
ARFSGSGSGTDFTLTISLPEPDAVYYCQQR SNWPPRITFGQGTRLEIK |
| 474 | B7-H3 CDR-H1 | IYNVH |
| 475 | B7-H3 CDR-H2 | TIFPGNGDTSYNQKFKD |
| 476 | B7-H3 CDR-H3 | WDDGNVGFAH |
| 477 | B7-H3 CDR-L1 | RASENINNYLT |
| 478 | B7-H3 CDR-L2 | HAKTLAE |
| 479 | B7-H3 CDR-L3 | QHHYGPPT |
| 480 | B7-H3 VH | QVQLQQPGAELVKPGASVKMSCKASGYFTIYNVHWIKTPGQGLEWMGTIFPGNGDTS
Y
NQKFKDKATLT TDKSSKTAYMQLNSLT SEDSAVYYCARWDDGNVGFAHWGQGLTVTVS
A |
| 481 | B7-H3 VL | DIQMTQSPASLSASVGETVTITCRASENINNYLTW FQQKQKSPQLLVYHAKTLAEGVPS |

| SEQ ID NO | Description | Sequence |
|-----------|-------------|---|
| | | RFSGSGSGTQFSLKINSLQPEDFGSYQCQHHYGTPTFGGGTKLEIK |
| 482 | B7-H3 VH | EVQLVQSGAEVKKPGASVKVSKASGYFTIYNVHWVRQAPGQGLEWMGTIFPGNGDTS
YNQKFKDKVTMTTDTSTSTAYMELSSLRSED TAVYYCARWDDGNVGF AHWGQGT LVTV
SS |
| 483 | B7-H3 VL | DIQMTQSPSSLSASVGDRTITCRASENINNYLTWFQQKQKSPQLLIYHAKTLAEGVP
SRFSGSGSGTDFLTITSSLPEDFATYYCQHHYGTPTFGGGTKVEIK |
| 484 | B7-H3 VH | EVQLVQSGAEVKKPGASVKVSKASGYFTIYNVHWIRQAPGQGLEWMGTIFPGNGDTS
Y
NQKFKDRATLTDDKSTKTAYMELRSLRSDDTAVYYCARWDDGNVGF AHWGQGT LVTVS
S |
| 485 | B7-H3 VL | DIQMTQSPSSLSASVGDRTITCRASENINNYLTWFQQKPGKAPKLLVYHAKTLAEGVPS
RFSGSGSGTQFTLTITSSLPEDFATYYCQHHYGTPTFGQGTKEIK |
| 486 | HER3 H | QVQLQQWAGALLKPSETLSLTCVAVGGSFSGYYWSWIRQPPGKLEWIGEINHSGSTNY
N
PSLKSRVTISVETSKNQFSLKLSSVTAADTAVYYCARDKWTWYFDLWGRGTLTVSSAST
KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL
YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKTHTCPPCPAPELLGGPS
VFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST
YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMT
KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMHEALHNHYTQKSLSLSPGK |
| 487 | HER3 L | DIEMTQSPDSLAVSLGERATINCRSSQSVLYSSSNRNLYAWYQQNPQPCKLLIYWASTR
ESGVPDRFSGSGSGTDFLTITSSLAEDVAVYYCQQYYSTPRTFGGQGTKEIKRTVAAPS
VFIFPPSDEQLKSGTASVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS
LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC |
| 488 | HER3 H | EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYVMAWVRQAPGKLEWVSSISSSGGWT
LY
ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRGLKMATIFDYWGQGT LVTVSSA
STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
LYSLSSVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVKCCVECPKPPAPPVAGPSVFL
FPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR
V
VSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ
VSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDSDGSFFLYSKLTVDKSRWQQGN
V
FSCSVMHEALHNHYTQKSLSLSPGK |
| 489 | HER3 L | QSALTQPASVSGSPGQSITISCTGTSSDVGSYNVWSWYQQHPGKAPKLIIEVSQRPSGV
SNRFSGSKSGNTASLTISGLQTEDEADYYCCSYAGSSIFVIFGGGTKVTVLGQPKAAPSVT
LFPPSSEELQANKATLVCLVDFYPGAVTVAWKADGSPVKVGVETTKPSKQSNNKYAASS
YLSLTPEQWKSHRSYSCRVTHEGSTVEKTVAPAEC |
| 490 | HER3 H | EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSAINSGGKSTY
YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARWGDEGFDIWGQGT LVTVSSA
STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
LYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKTHTCPPCPAPELLGGP
SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM
TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMHEALHNHYTQKSLSLSPGK |

| SEQ ID NO | Description | Sequence |
|-----------|-------------|--|
| 491 | HER3 L | DIQMTQSPSSLSASVGDRVTITCRASQGISNWLAWYQQKPGKAPKLLIYGASSLQSGVPS
RFGSGSGGTDFTLTISSLQPEDFATYYCQQYSSFPPTFGGQTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLS
KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC |
| 492 | HER3 H | QVQLVQSGAEVKKPGASVKVSCKASGYTFRSSYISWVRQAPGQGLEWMGWYAGTGSP
SYNQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARHRDYYNSLTWGGQTLVT
VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
QSSGLYSLSSVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK
SRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG |
| 493 | HER3 L | DIVMTQSPDSLAVSLGERATINCKSSQSVLNSGNQKNYLTWYQQKPGQPPKLLIYWASTR
ESGVPDRFSGSGSGGTDFTLTISSLQAEDVAVYYCQSDYSYPYTFGGQTKLEIKRTVAAPSV
FIFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSL
SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC |
| 494 | PTK7 CDR-H1 | TSNMGVG |
| 495 | PTK7 CDR-H2 | HIWWDDDKYYSPSLKS |
| 496 | PTK7 CDR-H3 | SNYGYAWFAY |
| 497 | PTK7 CDR-L1 | KASQDIYPYLN |
| 498 | PTK7 CDR-L2 | RTNRLLD |
| 499 | PTK7 CDR-L3 | LQYDEFPLT |
| 500 | PTK7 VH | QITLKESGPTLVKPTQTLTCTFSGFSLSTSNMGVGVIRQPPGKALEWLAHIWWDDDKY
YPSLKSRLTITKDTSKNQVLTMTNMDPVDATYYCVRSNYGYAWFAYWGQGTSLTVS
S |
| 501 | PTK7 VL | DIQMTQSPSSLSASVGDRVTITCKASQDIYPYLNWFQQKPGKAPKTLIYRTNRLLDGVPS
RFGSGSGGTDFTFITSSLQPEDATYYCLQYDEFPLTFGAGTKLEIK |
| 502 | PTK7 CDR-H1 | DYAVH |
| 503 | PTK7 CDR-H2 | VISTYNDYTYNNQDFKG |
| 504 | PTK7 CDR-H3 | GNSYFYALDY |
| 505 | PTK7 CDR-L1 | RASEVDSYGKSFMH |
| 506 | PTK7 CDR-L2 | RASNLES |
| 507 | PTK7 CDR-L3 | QQSNEDPWT |
| 508 | PTK7 VH | QVQLVQSGPEVKKPGASVKVSCKASGYTFTDYAVHWVRQAPGKRLEWIGVISTYNDYTY
NNQDFKGRVTMTRDTSASTAYMELSRRLSEDATVYYCARGNSYFYALDYWGQGTSLTV
SS |
| 509 | PTK7 VL | EIVLTQSPATLSLSPGERATLSCRASEVDSYGKSFMHYQQKPGQAPRLLIYRASNLES
GIPARFSGSGSGGTDFTLTISSLEPEDFAVYYCQQSNEDPWTFGGGTKLEIK |
| 510 | PTK7 CDR-H1 | RYWMS |
| 511 | PTK7 CDR-H2 | DLNPDSSAINYVDSVKG |
| 512 | PTK7 CDR-H3 | ITTLVPYTMDF |
| 513 | PTK7 CDR-L1 | ITNTDIDDDMN |
| 514 | PTK7 CDR-L2 | EGNGLRP |
| 515 | PTK7 CDR-L3 | LQSDNLPLT |
| 516 | PTK7 VH | EVQLVESGGGLVQPGGSLRLSCAASGFDPSRYWMSWVRQAPGKGLEWIGDLNPDSSAI
NY
VDSVKGRFTISRDNKNSLYLQMNSLRAEDATVYYCTLTITLVPYTMDFWGQGTSLTVSS |

| SEQ ID NO | Description | Sequence |
|-----------|-------------|--|
| 517 | PTK7 VL | ETTLTQSPAFMSATPGDKVNISCITNTDIDDDMNWYQQKPGEAAILLISEGNGLRPGIPPRF
SGSGYGTDFTLTINNIESEDAAYYFCLQSDNLPLTFGSGTKLEIK |
| 518 | LIV1 CDR-H1 | DYYMH |
| 519 | LIV1 CDR-H2 | WIDPENGDT EYGPKFQG |
| 520 | LIV1 CDR-H3 | HNAHYGTWFAY |
| 521 | LIV1 CDR-L1 | RSSQSLLHSSGNTYLE |
| 522 | LIV1 CDR-L2 | KISTRFS |
| 523 | LIV1 CDR-L3 | FQGSHVPYT |
| 524 | LIV1 VH | QVQLVQSGAEVKKPGASVKVSKASGLTIEDYYMHWVRQAPGQGLEWMGWIDPENGDT
EY
GPKFQGRVTMTRDTSINTAYMELSRLRSDDTAVYYCAVHNAHYGTWFAYWGQGLTVTS
S |
| 525 | LIV1 VL | DVVMTQSPLSLPVTLGQPASISCRSSQSLLHSSGNTYLEWYQQRPGQSPRPLIYKISTRFS
GVPDRFSGSGSGTDFTLKISRVEAEDVGYYCFQGSHPYTFGGGKTKVEIK |
| 526 | avb6 CDR-H1 | DYNVN |
| 527 | avb6 CDR-H2 | VINPKYGTTRYNQKFKG |
| 528 | avb6 CDR-H3 | GLNAWDY |
| 529 | avb6 CDR-L1 | GASENIYGALN |
| 530 | avb6 CDR-L2 | GATNLED |
| 531 | avb6 CDR-L3 | QNVLTTPYT |
| 532 | avb6 VH | QFQLVQSGAEVKKPGASVKVSKASGYSFTDYNVNWVRQAPGQGLEWIGVINPKYGTTR
Y
NQKFKGRATLTVDKSTSTAYMELSSLRSEDVAVYYCTRGLNAWDYWGQGLTVTVSS |
| 533 | avb6 VL | DIQMTQSPSSLSASVGDRTITCGASENIYGALNWKYQKPKAPKLLIYGATNLEDGVP
RFGSGSGRDTFTISSLPEDIATYYCQNVLTTPYTFGGGKTKLEIK |
| 534 | avb6 CDR-H1 | GYFMN |
| 535 | avb6 CDR-H2 | LINPYNGDSFYNQKFKG |
| 536 | avb6 CDR-H3 | GLRRDFDY |
| 537 | avb6 CDR-L1 | KSSQSLLDSDGKTYLN |
| 538 | avb6 CDR-L2 | LVSELD |
| 539 | avb6 CDR-L3 | WQGFTHFPRT |
| 540 | avb6 VH | QVQLVQSGAEVKKPGASVKVSKASGYSFSGYFMNWVRQAPGQGLEWMGLINPYNGD
SFY
NQKFKGRVTMTRQTSTSTVYMELSSLRSEDVAVYYCVRGLRRDFDYWGQGLTVTVSS |
| 541 | avb6 VL | DVVMTQSPLSLPVTLGQPASISCKSSQSLLDSDGKTYLNWLFQRPQGSPRRLIYLVSELD
SGVPDRFSGSGSGTDFTLKISRVEAEDVGYYCWQGFTHFPRTFGGGKTKLEIK |
| 542 | CD48 CDR-H1 | DFGMN |
| 543 | CD48 CDR-H2 | WINTFTGEPSYGNVFKG |
| 544 | CD48 CDR-H3 | RHGNGNVFDS |
| 545 | CD48 CDR-L1 | RASQSIGSNIH |
| 546 | CD48 CDR-L2 | YTSESIS |
| 547 | CD48 CDR-L3 | QQSNSWPLT |
| 548 | CD48 VH | QVQLVQSGSELKKPGASVKVSKASGYTFTDFGMNWVRQAPGQGLEWMGWINTFTGEP
SYGNVFKGRFVSLDTSVSTAYLQISSLKAEDTAVYYCARRHGNGNVFDSWGQGLTVTVS
S |
| 549 | CD48 VL | EIVLTQSPDFQSVTPKEKVTITCRASQSIGSNIHWYQKPKDQSPKLLIKYTSESISGVP
SRFSGSGSGTDFTLTINSLEAEDAATYYCQQSNSWPLTFGGGKTKVEIKR |

| SEQ ID NO | Description | Sequence |
|-----------|---------------------|--|
| 550 | PD-L1 CDR-H1 | TAAIS |
| 551 | PD-L1 CDR-H2 | GIIPFGKAHYAQKFQG |
| 552 | PD-L1 CDR-H3 | KFHFVSGSPFGMDV |
| 553 | PD-L1 CDR-L1 | RASQSVSSYLA |
| 554 | PD-L1 CDR-L2 | DASNRAT |
| 555 | PD-L1 CDR-L3 | QQRSNWPT |
| 556 | PD-L1 VH | QVQLVQSGAEVKKPGSSVKVSCKTSGDTFSTAAISWVRQAPGQGLEWMGGIIPFGKAHY
AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYFCARKFHFVSGSPFGMDVWGQGTTV
TVSS |
| 557 | PD-L1 VL | EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA
RFGSGSGTDFLTITSSLEPEDFAVYYCQQRSNWPTFGQGTKVEIK |
| 558 | IGF-1R CDR-H1 | SYAIS |
| 559 | IGF-1R CDR-H2 | GIIPFGTANYAQKFQG |
| 560 | IGF-1R CDR-H3 | APLRFLEWSTQDHYYYYYMDV |
| 561 | IGF-1R CDR-L1 | QGDSLRSYYAT |
| 562 | IGF-1R CDR-L2 | GENKRPS |
| 563 | IGF-1R CDR-L3 | KSRDGSGQHLV |
| 564 | IGF-1R VH | EVQLVQSGAEVKKPGSSVKVSCASGGTFSSYAISWVRQAPGQGLEWMGGIIPFGTANY
AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARAPLRFLEWSTQDHYYYYYMDV
WGKGTTVTVSS |
| 565 | IGF-1R VL | SSELTQDPAVSVALGQTVRITCQGDSLRSYYATWYQQKPGQAPILVIYGENKRPSGIPDR
FSGSSSGNTASLTITGAQAEADYYCKSRDGSGQHLVFGGGTKLTVL |
| 566 | Claudin-18.2 CDR-H1 | SYWIN |
| 567 | Claudin-18.2 CDR-H2 | NIYPSDSYTNYNQKFKD |
| 568 | Claudin-18.2 CDR-H3 | SWRGNSFDY |
| 569 | Claudin-18.2 CDR-L1 | KSSQSLLNSGNQKNYLT |
| 570 | Claudin-18.2 CDR-L2 | WASTRES |
| 571 | Claudin-18.2 CDR-L3 | QNDYSPFT |
| 572 | Claudin-18.2 VH | QVQLQQPGAELVRPGASVKLSCKASGYTFTSYWINWVKQRPGQGLEWIGNIYPSDSYTN
YNQKFKDKATLTVDKSSSTAYMQLSSPTSEDSAVYYCTRSWRGNSFDYWGQGTTTLTVSS |
| 573 | Claudin-18.2 VL | DIVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYWASTR
ESGVPDRFTGSGSGTDFLTITSSVQAEDLAVYYCQNDYSPFTFGSGTKLEIK |
| 574 | Claudin-18.2 CDR-H1 | NYGMN |
| 575 | Claudin-18.2 CDR-H2 | WINTNTGEPTYAEEFKG |
| 576 | Claudin-18.2 CDR-H3 | LGFGNAMDY |
| 577 | Claudin-18.2 CDR-L1 | KSSQSLLNSGNQKNYLT |
| 578 | Claudin-18.2 CDR-L2 | WASTRES |

| SEQ ID NO | Description | Sequence |
|-----------|---------------------|---|
| 579 | Claudin-18.2 CDR-L3 | QNDYSYPLT |
| 580 | Claudin-18.2 VH | QIQLVQSGPELKKPGETVKISCKASGYFTNYGMNWVKQAPGKGLKWMGWINTNTGEPT
Y
AEEFKGRFAFSLETSASTAYLQINNLIKNETATYFCARLGFGNAMDYWGQGTSTVTVSS |
| 581 | Claudin-18.2 VL | DIVMTQSPSSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYWASTR
ESGVPDRFTGSGSGTDFTLTISVQAEDLAVYYCQNDYSYPLTFGAGTKLELK |
| 582 | Nectin-4 CDR-H1 | SYNMN |
| 583 | Nectin-4 CDR-H2 | YISSSSSTIYYADSVKG |
| 584 | Nectin-4 CDR-H3 | AYYYGMDV |
| 585 | Nectin-4 CDR-L1 | RASQGISGWLA |
| 586 | Nectin-4 CDR-L2 | AASTLQS |
| 587 | Nectin-4 CDR-L3 | QQANSFPPT |
| 588 | Nectin-4 VH | EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYNMNWVRQAPGKGLEWVSYISSSSSTIY
Y
ADSVKGRFTISRDNKNSLSLQMNSLRDEDTAVYYCARAYYYYGMDVWGQGTSTVTVSS |
| 589 | Nectin-4 VL | DIQMTQSPSSVSASVGDRTITCRASQGISGWLAWYQQKPGKAPKFLIYAASTLQSGVPS
RFSGSGSGTDFTLTISLQPEDFATYYCQQANSFPPTFGGGTKVEIK |
| 590 | SLTRK6 CDR-H1 | SYGMH |
| 591 | SLTRK6 CDR-H2 | VIWYDGSNQYYADSVKG |
| 592 | SLTRK6 CDR-H3 | GLTSGRYGMDV |
| 593 | SLTRK6 CDR-L1 | RSSQSLLLSHGFNYLD |
| 594 | SLTRK6 CDR-L2 | LGSSRAS |
| 595 | SLTRK6 CDR-L3 | MQPLQIPWT |
| 596 | SLTRK6 VH | QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSN
QYY
ADSVKGRFTISRDNKNTLFLQMHSRAEDTAVYYCARGLTSGRYGMDVWGQGTSTVTVSS |
| 597 | SLTRK6 VL | DIVMTQSPLSLPVTGPGEPAISCRSSQSLLLSHGFNYLDWYLQKPGQSPQLLIYLGSSRAS
GVPDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQPLQIPWTFGQGTKEIK |
| 598 | CD228 CDR-H1 | SGYWN |
| 599 | CD228 CDR-H2 | YISDSGITYYNPSLKS |
| 600 | CD228 CDR-H3 | RTLATYYAMDY |
| 601 | CD228 CDR-L1 | RASQSLVHSDGNTYLH |
| 602 | CD228 CDR-L2 | RVSNRFS |
| 603 | CD228 CDR-L3 | SQSTHVPPT |

| SEQ ID NO | Description | Sequence |
|-----------|----------------------|--|
| 604 | CD228 VH | QVQLQESGPGLVKPSSETLSLTCTVSGDSITSGYWNWIRQPPGKGLEIYIGYISDSGITYYN
PSLKSRVTISRDTSKNQYSLKLSSVTAADTAVYYCARRTLATYYAMDYWGQGTLLTVSS |
| 605 | CD228 VL | DFVMTQSPSLPVTLGQPASISCRASQSLVHSDGNTYLHWYQQRPGQSPRLLIYRVSNRF
SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVPPTFGGQGTKLEIKR |
| 606 | CD142 (TF)
CDR-H1 | NYAMS |
| 607 | CD142 (TF)
CDR-H2 | SISGSGDYTTYTDSVKG |
| 608 | CD142 (TF)
CDR-H3 | SPWGYLDS |
| 609 | CD142 (TF)
CDR-L1 | RASQGISSRLA |
| 610 | CD142 (TF)
CDR-L2 | AASSLQS |
| 611 | CD142 (TF)
CDR-L3 | QQYNSYPYT |
| 612 | CD142 (TF) VH | EVQLLESGLLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSSISGSGDYT
Y
YTDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSPWGYLDSWGQGTLLTVSS |
| 613 | CD142 (TF) VL | DIQMTQSPPSLSASAGDRVITICRASQGISSRLAWYQQKPEKAPKSLIYAASSLQSGVPS
RFSGSGSGTDFTLTISLQPEDFATYYCQQYNSYPYTFGGQGTKLEIK |
| 614 | STn CDR-H1 | DHAIH |
| 615 | STn CDR-H2 | YFSPGNDDIKYNEKFRG |
| 616 | STn CDR-H3 | SLSTPY |
| 617 | STn CDR-L1 | KSSQSLLNRGNHKNYLT |
| 618 | STn CDR-L2 | WASTRES |
| 619 | STn CDR-L3 | QNDYTYPYT |
| 620 | STn VH | EVQLVQSGAEVKKPGASVKVSKASGYTFTDHAIIHWVRQAPGQGLEWMGYFSPGNDDI
KY
NEKFRGRVTMTADKSSSTAYMELRSLRSDDTAVYFCKRSLSTPYWGQGTLLTVSS |
| 621 | STn VL | DIVMTQSPDSLAVSLGERATINCKSSQSLLNRGNHKNYLTWYQQKPGQPPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISLQAEDVAVYYCQNDYTYPYTFGGQGTKVEIK |
| 622 | CD20 CDR-H1 | SYNMH |
| 623 | CD20 CDR-H2 | AIYPGNGDTSYNQKFKG |
| 624 | CD20 CDR-H3 | STYYGGDWYFNV |
| 625 | CD20 CDR-L1 | RASSSVSYIH |
| 626 | CD20 CDR-L2 | ATSNLAS |
| 627 | CD20 CDR-L3 | QQWTSNPPT |
| 628 | CD20 VH | QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDT
SY
NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFNVWGAGTTVT
SA |
| 629 | CD20 VL | QIVLSQSPAILASAPGEKVTMTCRASSSVSYIHWYQQKPGSSPKPIYATSNLASGVPVR
FSGSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFGGGTKLEIK |
| 630 | HER2 CDR-H1 | DTYIH |
| 631 | HER2 CDR-H2 | RIYPTNGYTRYADSVKG |

| SEQ ID NO | Description | Sequence |
|-----------|---------------|--|
| 632 | HER2 CDR-H3 | WGGDGFYAMDY |
| 633 | HER2 CDR-L1 | RASQDVNTAVA |
| 634 | HER2 CDR-L2 | SASFLYS |
| 635 | HER2 CDR-L3 | QQHYTTPPT |
| 636 | HER2 VH | EVQLVESGGGLVQP GGSRLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRY
ADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSS |
| 637 | HER2 VL | DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPS
RFGSGRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIK |
| 638 | CD79b CDR-H1 | SYWIE |
| 639 | CD79b CDR-H2 | EILPGGGDTNYNEIFKG |
| 640 | CD79b CDR-H3 | RVPIRLDY |
| 641 | CD79b CDR-L1 | KASQSVDEYEGDSFLN |
| 642 | CD79b CDR-L2 | AASNLES |
| 643 | CD79b CDR-L3 | QQSNEDPLT |
| 644 | CD79b VH | EVQLVESGGGLVQP GGSRLRLSCAASGYTFSSYIEWVRQAPGKGLEWIGEILPGGGDTN
YNEIFKGRATFSADTSKNTAYLQMNSLRAEDTAVYYCTRRVPIRLDYWGQGTLVTVSS |
| 645 | CD79b VL | DIQLTQSPSSLSASVGDRVTITCKASQSVDEYEGDSFLNWWYQQKPGKAPKLLIYAASNLES
GVPSRFGSGSGTDFTLTISLQPEDFATYYCQQSNEDPLTFGQGTKVEIK |
| 646 | NaPi2B CDR-H1 | DFAMS |
| 647 | NaPi2B CDR-H2 | TIGRVAFTYYPDSMKG |
| 648 | NaPi2B CDR-H3 | HRGFDVGHFDF |
| 649 | NaPi2B CDR-L1 | RSSETLVHSSGNTYLE |
| 650 | NaPi2B CDR-L2 | RVSNRFS |
| 651 | NaPi2B CDR-L3 | FQGSFNPLT |
| 652 | NaPi2B VH | EVQLVESGGGLVQP GGSRLRLSCAASGFSFSDFAMSWVRQAPGKGLEWVATIGRVAFTY
Y
PDSMKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHRGFDVGHFDFWGQGTLVTVSS |
| 653 | NaPi2B VL | DIQMTQSPSSLSASVGDRVTITCRSSETLVHSSGNTYLEWYQQKPGKAPKLLIYRVSNRF
SGVPSRFGSGSGTDFTLTISLQPEDFATYYCFQGSFNPLTFGQGTKVEIK |
| 654 | Muc16 CDR-H1 | NDYAWN |
| 655 | Muc16 CDR-H2 | YISYSGYTTYNPSLKS |
| 656 | Muc16 CDR-H3 | WTSGLDY |
| 657 | Muc16 CDR-L1 | KASDLIHNWLA |
| 658 | Muc16 CDR-L2 | GATSLET |
| 659 | Muc16 CDR-L3 | QQYWTPPFT |
| 660 | Muc16 VH | EVQLVESGGGLVQP GGSRLRLSCAASGYTNDYAWNWWVRQAPGKGLEWVGYSYSGYTT
Y
NPSLKSRTISRDT SKNTLYLQMNSLRAEDTAVYYCARWTSGLDYWGQGTLVTVSS |
| 661 | Muc16 VL | DIQMTQSPSSLSASVGDRVTITCKASDLIHNWLAWYQQKPGKAPKLLIYGATSLETGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCQQYWTPPFTFGQGTKVEIK |
| 662 | STEAP1 CDR-H1 | SDYAWN |
| 663 | STEAP1 CDR-H2 | YISNSGSTSYNPSLKS |

| SEQ ID NO | Description | Sequence |
|-----------|---------------|--|
| 664 | STEAP1 CDR-H3 | ERNYDYDDYYYAMDY |
| 665 | STEAP1 CDR-L1 | KSSQSLLYRSNQKNYLA |
| 666 | STEAP1 CDR-L2 | WASTRES |
| 667 | STEAP1 CDR-L3 | QQYYNYPRT |
| 668 | STEAP1 VH | EVQLVESGGGLVQPGGSLRLSCAVSGYSITSDYAWNWRQAPGKGLEWVGYSNSGST
SYNPSLKSRTISRDTSKNTLYLQMNSLRAEDTAVYYCARERNYDYDDYYYAMDYWGQG
TLVTSS |
| 669 | STEAP1 VL | DIQMTQSPSSLSASVGDRTITCKSSQSLLYRSNQKNYLAWYQQKPGKAPKLLIYWASTR
ESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYNYPRTFGQGTKVEIK |
| 670 | BCMA CDR-H1 | NYWMH |
| 671 | BCMA CDR-H2 | ATYRGHSDTYNQKFKG |
| 672 | BCMA CDR-H3 | GAIDGYDVLN |
| 673 | BCMA CDR-L1 | SASQDISNYLN |
| 674 | BCMA CDR-L2 | YTSNLHS |
| 675 | BCMA CDR-L3 | QQYRKLPWT |
| 676 | BCMA VH | QVQLVQSGAEVKKPGSSVKVSKASGGTFSNYWMHWVRQAPGQGLEWMGATYRGHS
DTYYNQKFKGRVTITADKSTSTAYMELSSLRSEDVAVYYCARGAIDGYDVLNWDGQGT
LTVSS |
| 677 | BCMA VL | DIQMTQSPSSLSASVGDRTITCSASQDISNYLNWYQQKPGKAPKLLIYYTSLHSGVPSR
FSGSGSGTDFTLTISSLQPEDFATYYCQQYRKLPWTFGGGKLEIK |
| 678 | c-Met CDR-H1 | AYTMH |
| 679 | c-Met CDR-H2 | WIKPNNGLANYAQKFQG |
| 680 | c-Met CDR-H3 | SEITTEFDY |
| 681 | c-Met CDR-L1 | KSSESVDSYANSFLH |
| 682 | c-Met CDR-L2 | RASTRES |
| 683 | c-Met CDR-L3 | QQSKEDPLT |
| 684 | c-Met VH | QVQLVQSGAEVKKPGASVKVSKASGYIFTAYTMHWVRQAPGQGLEWMGWIKPNNGLA
N
YAQKFQGRVTMTDTSISTAYMELSLRSDDTAVYYCARSEITTEFDYWGQGTSLTVSS |
| 685 | c-Met VL | DIVMTQSPDSLAVSLGERATINCKSSESVDSYANSFLHWYQQKPGQPPKLLIYRASTRE
SGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSKEDPLTFGGGKVEIK |
| 686 | EGFR CDR-H1 | SDFAWN |
| 687 | EGFR CDR-H2 | YISYSGNTRYQPSLKS |
| 688 | EGFR CDR-H3 | AGRGFPY |
| 689 | EGFR CDR-L1 | HSSQDINSNIG |
| 690 | EGFR CDR-L2 | HGTNLDD |
| 691 | EGFR CDR-L3 | VQYAQFPWT |
| 692 | EGFR VH | QVQLQESGPGLVKPSQTLSTCTVSGYISSDFAWNWRQPPGKGLEWMGYISYSGNTR
Y
QPSLKSRTISRDTSKNQFFLKLNSVTAADTATYYCVTAGRGFPYWGQGTSLTVSS |
| 693 | EGFR VL | DIQMTQSPSSMSVSVGDRTITCHSSQDINSNIGWLQQKPGKSFGLIYHGTNLDDGVPS
RFSGSGSGTDYTLTISSLQPEDFATYYCVQYAQFPWTFGGGKLEIK |

| SEQ ID NO | Description | Sequence |
|-----------|----------------|--|
| 694 | SLAMF7 CDR-H1 | DYYMA |
| 695 | SLAMF7 CDR-H2 | SINYDGSSTYYVDSVKG |
| 696 | SLAMF7 CDR-H3 | DRGYFDY |
| 697 | SLAMF7 CDR-L1 | RSSQSLVHSNGNTYLH |
| 698 | SLAMF7 CDR-L2 | KVSNRFS |
| 699 | SLAMF7 CDR-L3 | SQSTHVPPFT |
| 700 | SLAMF7 VH | EVQLVESGGGLVQPGGSLRLSCAASGFTFSDYYMAWVRQAPGKGLEWVASINYDGSST
Y
YVDSVKGRFTISRDNANSLYLQMNSLRAEDTAVYYCARDRGYFDYWGGQTTVTVSS |
| 701 | SLAMF7 VL | DVVMQTPLSLSVTPGPASISCRSSQSLVHSNGNTYLHWYLQKPGQSPQLLIYKVSNR
SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYFCSQSTHVPPFTFGGGTKVEIK |
| 702 | SLITRK6 CDR-H1 | SYGMH |
| 703 | SLITRK6 CDR-H2 | VIWYDGSNQYYADSVKG |
| 704 | SLITRK6 CDR-H3 | GLTSGRYGMDV |
| 705 | SLITRK6 CDR-L1 | RSSQSLLSHGFNYLD |
| 706 | SLITRK6 CDR-L2 | LGSSRAS |
| 707 | SLITRK6 CDR-L3 | MQPLQIPWT |
| 708 | SLITRK6 VH | QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSN
QYY
ADSVKGRFTISRDNKNTLFLQMHSRAEDTAVYYCARGLTSGRYGMDVWGQGTITVVS
S |
| 709 | SLITRK6 VL | DIVMTQSPLSLPVTPGEPASISCRSSQSLLSHGFNYLDWYLQKPGQSPQLLIYLGSSRA
SGVPDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQPLQIPWTFGGGTKVEIK |
| 710 | C4.4a CDR-H1 | NAWMS |
| 711 | C4.4a CDR-H2 | YISSSGSTIYYADSVKG |
| 712 | C4.4a CDR-H3 | EGLWAFDY |
| 713 | C4.4a CDR-L1 | TGSSSNIGAGYVWH |
| 714 | C4.4a CDR-L2 | DNNKRPS |
| 715 | C4.4a CDR-L3 | AAWDDRLNGPV |
| 716 | C4.4a VH | EVQLLES GGGLVQP GGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVSYISSSGSTIY
Y
ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAREGLWAFDYWGQGTITVTVSS |
| 717 | C4.4a VL | ESVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYVWHWYQQLPGTAPKLLIYDNNKRPSGV
PDRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDRLNGPVFGGGTKLTVL |
| 718 | GCC CDR-H1 | GYYSWS |
| 719 | GCC CDR-H2 | EINHRGNTNDNPSLKS |

| SEQ ID NO | Description | Sequence |
|-----------|---------------------------|--|
| 720 | GCC CDR-H3 | ERGYTYGNFDH |
| 721 | GCC CDR-L1 | RASQSVSRNLA |
| 722 | GCC CDR-L2 | GASTRAT |
| 723 | GCC CDR-L3 | QQYKTWPRT |
| 724 | GCC VH | QVQLQQWGAGLLKPSETLSLTCAVFGGSFSGYYWSWIRQPPGKGLEWIGEINHRGNTND
N
PSLKSRVTISVDTSKNQFALKLSSVTAADTAVYYCARERGYTYGNFDHWGQGTLTVSS |
| 725 | GCC VL | EIVMTQSPATLSVSPGERATLSCRASQSVSRNLAWYQQKPGQAPRLIYGASTRATGIP
ARFSGSGSGTEFTLTIGSLQSEDAVYYCQQYKTWPRTFGQGTNVEIK |
| 726 | Axl CDR-H1 | SYAMN |
| 727 | Axl CDR-H2 | TTSGSGASTYYADSVKG |
| 728 | Axl CDR-H3 | IWIAFDI |
| 729 | Axl CDR-L1 | RASQSVSSSYLA |
| 730 | Axl CDR-L2 | GASSRAT |
| 731 | Axl CDR-L3 | QQYGSSPYT |
| 732 | Axl VH | EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWRQAPGKGLEWVSTTSGSGAST
YY
ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKIWIWIAFDIWGQGTMTVTVSS |
| 733 | Axl VL | EIVLTQSPGTLTSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIYGASSRATGIP
DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPYTFGQGTKLEIK |
| 734 | gpNMB CDR-H1 | SFNYYWS |
| 735 | gpNMB CDR-H2 | YIYYSGSTYSNPSLKS |
| 736 | gpNMB CDR-H3 | GYNWNIFYDY |
| 737 | gpNMB CDR-L1 | RASQSVDDNNLV |
| 738 | gpNMB CDR-L2 | GASTRAT |
| 739 | gpNMB CDR-L3 | QQYNNWPPWT |
| 740 | gpNMB VH | QVQLQESGPGLVKPSQTLSTCTVSGGSISFNYYWSWIRHHPGKGLEWIGYIYYSGSTY
SNPSLKSRVTISVDTSKNQFSLTSSVTAADTAVYYCARGYNWNIFYDYWGQGTMTVTVSS |
| 741 | gpNMB VL | EIVMTQSPATLSVSPGERATLSCRASQSVDDNNLVWYQQKPGQAPRLIYGASTRATGIPA
RFSGSGSGTEFTLTISLQSEDAVYYCQQYNNWPPWTFGQGTKVEIK |
| 742 | Prolactin receptor CDR-H1 | TYWMH |
| 743 | Prolactin receptor CDR-H2 | EIDPSDSYSNQNQKFKD |
| 744 | Prolactin receptor CDR-H3 | NGGLGPAWFSY |
| 745 | Prolactin receptor CDR-L1 | KASQYVGTAVA |
| 746 | Prolactin receptor CDR-L2 | SASNRYT |
| 747 | Prolactin receptor CDR-L3 | QQYSSYPWT |
| 748 | Prolactin receptor VH | EVQLVQSGAEVKKPGSSVKVSCASGYTFTTYWMHWVRQAPGQGLEWIGEIDPSDSYS
NY |

| SEQ ID NO | Description | Sequence |
|-----------|-----------------------|---|
| | | NQKFKDRATLTVDKSTSTAYMELSSLRSED TAVYYCARNGGLGPAWFSYWGQGTLVTVS S |
| 749 | Prolactin receptor VL | DIQMTQSPSSVSASVGDRVITITCKASQYVGTAVAWYQQKPGKSPKLLIYSASNRYTGVP S RFSDSGSGTDFTLTITSLQPEDFATYFCQQYSSYPWTFGGGTKVEIK |
| 750 | FGFR2 CDR-H1 | SYAMS |
| 751 | FGFR2 CDR-H2 | AISGSGTSTYYADSVKG |
| 752 | FGFR2 CDR-H3 | VRYNWNHGDWFD P |
| 753 | FGFR2 CDR-L1 | SGSSSNIGNNYVS |
| 754 | FGFR2 CDR-L2 | ENYNRPA |
| 755 | FGFR2 CDR-L3 | SSWDDSLNYWV |
| 756 | FGFR2 VH | EVQLLES GGG LVQP GGS LRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGTSTY YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARVRYNWNHGDWFD PWGQGT LVTSS |
| 757 | FGFR2 VL | QSVLTQPPSASGTPGQRTVITSCSGSSSNIGNNYVSWYQQLPGTAPKLLIYENYNRPAGVP DRFSGSKSGTSASLAISGLRSEDEADYYCSSWDDSLNYWVFGGGTKLTVL |
| 758 | CDCP1 CDR-H1 | SYGMS |
| 759 | CDCP1 CDR-H2 | TISSGGSYKYYVDSVKG |
| 760 | CDCP1 CDR-H3 | HPDYDGVWFAY |
| 761 | CDCP1 CDR-L1 | SVSSSVFYVH |
| 762 | CDCP1 CDR-L2 | DTSKLAS |
| 763 | CDCP1 CDR-L3 | QQWNSNPPT |
| 764 | CDCP1 VH | EVQLVESGGGLVQP GGS LRLSCAASGFTFNSYGMWSVRQAPGKGLEWVATISSGGSYK YY VDSVKGRFTISRDN AKNSLYLQMNSLRAEDTAVYYCARHPDYDGVWFAYWGQGT LTVS S |
| 765 | CDCP1 VL | DIQMTQSPSSLSASVGDRVITITCSVSSSVFYVHWYQQKPGKAPKLLIYDTSKLASSGVPS RFSGSGSGTDFTFTITSLQPEDIATYYCQQWNSNPPTFGGGTKVEIK |
| 766 | CDCP1 CDR-H1 | SYGMS |
| 767 | CDCP1 CDR-H2 | TISSGGSYTYYPDSVKG |
| 768 | CDCP1 CDR-H3 | HPDYDGVWFAY |
| 769 | CDCP1 CDR-L1 | SVSSSVFYVH |
| 770 | CDCP1 CDR-L2 | DTSKLAS |
| 771 | CDCP1 CDR-L3 | QQWNSNPPT |
| 772 | CDCP1 VH | EVQLVESGGDLVKP GGS LKLSAASGFTFNSYGMWSVRQTPDKRLEWVATISSGGSYTY Y PDSVKGRFTISRDN AKNTLYLQMSSLKSED TAMYCARHPDYDGVWFAYWGQGT LTVS A |
| 773 | CDCP1 VL | QIVLTQSPAIMASPGKEVTMTCSVSSSVFYVHWYQQKSGTSPKRWIYDTSKLASGVPARF SGSGSGTSYSLTISMEADAATYYCQQWNSNPPTFGGGTKLEIK |
| 774 | CDCP1 CDR-H1 | SYMH |
| 775 | CDCP1 CDR-H2 | IINPSGGSTSYAQKFQG |
| 776 | CDCP1 CDR-H3 | DGVLRYFDWLLDY |
| 777 | CDCP1 CDR-L1 | RASQSVGSYLA |
| 778 | CDCP1 CDR-L2 | DASNRAT |
| 779 | CDCP1 CDR-L3 | QQRANVFT |
| 780 | CDCP1 VH | EVQLVQSGAEVKKPGASVKVSKASGYTFTSYMHVVRQAPQGGLWMIINPSGGST SY |

| SEQ ID NO | Description | Sequence |
|-----------|--------------|---|
| | | AQKFQGRVTMTRDTSTSTVYMELSSLRSED TAVYYCARDGVLRYFDWLLDYYYYMDVW
GKG
TTVTVSS |
| 781 | CDCP1 VL | EIVLTQSPATLSLSPGERATLSCRASQSVGSYLA WYQQRPGQAPRLIYDASNRATGIPA
RFSGSGSGTDFTLTISLLEPEDFAVYYCQQRANVFTFGQGTKVEIK |
| 782 | CDCP1 CDR-H1 | SYMH |
| 783 | CDCP1 CDR-H2 | IINPSGGSTSYAQKFQG |
| 784 | CDCP1 CDR-H3 | DAELRHFDHLLDYHYMDV |
| 785 | CDCP1 CDR-L1 | RASQSVGSYLA |
| 786 | CDCP1 CDR-L2 | DASNRAT |
| 787 | CDCP1 CDR-L3 | QQRAGEFT |
| 788 | CDCP1 VH | EVQLVQSGAEVKKPGASVKVSKASGYTFTSYMHVWRQAPGQGLEWMGIINPSGGST
SYAQKFQGRVTMTRDTSTSTVYMELSSLRSED TAVYYCARDAELRHFDHLLDYHYMDV
WGQGTITVTVSS |
| 789 | CDCP1 VL | EIVMTQSPATLSLSPGERATLSCRASQSVGSYLA WYQKPGQAPRLIYDASNRATGIPA
RFSGSGSGTDFTLTISLQPEDFAVYYCQQRAGEFTFGQGTKVEIK |
| 790 | ASCT2 VH | QVQLVQSGSELKKPGAPVKVSKASGYTFTFGMSWVRQAPGQGLKWMGWIHTYAGVP
IYGDDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYFCARRSDNYRYFFDYWGQGTITVTV
SS |
| 791 | ASCT2 VL | DIQMTQSPSSLSASLGDRVTITCRASQDIRNYLNWYQKPGKAPKLLIYYTSRLHSGVPSR
FSGSGSGTDYTLTISLQPEDFATYFCQQGHTLPPTFGQGTKLEIK |
| 792 | ASCT2 VH | QIQLVQSGPELKKPGAPVKISCKASGYTFTFGMSWVKQAPGQGLKWMGWIHTYAGVPI
YGDDFKGRFVFLDTSVSTAYLQISSVKAEDTATYFCARRSDNYRYFFDYWGQGTITLTVS
S |
| 793 | ASCT2 VL | DIQMTQSPSSLSASLGDRVTITCRASQDIRNYLNWYQKPGKAPKLLIYYTSRLHSGVPS
RFSGSGSGTDYTLTISLQPEDFATYFCQQGHTLPPTFGQGTKLEIK |
| 794 | ASCT2 CDR-H1 | NYMA |
| 795 | ASCT2 CDR-H2 | SITKGGGNTYYRDSVKG |
| 796 | ASCT2 CDR-H3 | QVTIAAVSTSYFDS |
| 797 | ASCT2 CDR-L1 | KTNQKVDYYGNSYVY |
| 798 | ASCT2 CDR-L2 | LASNLAS |
| 799 | ASCT2 CDR-L3 | QQRNLPT |
| 800 | ASCT2 VH | EVQLVESGGGLVQSGRSIRLSAASGFSFSNYMAWVRQAPSKGLEWVASITKGGGNTY
YRDSVKGRFTFSRDNAKSTLYLQMDSLRSED TATYYCARQVTIAAVSTSYFDSWGQGV
MTVSS |
| 801 | ASCT2 VL | DIVLTQSPALAVSLGQRATISCKTNQKVDYYGNSYVYWYQKPGQPKLLIYLASNLASGI
PARFSGRSGTDFTLTIDPVEADDTATYYCQQRNLPTFGAGTKLEIK |
| 802 | CD123 CDR-H1 | DYYMK |
| 803 | CD123 CDR-H2 | DIIPNGATFYNQKFKG |
| 804 | CD123 CDR-H3 | SHLLRASWFAY |
| 805 | CD123 CDR-L1 | KSSQSLLNSGNQKNYLT |
| 806 | CD123 CDR-L2 | WASTRES |
| 807 | CD123 CDR-L3 | QNDYSYPYT |
| 808 | CD123 VH | QVQLVQSGAEVKKPGASVKMSCKASGYTFTDYYMKWVKQAPGQGLEWIGDIIPNGATF
YNQKFKGKATLTVDRSISTAYMHLNRLRSDDTAVYYCTRSHLLRASWFAYWGQGTITVTVS
S |
| 809 | CD123 VL | DFVMTQSPDSLAVSLGERATINCKSSQSLLNSGNQKNYLTWYLQKPGQPPKLLIYWASTR
ESGVPDRFSGSGSGTDFTLTISLQAEDVAVYYCQNDYSYPYTFGQGTKLEIK |

| SEQ ID NO | Description | Sequence |
|-----------|--------------|--|
| 810 | GPC3 CDR-H1 | DYEMH |
| 811 | GPC3 CDR-H2 | WIGGIDPETGGTAYNQKFKG |
| 812 | GPC3 CDR-H3 | YYSFAY |
| 813 | GPC3 CDR-L1 | RSSQSIVHSNGNTYLQ |
| 814 | GPC3 CDR-L2 | KVSNRFS |
| 815 | GPC3 CDR-L3 | FQVSHVPYT |
| 816 | GPC3 VH | EVQLVQSGAEVKKPGATVKISCKVSGYTFTDYEMHWVQQAPGKGLEWMGGIDPETGGTAYNQKFKGRVTLTADKSTDTAYMELSSLRSED TAVYYCGRYYSFAYWGQGLTVTVSS |
| 817 | GPC3 VL | DVVM TQSPLSLPVT LGQPASISCRSSQSIVHSNANTYLQWFQQRPGQSPRLLIYKVS N R FSGVPDRFSGSGSGTDFTLKISRVEAEDVG VYYCFQVSHVPYTFGQGTKLEIK |
| 818 | B6A CDR-H1 | DYNVN |
| 819 | B6A CDR-H2 | VINPKYGTTRYNQKFKG |
| 820 | B6A CDR-H3 | GLNAWDY |
| 821 | B6A CDR-L1 | GA SENIYGALN |
| 822 | B6A CDR-L2 | GATNLED |
| 823 | B6A CDR-L3 | QNVLTTPYT |
| 824 | B6A VH | QFQLVQSGAEVKKPGASVKV SCKASGYSFTDYNVNWVRQAPGQGLEWIGVINPKYGTTRYNQKFKGRATLTVDKSTSTAYMELSSLRSED TAVYYCTRGLNAWDYWGQGLTVTVSS |
| 825 | B6A VL | DIQMTQSPSSLSASVGDRTITCGA SENIYGALN WYQQKPGKAPKLLIYGATNLEDGVP SRFSGSGSGRDTFTISSLQPEDIATYYCQNVLTTPYTFGQGTKLEIK |
| 826 | B6A CDR-H1 | GYFMN |
| 827 | B6A CDR-H2 | LINPYNGDSFYNQKFKG |
| 828 | B6A CDR-H3 | GLRRDFDY |
| 829 | B6A CDR-L1 | KSSQSLLDSDGKTYLN |
| 830 | B6A CDR-L2 | LVSELD S |
| 831 | B6A CDR-L3 | WQGTHFPRT |
| 832 | B6A VH | QVQLVQSGAEVKKPGASVKV SCKASGYSFSGYFMNWVRQAPGQGLEWMGLINPYNGDSFYNQKFKGRVTMTRQTSTSTVYME LSSLRSED TAVYYCVRGLRRDFDYWGQGLTVTVSS |
| 833 | B6A VL | DVVM TQSPLSLPVT LGQPASISCKSSQSLLDSDGKTYLNWLFQRP GQSPRRLIYLVS ELDSGVPDRFSGSGSGTDFTLKISRVEAEDVG VYYCWQGTHFPRTFGGGTKLEIK |
| 834 | PD-L1 CDR-H1 | TAAIS |
| 835 | PD-L1 CDR-H2 | GIPIFGKAHYAQKFQG |
| 836 | PD-L1 CDR-H3 | KFH FVSGSPFGMDV |
| 837 | PD-L1 CDR-L1 | RASQSVSSYLA |
| 838 | PD-L1 CDR-L2 | DASNRAT |
| 839 | PD-L1 CDR-L3 | QQR SNWPT |
| 840 | PD-L1 VH | QVQLVQSGAEVKKPGSSVKV SCKTSGDTFSTA AISWVRQAPGQGLEWMGGIPIFGKAHYAQKFQGRVTITADESTSTAYME LSSLRSED TAVYFCARKFH FVSGSPFGMDVWGQGT TVTVSS |
| 841 | PD-L1 VL | EIVLTQSPATLSLSPGERATLSCRASQSVSSYLA WYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFLTISSELPEDFAVYYCQQR SNWPTFGQGTKVEIK |
| 842 | TIGIT CDR-H1 | GTFSSY AIS |
| 843 | TIGIT CDR-H2 | SIPIFGTANYAQKFQG |
| 844 | TIGIT CDR-H3 | ARGPSEVGAILGYVWFDP |
| 845 | TIGIT CDR-L1 | RSSQSLLHSNGYNYLD |
| 846 | TIGIT CDR-L2 | LGSNRAS |

| SEQ ID NO | Description | Sequence |
|-----------|--------------|--|
| 847 | TIGIT CDR-L3 | MQARRIPIT |
| 848 | TIGIT VH | QVQLVQSGAEVKKPGSSVKVSKASGGTFSSYAIWVRQAPGQGLEWMGSIIPIFGTANY
AQKFQGRVTITADESTSTAYMELSSLRSEDVAVYYCARGPSEVGAILGYVWFDPWGQGT
LTVSS |
| 849 | TIGIT VL | DIVMTQSPSLPVTGPGEASISCRSSQSLLSNGYNYLDWYLQKPGQSPQLLIYLGSNRAS
GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQARRIPITFGGGTKVEIK |
| 850 | STN CDR-H1 | GYTFTDHAIHWV |
| 851 | STN CDR-H2 | FSPGNDDIKY |
| 852 | STN CDR-H3 | KRSLSTPY |
| 853 | STN CDR-L1 | QSLNLRGNHKNY |
| 854 | STN CDR-L2 | WASTRES |
| 855 | STN CDR-L3 | QNDYTPYT |
| 856 | STN VH | EVQLVQSGAEVKKPGASVKVSKASGYTFTDHAIHWVRQAPGQGLEWMGYFSPGNDDI
KYNEKFRGRVTMTADKSSSTAYMELRSLRSDDTAVYFCKRSLSTPYWGQGTLLTVSS |
| 857 | STN VL | DIVMTQSPDSLAVSLGERATINCKSSQSLNLRGNHKNYLTWYQQKPGQPPKLLIYWASTR
ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQNDYTPYTFGQGTKEIK |
| 858 | CD33 CDR-H1 | NYDIN |
| 859 | CD33 CDR-H2 | WIYPGDGSTKYNEKFA |
| 860 | CD33 CDR-H3 | GYEDAMDY |
| 861 | CD33 CDR-L1 | KASQDINSYLS |
| 862 | CD33 CDR-L2 | RANRLVD |
| 863 | CD33 CDR-L3 | LQYDEFPLT |
| 864 | CD33 VH | QVQLVQSGAE VKKPGASVKV SCKASGYTFT NYDINWVRQA PGQGLEWIGW
IYPGDGSTKY NEKFAKATL TADTSTAY MELRSLRSDDTAVYYCASGY
EDAMDYWGQG TTVTVSS |
| 865 | CD33 VL | DIQMTQSPS SLSASVGDRTV INCKASQDINSYLSWVQKPGKAPKTL IYRANRLVDGVP
S RFSGSGSGQDYTLT ISSLPEDFATYYCLQYDEFPLTFGGGTKEIK |
| 866 | NTBA CDR-H1 | NYGMN |
| 867 | NTBA CDR-H2 | WINTYSGEPYADDFKG |
| 868 | NTBA CDR-H3 | DYGRWYFDV |
| 869 | NTBA CDR-L1 | RASSSVSHMH |
| 870 | NTBA CDR-L2 | ATSNLAS |
| 871 | NTBA CDR-L3 | QQWSSTPRT |
| 872 | NTBA VH | QIQLVQSGSELKKPGASVKVSKASGYTFTNYGMNWVRQAPGQDLKWMGWINTYSGEP
RYADDFKGRFVFSLDKSVNTAYLQISSLKAEDTAVYYCARDYGRWYFDVWGQGTITVSS
S |
| 873 | NTBA VL | QIVLSQSPATLSLSPGERATMSCRASSSVSHMHWYQQKPGQAPRPWIYATSNLASGVP
A RFSGSGSGTDYTLTISSLEPEDFAVYYCQQWSSTPRTFGGGTKVEIK |
| 874 | BCMA CDR-H1 | DYYIH |
| 875 | BCMA CDR-H2 | YINPNSGYTNYAQKFQG |
| 876 | BCMA CDR-H3 | YMWERTGFFDF |
| 877 | BCMA CDR-L1 | LASEDISDDLA |
| 878 | BCMA CDR-L2 | TTSSLQS |
| 879 | BCMA CDR-L3 | QQTYKFPPT |
| 880 | BCMA VH | QVQLVQSGAEVKKPGASVKLSCKASGYTFTDYYIHWVRQAPGQGLEWIGYINPNSGYTN
Y AQKFQGRATMTADKSINTAYVELSRLRSDDTAVYFCTRYMWERTGFFDFWGQGTMTV
VSS |

| SEQ ID NO | Description | Sequence |
|-----------|-------------|--|
| 881 | BCMA VL | DIQMTQSPSSVSASVGDRTITCLASEDISDDLAWYQQKPGKAPKVLVYTTSSLQSGVPS
RFGSGSGTDFTLTISLQPEDFATYFCQQTYKFPPTFGGGTKVEIK |
| 882 | TF CDR-H1 | GFTFSNYA |
| 883 | TF CDR-H2 | ISGSGDYT |
| 884 | TF CDR-H3 | ARSPWGYLDS |
| 885 | TF CDR-L1 | QGISSR |
| 886 | TF CDR-L2 | AAS |
| 887 | TF CDR-L3 | QQYNSYPYT |
| 888 | TF VH | EVQLLES GGGLVQPGGSLRLS CAASGFTFSNYAMSWVRQAPGKGLEWVSSISGSGDYT
YYTDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSPWGYLDSWGQGT LTVS
S |
| 889 | TF VL | DIQMTQSPPSLSASAGDRVTITCRASQGISSRLAWYQQKPEKAPKSLIYAASSLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCQQYNSYPYTFGQGTKLEIK |

[0239] In some embodiments, the antibody is a non-targeted antibody, for example, a non-binding or control antibody.

Linkers

[0240] As described herein, linkers (L) are optional groups that connect D with Ab.

[0241] In some embodiments, the linker (L) has the formula $-M-(A)_a-(W)_w-(Y)_y-(X)-$, wherein:

M is a succinimide, a hydrolyzed succinimide, an amide, or a triazole;

X is from 1-10 amino acids; or

X is a 4-16 membered heteroalkylene, wherein X is optionally substituted with 1-3 independently selected R^X ;

each R^X is independently a C_2 - C_6 alkynyl group, $-NR^{X1}R^{X2}$, or a C_1 - C_6 alkyl group optionally substituted with hydroxyl, $-NR^{X1}R^{X2}$, guanidino, 1 or 2 $-CO_2H$ groups, $-C(=O)NR^{X1}R^{X2}$, urea, phenyl, naphthyl, indolyl, imidazolyl, $-SH$, $-SCH_3$, $-SeCH_3$, or 4-hydroxyphenyl optionally substituted with C_2 - C_6 alkenyl; or

two R^X attached to the same or adjacent carbon atom(s) of X, together with the carbon atom(s) to which they are attached form an unsubstituted 5-6 membered heterocyclyl;

each R^{X1} and R^{X2} are independently hydrogen or C_{1-6} alkyl;

A is a C_{2-10} alkylene optionally substituted with 1-3 R^{a1} ; or a 3 to 20 membered heteroalkylene optionally substituted with 1-3 R^{b1} ;

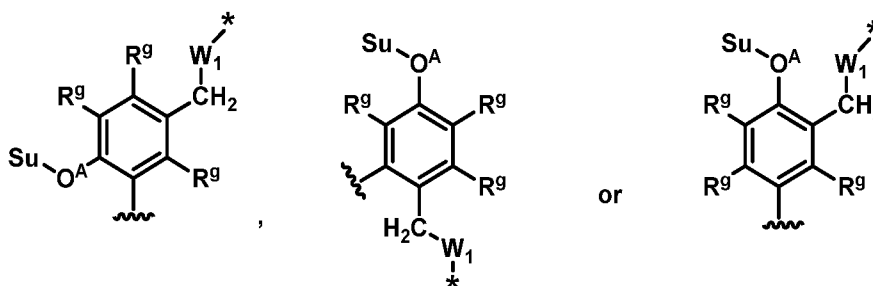
each R^{a1} is independently selected from the group consisting of: C_{1-6} alkyl, C_{1-6} haloalkyl, C_{1-6} alkoxy, C_{1-6} haloalkoxy, halogen, $-OH$, $=O$, $-NR^{d1}R^{e1}$, $-(C_{1-6} \text{ alkylene})-NR^{d1}R^{e1}$, $-C(=O)NR^{d1}R^{e1}$, $-C(=O)(C_{1-6} \text{ alkyl})$, and $-C(=O)O(C_{1-6} \text{ alkyl})$;

each R^{b1} is independently selected from the group consisting of: C_{1-6} alkyl, C_{1-6} haloalkyl, C_{1-6} alkoxy, C_{1-6} haloalkoxy, halogen, $-OH$, $=O$, $-NR^{d1}R^{e1}$, $-(C_{1-6} \text{ alkylene})-NR^{d1}R^{e1}$, $-C(=O)NR^{d1}R^{e1}$, $-C(=O)(C_{1-6} \text{ alkyl})$, and $-C(=O)O(C_{1-6} \text{ alkyl})$;

each R^{d1} and R^{e1} are independently hydrogen or C_{1-3} alkyl;

subscript a is 0 or 1;

W is from 2-6 amino acids or has the structure:



wherein Su is a Sugar moiety;

$-O^A$ represents the oxygen atom of a glycosidic bond;

each R^g is independently hydrogen, halogen, C_{1-6} alkoxy, $-N(C_{1-6} \text{ alkyl})_2$, $-NHC(=O)(C_{1-6} \text{ alkyl})$, $-CN$, $-CF_3$, acyl, carboxamido, C_{1-6} alkyl, or $-NO_2$;

W_1 is absent, $*-C(=O)-O-$, or $*-O-C(=O)-$;

~~~~~ represents covalent attachment to A or M;

\* represents covalent attachment to Y or X;

subscript w is 0 or 1;

Y is a self-immolative moiety, a non-self-immolative releasable moiety, or a non-cleavable moiety; and

subscript y is 0 or 1.

**[0242]** In some embodiments, subscript a is 0. In some embodiments, subscript a is 1. In some embodiments, subscript w is 0. In some embodiments, subscript w is 1. In some embodiments, subscript y is 0. In some embodiments, subscript y is 1. In some embodiments, subscripts  $a + y + w = 1$ . In some embodiments, subscripts  $a + y + w = 2$ . In some embodiments,

subscripts  $a + y + w = 3$ . In some embodiments, subscripts  $a + y + w = 0$  (i.e., the linker (L) is -M-X-).

**[0243]** In some embodiments, X is from 1-10 amino acids, for example, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 independently selected amino acids. In some embodiments, X is 1 amino acid. In some embodiments, X is 2 amino acids. In some embodiments, X is 3 amino acids. In some embodiments, X is 4 amino acids. In some embodiments, X is 5, 6, or 7 amino acids. In some embodiments, X is 8, 9, or 10 amino acids.

**[0244]** In some embodiments, the 1-10 amino acids of X are each independently selected from natural amino acids. In some embodiments, the 1-10 amino acids of X are each independently selected from non-natural amino acids. In some embodiments, the 1-10 amino acids of X are each independently selected from non-classical amino acids. In some embodiments, the 1-10 amino acids of X are each independently selected from a combination of natural amino acids, non-natural amino acids, and/or non-classical amino acids.

**[0245]** In some embodiments, X does not include any glycine residues. In some embodiments, X does not include any contiguous glycine residues, such as di-glycine, tri-glycine, tetra-glycine, penta-glycine, or hexa-glycine. In some embodiments, X includes one or more non-contiguous glycine residues.

**[0246]** In some embodiments, X is not a sortase enzyme recognition motif.

**[0247]** In some embodiments, X is not -Leu-Pro-\* -Thr-Gly-, -Gly-Thr-\* -Pro-Leu-, -Gly-Ser-\* -Pro-Leu-, -Gly-Thr-\* -Ala-Leu-, -Gly-Thr-\* -Pro-Leu-, -Gly-Ser-\* -Pro-Leu-, -Gly-Thr-\* -Ala-Leu-, -Thr-\* -Pro-Leu-, -Ser-\* -Pro-Leu-, -Thr-\* -Ala-Leu-, -Thr-\* -Pro-Leu-, -Ser-\* -Pro-Leu-, -Thr-\* -Ala-Leu-, -Gln-Pro-Gln-Thr-Asp-; wherein \* is any natural amino acid.

**[0248]** In some embodiments, X is not -Lys-Pro-Gly-Thr-Gly- or -Asp-Pro-Gln-Thr-Gln-.

**[0249]** In some embodiments, X is a 4-16 membered heteroalkylene optionally substituted with 1-3 independently selected  $R^X$ . In some embodiments, X is a 4-12 membered heteroalkylene optionally substituted with 1-3 independently selected  $R^X$ . In some embodiments, X is a 4-8 membered heteroalkylene optionally substituted with 1-3 independently selected  $R^X$ .

**[0250]** In some embodiments, X is a 4-16 membered heteroalkylene substituted with 1-3 independently selected  $R^X$ . In some embodiments, X is a 4-12 membered heteroalkylene

substituted with 1-3 independently selected  $R^X$ . In some embodiments, X is a 4-8 membered heteroalkylene substituted with 1-3 independently selected  $R^X$ .

**[0251]** In some embodiments, X is a 4-16 membered heteroalkylene substituted with 3 independently selected  $R^X$ . In some embodiments, X is a 4-12 membered heteroalkylene substituted with 3 independently selected  $R^X$ . In some embodiments, X is a 4-8 membered heteroalkylene substituted with 3 independently selected  $R^X$ .

**[0252]** In some embodiments, X is a 4-16 membered heteroalkylene substituted with 1 or 2 independently selected  $R^X$ . In some embodiments, X is a 4-12 membered heteroalkylene substituted with 1 or 2 independently selected  $R^X$ . In some embodiments, X is a 4-8 membered heteroalkylene substituted with 1 or 2 independently selected  $R^X$ .

**[0253]** In some embodiments, X is a 4-16 membered heteroalkylene substituted with 2 independently selected  $R^X$ . In some embodiments, X is a 4-12 membered heteroalkylene substituted with 2 independently selected  $R^X$ . In some embodiments, X is a 4-8 membered heteroalkylene substituted with 2 independently selected  $R^X$ .

**[0254]** In some embodiments, X is a 4-16 membered heteroalkylene substituted with 1  $R^X$ . In some embodiments, X is a 4-12 membered heteroalkylene substituted with 1  $R^X$ . In some embodiments, X is a 4-8 membered heteroalkylene substituted with 1  $R^X$ .

**[0255]** In some embodiments, each  $R^X$  is independently a  $C_2$ - $C_6$  alkynyl group,  $-NR^{X1}R^{X2}$ , or a  $C_1$ - $C_6$  alkyl group optionally substituted with hydroxyl,  $-NR^{X1}R^{X2}$ , guanidino, 1 or 2  $-CO_2H$  groups,  $-C(=O)NR^{X1}R^{X2}$ , urea, phenyl, naphthyl, indolyl, imidazolyl,  $-SH$ ,  $-SCH_3$ ,  $-SeCH_3$ , or 4-hydroxyphenyl optionally substituted with  $C_2$ - $C_6$  alkenyl; and each  $R^{X1}$  and  $R^{X2}$  are independently hydrogen or  $C_{1-6}$  alkyl.

**[0256]** In some embodiments, one  $R^X$  is a  $C_1$ - $C_6$  alkyl group optionally substituted with hydroxyl,  $-NR^{X1}R^{X2}$ , guanidino, 1 or 2  $-CO_2H$  groups,  $-C(=O)NR^{X1}R^{X2}$ , urea, phenyl, naphthyl, indolyl, imidazolyl,  $-SH$ ,  $-SCH_3$ ,  $-SeCH_3$ , or 4-hydroxyphenyl optionally substituted with  $C_2$ - $C_6$  alkenyl.

**[0257]** In some embodiments, one  $R^X$  is a  $C_1$ - $C_6$  alkyl group substituted with hydroxyl,  $-NR^{X1}R^{X2}$ , guanidino, 1 or 2  $-CO_2H$  groups,  $-C(=O)NR^{X1}R^{X2}$ , urea, phenyl, naphthyl, indolyl, imidazolyl,  $-SH$ ,  $-SCH_3$ ,  $-SeCH_3$ , or 4-hydroxyphenyl optionally substituted with  $C_2$ - $C_6$  alkenyl.

**[0258]** In some embodiments, one  $R^X$  is a  $C_1$ - $C_6$  alkyl group substituted with hydroxyl.

[0259] In some embodiments, one  $R^X$  is a  $C_1$ - $C_6$  alkyl group substituted with guanidino.

[0260] In some embodiments, one  $R^X$  is a  $C_1$ - $C_6$  alkyl group substituted with 1 or 2 - $CO_2H$  groups.

[0261] In some embodiments, one  $R^X$  is a  $C_1$ - $C_6$  alkyl group substituted with 1 - $CO_2H$  group.

[0262] In some embodiments, one  $R^X$  is a  $C_1$ - $C_6$  alkyl group substituted with 2 - $CO_2H$  groups.

[0263] In some embodiments, one  $R^X$  is a  $C_1$ - $C_6$  alkyl group substituted with urea.

[0264] In some embodiments, one  $R^X$  is a  $C_1$ - $C_6$  alkyl group substituted with phenyl.

[0265] In some embodiments, one  $R^X$  is a  $C_1$ - $C_6$  alkyl group substituted with naphthyl.

[0266] In some embodiments, one  $R^X$  is a  $C_1$ - $C_6$  alkyl group substituted with indolyl.

[0267] In some embodiments, one  $R^X$  is a  $C_1$ - $C_6$  alkyl group substituted with imidazolyl.

[0268] In some embodiments, one  $R^X$  is a  $C_1$ - $C_6$  alkyl group substituted with -SH, -SCH<sub>3</sub>, or -SeCH<sub>3</sub>.

[0269] In some embodiments, one  $R^X$  is a  $C_1$ - $C_6$  alkyl group substituted with 4-hydroxyphenyl optionally substituted with  $C_2$ - $C_6$  alkenyl.

[0270] In some embodiments, one  $R^X$  is a  $C_1$ - $C_6$  alkyl group substituted with -C(=O)NR<sup>X1</sup>R<sup>X2</sup>.

[0271] In some embodiments, one  $R^X$  is a  $C_1$ - $C_6$  alkyl group substituted with -NR<sup>X1</sup>R<sup>X2</sup>.

[0272] In some embodiments, one  $R^X$  is -NR<sup>X1</sup>R<sup>X2</sup>.

[0273] In some embodiments, R<sup>X1</sup> and R<sup>X2</sup> are each independently  $C_{1-6}$  alkyl. In some embodiments, R<sup>X1</sup> and R<sup>X2</sup> are each methyl. In some embodiments, R<sup>X1</sup> and R<sup>X2</sup> are each hydrogen. In some embodiments, one of R<sup>X1</sup> and R<sup>X2</sup> is hydrogen and the other of R<sup>X1</sup> and R<sup>X2</sup> is  $C_{1-6}$  alkyl. In some embodiments, one of R<sup>X1</sup> and R<sup>X2</sup> is hydrogen and the other of R<sup>X1</sup> and R<sup>X2</sup> is methyl.

[0274] In some embodiments, one  $R^X$  is a  $C_2$ - $C_6$  alkynyl group.

[0275] In some embodiments, X is substituted with two  $R^X$ ; wherein each  $R^X$  is an independently selected unsubstituted  $C_1$ - $C_6$  alkyl group.

**[0276]** In some embodiments, X is substituted with one  $R^X$ ; wherein  $R^X$  is an unsubstituted  $C_1$ - $C_6$  alkyl group.

**[0277]** In some embodiments, X is substituted with two  $R^X$ ; wherein the two  $R^X$  are attached to the same or adjacent carbon atom(s) of X, and together with the carbon atom(s) to which they are attached form an unsubstituted 5-6 membered heterocyclyl. In some embodiments, X is substituted with two  $R^X$ ; wherein the two  $R^X$  are attached to the same carbon atom of X, and together with the carbon atom to which they are attached form an unsubstituted 5-6 membered heterocyclyl. In some embodiments, X is substituted with two  $R^X$ ; wherein the two  $R^X$  are attached to adjacent carbon atoms of X, and together with the carbon atoms to which they are attached form an unsubstituted 5-6 membered heterocyclyl. In some embodiments, the two  $R^X$ , together with the carbon atom(s) to which they are attached form an unsubstituted 5-6 membered heterocyclyl selected from the group consisting of pyrrolidine, imidazolidine, piperidine, piperazine, and morpholine. In some embodiments, the two  $R^X$ , together with the carbon atom(s) to which they are attached form an unsubstituted pyrrolidine.

**[0278]** In some embodiments, X is substituted with two  $R^X$ ; wherein one  $R^X$  is a  $C_2$ - $C_6$  alkynyl group,  $-NR^{X1}R^{X2}$ , or a  $C_1$ - $C_6$  alkyl group optionally substituted with hydroxyl,  $-NR^{X1}R^{X2}$ , guanidino, 1 or 2  $-CO_2H$  groups,  $-C(=O)NR^{X1}R^{X2}$ , urea, phenyl, naphthyl, indolyl, imidazolyl,  $-SH$ ,  $-SCH_3$ ,  $-SeCH_3$ , or 4-hydroxyphenyl optionally substituted with  $C_2$ - $C_6$  alkenyl; wherein each  $R^{X1}$  and  $R^{X2}$  are independently hydrogen or  $C_{1-6}$  alkyl; and the other  $R^X$  is an unsubstituted  $C_1$ - $C_6$  alkyl group.

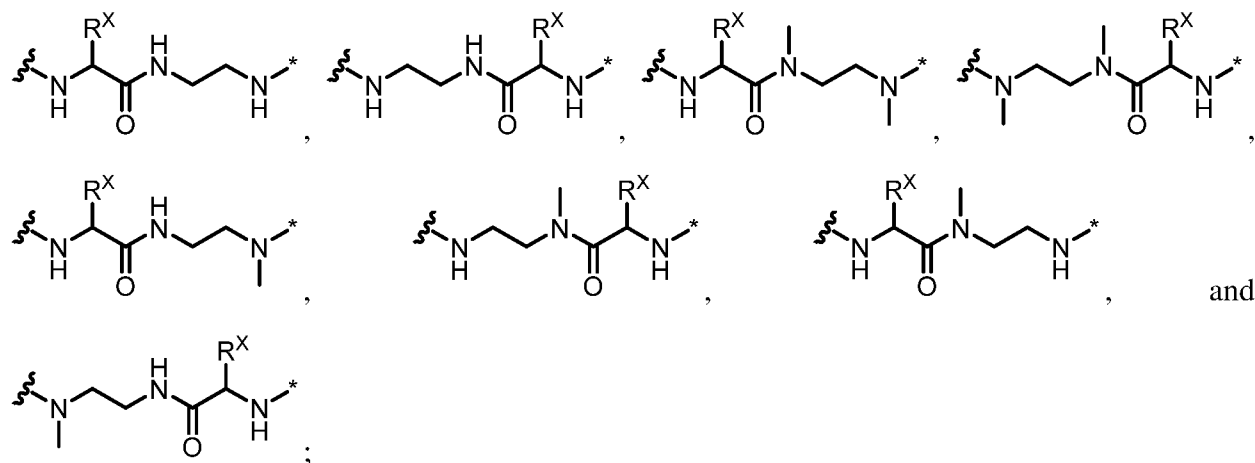
**[0279]** In some embodiments, X is substituted with one, two, or three methyl groups. In some embodiments, X is substituted with one or two (N)-methyl groups (i.e., X is substituted with methyl group on a nitrogen atom of X). In some embodiments, X is substituted with a geminal dimethyl group (two methyl groups attached to the same atom).

**[0280]** In some embodiments, X is  $-NH(C_2$ - $C_6$  alkylene) $NH$ - optionally substituted with  $C_1$ - $C_6$  alkyl. In some embodiments, X is  $-NH(C_2$ - $C_3$  alkylene) $NH$ - optionally substituted with  $C_1$ - $C_6$  alkyl. In some embodiments, X is  $-NH(C_2$ - $C_6$  alkylene) $NH$ - optionally substituted with two independently selected  $C_1$ - $C_6$  alkyl groups. In some embodiments, X is  $-NH(C_2$ - $C_3$  alkylene) $NH$ - optionally substituted with two independently selected  $C_1$ - $C_6$  alkyl groups. In some embodiments, X is  $##-NH(C_2$ - $C_6$  alkylene) $NH$ -(PEG2 to PEG4)-, wherein  $##$  indicates attachment to D.

[0281] In some embodiments, X is ##-NH(C<sub>2</sub>-C<sub>6</sub> alkylene)-, wherein ## indicates attachment to D. In some embodiments, X is ##-NH(C<sub>2</sub>-C<sub>6</sub> alkylene)-(PEG2 to PEG4)-, wherein ## indicates attachment to D. In some embodiments, X is ##-NH(C<sub>2</sub>-C<sub>6</sub> alkylene)NH-[(C(O)CH<sub>2</sub>NH)]<sub>1-2</sub>- or ##-NH(C<sub>2</sub>-C<sub>6</sub> alkylene)NH-[(C(O)CHR<sup>X</sup>NH)]<sub>1-3</sub>-, wherein R<sup>X</sup> is C<sub>1-3</sub> alkyl optionally substituted with -OH and ## indicates attachment to D. In some embodiments, X is ##-[NHCH<sub>2</sub>C(O)]<sub>1-3</sub>-NH(C<sub>2</sub>-C<sub>6</sub> alkylene)NH- or ##-[NHCHR<sup>X</sup>C(O)]<sub>1-3</sub>-NH(C<sub>2</sub>-C<sub>6</sub> alkylene)NH-, wherein R<sup>X</sup> is C<sub>1-3</sub> alkyl optionally substituted with -OH and ## indicates attachment to D. In some embodiments, X is ##-NR<sup>X</sup>(C<sub>2</sub>-C<sub>6</sub> alkylene)NR<sup>X</sup>-, wherein R<sup>X</sup> is C<sub>1-3</sub> alkyl and ## indicates attachment to D. In some embodiments, X is ##-[NHCH<sub>2</sub>C(O)]<sub>1-3</sub>- or ##-[NHCHR<sup>X</sup>C(O)]<sub>1-3</sub>-, wherein R<sup>X</sup> is C<sub>1-3</sub> alkyl optionally substituted with -OH and ## indicates attachment to D.

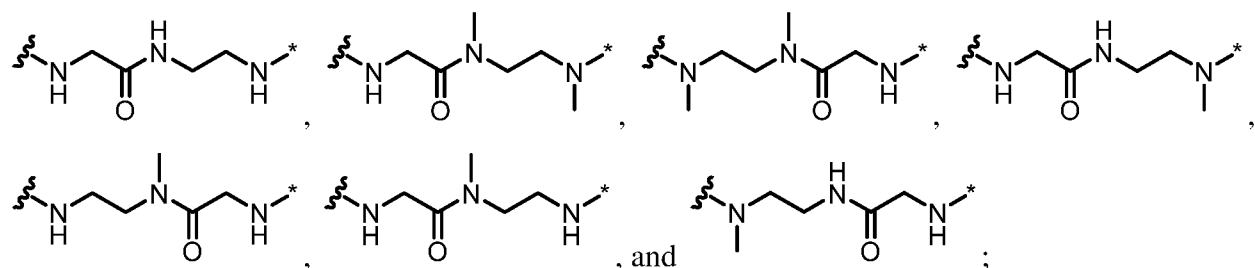
[0282] In some embodiments, X is an unsubstituted 4-16 membered heteroalkylene. In some embodiments, X is an unsubstituted 4-12 membered heteroalkylene. In some embodiments, X is an unsubstituted 4-8 membered heteroalkylene.

[0283] In some embodiments, X is selected from the group consisting of:



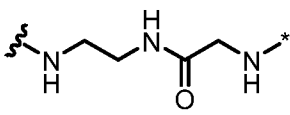
wherein the wavy line represents covalent attachment to Y, W, A, or M; and the \* represents covalent attachment to D.

[0284] In some embodiments, X is selected from the group consisting of:



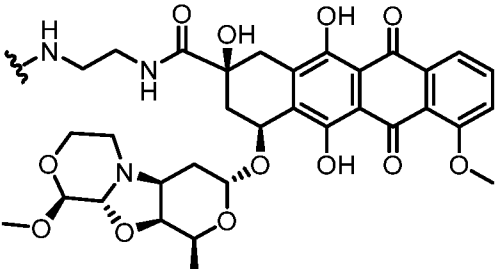


wherein the wavy line represents covalent attachment to Y, W, A, or M; and the \* represents covalent attachment to D.

[0285] In some embodiments, X is not ; wherein the wavy line represents covalent attachment to Y, W, A, or M; and the \* represents covalent attachment to D.

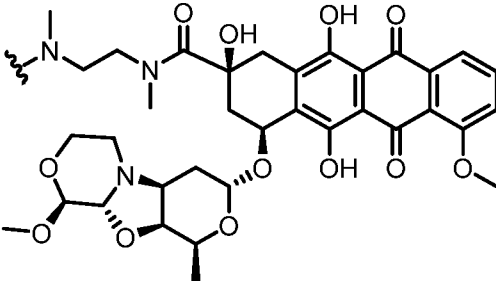
[0286] In some embodiments, X is not PEG1-PEG8. In some embodiments, X is not PEG1. In some embodiments, X is not PEG2. In some embodiments, X is not PEG3. In some embodiments, X is not PEG4. In some embodiments, X is not PEG5. In some embodiments, X is not PEG6. In some embodiments, X is not PEG7. In some embodiments, X is not PEG8.

[0287] In some embodiments, each D-X is:



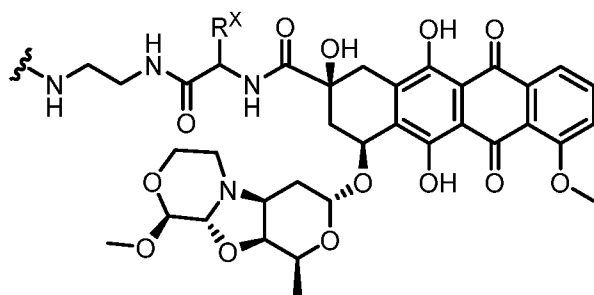
; wherein  represents covalent attachment to Y, W, A, or M.

[0288] In some embodiments, each D-X is:



; wherein  represents covalent attachment to Y, W, A, or M.

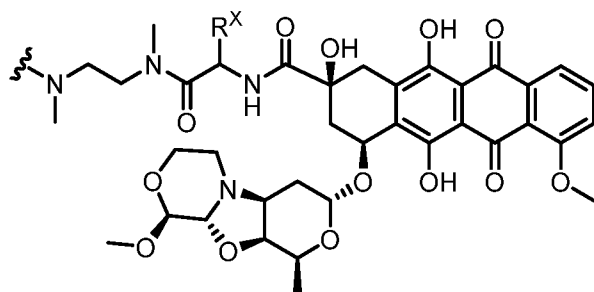
In some embodiments, each D-X is:



; wherein  represents covalent attachment

to Y, W, A, or M.

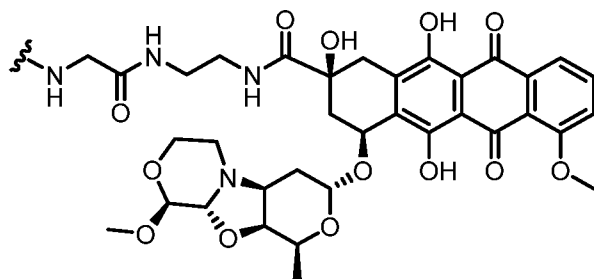
In some embodiments, each D-X is:



; wherein  represents covalent attachment

to Y, W, A, or M.

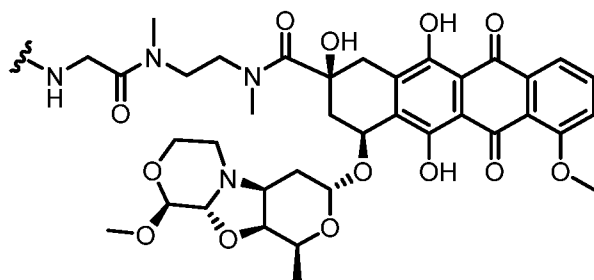
**[0289]** In some embodiments, each D-X is:



; wherein  represents covalent attachment

to Y, W, A, or M.

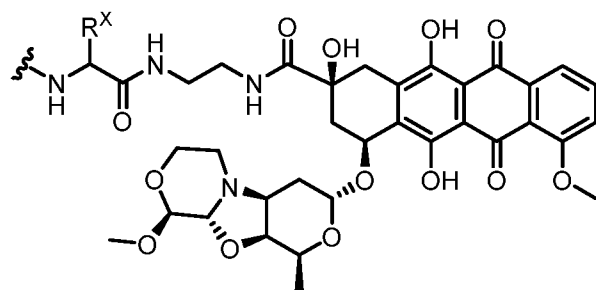
In some embodiments, each D-X is:



; wherein  represents covalent attachment

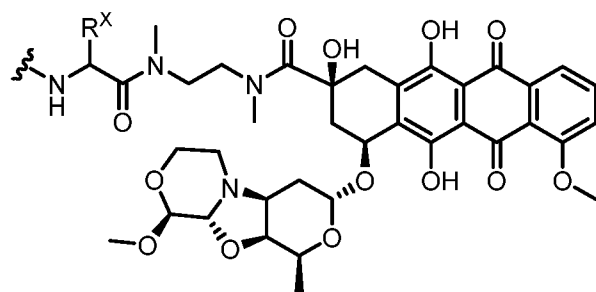
to Y, W, A, or M.

In some embodiments, each D-X is:



; wherein represents covalent attachment to Y, W, A, or M.

In some embodiments, each D-X is:



; wherein represents covalent attachment to Y, W, A, or M.

**[0290]** In some embodiments, subscript y is 0. In some embodiments subscript y is 1.

**[0291]** In some embodiments, Y is a self-immolative moiety, a non-self-immolative releasable moiety, or a non-cleavable moiety. In some embodiments, Y is a self-immolative moiety or a non-self-immolative releasable moiety. In some embodiments, Y is a self-immolative moiety. In some embodiments, Y is a non-self-immolative moiety.

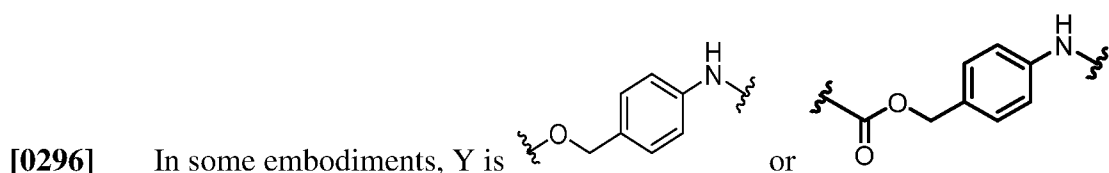
**[0292]** A non-self-immolative moiety is one which requires enzymatic cleavage, and in which part or all of the group remains bound to the Drug Unit after cleavage from the ADC, thereby forming free drug. Examples of a non-self-immolative moiety include, but are not limited to: -glycine-; -glycine-glycine-; and a p-aminobenzyl alcohol (PAB) optionally substituted with 1-4 substituents independently selected from halogen, C<sub>1</sub>-C<sub>6</sub> alkoxy, -N(C<sub>1</sub>-C<sub>6</sub> alkyl)<sub>2</sub>, -NHC(=O)(C<sub>1</sub>-C<sub>6</sub> alkyl), -CN, -CF<sub>3</sub>, acyl, carboxamido, C<sub>1</sub>-C<sub>6</sub> alkyl, or -NO<sub>2</sub>. When an ADC having Y is -glycine- or -glycine-glycine- undergoes enzymatic cleavage (for example, via a cancer-cell-associated protease or a lymphocyte-associated protease), the Drug Unit is cleaved from the ADC such that the free drug includes the glycine or glycine-glycine group from Y. In some embodiments, an independent hydrolysis reaction takes place within, or in proximity to, the target cell, further cleaving the glycine or glycine-glycine group from the free drug. For example,

an ADC with a non-self-immolative linker with a PAB optionally substituted with 1-4 substituents independently selected from halogen, cyano, and nitro, can undergo enzymatic cleavage of the linker (for example, via a cancer-cell-associated protease or a lymphocyte-associated protease), releasing a free drug which includes the optionally substituted PAB. This compound may further undergo 1,6-elimination of the PAB, removing any portion of Y from the free drug. *See, e.g.*, Told et al., 2002, *J. Org. Chem.* 67:1866-1872. In some embodiments, enzymatic cleavage of the non-self-immolative moiety, as described herein, does not result in any further hydrolysis step(s).

**[0293]** Other examples of self-immolative groups include, but are not limited to, aromatic compounds that are electronically similar to the PAB group such as 2-aminoimidazol-5-methanol derivatives (*see, e.g.*, Hay et al., 1999, *Bioorg. Med. Chem. Lett.* 9:2237), ortho or para-aminobenzylacetals, substituted and unsubstituted 4-aminobutyric acid amides (*see, e.g.*, Rodrigues et al., 1995, *Chemistry Biology* 2:223), appropriately substituted bicyclo[2.2.1] and bicyclo[2.2.2] ring systems (*see, e.g.*, Storm et al., 1972, *J. Amer. Chem. Soc.* 94:5815), 2-aminophenylpropionic acid amides (*see, e.g.*, Amsberry et al., 1990, *J. Org. Chem.* 55:5867), and elimination of amine-containing drugs that are substituted at the  $\alpha$ -position of glycine (*see, e.g.*, Kingsbury et al., 1984, *J. Med. Chem.* 27:1447).

**[0294]** In some embodiments, Y is a p-aminobenzyl alcohol (PAB) optionally substituted with 1-4 substituents independently selected from halogen, C<sub>1</sub>-C<sub>6</sub> alkoxy, -N(C<sub>1</sub>-C<sub>6</sub> alkyl)<sub>2</sub>, -NHC(=O)(C<sub>1</sub>-C<sub>6</sub> alkyl), -CN, -CF<sub>3</sub>, acyl, carboxamido, C<sub>1</sub>-C<sub>6</sub> alkyl, or -NO<sub>2</sub>. In some embodiments, Y is an unsubstituted p-aminobenzyl alcohol (PAB).

**[0295]** In some embodiments, Y is a para-aminobenzyloxy-carbonyl (PABC) group optionally substituted with a sugar moiety. In some embodiments, Y is -glycine- or -glycine-glycine-. In some embodiments, Y is a branched bis(hydroxymethyl)styrene (BHMS) unit, which is capable of incorporating (and releasing) multiple Drug Units.



**[0297]** In some embodiments, subscript w is 0. In some embodiments subscript w is 1.

**[0298]** In some embodiments, W is a single amino acid. In some embodiments, W is a single natural amino acid. In some embodiments, W is a peptide including from 2-6 amino acids,

wherein each amino acid is independently a natural or non-natural amino acid. In some embodiments, each amino acid is independently a natural amino acid. In some embodiments, W is a peptide including from 2-6 amino acids, wherein each amino acid is independently selected from non-natural amino acids. In some embodiments, W is a peptide including from 2-6 amino acids, wherein each amino acid is independently selected from non-classical amino acids. In some embodiments, W is a peptide including from 2-6 amino acids, wherein each amino acid is independently selected from a combination of natural amino acids, non-natural amino acids, and/or non-classical amino acids. In some embodiments, W is a peptide including from 1-3 amino acids, wherein each amino acid is independently selected from a combination of natural amino acids, non-natural amino acids, and/or non-classical amino acids. In some embodiments, W is a dipeptide. In some embodiments, W is a tripeptide. In some embodiments, W is a tetrapeptide. In some embodiments, W is a pentapeptide. In some embodiments, W is a hexapeptide.

**[0299]** In some embodiments, each amino acid of W is independently selected from the group consisting of valine, alanine,  $\beta$ -alanine, glycine, lysine, leucine, phenylalanine, proline, aspartic acid, serine, glutamic acid, homoserine methyl ether, aspartate methyl ester, N,N-dimethyl lysine, arginine, citrulline, isoleucine, histidine, threonine, O-methylserine, O-methylaspartic acid, O-methylglutamic acid, N-methyllysine, O-methyltyrosine, O-methylhistidine, and O-methylthreonine. In some embodiments, W is an aspartic acid. In some embodiments, W is a lysine. In some embodiments, W is a glycine. In some embodiments, W is an alanine. In some embodiments, W is aspartate methyl ester. In some embodiments, W is a N,N-dimethyl lysine. In some embodiments, W is a homoserine methyl ether. In some embodiments, W is a serine.

**[0300]** In some embodiments, W is a dipeptide selected from the group consisting of valine-alanine, valine-citrulline, and phenylalanine-lysine. In some embodiments, W is valine-alanine. In some embodiments, W is valine-citrulline. In some embodiments, W is phenylalanine-lysine.

**[0301]** In some embodiments, when W is from 2-6 amino acids, each amino acid is independently selected from group consisting of valine, alanine,  $\beta$ -alanine, lysine, leucine, phenylalanine, proline, aspartic acid, serine, glutamic acid, homoserine methyl ether, aspartate methyl ester, N,N-dimethyl lysine, arginine, valine-alanine, valine-citrulline, phenylalanine-lysine, and citrulline.

[0302] In some embodiments, W is from 2-6 amino acids; and the bond between W and X or between W and Y is enzymatically cleavable by a tumor-associated protease. In some embodiments, the tumor-associated protease is a cathepsin. In some embodiments, the tumor-associated protease is cathepsin B, C, or D.

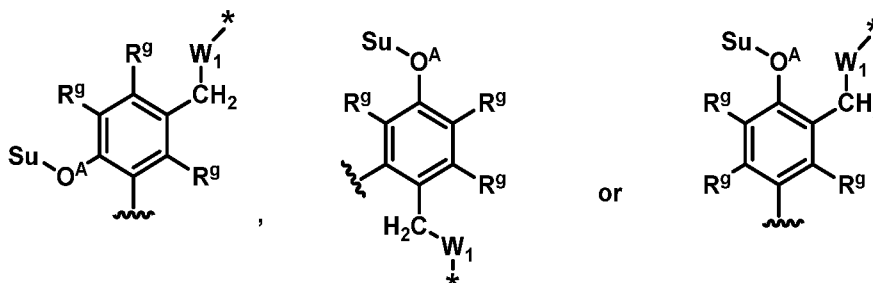
[0303] In some embodiments, W does not include any glycine residues. In some embodiments, W does not include any contiguous glycine residues, such as di-glycine, tri-glycine, tetra-glycine, penta-glycine, or hexa-glycine. In some embodiments, W includes one or more non-contiguous glycine residues.

[0304] In some embodiments, W is not a sortase enzyme recognition motif.

[0305] In some embodiments, W is not -Leu-Pro-\* -Thr-Gly-, -Gly-Thr-\* -Pro-Leu-, -Gly-Ser-\* -Pro-Leu-, -Gly-Thr-\* -Ala-Leu-, -Gly-Thr-\* -Pro-Leu-, -Gly-Ser-\* -Pro-Leu-, -Gly-Thr-\* -Ala-Leu-, -Thr-\* -Pro-Leu-, -Ser-\* -Pro-Leu-, -Thr-\* -Ala-Leu-, -Thr-\* -Pro-Leu-, -Ser-\* -Pro-Leu-, -Thr-\* -Ala-Leu-, -Gln-Pro-Gln-Thr-Asp-; wherein \* is any natural amino acid.

[0306] In some embodiments, W is not -Lys-Pro-Gly-Thr-Gly- or -Asp-Pro-Gln-Thr-Gln-.

[0307] In some embodiments, W has the structure of:



wherein Su is a Sugar moiety;

-O<sup>A</sup>- represents the oxygen atom of a glycosidic bond;

each R<sup>g</sup> is independently hydrogen, halogen, C<sub>1</sub>-C<sub>6</sub> alkoxy, -N(C<sub>1</sub>-C<sub>6</sub> alkyl)<sub>2</sub>, -NHC(=O)(C<sub>1</sub>-C<sub>6</sub> alkyl), -CN, -CF<sub>3</sub>, acyl, carboxamido, C<sub>1</sub>-C<sub>6</sub> alkyl, or -NO<sub>2</sub>;

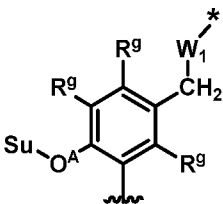
W<sub>1</sub> is absent, \*-C(=O)-O-, or \*-O-C(=O)-;

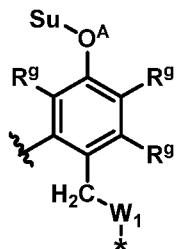
~~~~~ represents covalent attachment to A or M; and

the * represents covalent attachment to Y or X;

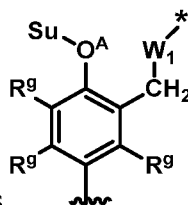
[0308] In some embodiments, -O^A- represents the oxygen atom of a glycosidic bond. In some embodiments, the glycosidic bond provides a β-glucuronidase or a α-mannosidase-

cleavage site. In some embodiments, the β -glucuronidase or a α -mannosidase-cleavage site is cleavable by human lysosomal β -glucuronidase or by human lysosomal α -mannosidase.

[0309] In some embodiments, W is . In some embodiments, W is



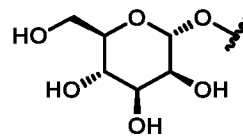
. In some embodiments, W is

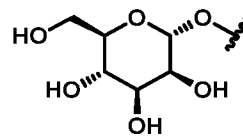


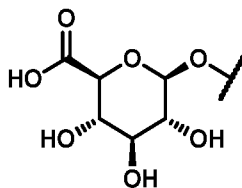
[0310] In some embodiments, each R^g is hydrogen. In some embodiments, one R^g is hydrogen, and the remaining R^g are independently halogen, C_1 - C_6 alkoxy, $-N(C_1$ - C_6 alkyl) $_2$, $-NHC(=O)(C_1$ - C_6 alkyl), $-CN$, $-CF_3$, acyl, carboxamido, C_1 - C_6 alkyl, or $-NO_2$. In some embodiments, two R^g are hydrogen, and the remaining R^g is halogen, C_1 - C_6 alkoxy, $-N(C_1$ - C_6 alkyl) $_2$, $-NHC(=O)(C_1$ - C_6 alkyl), $-CN$, $-CF_3$, acyl, carboxamido, C_1 - C_6 alkyl, or $-NO_2$.

[0311] In some embodiments, one R^g is halogen, C_1 - C_6 alkoxy, $-N(C_1$ - C_6 alkyl) $_2$, $-NHC(=O)(C_1$ - C_6 alkyl), $-CN$, $-CF_3$, acyl, carboxamido, C_1 - C_6 alkyl, or $-NO_2$, and the other R^g are hydrogen.

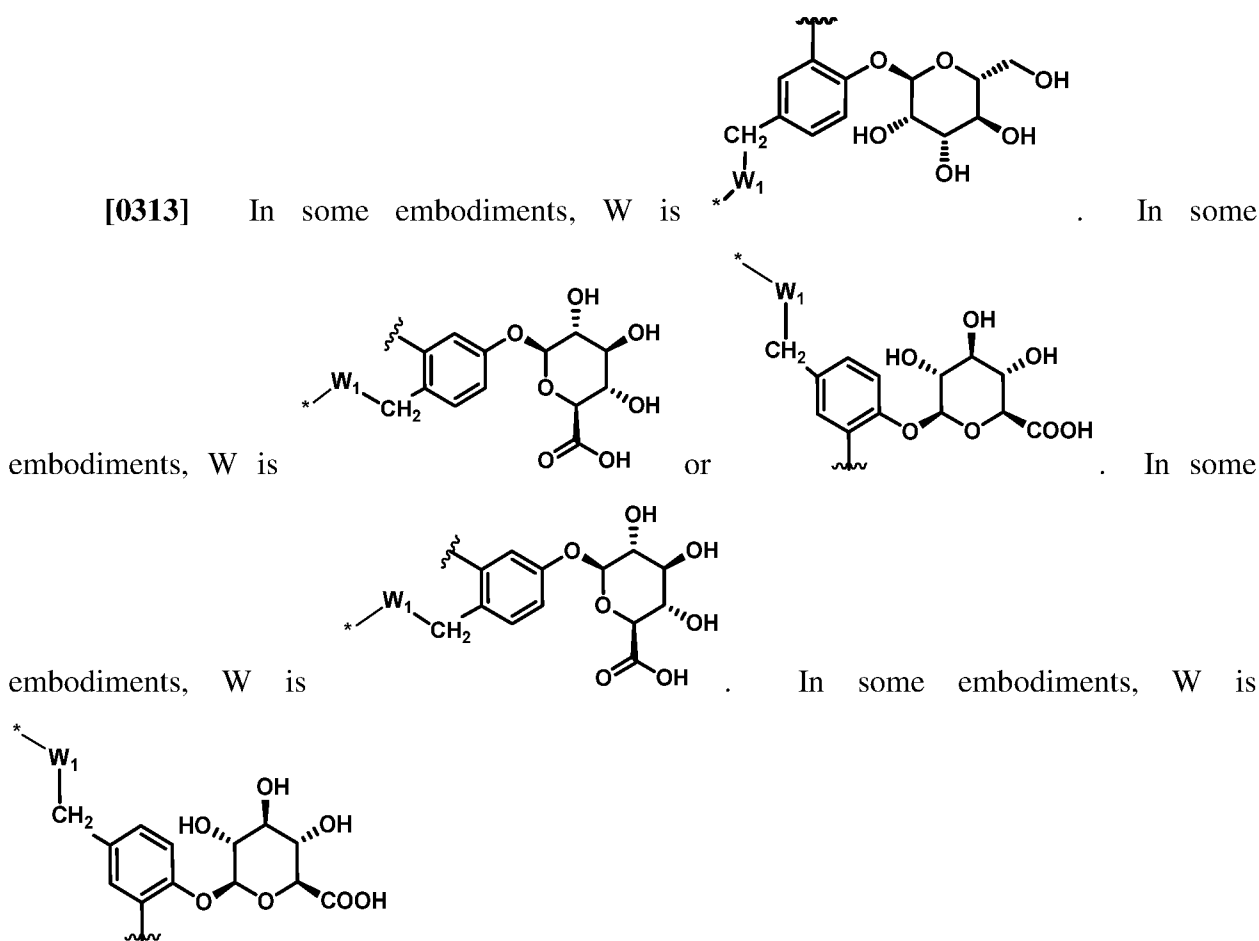
[0312] In some embodiments, O^A -Su is charged neutral at physiological pH. In some



embodiments, O^A -Su is mannose. In some embodiments, O^A -Su is . In some embodiments, O^A -Su comprises a carboxylate moiety. In some embodiments, O^A -Su is glucuronic



acid. In some embodiments, O^A -Su is



[0314] In some embodiments, W₁ is absent. In some embodiments, W₁ is *-C(=O)-O-. In some embodiments, W₁ is absent or *-O-C(=O)-. In some embodiments, W₁ is *-O-C(=O)-.

[0315] In some embodiments, W is a Cleavable Unit. In some embodiments, W is a Peptide Cleavable Unit. In some embodiments, W is a Glucuronide Unit.

[0316] In some embodiments,

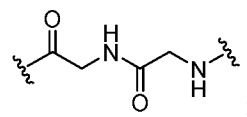
A is a C₂₋₁₀ alkylene optionally substituted with 1-3 R^{al};

each R^{al} is independently selected from the group consisting of: C₁₋₆ alkyl, C₁₋₆ haloalkyl, C₁₋₆ alkoxy, C₁₋₆ haloalkoxy, halogen, -OH, =O, -NR^{dl}R^{el}, -(C₁₋₆ alkylene)-NR^{dl}R^{el}, -C(=O)NR^{dl}R^{el}, -C(=O)(C₁₋₆ alkyl), and -C(=O)O(C₁₋₆ alkyl);

each R^{dl} and R^{el} are independently hydrogen or C₁₋₃ alkyl;

W is from 2-6 amino acids, wherein:

W is not a sortase enzyme recognition motif, and W does not include



Y is a self-immolative moiety, a non-self-immolative releasable moiety, or a non-cleavable moiety; and

L is optionally substituted with a PEG Unit from PEG1 to PEG72.

[0317] In some embodiments,

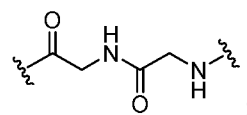
A is a C₂₋₁₀ alkylene optionally substituted with 1-3 R^{al};

each R^{al} is independently selected from the group consisting of: =O, -NR^{dl}R^{el}, -(C₁₋₆ alkylene)-NR^{dl}R^{el}, and -C(=O)NR^{dl}R^{el};

each R^{dl} and R^{el} are independently hydrogen or C₁₋₃ alkyl;

W is from 2-6 amino acids, wherein:

W is not a sortase enzyme recognition motif, and W does not include



Y is a self-immolative moiety, a non-self-immolative releasable moiety, or a non-cleavable moiety; and

L is optionally substituted with a PEG Unit from PEG1 to PEG72.

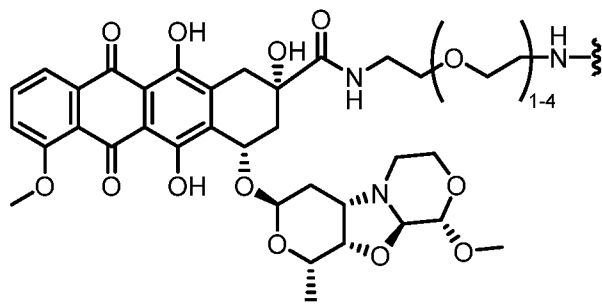
[0318] In some embodiments:

subscript y is 0;

subscript w is 0;

subscript a is 1; and

each D-X is:



wherein  represents covalent attachment to A.

[0319] In some embodiments, subscript a is 0. In some embodiments subscript a is 1.

[0320] In some embodiments, A is a C₂₋₁₀ alkylene optionally substituted with 1-3 R^{al}. In some embodiments, A is a C₄₋₁₀ alkylene optionally substituted with 1-3 R^{al}. In some embodiments, A is a C₂₋₁₀ alkylene substituted with one R^{al}. In some embodiments, A is a C₄₋₁₀ alkylene substituted with one R^{al}. In some embodiments, A is a C₄₋₈ alkylene substituted with one R^{al}.

[0321] In some embodiments, each R^{al} is independently selected from the group consisting of: C₁₋₆ alkyl, C₁₋₆ haloalkyl, C₁₋₆ alkoxy, C₁₋₆ haloalkoxy, halogen, -OH, =O, -NR^{dl}R^{el}, -C(=O)NR^{dl}R^{el}, -C(=O)(C₁₋₆ alkyl), and -C(=O)O(C₁₋₆ alkyl). In some embodiments, each R^{al} is C₁₋₆ alkyl. In some embodiments, each R^{al} is C₁₋₆ haloalkyl. In some embodiments, each R^{al} is C₁₋₆ alkoxy. In some embodiments, each R^{al} is C₁₋₆ haloalkoxy. In some embodiments, each R^{al} is halogen. In some embodiments, each R^{al} is -OH. In some embodiments, each R^{al} is =O. In some embodiments, each R^{al} is -NR^{dl}R^{el}. In some embodiments, each R^{al} is -(C₁₋₆ alkylene)-NR^{dl}R^{el}. In some embodiments, each R^{al} is -C(=O)NR^{dl}R^{el}. In some embodiments, each R^{al} is -C(=O)(C₁₋₆ alkyl). In some embodiments, each R^{al} is -C(=O)O(C₁₋₆ alkyl). In some embodiments, one occurrence of R^{al} is -NR^{dl}R^{el}. In some embodiments, one occurrence of R^{al} is -(C₁₋₆ alkylene)-NR^{dl}R^{el}. In some embodiments, one occurrence of R^{al} is -(C₁₋₂ alkylene)-NR^{dl}R^{el}. In some embodiments, A is a C₂₋₂₀ alkylene substituted with 1 or 2 R^{al}, each of which is =O.

[0322] In some embodiments, R^{dl} and R^{el} are independently hydrogen or C₁₋₃ alkyl. In some embodiments, one of R^{dl} and R^{el} is hydrogen, and the other of R^{dl} and R^{el} is C₁₋₃ alkyl. In some embodiments, R^{dl} and R^{el} are both hydrogen or C₁₋₃ alkyl. In some embodiments, R^{dl} and R^{el} are both C₁₋₃ alkyl. In some embodiments, R^{dl} and R^{el} are both methyl.

[0323] In some embodiments, A is an unsubstituted C₂₋₁₀ alkylene. In some embodiments, A is an unsubstituted C₂₋₆ alkylene. In some embodiments, A is an unsubstituted C₄₋₈ alkylene. In some embodiments, A is an unsubstituted C₄₋₁₀ alkylene.

[0324] In some embodiments, A is a 3 to 20 membered heteroalkylene optionally substituted with 1-3 R^{bl}. In some embodiments, A is a 3 to 12 membered heteroalkylene optionally substituted with 1-3 R^{bl}. In some embodiments, A is a 4 to 12 membered heteroalkylene optionally substituted with 1-3 R^{bl}. In some embodiments, A is a 4 to 8 membered heteroalkylene optionally substituted with 1-3 R^{bl}. In some embodiments, A is a 3 to 20 membered heteroalkylene substituted with one R^{bl}. In some embodiments, A is a 3 to 12 membered heteroalkylene

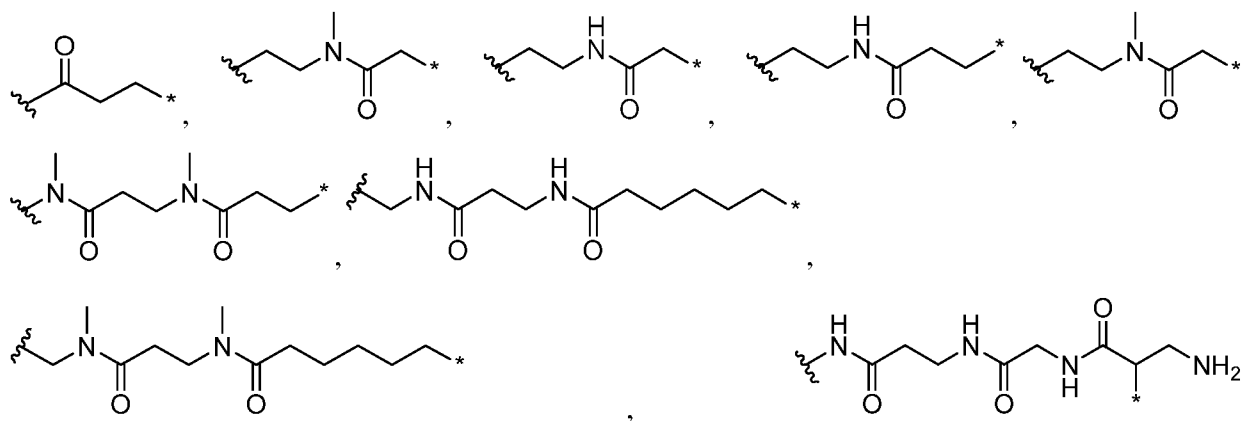
substituted with one R^{bl} . In some embodiments, A is a 4 to 12 membered heteroalkylene substituted with one R^{bl} . In some embodiments, A is a 4 to 8 membered heteroalkylene substituted with one R^{bl} .

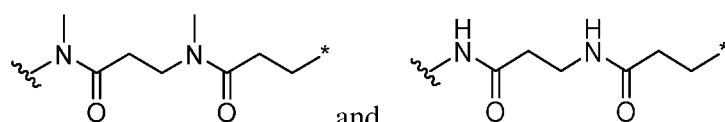
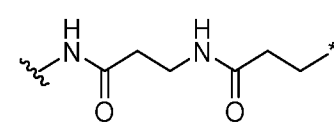
[0325] In some embodiments, each R^{bl} is independently selected from the group consisting of: C_{1-6} alkyl, C_{1-6} haloalkyl, C_{1-6} alkoxy, C_{1-6} haloalkoxy, halogen, $-OH$, $-NR^{dl}R^{el}$, $-(C_{1-6} \text{ alkylene})-NR^{dl}R^{el}$, $-C(=O)NR^{dl}R^{el}$, $-C(=O)(C_{1-6} \text{ alkyl})$, and $-C(=O)O(C_{1-6} \text{ alkyl})$. In some embodiments, each R^{bl} is C_{1-6} alkyl. In some embodiments, each R^{bl} is C_{1-6} haloalkyl. In some embodiments, each R^{bl} is C_{1-6} alkoxy. In some embodiments, each R^{bl} is C_{1-6} haloalkoxy. In some embodiments, each R^{bl} is halogen. In some embodiments, each R^{bl} is $-OH$. In some embodiments, each R^{bl} is $-NR^{dl}R^{el}$. In some embodiments, each R^{bl} is $-(C_{1-6} \text{ alkylene})-NR^{dl}R^{el}$. In some embodiments, each R^{bl} is $C(=O)NR^{dl}R^{el}$. In some embodiments, each R^{bl} is $-C(=O)(C_{1-6} \text{ alkyl})$. In some embodiments, each R^{bl} is $-C(=O)O(C_{1-6} \text{ alkyl})$. In some embodiments, one occurrence of R^{bl} is $-NR^{dl}R^{el}$. In some embodiments, one occurrence of R^{bl} is $-(C_{1-6} \text{ alkylene})-NR^{dl}R^{el}$. In some embodiments, one occurrence of R^{bl} is $-(C_{1-2} \text{ alkylene})-NR^{dl}R^{el}$.

[0326] In some embodiments, R^{dl} and R^{el} are independently hydrogen or C_{1-3} alkyl. In some embodiments, one of R^{dl} and R^{el} is hydrogen, and the other of R^{dl} and R^{el} is C_{1-3} alkyl. In some embodiments, R^{dl} and R^{el} are both hydrogen or C_{1-3} alkyl. In some embodiments, R^{dl} and R^{el} are both C_{1-3} alkyl. In some embodiments, R^{dl} and R^{el} are both methyl.

[0327] In some embodiments, A is a 3 to 20 membered heteroalkylene. In some embodiments, A is a 3 to 12 membered heteroalkylene. In some embodiments, A is a 4 to 12 membered heteroalkylene. In some embodiments, A is a 4 to 8 membered heteroalkylene.

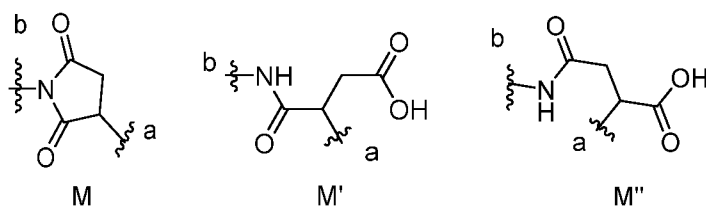
[0328] In some embodiments, A is selected from the group consisting of:

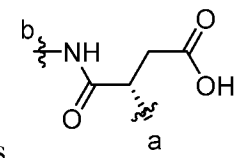


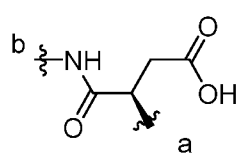

 and , wherein the wavy line represents covalent attachment to W, Y, or X, and * represents covalent linkage to M.

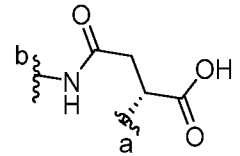
[0329] In some embodiments, A is selected from $-(CH_2)_{1-6}-$, $-C(O)(CH_2)_{1-6}-\#$, $-[NHC(O)(CH_2)_{1-4}]_{1-3}-\#$, and $-NH(CH_2)_{1-6}[NHC(O)(CH_2)_{1-4}]_{1-2}-\#$, wherein # indicates attachment to M.

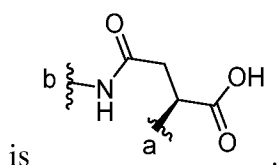
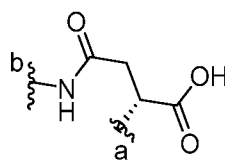
[0330] In some embodiments, M is a succinimide. In some embodiments, M is a hydrolyzed succinimide. It will be understood that a hydrolyzed succinimide may exist in two regioisomeric form(s). Those forms are exemplified below for hydrolysis of M, wherein the structures representing the regioisomers from that hydrolysis are formula M' and M''; wherein wavy line a indicates the point of covalent attachment to the antibody, and wavy line b indicates the point of covalent attachment to A.



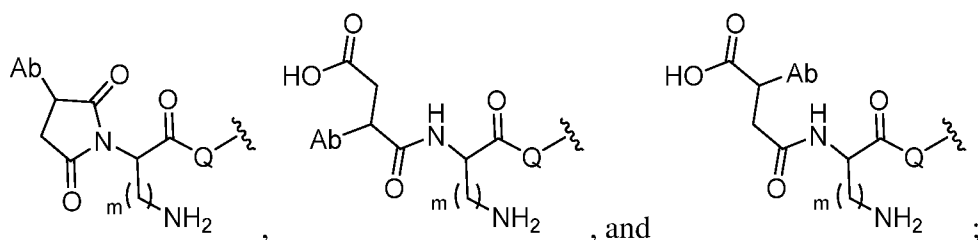
[0331] In some embodiments, M' is . In some embodiments, M' is



. In some embodiments, M'' is . In some embodiments, M''

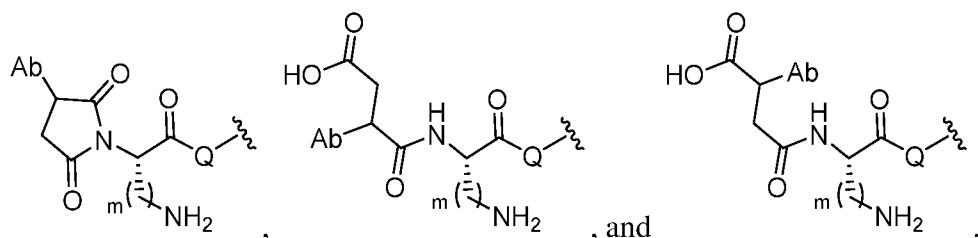


[0332] In some embodiments, $-M-A-$ is selected from the group consisting of:

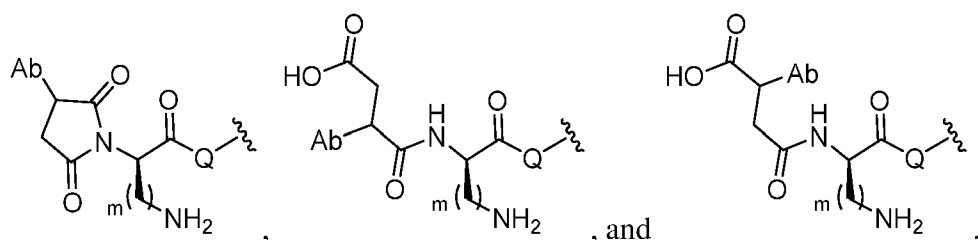


wherein subscript m is 1 or 2; Q is $-\text{NH}-(\text{C}_1\text{-C}_5 \text{ alkylene})-\text{C}(=\text{O})-$, or is absent;
wherein Ab is the antibody and the wavy line represents covalent attachment to W, Y, or X.

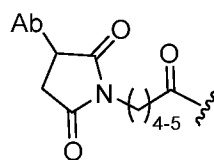
[0333] In some embodiments, $-\text{M-A}-$ is selected from the group consisting of:



[0334] In some embodiments, $-\text{M-A}-$ is selected from the group consisting of:



[0335] In some embodiments, Q is $-\text{NH}-\text{CH}_2-\text{C}(=\text{O})-$. In some embodiments, Q is absent.



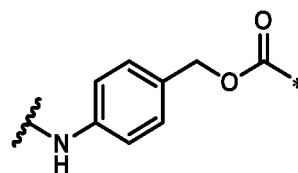
[0336] In some embodiments, $-\text{M-A}-$ is

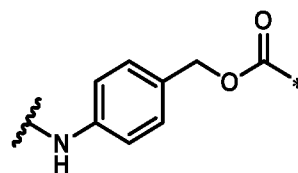
[0337] In some embodiments, $-\text{M}(\text{A})_a(\text{W})_w(\text{Y})_y(\text{X})-$ is a non-self-immolative releasable linker, which provides release of the free drug once the ADC has been internalized into the target cell. In some embodiments, $-\text{M}(\text{A})_a(\text{W})_w(\text{Y})_y(\text{X})-$ is a releasable linker, which provides release of the free drug with, or in the vicinity, of targeted cells. In some embodiments, releasable linkers possess a recognition site, such as a peptide cleavage site, sugar cleavage site, or disulfide cleavage site. In some embodiments, each releasable linker is a di-peptide. In some embodiments, each releasable linker is a disulfide. In some embodiments, each releasable linker is a hydrazone. In some embodiments, each releasable linker is independently selected from the

group consisting of Val-Cit-, -Phe-Lys-, and -Val-Ala-. In some embodiments, each releasable linker, when bound to a succinimide or hydrolyzed succinimide, is independently selected from the group consisting of succinimido-caproyl (mc), succinimido-caproyl-valine-citrulline (sc-vc), succinimido-caproyl-valine-citrulline-paraaminobenzyloxycarbonyl (sc-vc-PABC), and SDPr-vc (where “S” refers to succinimido).

[0338] In some embodiments, $-M-(A)_a-(W)_w-(Y)_y-(X)-$ comprises a non-cleavable linker. Non-cleavable linkers are known in the art and can be adapted for use with the ADCs described herein as the “Y” group. A non-cleavable linker is capable of linking a Drug Unit to an antibody in a generally stable and covalent manner and is substantially resistant to cleavage, such as acid-induced cleavage, light-induced cleavage, peptidase- or esterase-induced cleavage, and disulfide bond cleavage. The free drug can be released from the ADCs containing non-cleavable linkers via alternative mechanisms, such as proteolytic antibody degradation. In some embodiments, the Drug Unit can exert a biological effect as a part of the ADC (i.e., while still conjugated to the antibody via a linker).

[0339] Reagents that form non-cleavable linker-maleimide and non-cleavable linker-succinimide compounds are known in the art and can adapted for use herein. Exemplary reagents comprise a maleimido or haloacetyl-based moiety, such as 6-maleimidocaproic acid N-hydroxy succinimide ester (MCC), N-succinimidyl 4-(maleimidomethyl)cyclohexanecarboxylate (SMCC), N-succinimidyl-4-(N-maleimidomethyl)-cyclohexane-1-carboxy-(6-amidocaproate) (LC-SMCC), maleimidoundecanoic acid N-succinimidyl ester (KMUA), γ -maleimidobutyric acid N-succinimidyl ester (GMBS), ϵ -maleimidocaproic acid N-hydroxysuccinimide ester (EMCS), m -maleimidobenzoyl-N-hydroxysuccinimide ester (MBS), N-(α -maleimidoacetoxysuccinimide ester [AMAS], succinimidyl-6-(β -maleimidopropionamido)hexanoate (SMPH), N-succinimidyl-4-(p -maleimidophenyl)-butyrate (SMPB), and N-(p -maleimidophenyl)isocyanate (PMPI), N-succinimidyl-4-(iodoacetyl)-aminobenzoate (STAB), N-succinimidyl iodoacetate (SIA), N-succinimidyl bromoacetate (SBA) and N-succinimidyl 3-(bromoacetamido)propionate (SBAP). Additional “A-M” groups for use in the ADCs described herein can be found, for example, in U.S. Pat. No. 8,142,784, incorporated herein by reference in its entirety.

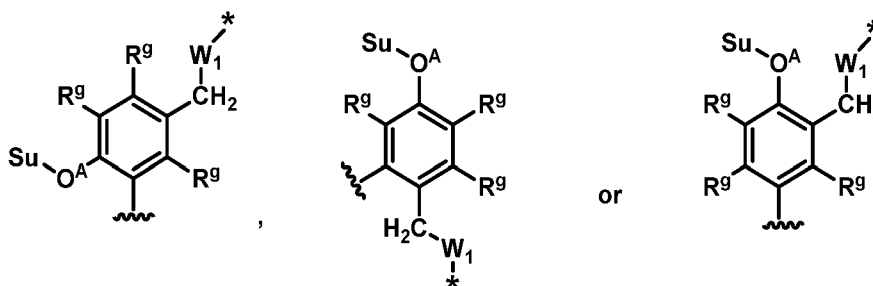


[0340] In some embodiments, Y is , wherein the wavy line represents connection to W, A, or M; and the * represents connection to X in the ADCs described herein.

[0341] In some embodiments, $-M-(A)_a-(W)_w-(Y)_y-(X)-$, comprises a non-releasable linker, wherein the free drug is released after the ADC has been internalized into the target cell and degraded, liberating the free drug.

[0342] In some embodiments, subscript y is 0; subscript w is 1; subscript a is 1; and M is a succinimide or a hydrolyzed succinimide.

[0343] In some embodiments, subscript y is 0; subscript w is 1; subscript a is 1; M is a succinimide or a hydrolyzed succinimide; and W has the structure of:



wherein Su is a Sugar moiety;

$-O^A-$ represents the oxygen atom of a glycosidic bond;

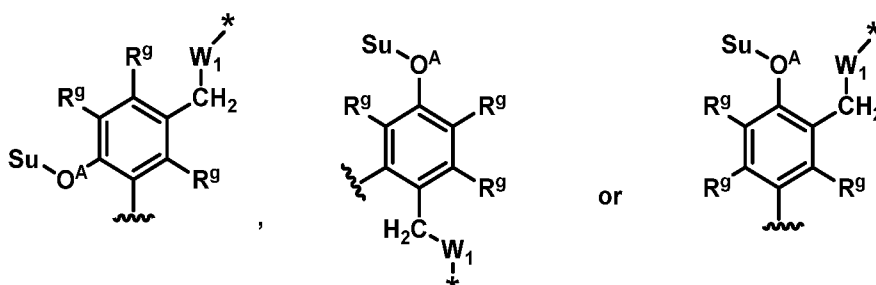
each R^g is independently hydrogen, halogen, C_1-C_6 alkoxy, $-N(C_1-C_6 \text{ alkyl})_2$, $-NHC(=O)(C_1-C_6 \text{ alkyl})$, $-CN$, $-CF_3$, acyl, carboxamido, C_1-C_6 alkyl, or $-NO_2$;

W_1 is absent;

the wavy line represents covalent attachment to A; and

the * represents covalent attachment to X.

[0344] In some embodiments, subscript y is 0; subscript w is 1; subscript a is 1; M is a succinimide or a hydrolyzed succinimide; and W has the structure of:



wherein Su is a Sugar moiety;

-O^A- represents the oxygen atom of a glycosidic bond;

each R^g is independently hydrogen, halogen, C₁-C₆ alkoxy, -N(C₁-C₆ alkyl)₂, -NHC(=O)(C₁-C₆ alkyl), -CN, -CF₃, acyl, carboxamido, C₁-C₆ alkyl, or -NO₂;

W_1 is *-C(=O)-O-;

the wavy line represents covalent attachment to A; and

the * represents covalent attachment to X.

[0345] In some embodiments, subscript y is 1; subscript w is 1; subscript a is 1; and M is a succinimide or a hydrolyzed succinimide. In some embodiments, Y is a PAB group and W is a dipeptide.

[0346] In some embodiments, A is covalently attached to M; Y is attached to X; and M is attached to Ab.

[0347] In some embodiments, A comprises PEG2-PEG8. In some embodiments, X comprises PEG2-PEG6. In some embodiments, only one of X and A comprises PEG2-PEG8. In some embodiments, X does not include PEG2-PEG8. In some embodiments, A does not include PEG2-PEG8. In some embodiments, X and A do not include PEG2-PEG8 as part of the X or A groups, respectively (i.e., X and/or A can be optionally substituted with PEG, as described herein).

[0348] In some embodiments, the linker (L) is substituted with a polyethylene glycol moiety selected from the group consisting of PEG2 to PEG20. In some embodiments, L is substituted with a polyethylene glycol moiety selected from the group consisting of PEG2, PEG4, PEG6, PEG8, PEG10, PEG12, PEG16, and PEG20. In some embodiments, L is not substituted with a polyethylene glycol moiety selected from the group consisting of PEG2 to PEG20.

[0349] In some embodiments, A is substituted with a polyethylene glycol moiety selected from the group consisting of PEG2 to PEG20. In some embodiments, W is substituted with a polyethylene glycol moiety selected from the group consisting of PEG2 to PEG20. In some

embodiments, Y is substituted with a polyethylene glycol moiety selected from the group consisting of PEG2 to PEG20. In some embodiments, X is substituted with a polyethylene glycol moiety selected from the group consisting of PEG2 to PEG20. In some embodiments, the linker (L) is substituted with one polyethylene glycol moiety. In some embodiments, the linker (L) is substituted with 2 or 3 independently selected polyethylene glycol moieties.

[0350] Polydisperse PEGs, monodisperse PEGs and discrete PEGs can be used to make the ADCs and intermediates thereof. Polydisperse PEGs are a heterogeneous mixture of sizes and molecular weights whereas monodisperse PEGs are typically purified from heterogeneous mixtures and therefore provide a single chain length and molecular weight. Discrete PEGs are synthesized in step-wise fashion and not via a polymerization process. Discrete PEGs provide a single molecule with defined and specified chain length. The number of $-\text{CH}_2\text{CH}_2\text{O}-$ subunits of a PEG Unit ranges, for example, from 8 to 24 or from 12 to 24, referred to as PEG8 to PEG24 and PEG12 to PEG24, respectively.

[0351] The PEG moieties provided herein, which are also referred to as PEG Units, comprise one or multiple polyethylene glycol chains. The polyethylene glycol chains are linked together, for example, in a linear, branched or star shaped configuration. Typically, at least one of the polyethylene glycol chains of a PEG Unit is derivatized at one end for covalent attachment to an appropriate site on a component of the ADC (e.g., L). Exemplary attachments to ADCs are by means of non-conditionally cleavable linkages or via conditionally cleavable linkages. Exemplary attachments are via amide linkage, ether linkages, ester linkages, hydrazone linkages, oxime linkages, disulfide linkages, peptide linkages or triazole linkages. In some embodiments, attachment to ADC is by means of a non-conditionally cleavable linkage. In some embodiments, attachment to the ADC is not via an ester linkage, hydrazone linkage, oxime linkage, or disulfide linkage. In some embodiments, attachment to the ADC is not via a hydrazone linkage.

[0352] A conditionally cleavable linkage refers to a linkage that is not substantially sensitive to cleavage while circulating in plasma but is sensitive to cleavage in an intracellular or intratumoral environment. A non-conditionally cleavable linkage is one that is not substantially sensitive to cleavage in any biologically relevant environment in a subject that is administered the ADC. Chemical hydrolysis of a hydrazone, reduction of a disulfide bond, and enzymatic cleavage of a peptide bond or glycosidic bond of a Glucuronide Unit as described by WO 2007/011968

(which is incorporated by reference in its entirety) are examples of conditionally cleavable linkages.

[0353] In some embodiments, the PEG Unit is directly attached to the ADC (or an intermediate thereof) at L. In those embodiments, the other terminus (or termini) of the PEG Unit is free and untethered (i.e., not covalently attached), and in some embodiments, is a methoxy, carboxylic acid, alcohol or other suitable functional group. The methoxy, carboxylic acid, alcohol or other suitable functional group acts as a cap for the terminal polyethylene glycol subunit of the PEG Unit. By untethered, it is meant that the PEG Unit will not be covalently attached at that untethered site to a Drug Unit, to an antibody, or to a linking component to a Drug Unit and/or an antibody. Such an arrangement can allow a PEG Unit of sufficient length to assume a parallel orientation with respect to the drug in conjugated form, i.e., as a Drug Unit (D). For those embodiments in which the PEG Unit comprises more than one polyethylene glycol chain, the multiple polyethylene glycol chains are independently chosen, e.g., are the same or different chemical moieties (e.g., polyethylene glycol chains of different molecular weight or number of $\text{CH}_2\text{CH}_2\text{O}$ - subunits). A PEG Unit having multiple polyethylene glycol chains is attached to the ADC at a single attachment site. The skilled artisan will understand that the PEG Unit, in addition to comprising repeating polyethylene glycol subunits, may also contain non-PEG material (e.g., to facilitate coupling of multiple polyethylene glycol chains to each other or to facilitate coupling to the ADC). Non-PEG material refers to the atoms in the PEG Unit that are not part of the repeating $\text{--CH}_2\text{CH}_2\text{O--}$ subunits. In some embodiments provided herein, the PEG Unit comprises two monomeric polyethylene glycol chains attached to each other via non-PEG elements. In other embodiments provided herein, the PEG Unit comprises two linear polyethylene glycol chains attached to a central core that is attached to the ADC (i.e., the PEG Unit itself is branched).

[0354] There are a number of PEG attachment methods available to those skilled in the art: see, for example: Goodson, et al. (1990) *Bio/Technology* 8:343 (PEGylation of interleukin-2 at its glycosylation site after site-directed mutagenesis); EP 0 401 384 (coupling PEG to G-CSF); Malik, et al., (1992) *Exp. Hematol.* 20:1028-1035 (PEGylation of GM-CSF using tresyl chloride); ACT Pub. No. WO 90/12874 (PEGylation of erythropoietin containing a recombinantly introduced cysteine residue using a cysteine-specific mPEG derivative); U.S. Pat. No. 5,757,078 (PEGylation of EPO peptides); U.S. Pat. No. 5,672,662 (Poly(ethylene glycol) and related polymers monosubstituted with propionic or butanoic acids and functional derivatives thereof for

biotechnical applications); U.S. Pat. No. 6,077,939 (PEGylation of an N-terminal α -carbon of a peptide); Veronese et al., (1985) *Appl. Biochem. Bioechnol* 11:141-142 (PEGylation of an N-terminal α -carbon of a peptide with PEG-nitrophenylcarbonate ("PEG-NPC") or PEG-trichlorophenylcarbonate); and Veronese (2001) *Biomaterials* 22:405-417 (Review article on peptide and protein PEGylation).

[0355] For example, a PEG Unit may be covalently bound to an amino acid residue via reactive groups of a polyethylene glycol-containing compound and the amino acid residue. Reactive groups of the amino acid residue include those that are reactive to an activated PEG molecule (e.g., a free amino or carboxyl group). For example, N-terminal amino acid residues and lysine (K) residues have a free amino group; and C-terminal amino acid residues have a free carboxyl group. Thiol groups (e.g., as found on cysteine residues) are also useful as a reactive group for forming a covalent attachment to a PEG. In addition, enzyme-assisted methods for introducing activated groups (e.g., hydrazide, aldehyde, and aromatic-amino groups) specifically at the C-terminus of a polypeptide have been described. See Schwarz, et al. (1990) *Methods Enzymol.* 184:160; Rose, et al. (1991) *Bioconjugate Chem.* 2:154; and Gaertner, et al. (1994) *J. Biol. Chem.* 269: 7224.

[0356] In some embodiments, a polyethylene glycol-containing compound forms a covalent attachment to an amino group using methoxylated PEG ("mPEG") having different reactive moieties. Non-limiting examples of such reactive moieties include succinimidyl succinate (SS), succinimidyl carbonate (SC), mPEG-imidate, para-nitrophenylcarbonate (NPC), succinimidyl propionate (SPA), and cyanuric chloride. Non-limiting examples of such mPEGs include mPEG-succinimidyl succinate (mPEG-SS), mPEG₂-succinimidyl succinate (mPEG₂-SS); mPEG-succinimidyl carbonate (mPEG-SC), mPEG₂-succinimidyl carbonate (mPEG₂-SC); mPEG-imidate, mPEG-para-nitrophenylcarbonate (mPEG-NPC), mPEG-imidate; mPEG₂-para-nitrophenylcarbonate (mPEG₂-NPC); mPEG-succinimidyl propionate (mPEG-SPA); mPEG₂-succinimidyl propionate (mPEG₂-SPA); mPEG-N-hydroxy-succinimide (mPEG-NHS); mPEG₂-N-hydroxy-succinimide (mPEG₂-NHS); mPEG-cyanuric chloride; mPEG₂-cyanuric chloride; mPEG₂-Lysinol-NPC, and mPEG₂-Lys-NHS.

[0357] Generally, at least one of the polyethylene glycol chains that make up the PEG is functionalized to provide covalent attachment to the ADC. Functionalization of the polyethylene glycol-containing compound that is the precursor to the PEG includes, for example,

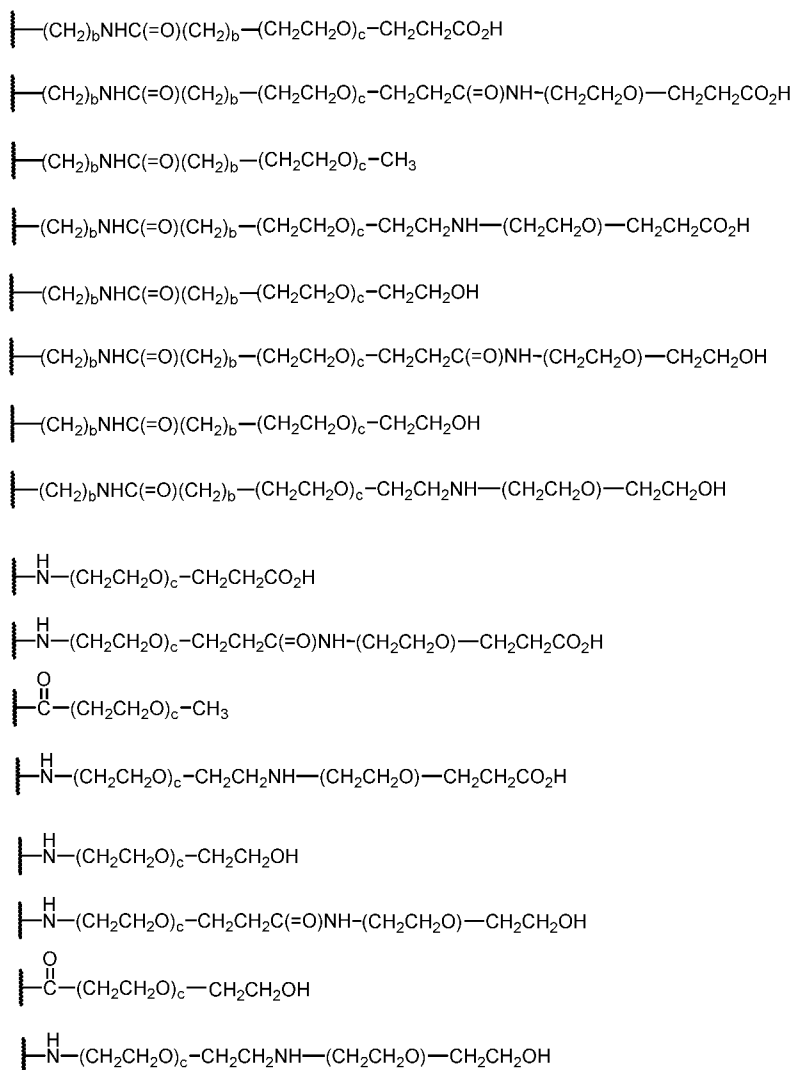
via an amine, thiol, NHS ester, maleimide, alkyne, azide, carbonyl, or other functional group. In some embodiments, the PEG further comprises non-PEG material (i.e., material not comprised of $-\text{CH}_2\text{CH}_2\text{O}-$) that provides coupling to the ADC or in constructing the polyethylene glycol-containing compound or PEG facilitates coupling of two or more polyethylene glycol chains.

[0358] In some embodiments, the presence of the PEG Unit in an ADC is capable of having two potential impacts upon the pharmacokinetics of the resulting ADC. One impact is a decrease in clearance (and consequent increase in exposure) that arises from the reduction in non-specific interactions induced by the exposed hydrophobic elements of the Drug Unit. The second impact is a decrease in volume and rate of distribution that sometimes arises from the increase in the molecular weight of the ADC. Increasing the number of polyethylene glycol subunits increases the hydrodynamic radius of a conjugate, typically resulting in decreased diffusivity. In turn, decreased diffusivity typically diminishes the ability of the ADC to penetrate into a tumor. See Schmidt and Wittrup, *Mol Cancer Ther* 2009; 8:2861-2871. Because of these two competing pharmacokinetic effects, it can be desirable to use a PEG Unit that is sufficiently large to decrease the ADC clearance thus increasing plasma exposure, but not so large as to greatly diminish its diffusivity to an extent that it interferes with the ability of the ADC to reach the intended target cell population. See, e.g., Examples 1, 18, and 21 of US 2016/0310612, which is incorporated by reference herein (e.g., for methodology for selecting an optimal size of a PEG Unit for a particular Drug Unit, Linker, and/or drug-linker compound).

[0359] In some embodiments, the PEG Unit comprises one or more linear polyethylene glycol chains each having at least 2 subunits, at least 3 subunits, at least 4 subunits, at least 5 subunits, at least 6 subunits, at least 7 subunits, at least 8 subunits, at least 9 subunits, at least 10 subunits, at least 11 subunits, at least 12 subunits, at least 13 subunits, at least 14 subunits, at least 15 subunits, at least 16 subunits, at least 17 subunits, at least 18 subunits, at least 19 subunits, at least 20 subunits, at least 21 subunits, at least 22 subunits, at least 23 subunits, or at least 24 subunits. In some embodiments, the PEG comprises a combined total of at least 8 subunits, at least 10 subunits, or at least 12 subunits. In some such embodiments, the PEG comprises no more than a combined total of about 72 subunits. In some such embodiments, the PEG comprises no more than a combined total of about 36 subunits. In some embodiments, the PEG comprises about 8 to about 24 subunits (referred to as PEG8 to PEG24).

[0360] In some embodiments, the PEG Unit comprises a combined total of from 2 to 72, 2 to 60, 2 to 48, 2 to 36 or 2 to 24 subunits, from 3 to 72, 3 to 60, 3 to 48, 3 to 36 or 3 to 24 subunits, from 4 to 72, 8 to 60, 4 to 48, 4 to 36 or 4 to 24 subunits, from 5 to 72, 5 to 60, 5 to 48, 5 to 36 or 5 to 24 subunits, from 6 to 72, 6 to 60, 6 to 48, 6 to 36 or 6 to 24 subunits, from 7 to 72, 7 to 60, 7 to 48, 7 to 36 or 7 to 24 subunits, from 8 to 72, 8 to 60, 8 to 48, 8 to 36 or 8 to 24 subunits, from 9 to 72, 9 to 60, 9 to 48, 9 to 36 or 9 to 24 subunits, from 10 to 72, 10 to 60, 10 to 48, 10 to 36 or 10 to 24 subunits, from 11 to 72, 11 to 60, 11 to 48, 11 to 36 or 11 to 24 subunits, from 12 to 72, 12 to 60, 12 to 48, 12 to 36 or 12 to 24 subunits, from 13 to 72, 13 to 60, 13 to 48, 13 to 36 or 13 to 24 subunits, from 14 to 72, 14 to 60, 14 to 48, 14 to 36 or 14 to 24 subunits, from 15 to 72, 15 to 60, 15 to 48, 15 to 36 or 15 to 24 subunits, from 16 to 72, 16 to 60, 16 to 48, 16 to 36 or 16 to 24 subunits, from 17 to 72, 17 to 60, 17 to 48, 17 to 36 or 17 to 24 subunits, from 18 to 72, 18 to 60, 18 to 48, 18 to 36 or 18 to 24 subunits, from 19 to 72, 19 to 60, 19 to 48, 19 to 36 or 19 to 24 subunits, from 20 to 72, 20 to 60, 20 to 48, 20 to 36 or 20 to 24 subunits, from 21 to 72, 21 to 60, 21 to 48, 21 to 36 or 21 to 24 subunits, from 22 to 72, 22 to 60, 22 to 48, 22 to 36 or 22 to 24 subunits, from 23 to 72, 23 to 60, 23 to 48, 23 to 36 or 23 to 24 subunits, or from 24 to 72, 24 to 60, 24 to 48, 24 to 36 or 24 subunits. In some embodiments, the PEG Unit comprises a combined total of from 2 to 24 subunits, 2 to 16 subunits, 2 to 12 subunits, 2 to 8 subunits, or 2 to 6 subunits.

[0361] Illustrative linear PEGs that can be used in any of the embodiments provided herein are as follows:



[0362] wherein the wavy line indicates the site of attachment to the ADC; each subscript b is independently selected from the group consisting of 2 to 12; and each subscript c is independently selected from the group consisting of 1 to 72, 8 to 72, 10 to 72, 12 to 72, 6 to 24, or 8 to 24. In some embodiments, each subscript b is 2 to 6. In some embodiments, each subscript c is about 2, about 4, about 8, about 12, or about 24.

[0363] In some embodiments, the sum of subscript b and subscript c (b+c) ranges from 6 to 72. In some embodiments, the sum of subscript b and subscript c (b+c) ranges from 8 to 72. In some embodiments, the sum of subscript b and subscript c (b+c) ranges from 10 to 72. In some embodiments, the sum of subscript b and subscript c (b+c) ranges from 12 to 72. In some embodiments, the sum of subscript b and subscript c (b+c) ranges from 6 to 24. In some embodiments, the sum of subscript b and subscript c (b+c) ranges from 8 to 24. In some

embodiments, the sum of subscript b and subscript c (b+c) ranges from 12 to 36. In some embodiments, the sum of subscript b and subscript c (b+c) ranges from 24 to 48. In some embodiments, the sum of subscript b and subscript c (b+c) ranges from 36 to 72. In some embodiments, the sum of subscript b and subscript c (b+c) is about 8, about 12, or about 24.

[0364] As described herein, the PEG Unit can be selected such that it improves clearance of the resultant ADC but does not significantly impact the ability of the ADC to penetrate into the tumor.

[0365] In some embodiments, the PEG moiety is from about 300 Daltons to about 5,000 Daltons; from about 300 Daltons to about 4,000 Daltons; from about 300 Daltons to about 3,000 Daltons; from about 300 Daltons to about 2,000 Daltons; from about 300 Daltons to about 1,000 Daltons; or any value in between. In some embodiments, the PEG moiety has at least 8, 10 or 12 subunits. In some embodiments, the PEG Unit is PEG8 to PEG72, for example, PEG8, PEG10, PEG12, PEG16, PEG20, PEG24, PEG28, PEG32, PEG36, PEG48, or PEG72.

[0366] In some embodiments, apart from the PEGylation of the ADC, there are no other PEG subunits present in the ADC (i.e., no PEG subunits are present as part of any of the other components of the conjugates and linkers provided herein, such as A and X). In some embodiments, apart from the PEG, there are no more than 8, no more than 7, no more than 6, no more than 5, no more than 4, no more than 3, no more than 2 or no more than 1 other polyethylene glycol (-CH₂CH₂O-) subunits present in the ADC, or intermediate thereof (i.e., no more than 8, 7, 6, 5, 4, 3, 2, or 1 other polyethylene glycol subunits in other components of the ADCs (or intermediates thereof) provided herein).

[0367] It will be appreciated that when referring to polyethylene glycol subunits of a PEG Unit, and depending on context, the number of subunits can represent an average number, e.g., when referring to a population of ADCs or intermediates thereto and/or using polydisperse PEGs.

Methods of Use of ADCs

[0368] In some embodiments, the ADCs described herein, or pharmaceutically acceptable salts thereof, are used to deliver the conjugated drug to a target cell. Without being bound by theory, in some embodiments, an ADC associates with an antigen on the surface of a target cell. The Drug Unit can then be released as free drug to induce its biological effect (such as

a cytotoxic effect). The Drug Unit can also remain attached to the antibody, or a portion of the antibody and/or linker, and induce its biological effect.

[0369] Some embodiments provide a method of treating a viral or bacterial infection in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of an ADC described herein, or a salt thereof.

[0370] Some embodiments provide a method of treating an autoimmune disorder in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of an ADC described herein, or a salt thereof.

[0371] Some embodiments provide a method of treating cancer in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of an ADC described herein, or a salt thereof.

[0372] Some embodiments provide a method of treating cancer in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of a composition comprising an ADC described herein, or a salt thereof.

[0373] Some embodiments provide a method of treating cancer in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of an ADC as described herein, or a salt thereof, in combination with another anticancer therapy (e.g., surgery and radiation therapy) and/or anticancer agent (e.g., an immunotherapy such as nivolumab or pembrolizumab). The ADCs described herein can be administered to the subject before, during, or after administration of the anticancer therapy and/or anticancer agent and/or surgery. In some embodiments, the ADCs described herein can be administered to the subject following treatment with radiation and/or after surgery.

[0374] Some embodiments provide a method for delaying or preventing acquired resistance to an anticancer agent, comprising administering to the subject a therapeutically effective amount of an ADC as described herein, or a salt thereof, to a patient at risk for developing or having acquired resistance to an anticancer agent. In some embodiments, the patient is administered a dose of the anticancer agent (e.g., at substantially the same time as a dose of an ADC as described herein, or a salt thereof is administered to the patient).

[0375] Some embodiments provide a method of delaying and/or preventing development of cancer resistant to an anticancer agent in a subject, comprising administering to

the subject a therapeutically effective amount of an ADC as described herein, or a salt thereof, before, during, or after administration of a therapeutically effective amount of the anticancer agent.

[0376] The ADCs described herein are useful for inhibiting the multiplication of a cancer cell, causing apoptosis in a cancer cell, for increasing phagocytosis of a cancer cell, and/or for treating cancer in a subject in need thereof. The ADCs can be used accordingly in a variety of settings for the treatment of cancers. The ADCs can be used to deliver a drug to a cancer cell. Without being bound by theory, in some embodiments, the antibody of an ADC binds to or associates with a cancer-cell-associated antigen. The antigen can be attached to a cancer cell or can be an extracellular matrix protein associated with the cancer cell. In some embodiments, the Drug Unit is cleaved from the ADC outside the cancer cell. In some embodiments, the Drug Unit remains attached to the antibody bound to the antigen.

[0377] In some embodiments, the antibody binds to the cancer cell. In some embodiments, the antibody binds to a cancer cell antigen which is on the surface of the cancer cell. In some embodiments, the antibody binds to a cancer cell antigen which is an extracellular matrix protein associated with the tumor cell or cancer cell. In some embodiments, the antibody of an ADC binds to or associates with a cancer-associated cell or an antigen on a cancer-associated cell. In some embodiments, the cancer-associated cell is a stromal cell in a tumor, for example, a cancer-associated fibroblast (CAF).

[0378] In some embodiments, the antibody of an ADC binds to or associates with an immune cell or an immune-cell-associated antigen. The antigen can be attached to an immune cell or can be an extracellular matrix protein associated with the immune cell. The drug can be released in proximity to the immune cell, thus recruiting/activating the immune cell to attack a cancer cell. In some embodiments, the Drug Unit is cleaved from the ADC outside the immune cell. In some embodiments, the Drug Unit remains attached to the antibody bound to the antigen. In some embodiments, the immune cell is a lymphocyte, an antigen-presenting cell, a natural killer (NK) cell, a neutrophil, an eosinophil, a basophil, a mast cell, an innate lymphoid cell, or a combination of any of the foregoing. In some embodiments, the immune cell is selected from the group consisting of B cells, plasma cells, T cells, NKT cells, gamma delta T cells, monocytes, macrophages, dendritic cells, natural killer (NK) cells, neutrophils, eosinophils, basophils, mast cells, and a combination of any of the foregoing.

[0379] The specificity of the antibody for a particular cancer cell can be important for determining those tumors or cancers that are most effectively treated. For example, ADCs that target a cancer cell antigen present on hematopoietic cancer cells in some embodiments treat hematologic malignancies. In some embodiments, ADCs target a cancer cell antigen present on abnormal cells of solid tumors for treating such solid tumors. In some embodiments an ADC are directed against abnormal cells of hematopoietic cancers such as, for example, lymphomas (Hodgkin Lymphoma and Non-Hodgkin Lymphomas) and leukemias.

[0380] Cancers, including, but not limited to, a tumor, metastasis, or other disease or disorder characterized by abnormal cells that are characterized by uncontrolled cell growth in some embodiments are treated or inhibited by administration of an ADC.

[0381] In some embodiments, the subject has previously undergone treatment for the cancer. In some embodiments, the prior treatment is surgery, radiation therapy, administration of one or more anticancer agents, or a combination of any of the foregoing.

[0382] In any of the methods described herein, the cancer is selected from the group consisting of: adenocarcinoma, adrenal gland cortical carcinoma, adrenal gland neuroblastoma, anus squamous cell carcinoma, appendix adenocarcinoma, bladder urothelial carcinoma, bile duct adenocarcinoma, bladder carcinoma, bladder urothelial carcinoma, bone chordoma, bone marrow leukemia lymphocytic chronic, bone marrow leukemia non-lymphocytic acute myelocytic, bone marrow lymph proliferative disease, bone marrow multiple myeloma, bone sarcoma, brain astrocytoma, brain glioblastoma, brain medulloblastoma, brain meningioma, brain oligodendroglioma, breast adenoid cystic carcinoma, breast carcinoma, breast ductal carcinoma in situ, breast invasive ductal carcinoma, breast invasive lobular carcinoma, breast metaplastic carcinoma, cervix neuroendocrine carcinoma, cervix squamous cell carcinoma, colon adenocarcinoma, colon carcinoid tumor, duodenum adenocarcinoma, endometrioid tumor, esophagus adenocarcinoma, esophagus and stomach carcinoma, eye intraocular melanoma, eye intraocular squamous cell carcinoma, eye lacrimal duct carcinoma, fallopian tube serous carcinoma, gallbladder adenocarcinoma, gallbladder glomus tumor, gastroesophageal junction adenocarcinoma, head and neck adenoid cystic carcinoma, head and neck carcinoma, head and neck neuroblastoma, head and neck squamous cell carcinoma, kidney chromophore carcinoma, kidney medullary carcinoma, kidney renal cell carcinoma, kidney renal papillary carcinoma, kidney sarcomatoid carcinoma, kidney urothelial carcinoma, kidney carcinoma, leukemia

lymphocytic, leukemia lymphocytic chronic, liver cholangiocarcinoma, liver hepatocellular carcinoma, liver carcinoma, lung adenocarcinoma, lung adenosquamous carcinoma, lung atypical carcinoid, lung carcinosarcoma, lung large cell neuroendocrine carcinoma, lung non-small cell lung carcinoma, lung sarcoma, lung sarcomatoid carcinoma, lung small cell carcinoma, lung small cell undifferentiated carcinoma, lung squamous cell carcinoma, upper aerodigestive tract squamous cell carcinoma, upper aerodigestive tract carcinoma, lymph node lymphoma diffuse large B cell, lymph node lymphoma follicular lymphoma, lymph node lymphoma mediastinal B-cell, lymph node lymphoma plasmablastic lung adenocarcinoma, lymphoma follicular lymphoma, lymphoma, non-Hodgkins, nasopharynx and paranasal sinuses undifferentiated carcinoma, ovary carcinoma, ovary carcinosarcoma, ovary clear cell carcinoma, ovary epithelial carcinoma, ovary granulosa cell tumor, ovary serous carcinoma, pancreas carcinoma, pancreas ductal adenocarcinoma, pancreas neuroendocrine carcinoma, peritoneum mesothelioma, peritoneum serous carcinoma, placenta choriocarcinoma, pleura mesothelioma, prostate acinar adenocarcinoma, prostate carcinoma, rectum adenocarcinoma, rectum squamous cell carcinoma, skin adnexal carcinoma, skin basal cell carcinoma, skin melanoma, skin Merkel cell carcinoma, skin squamous cell carcinoma, small intestine adenocarcinoma, small intestine gastrointestinal stromal tumors (GISTs), large intestine/colon carcinoma, large intestine adenocarcinoma, soft tissue angiosarcoma, soft tissue Ewing sarcoma, soft tissue hemangioendothelioma, soft tissue inflammatory myofibroblastic tumor, soft tissue leiomyosarcoma, soft tissue liposarcoma, soft tissue neuroblastoma, soft tissue paraganglioma, soft tissue perivascular epithelioid cell tumor, soft tissue sarcoma, soft tissue synovial sarcoma, stomach adenocarcinoma, stomach adenocarcinoma diffuse-type, stomach adenocarcinoma intestinal type, stomach adenocarcinoma intestinal type, stomach leiomyosarcoma, thymus carcinoma, thymus thymoma lymphocytic, thyroid papillary carcinoma, unknown primary adenocarcinoma, unknown primary carcinoma, unknown primary malignant neoplasm, lymphoid neoplasm, unknown primary melanoma, unknown primary sarcomatoid carcinoma, unknown primary squamous cell carcinoma, unknown undifferentiated neuroendocrine carcinoma, unknown primary undifferentiated small cell carcinoma, uterus carcinosarcoma, uterus endometrial adenocarcinoma, uterus endometrial adenocarcinoma endometrioid, uterus endometrial adenocarcinoma papillary serous, and uterus leiomyosarcoma.

[0383] In some embodiments, the subject is concurrently administered one or more additional anticancer agents with the ADCs described herein, or a salt thereof. In some

embodiments, the subject is concurrently receiving radiation therapy with the ADCs described herein, or a salt thereof. In some embodiments, the subject is administered one or more additional anticancer agents after administration of the ADCs described herein, or a salt thereof. In some embodiments, the subject receives radiation therapy after administration of the ADCs described herein, or a salt thereof.

[0384] In some embodiments, the subject has discontinued a prior therapy, for example, due to unacceptable or unbearable side effects, wherein the prior therapy was too toxic, or wherein the subject developed resistance to the prior therapy.

[0385] Some embodiments provide a method for delaying or preventing a disease or disorder, comprising administering to the subject a therapeutically effective amount of an ADC as described herein, or a salt thereof, and a vaccine against the disease or disorder, to a patient at risk for developing the disease or disorder. In some embodiments, the disease or disorder is cancer, as described herein. In some embodiments, the disease or disorder is a viral pathogen. In some embodiments, the vaccine is administered subcutaneously. In some embodiments, the vaccine is administered intramuscularly. In some embodiments, the ADC and the vaccine are administered via the same route (for example, the ADC and the vaccine are both administered subcutaneously). In some embodiments, the ADC, or a salt thereof, and the vaccine are administered via different routes. In some embodiments, the vaccine and the ADC, or a salt thereof, are provided in a single formulation. In some embodiments, the vaccine and the ADC, or a salt thereof, are provided in separate formulations.

[0386] In some embodiments, the ADCs described herein are present in the form of a salt. In some embodiments, the salt is a pharmaceutically acceptable salt.

Compositions and Methods of Administration of ADCs

[0387] Some embodiments provide an ADC composition comprising a distribution of ADCs, as described herein. In some embodiments, the composition comprises a distribution of ADCs, as described herein and at least one pharmaceutically acceptable carrier. In some embodiments, the route of administration is parenteral. Parenteral administration includes subcutaneous injections, intravenous, intramuscular, intrasternal injection or infusion techniques. In some embodiments, the compositions are administered parenterally. In one of those

embodiments, the ADCs are administered intravenously. Administration is typically through any convenient route, for example by infusion or bolus injection.

[0388] Compositions of an ADC are formulated so as to allow the ADC to be bioavailable upon administration of the composition to a subject. Compositions can be in the form of one or more injectable dosage units.

[0389] Materials used in preparing the compositions can be non-toxic in the amounts used. It will be evident to those of ordinary skill in the art that the optimal dosage of the active ingredient(s) in the composition will depend on a variety of factors. Relevant factors include, without limitation, the type of animal (*e.g.*, human), the particular form of the compound, the manner of administration, and the composition employed.

[0390] In some embodiments, the ADC composition is a solid, for example, as a lyophilized powder, suitable for reconstitution into a liquid prior to administration. In some embodiments, the ADC composition is a liquid composition, such as a solution or a suspension. A liquid composition or suspension is useful for delivery by injection and a lyophilized solid is suitable for reconstitution as a liquid or suspension using a diluent suitable for injection. In a composition administered by injection, one or more of a surfactant, preservative, wetting agent, dispersing agent, suspending agent, buffer, stabilizer and isotonic agent is typically included.

[0391] In some embodiments, the liquid compositions, whether they are solutions, suspensions or other like form, can also include one or more of the following: sterile diluents such as water for injection, saline solution, physiological saline, Ringer's solution, isotonic sodium chloride, fixed oils such as synthetic mono or diglycerides which can serve as the solvent or suspending medium, polyethylene glycols, glycerin, cyclodextrin, propylene glycol or other solvents; antibacterial agents such as benzyl alcohol or methyl paraben; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as amino acids, acetates, citrates or phosphates; detergents, such as nonionic surfactants, polyols; and agents for the adjustment of tonicity such as sodium chloride or dextrose. A parenteral composition is typically enclosed in ampoule, a disposable syringe or a multiple-dose vial made of glass, plastic or other material. In some embodiments, the sterile diluent comprises physiological saline. In some embodiments, the sterile diluent is physiological saline. In some embodiments, the composition described herein are liquid injectable compositions that are sterile.

[0392] The amount of the ADC that is effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, which is usually determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays are sometimes employed to help identify optimal dosage ranges. The precise dose to be employed in the compositions will also depend on the route of parenteral administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each subject's circumstances.

[0393] In some embodiments, the compositions comprise an effective amount of an ADC such that a suitable dosage will be obtained. Typically, this amount is at least about 0.01% of the ADC by weight of the composition.

[0394] In some embodiments, the compositions dosage of an ADC administered to a subject is from about 0.01 mg/kg to about 100 mg/kg, from about 1 to about 100 mg of a per kg or from about 0.1 to about 25 mg/kg of the subject's body weight. In some embodiments, the dosage administered to a subject is about 0.01 mg/kg to about 15 mg/kg of the subject's body weight. In some embodiments, the dosage administered to a subject is about 0.1 mg/kg to about 15 mg/kg of the subject's body weight. In some embodiments, the dosage administered to a subject is about 0.1 mg/kg to about 20 mg/kg of the subject's body weight. In some embodiments, the dosage administered is about 0.1 mg/kg to about 5 mg/kg or about 0.1 mg/kg to about 10 mg/kg of the subject's body weight. In some embodiments, the dosage administered is about 1 mg/kg to about 15 mg/kg of the subject's body weight. In some embodiments, the dosage administered is about 1 mg/kg to about 10 mg/kg of the subject's body weight. In some embodiments, the dosage administered is about 0.1 to about 4 mg/kg, about 0.1 to about 3.2 mg/kg, or about 0.1 to about 2.7 mg/kg of the subject's body weight over a treatment cycle.

[0395] The term "carrier" refers to a diluent, adjuvant or excipient, with which a compound is administered. Such pharmaceutical carriers are liquids. Water is an exemplary carrier when the compounds are administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions are also useful as liquid carriers for injectable solutions. Suitable pharmaceutical carriers also include glycerol, propylene, glycol, or ethanol. The present compositions, if desired, will in some embodiments also contain minor amounts of wetting or emulsifying agents, and/or pH buffering agents.

[0396] In some embodiments, the ADCs are formulated in accordance with routine procedures as a composition adapted for intravenous administration to animals, particularly human beings. Typically, the carriers or vehicles for intravenous administration are sterile isotonic aqueous buffer solutions. In some embodiments, the composition further comprises a local anesthetic, such as lignocaine, to ease pain at the site of the injection. In some embodiments, the ADC and the remainder of the formulation are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where an ADC is to be administered by infusion, it is sometimes dispensed, for example, with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the ADCs are administered by injection, an ampoule of sterile water for injection or saline is typically provided so that the ingredients can be mixed prior to administration.

[0397] The compositions are generally formulated as sterile, substantially isotonic and in full compliance with all Good Manufacturing Practice (GMP) regulations of the U.S. Food and Drug Administration.

Drug-Linker Intermediates (L^1 -D)

[0398] Some embodiments provide a compound having the formula L^1 -D, or a salt thereof, wherein:

L^1 is a linker intermediate having the formula $M^1-(A)_a-(W)_w-(Y)_y-(X)-$;

wherein A, W, Y, X, are as defined for the linker (L);

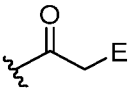
wherein subscripts a, w, and y, are each independently 0 or 1;

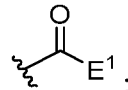
wherein the sum of subscripts a, w, and y, is 1, 2, or 3; and

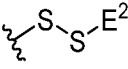
wherein D is as defined for the ADCs described herein.

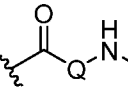
[0399] In some embodiments, M^1 comprises a functional group that will react with an antibody to form a covalent bond (the Ab-M bond). In some embodiments, M^1 is selected from the group consisting of maleimido, azido, C_2 - C_6 alkynyl, cycloalkynyl optionally substituted with 1 or 2 fluoro (e.g., cyclooctynyl or DIFO), sulfhydryl, succinimidyl esters (e.g., N-hydroxysuccinimidyl (NHS) or sulfo-NHS esters), 4-nitrophenyl esters, pentafluorophenyl esters, tetrafluorophenyl esters, anhydrides, acid chlorides, sulfonyl chlorides, isocyanates, isothiocyanates, alpha-haloketones, alpha-O-sulfonate (e.g., mesyl or tosyl) ketones, alkyl

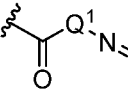
hydrazines, hydrazides, and hydroxylamines. In some embodiments, M^1 is selected from the group consisting of maleimido, azido, C_2 - C_6 alkynyl, cycloalkynyl optionally substituted with 1 or 2 fluoro (e.g., cyclooctynyl or DIFO), sulfhydryl, succinimidyl esters. Additional examples of functional groups that will react with an antibody to form a covalent bond are described in PCT Publication No. WO2016/040684, which is hereby incorporated by reference in its entirety.

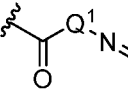
[0400] In some embodiments, M^1 is ; wherein the wavy line indicates the covalent bond to the remainder of L^1 (e.g., A, W, Y, or X); and wherein E is halogen or $-O(SO_2)-E'$; wherein E' is alkyl, aryl, or aryl substituted with alkyl, as described herein (e.g., tosyl or mesyl).

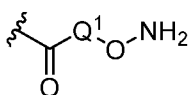
[0401] In some embodiments, M^1 is ; wherein the wavy line indicates the covalent bond to the remainder of L^1 (e.g., A, W, Y, or X); wherein E^1 is halogen, $-O-N$ -succinimide, $-O$ -(aryl), wherein the aryl is substituted with nitro, 4 or 5 fluoro, $-OC(=O)-O(C_1-C_6$ alkyl), or $-OC(=O)-O$ (aryl).

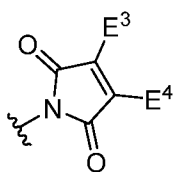
[0402] In some embodiments, M^1 is ; wherein the wavy line indicates the covalent bond to the remainder of L^1 (e.g., A, W, Y, or X); wherein E^2 is aryl or heteroaryl, as described herein.

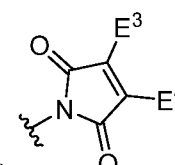
[0403] In some embodiments, M^1 is ; wherein the wavy line indicates the covalent bond to the remainder of L^1 (e.g., A, W, Y, or X); and wherein Q is a bond or C_1 - C_{10} alkylene.

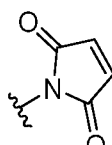
[0404] In some embodiments, M^1 is ; wherein the wavy line indicates the covalent bond to the remainder of L^1 (e.g., A, W, Y, or X); and wherein Q^1 is C_1 - C_{10} alkylene.

[0405] In some embodiments, M^1 is ; wherein the wavy line indicates the covalent bond to the remainder of L^1 (e.g., A, W, Y, or X); and wherein Q^1 is C_1 - C_{10} alkylene.

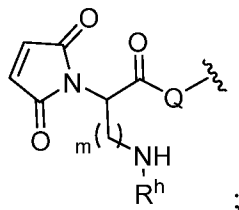
[0406] In some embodiments, M^1 is ; wherein the wavy line indicates the covalent bond to the remainder of L^1 (e.g., A, W, Y, or X); and wherein Q^1 is C_1 - C_{10} alkylene.

[0407] In some embodiments, M^1 is ; wherein the wavy line indicates the covalent bond to the remainder of L^1 (e.g., A, W, Y, or X); and wherein E^3 and E^4 are independently selected from the group consisting of hydrogen, halogen, C_1 - C_6 alkyl, and $-O(SO_2)-E^5$; wherein E^5 is alkyl, aryl, or aryl substituted with alkyl, as described herein (e.g., tosyl or mesyl)..

[0408] In some embodiments, M^1 is , and E^3 and E^4 are both hydrogen.

As such, in some embodiments M^1 is  (maleimido).

[0409] In some embodiments, $-M^1-A-$ is



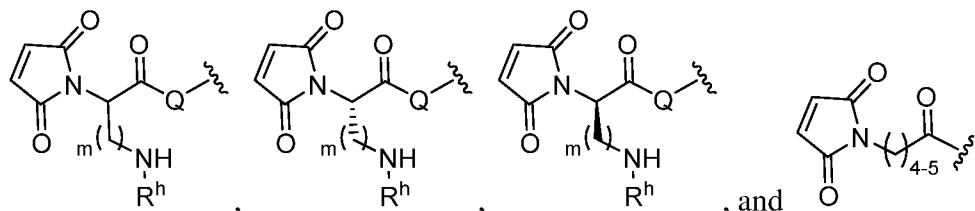
wherein subscript m is 1 or 2; Q is $-NH-(C_1-C_5 \text{ alkylene})-C(=O)-$ or is absent; R^h is hydrogen or a nitrogen protecting group;

wherein the wavy line represents covalent attachment to W, Y, or X.

[0410] In some embodiments, Q is $-NH-CH_2-C(=O)-$. In some embodiments, Q is absent.

[0411] In some embodiments, the nitrogen protecting group is an acid-labile protecting group. In some embodiments, the nitrogen protecting group is a carbamate protecting group. In some embodiments, the nitrogen protecting group is *t*-butyloxycarbonyl (Boc) or carboxybenzyl (Cbz).

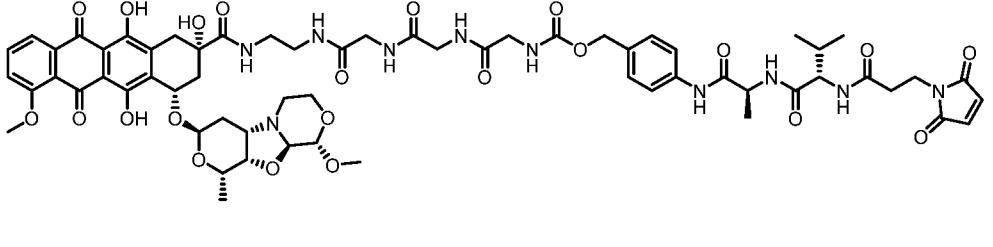
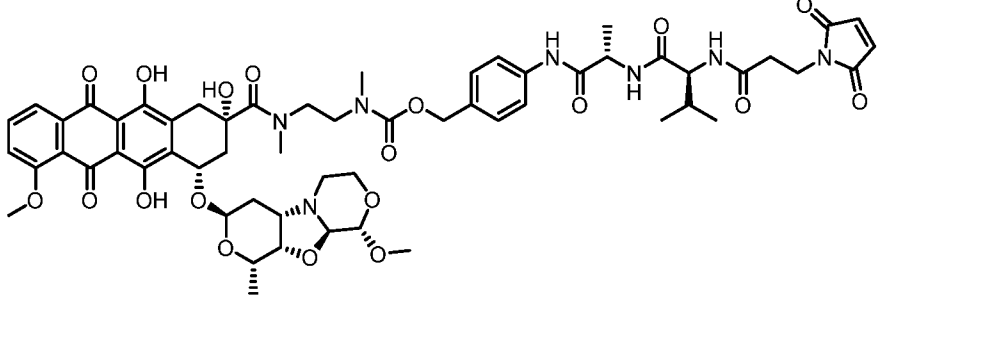
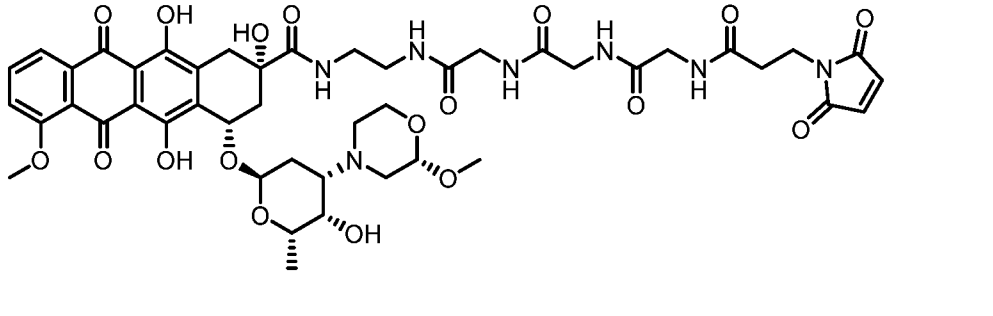
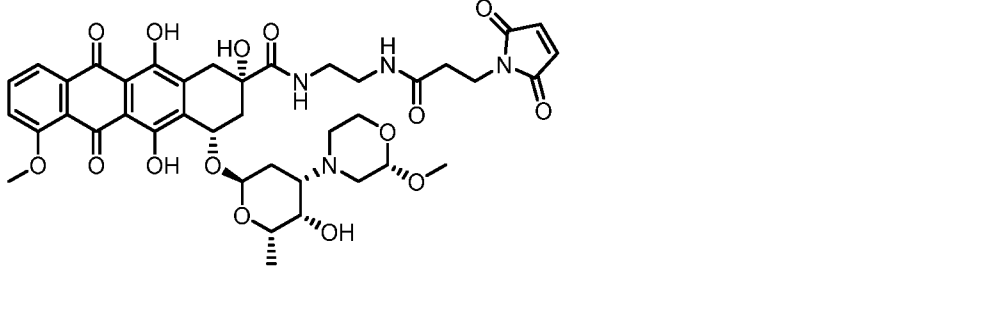
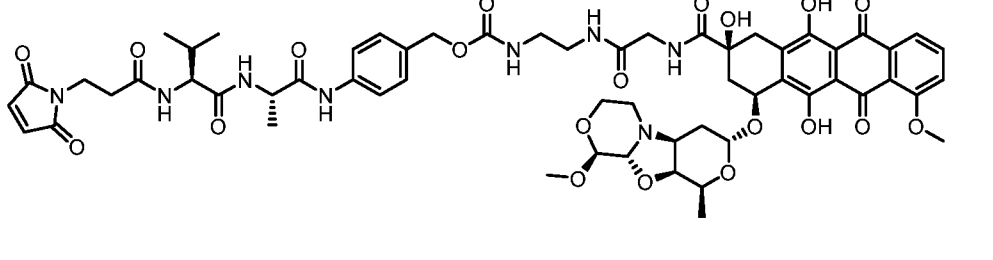
[0412] In some embodiments, $-M^1-A-$ is selected from the group consisting of:

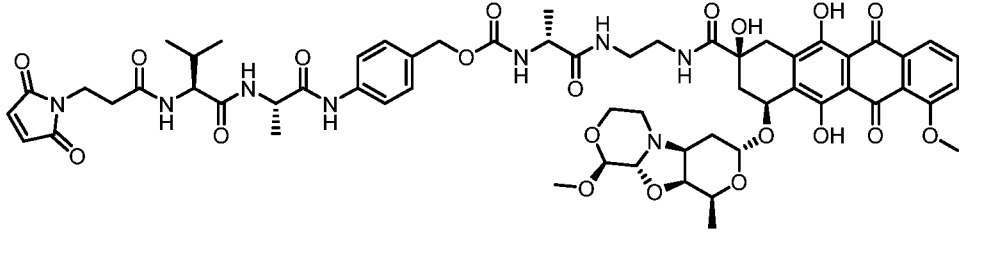
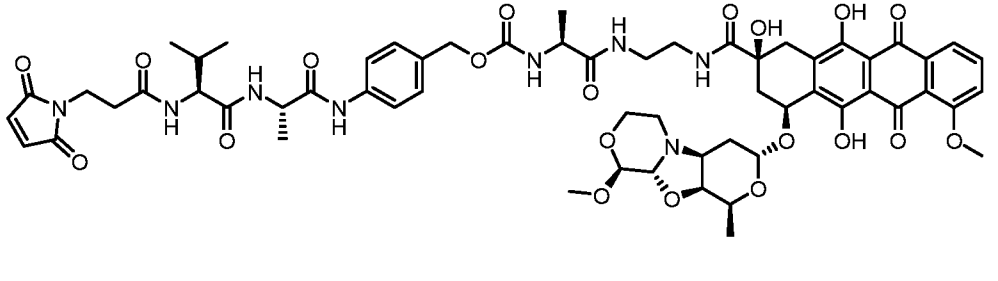
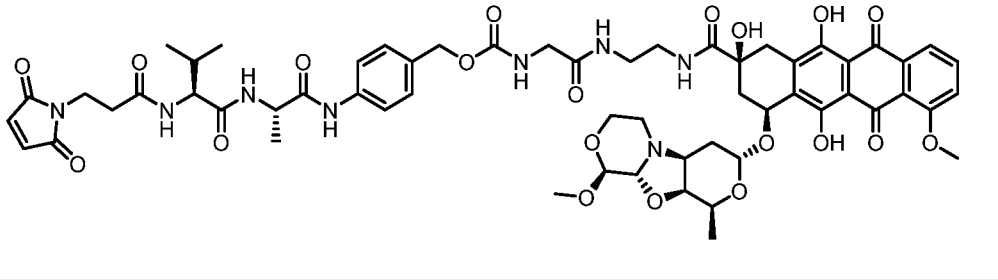
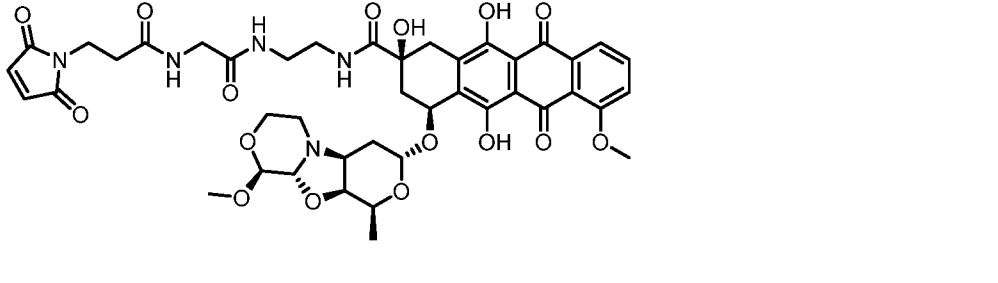
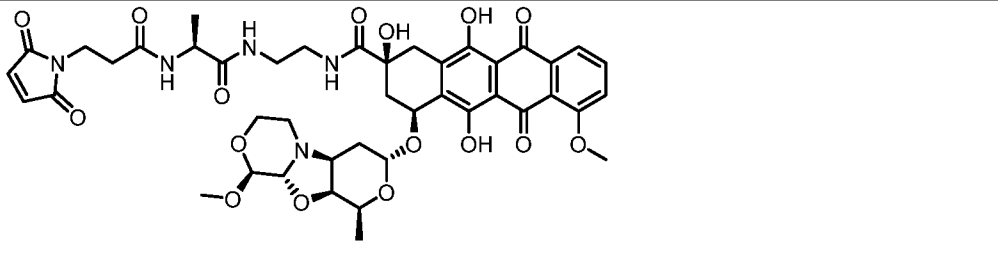


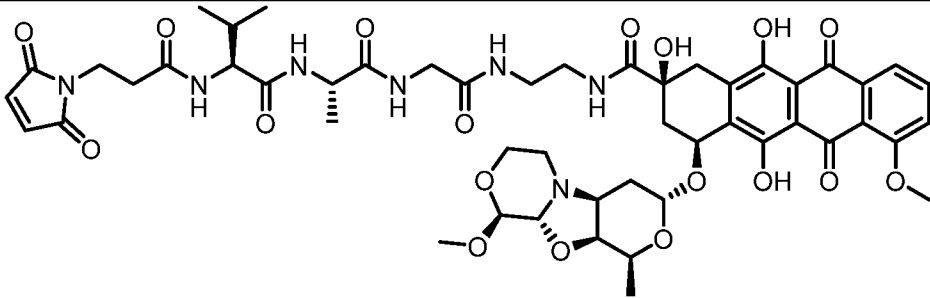
[0413] In some embodiments, the compound of L^1-D is selected from the compounds shown in Table 1, or a salt thereof.

TABLE 1

| Cmpd No. | Structure |
|----------|-----------|
| 14 | |
| 18 | |
| 21 | |
| 24 | |

| Cmpd No. | Structure |
|----------|--|
| 29 |  |
| 32 |  |
| 33 |  |
| 34 |  |
| 36 |  |

| Cmpd No. | Structure |
|----------|--|
| 38 |  <p>Chemical structure of compound 38: A complex molecule featuring a pyrazole ring connected via a linker to a chiral amide chain. This chain is further connected to a benzyl group, which is linked to another chiral amide chain. This second chain is connected to a complex polycyclic system, including a tetrahydropyran and a substituted benzene ring, which is finally linked to a complex polycyclic system, including a tetrahydropyran and a substituted benzene ring.</p> |
| 40 |  <p>Chemical structure of compound 40: A complex molecule featuring a pyrazole ring connected via a linker to a chiral amide chain. This chain is further connected to a benzyl group, which is linked to another chiral amide chain. This second chain is connected to a complex polycyclic system, including a tetrahydropyran and a substituted benzene ring, which is finally linked to a complex polycyclic system, including a tetrahydropyran and a substituted benzene ring.</p> |
| 42 |  <p>Chemical structure of compound 42: A complex molecule featuring a pyrazole ring connected via a linker to a chiral amide chain. This chain is further connected to a benzyl group, which is linked to another chiral amide chain. This second chain is connected to a complex polycyclic system, including a tetrahydropyran and a substituted benzene ring, which is finally linked to a complex polycyclic system, including a tetrahydropyran and a substituted benzene ring.</p> |
| 44 |  <p>Chemical structure of compound 44: A complex molecule featuring a pyrazole ring connected via a linker to a chiral amide chain. This chain is further connected to a benzyl group, which is linked to another chiral amide chain. This second chain is connected to a complex polycyclic system, including a tetrahydropyran and a substituted benzene ring, which is finally linked to a complex polycyclic system, including a tetrahydropyran and a substituted benzene ring.</p> |
| 46 |  <p>Chemical structure of compound 46: A complex molecule featuring a pyrazole ring connected via a linker to a chiral amide chain. This chain is further connected to a benzyl group, which is linked to another chiral amide chain. This second chain is connected to a complex polycyclic system, including a tetrahydropyran and a substituted benzene ring, which is finally linked to a complex polycyclic system, including a tetrahydropyran and a substituted benzene ring.</p> |

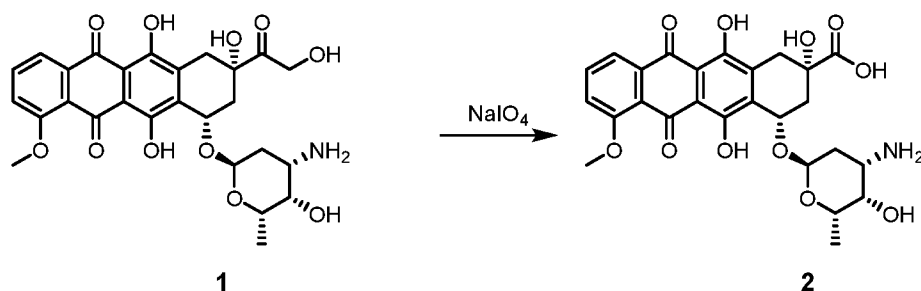
| Cmpd No. | Structure |
|----------|--|
| 48 |  |

[0414] In some embodiments, the compounds of Formula L¹-D described herein are present in the form of a salt. In some embodiments, the salt is a pharmaceutically acceptable salt.

EXAMPLES

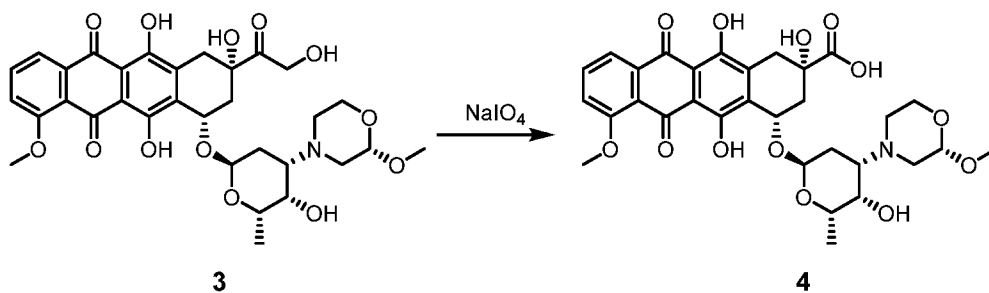
[0415] **Synthetic Procedures – General** All commercially available anhydrous solvents were used without further purification. Flash column chromatography was performed on a Biotage Isolera One flash purification system (Charlotte, NC). UPLC-MS systems consisted of either a Waters SQD2 mass detector interfaced to an Acquity Ultra Performance LC or a Waters Xevo G2 ToF interfaced to an Acquity H-class Ultra Performance LC. The HPLC column used for analysis was a CORTECS C18 2.1 x 50 mm, 1.6µm reversed-phase column. Analytes were eluted by running a gradient of 3% acetonitrile/97% water to 100% acetonitrile, at a flow rate of 0.5 mL/min. The organic acetonitrile (MeCN) and aqueous mobile phases were modified with either 0.1% (v/v) formic acid (**gradient 1**) or 10 mM ammonium chloride (NH₄Cl) in MeCN/water, pH 4.5 (**gradient 2**). Preparative HPLC was carried out using a Waters Prep 150 LC system paired with a 2998 photodiode array detector, using a C12 Phenomenex Synergi 10.0 x 250 mm, 4 µm, 80 Å reversed-phase column, and eluting with 0.1% (v/v) trifluoroacetic acid (TFA) or 10 mM NH₄Cl in water (solvent A) and 0.1% (v/v) TFA in MeCN or MeCN (solvent B). The purification methods generally consisted of linear gradients of solvent A to solvent B, ramping from 90% aqueous solvent A to 10% solvent A over 1 hour. The flow rate was 4.6 mL/min with monitoring by ultraviolet (UV) at 254 nm.

Example 1: (2S,4S)-4-(((2R,4S,5S,6S)-4-amino-5-hydroxy-6-methyltetrahydro-2H-pyran-2-yl)oxy)-2,5,12-trihydroxy-7-methoxy-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracene-2-carboxylic acid (2)



[0416] Doxorubicin (**1**, 14 mg, 26 μmol) was dissolved in a mixture of MeOH (3 mL) and H₂O (2 mL). A solution of sodium periodate (NaIO₄, 7 mg, 31 μmol) in H₂O (1 mL) was added to the above solution with stirring. After 1 hour, the solvents were removed under reduced pressure and the material was used in subsequent steps without further purification. Analytical UPLC-MS (gradient 1): HPLC retention time = 1.19 min; m/z (ESI+) calculated 530.17 [M+H]⁺; found 530.54.

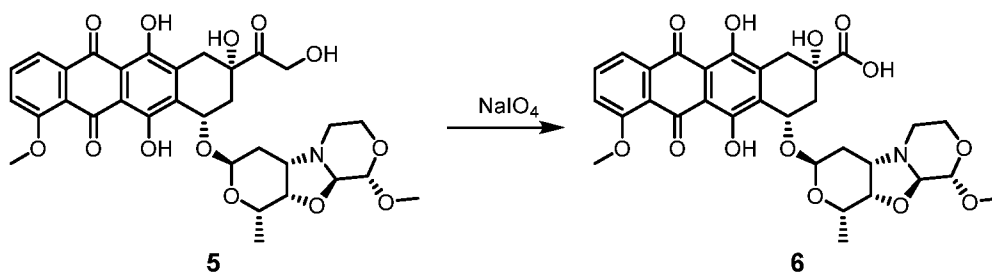
Example 2: (2S,4S)-2,5,12-trihydroxy-4-(((2R,4S,5S,6S)-5-hydroxy-4-((S)-2-methoxymorpholino)-6-methyltetrahydro-2H-pyran-2-yl)oxy)-7-methoxy-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracene-2-carboxylic acid (4)



[0417] Nemorubicin (**3**, MedChemExpress, 10 mg, 16 μmol) was dissolved in a mixture of MeOH (0.6 mL) and H₂O (0.4 mL). A solution of NaIO₄ (25 mg, 117 μmol) in H₂O (0.2 mL) was added to the above solution with stirring. After 1 hour, the solvents were removed under reduced pressure and the material was used in subsequent steps without further purification.

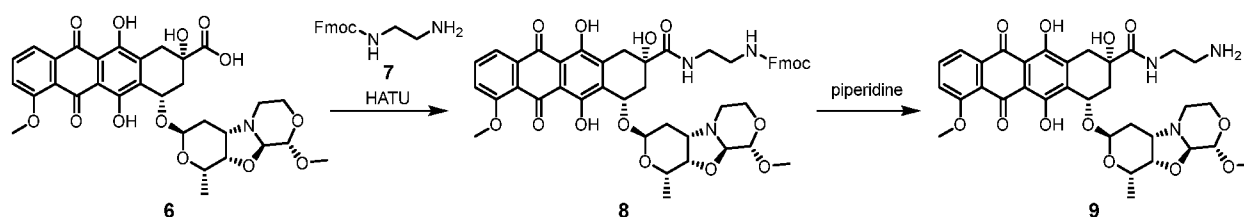
Analytical UPLC-MS (gradient 1): HPLC retention time = 1.30 min; m/z (ESI+) calculated 630.22 [M+H]⁺; found 630.46.

Example 3: (2S,4S)-2,5,12-trihydroxy-7-methoxy-4-(((1S,3R,4aS,9S,9aR,10aS)-9-methoxy-1-methyloctahydro-1H-pyrano[4',3':4,5]oxazolo[2,3-c][1,4]oxazin-3-yl)oxy)-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracene-2-carboxylic acid (6)



[0418] PNU-159682 (**5**, Levena Biopharma cat #, 50 mg, 78 μmol) was dissolved in a mixture of MeOH (3 mL) and H₂O (2 mL). A solution of NaIO₄ (25 mg, 117 μmol) in H₂O (1 mL) was added to the above solution with stirring. After 1 hour, the solvents were removed under reduced pressure and the material used in subsequent steps without further purification. Analytical UPLC-MS (gradient 1): HPLC retention time = 1.59 min; m/z (ESI+) calculated 628.20 [M+H]⁺; found 628.60.

Example 4: (2S,4S)-N-(2-aminoethyl)-2,5,12-trihydroxy-7-methoxy-4-(((1S,3R,4aS,9S,9aR,10aS)-9-methoxy-1-methyloctahydro-1H-pyrano[4',3':4,5]oxazolo[2,3-c][1,4]oxazin-3-yl)oxy)-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracene-2-carboxamide (9)



(9H-fluoren-9-yl)methyl (2-((2S,4S)-2,5,12-trihydroxy-7-methoxy-4-(((1S,3R,4aS,9S,9aR,10aS)-9-methoxy-1-methyloctahydro-1H-pyrano[4',3':4,5]oxazolo[2,3-

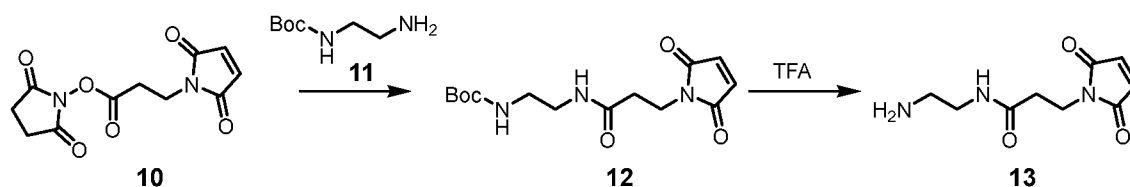
c][1,4]oxazin-3-yl)oxy)-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracene-2-carboxamido)ethyl)carbamate (8):

[0419] PNU-OH (6, 28 mg, 45 μ mol) and 1-[bis(dimethylamino)methylene]-1H-1,2,3-triazolo[4,5-b]pyridinium 3-oxid hexafluorophosphate, N-[(Dimethylamino)-1H-1,2,3-triazolo[4,5-b]pyridin-1-ylmethylene]-N-methylmethanaminium hexafluorophosphate N-oxide (HATU, 34 mg, 90 μ mol) were dissolved in anhydrous N,N-dimethylformamide (DMF, 0.90 mL). N-Fmoc-ethylenediamine hydrochloride (7, Santa Cruz Biotech, 25 mg, 90 μ mol) was added to the above solution as a solid, followed by the addition of N,N-diisopropylethylamine (DIPEA, 31 μ L, 179 μ mol). After 15 minutes, the reaction mixture was diluted with 0.5 mL MeCN and 0.5 mL 0.05% (v/v) aqueous TFA, and purified by preparative LC using TFA as mobile phase modifier to provide 8 (13 mg, 33%). Analytical UPLC-MS (gradient 1): HPLC retention time = 2.26 min; m/z (ESI+) calculated 892.33 [M+H]⁺; found 892.48.

(2S,4S)-N-(2-aminoethyl)-2,5,12-trihydroxy-7-methoxy-4-(((1S,3R,4aS,9S,9aR,10aS)-9-methoxy-1-methyloctahydro-1H-pyrano[4',3':4,5]oxazolo[2,3-c][1,4]oxazin-3-yl)oxy)-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracene-2-carboxamide (9):

[0420] Fmoc-EDA-PNU (8, 5 mg, 6 μ mol) was dissolved in a mixture of DMF (0.18 mL) and piperidine (45 μ L). After 15 minutes, the reaction mixture was diluted with 0.5 mL MeCN and 0.5 mL 0.05% (v/v) aqueous TFA, and purified by preparative LC using TFA as mobile phase modifier to provide 9 (2.4 mg, 60%). Analytical UPLC-MS (gradient 1): HPLC retention time = 1.24 min; m/z (ESI+) calculated 670.26 [M+H]⁺; found 670.41.

Example 5: N-(2-aminoethyl)-3-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)propanamide (13)



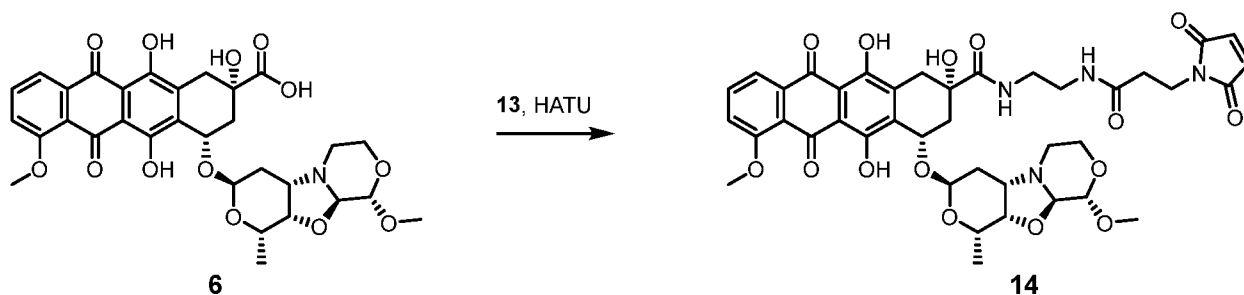
tert-butyl (2-(3-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)propanamido)ethyl)carbamate (12):

[0421] A flame dried flask was charged with 3-(maleimido)propionic acid N-hydroxysuccinimide ester (mp-OSu **10**, 50 mg, 188 μmol), anhydrous DMF (0.75 mL), and DIPEA (101 μL , 564 μmol). N-Boc-ethylenediamine (**11**, 169 μmol , 27 μL) was diluted in minimal volume of DMF and added dropwise to the mp-OSu solution with stirring. The reaction was quenched after 30 minutes by adding 101 μL glacial acetic acid (AcOH), and the reaction mixture was diluted with minimal volume of 1:1 MeCN:0.05% (v/v) aqueous TFA, and purified by preparative LC using TFA as mobile phase modifier to provide **12** (34 mg, **58%**). Analytical UPLC-MS (gradient 1): HPLC retention time = 1.28 min; m/z (ESI+) calculated 334.14 [M+Na]⁺; found 334.39.

N-(2-aminoethyl)-3-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)propanamide (13):

[0422] mp-EDA-Boc (**12**, 34 mg, 108 μmol) was dissolved in anhydrous dichloromethane (DCM, 0.8 mL) and cooled to 0°C using an ice bath. TFA (0.2 mL) was added dropwise to the above solution with stirring. After 1 hour, the solvents were removed under reduced pressure and the crude product was used in subsequent steps without further purification. Analytical UPLC-MS (gradient 1): HPLC retention time = 0.42 min; m/z (ESI+) calculated 234.19 [M+Na]⁺; found 234.08.

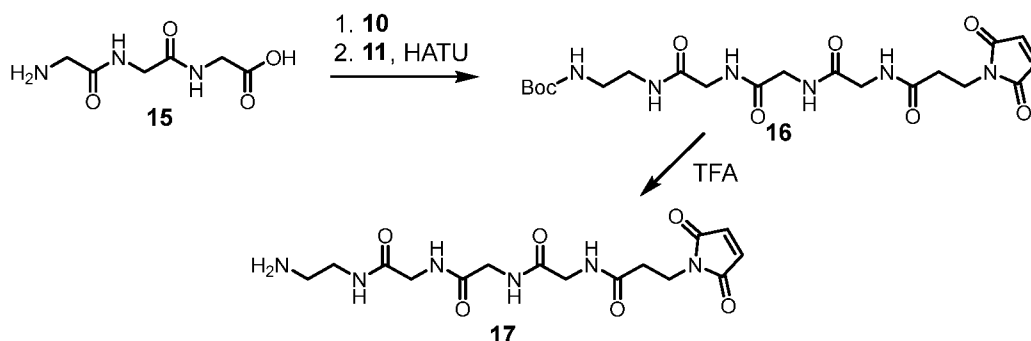
Example 6: (2S,4S)-N-(2-(3-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)propanamido)ethyl)-2,5,12-trihydroxy-7-methoxy-4-(((1S,3R,4aS,9S,9aR,10aS)-9-methoxy-1-methyloctahydro-1H-pyrano[4',3':4,5]oxazolo[2,3-c][1,4]oxazin-3-yl)oxy)-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracene-2-carboxamide (14)



[0423] PNU-OH (**6**, 10 mg, 16 μmol) and HATU (6 mg, 16 μmol) were dissolved in anhydrous DMF (0.17 mL). mp-EDA (**13**, 3 mg, 16 μmol), as a solution in DMF (0.17 mL) was

added to the above solution with stirring, followed by the addition of DIPEA (8 μ L, 48 μ mol). After 15 minutes, the reaction mixture was diluted with 0.5 mL MeCN and 0.5 mL 10 mM aqueous NH_4Cl , and purified by preparative LC using NH_4Cl as mobile phase modifier to provide **14** (4 mg, 30%). Analytical UPLC-MS (gradient 2): HPLC retention time = 1.72 min; m/z (ESI+) calculated 821.29 $[\text{M}+\text{H}]^+$; found 821.65.

Example 7: N-(2-((2-((2-((2-aminoethyl)amino)-2-oxoethyl)amino)-2-oxoethyl)amino)-2-oxoethyl)-3-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)propenamide (17)



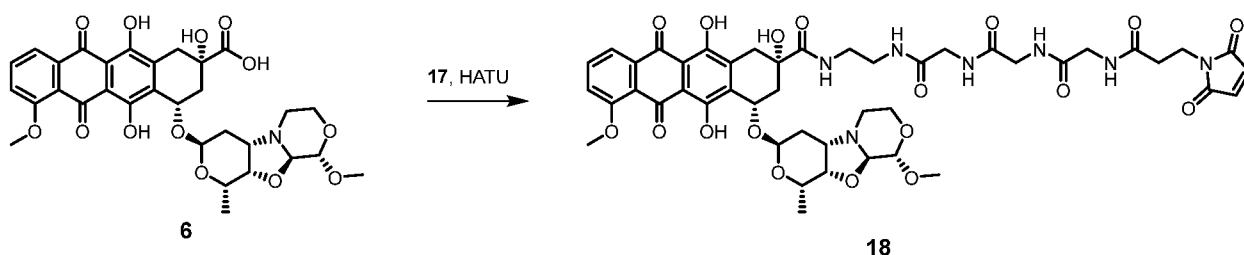
tert-butyl (15-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)-4,7,10,13-tetraoxo-3,6,9,12-tetraazapentadecyl)carbamate (16):

[0424] A flame-dried flask was charged with H-Gly₃-OH (**15**, 71 mg, 376 μ mol), mp-OSu (**10**, 100 mg, 376 μ mol), and anhydrous dimethylsulfoxide (DMSO, 3.76 mL). DIPEA (262 μ L, 1.5 mmol) was added to the above solution, and the reaction mixture was stirred overnight under N_2 . HATU (157 mg, 414 μ mol) was then added to the reaction mixture followed by Boc-EDA (**11**, 60 μ L, 376 μ mol). After 30 minutes, the reaction mixture was directly loaded onto a preparative LC and the desired product purified, using TFA as the mobile phase modifier to provide **16** (91 mg, 50%). Analytical UPLC-MS (gradient 1): HPLC retention time = 1.06 min; m/z (ESI+) calculated 483.22 $[\text{M}+\text{H}]^+$; found 483.47.

N-(2-((2-((2-((2-aminoethyl)amino)-2-oxoethyl)amino)-2-oxoethyl)amino)-2-oxoethyl)-3-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)propenamide (17):

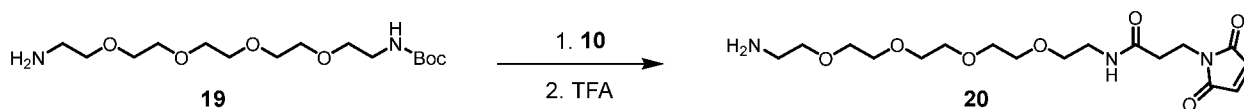
[0425] mp-Gly₃-EDA-Boc (**16**, 91 mg, 188 μ mol) was dissolved in anhydrous DCM (1.6 mL) and cooled to 0°C. TFA (0.4 mL) was added dropwise to this solution with stirring. After 1 hour, the solvents were removed under reduced pressure and the crude product was used in subsequent steps without further purification. Analytical UPLC-MS (gradient 1): HPLC retention time = 0.43 min; m/z (ESI+) calculated 383.17 [M+H]⁺; found 383.36.

Example 8: (2S,4S)-N-(15-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)-4,7,10,13-tetraoxo-3,6,9,12-tetraazapentadecyl)-2,5,12-trihydroxy-7-methoxy-4-(((1S,3R,4aS,9S,9aR,10aS)-9-methoxy-1-methyloctahydro-1H-pyrano[4',3':4,5]oxazolo[2,3-c][1,4]oxazin-3-yl)oxy)-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracene-2-carboxamide (18)



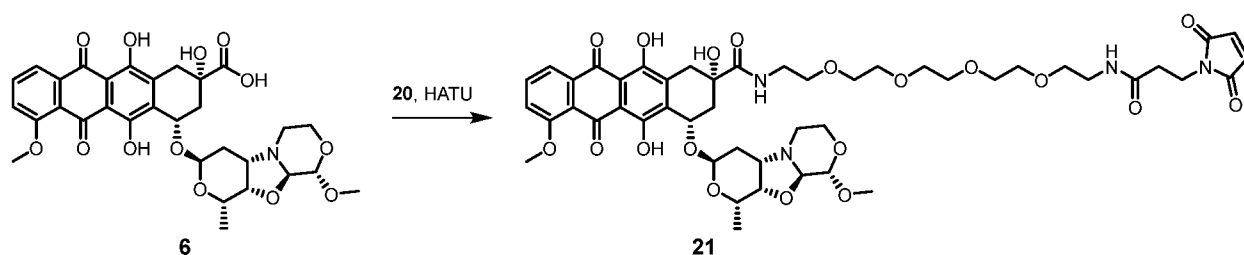
[0426] PNU-OH (**6**, 5 mg, 8 μ mol) and HATU (3 mg, 7 μ mol) were dissolved in anhydrous DMF (0.2 mL). mp-Gly₃-EDA (**17**, 3 mg, 6 μ mol), as solution in DMF (0.2 mL), was added to the above solution with stirring, followed by the addition of DIPEA (4 μ L, 25 μ mol). After 15 minutes, the reaction mixture was diluted with 0.5 mL MeCN and 0.5 mL 10 mM aqueous NH₄Cl, and purified by preparative LC using NH₄Cl as mobile phase modifier to provide **18** (4 mg, **30%**). Analytical UPLC-MS (gradient 2): HPLC retention time = 1.48 min; m/z (ES+) calculated 992.35 [M+H]⁺; found 992.87.

Example 9: N-(14-amino-3,6,9,12-tetraoxatetradecyl)-3-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)propenamide (20)



[0427] A flame-dried flask was charged with mp-OSu (**10**, 25 mg, 94 μ mol), anhydrous DMF (0.94 mL), and DIPEA (65 μ L, 376 μ mol). Boc-PEG₄-NH₂ (**19**, 30 μ L, 94 μ mol) was dissolved in minimal volume of DMF and added dropwise to the mp-OSu solution with stirring. The solvents were removed under reduced pressure, and the resulting residue was then re-dissolved in 0.8 mL DCM and 0.2 mL TFA. After 30 minutes, the volatiles were removed under reduced pressure, the resulting residue was re-solubilized in minimal volume of 1:1 MeCN: 0.05% (v/v) aqueous TFA, and purified by preparative LC using TFA as mobile phase modifier to provide **20** (40 mg, **87%**). Analytical UPLC-MS (gradient 1): HPLC retention time = 0.71 min; m/z (ESI+) calculated 388.21 [M+H]⁺; found 388.39.

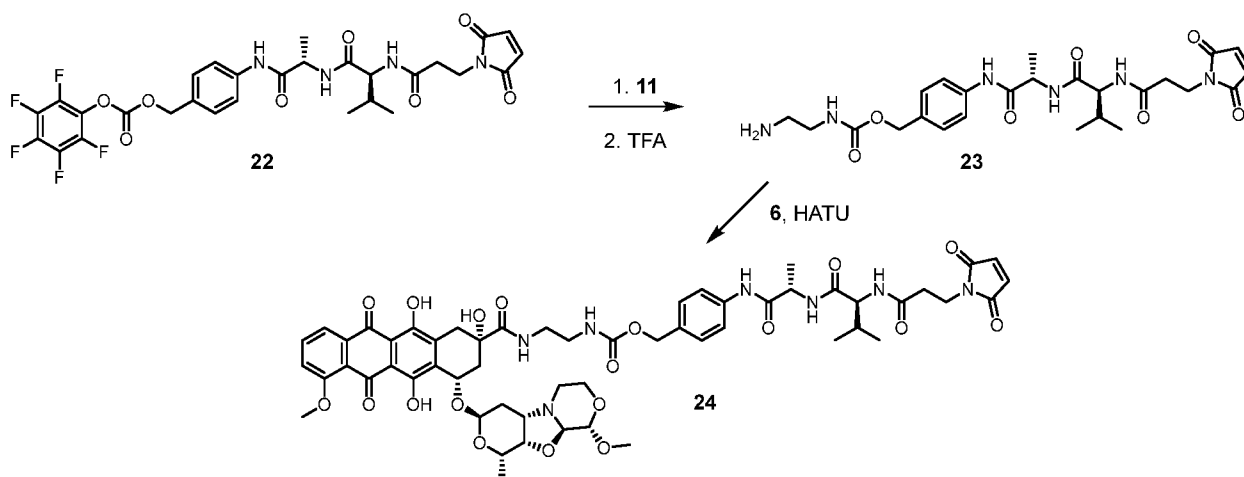
Example 10: (2S,4S)-N-(18-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)-16-oxo-3,6,9,12-tetraoxa-15-aza-octadecyl)-2,5,12-trihydroxy-7-methoxy-4-(((1S,3R,4aS,9S,9aR,10aS)-9-methoxy-1-methyloctahydro-1H-pyrano[4',3':4,5]oxazolol[2,3-c][1,4]oxazin-3-yl)oxy)-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracene-2-carboxamide (21)



[0428] PNU-OH (**6**, 5 mg, 8 μ mol) and HATU (1.7 mg, 4.3 μ mol) were dissolved in anhydrous DMF (0.13 mL). mp-PEG₄-NH₂ (**20**, 1.7 mg, 4.3 μ mol) was added as a solution in DMF (0.13 mL), followed by the addition of DIPEA (3 μ L, 17 μ mol). After 15 minutes, the reaction mixture was diluted with 0.5 mL MeCN and 0.5 mL 0.05% (v/v) aqueous TFA, and purified by preparative LC using TFA as mobile phase modifier to provide **21** (2.2 mg, **51%**). Analytical UPLC-MS (gradient 1): HPLC retention time = 1.65 min; m/z (ESI+) calculated 997.40 [M+H]⁺; found 997.92.

Example 11: 4-((S)-2-((S)-2-(3-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)propanamido)-3-methylbutanamido)propanamido)benzyl (2-((2S,4S)-2,5,12-trihydroxy-7-methoxy-4-(((1S,3R,4aS,9S,9aR,10aS)-9-methoxy-1-methyloctahydro-1H-pyrano[4',3':4,5]oxazolol[2,3-

c][1,4]oxazin-3-yl)oxy)-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracene-2-carboxamido)ethyl)carbamate (24)



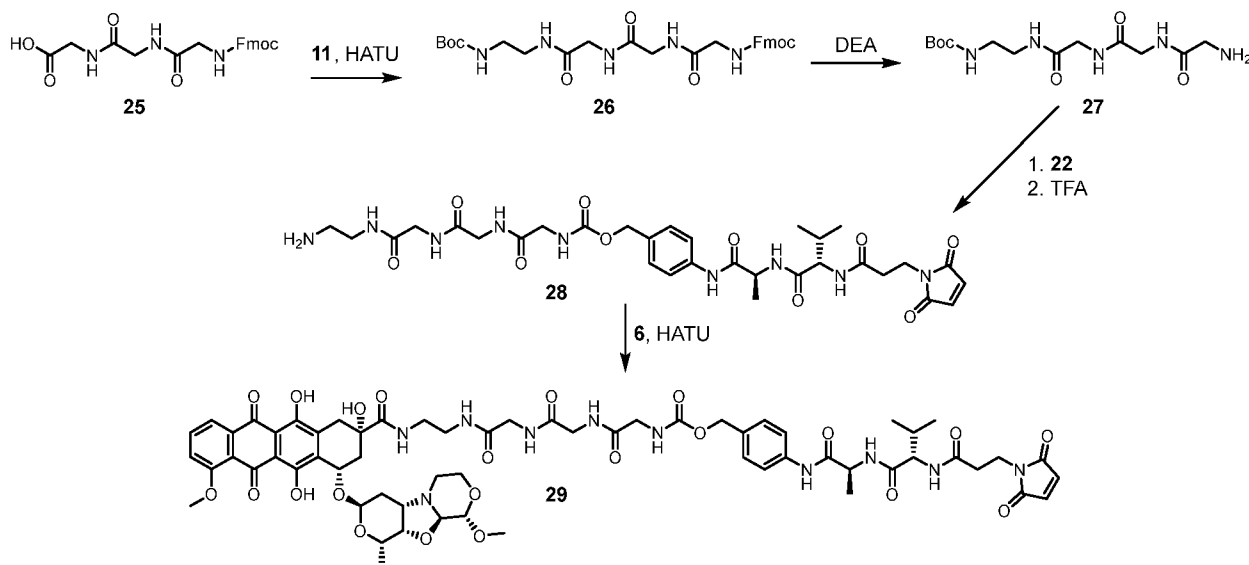
4-((S)-2-((S)-2-(3-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)propanamido)-3-methylbutanamido)propanamido)benzyl (2-aminoethyl)carbamate (23):

[0429] A flame-dried flask was charged with mp-ValAlaPAB-OPFP (**22**, 25 mg, 38 μ mol) and Boc-EDA (**11**, 7 μ L, 42 μ mol) in anhydrous DMF (0.38 mL). DIPEA (27 μ L, 153 μ mol) was added to the above solution with stirring. After 30 minutes, solvents were removed under reduced pressure and the resulting residue was resolubilized in DCM (0.3 mL) and TFA (76 μ L) for an additional 30 minutes. The volatiles were removed under reduced pressure, and the resulting residue was re-dissolved in minimal volume of 1:1 MeCN: 0.05% (v/v) aqueous TFA, and purified by preparative LC using TFA as mobile phase modifier to provide **23** (8 mg, **33%**). Analytical UPLC-MS (gradient 1): HPLC retention time = 0.93 min; m/z (ESI+) calculated 531.26 [M+H]⁺; found 531.58.

4-((S)-2-((S)-2-(3-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)propanamido)-3-methylbutanamido)propanamido)benzyl (2-((2S,4S)-2,5,12-trihydroxy-7-methoxy-4-(((1S,3R,4aS,9S,9aR,10aS)-9-methoxy-1-methyloctahydro-1H-pyrano[4',3':4,5]oxazolo[2,3-c][1,4]oxazin-3-yl)oxy)-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracene-2-carboxamido)ethyl)carbamate (24):

[0430] PNU-OH (**6**, 5.4 mg, 8.6 μ mol) and HATU (3.6 mg, 9.5 μ mol) were dissolved in anhydrous DMF (0.34 mL). mp-ValAlaPAB-EDA (**23**, 4.6 mg, 8.6 μ mol) was added as a solution in DMF (0.34 mL) followed by the addition of DIPEA (6.0 μ L, 34 μ mol). After 15 minutes, the reaction mixture was diluted with 0.5 mL MeCN and 0.5 mL 10 mM aqueous NH_4Cl , and purified by preparative LC using NH_4Cl as mobile phase modifier to provide **24** (0.8 mg, 8%). Analytical UPLC-MS (gradient 2): HPLC retention time = 1.83 min; m/z (ESI+) calculated 1140.44 $[\text{M}+\text{H}]^+$; found 1140.75.

Example 12: 4-((S)-2-((S)-2-(3-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)propanamido)-3-methylbutanamido)propanamido)benzyl (1,6,9,12-tetraoxo-1-((2S,4S)-2,5,12-trihydroxy-7-methoxy-4-(((1S,3R,4aS,9S,9aR,10aS)-9-methoxy-1-methyloctahydro-1H-pyrano[4',3':4,5]oxazolo[2,3-c][1,4]oxazin-3-yl)oxy)-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracen-2-yl)-2,5,8,11-tetraazatridecan-13-yl)carbamate (**29**)



(9H-fluoren-9-yl)methyl (2,2-dimethyl-4,9,12,15-tetraoxo-3-oxa-5,8,11,14-tetraazahexadecan-16-yl)carbamate (26**):**

[0431] Fmoc-Gly₃-OH (**25**, 50 mg, 122 μ mol) and HATU (46 mg, 122 μ mol) were dissolved in anhydrous DMF (1.2 mL). Boc-EDA (**11**, 19 μ L, 122 μ mol) was added to this solution with stirring, followed by the addition of DIPEA (85 μ L, 486 μ mol). After 15 minutes, the volatiles were removed under reduced pressure and the crude product was purified by flash chromatography

over silica gel (2%-20% MeOH in DCM linear gradient) to provide **26** (66 mg, **99%**). Analytical UPLC-MS (gradient 1): HPLC retention time = 1.79 min; m/z (ESI+) calculated 554.26 [M+H]⁺; found 554.45.

tert-butyl (2-(2-(2-(2-aminoacetamido)acetamido)acetamido)ethyl)carbamate (27):

[0432] Boc-EDA-Gly₃-Fmoc (**26**, 66 mg, 119 μmol) was dissolved in a premixed solution of 1:1 (v/v) DCM and diethylamine (1.21 mL each). After 30 minutes, MeOH was added dropwise to the reaction mixture until all precipitate dissolved. MTBE was subsequently added dropwise until significant precipitation was observed, then the reaction was cooled to -20 °C and stirred for 1 hour. The resulting solid was collected using a fritted funnel, resolubilized in MeOH, and dried to provide **27** (28 mg, **71%**). This crude product was used in subsequent steps without further purification. Analytical UPLC-MS (gradient 1): HPLC retention time = 0.78 min; m/z (ESI+) calculated 332.20 [M+H]⁺; found 332.31.

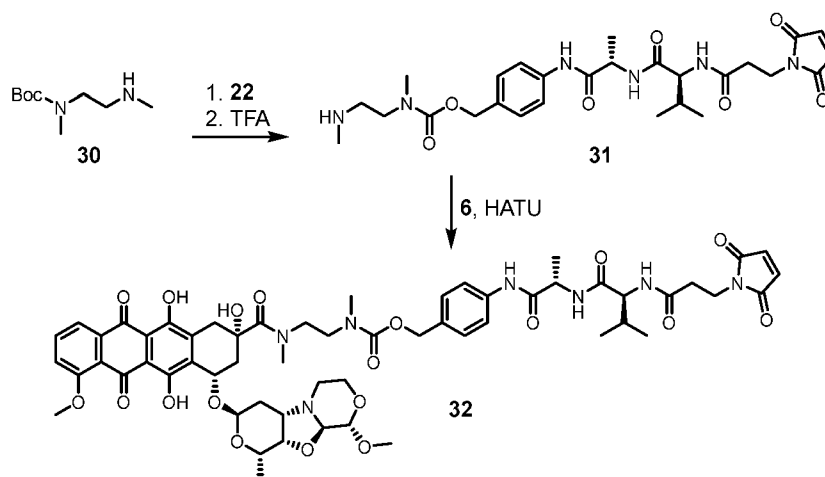
4-((S)-2-((S)-2-(3-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)propanamido)-3-methylbutanamido)propanamido)benzyl (2-((2-((2-((2-aminoethyl)amino)-2-oxoethyl)amino)-2-oxoethyl)amino)-2-oxoethyl)carbamate (28):

[0433] A flame-dried flask was charged with mp-ValAlaPAB-OPFP (**22**, 55 mg, 84 μmol) and Boc-EDA-Gly₃ (**27**, 28 mg, 84 μmol) in anhydrous DMF (0.85 mL). DIPEA (59 μL, 338 μmol) was added to the above solution with stirring. After 30 minutes, solvents were removed under reduced pressure and the resulting residue was resolubilized in DCM (0.68 mL) and TFA (0.17 μL), and stirred for an additional 30 minutes. The volatiles were removed under reduced pressure, and the resulting residue was re-dissolved in minimal volume of 1:1 MeCN: 0.05% (v/v) aqueous TFA, and purified by preparative LC using TFA as mobile phase modifier to provide **28** (38 mg, **64%**). Analytical UPLC-MS (gradient 1): HPLC retention time = 0.92 min; m/z (ESI+) calculated 702.32 [M+H]⁺; found 702.30.

4-((S)-2-((S)-2-(3-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)propanamido)-3-methylbutanamido)propanamido)benzyl (1,6,9,12-tetraoxo-1-((2S,4S)-2,5,12-trihydroxy-7-methoxy-4-(((1S,3R,4aS,9S,9aR,10aS)-9-methoxy-1-methyloctahydro-1H-pyrano[4',3':4,5]oxazolo[2,3-c][1,4]oxazin-3-yl)oxy)-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracen-2-yl)-2,5,8,11-tetraazatridecan-13-yl)carbamate (29):

[0434] PNU-OH (**6**, 10 mg, 16 μ mol) and HATU (6 mg, 16 μ mol) were dissolved in anhydrous DMF (0.32 mL). mp-ValAlaPAB-EDA-Gly₃ (**28**, 11 mg, 16 μ mol) was added as a solution in DMF (0.2 mL) to the above solution, followed by the addition of DIPEA (11 μ L, 64 μ mol). After 15 minutes, the reaction mixture was diluted with 0.5 mL MeCN and 0.5 mL 10 mM aqueous NH₄Cl and purified by preparative LC using NH₄Cl as mobile phase modifier to provide **29** (11 mg, **53%**). Analytical UPLC-MS (gradient 2): HPLC retention time = 1.58 min; m/z (ESI+) calculated 1311.51 [M+H]⁺; found 1311.87.

Example 13: 4-((S)-2-((S)-2-(3-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)propanamido)-3-methylbutanamido)propanamido)benzyl methyl(2-((2S,4S)-2,5,12-trihydroxy-7-methoxy-4-(((1S,3R,4aS,9S,9aR,10aS)-9-methoxy-1-methyloctahydro-1H-pyranof[4',3':4,5]oxazolof[2,3-c][1,4]oxazin-3-yl)oxy)-N-methyl-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracene-2-carboxamido)ethyl)carbamate (**32**)



4-((S)-2-((S)-2-(3-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)propanamido)-3-methylbutanamido)propanamido)benzyl methyl(2-(methylamino)ethyl)carbamate (31**):**

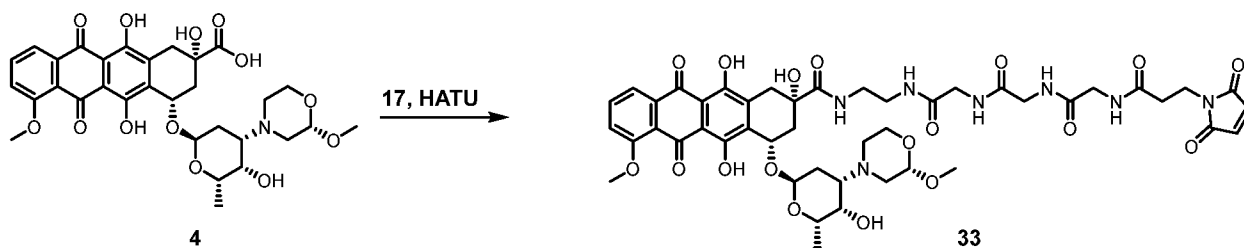
[0435] A flame-dried flask was charged with mp-ValAlaPAB-OPFP (**22**, 20 mg, 31 μ mol) and Boc-N,N-DiMeEDA (**30**, 13 μ L, 61 μ mol) in anhydrous DMF (0.23 mL). DIPEA (21 μ L, 122 μ mol) was added to the above solution with stirring. After 30 minutes, the solvents were removed under reduced pressure and the resulting residue was resolubilized in DCM (0.18 mL) and TFA (46 μ L), and stirred for an additional 30 minutes. The volatiles were removed under

reduced pressure, and the resulting residue was dissolved in minimal volume of 1:1 MeCN: 0.05% (v/v) aqueous TFA, and purified by preparative LC using TFA as mobile phase modifier to provide **31** (3.1 mg, **18%**). Analytical UPLC-MS (gradient 1): HPLC retention time = 0.96 min; m/z (ESI+) calculated 559.29 [M+H]⁺; found 559.10.

4-((S)-2-(((S)-2-(3-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)propanamido)-3-methylbutanamido)propanamido)benzyl methyl(2-((2S,4S)-2,5,12-trihydroxy-7-methoxy-4-(((1S,3R,4aS,9S,9aR,10aS)-9-methoxy-1-methyloctahydro-1H-pyrano[4',3':4,5]oxazolo[2,3-c][1,4]oxazin-3-yl)oxy)-N-methyl-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracene-2-carboxamido)ethyl)carbamate (32):

[0436] PNU-OH (**6**, 5.2 mg, 8.3 μmol) and HATU (3.2 mg, 8.3 μmol) were dissolved in anhydrous DMF (0.14 mL). mp-ValAlaPAB-N,N-DiMeEDA (**31**, 3.1 mg, 5.5 μmol) was added as a solution in DMF (0.14 mL), followed by the addition of DIPEA (3.9 μL, 22 μmol). After 15 minutes, the reaction mixture was diluted with 0.5 mL MeCN and 0.5 mL 0.05% (v/v) aqueous TFA, and purified by preparative LC using TFA as mobile phase modifier to provide **32** (2.1 mg, **33%**). Analytical UPLC-MS (gradient 1): HPLC retention time = 1.83 min; m/z (ESI+) calculated 1168.47 [M+H]⁺; found 1168.65.

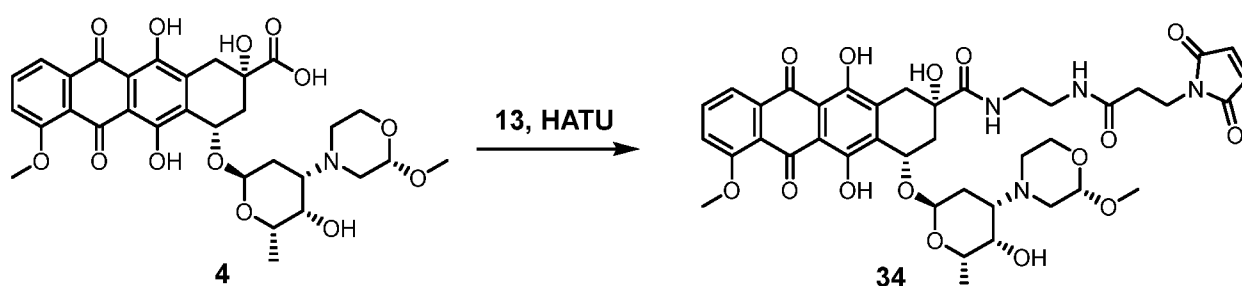
Example 14: (2S,4S)-N-(15-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)-4,7,10,13-tetraoxo-3,6,9,12-tetraazapentadecyl)-2,5,12-trihydroxy-4-(((2R,4S,5S,6S)-5-hydroxy-4-((S)-2-methoxymorpholino)-6-methyltetrahydro-2H-pyran-2-yl)oxy)-7-methoxy-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracene-2-carboxamide (33)



[0437] Nemorubicin-OH (**4**, 3.7 mg, 5.9 μmol) and HATU (2.5 mg, 6.5 μmol) were dissolved in anhydrous DMF (0.15 mL). mp-Gly₃-EDA (**17**, 2.9 mg, 5.9 μmol) as a solution in DMF (0.15 mL) was added to this solution with stirring, followed by the addition of DIPEA (4

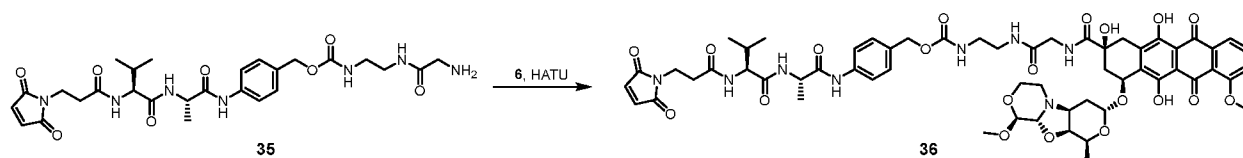
μL , 24 μmol). After 15 minutes, the reaction mixture was diluted with minimal volume of 1:1 MeCN: 0.05% (v/v) aqueous TFA, and purified by preparative LC using TFA as mobile phase modifier to provide **33** (1.0 mg, **17%**). Analytical UPLC-MS (gradient 1): HPLC retention time = 1.19 min; m/z (ESI+) calculated 994.37 $[\text{M}+\text{H}]^+$; found 995.07.

Example 15: (2S,4S)-N-(2-(3-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)propanamido)ethyl)-2,5,12-trihydroxy-4-(((2R,4S,5S,6S)-5-hydroxy-4-((S)-2-methoxymorpholino)-6-methyltetrahydro-2H-pyran-2-yl)oxy)-7-methoxy-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracene-2-carboxamide (34)



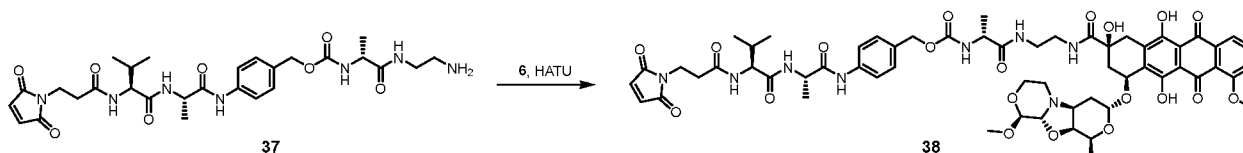
[0438] Nemorubicin-OH (**4**, 23 mg, 37 μmol) and HATU (21 mg, 55 μmol) were dissolved in anhydrous DMF (0.73 mL). mp-EDA (**13**, 12 mg, 37 μmol) as a solution in DMF (0.12 mL) was added to the above solution with stirring, followed by the addition of DIPEA (25 μL , 148 μmol). After 15 minutes, the reaction mixture was diluted with 0.5 mL MeCN and 0.5 mL 0.05% (v/v) aqueous TFA, and purified by preparative LC using TFA as mobile phase modifier to provide **34** (7.0 mg, **23%**). Analytical UPLC-MS (gradient 1): HPLC retention time = 1.54 min; m/z (ESI+) calculated 823.30 $[\text{M}+\text{H}]^+$; found 823.37.

Example 16: 4-((S)-2-(((S)-2-(3-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)propanamido)-3-methylbutanamido)propanamido)benzyl (2-(2-((2S,4S)-2,5,12-trihydroxy-7-methoxy-4-(((1S,3R,4aS,9S,9aR,10aS)-9-methoxy-1-methyloctahydro-1H-pyrano[4',3':4,5]oxazolo[2,3-c][1,4]oxazin-3-yl)oxy)-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracene-2-carboxamido)acetamido)ethyl)carbamate (36)



[0439] mp-ValAlaPAB-EDA-Gly (**35**, 9 mg, 15 μ mol), PNU-OH (**6**, 9 mg, 15 μ mol) and HATU (6 mg, 15 μ mol) were dissolved in anhydrous DMF (0.30 mL). The reaction was cooled to 0 °C followed by the addition of DIPEA (8 μ L, 44 μ mol). After 15 minutes, the reaction mixture was quenched with 8 μ L of AcOH, diluted with 0.5 mL MeCN and 0.5 mL 10 mM aqueous NH_4OAc , then purified by preparative LC using NH_4OAc as mobile phase modifier to provide **36** (2 mg, **13%**). Analytical UPLC-MS (gradient 2): HPLC retention time = 1.72 min; m/z (ESI+) calculated 1197.46 $[\text{M}+\text{H}]^+$; found 1197.80.

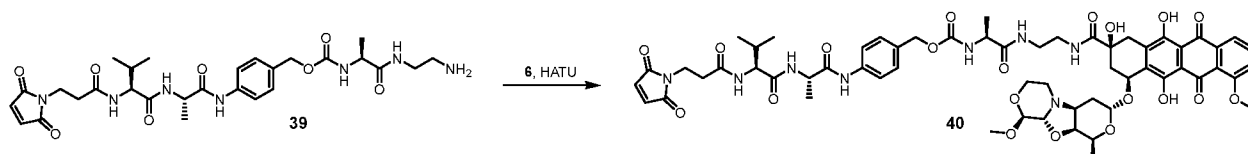
Example 17: 4-((S)-2-((S)-2-(3-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)propanamido)-3-methylbutanamido)propanamido)benzyl ((R)-1-oxo-1-((2-((2S,4S)-2,5,12-trihydroxy-7-methoxy-4-(((1S,3R,4aS,9S,9aR,10aS)-9-methoxy-1-methyloctahydro-1H-pyrano[4',3':4,5]oxazolo[2,3-c][1,4]oxazin-3-yl)oxy)-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracene-2-carboxamido)ethyl)amino)propan-2-yl)carbamate (**38**)



[0440] mp-ValAlaPAB-Ala(D)-EDA (**37**, 9 mg, 15 μ mol), PNU-OH (**6**, 9 mg, 15 μ mol) and HATU (6 mg, 15 μ mol) were dissolved in anhydrous DMF (0.30 mL). The reaction was cooled to 0 °C followed by the addition of DIPEA (8 μ L, 44 μ mol). After 15 minutes, the reaction mixture was quenched with 8 μ L of AcOH, diluted with 0.5 mL MeCN and 0.5 mL 10 mM aqueous NH_4OAc , then purified by preparative LC using NH_4OAc as mobile phase modifier to provide **38** (4 mg, **24%**). Analytical UPLC-MS (gradient 2): HPLC retention time = 1.73 min; m/z (ESI+) calculated 1211.48 $[\text{M}+\text{H}]^+$; found 1211.85.

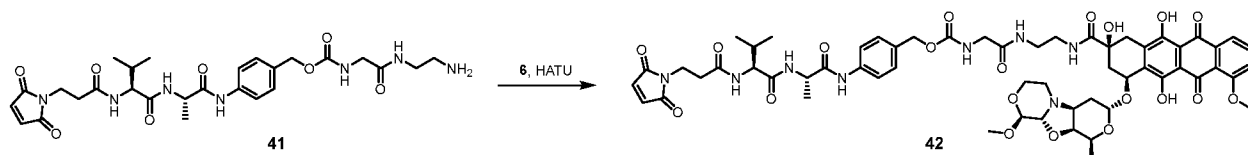
Example 18: 4-((S)-2-((S)-2-(3-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)propanamido)-3-methylbutanamido)propanamido)benzyl ((S)-1-oxo-1-((2-((2S,4S)-2,5,12-trihydroxy-7-methoxy-

4-(((1S,3R,4aS,9S,9aR,10aS)-9-methoxy-1-methyloctahydro-1H-pyrano[4',3':4,5]oxazolo[2,3-c][1,4]oxazin-3-yl)oxy)-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracene-2-carboxamido)ethyl)amino)propan-2-yl)carbamate (40)



[0441] mp-ValAlaPAB-Ala-EDA (**39**, 9 mg, 15 μ mol), PNU-OH (**6**, 9 mg, 15 μ mol) and HATU (6 mg, 15 μ mol) were dissolved in anhydrous DMF (0.30 mL). The reaction was cooled to 0 °C followed by the addition of DIPEA (8 μ L, 44 μ mol). After 15 minutes, the reaction mixture was quenched with 8 μ L of AcOH, diluted with 0.5 mL MeCN and 0.5 mL 10 mM aqueous NH₄OAc, then purified by preparative LC using NH₄OAc as mobile phase modifier to provide **40** (4 mg, **24%**). Analytical UPLC-MS (gradient 2): HPLC retention time = 1.76 min; m/z (ESI+) calculated 1211.48 [M+H]⁺; found 1211.85.

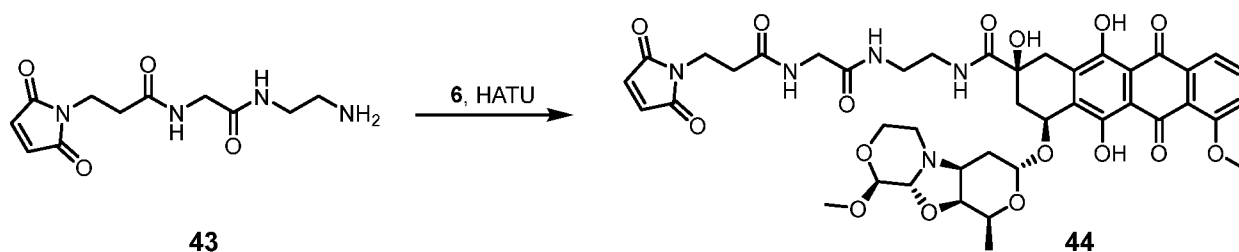
Example 19: 4-((S)-2-((S)-2-(3-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)propanamido)-3-methylbutanamido)propanamido)benzyl (2-oxo-2-((2-((2S,4S)-2,5,12-trihydroxy-7-methoxy-4-(((1S,3R,4aS,9S,9aR,10aS)-9-methoxy-1-methyloctahydro-1H-pyrano[4',3':4,5]oxazolo[2,3-c][1,4]oxazin-3-yl)oxy)-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracene-2-carboxamido)ethyl)amino)ethyl)carbamate (42)



[0442] mp-ValAlaPAB-Gly-EDA (**41**, 9 mg, 15 μ mol), PNU-OH (**6**, 9 mg, 15 μ mol) and HATU (6 mg, 15 μ mol) were dissolved in anhydrous DMF (0.30 mL). The reaction was cooled to 0 °C followed by the addition of DIPEA (8 μ L, 44 μ mol). After 15 minutes, the reaction mixture was quenched with 8 μ L of AcOH, diluted with 0.5 mL MeCN and 0.5 mL 10 mM aqueous NH₄OAc, then purified by preparative LC using NH₄OAc as mobile phase modifier to provide **42**

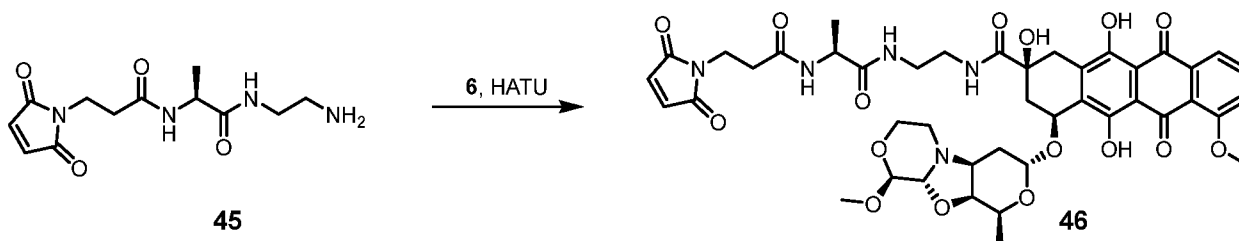
(4 mg, **24%**). Analytical UPLC-MS (gradient 2): HPLC retention time = 1.71 min; m/z (ESI+) calculated 1197.46 [M+H]⁺; found 1197.80.

Example 20: (2S,4S)-N-(2-(2-(3-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)propanamido)acetamido)ethyl)-2,5,12-trihydroxy-7-methoxy-4-(((1S,3R,4aS,9S,9aR,10aS)-9-methoxy-1-methyloctahydro-1H-pyrano[4',3':4,5]oxazolo[2,3-c][1,4]oxazin-3-yl)oxy)-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracene-2-carboxamide (**44**)



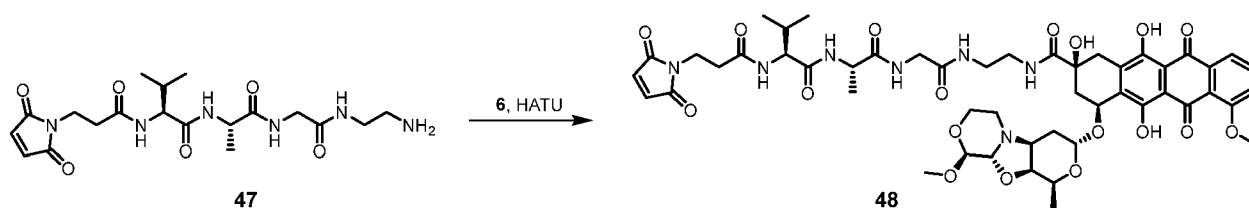
[0443] PNU-OH (**6**, 17 mg, 27 μ mol) and HATU (10 mg, 27 μ mol) were dissolved in anhydrous DMF (0.30 mL) and cooled to 0 °C. DIPEA (14 μ L, 81 μ mol) was added the reaction was allowed to preactivate for 5 minutes. mp-Gly-EDA (**43**, 7 mg, 27 μ mol) was added with minimal DMF. After 15 minutes, the reaction mixture was quenched with 14 μ L of AcOH, diluted with 0.5 mL MeCN and 0.5 mL 10 mM aqueous NH₄OAc, then purified by preparative LC using NH₄OAc as mobile phase modifier to provide **44** (1 mg, **4%**). Analytical UPLC-MS (gradient 2): HPLC retention time = 1.57 min; m/z (ESI+) calculated 878.31 [M+H]⁺; found 878.59.

Example 21: (2S,4S)-N-(2-((S)-2-(3-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)propanamido)propanamido)ethyl)-2,5,12-trihydroxy-7-methoxy-4-(((1S,3R,4aS,9S,9aR,10aS)-9-methoxy-1-methyloctahydro-1H-pyrano[4',3':4,5]oxazolo[2,3-c][1,4]oxazin-3-yl)oxy)-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracene-2-carboxamide (**46**)



[0444] mp-Ala-EDA (**45**, 4 mg, 13 μ mol), PNU-OH (**6**, 7 mg, 12 μ mol) and HATU (5 mg, 12 μ mol) were dissolved in anhydrous DMF (0.26 mL). The reaction was cooled to 0 °C followed by the addition of DIPEA (7 μ L, 39 μ mol). After 15 minutes, the reaction mixture was quenched with 7 μ L of AcOH, diluted with 0.5 mL MeCN and 0.5 mL 10 mM aqueous NH₄OAc, then purified by preparative LC using NH₄OAc as mobile phase modifier to provide **46** (3 mg, **24%**). Analytical UPLC-MS (gradient 2): HPLC retention time = 1.61 min; m/z (ESI+) calculated 892.33 [M+H]⁺; found 892.55.

Example 22: (2S,4S)-N-((8S,11S)-15-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)-11-isopropyl-8-methyl-4,7,10,13-tetraoxo-3,6,9,12-tetraazapentadecyl)-2,5,12-trihydroxy-7-methoxy-4-(((1S,3R,4aS,9S,9aR,10aS)-9-methoxy-1-methyloctahydro-1H-pyranof[4',3':4,5]oxazolof[2,3-c][1,4]oxazin-3-yl)oxy)-6,11-dioxo-1,2,3,4,6,11-hexahydrotetracene-2-carboxamide (48)



[0445] mp-ValAlaGly-EDA (**47**, 6 mg, 14 μ mol), PNU-OH (**6**, 9 mg, 114 μ mol) and HATU (5 mg, 14 μ mol) were dissolved in anhydrous DMF (0.28 mL). The reaction was cooled to 0 °C followed by the addition of DIPEA (7 μ L, 42 μ mol). After 15 minutes, the reaction mixture was quenched with 7 μ L of AcOH, diluted with 0.5 mL MeCN and 0.5 mL 10 mM aqueous NH₄OAc, then purified by preparative LC using NH₄OAc as mobile phase modifier to provide **48** (1.4 mg, **10%**). Analytical UPLC-MS (gradient 2): HPLC retention time = 1.61 min; m/z (ESI+) calculated 1048.41 [M+H]⁺; found 1048.68.

In vitro assays

[0446] Cell culture of cell lines as listed in Table 2-4 in log-phase growth were seeded in 96-well plates and grown for 24 h in cell culture media containing 150 μ L RPMI 1640 supplemented with 20% FBS (see *Mol. Cancer Ther.*, **2016**, 15(5), 938-945 and *Mol. Cancer Ther.*, **2018**, 17(8), 1752-1760). Serial dilutions of free drugs or antibody-drug conjugates (final concentration between 0.004nM and 1 μ M) in cell culture media were prepared at 4x working

concentrations; 50 μ L of each dilution was added to the 96-well plates. Following addition of the drug or ADC, the cells were incubated with test articles (free drugs or ADCs) for 4 d at 37 °C. After 96 h, growth inhibition was assessed by CellTiter-Glo® (Promega, Madison, WI) and luminescence was measured on a plate reader (brand, model). The IC₅₀ values, determined in triplicate, are defined herein as the concentration that results in a 50% reduction in cell growth relative to untreated controls.

(A) Anthracycline free drugs

[0447] Cells were treated for 96 hours with anthracycline analogues listed in Table 2, and then assessed for viability as described in the procedures as described above. The IC₅₀ ranges are as follows: A denotes IC₅₀ < 10 nM; B denotes 10 nM $\leq$ IC₅₀ < 100 nM; C denotes 100 nM $\leq$ IC₅₀ < 1000 nM; D denotes IC₅₀ $\geq$ 1000 nM. ND denotes value not determined with that assay for the specified compound.

TABLE 2.

| Compound No. | Drug | IC ₅₀ (nM) | | | | |
|--------------|--------------------------|-----------------------|-----------------|---------------|-----------|-------------------|
| | | L540cy, HL | 786-O, MDR+ RCC | BxPC3, PancCa | HL60, AML | HL60/RV, MDR+ AML |
| 1 | DOX | B | B | C | B | C |
| 2 | DOX-COOH | D | D | D | D | D |
| 3 | Nemorubicin | A | A | A | ND | ND |
| 4 | Nemorubicin-COOH | B | B | B | ND | ND |
| 5 | PNU-159682 | A | A | A | A | A |
| 6 | PNU-COOH | A | A | B | B | B |
| 9 | PNU-EDA | A | A | A | A | C |
| -- | PNU-EDA-Gly ₃ | B | B | B | B | C |

[0448] Doxorubicin (**1**) displayed cytotoxic activity on the cancer lines tested with IC₅₀ values in the range of 13-390 nM. Oxidation of doxorubicin to form the carboxylic acid derivative (DOX-COOH, **2**) resulted in complete loss of cytotoxic activity wherein the IC₅₀s are $\geq$ 1000 nM. Nemorubicin (**3**), which displayed 2-3 nM potency, lost roughly one order of magnitude in potency

upon oxidation to the corresponding nemorubicin-COOH derivative (**4**). PNU-159682 (**5**) was the most potent analogue tested with IC₅₀s around 0.01 nM for most of the cell lines tested, and the lowest in the case of 786-O with an IC₅₀ value of <0.004 nM. Oxidation of PNU-159682 to the carboxylic acid derivative (PNU-COOH, **6**) reduced potency slightly to the range of 5-19 nM. Elaboration of the PNU-COOH derivative by amide coupling to an ethylene diamine linker yielded the PNU-EDA derivative (**9**), which has an increased potency in 4 of 5 cell lines relative to PNU-159682. Further elaboration of Compound **9** with a glycine tripeptide (PNU-EDA-Gly₃, commercially available), however, led to a reduced potency relative to **9**, with IC₅₀s ranging from 13-890 nM.

(B) In vitro assays – anthracycline ADCs.

[0449] ADCs were prepared by full reduction of interchain disulfides to reveal 8-conjugatable cysteines/antibody, and subsequent alkylation with the maleimide-containing drug-linkers (Compounds **14**, **18**, **21**, **24**, **29**, **32**, **33**, **34**, and **48**) according to the procedures described in *Mol. Cancer Ther.* 2018, 17(8). 1752-1760. Conjugates of antibody cOKT9 were prepared with anthracycline linkers. Cancer cell lines were treated with cOKT9 ADCs (average DAR of 8:1) for 96 h and then assessed for viability. The IC₅₀s are shown in Table 3. The IC₅₀ ranges are as follows: A denotes IC₅₀ < 10 ng/mL; B denotes 10 ng/mL ≤ IC₅₀ < 100 ng/mL; C denotes 100 ng/mL ≤ IC₅₀ < 1000 ng/mL; D denotes IC₅₀ ≥ 1000 ng/mL. ND denotes value not determined with that assay for the specified compound.

TABLE 3.

| cOKT9 ADCs
No. | Drug linker | IC ₅₀ (ng/mL) | | | | |
|-------------------|-------------------------------|--------------------------|-----------------------|------------------|--------------|----------------------|
| | | L540cy,
HL | 786-O,
MDR+
RCC | BxPC3,
PancCa | HL60,
AML | HL60/RV,
MDR+ AML |
| 24 | VA-EDA-PNU | A | B | A | B | B |
| 32 | VA-DMED-PNU | B | C | B | B | C |
| 29 | VA-Gly ₃ -EDA-PNU | A | B | A | B | D |
| 18 | mp-Gly ₃ -EDA-PNU | A | A | A | B | D |
| 14 | mp-EDA-PNU | A | A | A | C | D |
| 21 | mp-PEG ₄ -PNU | A | A | A | C | D |
| 33 | mp-Gly ₃ -EDA-Nemo | D | D | D | D | D |
| 34 | mp-EDA-Nemo | D | D | D | ND | ND |
| 48 | mp-VAG-EDA-PNU | A | B | A | ND | ND |

[0450] The results summarized in Table 3 show that, the conjugates bearing nemorubicin linkers **33** & **34** were inactive across the panel of cancer cell lines tested. In contrast, conjugates bearing PNU drug-linkers **24**, **32**, **29**, **18**, **14**, and **21** were active on L540cy, 786-O, BxPC3, and HL60 cell lines, and conjugate **48** was active on L540cy, 786-O, and BxPC3, with IC₅₀s ranging from 1-150 ng/ml. On the multidrug resistant HL60/RV cell line, only the conjugates bearing PNU drug-linkers **24** and **32** were active.

[0451] Anti-CD30 ADCs comprising cAC10 antibody conjugated to drug-linkers **24**, **32**, **29**, **18**, **14**, and **48** with an average DAR of 4 were prepared for evaluation on a CD30-expressing lymphoma cell line panel. As shown in the data summarized in Table 4, the conjugate bearing doxorubicin linker **33** was inactive with IC₅₀ values > 20,000 ng/ml, the highest dose tested. Anti-CD30 conjugates bearing the PNU linkers **24**, **32**, **29**, **18**, and **14** were active on L540cy, DEL, and Karpas299 lymphoma cell lines, and conjugate **48** was active on L540cy and DEL cell lines, with IC₅₀s ranging from 0.2-4 ng/mL. On the multidrug resistant L428 lymphoma cell line, anti-CD30 conjugates containing PNU linkers **32**, **18**, and **14** displayed activity with IC₅₀s ranging from 3-610 ng/ml. All anti-CD30 PNU conjugates appeared to possess immunological specificity, wherein the IC₅₀s are generally 1-2 log units lower on CD30-negative Ramos NHL cell line as compared to the CD30 positive cell lines. The IC₅₀ ranges are as follows: A denotes IC₅₀ < 1 ng/mL; B denotes 1 ng/mL ≤ IC₅₀ < 10 ng/mL; C denotes 10 ng/mL ≤ IC₅₀ < 100 ng/mL; D denotes 100 ng/mL ≤ IC₅₀ < 500 ng/mL; E denotes IC₅₀ ≥ 500 ng/mL.

TABLE 4.

| cAC10
ADC No. | Drug linker | IC ₅₀ (ng/mL) | | | | |
|------------------|----------------------------------|--------------------------|------------------|--------------|--------------------|---------------------|
| | | L540cy,
HL | L428,
MDR+ HL | DEL,
ALCL | Karpas299,
ALCL | Ramos,
CD30- NHL |
| 24 | VA-EDA-PNU | B | E | A | B | D |
| 32 | VA-DMED-PNU | C | E | B | B | D |
| 29 | VA-Gly ₃ -EDA-
PNU | B | E | A | A | E |
| 18 | mp-Gly ₃ -EDA-
PNU | B | D | A | A | D |
| 14 | mp-EDA-PNU | B | B | B | A | E |
| 48 | mp-VAG-EDA-
PNU | A | ND | A | ND | ND |

In vivo xenograft models

[0452] All experiments were conducted in concordance with the Animal Care and Use Committee in a facility fully accredited by the Association for Assessment and Accreditation of Laboratory Animal Care. Efficacy experiments were conducted using the L540cy Hodgkin's lymphoma and DEL/BVR anaplastic large cell lymphoma xenograft models (*Mol. Cancer Ther.*, **2018**, 17(8), 1752-1760). Tumor cells, as a cell suspension, were implanted subcutaneously in immune-compromised SCID female mice. Upon tumor engraftment, the mice were randomized into study groups when the average tumor volume reached about 100 mm³. The ADCs were dosed once via intraperitoneal injection. Tumor volume as a function of time was determined using the formula $(L \times W^2)/2$. Animals were euthanized when tumor volumes reached 1000 mm³.

(A) L540cy CD30+ Hodgkin lymphoma xenograft model

[0453] Anti-CD30 conjugates bearing PNU drug-linkers **29**, **18**, and **14** were evaluated in a CD30-expressing xenograft model as described above. cAC10 antibody with the S239C mutation is conjugated to the PNU drug linkers with an average DAR of 2 to minimize the effects of ADC pharmacokinetics. Tumor-bearing mice were administered a single dose intraperitoneally (i.p.) of test article once the average tumor volume reached 100 mm³ (typically on day 8). All three test articles were active with a majority of animals in a complete regression as shown in Figure 1. Untreated mice were used as negative controls.

(B) DEL/BVR MDR+, CD30+ anaplastic large cell lymphoma

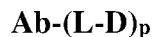
[0454] Anti-CD30 conjugates bearing PNU drug-linkers **29**, **18**, and **14** were further evaluated in a DEL/BVR MDR+, CD30+ anaplastic large cell lymphoma xenograft model. cAC10 antibody with the S239C mutation is conjugated to the PNU drug linkers with an average DAR of 2 to minimize the effects of ADC pharmacokinetics. Tumor-bearing mice were administered a 3 mg/kg single dose intraperitoneally (i.p.) of test article once the average tumor volume reached 100 mm³ (typically on day 4). Conjugates bearing PNU linkers **18** and **14** were shown to be efficacious in suppressing tumor growth, wherein almost all animals were in durable, complete regression at 18 days post treatment. However, the conjugate comprising PNU linker **29** appeared to be non-efficacious, and only provided minimal tumor growth delay (Figure 2). Untreated mice were used as negative controls.

[0455] The contents of each of the references cited in the present disclosure are hereby incorporated by reference in their entirety.

[0456] A number of embodiments of the present disclosure have been described. Nevertheless, it will be understood that various modifications may be made without departing from the spirit and scope of the disclosure. Accordingly, other embodiments are within the scope of the following claims.

WHAT IS CLAIMED IS:

1. An antibody drug conjugate (ADC) having the structure:



or a salt thereof;

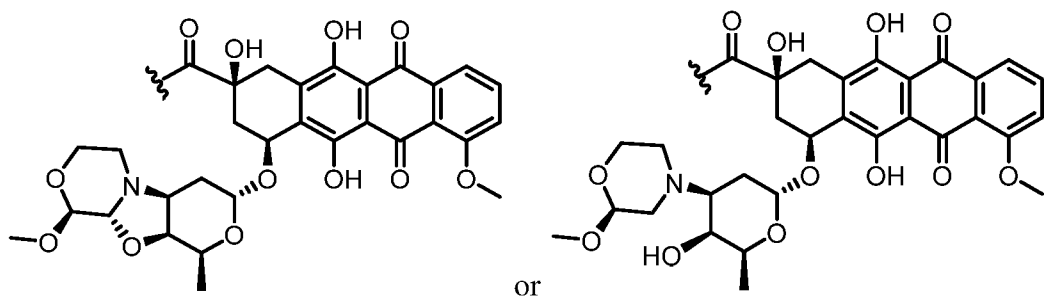
wherein:

Ab is an antibody;

wherein each L is covalently attached to Ab via a sulfur atom of a cysteine residue or an ϵ -amino group of a lysine residue in Ab;

subscript p is an integer from 1 to 16;

each D is:



wherein  represents covalent attachment to L;

each L has the formula $-\text{M}-(\text{A})_a-(\text{W})_w-(\text{Y})_y-(\text{X})-$, wherein:

M is a succinimide, a hydrolyzed succinimide, an amide, or a triazole, wherein M is covalently attached to Ab;

subscript a is 0 or 1;

subscript y is 0 or 1;

subscript w is 0 or 1;

A is a C_{2-10} alkylene optionally substituted with 1-3 R^{al} ; or a 3 to 20 membered heteroalkylene optionally substituted with 1-3 R^{bl} ;

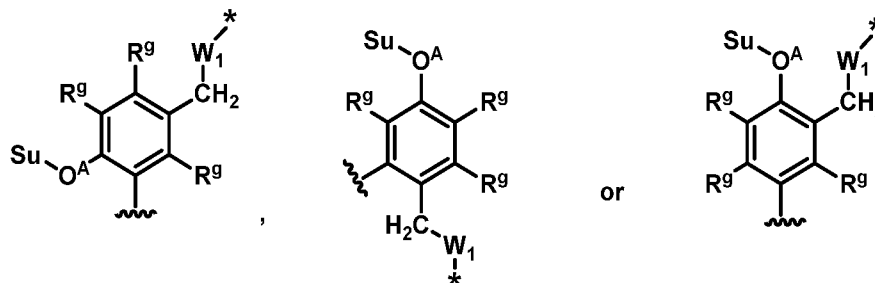
each R^{al} is independently selected from the group consisting of: C_{1-6} alkyl, C_{1-6} haloalkyl, C_{1-6} alkoxy, C_{1-6} haloalkoxy, halogen, $-\text{OH}$, $=\text{O}$, $-\text{NR}^{\text{dl}}\text{R}^{\text{el}}$, $-(\text{C}_{1-6} \text{ alkylene})-\text{NR}^{\text{dl}}\text{R}^{\text{el}}$, $-\text{C}(=\text{O})\text{NR}^{\text{dl}}\text{R}^{\text{el}}$, $-\text{C}(=\text{O})(\text{C}_{1-6} \text{ alkyl})$, and $-\text{C}(=\text{O})\text{O}(\text{C}_{1-6} \text{ alkyl})$;

each R^{b1} is independently selected from the group consisting of: C_{1-6} alkyl, C_{1-6} haloalkyl, C_{1-6} alkoxy, C_{1-6} haloalkoxy, halogen, $-OH$, $-NR^{d1}R^{e1}$, $-(C_{1-6} \text{ alkylene})-NR^{d1}R^{e1}$, $-C(=O)NR^{d1}R^{e1}$, $-C(=O)(C_{1-6} \text{ alkyl})$, and $-C(=O)O(C_{1-6} \text{ alkyl})$;

each R^{d1} and R^{e1} are independently hydrogen or C_{1-3} alkyl;

W is from 1-6 amino acids; or

W has the structure:



wherein Su is a Sugar moiety;

$-O^A$ represents the oxygen atom of a glycosidic bond;

each R^g is independently hydrogen, halogen, C_{1-6} alkoxy, $-N(C_{1-6} \text{ alkyl})_2$, $-NHC(=O)(C_{1-6} \text{ alkyl})$, $-CN$, $-CF_3$, acyl, carboxamido, C_{1-6} alkyl, or $-NO_2$;

W^1 is absent, $*-C(=O)-O-$, or $*-O-C(=O)-$;

represents covalent attachment to A or M;

* represents covalent attachment to Y or X;

Y is a self-immolative moiety, a non-self-immolative releasable moiety, or a non-cleavable moiety;

X is a 4-16 membered heteroalkylene, wherein X is optionally substituted with 1-3 independently selected R^X ;

each R^X is independently a C_{2-6} alkynyl group, $-NR^{X1}R^{X2}$, or a C_{1-6} alkyl group optionally substituted with hydroxyl, $-NR^{X1}R^{X2}$, guanidino, 1 or 2 $-CO_2H$ groups, $-C(=O)NR^{X1}R^{X2}$, urea, phenyl, naphthyl, indolyl, imidazolyl, $-SH$, $-SCH_3$, $-SeCH_3$, or 4-hydroxyphenyl optionally substituted with C_{2-6} alkenyl; or

two R^X attached to the same or adjacent carbon atom(s) of X, together with the carbon atom(s) to which they are attached form an unsubstituted 5-6 membered heterocyclyl;

each R^{X1} and R^{X2} are independently hydrogen or C_{1-6} alkyl; and

L is optionally substituted with a PEG Unit from PEG1 to PEG72.

2. The ADC of claim 1, wherein M is a succinimide.
3. The ADC of claim 1, wherein M is a hydrolyzed succinimide.
4. The ADC of claim 1, wherein M is an amide.
5. The ADC of claim 1, wherein M is a triazole.
6. The ADC of any one of claims 1-5, wherein subscript a is 1.
7. The ADC of any one of claims 1-6, wherein A is C₂₋₁₀ alkylene optionally substituted with 1-3 R^{al}.
8. The ADC of any one of claims 1-7, wherein A is C₂₋₁₀ alkylene substituted with 1-3 R^{al}.
9. The ADC of any one of claims 1-8, wherein A is C₂₋₁₀ alkylene substituted with one R^{al}.
10. The ADC of any one of claims 1-9, wherein A is C₄₋₁₀ alkylene substituted with one R^{al}.
11. The ADC of any one of claims 1-7, wherein A is unsubstituted C₂₋₁₀ alkylene.
12. The ADC of any one of claims 1-6, wherein A is a 3 to 20 membered heteroalkylene optionally substituted with 1-3 R^{bl}.
13. The ADC of any one of claims 1-6 or 12, wherein A is a 4 to 12 membered heteroalkylene optionally substituted with 1-3 R^{bl}.

14. The ADC of any one of claims 1-6 or 12-13, wherein A is a 3 to 20 membered heteroalkylene substituted with one R^{b1}.

15. The ADC of any one of claims 1-6 or 12-14, wherein A is a 4 to 12 membered heteroalkylene substituted with one R^{b1}.

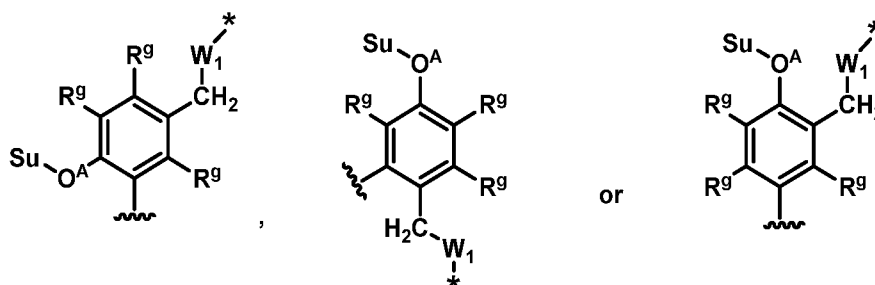
16. The ADC of any one of claims 1-6 or 12, wherein A is an unsubstituted 3 to 20 membered heteroalkylene.

17. The ADC of any one of claims 1-6, wherein A is selected from $-(CH_2)_{1-6}-$, $-C(O)(CH_2)_{1-6}-\#$, $-[NHC(O)(CH_2)_{1-4}]_{1-3}-\#$, and $-NH(CH_2)_{1-6}[NHC(O)(CH_2)_{1-4}]_{1-2}-\#$, wherein # indicates attachment to M.

18. The ADC of any one of claims 1-5, wherein subscript a is 0.

19. The ADC of any one of claims 1-18, wherein subscript w is 1.

20. The ADC of any one of claims 1-19, wherein W has the structure:



wherein Su is a Sugar moiety;

$-O^A-$ represents the oxygen atom of a glycosidic bond;

each R^g is independently hydrogen, halogen, C₁-C₆ alkoxy, $-N(C_1-C_6 \text{ alkyl})_2$, $-NHC(=O)(C_1-C_6 \text{ alkyl})$, $-CN$, $-CF_3$, acyl, carboxamido, C₁-C₆ alkyl, or $-NO_2$;

W¹ is absent, $*-C(=O)-O-$, or $*-O-C(=O)-$;

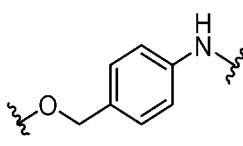
~~~~~ represents covalent attachment to A or M; and

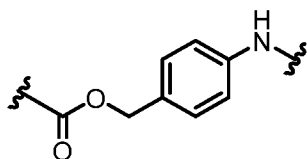
\* represents covalent attachment to Y or X.

21. The ADC of any one of claims 1-20, wherein  $W^1$  is absent.
22. The ADC of any one of claims 1-20, wherein  $W^1$  is  $^*-C(=O)-O-$ .
23. The ADC of any one of claims 1-20, wherein  $W^1$  is  $^*-O-C(=O)-$ .
24. The ADC of any one of claims 1-23, wherein one  $R^g$  is halogen,  $C_1-C_6$  alkoxy,  $-N(C_1-C_6 \text{ alkyl})_2$ ,  $-NHC(=O)(C_1-C_6 \text{ alkyl})$ ,  $-CN$ ,  $-CF_3$ , acyl, carboxamido,  $C_1-C_6$  alkyl, or  $-NO_2$ , and the remaining  $R^g$  are hydrogen.
25. The ADC of any one of claims 1-23, wherein each  $R^g$  is hydrogen.
26. The ADC of any one of claims 1-19, wherein  $W$  is from 2-6 amino acids.
27. The ADC of any one of claims 1-19, wherein  $W$  is from 1-3 amino acids.
28. The ADC of any one of claims 1-19 or 26-27, wherein each amino acid in  $W$  is independently selected from the group consisting of alanine, glycine, lysine, serine, aspartic acid, aspartate methyl ester, N,N-dimethyl-lysine, phenylalanine, citrulline, valine, asparagine, homoserine methyl ether, isoleucine, leucine, glutamic acid, histidine, arginine, threonine, O-methylserine, O-methylaspartic acid, O-methylglutamic acid, N-methyllysine, O-methyltyrosine, O-methylhistidine, and O-methylthreonine.
29. The ADC of any one of claims 1-19 or 26-28, wherein  $W$  is a dipeptide.
30. The ADC of claim 27, wherein  $W$  is not  $-Gly-Gly-$ ,  $-Val-Ala-$ ,  $-Val-Cit-$ , or  $-Asp-Ala-$ .
31. The ADC of any one of claims 1-19 or 26-28, wherein  $W$  is a tripeptide.
32. The ADC of claim 31, wherein  $W$  is not tri-glycine.
33. The ADC of any one of claims 1-19 or 26-28, wherein  $W$  is a tetrapeptide.



34. The ADC of claim 33, wherein W is not tetra-glycine.
35. The ADC of any one of claims 1-19 or 26-28, wherein W is a pentapeptide.
36. The ADC of claim 35, wherein W is not penta-glycine.
37. The ADC of any one of claims 1-19 or 26-28, wherein W is a hexapeptide.
38. The ADC of claim 37, wherein W is not hexa-glycine.
39. The ADC of any one of claims 1-19 or 26-38, wherein W is not a sortase recognition motif.
40. The ADC of claim 39, wherein W is not -Leu-Pro-\*\*-Thr-Gly-, -Gly-Thr-\*\*-Pro-Leu-, -Gly-Ser-\*\*-Pro-Leu-, -Gly-Thr-\*\*-Ala-Leu-, -Gly-Thr-\*\*-Pro-Leu-, -Gly-Ser-\*\*-Pro-Leu-, -Gly-Thr-\*\*-Ala-Leu-, -Thr-\*\*-Pro-Leu-, -Ser-\*\*-Pro-Leu-, -Thr-\*\*-Ala-Leu-, -Thr-\*\*-Pro-Leu-, -Ser-\*\*-Pro-Leu-, -Thr-\*\*-Ala-Leu-, or -Gln-Pro-Gln-Thr-Asp-; wherein \*\* is any natural amino acid.
41. The ADC of claim 40, wherein W is not -Lys-Pro-Gly-Thr-Gly- or -Asp-Pro-Gln-Thr-Gln-.
42. The ADC of any one of claims 1-18, wherein subscript w is 0.
43. The ADC of any one of claims 1-42, wherein subscript y is 1.
44. The ADC of any one of claims 1-43, wherein Y is a self-immolative moiety.

45. The ADC of any one of claims 1-44, wherein Y is  or



46. The ADC of any one of claims 1-43, wherein Y is a non-cleavable moiety.
47. The ADC of any one of claims 1-43 or 46, wherein Y is a cyclohexanecarboxyl, undecanoyl, caproyl, hexanoyl, butanoyl, or propionyl group.
48. The ADC of any one of claims 1-43 or 46, wherein Y is PEG4 to PEG12.
49. The ADC of any one of claims 1-42, wherein subscript y is 0.
50. The ADC of any one of claims 1-49, wherein X is a 4-16 membered heteroalkylene optionally substituted with 1-3 independently selected  $R^X$ .
51. The ADC of any one of claims 1-50, wherein X is a 4-12 membered heteroalkylene optionally substituted with 1-3 independently selected  $R^X$ .
52. The ADC of any one of claims 1-51, wherein X is a 4-8 membered heteroalkylene optionally substituted with 1-3 independently selected  $R^X$ .
53. The ADC of any one of claims 1-50, wherein X is a 4-16 membered heteroalkylene substituted with 1 or 2 independently selected  $R^X$ .
54. The ADC of any one of claims 1-51, wherein X is a 4-12 membered heteroalkylene substituted with 1 or 2 independently selected  $R^X$ .

55. The ADC of any one of claims 1-54, wherein X is a 4-8 membered heteroalkylene substituted with 1 or 2 independently selected  $R^X$ .

56. The ADC of any one of claims 1-50, wherein X is a 4-16 membered heteroalkylene substituted with 1  $R^X$ .

57. The ADC of any one of claims 1-51, wherein X is a 4-12 membered heteroalkylene substituted with 1  $R^X$ .

58. The ADC of any one of claims 1-57, wherein X is a 4-8 membered heteroalkylene substituted with 1  $R^X$ .

59. The ADC of any one of claims 1-58, wherein each  $R^X$  is independently a  $C_2$ - $C_6$  alkynyl group,  $-NR^{X1}R^{X2}$ , or a  $C_1$ - $C_6$  alkyl group optionally substituted with hydroxyl,  $-NR^{X1}R^{X2}$ , guanidino, 1 or 2  $-CO_2H$  groups,  $-C(=O)NR^{X1}R^{X2}$ , urea, phenyl, naphthyl, indolyl, imidazolyl,  $-SH$ ,  $-SCH_3$ ,  $-SeCH_3$ , or 4-hydroxyphenyl optionally substituted with  $C_2$ - $C_6$  alkenyl; and

60. each  $R^{X1}$  and  $R^{X2}$  are independently hydrogen or  $C_{1-6}$  alkyl.

61. The ADC of any one of claims 1-59, wherein one  $R^X$  is a  $C_1$ - $C_6$  alkyl group optionally substituted with hydroxyl,  $-NR^{X1}R^{X2}$ , guanidino, 1 or 2  $-CO_2H$  groups,  $-C(=O)NR^{X1}R^{X2}$ , urea, phenyl, naphthyl, indolyl, imidazolyl,  $-SH$ ,  $-SCH_3$ ,  $-SeCH_3$ , or 4-hydroxyphenyl optionally substituted with  $C_2$ - $C_6$  alkenyl.

62. The ADC of any one of claims 1-60, wherein one  $R^X$  is a  $C_1$ - $C_6$  alkyl group substituted with hydroxyl,  $-NR^{X1}R^{X2}$ , guanidino, 1 or 2  $-CO_2H$  groups,  $-C(=O)NR^{X1}R^{X2}$ , urea, phenyl, naphthyl, indolyl, imidazolyl,  $-SH$ ,  $-SCH_3$ ,  $-SeCH_3$ , or 4-hydroxyphenyl optionally substituted with  $C_2$ - $C_6$  alkenyl.

63. The ADC of any one of claims 1-61, wherein one  $R^X$  is a  $C_1$ - $C_6$  alkyl group substituted with hydroxyl.

64. The ADC of any one of claims 1-61, wherein one R<sup>X</sup> is a C<sub>1</sub>-C<sub>6</sub> alkyl group substituted with guanidino.

65. The ADC of any one of claims 1-61, wherein one R<sup>X</sup> is a C<sub>1</sub>-C<sub>6</sub> alkyl group substituted with 1 or 2 -CO<sub>2</sub>H groups.

66. The ADC of any one of claims 1-61 or 64, wherein one R<sup>X</sup> is a C<sub>1</sub>-C<sub>6</sub> alkyl group substituted with 1 -CO<sub>2</sub>H group.

67. The ADC of any one of claims 1-61 or 64, wherein one R<sup>X</sup> is a C<sub>1</sub>-C<sub>6</sub> alkyl group substituted with 2 -CO<sub>2</sub>H groups.

68. The ADC of any one of claims 1-61, wherein one R<sup>X</sup> is a C<sub>1</sub>-C<sub>6</sub> alkyl group substituted with urea.

69. The ADC of any one of claims 1-61, wherein one R<sup>X</sup> is a C<sub>1</sub>-C<sub>6</sub> alkyl group substituted with phenyl.

70. The ADC of any one of claims 1-61, wherein one R<sup>X</sup> is a C<sub>1</sub>-C<sub>6</sub> alkyl group substituted with naphthyl.

71. The ADC of any one of claims 1-61, wherein one R<sup>X</sup> is a C<sub>1</sub>-C<sub>6</sub> alkyl group substituted with indolyl.

72. The ADC of any one of claims 1-61, wherein one R<sup>X</sup> is a C<sub>1</sub>-C<sub>6</sub> alkyl group substituted with imidazolyl.

73. The ADC of any one of claims 1-61, wherein one R<sup>X</sup> is a C<sub>1</sub>-C<sub>6</sub> alkyl group substituted with -SH, -SCH<sub>3</sub>, or -SeCH<sub>3</sub>.

74. The ADC of any one of claims 1-61, wherein one R<sup>X</sup> is a C<sub>1</sub>-C<sub>6</sub> alkyl group substituted with 4-hydroxyphenyl optionally substituted with C<sub>2</sub>-C<sub>6</sub> alkenyl.

75. The ADC of any one of claims 1-61, wherein one  $R^X$  is a  $C_1$ - $C_6$  alkyl group substituted with  $-C(=O)NR^{X1}R^{X2}$ .

76. The ADC of any one of claims 1-61, wherein one  $R^X$  is a  $C_1$ - $C_6$  alkyl group substituted with  $-NR^{X1}R^{X2}$ .

77. The ADC of any one of claims 1-58, wherein one  $R^X$  is  $-NR^{X1}R^{X2}$ .

78. The ADC of any one of claims 1-61 or 74-76, wherein  $R^{X1}$  and  $R^{X2}$  are each independently  $C_{1-6}$  alkyl.

79. The ADC of any one of claims 1-60 or 74-77, wherein  $R^{X1}$  and  $R^{X2}$  are each methyl.

80. The ADC of any one of claims 1-61 or 74-76, wherein  $R^{X1}$  and  $R^{X2}$  are each hydrogen.

81. The ADC of any one of claims 1-76, wherein one of  $R^{X1}$  and  $R^{X2}$  is hydrogen and the other of  $R^{X1}$  and  $R^{X2}$  is  $C_{1-6}$  alkyl.

82. The ADC of any one of claims 1-76 or 80, wherein one of  $R^{X1}$  and  $R^{X2}$  is hydrogen and the other of  $R^{X1}$  and  $R^{X2}$  is methyl.

83. The ADC of any one of claims 1-59, wherein one  $R^X$  is a  $C_2$ - $C_6$  alkynyl group.

84. The ADC of any one of claims 1-55, wherein X is substituted with two  $R^X$ ; wherein each  $R^X$  is an independently selected unsubstituted  $C_1$ - $C_6$  alkyl group.

85. The ADC of any one of claims 1-55, wherein X is substituted with two  $R^X$ ; wherein the two  $R^X$  are attached to the same or adjacent carbon atom(s) of X; and the two  $R^X$  together with the carbon atom(s) to which they are attached form an unsubstituted 5-6 membered heterocyclyl.

86. The ADC of any one of claims 1-55 or 84, wherein X is substituted with two R<sup>X</sup>; wherein the two R<sup>X</sup> are attached to adjacent carbon atom(s) of X; and the two R<sup>X</sup> together with the carbon atom(s) to which they are attached form an unsubstituted 5-6 membered heterocyclyl.

87. The ADC of any one of claims 1-55 or 84-85, wherein X is substituted with two R<sup>X</sup>; wherein the two R<sup>X</sup> are attached to adjacent carbon atom(s) of X; and the two R<sup>X</sup> together with the carbon atom(s) to which they are attached form an unsubstituted pyrrolidine.

88. The ADC of any one of claims 1-55 or 84, wherein X is substituted with two R<sup>X</sup>; wherein the two R<sup>X</sup> are attached to the same carbon atom of X; and the two R<sup>X</sup> together with the carbon atom to which they are attached form an unsubstituted 5-6 membered heterocyclyl.

89. The ADC of any one of claims 1-59, wherein X is substituted with one R<sup>X</sup>; wherein R<sup>X</sup> is an unsubstituted C<sub>1</sub>-C<sub>6</sub> alkyl group.

90. The ADC of any one of claims 1-50, wherein X is -NH(C<sub>2</sub>-C<sub>6</sub> alkylene)NH- optionally substituted with C<sub>1</sub>-C<sub>6</sub> alkyl.

91. The ADC of any one of claims 1-50, wherein X is -NH(C<sub>2</sub>-C<sub>3</sub> alkylene)NH- optionally substituted with C<sub>1</sub>-C<sub>6</sub> alkyl.

92. The ADC of any one of claims 1-50, wherein X is -NH(C<sub>2</sub>-C<sub>6</sub> alkylene)NH- optionally substituted with two independently selected C<sub>1</sub>-C<sub>6</sub> alkyl groups.

93. The ADC of any one of claims 1-50, wherein X is -NH(C<sub>2</sub>-C<sub>3</sub> alkylene)NH- optionally substituted with two independently selected C<sub>1</sub>-C<sub>6</sub> alkyl groups.

94. The ADC of any one of claims 1-50, wherein X is ##-NH(C<sub>2</sub>-C<sub>6</sub> alkylene)NH-(PEG2 to PEG4)-, wherein ## indicates attachment to D.

95. The ADC of any one of claims 1-50, wherein X is ##-NH(C<sub>2</sub>-C<sub>6</sub> alkylene)-, wherein ## indicates attachment to D.

96. The ADC of any one of claims 1-50, wherein X is ##-NH(C<sub>2</sub>-C<sub>6</sub> alkylene)-(PEG2 to PEG4)-, wherein ## indicates attachment to D.

97. The ADC of any one of claims 1-50, wherein X is ##-NH(C<sub>2</sub>-C<sub>6</sub> alkylene)NH-[(C(O)CH<sub>2</sub>NH)]<sub>1-2</sub>- or ##-NH(C<sub>2</sub>-C<sub>6</sub> alkylene)NH-[(C(O)CHR<sup>X</sup>NH)]<sub>1-3</sub>-, wherein R<sup>X</sup> is C<sub>1-3</sub> alkyl optionally substituted with -OH and ## indicates attachment to D.

98. The ADC of any one of claims 1-50, wherein X is ##-[NHCH<sub>2</sub>C(O)]<sub>1-3</sub>-NH(C<sub>2</sub>-C<sub>6</sub> alkylene)NH- or ##-[NHCHR<sup>X</sup>C(O)]<sub>1-3</sub>-NH(C<sub>2</sub>-C<sub>6</sub> alkylene)NH-, wherein R<sup>X</sup> is C<sub>1-3</sub> alkyl optionally substituted with -OH and ## indicates attachment to D.

99. The ADC of any one of claims 1-50, wherein X is ##-NR<sup>X</sup>(C<sub>2</sub>-C<sub>6</sub> alkylene)NR<sup>X</sup>-, wherein R<sup>X</sup> is C<sub>1-3</sub> alkyl and ## indicates attachment to D.

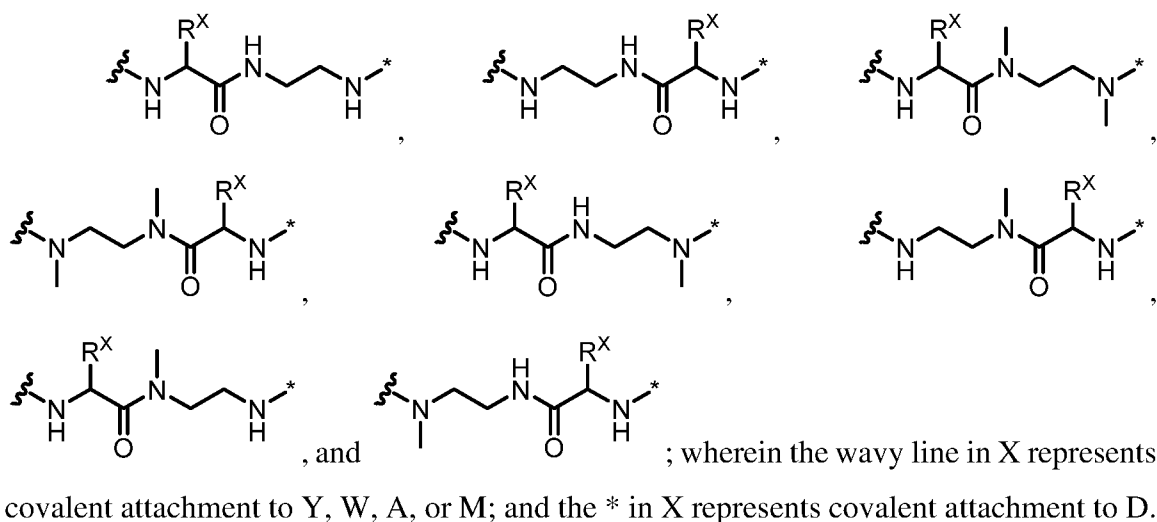
100. The ADC of any one of claims 1-50, wherein X is ##-[NHCH<sub>2</sub>C(O)]<sub>1-3</sub>- or ##-[NHCHR<sup>X</sup>C(O)]<sub>1-3</sub>-, wherein R<sup>X</sup> is C<sub>1-3</sub> alkyl optionally substituted with -OH and ## indicates attachment to D.

101. The ADC of any one of claims 1-50, wherein X is an unsubstituted 4-16 membered heteroalkylene.

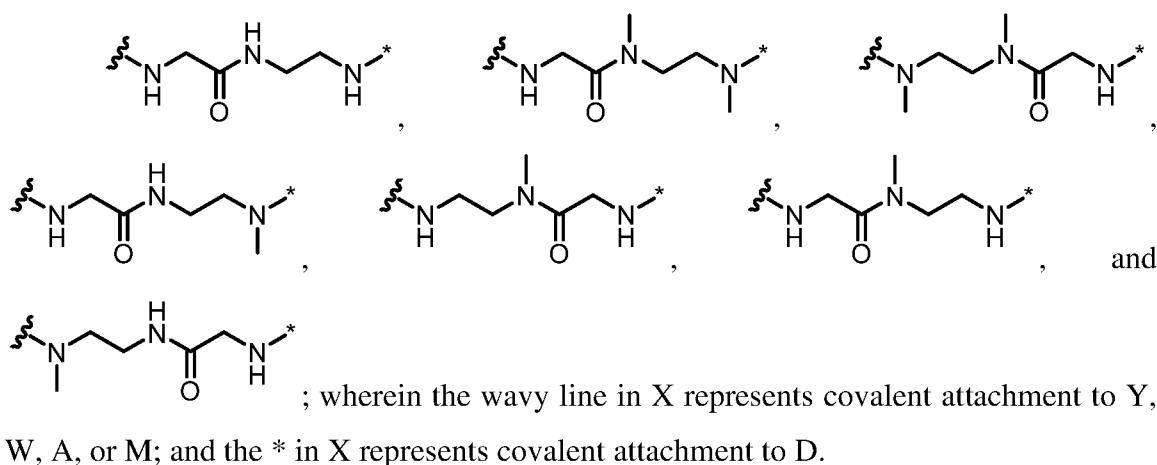
102. The ADC of any one of claims 1-50 or 100, wherein X is an unsubstituted 4-12 membered heteroalkylene.

103. The ADC of any one of claims 1-50 or 100-101, wherein X is an unsubstituted 4-8 membered heteroalkylene.

104. The ADC of any one of claims 1-50, wherein X is selected from the group consisting of:



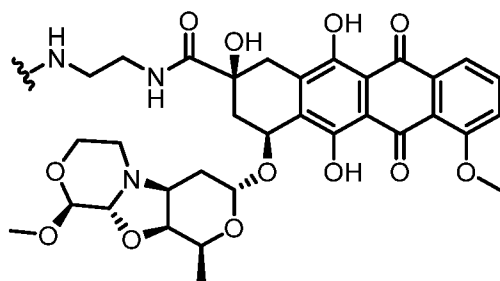
105. The ADC of any one of claims 1-50, wherein X is selected from the group consisting of:



106. The ADC of any one of claims 1-50, wherein X is not ; wherein the wavy line in X represents covalent attachment to Y, W, A, or M; and the \* in X represents covalent attachment to D.

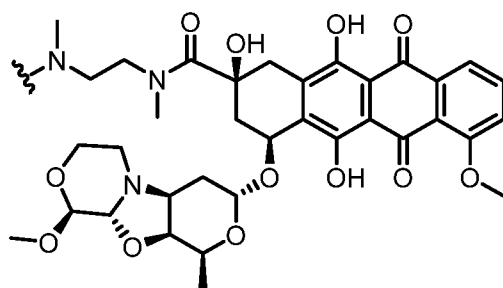
107. The ADC of any one of claims 1-50, wherein each D-X is:





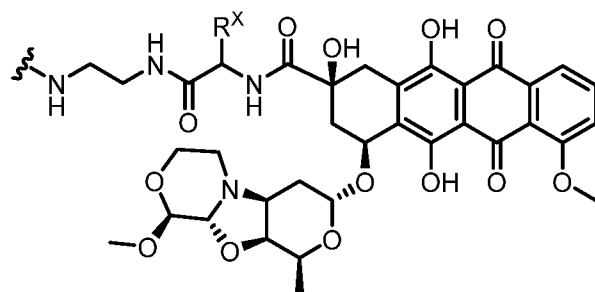
; wherein  represents covalent attachment to Y, W, A, or M.

108. The ADC of any one of claims 1-50, wherein each D-X is:



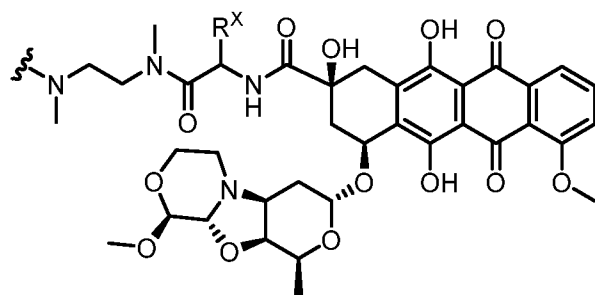
; wherein  represents covalent attachment to Y, W, A, or M.

109. The ADC of any one of claims 1-50, wherein each D-X is:



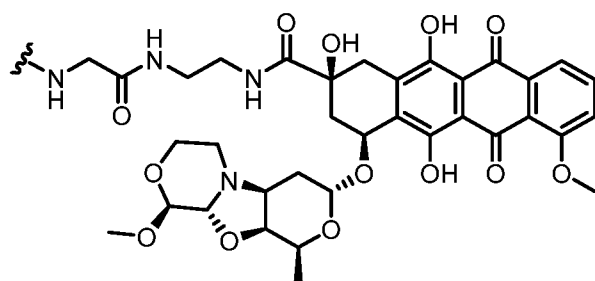
; wherein  represents covalent attachment to Y, W, A, or M.

110. The ADC of any one of claims 1-50, wherein each D-X is:



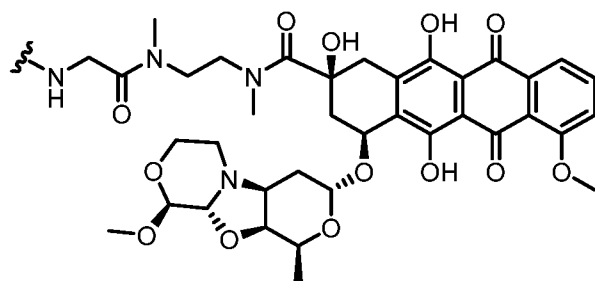
; wherein  represents covalent attachment to Y, W, A, or M.

111. The ADC of any one of claims 1-50, wherein each D-X is:



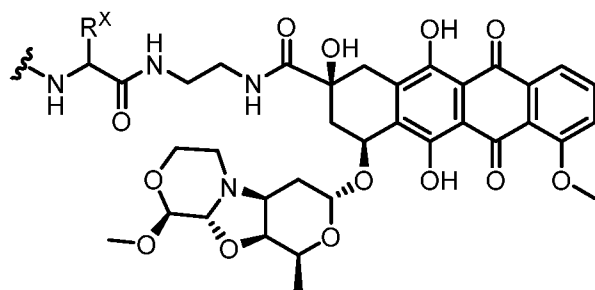
; wherein  represents covalent attachment to Y, W, A, or M.

112. The ADC of any one of claims 1-50, wherein each D-X is:



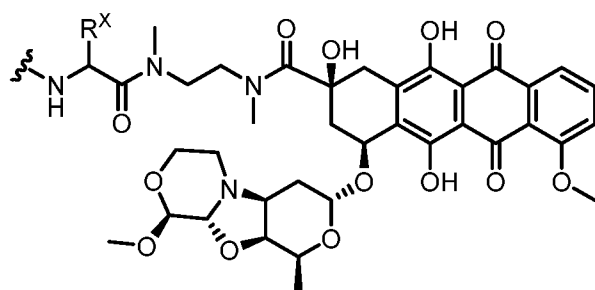
; wherein  represents covalent attachment to Y, W, A, or M.

113. The ADC of any one of claims 1-50, wherein each D-X is:



; wherein  represents covalent attachment to Y, W, A, or M.

114. The ADC of any one of claims 1-50, wherein each D-X is:



; wherein  represents covalent attachment to Y, W, A, or M.

115. The ADC of claim 1, wherein:

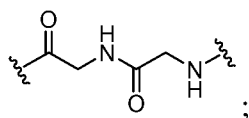
A is a C<sub>2-10</sub> alkylene optionally substituted with 1-3 R<sup>a1</sup>;

each R<sup>a1</sup> is independently selected from the group consisting of: C<sub>1-6</sub> alkyl, C<sub>1-6</sub> haloalkyl, C<sub>1-6</sub> alkoxy, C<sub>1-6</sub> haloalkoxy, halogen, -OH, =O, -NR<sup>d1</sup>R<sup>e1</sup>, -(C<sub>1-6</sub> alkylene)-NR<sup>d1</sup>R<sup>e1</sup>, -C(=O)NR<sup>d1</sup>R<sup>e1</sup>, -C(=O)(C<sub>1-6</sub> alkyl), and -C(=O)O(C<sub>1-6</sub> alkyl);

each R<sup>d1</sup> and R<sup>e1</sup> are independently hydrogen or C<sub>1-3</sub> alkyl;

W is from 2-6 amino acids, wherein:

W is not a sortase enzyme recognition motif, and W does not include



Y is a self-immolative moiety, a non-self-immolative releasable moiety, or a non-cleavable moiety; and

L is optionally substituted with a PEG Unit from PEG1 to PEG72.

116. The ADC of any one of claims 1-114, wherein L is substituted with a PEG Unit from PEG1 to PEG72.

117. The ADC of any one of claims 1-115, wherein A is substituted with a PEG Unit from PEG1 to PEG72.

118. The ADC of any one of claims 1-115, wherein L is not substituted with a PEG Unit from PEG1 to PEG72.

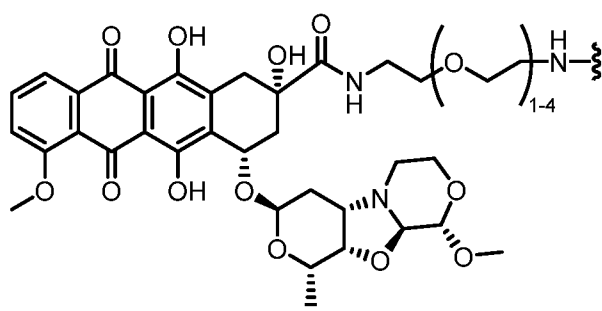
119. The ADC of claim 1, wherein:

subscript y is 0;

subscript w is 0;

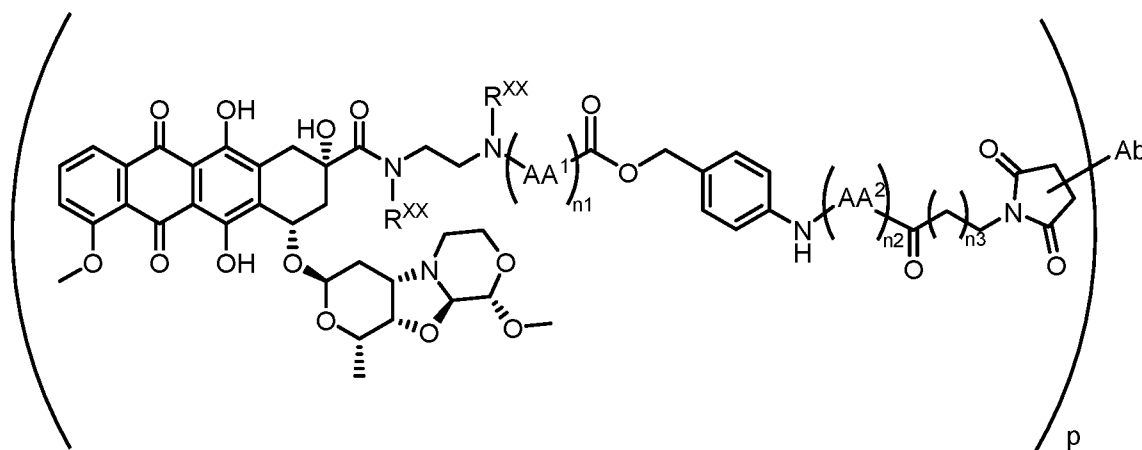
subscript a is 1; and

each D-X is:



wherein  represents covalent attachment to Y, W, A, or M.

120. An ADC having the structure:



wherein:

each R<sup>XX</sup> is independently hydrogen or C<sub>1-3</sub> alkyl;

n<sub>1</sub> is an integer from 0 to 4;

n<sub>2</sub> is an integer from 1 to 4;

n<sub>3</sub> is an integer from 1 to 4;

each AA<sup>1</sup> is independently selected from the group consisting of alanine, glycine, lysine, serine, aspartic acid, aspartate methyl ester, N,N-dimethyl-lysine, phenylalanine, citrulline, valine, asparagine, homoserine methyl ether, isoleucine, leucine, glutamic acid, histidine, arginine, threonine, O-methylserine, O-methylaspartic acid, O-methylglutamic acid, N-methyllysine, O-methyltyrosine, O-methylhistidine, and O-methylthreonine;

each AA<sup>2</sup> is independently selected from the group consisting of alanine, glycine, lysine, serine, aspartic acid, aspartate methyl ester, N,N-dimethyl-lysine, phenylalanine, citrulline, valine, asparagine, homoserine methyl ether, isoleucine, leucine, glutamic acid, histidine, arginine, threonine, O-methylserine, O-methylaspartic acid, O-methylglutamic acid, N-methyllysine, O-methyltyrosine, O-methylhistidine, and O-methylthreonine;

Ab is an antibody; and

p is an integer from 1 to 16.

121. The ADC of claim 121, wherein each AA<sup>1</sup> is independently selected from the group consisting of alanine, glycine, valine, and serine.

122. The ADC of claim 120 or 121, wherein n<sub>1</sub> is 0.

123. The ADC of claim 120 or 121, n<sub>1</sub> is 1.

124. The ADC of claim 120 or 121, n<sub>1</sub> is 2.

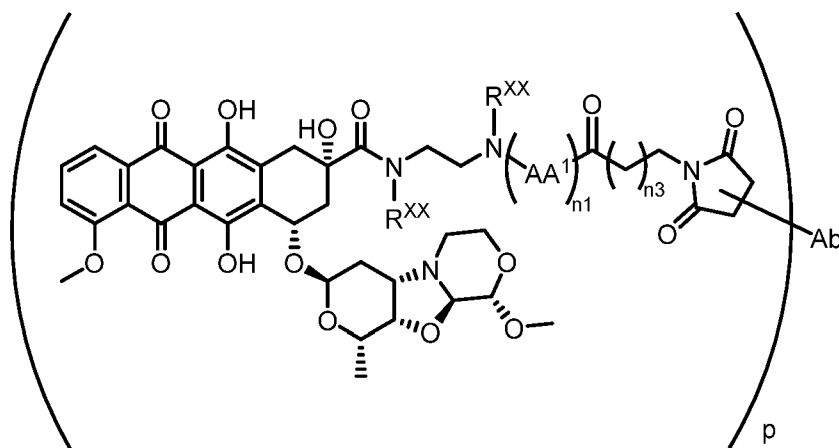
125. The ADC of claim 120 or 121, n<sub>1</sub> is 3.

126. The ADC of any one of claims 120-125, wherein each AA<sup>2</sup> is independently selected from the group consisting of alanine, glycine, valine, serine, leucine, and aspartic acid. In some embodiments, each AA<sup>2</sup> is independently selected from the group consisting of alanine and valine.

127. The ADC of any one of claims 120-126, wherein n<sub>2</sub> is 2.

128. The ADC of claim 127, wherein (AA<sup>2</sup>)<sub>n<sub>2</sub></sub> is -Ala-Val-.

129. An ADC having the structure:



wherein:

each R<sup>XX</sup> is independently hydrogen or C<sub>1-3</sub> alkyl;

n<sub>1</sub> is an integer from 0 to 4;

each AA<sup>1</sup> is independently selected from the group consisting of alanine, glycine, lysine, serine, aspartic acid, aspartate methyl ester, N,N-dimethyl-lysine, phenylalanine, citrulline, valine, asparagine, homoserine methyl ether, isoleucine, leucine, glutamic acid, histidine, arginine, threonine, O-methylserine, O-methylaspartic acid, O-methylglutamic acid, N-methyllysine, O-methyltyrosine, O-methylhistidine, and O-methylthreonine;

n<sub>3</sub> is an integer from 1 to 4;

Ab is an antibody; and

p is an integer from 1 to 16.

130. The ADC of claim 129, wherein  $n_1$  is 0.

131. The ADC of claim 129,  $n_1$  is 1.

132. The ADC of claim 129,  $n_1$  is 2.

133. The ADC of claim 129,  $n_1$  is 3.

134. The ADC of claim 129, wherein when  $n_1$  is 3, at least one  $AA^1$  is not glycine.

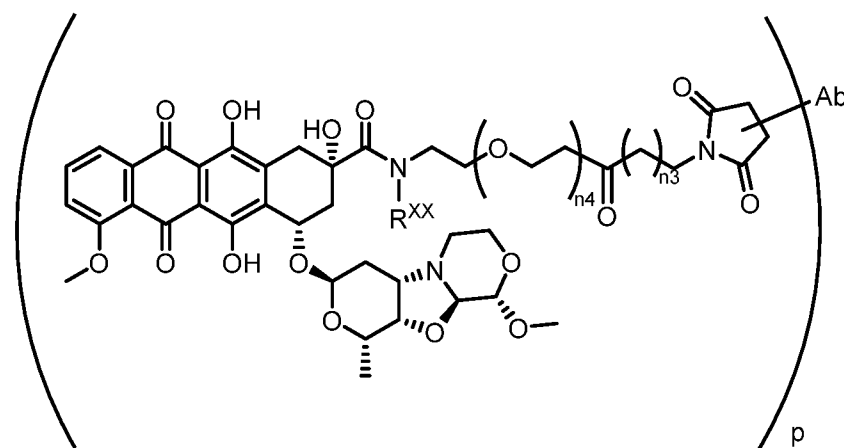
135. The ADC of any one of claims 129-134, wherein each  $AA^1$  is independently selected from the group consisting of alanine, glycine, valine, serine, leucine, arginine, and aspartic acid. In some embodiments, each  $AA^1$  is independently selected from the group consisting of alanine, glycine, valine, and serine.

136. The ADC of claim 129, wherein

$n_1$  is 3; and

each  $AA^1$  is independently selected from the group consisting of alanine, glycine, valine, serine, leucine, arginine, and aspartic acid; and wherein at least one  $AA^1$  is not glycine.

137. An ADC having the structure:



wherein:

$R^{XX}$  is hydrogen or  $C_{1-3}$  alkyl;

n4 is an integer from 2 to 8;

n3 is an integer from 1 to 4;

Ab is an antibody; and

p is an integer from 1 to 16.

138. The ADC of claim 137, wherein n4 is an integer from 3 to 6.
139. The ADC of any one of claims 120-138, wherein n3 is 1.
140. The ADC of any one of claims 1-139, wherein the antibody is a humanized antibody.
141. The ADC of any one of claims 1-140, wherein the antibody is a monoclonal antibody.
142. The ADC of any one of claims 1-141, wherein the antibody is fucosylated.
143. The ADC of any one of claims 1-141, wherein the antibody is afucosylated.
144. The ADC of any one of claims 1-143, wherein each L is covalently attached to Ab via a sulfur atom of a cysteine residue.
145. The ADC of any one of claims 1-143, wherein each L is covalently attached to Ab via an  $\epsilon$ -amino group of a lysine residue.
146. The ADC of any one of claims 1-145, wherein subscript p is an integer from 1 to 8.
147. The ADC of any one of claims 1-145, wherein subscript p is an integer from 4 to 12.



148. The ADC of any one of claims 1-145, wherein subscript p is an integer from 8 to 16.

149. The ADC of any one of claims 1-147, wherein subscript p is 2, 4, 6, or 8.

150. A composition comprising a distribution of the ADCs of any one of claims 1-139, or a salt thereof.

151. The composition of claim 150, further comprising at least one pharmaceutically acceptable carrier.

152. A method of treating cancer in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of the ADC of any one of claims 1-139, or a salt thereof.

153. A method of treating cancer in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of the composition of claim 150 or 151.

154. A method of treating an autoimmune disorder in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of the ADC of any one of claims 1-139, or a salt thereof.

155. A method of treating an autoimmune disorder in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of the composition of claim 150 or 151.

Figure 1 - L540cy HL xenograft model  
DAR 2 - 1 mg/kg single dose (n=6)

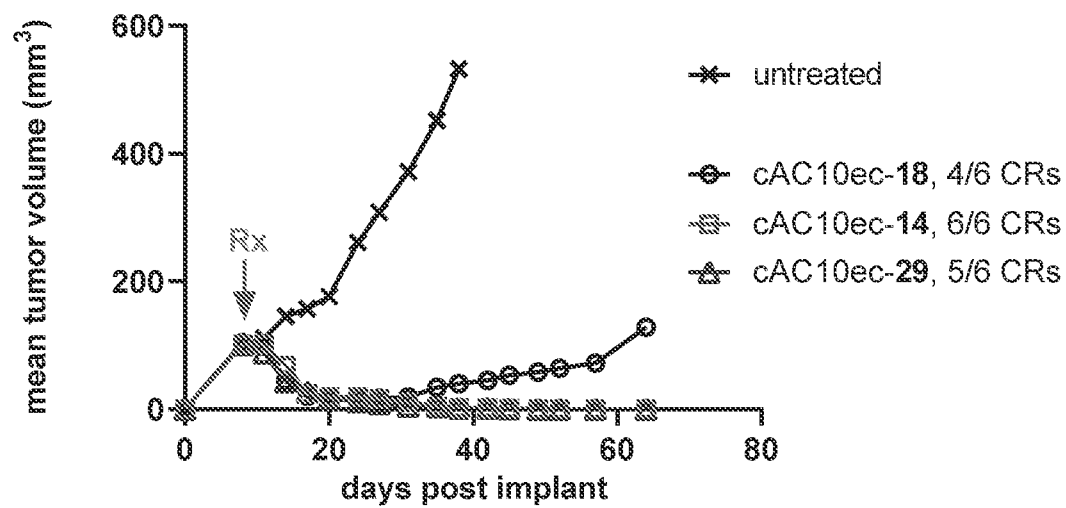
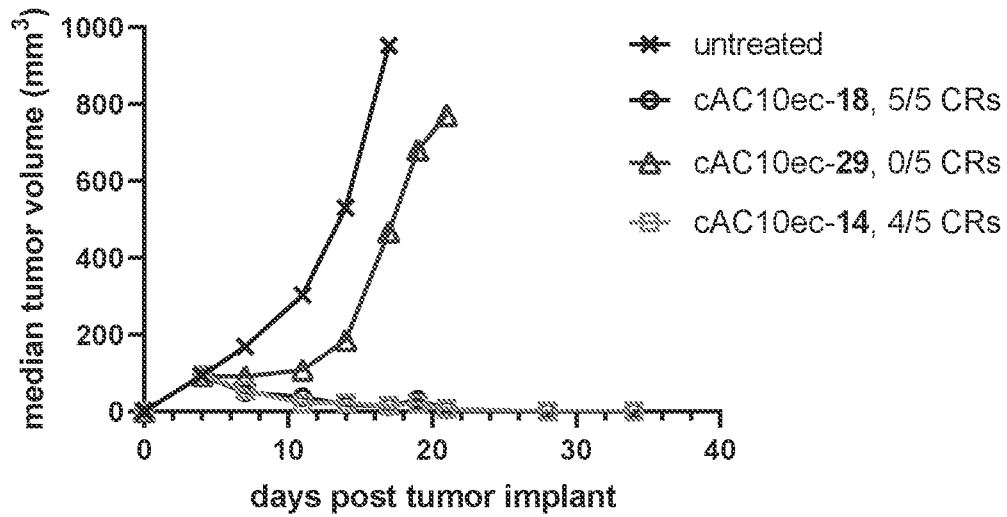


Figure 2 - DEL/BVR ALCL xenograft model  
DAR 2 - 3 mg/kg single dose (n=5)



## SEQUENCE LISTING

<110> SEAGEN INC.

<120> ANTHRACYCLINE ANTIBODY CONJUGATES

<130> SGENE.005WO

<150> 63/194,606

<151> 2021-05-28

<160> 889

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1

Asp Tyr Tyr Ile Thr

1 5

<210> 2

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2

Trp Ile Tyr Pro Gly Ser Gly Asn Thr Lys Tyr Asn Glu Lys Phe Lys

1 5 10 15

Gly

<210> 3

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 3

Tyr Gly Asn Tyr Trp Phe Ala Tyr  
1 5

<210> 4

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 4

Lys Ala Ser Gln Ser Val Asp Phe Asp Gly Asp Ser Tyr Met Asn  
1 5 10 15

<210> 5

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 5

Ala Ala Ser Asn Leu Glu Ser  
1 5

<210> 6

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 6

Gln Gln Ser Asn Glu Asp Pro Trp Thr  
1 5

<210> 7

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 7

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

<210> 8

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 8

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

<210> 9

<211> 447  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 9

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Gln | Ile | Gln | Leu | Gln | Gln | Ser | Gly | Pro | Glu | Val | Val | Lys | Pro | Gly | Ala |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Ser | Val | Lys | Ile | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Thr | Phe | Thr | Asp | Tyr |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |  |  |
| Tyr | Ile | Thr | Trp | Val | Lys | Gln | Lys | Pro | Gly | Gln | Gly | Leu | Glu | Trp | Ile |  |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     |     | 45  |     |  |  |
| Gly | Trp | Ile | Tyr | Pro | Gly | Ser | Gly | Asn | Thr | Lys | Tyr | Asn | Glu | Lys | Phe |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Lys | Gly | Lys | Ala | Thr | Leu | Thr | Val | Asp | Thr | Ser | Ser | Ser | Thr | Ala | Phe |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |
| Met | Gln | Leu | Ser | Ser | Leu | Thr | Ser | Glu | Asp | Thr | Ala | Val | Tyr | Phe | Cys |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |  |  |
| Ala | Asn | Tyr | Gly | Asn | Tyr | Trp | Phe | Ala | Tyr | Trp | Gly | Gln | Gly | Thr | Gln |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |  |
| Val | Thr | Val | Ser | Ala | Ala | Ser | Thr | Lys | Gly | Pro | Ser | Val | Phe | Pro | Leu |  |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     | 125 |     |  |  |
| Ala | Pro | Ser | Ser | Lys | Ser | Thr | Ser | Gly | Gly | Thr | Ala | Ala | Leu | Gly | Cys |  |  |
|     |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Leu | Val | Lys | Asp | Tyr | Phe | Pro | Glu | Pro | Val | Thr | Val | Ser | Trp | Asn | Ser |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Gly | Ala | Leu | Thr | Ser | Gly | Val | His | Thr | Phe | Pro | Ala | Val | Leu | Gln | Ser |  |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Ser | Gly | Leu | Tyr | Ser | Leu | Ser | Ser | Val | Val | Thr | Val | Pro | Ser | Ser | Ser |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |  |  |
| Leu | Gly | Thr | Gln | Thr | Tyr | Ile | Cys | Asn | Val | Asn | His | Lys | Pro | Ser | Asn |  |  |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |  |  |
| Thr | Lys | Val | Asp | Lys | Lys | Val | Glu | Pro | Lys | Ser | Cys | Asp | Lys | Thr | His |  |  |
|     |     |     | 210 |     |     | 215 |     |     |     |     |     | 220 |     |     |     |  |  |
| Thr | Cys | Pro | Pro | Cys | Pro | Ala | Pro | Glu | Leu | Leu | Gly | Gly | Pro | Ser | Val |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Phe | Leu | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Thr | Leu | Met | Ile | Ser | Arg | Thr |  |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |  |  |
| Pro | Glu | Val | Thr | Cys | Val | Val | Val | Asp | Val | Ser | His | Glu | Asp | Pro | Glu |  |  |
|     |     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |  |  |
| Val | Lys | Phe | Asn | Trp | Tyr | Val | Asp | Gly | Val | Glu | Val | His | Asn | Ala | Lys |  |  |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |  |  |
| Thr | Lys | Pro | Arg | Glu | Glu | Gln | Tyr | Asn | Ser | Thr | Tyr | Arg | Val | Val | Ser |  |  |
|     |     |     | 290 |     |     | 295 |     |     |     |     |     | 300 |     |     |     |  |  |
| Val | Leu | Thr | Val | Leu | His | Gln | Asp | Trp | Leu | Asn | Gly | Lys | Glu | Tyr | Lys |  |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |  |
| Cys | Lys | Val | Ser | Asn | Lys | Ala | Leu | Pro | Ala | Pro | Ile | Glu | Lys | Thr | Ile |  |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |  |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Lys | Ala | Lys | Gly | Gln | Pro | Arg | Glu | Pro | Gln | Val | Tyr | Thr | Leu | Pro |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Pro | Ser | Arg | Asp | Glu | Leu | Thr | Lys | Asn | Gln | Val | Ser | Leu | Thr | Cys | Leu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Val | Lys | Gly | Phe | Tyr | Pro | Ser | Asp | Ile | Ala | Val | Glu | Trp | Glu | Ser | Asn |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Gly | Gln | Pro | Glu | Asn | Asn | Tyr | Lys | Thr | Thr | Pro | Pro | Val | Leu | Asp | Ser |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Asp | Gly | Ser | Phe | Phe | Leu | Tyr | Ser | Lys | Leu | Thr | Val | Asp | Lys | Ser | Arg |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     |     | 415 |     |
| Trp | Gln | Gln | Gly | Asn | Val | Phe | Ser | Cys | Ser | Val | Met | His | Glu | Ala | Leu |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| His | Asn | His | Tyr | Thr | Gln | Lys | Ser | Leu | Ser | Leu | Ser | Pro | Gly | Lys |     |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |

<210> 10

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 10

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ile | Gln | Leu | Gln | Gln | Ser | Gly | Pro | Glu | Val | Val | Lys | Pro | Gly | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Val | Lys | Ile | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Thr | Phe | Thr | Asp | Tyr |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Tyr | Ile | Thr | Trp | Val | Lys | Gln | Lys | Pro | Gly | Gln | Gly | Leu | Glu | Trp | Ile |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Gly | Trp | Ile | Tyr | Pro | Gly | Ser | Gly | Asn | Thr | Lys | Tyr | Asn | Glu | Lys | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Gly | Lys | Ala | Thr | Leu | Thr | Val | Asp | Thr | Ser | Ser | Ser | Thr | Ala | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Met | Gln | Leu | Ser | Ser | Leu | Thr | Ser | Glu | Asp | Thr | Ala | Val | Tyr | Phe | Cys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ala | Asn | Tyr | Gly | Asn | Tyr | Trp | Phe | Ala | Tyr | Trp | Gly | Gln | Gly | Thr | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Thr | Val | Ser | Ala | Ala | Ser | Thr | Lys | Gly | Pro | Ser | Val | Phe | Pro | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Pro | Ser | Ser | Lys | Ser | Thr | Ser | Gly | Gly | Thr | Ala | Ala | Leu | Gly | Cys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Val | Lys | Asp | Tyr | Phe | Pro | Glu | Pro | Val | Thr | Val | Ser | Trp | Asn | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |
| Gly | Ala | Leu | Thr | Ser | Gly | Val | His | Thr | Phe | Pro | Ala | Val | Leu | Gln | Ser |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Gly | Leu | Tyr | Ser | Leu | Ser | Ser | Val | Val | Thr | Val | Pro | Ser | Ser | Ser |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Gly | Thr | Gln | Thr | Tyr | Ile | Cys | Asn | Val | Asn | His | Lys | Pro | Ser | Asn |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |
| Thr | Lys | Val | Asp | Lys | Lys | Val | Glu | Pro | Lys | Ser | Cys | Asp | Lys | Thr | His |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |
| Thr | Cys | Pro | Pro | Cys | Pro | Ala | Pro | Glu | Leu | Leu | Gly | Gly | Pro | Ser | Val |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Phe | Leu | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Thr | Leu | Met | Ile | Ser | Arg | Thr |  |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |
| Pro | Glu | Val | Thr | Cys | Val | Val | Val | Asp | Val | Ser | His | Glu | Asp | Pro | Glu |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |
| Val | Lys | Phe | Asn | Trp | Tyr | Val | Asp | Gly | Val | Glu | Val | His | Asn | Ala | Lys |  |  |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |  |  |
| Thr | Lys | Pro | Arg | Glu | Glu | Gln | Tyr | Asn | Ser | Thr | Tyr | Arg | Val | Val | Ser |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |
| Val | Leu | Thr | Val | Leu | His | Gln | Asp | Trp | Leu | Asn | Gly | Lys | Glu | Tyr | Lys |  |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |  |
| Cys | Lys | Val | Ser | Asn | Lys | Ala | Leu | Pro | Ala | Pro | Ile | Glu | Lys | Thr | Ile |  |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |  |
| Ser | Lys | Ala | Lys | Gly | Gln | Pro | Arg | Glu | Pro | Gln | Val | Tyr | Thr | Leu | Pro |  |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |  |
| Pro | Ser | Arg | Asp | Glu | Leu | Thr | Lys | Asn | Gln | Val | Ser | Leu | Thr | Cys | Leu |  |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |  |  |
| Val | Lys | Gly | Phe | Tyr | Pro | Ser | Asp | Ile | Ala | Val | Glu | Trp | Glu | Ser | Asn |  |  |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |  |
| Gly | Gln | Pro | Glu | Asn | Asn | Tyr | Lys | Thr | Thr | Pro | Pro | Val | Leu | Asp | Ser |  |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |  |
| Asp | Gly | Ser | Phe | Phe | Leu | Tyr | Ser | Lys | Leu | Thr | Val | Asp | Lys | Ser | Arg |  |  |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |  |  |
| Trp | Gln | Gln | Gly | Asn | Val | Phe | Ser | Cys | Ser | Val | Met | His | Glu | Ala | Leu |  |  |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |  |
| His | Asn | His | Tyr | Thr | Gln | Lys | Ser | Leu | Ser | Leu | Ser | Pro | Gly |     |     |  |  |
|     | 435 |     |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |  |

<210> 11

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 11

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Asp | Ile | Val | Leu | Thr | Gln | Ser | Pro | Ala | Ser | Leu | Ala | Val | Ser | Leu | Gly |  |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |  |
| Gln | Arg | Ala | Thr | Ile | Ser | Cys | Lys | Ala | Ser | Gln | Ser | Val | Asp | Phe | Asp |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Gly | Asp | Ser | Tyr | Met | Asn | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Gln | Pro | Pro |  |  |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |  |
| Lys | Val | Leu | Ile | Tyr | Ala | Ala | Ser | Asn | Leu | Glu | Ser | Gly | Ile | Pro | Ala |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Asn | Ile | His |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Val | Glu | Glu | Glu | Asp | Ala | Ala | Thr | Tyr | Tyr | Cys | Gln | Gln | Ser | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Asp | Pro | Trp | Thr | Phe | Gly | Gly | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Thr | Val | Ala | Ala | Pro | Ser | Val | Phe | Ile | Phe | Pro | Pro | Ser | Asp | Glu | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Lys | Ser | Gly | Thr | Ala | Ser | Val | Val | Cys | Leu | Leu | Asn | Asn | Phe | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Pro | Arg | Glu | Ala | Lys | Val | Gln | Trp | Lys | Val | Asp | Asn | Ala | Leu | Gln | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Asn | Ser | Gln | Glu | Ser | Val | Thr | Glu | Gln | Asp | Ser | Lys | Asp | Ser | Thr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Tyr | Ser | Leu | Ser | Ser | Thr | Leu | Thr | Leu | Ser | Lys | Ala | Asp | Tyr | Glu | Lys |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| His | Lys | Val | Tyr | Ala | Cys | Glu | Val | Thr | His | Gln | Gly | Leu | Ser | Ser | Pro |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Thr | Lys | Ser | Phe | Asn | Arg | Gly | Glu | Cys |     |     |     |     |     |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     |     |     |     |     |

<210> 12

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 12

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

<210> 13

<211> 111  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 13

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

<210> 14  
<211> 448  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 14

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 130 |     | 135 |     | 140 |     |     |     |     |     |     |     |     |     |     |     |
| Cys | Leu | Val | Lys | Asp | Tyr | Phe | Pro | Glu | Pro | Val | Thr | Val | Ser | Trp | Asn |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Gly | Ala | Leu | Thr | Ser | Gly | Val | His | Thr | Phe | Pro | Ala | Val | Leu | Gln |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |
| Ser | Ser | Gly | Leu | Tyr | Ser | Leu | Ser | Ser | Val | Val | Thr | Val | Pro | Ser | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Leu | Gly | Thr | Gln | Thr | Tyr | Ile | Cys | Asn | Val | Asn | His | Lys | Pro | Ser |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Asn | Thr | Lys | Val | Asp | Lys | Lys | Val | Glu | Pro | Lys | Ser | Cys | Asp | Lys | Thr |
| 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| His | Thr | Cys | Pro | Pro | Cys | Pro | Ala | Pro | Glu | Leu | Leu | Gly | Gly | Pro | Ser |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     | 240 |
| Val | Phe | Leu | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Thr | Leu | Met | Ile | Ser | Arg |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Thr | Pro | Glu | Val | Thr | Cys | Val | Val | Val | Asp | Val | Ser | His | Glu | Asp | Pro |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Glu | Val | Lys | Phe | Asn | Trp | Tyr | Val | Asp | Gly | Val | Glu | Val | His | Asn | Ala |
|     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Lys | Thr | Lys | Pro | Arg | Glu | Glu | Gln | Tyr | Asn | Ser | Thr | Tyr | Arg | Val | Val |
| 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |
| Ser | Val | Leu | Thr | Val | Leu | His | Gln | Asp | Trp | Leu | Asn | Gly | Lys | Glu | Tyr |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     | 320 |
| Lys | Cys | Lys | Val | Ser | Asn | Lys | Ala | Leu | Pro | Ala | Pro | Ile | Glu | Lys | Thr |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Ile | Ser | Lys | Ala | Lys | Gly | Gln | Pro | Arg | Glu | Pro | Gln | Val | Tyr | Thr | Leu |
|     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |     |
| Pro | Pro | Ser | Arg | Asp | Glu | Leu | Thr | Lys | Asn | Gln | Val | Ser | Leu | Thr | Cys |
|     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |     |
| Leu | Val | Lys | Gly | Phe | Tyr | Pro | Ser | Asp | Ile | Ala | Val | Glu | Trp | Glu | Ser |
| 370 |     |     |     |     | 375 |     |     |     | 380 |     |     |     |     |     |     |
| Asn | Gly | Gln | Pro | Glu | Asn | Asn | Tyr | Lys | Thr | Thr | Pro | Pro | Val | Leu | Asp |
| 385 |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     |     | 400 |
| Ser | Asp | Gly | Ser | Phe | Phe | Leu | Tyr | Ser | Lys | Leu | Thr | Val | Asp | Lys | Ser |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |     |
| Arg | Trp | Gln | Gln | Gly | Asn | Val | Phe | Ser | Cys | Ser | Val | Met | His | Glu | Ala |
|     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |     |     |
| Leu | His | Asn | His | Tyr | Thr | Gln | Lys | Ser | Leu | Ser | Leu | Ser | Pro | Gly | Lys |
|     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |     |

<210> 15

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 15

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Val | Met | Thr | Gln | Ser | Pro | Asp | Ser | Leu | Ala | Val | Ser | Leu | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Glu | Arg | Ala | Thr | Ile | Asn | Cys | Arg | Ala | Ser | Lys | Ser | Val | Ser | Thr | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Tyr | Ser | Phe | Met | His | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Gln | Pro | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Leu | Leu | Ile | Tyr | Leu | Ala | Ser | Asn | Leu | Glu | Ser | Gly | Val | Pro | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr | Ile | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Ser | Leu | Gln | Ala | Glu | Asp | Val | Ala | Val | Tyr | Tyr | Cys | Gln | His | Ser | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Val | Pro | Trp | Thr | Phe | Gly | Gln | Gly | Thr | Lys | Val | Glu | Ile | Lys | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Val | Ala | Ala | Pro | Ser | Val | Phe | Ile | Phe | Pro | Pro | Ser | Asp | Glu | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Leu | Lys | Ser | Gly | Thr | Ala | Ser | Val | Val | Cys | Leu | Leu | Asn | Asn | Phe | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Arg | Glu | Ala | Lys | Val | Gln | Trp | Lys | Val | Asp | Asn | Ala | Leu | Gln | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Asn | Ser | Gln | Glu | Ser | Val | Thr | Glu | Gln | Asp | Ser | Lys | Asp | Ser | Thr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Tyr | Ser | Leu | Ser | Ser | Thr | Leu | Thr | Leu | Ser | Lys | Ala | Asp | Tyr | Glu | Lys |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| His | Lys | Val | Tyr | Ala | Cys | Glu | Val | Thr | His | Gln | Gly | Leu | Ser | Ser | Pro |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Val | Thr | Lys | Ser | Phe | Asn | Arg | Gly | Glu | Cys |     |     |     |     |     |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     |     |     |     |     |

<210> 16

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 16

Asn Tyr Gly Met Asn

1

5

<210> 17

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 17

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Thr Asp Asp Phe Lys

1 5 10 15

Gly

<210> 18

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 18

Gly Gly Phe Gly Ser Ser Tyr Trp Tyr Phe Asp Val

1 5 10

<210> 19

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 19

Lys Ala Ser Gln Asp Val Ser Ile Ala Val Ala

1 5 10

<210> 20

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 20

Ser Ala Ser Tyr Arg Tyr Thr

1 5

<210> 21

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 21

Gln Gln His Tyr Ile Thr Pro Leu Thr  
1 5

<210> 22

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 22

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

<210> 23

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 23

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ala | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys | Ala | Pro | Lys | Leu | Leu | Ile |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Ser | Ala | Ser | Tyr | Arg | Tyr | Thr | Gly | Val | Pro | Asp | Arg | Phe | Ser | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr | Ile | Ser | Ser | Leu | Gln | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Asp | Phe | Ala | Val | Tyr | Tyr | Cys | Gln | Gln | His | Tyr | Ile | Thr | Pro | Leu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Phe | Gly | Ala | Gly | Thr | Lys | Val | Glu | Ile | Lys |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

<210> 24  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 24  
 Thr Ala Gly Met Gln  
 1 5

<210> 25  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 25  
 Trp Ile Asn Thr His Ser Gly Val Pro Lys Tyr Ala Glu Asp Phe Lys  
 1 5 10 15  
 Gly

<210> 26  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 26  
 Ser Gly Phe Gly Ser Ser Tyr Trp Tyr Phe Asp Val



1 5 10

<210> 27  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 27  
Lys Ala Ser Gln Asp Val Ser Thr Ala Val Ala  
1 5 10

<210> 28  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 28  
Ser Ala Ser Tyr Arg Tyr Thr  
1 5

<210> 29  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 29  
Gln Gln His Tyr Ile Thr Pro Leu Thr  
1 5

<210> 30  
<211> 121  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 30

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

<210> 31

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 31

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

<210> 32

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 32

Ser Gln Asn Ile Tyr  
1 5

<210> 33

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 33

Tyr Ile Glu Pro Tyr Asn Val Val Pro Met Tyr Asn Pro Lys Phe Lys  
1 5 10 15  
Gly

<210> 34

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 34

Ser Gly Ser Ser Asn Phe Asp Tyr  
1 5

<210> 35

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 35

Ser Ala Ser Ser Ser Ile Ser Ser His Tyr Leu His  
1 5 10

<210> 36

<211> 7

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 36  
Arg Thr Ser Asn Leu Ala Ser  
1 5

<210> 37  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 37  
Gln Gln Gly Ser Ser Leu Pro Leu Thr  
1 5

<210> 38  
<211> 117  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 38  
Glu Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1 5 10 15  
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Ser Gln  
20 25 30  
Asn Ile Tyr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile  
35 40 45  
Gly Tyr Ile Glu Pro Tyr Asn Val Val Pro Met Tyr Asn Pro Lys Phe  
50 55 60  
Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr  
65 70 75 80  
Leu Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Arg Ser Gly Ser Ser Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
100 105 110  
Val Thr Val Ser Ser  
115

<210> 39  
<211> 108  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 39  
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15  
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Ile Ser Ser His  
20 25 30  
Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Leu Leu  
35 40 45  
Ile Tyr Arg Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser  
50 55 60  
Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln  
65 70 75 80  
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Ser Ser Leu Pro  
85 90 95  
Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 40  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 40  
Asn Tyr Ala Met His  
1 5

<210> 41  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 41  
Leu Ile Trp Tyr Asp Gly Ser Asn Lys Phe Tyr Gly Asp Ser Val Lys  
1 5 10 15

Gly

<210> 42  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 42  
Glu Gly Ser Gly His Tyr  
1 5

<210> 43  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 43  
Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala  
1 5 10

<210> 44  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 44  
Asp Ala Ser Ser Leu Glu Ser  
1 5

<210> 45  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 45

Gln Gln Phe Asn Ser Tyr Pro Ile Thr

1

5

<210> 46

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 46

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr

20

25

30

Ala Met His Trp Val Arg Gln Ala Pro Gly Glu Gly Leu Glu Trp Val

35

40

45

Ala Leu Ile Trp Tyr Asp Gly Ser Asn Lys Phe Tyr Gly Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Ser Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Glu Gly Ser Gly His Tyr Trp Gly Gln Gly Thr Leu Val Thr

100

105

110

Val Ser Ser

115

<210> 47

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 47

Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala

20

25

30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Ser Leu Ile

35

40

45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly

50

55

60

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr | Ile | Ser | Ser | Leu | Gln | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Asp | Phe | Ala | Thr | Tyr | Tyr | Cys | Gln | Gln | Phe | Asn | Ser | Tyr | Pro | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Phe | Gly | Gln | Gly | Thr | Arg | Leu | Glu | Ile | Lys |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

<210> 48  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 48  
 Asn Tyr Ala Met Ser  
 1 5

<210> 49  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 49  
 Tyr Ile Ser Pro Gly Gly Asp Tyr Ile Tyr Tyr Ala Asp Ser Val Lys  
 1 5 10 15  
 Gly

<210> 50  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 50  
 Asp Arg Arg His Tyr Gly Ser Tyr Ala Met Asp Tyr  
 1 5 10

<210> 51



<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 51  
Arg Ser Ser Lys Ser Leu Leu His Ser Asn Leu Asn Thr Tyr Leu Tyr  
1 5 10 15

<210> 52  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 52  
Arg Met Ser Asn Leu Ala Ser  
1 5

<210> 53  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 53  
Met Gln His Leu Glu Tyr Pro Phe Thr  
1 5

<210> 54  
<211> 121  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 54  
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr

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

<210> 55

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 55

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

<210> 56

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 56

Thr Tyr Ala Phe His

1 5

<210> 57  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 57  
Gly Ile Val Pro Ile Phe Gly Thr Leu Lys Tyr Ala Gln Lys Phe Gln  
1 5 10 15  
Asp

<210> 58  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 58  
Ala Ile Gln Leu Glu Gly Arg Pro Phe Asp His  
1 5 10

<210> 59  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 59  
Arg Ala Ser Gln Gly Ile Thr Ser Tyr Leu Ala  
1 5 10

<210> 60  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 60

Ala Ala Ser Ala Leu Gln Ser  
1 5

<210> 61

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 61

Gln Gln Val Asn Arg Gly Ala Ala Ile Thr  
1 5 10

<210> 62

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 62

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

<210> 63

<211> 108

<212> PRT

### <213> Artificial Sequence

$\langle 220 \rangle$

<223> Synthetic

<400> 63

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

<210> 64

<211> 5

&lt;212&gt; PRT

### <213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Synthetic

<400> 64

Thr Tyr Ala Phe His  
1 5

<210> 65

<211> 17

&lt;212&gt; PRT

### <213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Synthetic

<400> 65

Gly Ile Val Pro Ile Phe Gly Thr Leu Lys Tyr Ala Gln Lys Phe Gln  
1 5 10 15  
Asp

<210> 66  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 66  
Ala Ile Gln Leu Glu Gly Arg Pro Phe Asp His  
1 5 10

<210> 67  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 67  
Arg Ala Ser Gln Gly Ile Thr Ser Tyr Leu Ala  
1 5 10

<210> 68  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 68  
Ala Ala Ser Ala Leu Gln Ser  
1 5

<210> 69  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 69  
Gln Gln Val Asn Arg Gly Ala Ala Ile Thr  
1 5 10

<210> 70  
 <211> 120  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 70  
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
 1 5 10 15  
 Ser Val Arg Val Ser Cys Arg Ala Ser Gly Gly Ser Ser Thr Thr Tyr  
 20 25 30  
 Ala Phe His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
 35 40 45  
 Gly Gly Ile Val Pro Ile Phe Gly Thr Leu Lys Tyr Ala Gln Lys Phe  
 50 55 60  
 Gln Asp Arg Val Thr Leu Thr Ala Asp Lys Ser Thr Gly Thr Ala Tyr  
 65 70 75 80  
 Met Glu Leu Asn Ser Leu Arg Leu Asp Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Arg Ala Ile Gln Leu Glu Gly Arg Pro Phe Asp His Trp Gly Gln  
 100 105 110  
 Gly Thr Gln Val Thr Val Ser Ala  
 115 120

<210> 71  
 <211> 108  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 71  
 Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Thr Ser Tyr  
 20 25 30  
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45  
 Tyr Ala Ala Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Arg Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Val Asn Arg Gly Ala Ala  
 85 90 95

Ile Thr Phe Gly His Gly Thr Arg Leu Asp Ile Lys  
100 105

<210> 72  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 72  
Arg Tyr Thr Met His  
1 5

<210> 73  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 73  
Val Ile Ser Phe Asp Gly Ser Asn Lys Tyr Tyr Val Asp Ser Val Lys  
1 5 10 15  
Gly

<210> 74  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 74  
Glu Ala Arg Gly Ser Tyr Ala Phe Asp Ile  
1 5 10

<210> 75  
<211> 11  
<212> PRT  
<213> Artificial Sequence



<220>

<223> Synthetic

<400> 75

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala  
1 5 10

<210> 76

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 76

Asp Ala Ser Asn Arg Ala Thr  
1 5

<210> 77

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 77

Gln Gln Arg Ser Asn Trp Pro Pro Phe Thr  
1 5 10

<210> 78

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 78

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 50  |     | 55  |     | 60  |     |     |     |     |     |     |     |     |     |     |     |
| Lys | Gly | Arg | Phe | Thr | Ile | Ser | Arg | Asp | Asn | Ser | Glu | Asn | Thr | Leu | Tyr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Gln | Val | Asn | Ile | Leu | Arg | Ala | Glu | Asp | Thr | Ala | Val | Tyr | Tyr | Cys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Arg | Glu | Ala | Arg | Gly | Ser | Tyr | Ala | Phe | Asp | Ile | Trp | Gly | Gln | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Met | Val | Thr | Val | Ser | Ser |     |     |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 79  
 <211> 108  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|                                                                 |
|-----------------------------------------------------------------|
| <400> 79                                                        |
| Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly |
| 1 5 10 15                                                       |
| Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr |
| 20 25 30                                                        |
| Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile |
| 35 40 45                                                        |
| Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly |
| 50 55 60                                                        |
| Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro |
| 65 70 75 80                                                     |
| Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro |
| 85 90 95                                                        |
| Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys                 |
| 100 105                                                         |

<210> 80  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|                     |
|---------------------|
| <400> 80            |
| Ser Phe Trp Met His |
| 1 5                 |

<210> 81

<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 81  
Tyr Ile Asn Pro Arg Ser Gly Tyr Thr Glu Tyr Asn Glu Ile Phe Arg  
1 5 10 15  
Asp

<210> 82  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 82  
Phe Leu Gly Arg Gly Ala Met Asp Tyr  
1 5

<210> 83  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 83  
Arg Ala Ser Gln Asp Ile Ser Asn Tyr Leu Ala  
1 5 10

<210> 84  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 84  
Tyr Thr Ser Lys Ile His Ser

1

5

<210> 85

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 85

Gln Gln Gly Asn Thr Phe Pro Tyr Thr

1

5

<210> 86

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 86

Gln Val Gln Leu Gln Gln Ser Gly Gly Glu Leu Ala Lys Pro Gly Ala

1

5

10

15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Ser Phe

20

25

30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile

35

40

45

Gly Tyr Ile Asn Pro Arg Ser Gly Tyr Thr Glu Tyr Asn Glu Ile Phe

50

55

60

Arg Asp Lys Ala Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr

65

70

75

80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Ser Phe Leu Gly Arg Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr

100

105

110

Thr Val Thr Val Ser Ser

115

<210> 87

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 87

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

<210> 88

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 88

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ser | Ser | Tyr | Tyr | Trp | Gly |
| 1   |     |     |     | 5   |     |     |

<210> 89

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 89

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ile | Tyr | Tyr | Asn | Gly | Ser | Thr | Tyr | Tyr | Ser | Pro | Ser | Leu | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

<210> 90

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 90

Gln Gly Tyr Asp Ile Lys Ile Asn Ile Asp Val  
1 5 10

<210> 91

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 91

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala  
1 5 10

<210> 92

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 92

Val Ala Ser Asn Arg Ala Thr  
1 5

<210> 93

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 93

Gln Gln Arg Ser Asn Trp Pro Leu Thr  
1 5

<210> 94

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 94

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

<210> 95

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 95

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

<210> 96

<211> 5

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 96  
Ser Ser Trp Met Asn  
1 5

<210> 97  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 97  
Arg Ile Tyr Pro Gly Asp Gly Asn Thr His Tyr Ala Gln Lys Phe Gln  
1 5 10 15  
Gly

<210> 98  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 98  
Gly Tyr Leu Asp Pro Met Asp Tyr  
1 5

<210> 99  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 99  
Gln Ala Ser Gln Gly Ile Asn Asn Tyr Leu Asn  
1 5 10



<210> 100  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 100  
Tyr Thr Ser Gly Leu His Ala  
1 5

<210> 101  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 101  
Gln Gln Tyr Ser Ile Leu Pro Trp Thr  
1 5

<210> 102  
<211> 117  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 102  
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
1 5 10 15  
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Ser Ser  
20 25 30  
Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45  
Gly Arg Ile Tyr Pro Gly Asp Gly Asn Thr His Tyr Ala Gln Lys Phe  
50 55 60  
Gln Gly Arg Val Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr  
65 70 75 80  
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Gly Glu Gly Tyr Leu Asp Pro Met Asp Tyr Trp Gly Gln Gly Thr Leu

|                     |     |     |     |
|---------------------|-----|-----|-----|
|                     | 100 | 105 | 110 |
| Val Thr Val Ser Ser |     |     |     |
| 115                 |     |     |     |

<210> 103  
 <211> 107  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 103  
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Gly Ile Asn Asn Tyr  
 20 25 30  
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45  
 His Tyr Thr Ser Gly Leu His Ala Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro  
 65 70 75 80  
 Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ile Leu Pro Trp  
 85 90 95  
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
 100 105

<210> 104  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 104  
 Ser Tyr Gly Met His  
 1 5

<210> 105  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 105

Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys  
1 5 10 15  
Gly

<210> 106

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 106

Asp Met Gly  
1

<210> 107

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 107

Arg Thr Ser Gln Ser Ile Ser Ser Tyr Leu Asn  
1 5 10

<210> 108

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 108

Trp Ala Ser Thr Arg Glu Ser  
1 5

<210> 109

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 109

Gln Gln Ser Tyr Asp Ile Pro Tyr Thr  
1 5

<210> 110

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 110

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

<210> 111

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 111

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asn | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Gln | Pro | Pro | Lys | Leu | Leu | Ile |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Trp | Ala | Ser | Thr | Arg | Glu | Ser | Gly | Val | Pro | Asp | Arg | Phe | Ser | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr | Ile | Ser | Ser | Leu | Gln | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Asp | Ser | Ala | Thr | Tyr | Tyr | Cys | Gln | Gln | Ser | Tyr | Asp | Ile | Pro | Tyr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Phe | Gly | Gln | Gly | Thr | Lys | Leu | Glu | Ile | Lys |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

<210> 112  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 112  
 Asn Tyr Trp Met Ser  
 1 5

<210> 113  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 113  
 Asn Ile Lys Gln Asp Gly Ser Glu Lys Phe Tyr Ala Asp Ser Val Lys  
 1 5 10 15  
 Gly

<210> 114  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 114  
 Val Gly Pro Ser Trp Glu Gln Asp Tyr

1 5

<210> 115  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 115  
Thr Gly Ser Ser Ser Asn Ile Gly Ser Tyr Tyr Gly Val His  
1 5 10

<210> 116  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 116  
Ser Asp Thr Asn Arg Pro Ser  
1 5

<210> 117  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 117  
Gln Ser Tyr Asp Lys Gly Phe Gly His Arg Val  
1 5 10

<210> 118  
<211> 118  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 118

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

<210> 119

<211> 94

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 119

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

<210> 120

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 120  
Ser Tyr Ala Ile Ser  
1 5

<210> 121  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 121  
Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln  
1 5 10 15  
Gly

<210> 122  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 122  
Gly Leu Leu Trp Asn Tyr  
1 5

<210> 123  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 123  
Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala  
1 5 10

<210> 124  
<211> 7  
<212> PRT  
<213> Artificial Sequence



<220>

<223> Synthetic

<400> 124

Gly Ala Ser Thr Thr Ala Ser

1

5

<210> 125

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 125

Gln Gln Tyr Asn Asn Trp Pro Pro Ala Tyr Thr

1

5

10

<210> 126

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 126

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser

1

5

10

15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr

20

25

30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35

40

45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe

50

55

60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr

65

70

75

80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Gly Leu Leu Trp Asn Tyr Trp Gly Gln Gly Thr Leu Val Thr

100

105

110

Val Ser Ser

115

<210> 127

<211> 109  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 127  
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly  
1 5 10 15  
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn  
20 25 30  
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Ile Ile  
35 40 45  
Tyr Gly Ala Ser Thr Thr Ala Ser Gly Ile Pro Ala Arg Phe Ser Ala  
50 55 60  
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser  
65 70 75 80  
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Pro  
85 90 95  
Ala Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
100 105

<210> 128  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 128  
Asn Tyr Gly Met Asn  
1 5

<210> 129  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 129  
Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Gly Glu Asp Phe Lys  
1 5 10 15  
Gly

<210> 130  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 130  
Phe Gly Asn Tyr Val Asp Tyr  
1 5

<210> 131  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 131  
Arg Ser Ser Lys Asn Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr  
1 5 10 15

<210> 132  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 132  
Gln Met Ser Asn Leu Ala Ser  
1 5

<210> 133  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 133

Ala Gln Asn Leu Glu Ile Pro Arg Thr  
1 5

<210> 134

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 134

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

<210> 135

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 135

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Val | Met | Thr | Gln | Ser | Pro | Leu | Ser | Leu | Pro | Val | Thr | Pro | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Glu | Pro | Ala | Ser | Ile | Ser | Cys | Arg | Ser | Ser | Lys | Asn | Leu | Leu | His | Ser |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Asn | Gly | Ile | Thr | Tyr | Leu | Tyr | Trp | Tyr | Leu | Gln | Lys | Pro | Gly | Gln | Ser |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Pro | Gln | Leu | Leu | Ile | Tyr | Gln | Met | Ser | Asn | Leu | Ala | Ser | Gly | Val | Pro |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Asp | Arg | Phe | Ser | Ser | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Lys | Ile |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Arg | Val | Glu | Ala | Glu | Asp | Val | Gly | Val | Tyr | Tyr | Cys | Ala | Gln | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Glu | Ile | Pro | Arg | Thr | Phe | Gly | Gln | Gly | Thr | Lys | Val | Glu | Ile | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

<210> 136  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 136  
 Lys Tyr Gly Met Asn  
 1 5

<210> 137  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 137  
 Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly Asp Asp Phe Lys  
 1 5 10 15  
 Gly

<210> 138  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 138  
 Phe Gly Ser Ala Val Asp Tyr  
 1 5

<210> 139  
 <211> 16  
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 139

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Ser | Lys | Ser | Leu | Leu | His | Ser | Asn | Gly | Ile | Thr | Tyr | Leu | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

<210> 140

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 140

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| Gln | Met | Ser | Asn | Arg | Ala | Ser |
| 1   |     |     | 5   |     |     |     |

<210> 141

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 141

|     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gln | Asn | Leu | Glu | Leu | Pro | Arg | Thr |
| 1   |     |     | 5   |     |     |     |     |     |

<210> 142

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 142

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ile | Gln | Leu | Val | Gln | Ser | Gly | Pro | Glu | Val | Lys | Lys | Pro | Gly | Glu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Val | Lys | Ile | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Thr | Phe | Thr | Lys | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Met | Asn | Trp | Val | Lys | Gln | Ala | Pro | Gly | Gln | Gly | Leu | Lys | Trp | Met |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Gly | Trp | Ile | Asn | Thr | Tyr | Thr | Glu | Glu | Pro | Thr | Tyr | Gly | Asp | Asp | Phe |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Lys | Gly | Arg | Phe | Thr | Phe | Thr | Leu | Asp | Thr | Ser | Thr | Ser | Thr | Ala | Tyr |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |
| Leu | Glu | Ile | Ser | Ser | Leu | Arg | Ser | Glu | Asp | Thr | Ala | Thr | Tyr | Phe | Cys |  |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Ala | Arg | Phe | Gly | Ser | Ala | Val | Asp | Tyr | Trp | Gly | Gln | Gly | Thr | Leu | Val |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Thr | Val | Ser | Ser |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

<210> 143  
 <211> 113  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| <400> 143 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| Asp       | Ile | Val | Met | Thr | Gln | Ser | Ala | Leu | Ser | Asn | Pro | Val | Thr | Leu | Gly |  |  |
| 1         |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Glu       | Ser | Gly | Ser | Ile | Ser | Cys | Arg | Ser | Ser | Lys | Ser | Leu | Leu | His | Ser |  |  |
|           |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |  |
| Asn       | Gly | Ile | Thr | Tyr | Leu | Tyr | Trp | Tyr | Leu | Gln | Lys | Pro | Gly | Gln | Ser |  |  |
|           |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Pro       | Gln | Leu | Leu | Ile | Tyr | Gln | Met | Ser | Asn | Arg | Ala | Ser | Gly | Val | Pro |  |  |
|           | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |  |
| Asp       | Arg | Phe | Ser | Ser | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Lys | Ile |  |  |
| 65        |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |  |
| Ser       | Arg | Val | Glu | Ala | Glu | Asp | Val | Gly | Val | Tyr | Tyr | Cys | Ala | Gln | Asn |  |  |
|           |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |  |
| Leu       | Glu | Leu | Pro | Arg | Thr | Phe | Gly | Gln | Gly | Thr | Lys | Leu | Glu | Met | Lys |  |  |
|           |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Arg       |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

<210> 144  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 144  
 Asp Tyr Ser Met His

1 5

<210> 145  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 145  
Trp Ile Asn Thr Glu Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe Lys  
1 5 10 15  
Gly

<210> 146  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 146  
Thr Ala Val Tyr  
1

<210> 147  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 147  
Arg Ala Ser Gln Glu Ile Ser Val Ser Leu Ser  
1 5 10

<210> 148  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>



<223> Synthetic

<400> 148

Ala Thr Ser Thr Leu Asp Ser  
1 5

<210> 149

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 149

Leu Gln Tyr Ala Ser Tyr Pro Trp Thr  
1 5

<210> 150

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 150

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

<210> 151

<211> 108

<212> PRT



<210> 154  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 154  
Asp Tyr Gly Arg Trp Tyr Phe Asp Val  
1 5

<210> 155  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 155  
Arg Ala Ser Ser Ser Val Ser His Met His  
1 5 10

<210> 156  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 156  
Ala Thr Ser Asn Leu Ala Ser  
1 5

<210> 157  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 157  
Gln Gln Trp Ser Ser Thr Pro Arg Thr  
1 5

<210> 158  
<211> 118  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 158  
Gln Ile Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala  
1 5 10 15  
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr  
20 25 30  
Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Asp Leu Lys Trp Met  
35 40 45  
Gly Trp Ile Asn Thr Tyr Ser Gly Glu Pro Arg Tyr Ala Asp Asp Phe  
50 55 60  
Lys Gly Arg Phe Val Phe Ser Leu Asp Lys Ser Val Asn Thr Ala Tyr  
65 70 75 80  
Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Arg Asp Tyr Gly Arg Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr  
100 105 110  
Thr Val Thr Val Ser Ser  
115

<210> 159  
<211> 107  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 159  
Gln Ile Val Leu Ser Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15  
Glu Arg Ala Thr Met Ser Cys Arg Ala Ser Ser Ser Val Ser His Met  
20 25 30  
His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Trp Ile Tyr  
35 40 45  
Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser  
50 55 60  
Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu  
65 70 75 80  
Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Thr Pro Arg Thr  
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg  
100 105

<210> 160

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 160

Arg Tyr Trp Met Ser  
1 5

<210> 161

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 161

Glu Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu Lys  
1 5 10 15  
Asp

<210> 162

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 162

Pro Asp Gly Asn Tyr Trp Tyr Phe Asp Val  
1 5 10

<210> 163

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 163

Lys Ala Ser Gln Asp Val Gly Ile Ala Val Ala  
1 5 10

<210> 164

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 164

Trp Ala Ser Thr Arg His Thr  
1 5

<210> 165

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 165

Gln Gln Tyr Ser Ser Tyr Pro Tyr Thr  
1 5

<210> 166

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 166

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 50  |     | 55  |     | 60  |     |     |     |     |     |     |     |     |     |     |     |
| Lys | Asp | Lys | Phe | Ile | Ile | Ser | Arg | Asp | Asn | Ala | Lys | Asn | Ser | Leu | Tyr |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     |     | 80  |
| Leu | Gln | Met | Asn | Ser | Leu | Arg | Ala | Glu | Asp | Thr | Ala | Val | Tyr | Tyr | Cys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ala | Arg | Pro | Asp | Gly | Asn | Tyr | Trp | Tyr | Phe | Asp | Val | Trp | Gly | Gln | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Leu | Val | Thr | Val | Ser | Ser |     |     |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 167  
 <211> 108  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|                                                                 |
|-----------------------------------------------------------------|
| <400> 167                                                       |
| Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly |
| 1 5 10 15                                                       |
| Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Ile Ala |
| 20 25 30                                                        |
| Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile |
| 35 40 45                                                        |
| Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Ser Gly |
| 50 55 60                                                        |
| Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro |
| 65 70 75 80                                                     |
| Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser Tyr Pro Tyr |
| 85 90 95                                                        |
| Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg                 |
| 100 105                                                         |

<210> 168  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|                     |
|---------------------|
| <400> 168           |
| Ser Phe Ala Met Ser |
| 1 5                 |

<210> 169

<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 169  
Ala Ile Ser Gly Ser Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val Lys  
1 5 10 15  
Gly

<210> 170  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 170  
Asp Lys Ile Leu Trp Phe Gly Glu Pro Val Phe Asp Tyr  
1 5 10

<210> 171  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 171  
Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala  
1 5 10

<210> 172  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 172  
Asp Ala Ser Asn Arg Ala Thr



1

5

<210> 173

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 173

Gln Gln Arg Ser Asn Trp Pro Pro Thr  
1 5

<210> 174

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 174

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

<210> 175

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 175

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

<210> 176

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 176

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| Ser | Tyr | Arg | Met | His |
| 1   |     |     |     | 5   |

<210> 177

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 177

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ile | Asn | Pro | Ser | Thr | Gly | Tyr | Thr | Glu | Tyr | Asn | Gln | Lys | Phe | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 178

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 178

Gly Gly Gly Val Phe Asp Tyr

1

5

<210> 179

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 179

Ser Ala Ser Ser Ser Ile Ser Tyr Met His

1

5

10

<210> 180

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 180

Thr Thr Ser Asn Leu Ala Ser

1

5

<210> 181

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 181

His Gln Arg Ser Thr Tyr Pro Leu Thr

1

5

<210> 182

<211> 116

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 182  
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
1 5 10 15  
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
20 25 30  
Arg Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile  
35 40 45  
Gly Tyr Ile Asn Pro Ser Thr Gly Tyr Thr Glu Tyr Asn Gln Lys Phe  
50 55 60  
Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr  
65 70 75 80  
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Arg Gly Gly Gly Val Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110  
Thr Val Ser Ser  
115

<210> 183  
<211> 106  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 183  
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly  
1 5 10 15  
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Ile Ser Tyr Met  
20 25 30  
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr  
35 40 45  
Thr Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser  
50 55 60  
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp  
65 70 75 80  
Asp Phe Ala Thr Tyr Tyr Cys His Gln Arg Ser Thr Tyr Pro Leu Thr  
85 90 95  
Phe Gly Gln Gly Thr Lys Val Glu Val Lys  
100 105

<210> 184  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 184  
Ser Tyr Trp Met  
1

<210> 185  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 185  
Glu Ile Ile Pro Ile Asn Gly His Thr Asn Tyr Asn Glu Lys Phe Lys  
1 5 10 15  
Ser

<210> 186  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 186  
Gly Gly Tyr Tyr Tyr Gly Ser Arg Asp Tyr Phe Asp Tyr  
1 5 10

<210> 187  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 187

Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn  
1 5 10 15

<210> 188

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 188

Ala Ala Ser Asp Leu Glu Ser  
1 5

<210> 189

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 189

Gln Gln Ser His Glu Asp Pro Phe Thr  
1 5

<210> 190

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 190

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Ala | Arg | Gly | Gly | Tyr | Tyr | Tyr | Tyr | Gly | Ser | Arg | Asp | Tyr | Phe | Asp | Tyr |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Trp | Gly | Gln | Gly | Thr | Thr | Leu | Thr | Val | Ser | Ser |     |     |     |     |     |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |  |  |

<210> 191  
 <211> 111  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| <400> 191 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| Asp       | Ile | Val | Leu | Thr | Gln | Ser | Pro | Ala | Ser | Leu | Ala | Val | Ser | Leu | Gly |  |  |
| 1         |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Gln       | Arg | Ala | Thr | Ile | Ser | Cys | Lys | Ala | Ser | Gln | Ser | Val | Asp | Tyr | Asp |  |  |
|           |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Gly       | Asp | Ser | Tyr | Met | Asn | Trp | Tyr | Gln | Gln | Ile | Pro | Gly | Gln | Pro | Pro |  |  |
|           |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Lys       | Leu | Leu | Ile | Tyr | Ala | Ala | Ser | Asp | Leu | Glu | Ser | Gly | Ile | Pro | Ala |  |  |
|           | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |  |
| Arg       | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Asn | Ile | His |  |  |
| 65        |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |  |
| Pro       | Val | Glu | Glu | Glu | Asp | Ala | Ala | Thr | Tyr | Tyr | Cys | Gln | Gln | Ser | His |  |  |
|           |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Glu       | Asp | Pro | Phe | Thr | Phe | Gly | Gly | Gly | Thr | Lys | Leu | Glu | Ile | Lys |     |  |  |
|           |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |

<210> 192  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|           |     |     |     |
|-----------|-----|-----|-----|
| <400> 192 |     |     |     |
| Ser       | Tyr | Trp | Met |
| 1         |     |     |     |

<210> 193  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 193

Glu Ile Ile Pro Ile Phe Gly His Thr Asn Tyr Asn Glu Lys Phe Lys  
1 5 10 15

Ser

<210> 194

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 194

Gly Gly Tyr Tyr Tyr Tyr Pro Arg Gln Gly Phe Leu Asp Tyr  
1 5 10

<210> 195

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 195

Lys Ala Ser Gln Ser Val Asp Tyr Asp Ser Gly Asp Ser Tyr Met Asn  
1 5 10 15

<210> 196

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 196

Ala Ala Ser Asp Leu Glu Ser  
1 5

<210> 197



<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 197  
Gln Gln Ser His Glu Asp Pro Phe Thr  
1 5

<210> 198  
<211> 123  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 198  
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30  
Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Gly Glu Ile Ile Pro Ile Phe Gly His Thr Asn Tyr Asn Glu Lys Phe  
50 55 60  
Lys Ser Arg Phe Thr Ile Ser Leu Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Arg Gly Gly Tyr Tyr Tyr Tyr Pro Arg Gln Gly Phe Leu Asp Tyr  
100 105 110  
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
115 120

<210> 199  
<211> 111  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 199  
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly  
1 5 10 15

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

<210> 200  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 200  
 Tyr Gly Met Asn  
 1

<210> 201  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 201  
 Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Ala Asp Ser Val Lys Gly  
 1 5 10 15

<210> 202  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 202  
 Gly Pro Gly Met Asp Val

1 5

<210> 203  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 203  
Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu  
1 5 10 15  
Ala

<210> 204  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 204  
Trp Ala Ser Thr Arg Glu Ser  
1 5

<210> 205  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 205  
Gln Gln Tyr Tyr Ser Thr Pro Gln Leu Thr  
1 5 10

<210> 206  
<211> 112  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 206

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

<210> 207

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 207

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

Ile Lys

<210> 208

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 208

Thr Ser Gly Met Gly Val Gly

1

5

<210> 209

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 209

His Ile Trp Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ala Leu Lys Ser

1

5

10

15

<210> 210

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 210

Met Glu Leu Trp Ser Tyr Tyr Phe Asp Tyr

1

5

10

<210> 211

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 211

Ser Ala Ser Ser Ser Val Ser Tyr Met His

1

5

10

<210> 212

<211> 7

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 212  
Asp Thr Ser Lys Leu Ala Ser  
1 5

<210> 213  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 213  
Phe Gln Gly Ser Val Tyr Pro Phe Thr  
1 5

<210> 214  
<211> 120  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 214  
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln  
1 5 10 15  
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Thr Ser  
20 25 30  
Gly Met Gly Val Gly Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu  
35 40 45  
Trp Ile Gly His Ile Trp Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ala  
50 55 60  
Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe  
65 70 75 80  
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr  
85 90 95  
Cys Ala Arg Met Glu Leu Trp Ser Tyr Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110  
Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 215  
<211> 107  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 215  
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15  
Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Ser Tyr Met  
20 25 30  
His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr  
35 40 45  
Asp Thr Ser Lys Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser  
50 55 60  
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu  
65 70 75 80  
Asp Val Ala Val Tyr Tyr Cys Phe Gln Gly Ser Val Tyr Pro Phe Thr  
85 90 95  
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg  
100 105

<210> 216  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 216  
Asn Tyr Gly Met Asn  
1 5

<210> 217  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 217  
Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Ala Phe Lys  
1 5 10 15

Gly

<210> 218

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 218

Asp Tyr Gly Asp Tyr Gly Met Asp Tyr  
1 5

<210> 219

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 219

Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Phe Met His  
1 5 10 15

<210> 220

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 220

Leu Ala Ser Asn Leu Glu Ser  
1 5

<210> 221

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic



<400> 221

Gln His Ser Arg Glu Val Pro Trp Thr  
1 5

<210> 222

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 222

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

<210> 223

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 223

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly  
1 5 10 15  
Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Lys Ser Val Ser Thr Ser  
20 25 30  
Gly Tyr Ser Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro  
35 40 45  
Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Asp  
50 55 60

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr | Ile | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Leu | Gln | Ala | Glu | Asp | Val | Ala | Val | Tyr | Tyr | Cys | Gln | His | Ser | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Val | Pro | Trp | Thr | Phe | Gly | Gln | Gly | Thr | Lys | Val | Glu | Ile | Lys |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

<210> 224  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 224  
 Ser Gly Tyr Ser Trp His  
 1 5

<210> 225  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 225  
 Tyr Ile His Ser Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser  
 1 5 10 15

<210> 226  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 226  
 Tyr Asp Asp Tyr Phe Glu Tyr  
 1 5

<210> 227  
 <211> 11  
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 227

Lys Ala Ser Gln Asn Val Gly Phe Asn Val Ala  
1 5 10

<210> 228

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 228

Ser Ala Ser Tyr Arg Tyr Ser  
1 5

<210> 229

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 229

Gln Gln Tyr Asn Trp Tyr Pro Phe Thr  
1 5

<210> 230

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 230

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



<210> 233  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 233  
Glu Ile Leu Pro Gly Thr Gly Arg Thr Ile Tyr Asn Glu Lys Phe Lys  
1 5 10 15  
Gly

<210> 234  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 234  
Arg Asp Tyr Tyr Gly Asn Phe Tyr Tyr Ala Met Asp Tyr  
1 5 10

<210> 235  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 235  
Ser Ala Ser Gln Gly Ile Asn Asn Tyr Leu Asn  
1 5 10

<210> 236  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 236

Tyr Thr Ser Thr Leu Gln Ser  
1 5

<210> 237

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 237

Gln Gln Tyr Ser Lys Leu Pro Arg Thr  
1 5

<210> 238

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 238

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

<210> 239

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 239

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

<210> 240

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 240

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| Thr | Tyr | Gly | Met | Gly | Val | Gly |
| 1   |     |     |     | 5   |     |     |

<210> 241

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 241

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ile | Trp | Trp | Ser | Glu | Asp | Lys | His | Tyr | Ser | Pro | Ser | Leu | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

<210> 242

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 242

Ile Asp Tyr Gly Asn Asp Tyr Ala Phe Thr Tyr  
1 5 10

<210> 243

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 243

Arg Ser Ser Lys Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr  
1 5 10 15

<210> 244

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 244

Gln Met Ser Asn Leu Ala Ser  
1 5

<210> 245

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 245

Ala Gln Asn Leu Glu Leu Pro Tyr Thr  
1 5

<210> 246

<211> 121



<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 246

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

<210> 247  
<211> 112  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 247

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

<210> 248  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 248  
Arg Tyr Thr Met His  
1 5

<210> 249  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 249  
Val Ile Ser Phe Asp Gly Ser Asn Lys Tyr Tyr Val Asp Ser Val Lys  
1 5 10 15  
Gly

<210> 250  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 250  
Glu Ala Arg Gly Ser Tyr Ala Phe Asp Ile  
1 5 10

<210> 251  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 251

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala  
1 5 10

<210> 252

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 252

Asp Ala Ser Asn Arg Ala Thr  
1 5

<210> 253

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 253

Gln Gln Arg Ser Asn Trp Pro Pro Phe Thr  
1 5 10

<210> 254

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 254

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ala | Arg | Glu | Ala | Arg | Gly | Ser | Tyr | Ala | Phe | Asp | Ile | Trp | Gly | Gln | Gly |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Thr | Met | Val | Thr | Val | Ser | Ser |     |     |     |     |     |     |     |     |     |  |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |  |

<210> 255  
 <211> 108  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| <400> 255 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Glu       | Ile | Val | Leu | Thr | Gln | Ser | Pro | Ala | Thr | Leu | Ser | Leu | Ser | Pro | Gly |  |
| 1         |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Glu       | Arg | Ala | Thr | Leu | Ser | Cys | Arg | Ala | Ser | Gln | Ser | Val | Ser | Ser | Tyr |  |
|           |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu       | Ala | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Gln | Ala | Pro | Arg | Leu | Leu | Ile |  |
|           |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Tyr       | Asp | Ala | Ser | Asn | Arg | Ala | Thr | Gly | Ile | Pro | Ala | Arg | Phe | Ser | Gly |  |
|           | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ser       | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr | Ile | Ser | Ser | Leu | Glu | Pro |  |
| 65        |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Glu       | Asp | Phe | Ala | Val | Tyr | Tyr | Cys | Gln | Gln | Arg | Ser | Asn | Trp | Pro | Pro |  |
|           |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Phe       | Thr | Phe | Gly | Pro | Gly | Thr | Lys | Val | Asp | Ile | Lys |     |     |     |     |  |
|           |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |  |

<210> 256  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|           |     |     |     |     |
|-----------|-----|-----|-----|-----|
| <400> 256 |     |     |     |     |
| Ser       | Phe | Gly | Met | His |
| 1         |     |     | 5   |     |

<210> 257  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 257

Tyr Ile Ser Ser Gly Ser Phe Thr Ile Tyr Tyr Ala Asp Ser Val Lys  
1 5 10 15

Gly

<210> 258

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 258

Met Arg Lys Gly Tyr Ala Met Asp Tyr  
1 5

<210> 259

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 259

Arg Ser Ser Gln Ile Ile Ile His Ser Asp Gly Asn Thr Tyr Leu Glu  
1 5 10 15

<210> 260

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 260

Lys Val Ser Asn Arg Phe Ser  
1 5

<210> 261

<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 261  
Phe Gln Gly Ser His Val Pro His Thr  
1 5

<210> 262  
<211> 118  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 262  
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe  
20 25 30  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Ala Tyr Ile Ser Ser Gly Ser Phe Thr Ile Tyr Tyr Ala Asp Ser Val  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Arg Met Arg Lys Gly Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr  
100 105 110  
Leu Val Thr Val Ser Ser  
115

<210> 263  
<211> 112  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 263  
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly  
1 5 10 15

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

<210> 264  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 264  
 Asn Tyr Gly Val Asn  
 1 5

<210> 265  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 265  
 Trp Ile Asn Pro Asn Thr Gly Glu Pro Thr Phe Asp Asp Asp Phe Lys  
 1 5 10 15  
 Gly

<210> 266  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 266  
Ser Arg Gly Lys Asn Glu Ala Trp Phe Ala Tyr  
1 5 10

<210> 267  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 267  
Arg Ser Ser Gln Ser Leu Val His Arg Asn Gly Asn Thr Tyr Leu His  
1 5 10 15

<210> 268  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 268  
Thr Val Ser Asn Arg Phe Ser  
1 5

<210> 269  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 269  
Ser Gln Ser Ser His Val Pro Pro Thr  
1 5

<210> 270  
<211> 120  
<212> PRT  
<213> Artificial Sequence

<220>



<223> Synthetic

<400> 270

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

<210> 271

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 271

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

<210> 272

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 272

Thr Tyr Trp Met Ser

1 5

<210> 273

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 273

Glu Ile His Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu Lys

1 5 10 15

Asp

<210> 274

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 274

Leu Tyr Phe Gly Phe Pro Trp Phe Ala Tyr

1 5 10

<210> 275

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 275

Lys Ala Ser Gln Asp Val Gly Thr Ser Val Ala

1 5 10

<210> 276  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 276  
Trp Thr Ser Thr Arg His Thr  
1 5

<210> 277  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 277  
Gln Gln Tyr Ser Leu Tyr Arg Ser  
1 5

<210> 278  
<211> 119  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 278  
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe Thr Thr Tyr  
20 25 30  
Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45  
Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu  
50 55 60  
Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Phe  
65 70 75 80  
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys  
85 90 95  
Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala Tyr Trp Gly Gln Gly  
100 105 110  
Thr Pro Val Thr Val Ser Ser

<210> 279  
 <211> 106  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 279  
 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Ser  
 20 25 30  
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45  
 Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu Tyr Arg Ser  
 85 90 95  
 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
 100 105

<210> 280  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 280  
 Tyr Tyr Gly Met Asn  
 1 5

<210> 281  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 281

Trp Ile Asp Thr Thr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe Gln  
1 5 10 15  
Gly

<210> 282  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 282  
Arg Gly Pro Tyr Asn Trp Tyr Phe Asp Val  
1 5 10

<210> 283  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 283  
Arg Ser Ser Lys Ser Leu Leu His Ser Asn Gly Asn Thr Tyr Leu Tyr  
1 5 10 15

<210> 284  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 284  
Arg Met Ser Asn Leu Val Ser  
1 5

<210> 285  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 285

Leu Gln His Leu Glu Tyr Pro Phe Thr  
1 5

<210> 286

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 286

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

<210> 287

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 287

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Gln | Leu | Leu | Ile | Tyr | Arg | Met | Ser | Asn | Leu | Val | Ser | Gly | Val | Pro |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Ala | Phe | Thr | Leu | Arg | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Arg | Val | Glu | Ala | Glu | Asp | Val | Gly | Val | Tyr | Tyr | Cys | Leu | Gln | His |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Glu | Tyr | Pro | Phe | Thr | Phe | Gly | Pro | Gly | Thr | Lys | Leu | Glu | Leu | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

<210> 288  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 288  
 Asn Tyr Gly Met Asn  
 1 5

<210> 289  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 289  
 Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe Lys  
 1 5 10 15  
 Gly

<210> 290  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 290  
 Ile Gly Asp Ser Ser Pro Ser Asp Tyr  
 1 5

<210> 291  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 291  
Lys Ala Ser Gln Ser Val Ser Asn Asp Val Val  
1 5 10

<210> 292  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 292  
Tyr Ala Ser Asn Arg Tyr Thr  
1 5

<210> 293  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 293  
Gln Gln Asp Tyr Thr Ser Pro Trp Thr  
1 5

<210> 294  
<211> 118  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 294  
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala



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

<210> 295  
 <211> 107  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| <400> 295 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Glu       | Ile | Val | Met | Thr | Gln | Ser | Pro | Ala | Thr | Leu | Ser | Val | Ser | Pro | Gly |  |
| 1         |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Glu       | Arg | Ala | Thr | Leu | Ser | Cys | Lys | Ala | Ser | Gln | Ser | Val | Ser | Asn | Asp |  |
|           |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |
| Val       | Val | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Gln | Ala | Pro | Arg | Leu | Leu | Ile |  |
|           |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Tyr       | Tyr | Ala | Ser | Asn | Arg | Tyr | Thr | Gly | Ile | Pro | Ala | Arg | Phe | Ser | Gly |  |
|           | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ser       | Gly | Ser | Gly | Thr | Glu | Phe | Thr | Leu | Thr | Ile | Ser | Ser | Leu | Gln | Ser |  |
| 65        |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Glu       | Asp | Phe | Ala | Val | Tyr | Tyr | Cys | Gln | Gln | Asp | Tyr | Thr | Ser | Pro | Trp |  |
|           |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Thr       | Phe | Gly | Gln | Gly | Thr | Lys | Leu | Glu | Ile | Lys |     |     |     |     |     |  |
|           |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |  |

<210> 296  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 296

Ser Tyr Trp Ile Glu  
1 5

<210> 297

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 297

Glu Ile Leu Pro Gly Ser Gly Asn Thr Tyr Tyr Asn Glu Arg Phe Lys  
1 5 10 15  
Asp

<210> 298

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 298

Arg Ala Ala Ala Tyr Tyr Ser Asn Pro Glu Trp Phe Ala Tyr  
1 5 10

<210> 299

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 299

Thr Ala Ser Ser Ser Val Asn Ser Phe Tyr Leu His  
1 5 10

<210> 300

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 300

Ser Thr Ser Asn Leu Ala Ser

1

5

<210> 301

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 301

His Gln Tyr His Arg Ser Pro Tyr Thr

1

5

<210> 302

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 302

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser

1

5

10

15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr

20

25

30

Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35

40

45

Gly Glu Ile Leu Pro Gly Ser Gly Asn Thr Tyr Tyr Asn Glu Arg Phe

50

55

60

Lys Asp Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr

65

70

75

80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Arg Ala Ala Ala Tyr Tyr Ser Asn Pro Glu Trp Phe Ala Tyr

100

105

110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 303

<211> 108  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 303  
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15  
Glu Arg Ala Thr Leu Ser Cys Thr Ala Ser Ser Ser Val Asn Ser Phe  
20 25 30  
Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Leu Ala Pro Arg Leu Leu  
35 40 45  
Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Ile Pro Asp Arg Phe Ser  
50 55 60  
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80  
Pro Glu Asp Phe Ala Val Tyr Tyr Cys His Gln Tyr His Arg Ser Pro  
85 90 95  
Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
100 105

<210> 304  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 304  
Ser Tyr Trp Met Gln  
1 5

<210> 305  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 305  
Thr Ile Tyr Pro Gly Asp Gly Asp Thr Thr Tyr Thr Gln Lys Phe Gln  
1 5 10 15  
Gly

<210> 306  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 306  
Tyr Asp Ala Pro Gly Tyr Ala Met Asp Tyr  
1 5 10

<210> 307  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 307  
Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Ala  
1 5 10

<210> 308  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 308  
Tyr Thr Ser Thr Leu His Pro  
1 5

<210> 309  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 309

Leu Gln Tyr Asp Asn Leu Leu Tyr Thr  
1 5

<210> 310

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 310

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

<210> 311

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 311

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Gln | Met | Thr | Gln | Ser | Pro | Ser | Ser | Leu | Ser | Ala | Ser | Val | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asp | Arg | Val | Thr | Ile | Thr | Cys | Arg | Ala | Ser | Gln | Asp | Ile | Asn | Asn | Tyr |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Leu | Ala | Trp | Tyr | Gln | His | Lys | Pro | Gly | Lys | Gly | Pro | Lys | Leu | Leu | Ile |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| His | Tyr | Thr | Ser | Thr | Leu | His | Pro | Gly | Ile | Pro | Ser | Arg | Phe | Ser | Gly |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Ser | Gly | Ser | Gly | Arg | Asp | Tyr | Ser | Phe | Ser | Ile | Ser | Ser | Leu | Glu | Pro |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |

Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Asn Leu Leu Tyr  
85 90 95  
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
100 105

<210> 312  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 312  
Arg Asp Phe Ala Trp Asn  
1 5

<210> 313  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 313  
Tyr Ile Ser Tyr Asn Gly Asn Thr Arg Tyr Gln Pro Ser Leu Lys Ser  
1 5 10 15

<210> 314  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 314  
Ala Ser Arg Gly Phe Pro Tyr  
1 5

<210> 315  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 315

His Ser Ser Gln Asp Ile Asn Ser Asn Ile Gly  
1 5 10

<210> 316

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 316

His Gly Thr Asn Leu Asp Asp  
1 5

<210> 317

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 317

Val Gln Tyr Ala Gln Phe Pro Trp Thr  
1 5

<210> 318

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 318

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



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 50  |     | 55  |     | 60  |     |     |     |     |     |     |     |     |     |     |     |
| Lys | Ser | Arg | Ile | Thr | Ile | Ser | Arg | Asp | Thr | Ser | Lys | Asn | Gln | Phe | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Lys | Leu | Asn | Ser | Val | Thr | Ala | Ala | Asp | Thr | Ala | Thr | Tyr | Tyr | Cys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Thr | Ala | Ser | Arg | Gly | Phe | Pro | Tyr | Trp | Gly | Gln | Gly | Thr | Leu | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Val | Ser | Ser |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 319  
 <211> 107  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 319 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Asp       | Ile | Gln | Met | Thr | Gln | Ser | Pro | Ser | Ser | Met | Ser | Val | Ser | Val | Gly |
| 1         |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp       | Arg | Val | Thr | Ile | Thr | Cys | His | Ser | Ser | Gln | Asp | Ile | Asn | Ser | Asn |
|           |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile       | Gly | Trp | Leu | Gln | Gln | Lys | Pro | Gly | Lys | Ser | Phe | Lys | Gly | Leu | Ile |
|           |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Tyr       | His | Gly | Thr | Asn | Leu | Asp | Asp | Gly | Val | Pro | Ser | Arg | Phe | Ser | Gly |
|           | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ser       | Gly | Ser | Gly | Thr | Asp | Tyr | Thr | Leu | Thr | Ile | Ser | Ser | Leu | Gln | Pro |
| 65        |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Glu       | Asp | Phe | Ala | Thr | Tyr | Tyr | Cys | Val | Gln | Tyr | Ala | Gln | Phe | Pro | Trp |
|           |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Thr       | Phe | Gly | Gly | Gly | Thr | Lys | Leu | Glu | Ile | Lys |     |     |     |     |     |
|           |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

<210> 320  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|           |     |     |     |     |     |
|-----------|-----|-----|-----|-----|-----|
| <400> 320 |     |     |     |     |     |
| Arg       | Asp | Phe | Ala | Trp | Asn |
| 1         |     |     |     | 5   |     |

<210> 321

<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 321  
Tyr Ile Ser Tyr Asn Gly Asn Thr Arg Tyr Gln Pro Ser Leu Lys Ser  
1 5 10 15

<210> 322  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 322  
Ala Ser Arg Gly Phe Pro Tyr  
1 5

<210> 323  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 323  
His Ser Ser Gln Asp Ile Asn Ser Asn Ile Gly  
1 5 10

<210> 324  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 324  
His Gly Thr Asn Leu Asp Asp  
1 5

<210> 325  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 325  
Val Gln Tyr Ala Gln Phe Pro Trp Thr  
1 5

<210> 326  
<211> 116  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 326  
Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln  
1 5 10 15  
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Ser Arg Asp  
20 25 30  
Phe Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp  
35 40 45  
Met Gly Tyr Ile Ser Tyr Asn Gly Asn Thr Arg Tyr Gln Pro Ser Leu  
50 55 60  
Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Phe  
65 70 75 80  
Leu Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Thr Tyr Tyr Cys  
85 90 95  
Val Thr Ala Ser Arg Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110  
Thr Val Ser Ser  
115

<210> 327  
<211> 107  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 327

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

<210> 328

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 328

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| Asn | Tyr | Gly | Val | His |
| 1   |     |     | 5   |     |

<210> 329

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 329

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Trp | Ser | Gly | Gly | Asn | Thr | Asp | Tyr | Asn | Thr | Pro | Phe | Thr | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

<210> 330

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 330

Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr  
1 5 10

<210> 331

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 331

Arg Ala Ser Gln Ser Ile Gly Thr Asn Ile His  
1 5 10

<210> 332

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 332

Tyr Ala Ser Glu Ser Ile Ser  
1 5

<210> 333

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 333

Gln Gln Asn Asn Asn Trp Pro Thr Thr  
1 5

<210> 334

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 334

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

<210> 335

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 335

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

<210> 336

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 336

Gly Tyr Phe Met Asn

1

5

<210> 337

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 337

Arg Ile His Pro Tyr Asp Gly Asp Thr Phe Tyr Asn Gln Lys Phe Gln

1

5

10

15

Gly

<210> 338

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 338

Tyr Asp Gly Ser Arg Ala Met Asp Tyr

1

5

<210> 339

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 339

Lys Ala Ser Gln Ser Val Ser Phe Ala Gly Thr Ser Leu Met His

1

5

10

15

<210> 340  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 340  
Arg Ala Ser Asn Leu Glu Ala  
1 5

<210> 341  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 341  
Gln Gln Ser Arg Glu Tyr Pro Tyr Thr  
1 5

<210> 342  
<211> 118  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 342  
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Val Lys Pro Gly Ala  
1 5 10 15  
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr  
20 25 30  
Phe Met Asn Trp Val Lys Gln Ser Pro Gly Gln Ser Leu Glu Trp Ile  
35 40 45  
Gly Arg Ile His Pro Tyr Asp Gly Asp Thr Phe Tyr Asn Gln Lys Phe  
50 55 60  
Gln Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Asn Thr Ala His  
65 70 75 80  
Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Phe Ala Val Tyr Tyr Cys  
85 90 95  
Thr Arg Tyr Asp Gly Ser Arg Ala Met Asp Tyr Trp Gly Gln Gly Thr  
100 105 110  
Thr Val Thr Val Ser Ser



<210> 343  
 <211> 111  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 343  
 Asp Ile Val Leu Thr Gln Ser Pro Leu Ser Leu Ala Val Ser Leu Gly  
 1 5 10 15  
 Gln Pro Ala Ile Ile Ser Cys Lys Ala Ser Gln Ser Val Ser Phe Ala  
 20 25 30  
 Gly Thr Ser Leu Met His Trp Tyr His Gln Lys Pro Gly Gln Gln Pro  
 35 40 45  
 Arg Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ala Gly Val Pro Asp  
 50 55 60  
 Arg Phe Ser Gly Ser Gly Ser Lys Thr Asp Phe Thr Leu Thr Ile Ser  
 65 70 75 80  
 Pro Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Arg  
 85 90 95  
 Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
 100 105 110

<210> 344  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 344  
 Gly Tyr Gly Leu Ser  
 1 5

<210> 345  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 345

Met Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Ala Asp Ser Val Lys  
1 5 10 15  
Gly

<210> 346  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 346  
His Gly Asp Asp Pro Ala Trp Phe Ala Tyr  
1 5 10

<210> 347  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 347  
Ser Val Ser Ser Ser Ile Ser Ser Asn Asn Leu His  
1 5 10

<210> 348  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 348  
Gly Thr Ser Asn Leu Ala Ser  
1 5

<210> 349  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 349

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Gln | Trp | Ser | Ser | Tyr | Pro | Tyr | Met | Tyr | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

<210> 350

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 350

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

<210> 351

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 351

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Gln | Leu | Thr | Gln | Ser | Pro | Ser | Ser | Leu | Ser | Ala | Ser | Val | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Arg | Val | Thr | Ile | Thr | Cys | Ser | Val | Ser | Ser | Ser | Ile | Ser | Ser | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Leu | His | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys | Ala | Pro | Lys | Pro | Trp |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Tyr | Gly | Thr | Ser | Asn | Leu | Ala | Ser | Gly | Val | Pro | Ser | Arg | Phe | Ser |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Ser | Gly | Ser | Gly | Thr | Asp | Tyr | Thr | Phe | Thr | Ile | Ser | Ser | Leu | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Glu | Asp | Ile | Ala | Thr | Tyr | Tyr | Cys | Gln | Gln | Trp | Ser | Ser | Tyr | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Met | Tyr | Thr | Phe | Gly | Gln | Gly | Thr | Lys | Val | Glu | Ile | Lys |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

<210> 352  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 352  
 Asn Tyr Trp Met Asn  
 1 5

<210> 353  
 <211> 19  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 353  
 Glu Ile Arg Leu Lys Ser Asn Asn Tyr Thr Thr His Tyr Ala Glu Ser  
 1 5 10 15  
 Val Lys Gly

<210> 354  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 354  
 His Tyr Tyr Phe Asp Tyr  
 1 5

<210> 355  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 355  
Arg Ser Ser Lys Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Phe Phe  
1 5 10 15

<210> 356  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 356  
Gln Met Ser Asn Leu Ala Ser  
1 5

<210> 357  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 357  
Ala Gln Asn Leu Glu Leu Pro Pro Thr  
1 5

<210> 358  
<211> 117  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 358  
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

<210> 359  
 <211> 112  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| <400> 359 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Asp       | Ile | Val | Met | Thr | Gln | Ser | Pro | Leu | Ser | Asn | Pro | Val | Thr | Pro | Gly |  |
| 1         |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Glu       | Pro | Ala | Ser | Ile | Ser | Cys | Arg | Ser | Ser | Lys | Ser | Leu | Leu | His | Ser |  |
|           |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Asn       | Gly | Ile | Thr | Tyr | Phe | Phe | Trp | Tyr | Leu | Gln | Lys | Pro | Gly | Gln | Ser |  |
|           | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Pro       | Gln | Leu | Leu | Ile | Tyr | Gln | Met | Ser | Asn | Leu | Ala | Ser | Gly | Val | Pro |  |
|           | 50  |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |     |  |
| Asp       | Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Arg | Ile |  |
| 65        |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |
| Ser       | Arg | Val | Glu | Ala | Glu | Asp | Val | Gly | Val | Tyr | Tyr | Cys | Ala | Gln | Asn |  |
|           |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |     |  |
| Leu       | Glu | Leu | Pro | Pro | Thr | Phe | Gly | Gln | Gly | Thr | Lys | Val | Glu | Ile | Lys |  |
|           |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |

<210> 360  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 360  
Ser Tyr Trp Ile Gly  
1 5

<210> 361  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 361  
Ile Ile Asp Pro Gly Asp Ser Arg Thr Arg Tyr Ser Pro Ser Phe Gln  
1 5 10 15  
Gly

<210> 362  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 362  
Gly Gln Leu Tyr Gly Gly Thr Tyr Met Asp Gly  
1 5 10

<210> 363  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 363  
Thr Gly Thr Ser Ser Asp Ile Gly Gly Tyr Asn Ser Val Ser  
1 5 10

<210> 364  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 364

Gly Val Asn Asn Arg Pro Ser

1

5

<210> 365

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 365

Ser Ser Tyr Asp Ile Glu Ser Ala Thr Pro Val

1

5

10

<210> 366

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 366

Gln Val Glu Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu

1

5

10

15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr

20

25

30

Trp Ile Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met

35

40

45

Gly Ile Ile Asp Pro Gly Asp Ser Arg Thr Arg Tyr Ser Pro Ser Phe

50

55

60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr

65

70

75

80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys

85

90

95

Ala Arg Gly Gln Leu Tyr Gly Gly Thr Tyr Met Asp Gly Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 367



<211> 111  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 367  
Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln  
1 5 10 15  
Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Ile Gly Gly Tyr  
20 25 30  
Asn Ser Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu  
35 40 45  
Met Ile Tyr Gly Val Asn Asn Arg Pro Ser Gly Val Ser Asn Arg Phe  
50 55 60  
Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu  
65 70 75 80  
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Asp Ile Glu  
85 90 95  
Ser Ala Thr Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu  
100 105 110

<210> 368  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 368  
Ala Tyr Asn Ile His  
1 5

<210> 369  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 369  
Ser Phe Asp Pro Tyr Asp Gly Gly Ser Ser Tyr Asn Gln Lys Phe Lys  
1 5 10 15  
Asp

<210> 370  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 370  
Gly Trp Tyr Tyr Phe Asp Tyr  
1 5

<210> 371  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 371  
Arg Ala Ser Lys Ser Ile Ser Lys Tyr Leu Ala  
1 5 10

<210> 372  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 372  
Ser Gly Ser Thr Leu Gln Ser  
1 5

<210> 373  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 373

Gln Gln His Asp Glu Ser Pro Tyr Thr  
1 5

<210> 374

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 374

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

<210> 375

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 375

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Asp | Ala | Ala | Tyr | Tyr | Phe | Cys | Gln | Gln | His | Asp | Glu | Ser | Pro | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Phe | Gly | Glu | Gly | Thr | Lys | Val | Glu | Ile | Lys |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

<210> 376  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|           |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|
| <400> 376 |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |
| Gly       | Ser | Ile | Lys | Ser | Gly | Ser | Tyr | Tyr | Trp | Gly |  |  |  |  |  |
| 1         |     |     |     | 5   |     |     |     |     | 10  |     |  |  |  |  |  |

<210> 377  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 377 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Asn       | Ile | Tyr | Tyr | Ser | Gly | Ser | Thr | Tyr | Tyr | Asn | Pro | Ser | Leu | Arg | Ser |
| 1         |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

<210> 378  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|           |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| <400> 378 |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
| Ala       | Arg | Glu | Gly | Ser | Tyr | Pro | Asn | Gln | Phe | Asp | Pro |  |  |  |  |
| 1         |     |     |     | 5   |     |     |     |     | 10  |     |     |  |  |  |  |

<210> 379  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 379

Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala  
1 5 10

<210> 380

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 380

Gly Ala Ser Thr Arg Ala Thr  
1 5

<210> 381

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 381

Gln Gln Tyr His Ser Phe Pro Phe Thr  
1 5

<210> 382

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 382

Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15  
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Lys Ser Gly  
20 25 30  
Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu  
35 40 45  
Trp Ile Gly Asn Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 50  |     | 55  |     | 60  |     |     |     |     |     |     |     |     |     |     |     |
| Leu | Arg | Ser | Arg | Val | Thr | Ile | Ser | Val | Asp | Thr | Ser | Lys | Asn | Gln | Phe |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Ser | Leu | Lys | Leu | Ser | Ser | Val | Thr | Ala | Ala | Asp | Thr | Ala | Val | Tyr | Tyr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Cys | Ala | Arg | Glu | Gly | Ser | Tyr | Pro | Asn | Gln | Phe | Asp | Pro | Trp | Gly | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Thr | Leu | Val | Thr | Val | Ser | Ser |     |     |     |     |     |     |     |     |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |     |     |

<210> 383  
 <211> 107  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|                                                                 |
|-----------------------------------------------------------------|
| <400> 383                                                       |
| Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly |
| 1 5 10 15                                                       |
| Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn |
| 20 25 30                                                        |
| Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile |
| 35 40 45                                                        |
| Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly |
| 50 55 60                                                        |
| Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser |
| 65 70 75 80                                                     |
| Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr His Ser Phe Pro Phe |
| 85 90 95                                                        |
| Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys                     |
| 100 105                                                         |

<210> 384  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|                     |
|---------------------|
| <400> 384           |
| Ser Phe Gly Met His |
| 1 5                 |

<210> 385

<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 385  
Tyr Ile Ser Ser Asp Ser Ser Ala Ile Tyr Tyr  
1 5 10

<210> 386  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 386  
Gly Arg Glu Asn Ile Tyr Tyr Gly Ser Arg Leu Asp  
1 5 10

<210> 387  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 387  
Lys Ala Ser Gln Asn Val Asp  
1 5

<210> 388  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 388  
Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp  
1 5 10

<210> 389  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 389  
Gln Gln Tyr Asn Asn Tyr Pro Phe Thr Phe Gly Ser  
1 5 10

<210> 390  
<211> 122  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 390  
Asp Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
Ser Arg Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe  
20 25 30  
Gly Met His Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu Trp Val  
35 40 45  
Ala Tyr Ile Ser Ser Asp Ser Ser Ala Ile Tyr Tyr Ala Asp Thr Val  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Pro Lys Asn Thr Leu Phe  
65 70 75 80  
Leu Gln Met Thr Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys  
85 90 95  
Gly Arg Gly Arg Glu Asn Ile Tyr Tyr Gly Ser Arg Leu Asp Tyr Trp  
100 105 110  
Gly Gln Gly Thr Thr Leu Thr Val Ser Ser  
115 120

<210> 391  
<211> 107  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 391



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

<210> 392

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 392

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Tyr | Trp | Met | Gln | Trp | Val | Arg | Gln | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

<210> 393

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 393

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ile | Tyr | Pro | Gly | Asp | Gly | Asp | Thr | Arg | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

<210> 394

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 394  
Arg Gly Ile Pro Arg Leu Trp Tyr Phe Asp Val Met  
1 5 10

<210> 395  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 395  
Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser  
1 5 10

<210> 396  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 396  
Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser  
1 5 10

<210> 397  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 397  
Gln Gln Gly Asn Thr Leu Pro Pro Phe Thr Gly Gly  
1 5 10

<210> 398  
<211> 122  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 398

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

<210> 399

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 399

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

<210> 400

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 400

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Tyr | Gly | Met | Ser | Trp | Val | Arg | Gln | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

<210> 401

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 401

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Asn | Ser | Gly | Gly | Ser | Asn | Thr | Tyr | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

<210> 402

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 402

|     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Asp | Gly | Gly | Ala | Met | Asp | Tyr | Trp |
| 1   |     |     |     | 5   |     |     |     |     |

<210> 403

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 403

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Thr | Cys | Arg | Ala | Ser | Glu | Ser | Ile | Tyr | Ser | Tyr | Leu | Ala |
| 1   |     |     |     | 5   |     |     |     |     |     |     |     | 10  |     |

<210> 404

<211> 7

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 404  
Asn Thr Lys Thr Leu Pro Glu  
1 5

<210> 405  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 405  
His His Tyr Gly Thr Pro Pro Trp Thr Phe Gly  
1 5 10

<210> 406  
<211> 117  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 406  
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30  
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Ala Thr Ile Asn Ser Gly Gly Ser Asn Thr Tyr Tyr Pro Asp Ser Leu  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Arg His Asp Gly Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr  
100 105 110  
Val Thr Val Ser Ser  
115

<210> 407  
<211> 108  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 407  
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15  
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Ser Ile Tyr Ser Tyr  
20 25 30  
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Val  
35 40 45  
Tyr Asn Thr Lys Thr Leu Pro Glu Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60  
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80  
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His His Tyr Gly Thr Pro Pro  
85 90 95  
Trp Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys  
100 105

<210> 408  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 408  
Ser Phe Gly Met His Trp Val Arg Gln Ala  
1 5 10

<210> 409  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 409  
Ile Ser Ser Gly Ser Gly Thr Ile Tyr Tyr Ala Asp Thr Val Lys Gly  
1 5 10 15

Arg Phe Thr Ile  
20

<210> 410  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 410  
His Gly Tyr Arg Tyr Glu Gly Phe Asp Tyr Trp Gly  
1 5 10

<210> 411  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 411  
Ile Thr Cys Lys Ala Ser Gln Asn Val Asp Thr Asn Val Ala  
1 5 10

<210> 412  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 412  
Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser  
1 5 10

<210> 413  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 413

Gln Gln Tyr Asn Asn Tyr Pro Phe Thr Phe Gly Gln  
1 5 10

<210> 414

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 414

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

<210> 415

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 415

Asp Ile Gln Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly  
1 5 10 15  
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Asp Thr Asn  
20 25 30  
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile  
35 40 45  
Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr | Ile | Ser | Ser | Leu | Gln | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Asp | Phe | Ala | Glu | Tyr | Phe | Cys | Gln | Gln | Tyr | Asn | Asn | Tyr | Pro | Phe |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Phe | Gly | Gln | Gly | Thr | Lys | Leu | Glu | Ile | Lys |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

<210> 416  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 416  
 Asn Tyr Val Met His  
 1 5

<210> 417  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 417  
 Tyr Ile Asn Pro Tyr Asn Asp Asp Val Lys Tyr Asn Glu Lys Phe Lys  
 1 5 10 15  
 Gly

<210> 418  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 418  
 Trp Gly Tyr Tyr Gly Ser Pro Leu Tyr Tyr Phe Asp Tyr  
 1 5 10

<210> 419

<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 419  
Arg Ala Ser Ser Arg Leu Ile Tyr Met His  
1 5 10

<210> 420  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 420  
Ala Thr Ser Asn Leu Ala Ser  
1 5

<210> 421  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 421  
Gln Gln Trp Asn Ser Asn Pro Pro Thr  
1 5

<210> 422  
<211> 122  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 422  
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala  
1 5 10 15  
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr

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

<210> 423

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 423

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

<210> 424

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 424

Asn Tyr Val Met His

1 5

<210> 425  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 425  
Tyr Ile Asn Pro Tyr Asn Asp Asp Val Lys Tyr Asn Glu Lys Phe Lys  
1 5 10 15  
Gly

<210> 426  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 426  
Trp Gly Tyr Tyr Gly Ser Pro Leu Tyr Tyr Phe Asp Tyr  
1 5 10

<210> 427  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 427  
Arg Ala Ser Ser Arg Leu Ile Tyr Met His  
1 5 10

<210> 428  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 428

Ala Thr Ser Asn Leu Ala Ser  
1 5

<210> 429

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 429

Gln Gln Trp Asn Ser Asn Pro Pro Thr  
1 5

<210> 430

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 430

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

<210> 431

<211> 106

<212> PRT

Tyr Ile Asn Pro Asn Ser Arg Asn Thr Asp Tyr Ala Gln Lys Phe Gln  
1 5 10 15  
Gly

<210> 434  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 434  
Tyr Ser Gly Ser Thr Pro Tyr Trp Tyr Phe Asp Val  
1 5 10

<210> 435  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 435  
Arg Ala Ser Ser Ser Val Ser Tyr Met Asn  
1 5 10

<210> 436  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 436  
Ala Thr Ser Asn Leu Ala Ser  
1 5

<210> 437  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 437  
Gln Gln Trp Ser Ser Asn Pro Leu Thr  
1 5

<210> 438  
<211> 121  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 438  
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
1 5 10 15  
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr  
20 25 30  
Thr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45  
Gly Tyr Ile Asn Pro Asn Ser Arg Asn Thr Asp Tyr Ala Gln Lys Phe  
50 55 60  
Gln Gly Arg Val Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr  
65 70 75 80  
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Arg Tyr Ser Gly Ser Thr Pro Tyr Trp Tyr Phe Asp Val Trp Gly  
100 105 110  
Gln Gly Thr Thr Val Thr Val Ser Ser  
115 120

<210> 439  
<211> 107  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 439  
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15  
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Phe Asn  
20 25 30  
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Ala Leu Ile  
35 40 45  
Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60  
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80  
Glu Asp Phe Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Trp Tyr Pro Phe  
85 90 95



Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
100 105

<210> 440

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 440

Gly Tyr Thr Phe Ser Ser Tyr Trp Met His  
1 5 10

<210> 441

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 441

Leu Ile His Pro Asp Ser Gly Ser Thr Asn Tyr Asn Glu Met Phe Lys  
1 5 10 15  
Asn

<210> 442

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 442

Gly Gly Arg Leu Tyr Phe Asp  
1 5

<210> 443

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 443

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Ser | Gln | Ser | Leu | Val | His | Ser | Asn | Gly | Asp | Thr | Tyr | Leu | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

<210> 444

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 444

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| Lys | Val | Ser | Asn | Arg | Phe | Ser |
| 1   |     |     |     | 5   |     |     |

<210> 445

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 445

|     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gln | Ser | Thr | His | Val | Pro | Tyr | Thr |
| 1   |     |     |     | 5   |     |     |     |     |

<210> 446

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 446

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 50  |     | 55  |     | 60  |     |     |     |     |     |     |     |     |     |     |     |
| Lys | Asn | Arg | Ala | Thr | Leu | Thr | Val | Asp | Arg | Ser | Thr | Ser | Thr | Ala | Tyr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Glu | Leu | Ser | Ser | Leu | Arg | Ser | Glu | Asp | Thr | Ala | Val | Tyr | Phe | Cys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Gly | Gly | Gly | Arg | Leu | Tyr | Phe | Asp | Tyr | Trp | Gly | Gln | Gly | Thr | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Thr | Val | Ser | Ser |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 447  
 <211> 112  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|                                                                 |
|-----------------------------------------------------------------|
| <400> 447                                                       |
| Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly |
| 1 5 10 15                                                       |
| Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser |
| 20 25 30                                                        |
| Asn Gly Asp Thr Tyr Leu Arg Trp Tyr Leu Gln Lys Pro Gly Gln Ser |
| 35 40 45                                                        |
| Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro |
| 50 55 60                                                        |
| Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile |
| 65 70 75 80                                                     |
| Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Ser |
| 85 90 95                                                        |
| Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys |
| 100 105 110                                                     |

<210> 448  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|                                         |
|-----------------------------------------|
| <400> 448                               |
| Gly Tyr Thr Phe Ser Ser Tyr Trp Met His |
| 1 5 10                                  |

<210> 449

<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 449  
Leu Ile His Pro Glu Ser Gly Ser Thr Asn Tyr Asn Glu Met Phe Lys  
1 5 10 15  
Asn

<210> 450  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 450  
Gly Gly Arg Leu Tyr Phe Asp Tyr  
1 5

<210> 451  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 451  
Arg Ser Ser Gln Ser Leu Val His Ser Asn Gln Asp Thr Tyr Leu Arg  
1 5 10 15

<210> 452  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 452  
Lys Val Ser Asn Arg Phe Ser

1

5

<210> 453

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 453

Ser Gln Ser Thr His Val Pro Tyr Thr

1

5

<210> 454

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 454

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser

1

5

10

15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Ser Tyr

20

25

30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile

35

40

45

Gly Leu Ile His Pro Glu Ser Gly Ser Thr Asn Tyr Asn Glu Met Phe

50

55

60

Lys Asn Arg Ala Thr Leu Thr Val Asp Arg Ser Thr Ser Thr Ala Tyr

65

70

75

80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Gly Gly Gly Arg Leu Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr

100

105

110

Val Thr Val Ser Ser

115

<210> 455

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 455

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

Lys

<210> 456

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 456

|     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Gly | Tyr | Ser | Ile | Thr | Ser | Gly | Tyr | Ser | Trp | His |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |

<210> 457

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 457

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ile | His | Ser | Ser | Gly | Ser | Thr | Asn | Tyr | Asn | Pro | Ser | Leu | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

<210> 458

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 458

Tyr Asp Asp Tyr Phe Glu Tyr

1

5

<210> 459

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 459

Lys Ala Ser Gln Asn Val Gly Phe Asn Val Ala Trp

1

5

10

<210> 460

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 460

Ser Ala Ser Tyr Arg Tyr Ser

1

5

<210> 461

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 461

Gln Gln Tyr Asn Trp Tyr Pro Phe Thr

1

5

<210> 462

<211> 116

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 462

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

<210> 463  
<211> 108  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 463

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



<210> 464  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 464  
Asn Tyr Asp Ile Asn  
1 5

<210> 465  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 465  
Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Ser Thr Gln Tyr Asn Glu  
1 5 10 15  
Lys Phe Lys Gly  
20

<210> 466  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 466  
Gln Thr Thr Gly Thr Trp Phe Ala Tyr  
1 5

<210> 467  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 467

Arg Ala Ser Gln Ser Ile Ser Asp Tyr Leu Tyr  
1 5 10

<210> 468

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 468

Tyr Ala Ser Gln Ser Ile Ser  
1 5

<210> 469

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 469

Cys Gln Asn Gly His Ser Phe Pro Leu  
1 5

<210> 470

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 470

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Ala | Arg | Gln | Thr | Thr | Gly | Thr | Trp | Phe | Ala | Tyr | Trp | Gly | Gln | Gly | Thr |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Leu | Val | Thr | Val | Ser | Ser |     |     |     |     |     |     |     |     |     |     |  |  |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

<210> 471  
 <211> 107  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| <400> 471 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| Glu       | Ile | Val | Met | Thr | Gln | Ser | Pro | Ala | Thr | Leu | Ser | Val | Ser | Pro | Gly |  |  |
| 1         |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Glu       | Arg | Val | Thr | Leu | Ser | Cys | Arg | Ala | Ser | Gln | Ser | Ile | Ser | Asp | Tyr |  |  |
|           |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Leu       | Tyr | Trp | Tyr | Gln | Gln | Lys | Ser | His | Glu | Ser | Pro | Arg | Leu | Leu | Ile |  |  |
|           |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Lys       | Tyr | Ala | Ser | Gln | Ser | Ile | Ser | Gly | Ile | Pro | Ala | Arg | Phe | Ser | Gly |  |  |
|           | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |  |
| Ser       | Gly | Ser | Gly | Ser | Glu | Phe | Thr | Leu | Thr | Ile | Asn | Ser | Val | Glu | Pro |  |  |
| 65        |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |  |
| Glu       | Asp | Val | Gly | Val | Tyr | Tyr | Cys | Gln | Asn | Gly | His | Ser | Phe | Pro | Leu |  |  |
|           |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |  |
| Thr       | Phe | Gly | Gln | Gly | Thr | Lys | Leu | Glu | Leu | Lys |     |     |     |     |     |  |  |
|           |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |  |  |

<210> 472  
 <211> 119  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| <400> 472 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| Gln       | Val | Gln | Leu | Gln | Gln | Ser | Gly | Ala | Glu | Val | Lys | Lys | Pro | Gly | Ser |  |  |
| 1         |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Ser       | Val | Lys | Val | Ser | Cys | Lys | Ala | Ser | Gly | Gly | Thr | Phe | Ser | Ser | Tyr |  |  |
|           |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |  |
| Ala       | Ile | Ser | Trp | Val | Arg | Gln | Ala | Pro | Gly | Gln | Gly | Leu | Glu | Trp | Met |  |  |
|           |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Gly       | Gly | Ile | Ile | Pro | Ile | Leu | Gly | Ile | Ala | Asn | Tyr | Ala | Gln | Lys | Phe |  |  |
|           | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |  |  |
| Gln       | Gly | Arg | Val | Thr | Ile | Thr | Ala | Asp | Glu | Ser | Thr | Ser | Thr | Ala | Tyr |  |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Met | Glu | Leu | Ser | Ser | Leu | Arg | Ser | Glu | Asp | Thr | Ala | Val | Tyr | Tyr | Cys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Arg | Gly | Gly | Ser | Gly | Ser | Tyr | His | Met | Asp | Val | Trp | Gly | Lys | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Thr | Val | Thr | Val | Ser | Ser |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 115 |

<210> 473  
 <211> 109  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 473 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Glu       | Ile | Val | Leu | Thr | Gln | Ser | Pro | Ala | Thr | Leu | Ser | Leu | Ser | Pro | Gly |
| 1         |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu       | Arg | Ala | Thr | Leu | Ser | Cys | Arg | Ala | Ser | Gln | Ser | Val | Ser | Ser | Tyr |
|           |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu       | Ala | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Gln | Ala | Pro | Arg | Leu | Leu | Ile |
|           |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr       | Asp | Ala | Ser | Asn | Arg | Ala | Thr | Gly | Ile | Pro | Ala | Arg | Phe | Ser | Gly |
|           | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser       | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr | Ile | Ser | Ser | Leu | Glu | Pro |
| 65        |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu       | Asp | Phe | Ala | Val | Tyr | Tyr | Cys | Gln | Gln | Arg | Ser | Asn | Trp | Pro | Pro |
|           |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg       | Ile | Thr | Phe | Gly | Gln | Gly | Thr | Arg | Leu | Glu | Ile | Lys |     |     |     |
|           |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

<210> 474  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|           |     |     |     |     |
|-----------|-----|-----|-----|-----|
| <400> 474 |     |     |     |     |
| Ile       | Tyr | Asn | Val | His |
| 1         |     |     |     | 5   |

<210> 475  
 <211> 17  
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 475

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ile | Phe | Pro | Gly | Asn | Gly | Asp | Thr | Ser | Tyr | Asn | Gln | Lys | Phe | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 476

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 476

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Asp | Asp | Gly | Asn | Val | Gly | Phe | Ala | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

<210> 477

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 477

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ala | Ser | Glu | Asn | Ile | Asn | Asn | Tyr | Leu | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

<210> 478

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 478

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| His | Ala | Lys | Thr | Leu | Ala | Glu |
| 1   |     |     |     | 5   |     |     |

<210> 479  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 479  
Gln His His Tyr Gly Thr Pro Pro Thr  
1 5

<210> 480  
<211> 119  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 480  
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala  
1 5 10 15  
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ile Tyr  
20 25 30  
Asn Val His Trp Ile Lys Gln Thr Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45  
Gly Thr Ile Phe Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
50 55 60  
Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Lys Thr Ala Tyr  
65 70 75 80  
Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
85 90 95  
Ala Arg Trp Asp Asp Gly Asn Val Gly Phe Ala His Trp Gly Gln Gly  
100 105 110  
Thr Leu Val Thr Val Ser Ala  
115

<210> 481  
<211> 107  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 481

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

<210> 482

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 482

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

<210> 483

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 483

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

<210> 484

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 484

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

<210> 485

<211> 107

<212> PRT

<213> Artificial Sequence



<220>

<223> Synthetic

<400> 485

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

<210> 486

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 486

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gln | Val | Gln | Leu | Gln | Gln | Trp | Gly | Ala | Gly | Leu | Leu | Lys | Pro | Ser | Glu |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Thr | Leu | Ser | Leu | Thr | Cys | Ala | Val | Tyr | Gly | Gly | Ser | Phe | Ser | Gly | Tyr |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Tyr | Trp | Ser | Trp | Ile | Arg | Gln | Pro | Pro | Gly | Lys | Gly | Leu | Glu | Trp | Ile |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Gly | Glu | Ile | Asn | His | Ser | Gly | Ser | Thr | Asn | Tyr | Asn | Pro | Ser | Leu | Lys |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ser | Arg | Val | Thr | Ile | Ser | Val | Glu | Thr | Ser | Lys | Asn | Gln | Phe | Ser | Leu |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Lys | Leu | Ser | Ser | Val | Thr | Ala | Ala | Asp | Thr | Ala | Val | Tyr | Tyr | Cys | Ala |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Arg | Asp | Lys | Trp | Thr | Trp | Tyr | Phe | Asp | Leu | Trp | Gly | Arg | Gly | Thr | Leu |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Val | Thr | Val | Ser | Ser | Ala | Ser | Thr | Lys | Gly | Pro | Ser | Val | Phe | Pro | Leu |  |
|     |     | 115 |     |     |     |     |     | 120 |     |     |     | 125 |     |     |     |  |
| Ala | Pro | Ser | Ser | Lys | Ser | Thr | Ser | Gly | Gly | Thr | Ala | Ala | Leu | Gly | Cys |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Leu | Val | Lys | Asp | Tyr | Phe | Pro | Glu | Pro | Val | Thr | Val | Ser | Trp | Asn | Ser |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Gly | Ala | Leu | Thr | Ser | Gly | Val | His | Thr | Phe | Pro | Ala | Val | Leu | Gln | Ser |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Ser | Gly | Leu | Tyr | Ser | Leu | Ser | Ser | Val | Val | Thr | Val | Pro | Ser | Ser | Ser |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Leu | Gly | Thr | Gln | Thr | Tyr | Ile | Cys | Asn | Val | Asn | His | Lys | Pro | Ser | Asn |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |
| Thr | Lys | Val | Asp | Lys | Arg | Val | Glu | Pro | Lys | Ser | Cys | Asp | Lys | Thr | His |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |
| Thr | Cys | Pro | Pro | Cys | Pro | Ala | Pro | Glu | Leu | Leu | Gly | Gly | Pro | Ser | Val |  |  |
| 225 |     |     |     | 230 |     |     |     | 235 |     |     |     |     |     |     | 240 |  |  |
| Phe | Leu | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Thr | Leu | Met | Ile | Ser | Arg | Thr |  |  |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |  |  |
| Pro | Glu | Val | Thr | Cys | Val | Val | Val | Asp | Val | Ser | His | Glu | Asp | Pro | Glu |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |
| Val | Lys | Phe | Asn | Trp | Tyr | Val | Asp | Gly | Val | Glu | Val | His | Asn | Ala | Lys |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |
| Thr | Lys | Pro | Arg | Glu | Glu | Gln | Tyr | Asn | Ser | Thr | Tyr | Arg | Val | Val | Ser |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |
| Val | Leu | Thr | Val | Leu | His | Gln | Asp | Trp | Leu | Asn | Gly | Lys | Glu | Tyr | Lys |  |  |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |  |  |
| Cys | Lys | Val | Ser | Asn | Lys | Ala | Leu | Pro | Ala | Pro | Ile | Glu | Lys | Thr | Ile |  |  |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |  |  |
| Ser | Lys | Ala | Lys | Gly | Gln | Pro | Arg | Glu | Pro | Gln | Val | Tyr | Thr | Leu | Pro |  |  |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |  |
| Pro | Ser | Arg | Glu | Glu | Met | Thr | Lys | Asn | Gln | Val | Ser | Leu | Thr | Cys | Leu |  |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |  |
| Val | Lys | Gly | Phe | Tyr | Pro | Ser | Asp | Ile | Ala | Val | Glu | Trp | Glu | Ser | Asn |  |  |
|     | 370 |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |     |  |  |
| Gly | Gln | Pro | Glu | Asn | Asn | Tyr | Lys | Thr | Thr | Pro | Pro | Val | Leu | Asp | Ser |  |  |
| 385 |     |     |     | 390 |     |     |     |     |     | 395 |     |     |     |     | 400 |  |  |
| Asp | Gly | Ser | Phe | Phe | Leu | Tyr | Ser | Lys | Leu | Thr | Val | Asp | Lys | Ser | Arg |  |  |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     |     | 415 |     |  |  |
| Trp | Gln | Gln | Gly | Asn | Val | Phe | Ser | Cys | Ser | Val | Met | His | Glu | Ala | Leu |  |  |
|     |     | 420 |     |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |  |
| His | Asn | His | Tyr | Thr | Gln | Lys | Ser | Leu | Ser | Leu | Ser | Pro | Gly | Lys |     |  |  |
|     | 435 |     |     |     |     | 440 |     |     |     |     |     | 445 |     |     |     |  |  |

<210> 487

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 487

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Asn | Arg | Asn | Tyr | Leu | Ala | Trp | Tyr | Gln | Gln | Asn | Pro | Gly | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Pro | Lys | Leu | Leu | Ile | Tyr | Trp | Ala | Ser | Thr | Arg | Glu | Ser | Gly | Val |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Asp | Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Ser | Ser | Leu | Gln | Ala | Glu | Asp | Val | Ala | Val | Tyr | Tyr | Cys | Gln | Gln |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Tyr | Ser | Thr | Pro | Arg | Thr | Phe | Gly | Gln | Gly | Thr | Lys | Val | Glu | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Arg | Thr | Val | Ala | Ala | Pro | Ser | Val | Phe | Ile | Phe | Pro | Pro | Ser | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Gln | Leu | Lys | Ser | Gly | Thr | Ala | Ser | Val | Val | Cys | Leu | Leu | Asn | Asn |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Tyr | Pro | Arg | Glu | Ala | Lys | Val | Gln | Trp | Lys | Val | Asp | Asn | Ala | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Ser | Gly | Asn | Ser | Gln | Glu | Ser | Val | Thr | Glu | Gln | Asp | Ser | Lys | Asp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Thr | Tyr | Ser | Leu | Ser | Ser | Thr | Leu | Thr | Leu | Ser | Lys | Ala | Asp | Tyr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Lys | His | Lys | Val | Tyr | Ala | Cys | Glu | Val | Thr | His | Gln | Gly | Leu | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Pro | Val | Thr | Lys | Ser | Phe | Asn | Arg | Gly | Glu | Cys |     |     |     |     |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

<210> 488

<211> 445

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 488

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



<400> 489

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ser | Ala | Leu | Thr | Gln | Pro | Ala | Ser | Val | Ser | Gly | Ser | Pro | Gly | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ile | Thr | Ile | Ser | Cys | Thr | Gly | Thr | Ser | Ser | Asp | Val | Gly | Ser | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Val | Val | Ser | Trp | Tyr | Gln | Gln | His | Pro | Gly | Lys | Ala | Pro | Lys | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ile | Tyr | Glu | Val | Ser | Gln | Arg | Pro | Ser | Gly | Val | Ser | Asn | Arg | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Gly | Ser | Lys | Ser | Gly | Asn | Thr | Ala | Ser | Leu | Thr | Ile | Ser | Gly | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gln | Thr | Glu | Asp | Glu | Ala | Asp | Tyr | Tyr | Cys | Cys | Ser | Tyr | Ala | Gly | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Ile | Phe | Val | Ile | Phe | Gly | Gly | Gly | Thr | Lys | Val | Thr | Val | Leu | Gly |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Pro | Lys | Ala | Ala | Pro | Ser | Val | Thr | Leu | Phe | Pro | Pro | Ser | Ser | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Leu | Gln | Ala | Asn | Lys | Ala | Thr | Leu | Val | Cys | Leu | Val | Ser | Asp | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Tyr | Pro | Gly | Ala | Val | Thr | Val | Ala | Trp | Lys | Ala | Asp | Gly | Ser | Pro | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Val | Gly | Val | Glu | Thr | Thr | Lys | Pro | Ser | Lys | Gln | Ser | Asn | Asn | Lys |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Tyr | Ala | Ala | Ser | Ser | Tyr | Leu | Ser | Leu | Thr | Pro | Glu | Gln | Trp | Lys | Ser |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| His | Arg | Ser | Tyr | Ser | Cys | Arg | Val | Thr | His | Glu | Gly | Ser | Thr | Val | Glu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Thr | Val | Ala | Pro | Ala | Glu | Cys | Ser |     |     |     |     |     |     |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     |     |     |     |     |

<210> 490

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 490

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Val | Gln | Leu | Leu | Glu | Ser | Gly | Gly | Gly | Leu | Val | Gln | Pro | Gly | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Leu | Arg | Leu | Ser | Cys | Ala | Ala | Ser | Gly | Phe | Thr | Phe | Ser | Ser | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Met | Ser | Trp | Val | Arg | Gln | Ala | Pro | Gly | Lys | Gly | Leu | Glu | Trp | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ala | Ile | Asn | Ser | Gln | Gly | Lys | Ser | Thr | Tyr | Tyr | Ala | Asp | Ser | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Gly | Arg | Phe | Thr | Ile | Ser | Arg | Asp | Asn | Ser | Lys | Asn | Thr | Leu | Tyr |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Leu | Gln | Met | Asn | Ser | Leu | Arg | Ala | Glu | Asp | Thr | Ala | Val | Tyr | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |
| Ala | Arg | Trp | Gly | Asp | Glu | Gly | Phe | Asp | Ile | Trp | Gly | Gln | Gly | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 | Leu |
| Val | Thr | Val | Ser | Ser | Ala | Ser | Thr | Lys | Gly | Pro | Ser | Val | Phe | Pro |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     | Leu |
| Ala | Pro | Ser | Ser | Lys | Ser | Thr | Ser | Gly | Gly | Thr | Ala | Ala | Leu | Gly |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     | Cys |
| Leu | Val | Lys | Asp | Tyr | Phe | Pro | Glu | Pro | Val | Thr | Val | Ser | Trp | Asn |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Ala | Leu | Thr | Ser | Gly | Val | His | Thr | Phe | Pro | Ala | Val | Leu | Gln |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |
| Ser | Gly | Leu | Tyr | Ser | Leu | Ser | Ser | Val | Val | Thr | Val | Pro | Ser | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |     | Ser |
| Leu | Gly | Thr | Gln | Thr | Tyr | Ile | Cys | Asn | Val | Asn | His | Lys | Pro | Ser |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     | Asn |
| Thr | Lys | Val | Asp | Lys | Arg | Val | Glu | Pro | Lys | Ser | Cys | Asp | Lys | Thr |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     | His |
| Thr | Cys | Pro | Pro | Cys | Pro | Ala | Pro | Glu | Leu | Leu | Gly | Gly | Pro | Ser |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |
| Phe | Leu | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Thr | Leu | Met | Ile | Ser | Arg |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |
| Pro | Glu | Val | Thr | Cys | Val | Val | Val | Asp | Val | Ser | His | Glu | Asp | Pro |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     | 270 |     | Glu |
| Val | Lys | Phe | Asn | Trp | Tyr | Val | Asp | Gly | Val | Glu | Val | His | Asn | Ala |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     | Lys |
| Thr | Lys | Pro | Arg | Glu | Glu | Gln | Tyr | Asn | Ser | Thr | Tyr | Arg | Val | Val |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     | Ser |
| Val | Leu | Thr | Val | Leu | His | Gln | Asp | Trp | Leu | Asn | Gly | Lys | Glu | Tyr |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |
| Cys | Lys | Val | Ser | Asn | Lys | Ala | Leu | Pro | Ala | Pro | Ile | Glu | Lys | Thr |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |
| Ser | Lys | Ala | Lys | Gly | Gln | Pro | Arg | Glu | Pro | Gln | Val | Tyr | Thr | Leu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 | Pro |
| Pro | Ser | Arg | Glu | Glu | Met | Thr | Lys | Asn | Gln | Val | Ser | Leu | Thr | Cys |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     | Leu |
| Val | Lys | Gly | Phe | Tyr | Pro | Ser | Asp | Ile | Ala | Val | Glu | Trp | Glu | Ser |
|     | 370 |     |     |     |     | 375 |     |     |     | 380 |     |     |     | Asn |
| Gly | Gln | Pro | Glu | Asn | Asn | Tyr | Lys | Thr | Thr | Pro | Pro | Val | Leu | Asp |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |
| Asp | Gly | Ser | Phe | Phe | Leu | Tyr | Ser | Lys | Leu | Thr | Val | Asp | Lys | Ser |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     |     | 415 |
| Trp | Gln | Gln | Gly | Asn | Val | Phe | Ser | Cys | Ser | Val | Met | His | Glu | Ala |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 | Leu |
| His | Asn | His | Tyr | Thr | Gln | Lys | Ser | Leu | Ser | Leu | Ser | Pro | Gly | Lys |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |

<211> 214  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 491

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Gln | Met | Thr | Gln | Ser | Pro | Ser | Ser | Leu | Ser | Ala | Ser | Val | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asp | Arg | Val | Thr | Ile | Thr | Cys | Arg | Ala | Ser | Gln | Gly | Ile | Ser | Asn | Trp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Leu | Ala | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys | Ala | Pro | Lys | Leu | Leu | Ile |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Tyr | Gly | Ala | Ser | Ser | Leu | Gln | Ser | Gly | Val | Pro | Ser | Arg | Phe | Ser | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr | Ile | Ser | Ser | Leu | Gln | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Asp | Phe | Ala | Thr | Tyr | Tyr | Cys | Gln | Gln | Tyr | Ser | Ser | Phe | Pro | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Phe | Gly | Gln | Gly | Thr | Lys | Val | Glu | Ile | Lys | Arg | Thr | Val | Ala | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Pro | Ser | Val | Phe | Ile | Phe | Pro | Pro | Ser | Asp | Glu | Gln | Leu | Lys | Ser | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Thr | Ala | Ser | Val | Val | Cys | Leu | Leu | Asn | Asn | Phe | Tyr | Pro | Arg | Glu | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Val | Gln | Trp | Lys | Val | Asp | Asn | Ala | Leu | Gln | Ser | Gly | Asn | Ser | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Glu | Ser | Val | Thr | Glu | Gln | Asp | Ser | Lys | Asp | Ser | Thr | Tyr | Ser | Leu | Ser |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Thr | Leu | Thr | Leu | Ser | Lys | Ala | Asp | Tyr | Glu | Lys | His | Lys | Val | Tyr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Cys | Glu | Val | Thr | His | Gln | Gly | Leu | Ser | Ser | Pro | Val | Thr | Lys | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |
| Phe | Asn | Arg | Gly | Glu | Cys |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 210 |

<210> 492  
<211> 449  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 492

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Gln | Leu | Val | Gln | Ser | Gly | Ala | Glu | Val | Lys | Lys | Pro | Gly | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Val | Lys | Val | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Thr | Phe | Arg | Ser | Ser |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Ile | Ser | Trp | Val | Arg | Gln | Ala | Pro | Gly | Gln | Gly | Leu | Glu | Trp | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Trp | Ile | Tyr | Ala | Gly | Thr | Gly | Ser | Pro | Ser | Tyr | Asn | Gln | Lys | Leu |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Gly | Arg | Val | Thr | Met | Thr | Thr | Asp | Thr | Ser | Thr | Ser | Thr | Ala | Tyr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Met | Glu | Leu | Arg | Ser | Leu | Arg | Ser | Asp | Asp | Thr | Ala | Val | Tyr | Tyr | Cys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Arg | His | Arg | Asp | Tyr | Tyr | Ser | Asn | Ser | Leu | Thr | Tyr | Trp | Gly | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Thr | Leu | Val | Thr | Val | Ser | Ser | Ala | Ser | Thr | Lys | Gly | Pro | Ser | Val |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Phe | Pro | Leu | Ala | Pro | Ser | Ser | Lys | Ser | Thr | Ser | Gly | Gly | Thr | Ala | Ala |
|     |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Gly | Cys | Leu | Val | Lys | Asp | Tyr | Phe | Pro | Glu | Pro | Val | Thr | Val | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Trp | Asn | Ser | Gly | Ala | Leu | Thr | Ser | Gly | Val | His | Thr | Phe | Pro | Ala | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Gln | Ser | Ser | Gly | Leu | Tyr | Ser | Leu | Ser | Ser | Val | Val | Thr | Val | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Ser | Ser | Leu | Gly | Thr | Gln | Thr | Tyr | Ile | Cys | Asn | Val | Asn | His | Lys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Ser | Asn | Thr | Lys | Val | Asp | Lys | Lys | Val | Glu | Pro | Lys | Ser | Cys | Asp |
|     |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Thr | His | Thr | Cys | Pro | Pro | Cys | Pro | Ala | Pro | Glu | Leu | Leu | Gly | Gly |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Pro | Ser | Val | Phe | Leu | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Thr | Leu | Met | Ile |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ser | Arg | Thr | Pro | Glu | Val | Thr | Cys | Val | Val | Val | Asp | Val | Ser | His | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asp | Pro | Glu | Val | Lys | Phe | Asn | Trp | Tyr | Val | Asp | Gly | Val | Glu | Val | His |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asn | Ala | Lys | Thr | Lys | Pro | Arg | Glu | Glu | Gln | Tyr | Asn | Ser | Thr | Tyr | Arg |
|     |     |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Val | Val | Ser | Val | Leu | Thr | Val | Leu | His | Gln | Asp | Trp | Leu | Asn | Gly | Lys |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Glu | Tyr | Lys | Cys | Lys | Val | Ser | Asn | Lys | Ala | Leu | Pro | Ala | Pro | Ile | Glu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Lys | Thr | Ile | Ser | Lys | Ala | Lys | Gly | Gln | Pro | Arg | Glu | Pro | Gln | Val | Tyr |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Thr | Leu | Pro | Pro | Ser | Arg | Asp | Glu | Leu | Thr | Lys | Asn | Gln | Val | Ser | Leu |
|     |     |     | 355 |     |     |     |     | 360 |     |     |     | 365 |     |     |     |
| Thr | Cys | Leu | Val | Lys | Gly | Phe | Tyr | Pro | Ser | Asp | Ile | Ala | Val | Glu | Trp |
|     |     |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |     |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |  |
| Glu | Ala | Leu | His | Asn | His | Tyr | Thr | Gln | Lys | Ser | Leu | Ser | Leu | Ser | Pro |  |  |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |  |
| Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

<210> 493  
 <211> 220  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| <400> 493 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| Asp       | Ile | Val | Met | Thr | Gln | Ser | Pro | Asp | Ser | Leu | Ala | Val | Ser | Leu | Gly |  |  |
| 1         |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |  |
| Glu       | Arg | Ala | Thr | Ile | Asn | Cys | Lys | Ser | Ser | Gln | Ser | Val | Leu | Asn | Ser |  |  |
|           |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Gly       | Asn | Gln | Lys | Asn | Tyr | Leu | Thr | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Gln |  |  |
|           |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |  |
| Pro       | Pro | Lys | Leu | Leu | Ile | Tyr | Trp | Ala | Ser | Thr | Arg | Glu | Ser | Gly | Val |  |  |
|           |     | 50  |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |  |  |
| Pro       | Asp | Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr |  |  |
| 65        |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |  |  |
| Ile       | Ser | Ser | Leu | Gln | Ala | Glu | Asp | Val | Ala | Val | Tyr | Tyr | Cys | Gln | Ser |  |  |
|           |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |  |
| Asp       | Tyr | Ser | Tyr | Pro | Tyr | Thr | Phe | Gly | Gln | Gly | Thr | Lys | Leu | Glu | Ile |  |  |
|           |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Lys       | Arg | Thr | Val | Ala | Ala | Pro | Ser | Val | Phe | Ile | Phe | Pro | Pro | Ser | Asp |  |  |
|           |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Glu       | Gln | Leu | Lys | Ser | Gly | Thr | Ala | Ser | Val | Val | Cys | Leu | Leu | Asn | Asn |  |  |
|           |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Phe       | Tyr | Pro | Arg | Glu | Ala | Lys | Val | Gln | Trp | Lys | Val | Asp | Asn | Ala | Leu |  |  |
| 145       |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Gln       | Ser | Gly | Asn | Ser | Gln | Glu | Ser | Val | Thr | Glu | Gln | Asp | Ser | Lys | Asp |  |  |
|           |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |  |
| Ser       | Thr | Tyr | Ser | Leu | Ser | Ser | Thr | Leu | Thr | Leu | Ser | Lys | Ala | Asp | Tyr |  |  |
|           |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |     |  |  |
| Glu       | Lys | His | Lys | Val | Tyr | Ala | Cys | Glu | Val | Thr | His | Gln | Gly | Leu | Ser |  |  |
|           |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |  |
| Ser       | Pro | Val | Thr | Lys | Ser | Phe | Asn | Arg | Gly | Glu | Cys |     |     |     |     |  |  |
|           |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |

<210> 494  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 494

Thr Ser Asn Met Gly Val Gly

1

5

<210> 495

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 495

His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Ser Pro Ser Leu Lys Ser

1

5

10

15

<210> 496

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 496

Ser Asn Tyr Gly Tyr Ala Trp Phe Ala Tyr

1

5

10

<210> 497

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 497

Lys Ala Ser Gln Asp Ile Tyr Pro Tyr Leu Asn

1

5

10

<210> 498

<211> 7

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 498  
Arg Thr Asn Arg Leu Leu Asp  
1 5

<210> 499  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 499  
Leu Gln Tyr Asp Glu Phe Pro Leu Thr  
1 5

<210> 500  
<211> 120  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 500  
Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln  
1 5 10 15  
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser  
20 25 30  
Asn Met Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu  
35 40 45  
Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Ser Pro Ser  
50 55 60  
Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val  
65 70 75 80  
Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr  
85 90 95  
Cys Val Arg Ser Asn Tyr Gly Tyr Ala Trp Phe Ala Tyr Trp Gly Gln  
100 105 110  
Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 501  
<211> 107  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 501  
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15  
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Tyr Pro Tyr  
20 25 30  
Leu Asn Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Thr Leu Ile  
35 40 45  
Tyr Arg Thr Asn Arg Leu Leu Asp Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60  
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80  
Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Glu Phe Pro Leu  
85 90 95  
Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys  
100 105

<210> 502  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 502  
Asp Tyr Ala Val His  
1 5

<210> 503  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 503  
Val Ile Ser Thr Tyr Asn Asp Tyr Thr Tyr Asn Asn Gln Asp Phe Lys  
1 5 10 15

Gly

<210> 504  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 504  
Gly Asn Ser Tyr Phe Tyr Ala Leu Asp Tyr  
1 5 10

<210> 505  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 505  
Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly Lys Ser Phe Met His  
1 5 10 15

<210> 506  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 506  
Arg Ala Ser Asn Leu Glu Ser  
1 5

<210> 507  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 507

Gln Gln Ser Asn Glu Asp Pro Trp Thr  
1 5

<210> 508

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 508

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

<210> 509

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 509

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15  
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr  
20 25 30  
Gly Lys Ser Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro  
35 40 45  
Arg Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala  
50 55 60

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr | Ile | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Leu | Glu | Pro | Glu | Asp | Phe | Ala | Val | Tyr | Tyr | Cys | Gln | Gln | Ser | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Asp | Pro | Trp | Thr | Phe | Gly | Gly | Gly | Thr | Lys | Leu | Glu | Ile | Lys |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

<210> 510  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 510  
 Arg Tyr Trp Met Ser  
 1 5

<210> 511  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 511  
 Asp Leu Asn Pro Asp Ser Ser Ala Ile Asn Tyr Val Asp Ser Val Lys  
 1 5 10 15  
 Gly

<210> 512  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 512  
 Ile Thr Thr Leu Val Pro Tyr Thr Met Asp Phe  
 1 5 10

<210> 513

<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 513  
Ile Thr Asn Thr Asp Ile Asp Asp Asp Met Asn  
1 5 10

<210> 514  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 514  
Glu Gly Asn Gly Leu Arg Pro  
1 5

<210> 515  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 515  
Leu Gln Ser Asp Asn Leu Pro Leu Thr  
1 5

<210> 516  
<211> 120  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 516  
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg Tyr



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

<210> 517  
 <211> 107  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

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

<210> 518  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 518  
 Asp Tyr Tyr Met His

1 5

<210> 519  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 519  
Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Gly Pro Lys Phe Gln  
1 5 10 15  
Gly

<210> 520  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 520  
His Asn Ala His Tyr Gly Thr Trp Phe Ala Tyr  
1 5 10

<210> 521  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 521  
Arg Ser Ser Gln Ser Leu Leu His Ser Ser Gly Asn Thr Tyr Leu Glu  
1 5 10 15

<210> 522  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 522

Lys Ile Ser Thr Arg Phe Ser  
1 5

<210> 523

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 523

Phe Gln Gly Ser His Val Pro Tyr Thr  
1 5

<210> 524

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 524

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

<210> 525

<211> 112

<212> PRT

Val Ile Asn Pro Lys Tyr Gly Thr Thr Arg Tyr Asn Gln Lys Phe Lys  
1 5 10 15  
Gly

<210> 528  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 528  
Gly Leu Asn Ala Trp Asp Tyr  
1 5

<210> 529  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 529  
Gly Ala Ser Glu Asn Ile Tyr Gly Ala Leu Asn  
1 5 10

<210> 530  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 530  
Gly Ala Thr Asn Leu Glu Asp  
1 5

<210> 531  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 531  
Gln Asn Val Leu Thr Thr Pro Tyr Thr  
1 5

<210> 532  
<211> 116  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 532  
Gln Phe Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1 5 10 15  
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr  
20 25 30  
Asn Val Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile  
35 40 45  
Gly Val Ile Asn Pro Lys Tyr Gly Thr Thr Arg Tyr Asn Gln Lys Phe  
50 55 60  
Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr  
65 70 75 80  
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Thr Arg Gly Leu Asn Ala Trp Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110  
Thr Val Ser Ser  
115

<210> 533  
<211> 107  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 533  
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15  
Asp Arg Val Thr Ile Thr Cys Gly Ala Ser Glu Asn Ile Tyr Gly Ala  
20 25 30  
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45  
Tyr Gly Ala Thr Asn Leu Glu Asp Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60  
Ser Gly Ser Gly Arg Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80  
Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Asn Val Leu Thr Thr Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
100 105

<210> 534

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 534

Gly Tyr Phe Met Asn  
1 5

<210> 535

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 535

Leu Ile Asn Pro Tyr Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe Lys  
1 5 10 15  
Gly

<210> 536

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 536

Gly Leu Arg Arg Asp Phe Asp Tyr  
1 5

<210> 537

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 537

Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn  
1 5 10 15

<210> 538

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 538

Leu Val Ser Glu Leu Asp Ser  
1 5

<210> 539

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 539

Trp Gln Gly Thr His Phe Pro Arg Thr  
1 5

<210> 540

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 540

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



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 50  |     | 55  |     | 60  |     |     |     |     |     |     |     |     |     |     |     |
| Lys | Gly | Arg | Val | Thr | Met | Thr | Arg | Gln | Thr | Ser | Thr | Ser | Thr | Val | Tyr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Met | Glu | Leu | Ser | Ser | Leu | Arg | Ser | Glu | Asp | Thr | Ala | Val | Tyr | Tyr | Cys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Arg | Gly | Leu | Arg | Arg | Asp | Phe | Asp | Tyr | Trp | Gly | Gln | Gly | Thr | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Thr | Val | Ser | Ser |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 541  
 <211> 112  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|                                                                 |
|-----------------------------------------------------------------|
| <400> 541                                                       |
| Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly |
| 1 5 10 15                                                       |
| Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser |
| 20 25 30                                                        |
| Asp Gly Lys Thr Tyr Leu Asn Trp Leu Phe Gln Arg Pro Gly Gln Ser |
| 35 40 45                                                        |
| Pro Arg Arg Leu Ile Tyr Leu Val Ser Glu Leu Asp Ser Gly Val Pro |
| 50 55 60                                                        |
| Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile |
| 65 70 75 80                                                     |
| Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly |
| 85 90 95                                                        |
| Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys |
| 100 105 110                                                     |

<210> 542  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|                     |
|---------------------|
| <400> 542           |
| Asp Phe Gly Met Asn |
| 1 5                 |

<210> 543

<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 543  
Trp Ile Asn Thr Phe Thr Gly Glu Pro Ser Tyr Gly Asn Val Phe Lys  
1 5 10 15  
Gly

<210> 544  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 544  
Arg His Gly Asn Gly Asn Val Phe Asp Ser  
1 5 10

<210> 545  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 545  
Arg Ala Ser Gln Ser Ile Gly Ser Asn Ile His  
1 5 10

<210> 546  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 546  
Tyr Thr Ser Glu Ser Ile Ser

1

5

<210> 547

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 547

Gln Gln Ser Asn Ser Trp Pro Leu Thr

1

5

<210> 548

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 548

Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala

1

5

10

15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Phe

20

25

30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35

40

45

Gly Trp Ile Asn Thr Phe Thr Gly Glu Pro Ser Tyr Gly Asn Val Phe

50

55

60

Lys Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr

65

70

75

80

Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Arg His Gly Asn Gly Asn Val Phe Asp Ser Trp Gly Gln Gly

100

105

110

Thr Leu Val Thr Val Ser Ser

115

<210> 549

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 549

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

<210> 550

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 550

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| Thr | Ala | Ala | Ile | Ser |
| 1   |     |     | 5   |     |

<210> 551

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 551

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ile | Ile | Pro | Ile | Phe | Gly | Lys | Ala | His | Tyr | Ala | Gln | Lys | Phe | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 552

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 552

Lys Phe His Phe Val Ser Gly Ser Pro Phe Gly Met Asp Val

1

5

10

<210> 553

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 553

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala

1

5

10

<210> 554

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 554

Asp Ala Ser Asn Arg Ala Thr

1

5

<210> 555

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 555

Gln Gln Arg Ser Asn Trp Pro Thr

1

5

<210> 556

<211> 123

<212> PRT

### <213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Synthetic

<400> 556

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

<210> 557

<211> 106

&lt;212&gt; PRT

### <213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Synthetic

<400> 557

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

<210> 558  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 558  
Ser Tyr Ala Ile Ser  
1 5

<210> 559  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 559  
Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln  
1 5 10 15  
Gly

<210> 560  
<211> 21  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 560  
Ala Pro Leu Arg Phe Leu Glu Trp Ser Thr Gln Asp His Tyr Tyr Tyr  
1 5 10 15  
Tyr Tyr Met Asp Val  
20

<210> 561  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 561

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Thr  
1 5 10

<210> 562

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 562

Gly Glu Asn Lys Arg Pro Ser  
1 5

<210> 563

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 563

Lys Ser Arg Asp Gly Ser Gly Gln His Leu Val  
1 5 10

<210> 564

<211> 130

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 564

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
1 5 10 15  
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr  
20 25 30  
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45  
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe  
50 55 60  
Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Met | Glu | Leu | Ser | Ser | Leu | Arg | Ser | Glu | Asp | Thr | Ala | Val | Tyr | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  | Cys |
| Ala | Arg | Ala | Pro | Leu | Arg | Phe | Leu | Glu | Trp | Ser | Thr | Gln | Asp | His |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 | Tyr |
| Tyr | Tyr | Tyr | Tyr | Met | Asp | Val | Trp | Gly | Lys | Gly | Thr | Thr | Val | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     | Val |
| Ser | Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     | 130 |     |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 565  
 <211> 108  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 565 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ser       | Ser | Glu | Leu | Thr | Gln | Asp | Pro | Ala | Val | Ser | Val | Ala | Leu | Gly |
| 1         |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  | Gln |
| Thr       | Val | Arg | Ile | Thr | Cys | Gln | Gly | Asp | Ser | Leu | Arg | Ser | Tyr | Tyr |
|           |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  | Ala |     |
| Thr       | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Gln | Ala | Pro | Ile | Leu | Val | Ile |
|           |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     | Tyr |     |
| Gly       | Glu | Asn | Lys | Arg | Pro | Ser | Gly | Ile | Pro | Asp | Arg | Phe | Ser | Gly |
|           | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     | Ser |     |
| Ser       | Ser | Gly | Asn | Thr | Ala | Ser | Leu | Thr | Ile | Thr | Gly | Ala | Gln | Ala |
| 65        |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  | Glu |
| Asp       | Glu | Ala | Asp | Tyr | Tyr | Cys | Lys | Ser | Arg | Asp | Gly | Ser | Gly | Gln |
|           |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  | His |
| Leu       | Val | Phe | Gly | Gly | Gly | Thr | Lys | Leu | Thr | Val | Leu |     |     |     |
|           |     | 100 |     |     |     |     |     | 105 |     |     |     |     |     |     |

<210> 566  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|                     |
|---------------------|
| <400> 566           |
| Ser Tyr Trp Ile Asn |
| 1 5                 |

<210> 567

<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 567  
Asn Ile Tyr Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe Lys  
1 5 10 15  
Asp

<210> 568  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 568  
Ser Trp Arg Gly Asn Ser Phe Asp Tyr  
1 5

<210> 569  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 569  
Lys Ser Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu  
1 5 10 15  
Thr

<210> 570  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 570

Trp Ala Ser Thr Arg Glu Ser  
1 5

<210> 571

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 571

Gln Asn Asp Tyr Ser Tyr Pro Phe Thr  
1 5

<210> 572

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 572

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

<210> 573

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 573

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

Lys

<210> 574

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 574

|     |     |     |     |     |  |
|-----|-----|-----|-----|-----|--|
| Asn | Tyr | Gly | Met | Asn |  |
| 1   |     |     |     | 5   |  |

<210> 575

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 575

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ile | Asn | Thr | Asn | Thr | Gly | Glu | Pro | Thr | Tyr | Ala | Glu | Glu | Phe | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Gly

<210> 576  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 576  
Leu Gly Phe Gly Asn Ala Met Asp Tyr  
1 5

<210> 577  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 577  
Lys Ser Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu  
1 5 10 15  
Thr

<210> 578  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 578  
Trp Ala Ser Thr Arg Glu Ser  
1 5

<210> 579  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 579

Gln Asn Asp Tyr Ser Tyr Pro Leu Thr  
1 5

<210> 580

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 580

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

<210> 581

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 581

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ser | Ser | Val | Gln | Ala | Glu | Asp | Leu | Ala | Val | Tyr | Tyr | Cys | Gln | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Tyr | Ser | Tyr | Pro | Leu | Thr | Phe | Gly | Ala | Gly | Thr | Lys | Leu | Glu | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 582  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 582  
 Ser Tyr Asn Met Asn  
 1 5

<210> 583  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 583  
 Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys  
 1 5 10 15  
 Gly

<210> 584  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 584  
 Ala Tyr Tyr Tyr Gly Met Asp Val  
 1 5

<210> 585

<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 585  
Arg Ala Ser Gln Gly Ile Ser Gly Trp Leu Ala  
1 5 10

<210> 586  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 586  
Ala Ala Ser Thr Leu Gln Ser  
1 5

<210> 587  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 587  
Gln Gln Ala Asn Ser Phe Pro Pro Thr  
1 5

<210> 588  
<211> 117  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 588  
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr





1 5

<210> 591  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 591  
Val Ile Trp Tyr Asp Gly Ser Asn Gln Tyr Tyr Ala Asp Ser Val Lys  
1 5 10 15  
Gly

<210> 592  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 592  
Gly Leu Thr Ser Gly Arg Tyr Gly Met Asp Val  
1 5 10

<210> 593  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 593  
Arg Ser Ser Gln Ser Leu Leu Leu Ser His Gly Phe Asn Tyr Leu Asp  
1 5 10 15

<210> 594  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 594

Leu Gly Ser Ser Arg Ala Ser  
1 5

<210> 595

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 595

Met Gln Pro Leu Gln Ile Pro Trp Thr  
1 5

<210> 596

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 596

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

<210> 597

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 597

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

<210> 598

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 598

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| Ser | Gly | Tyr | Trp | Asn |
| 1   |     |     |     | 5   |

<210> 599

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 599

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ile | Ser | Asp | Ser | Gly | Ile | Thr | Tyr | Tyr | Asn | Pro | Ser | Leu | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

<210> 600

<211> 11

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 600  
Arg Thr Leu Ala Thr Tyr Tyr Ala Met Asp Tyr  
1 5 10

<210> 601  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 601  
Arg Ala Ser Gln Ser Leu Val His Ser Asp Gly Asn Thr Tyr Leu His  
1 5 10 15

<210> 602  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 602  
Arg Val Ser Asn Arg Phe Ser  
1 5

<210> 603  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 603  
Ser Gln Ser Thr His Val Pro Pro Thr  
1 5

<210> 604  
<211> 119  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 604  
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15  
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Thr Ser Gly  
20 25 30  
Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Tyr Ile  
35 40 45  
Gly Tyr Ile Ser Asp Ser Gly Ile Thr Tyr Tyr Asn Pro Ser Leu Lys  
50 55 60  
Ser Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Tyr Ser Leu  
65 70 75 80  
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95  
Arg Arg Thr Leu Ala Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly  
100 105 110  
Thr Leu Val Thr Val Ser Ser  
115

<210> 605  
<211> 113  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 605  
Asp Phe Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly  
1 5 10 15  
Gln Pro Ala Ser Ile Ser Cys Arg Ala Ser Gln Ser Leu Val His Ser  
20 25 30  
Asp Gly Asn Thr Tyr Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ser  
35 40 45  
Pro Arg Leu Leu Ile Tyr Arg Val Ser Asn Arg Phe Ser Gly Val Pro  
50 55 60  
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile  
65 70 75 80  
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Ser  
85 90 95  
Thr His Val Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
100 105 110

Arg

<210> 606  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 606  
Asn Tyr Ala Met Ser  
1 5

<210> 607  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 607  
Ser Ile Ser Gly Ser Gly Asp Tyr Thr Tyr Tyr Thr Asp Ser Val Lys  
1 5 10 15  
Gly

<210> 608  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 608  
Ser Pro Trp Gly Tyr Tyr Leu Asp Ser  
1 5

<210> 609  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 609

Arg Ala Ser Gln Gly Ile Ser Ser Arg Leu Ala  
1 5 10

<210> 610

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 610

Ala Ala Ser Ser Leu Gln Ser  
1 5

<210> 611

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 611

Gln Gln Tyr Asn Ser Tyr Pro Tyr Thr  
1 5

<210> 612

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 612

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



|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| 50  |     | 55  |     | 60  |
| Lys | Gly | Arg | Phe | Thr |
| 65  |     | 70  |     | 75  |
| Leu | Gln | Met | Asn | Ser |
|     |     | 85  |     | 90  |
| Ala | Arg | Ser | Pro | Trp |
|     |     | 100 |     | 105 |
| Leu | Val | Thr | Val | Ser |
|     |     | 115 |     |     |

<210> 613  
 <211> 107  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|                                                                 |
|-----------------------------------------------------------------|
| <400> 613                                                       |
| Asp Ile Gln Met Thr Gln Ser Pro Pro Ser Leu Ser Ala Ser Ala Gly |
| 1 5 10 15                                                       |
| Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Arg |
| 20 25 30                                                        |
| Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile |
| 35 40 45                                                        |
| Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly |
| 50 55 60                                                        |
| Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro |
| 65 70 75 80                                                     |
| Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Tyr |
| 85 90 95                                                        |
| Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys                     |
| 100 105                                                         |

<210> 614  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|                     |
|---------------------|
| <400> 614           |
| Asp His Ala Ile His |
| 1 5                 |

<210> 615

<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 615  
Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe Arg  
1 5 10 15  
Gly

<210> 616  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 616  
Ser Leu Ser Thr Pro Tyr  
1 5

<210> 617  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 617  
Lys Ser Ser Gln Ser Leu Leu Asn Arg Gly Asn His Lys Asn Tyr Leu  
1 5 10 15  
Thr

<210> 618  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 618

Trp Ala Ser Thr Arg Glu Ser  
1 5

<210> 619

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 619

Gln Asn Asp Tyr Thr Tyr Pro Tyr Thr  
1 5

<210> 620

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 620

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

<210> 621

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 621

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

Lys

<210> 622

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 622

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| Ser | Tyr | Asn | Met | His |
| 1   |     |     |     | 5   |

<210> 623

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 623

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ile | Tyr | Pro | Gly | Asn | Gly | Asp | Thr | Ser | Tyr | Asn | Gln | Lys | Phe | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Gly

<210> 624  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 624  
Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val  
1 5 10

<210> 625  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 625  
Arg Ala Ser Ser Ser Val Ser Tyr Ile His  
1 5 10

<210> 626  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 626  
Ala Thr Ser Asn Leu Ala Ser  
1 5

<210> 627  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 627  
Gln Gln Trp Thr Ser Asn Pro Pro Thr  
1 5

<210> 628  
<211> 121  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 628  
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala  
1 5 10 15  
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
20 25 30  
Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile  
35 40 45  
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
50 55 60  
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr  
65 70 75 80  
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
85 90 95  
Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly  
100 105 110  
Ala Gly Thr Thr Val Thr Val Ser Ala  
115 120

<210> 629  
<211> 106  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 629  
Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly  
1 5 10 15  
Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile  
20 25 30  
His Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr  
35 40 45  
Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser  
50 55 60  
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu  
65 70 75 80  
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn Pro Pro Thr  
85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
100 105

<210> 630

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 630

Asp Thr Tyr Ile His

1 5

<210> 631

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 631

Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 632

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 632

Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr

1 5 10

<210> 633

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 633

Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala  
1 5 10

<210> 634

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 634

Ser Ala Ser Phe Leu Tyr Ser  
1 5

<210> 635

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 635

Gln Gln His Tyr Thr Thr Pro Pro Thr  
1 5

<210> 636

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 636

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



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 50  |     | 55  |     | 60  |     |     |     |     |     |     |     |     |     |     |     |
| Lys | Gly | Arg | Phe | Thr | Ile | Ser | Ala | Asp | Thr | Ser | Lys | Asn | Thr | Ala | Tyr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Gln | Met | Asn | Ser | Leu | Arg | Ala | Glu | Asp | Thr | Ala | Val | Tyr | Tyr | Cys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Arg | Trp | Gly | Gly | Asp | Gly | Phe | Tyr | Ala | Met | Asp | Tyr | Trp | Gly | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Thr | Leu | Val | Thr | Val | Ser | Ser |     |     |     |     |     |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

<210> 637  
 <211> 107  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|                                                                 |
|-----------------------------------------------------------------|
| <400> 637                                                       |
| Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly |
| 1 5 10 15                                                       |
| Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala |
| 20 25 30                                                        |
| Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile |
| 35 40 45                                                        |
| Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly |
| 50 55 60                                                        |
| Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro |
| 65 70 75 80                                                     |
| Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro |
| 85 90 95                                                        |
| Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys                     |
| 100 105                                                         |

<210> 638  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|                     |
|---------------------|
| <400> 638           |
| Ser Tyr Trp Ile Glu |
| 1 5                 |

<210> 639

<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 639  
Glu Ile Leu Pro Gly Gly Gly Asp Thr Asn Tyr Asn Glu Ile Phe Lys  
1 5 10 15  
Gly

<210> 640  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 640  
Arg Val Pro Ile Arg Leu Asp Tyr  
1 5

<210> 641  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 641  
Lys Ala Ser Gln Ser Val Asp Tyr Glu Gly Asp Ser Phe Leu Asn  
1 5 10 15

<210> 642  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 642  
Ala Ala Ser Asn Leu Glu Ser

1

5

<210> 643

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 643

Gln Gln Ser Asn Glu Asp Pro Leu Thr

1

5

<210> 644

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 644

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Ser Ser Tyr

20

25

30

Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile

35

40

45

Gly Glu Ile Leu Pro Gly Gly Gly Asp Thr Asn Tyr Asn Glu Ile Phe

50

55

60

Lys Gly Arg Ala Thr Phe Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Thr Arg Arg Val Pro Ile Arg Leu Asp Tyr Trp Gly Gln Gly Thr Leu

100

105

110

Val Thr Val Ser Ser

115

<210> 645

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 645

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

<210> 646

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 646

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| Asp | Phe | Ala | Met | Ser |
| 1   |     |     |     | 5   |

<210> 647

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 647

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ile | Gly | Arg | Val | Ala | Phe | His | Thr | Tyr | Tyr | Pro | Asp | Ser | Met | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 648

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 648

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Arg | Gly | Phe | Asp | Val | Gly | His | Phe | Asp | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

<210> 649

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 649

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Ser | Glu | Thr | Leu | Val | His | Ser | Ser | Gly | Asn | Thr | Tyr | Leu | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

<210> 650

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 650

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| Arg | Val | Ser | Asn | Arg | Phe | Ser |
| 1   |     |     | 5   |     |     |     |

<210> 651

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 651

|     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Gln | Gly | Ser | Phe | Asn | Pro | Leu | Thr |
| 1   |     |     |     | 5   |     |     |     |     |

<210> 652

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 652

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

<210> 653

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 653

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

<210> 654  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 654  
Asn Asp Tyr Ala Trp Asn  
1 5

<210> 655  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 655  
Tyr Ile Ser Tyr Ser Gly Tyr Thr Thr Tyr Asn Pro Ser Leu Lys Ser  
1 5 10 15

<210> 656  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 656  
Trp Thr Ser Gly Leu Asp Tyr  
1 5

<210> 657  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 657  
Lys Ala Ser Asp Leu Ile His Asn Trp Leu Ala  
1 5 10

<210> 658  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 658  
Gly Ala Thr Ser Leu Glu Thr  
1 5

<210> 659  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 659  
Gln Gln Tyr Trp Thr Thr Pro Phe Thr  
1 5

<210> 660  
<211> 116  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 660  
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Ser Ile Thr Asn Asp  
20 25 30  
Tyr Ala Trp Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp  
35 40 45  
Val Gly Tyr Ile Ser Tyr Ser Gly Tyr Thr Thr Tyr Asn Pro Ser Leu  
50 55 60  
Lys Ser Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Arg Trp Thr Ser Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val



|                 |     |     |     |
|-----------------|-----|-----|-----|
|                 | 100 | 105 | 110 |
| Thr Val Ser Ser |     |     |     |
| 115             |     |     |     |

<210> 661  
 <211> 107  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 661  
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Asp Leu Ile His Asn Trp  
 20 25 30  
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45  
 Tyr Gly Ala Thr Ser Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Thr Thr Pro Phe  
 85 90 95  
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
 100 105

<210> 662  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 662  
 Ser Asp Tyr Ala Trp Asn  
 1 5

<210> 663  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 663

Tyr Ile Ser Asn Ser Gly Ser Thr Ser Tyr Asn Pro Ser Leu Lys Ser  
1 5 10 15

<210> 664

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 664

Glu Arg Asn Tyr Asp Tyr Asp Asp Tyr Tyr Tyr Ala Met Asp Tyr  
1 5 10 15

<210> 665

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 665

Lys Ser Ser Gln Ser Leu Leu Tyr Arg Ser Asn Gln Lys Asn Tyr Leu  
1 5 10 15

Ala

<210> 666

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 666

Trp Ala Ser Thr Arg Glu Ser  
1 5

<210> 667

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 667

Gln Gln Tyr Tyr Asn Tyr Pro Arg Thr  
1 5

<210> 668

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 668

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

<210> 669

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 669

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Asn | Gln | Lys | Asn | Tyr | Leu | Ala | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Pro | Lys | Leu | Leu | Ile | Tyr | Trp | Ala | Ser | Thr | Arg | Glu | Ser | Gly | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Ser | Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Ser | Ser | Leu | Gln | Pro | Glu | Asp | Phe | Ala | Thr | Tyr | Tyr | Cys | Gln | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Tyr | Asn | Tyr | Pro | Arg | Thr | Phe | Gly | Gln | Gly | Thr | Lys | Val | Glu | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Lys

<210> 670  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 670  
 Asn Tyr Trp Met His  
 1 5

<210> 671  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 671  
 Ala Thr Tyr Arg Gly His Ser Asp Thr Tyr Tyr Asn Gln Lys Phe Lys  
 1 5 10 15  
 Gly

<210> 672  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 672  
Gly Ala Ile Tyr Asp Gly Tyr Asp Val Leu Asp Asn  
1 5 10

<210> 673  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 673  
Ser Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn  
1 5 10

<210> 674  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 674  
Tyr Thr Ser Asn Leu His Ser  
1 5

<210> 675  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 675  
Gln Gln Tyr Arg Lys Leu Pro Trp Thr  
1 5

<210> 676  
<211> 121  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 676

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

<210> 677

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 677

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

<210> 678

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 678

Ala Tyr Thr Met His

1 5

<210> 679

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 679

Trp Ile Lys Pro Asn Asn Gly Leu Ala Asn Tyr Ala Gln Lys Phe Gln

1 5 10 15

Gly

<210> 680

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 680

Ser Glu Ile Thr Thr Glu Phe Asp Tyr

1 5

<210> 681

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 681

Lys Ser Ser Glu Ser Val Asp Ser Tyr Ala Asn Ser Phe Leu His

1 5 10 15

<210> 682  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 682  
Arg Ala Ser Thr Arg Glu Ser  
1 5

<210> 683  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 683  
Gln Gln Ser Lys Glu Asp Pro Leu Thr  
1 5

<210> 684  
<211> 118  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 684  
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1 5 10 15  
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Ala Tyr  
20 25 30  
Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45  
Gly Trp Ile Lys Pro Asn Asn Gly Leu Ala Asn Tyr Ala Gln Lys Phe  
50 55 60  
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr  
65 70 75 80  
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Arg Ser Glu Ile Thr Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110  
Leu Val Thr Val Ser Ser



<210> 685  
 <211> 111  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 685  
 Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly  
 1 5 10 15  
 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Glu Ser Val Asp Ser Tyr  
 20 25 30  
 Ala Asn Ser Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro  
 35 40 45  
 Lys Leu Leu Ile Tyr Arg Ala Ser Thr Arg Glu Ser Gly Val Pro Asp  
 50 55 60  
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser  
 65 70 75 80  
 Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Lys  
 85 90 95  
 Glu Asp Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
 100 105 110

<210> 686  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 686  
 Ser Asp Phe Ala Trp Asn  
 1 5

<210> 687  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 687

Tyr Ile Ser Tyr Ser Gly Asn Thr Arg Tyr Gln Pro Ser Leu Lys Ser  
1 5 10 15

<210> 688

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 688

Ala Gly Arg Gly Phe Pro Tyr  
1 5

<210> 689

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 689

His Ser Ser Gln Asp Ile Asn Ser Asn Ile Gly  
1 5 10

<210> 690

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 690

His Gly Thr Asn Leu Asp Asp  
1 5

<210> 691

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 691

Val Gln Tyr Ala Gln Phe Pro Trp Thr  
1 5

<210> 692

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 692

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

<210> 693

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 693

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Met Ser Val Ser Val Gly  
1 5 10 15  
Asp Arg Val Thr Ile Thr Cys His Ser Ser Gln Asp Ile Asn Ser Asn  
20 25 30  
Ile Gly Trp Leu Gln Gln Lys Pro Gly Lys Ser Phe Lys Gly Leu Ile  
35 40 45  
Tyr His Gly Thr Asn Leu Asp Asp Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gly | Ser | Gly | Thr | Asp | Tyr | Thr | Leu | Thr | Ile | Ser | Ser | Leu | Gln | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Asp | Phe | Ala | Thr | Tyr | Tyr | Cys | Val | Gln | Tyr | Ala | Gln | Phe | Pro | Trp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Phe | Gly | Gly | Gly | Thr | Lys | Leu | Glu | Ile | Lys |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

<210> 694  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 694  
 Asp Tyr Tyr Met Ala  
 1 5

<210> 695  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 695  
 Ser Ile Asn Tyr Asp Gly Ser Ser Thr Tyr Tyr Val Asp Ser Val Lys  
 1 5 10 15  
 Gly

<210> 696  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 696  
 Asp Arg Gly Tyr Tyr Phe Asp Tyr  
 1 5

<210> 697

<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 697  
Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His  
1 5 10 15

<210> 698  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 698  
Lys Val Ser Asn Arg Phe Ser  
1 5

<210> 699  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 699  
Ser Gln Ser Thr His Val Pro Pro Phe Thr  
1 5 10

<210> 700  
<211> 117  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 700  
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr



<400> 702  
Ser Tyr Gly Met His  
1 5

<210> 703  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 703  
Val Ile Trp Tyr Asp Gly Ser Asn Gln Tyr Tyr Ala Asp Ser Val Lys  
1 5 10 15  
Gly

<210> 704  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 704  
Gly Leu Thr Ser Gly Arg Tyr Gly Met Asp Val  
1 5 10

<210> 705  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 705  
Arg Ser Ser Gln Ser Leu Leu Leu Ser His Gly Phe Asn Tyr Leu Asp  
1 5 10 15

<210> 706  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 706

Leu Gly Ser Ser Arg Ala Ser

1

5

<210> 707

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 707

Met Gln Pro Leu Gln Ile Pro Trp Thr

1

5

<210> 708

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 708

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Gln Tyr Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe

65

70

75

80

Leu Gln Met His Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Gly Leu Thr Ser Gly Arg Tyr Gly Met Asp Val Trp Gly Gln

100

105

110

Gly Thr Thr Val Thr Val Ser Ser

115

120

<210> 709



<211> 112  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 709  
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly  
1 5 10 15  
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Leu Ser  
20 25 30  
His Gly Phe Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser  
35 40 45  
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Ser Arg Ala Ser Gly Val Pro  
50 55 60  
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile  
65 70 75 80  
Ser Arg Val Glu Ala Glu Asp Val Gly Leu Tyr Tyr Cys Met Gln Pro  
85 90 95  
Leu Gln Ile Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105 110

<210> 710  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 710  
Asn Ala Trp Met Ser  
1 5

<210> 711  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 711  
Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys  
1 5 10 15  
Gly

<210> 712  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 712  
Glu Gly Leu Trp Ala Phe Asp Tyr  
1 5

<210> 713  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 713  
Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Val Val His  
1 5 10

<210> 714  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 714  
Asp Asn Asn Lys Arg Pro Ser  
1 5

<210> 715  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 715

Ala Ala Trp Asp Asp Arg Leu Asn Gly Pro Val  
1 5 10

<210> 716

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 716

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

<210> 717

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 717

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Glu | Asp | Glu | Ala | Asp | Tyr | Tyr | Cys | Ala | Ala | Trp | Asp | Asp | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Asn | Gly | Pro | Val | Phe | Gly | Gly | Gly | Thr | Lys | Leu | Thr | Val | Leu |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

<210> 718  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 718  
 Gly Tyr Tyr Trp Ser  
 1 5

<210> 719  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 719  
 Glu Ile Asn His Arg Gly Asn Thr Asn Asp Asn Pro Ser Leu Lys Ser  
 1 5 10 15

<210> 720  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 720  
 Glu Arg Gly Tyr Thr Tyr Gly Asn Phe Asp His  
 1 5 10

<210> 721  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 721

Arg Ala Ser Gln Ser Val Ser Arg Asn Leu Ala  
1 5 10

<210> 722

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 722

Gly Ala Ser Thr Arg Ala Thr  
1 5

<210> 723

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 723

Gln Gln Tyr Lys Thr Trp Pro Arg Thr  
1 5

<210> 724

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 724

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| 50  |     | 55  |     | 60  |     |     |     |     |     |     |     |     |     |     |     |  |
| Ser | Arg | Val | Thr | Ile | Ser | Val | Asp | Thr | Ser | Lys | Asn | Gln | Phe | Ala | Leu |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Lys | Leu | Ser | Ser | Val | Thr | Ala | Ala | Asp | Thr | Ala | Val | Tyr | Tyr | Cys | Ala |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Arg | Glu | Arg | Gly | Tyr | Thr | Tyr | Gly | Asn | Phe | Asp | His | Trp | Gly | Gln | Gly |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Thr | Leu | Val | Thr | Val | Ser | Ser |     |     |     |     |     |     |     |     |     |  |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |  |

<210> 725  
 <211> 107  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| <400> 725 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Glu       | Ile | Val | Met | Thr | Gln | Ser | Pro | Ala | Thr | Leu | Ser | Val | Ser | Pro | Gly |  |
| 1         |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Glu       | Arg | Ala | Thr | Leu | Ser | Cys | Arg | Ala | Ser | Gln | Ser | Val | Ser | Arg | Asn |  |
|           |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu       | Ala | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Gln | Ala | Pro | Arg | Leu | Leu | Ile |  |
|           |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Tyr       | Gly | Ala | Ser | Thr | Arg | Ala | Thr | Gly | Ile | Pro | Ala | Arg | Phe | Ser | Gly |  |
|           | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Ser       | Gly | Ser | Gly | Thr | Glu | Phe | Thr | Leu | Thr | Ile | Gly | Ser | Leu | Gln | Ser |  |
| 65        |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Glu       | Asp | Phe | Ala | Val | Tyr | Tyr | Cys | Gln | Gln | Tyr | Lys | Thr | Trp | Pro | Arg |  |
|           |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Thr       | Phe | Gly | Gln | Gly | Thr | Asn | Val | Glu | Ile | Lys |     |     |     |     |     |  |
|           |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |  |

<210> 726  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|           |     |     |     |     |
|-----------|-----|-----|-----|-----|
| <400> 726 |     |     |     |     |
| Ser       | Tyr | Ala | Met | Asn |
| 1         |     |     | 5   |     |

<210> 727

<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 727  
Thr Thr Ser Gly Ser Gly Ala Ser Thr Tyr Tyr Ala Asp Ser Val Lys  
1 5 10 15  
Gly

<210> 728  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 728  
Ile Trp Ile Ala Phe Asp Ile  
1 5

<210> 729  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 729  
Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala  
1 5 10

<210> 730  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 730  
Gly Ala Ser Ser Arg Ala Thr

1

5

<210> 731

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 731

Gln Gln Tyr Gly Ser Ser Pro Tyr Thr  
1 5

<210> 732

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 732

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

<210> 733

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic



<400> 733

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

<210> 734

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 734

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| Ser | Phe | Asn | Tyr | Tyr | Trp | Ser |
| 1   |     |     |     | 5   |     |     |

<210> 735

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 735

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ile | Tyr | Tyr | Ser | Gly | Ser | Thr | Tyr | Ser | Asn | Pro | Ser | Leu | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

<210> 736

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 736

Gly Tyr Asn Trp Asn Tyr Phe Asp Tyr  
1 5

<210> 737

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 737

Arg Ala Ser Gln Ser Val Asp Asn Asn Leu Val  
1 5 10

<210> 738

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 738

Gly Ala Ser Thr Arg Ala Thr  
1 5

<210> 739

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 739

Gln Gln Tyr Asn Asn Trp Pro Pro Trp Thr  
1 5 10

<210> 740

<211> 119

<212> PRT

<213> Artificial Sequence

## <223> Synthetic

[illegible]

$\langle 211 \rangle$  108

&lt;212&gt; PRT

## <213> Artificial Sequence

<223> Synthetic

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

<211> 5

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 742  
Thr Tyr Trp Met His  
1 5

<210> 743  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 743  
Glu Ile Asp Pro Ser Asp Ser Tyr Ser Asn Tyr Asn Gln Lys Phe Lys  
1 5 10 15  
Asp

<210> 744  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 744  
Asn Gly Gly Leu Gly Pro Ala Trp Phe Ser Tyr  
1 5 10

<210> 745  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 745  
Lys Ala Ser Gln Tyr Val Gly Thr Ala Val Ala  
1 5 10

<210> 746  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 746  
Ser Ala Ser Asn Arg Tyr Thr  
1 5

<210> 747  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 747  
Gln Gln Tyr Ser Ser Tyr Pro Trp Thr  
1 5

<210> 748  
<211> 120  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 748  
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
1 5 10 15  
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr  
20 25 30  
Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile  
35 40 45  
Gly Glu Ile Asp Pro Ser Asp Ser Tyr Ser Asn Tyr Asn Gln Lys Phe  
50 55 60  
Lys Asp Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr  
65 70 75 80  
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Arg Asn Gly Gly Leu Gly Pro Ala Trp Phe Ser Tyr Trp Gly Gln

|     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     | 100 |     |     |     | 105 |     | 110 |
| Gly | Thr | Leu | Val | Thr | Val | Ser | Ser |     |
|     |     | 115 |     |     |     | 120 |     |     |

<210> 749  
 <211> 107  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 749  
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Tyr Val Gly Thr Ala  
 20 25 30  
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Leu Leu Ile  
 35 40 45  
 Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Asp  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Trp  
 85 90 95  
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
 100 105

<210> 750  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 750  
 Ser Tyr Ala Met Ser  
 1 5

<210> 751  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 751

Ala Ile Ser Gly Ser Gly Thr Ser Thr Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 752

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 752

Val Arg Tyr Asn Trp Asn His Gly Asp Trp Phe Asp Pro

1 5 10

<210> 753

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 753

Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser

1 5 10

<210> 754

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 754

Glu Asn Tyr Asn Arg Pro Ala

1 5

<210> 755

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 755

Ser Ser Trp Asp Asp Ser Leu Asn Tyr Trp Val  
1 5 10

<210> 756

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 756

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

<210> 757

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 757

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln  
1 5 10 15  
Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn  
20 25 30



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Val | Ser | Trp | Tyr | Gln | Gln | Leu | Pro | Gly | Thr | Ala | Pro | Lys | Leu | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Tyr | Glu | Asn | Tyr | Asn | Arg | Pro | Ala | Gly | Val | Pro | Asp | Arg | Phe | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Ser | Lys | Ser | Gly | Thr | Ser | Ala | Ser | Leu | Ala | Ile | Ser | Gly | Leu | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Glu | Asp | Glu | Ala | Asp | Tyr | Tyr | Cys | Ser | Ser | Trp | Asp | Asp | Ser | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Tyr | Trp | Val | Phe | Gly | Gly | Gly | Thr | Lys | Leu | Thr | Val | Leu |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

<210> 758  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 758  
 Ser Tyr Gly Met Ser  
 1 5

<210> 759  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 759  
 Thr Ile Ser Ser Gly Gly Ser Tyr Lys Tyr Tyr Val Asp Ser Val Lys  
 1 5 10 15  
 Gly

<210> 760  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 760  
 His Pro Asp Tyr Asp Gly Val Trp Phe Ala Tyr



<400> 764

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

<210> 765

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 765

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

<210> 766

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 766

Ser Tyr Gly Met Ser  
1 5

<210> 767

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 767

Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val Lys  
1 5 10 15  
Gly

<210> 768

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 768

His Pro Asp Tyr Asp Gly Val Trp Phe Ala Tyr  
1 5 10

<210> 769

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 769

Ser Val Ser Ser Ser Val Phe Tyr Val His  
1 5 10

<210> 770

<211> 7

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 770  
Asp Thr Ser Lys Leu Ala Ser  
1 5

<210> 771  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 771  
Gln Gln Trp Asn Ser Asn Pro Pro Thr  
1 5

<210> 772  
<211> 120  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 772  
Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly  
1 5 10 15  
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ser Tyr  
20 25 30  
Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Trp Val  
35 40 45  
Ala Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys  
85 90 95  
Ala Arg His Pro Asp Tyr Asp Gly Val Trp Phe Ala Tyr Trp Gly Gln  
100 105 110  
Gly Thr Leu Val Thr Val Ser Ala  
115 120

<210> 773  
<211> 105  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 773  
Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ala Ser Pro Gly Glu  
1 5 10 15  
Lys Val Thr Met Thr Cys Ser Val Ser Ser Ser Val Phe Tyr Val His  
20 25 30  
Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp  
35 40 45  
Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly  
50 55 60  
Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp  
65 70 75 80  
Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Asn Ser Asn Pro Pro Thr Phe  
85 90 95  
Gly Gly Gly Thr Lys Leu Glu Ile Lys  
100 105

<210> 774  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 774  
Ser Tyr Tyr Met His  
1 5

<210> 775  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 775  
Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe Gln  
1 5 10 15

Gly

<210> 776  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 776  
Asp Gly Val Leu Arg Tyr Phe Asp Trp Leu Leu Asp Tyr Tyr Tyr Tyr  
1 5 10 15

<210> 777  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 777  
Arg Ala Ser Gln Ser Val Gly Ser Tyr Leu Ala  
1 5 10

<210> 778  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 778  
Asp Ala Ser Asn Arg Ala Thr  
1 5

<210> 779  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 779

Gln Gln Arg Ala Asn Val Phe Thr  
1 5

<210> 780

<211> 128

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 780

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

<210> 781

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 781

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15  
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Tyr  
20 25 30  
Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile  
35 40 45  
Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly  
50 55 60



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr | Ile | Ser | Ser | Leu | Glu | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Asp | Phe | Ala | Val | Tyr | Tyr | Cys | Gln | Gln | Arg | Ala | Asn | Val | Phe | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Gly | Gln | Gly | Thr | Lys | Val | Glu | Ile | Lys |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

<210> 782  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 782  
 Ser Tyr Tyr Met His  
 1 5

<210> 783  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 783  
 Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe Gln  
 1 5 10 15  
 Gly

<210> 784  
 <211> 19  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 784  
 Asp Ala Glu Leu Arg His Phe Asp His Leu Leu Asp Tyr His Tyr Tyr  
 1 5 10 15  
 Met Asp Val

<210> 785  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 785  
Arg Ala Ser Gln Ser Val Gly Ser Tyr Leu Ala  
1 5 10

<210> 786  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 786  
Asp Ala Ser Asn Arg Ala Thr  
1 5

<210> 787  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 787  
Gln Gln Arg Ala Gln Glu Phe Thr  
1 5

<210> 788  
<211> 128  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 788  
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

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

<210> 789  
 <211> 106  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 789

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

<210> 790  
 <211> 120  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 790

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

<210> 791

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 791

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

<210> 792

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 792

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

<210> 793

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 793

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

<210> 794

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 794

Asn Tyr Tyr Met Ala

1

5

<210> 795

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 795

Ser Ile Thr Lys Gly Gly Gly Asn Thr Tyr Tyr Arg Asp Ser Val Lys

1

5

10

15

Gly

<210> 796

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 796

Gln Val Thr Ile Ala Ala Val Ser Thr Ser Tyr Phe Asp Ser

1

5

10

<210> 797

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 797

Lys Thr Asn Gln Lys Val Asp Tyr Tyr Gly Asn Ser Tyr Val Tyr

1

5

10

15

<210> 798  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 798  
Leu Ala Ser Asn Leu Ala Ser  
1 5

<210> 799  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 799  
Gln Gln Ser Arg Asn Leu Pro Tyr Thr  
1 5

<210> 800  
<211> 123  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 800  
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Arg  
1 5 10 15  
Ser Ile Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Asn Tyr  
20 25 30  
Tyr Met Ala Trp Val Arg Gln Ala Pro Ser Lys Gly Leu Glu Trp Val  
35 40 45  
Ala Ser Ile Thr Lys Gly Gly Gly Asn Thr Tyr Tyr Arg Asp Ser Val  
50 55 60  
Lys Gly Arg Phe Thr Phe Ser Arg Asp Asn Ala Lys Ser Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Asp Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys  
85 90 95  
Ala Arg Gln Val Thr Ile Ala Ala Val Ser Thr Ser Tyr Phe Asp Ser  
100 105 110  
Trp Gly Gln Gly Val Met Val Thr Val Ser Ser

115

120

<210> 801  
 <211> 110  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 801  
 Asp Ile Val Leu Thr Gln Ser Pro Ala Leu Ala Val Ser Leu Gly Gln  
 1 5 10 15  
 Arg Ala Thr Ile Ser Cys Lys Thr Asn Gln Lys Val Asp Tyr Tyr Gly  
 20 25 30  
 Asn Ser Tyr Val Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Gln Pro Lys  
 35 40 45  
 Leu Leu Ile Tyr Leu Ala Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg  
 50 55 60  
 Phe Ser Gly Arg Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asp Pro  
 65 70 75 80  
 Val Glu Ala Asp Asp Thr Ala Thr Tyr Tyr Cys Gln Gln Ser Arg Asn  
 85 90 95  
 Leu Pro Tyr Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 100 105 110

<210> 802  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 802  
 Asp Tyr Tyr Met Lys  
 1 5

<210> 803  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 803



Asp Ile Ile Pro Ser Asn Gly Ala Thr Phe Tyr Asn Gln Lys Phe Lys  
1 5 10 15  
Gly

<210> 804  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 804  
Ser His Leu Leu Arg Ala Ser Trp Phe Ala Tyr  
1 5 10

<210> 805  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 805  
Lys Ser Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu  
1 5 10 15  
Thr

<210> 806  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 806  
Trp Ala Ser Thr Arg Glu Ser  
1 5

<210> 807  
<211> 9  
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 807

Gln Asn Asp Tyr Ser Tyr Pro Tyr Thr  
1 5

<210> 808

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 808

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

<210> 809

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 809

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Asn | Gln | Lys | Asn | Tyr | Leu | Thr | Trp | Tyr | Leu | Gln | Lys | Pro | Gly | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Pro | Lys | Leu | Leu | Ile | Tyr | Trp | Ala | Ser | Thr | Arg | Glu | Ser | Gly | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Asp | Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Ser | Ser | Leu | Gln | Ala | Glu | Asp | Val | Ala | Val | Tyr | Tyr | Cys | Gln | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Tyr | Ser | Tyr | Pro | Tyr | Thr | Phe | Gly | Gln | Gly | Thr | Lys | Leu | Glu | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Lys

<210> 810  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 810  
 Asp Tyr Glu Met His  
 1 5

<210> 811  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 811  
 Trp Ile Gly Gly Ile Asp Pro Glu Thr Gly Gly Thr Ala Tyr Asn Gln  
 1 5 10 15  
 Lys Phe Lys Gly  
 20

<210> 812  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 812

Tyr Tyr Ser Phe Ala Tyr  
1 5

<210> 813

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 813

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Gln  
1 5 10 15

<210> 814

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 814

Lys Val Ser Asn Arg Phe Ser  
1 5

<210> 815

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 815

Phe Gln Val Ser His Val Pro Tyr Thr  
1 5

<210> 816

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 816

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

<210> 817

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 817

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

<210> 818

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 818

Asp Tyr Asn Val Asn

1 5

<210> 819

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 819

Val Ile Asn Pro Lys Tyr Gly Thr Thr Arg Tyr Asn Gln Lys Phe Lys

1 5 10 15

Gly

<210> 820

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 820

Gly Leu Asn Ala Trp Asp Tyr

1 5

<210> 821

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 821

Gly Ala Ser Glu Asn Ile Tyr Gly Ala Leu Asn

1 5 10

<210> 822  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 822  
Gly Ala Thr Asn Leu Glu Asp  
1 5

<210> 823  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 823  
Gln Asn Val Leu Thr Thr Pro Tyr Thr  
1 5

<210> 824  
<211> 116  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 824  
Gln Phe Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1 5 10 15  
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr  
20 25 30  
Asn Val Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile  
35 40 45  
Gly Val Ile Asn Pro Lys Tyr Gly Thr Thr Arg Tyr Asn Gln Lys Phe  
50 55 60  
Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr  
65 70 75 80  
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Thr Arg Gly Leu Asn Ala Trp Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110  
Thr Val Ser Ser

<210> 825  
 <211> 107  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 825  
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Thr Cys Gly Ala Ser Glu Asn Ile Tyr Gly Ala  
 20 25 30  
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45  
 Tyr Gly Ala Thr Asn Leu Glu Asp Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Arg Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Asn Val Leu Thr Thr Pro Tyr  
 85 90 95  
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
 100 105

<210> 826  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 826  
 Gly Tyr Phe Met Asn  
 1 5

<210> 827  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 827



Leu Ile Asn Pro Tyr Asn Gly Asp Ser Phe Tyr Asn Gln Lys Phe Lys  
1 5 10 15  
Gly

<210> 828  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 828  
Gly Leu Arg Arg Asp Phe Asp Tyr  
1 5

<210> 829  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 829  
Gly Leu Arg Arg Asp Phe Asp Tyr  
1 5

<210> 830  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 830  
Leu Val Ser Glu Leu Asp Ser  
1 5

<210> 831  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 831

Trp Gln Gly Thr His Phe Pro Arg Thr  
1 5

<210> 832

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 832

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

<210> 833

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 833

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Arg | Arg | Leu | Ile | Tyr | Leu | Val | Ser | Glu | Leu | Asp | Ser | Gly | Val | Pro |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Lys | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Arg | Val | Glu | Ala | Glu | Asp | Val | Gly | Val | Tyr | Tyr | Cys | Trp | Gln | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | His | Phe | Pro | Arg | Thr | Phe | Gly | Gly | Gly | Thr | Lys | Leu | Glu | Ile | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

<210> 834  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 834  
 Thr Ala Ala Ile Ser  
 1 5

<210> 835  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 835  
 Gly Ile Ile Pro Ile Phe Gly Lys Ala His Tyr Ala Gln Lys Phe Gln  
 1 5 10 15  
 Gly

<210> 836  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 836  
 Lys Phe His Phe Val Ser Gly Ser Pro Phe Gly Met Asp Val  
 1 5 10

<210> 837  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 837  
Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala  
1 5 10

<210> 838  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 838  
Asp Ala Ser Asn Arg Ala Thr  
1 5

<210> 839  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 839  
Gln Gln Arg Ser Asn Trp Pro Thr  
1 5

<210> 840  
<211> 123  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 840  
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser

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

<210> 841  
 <211> 106  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

|           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| <400> 841 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Glu       | Ile | Val | Leu | Thr | Gln | Ser | Pro | Ala | Thr | Leu | Ser | Leu | Ser | Pro | Gly |  |
| 1         |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Glu       | Arg | Ala | Thr | Leu | Ser | Cys | Arg | Ala | Ser | Gln | Ser | Val | Ser | Ser | Tyr |  |
|           |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |
| Leu       | Ala | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Gln | Ala | Pro | Arg | Leu | Leu | Ile |  |
|           |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Tyr       | Asp | Ala | Ser | Asn | Arg | Ala | Thr | Gly | Ile | Pro | Ala | Arg | Phe | Ser | Gly |  |
|           | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ser       | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr | Ile | Ser | Ser | Leu | Glu | Pro |  |
| 65        |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Glu       | Asp | Phe | Ala | Val | Tyr | Tyr | Cys | Gln | Gln | Arg | Ser | Asn | Trp | Pro | Thr |  |
|           |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Phe       | Gly | Gln | Gly | Thr | Lys | Val | Glu | Ile | Lys |     |     |     |     |     |     |  |
|           |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |     |  |

<210> 842  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 842  
Gly Thr Phe Ser Ser Tyr Ala Ile Ser  
1 5

<210> 843  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 843  
Ser Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln  
1 5 10 15  
Gly

<210> 844  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 844  
Ala Arg Gly Pro Ser Glu Val Gly Ala Ile Leu Gly Tyr Val Trp Phe  
1 5 10 15  
Asp Pro

<210> 845  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 845  
Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp  
1 5 10 15

<210> 846  
<211> 7

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 846  
Leu Gly Ser Asn Arg Ala Ser  
1 5

<210> 847  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 847  
Met Gln Ala Arg Arg Ile Pro Ile Thr  
1 5

<210> 848  
<211> 125  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 848  
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
1 5 10 15  
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr  
20 25 30  
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45  
Gly Ser Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe  
50 55 60  
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr  
65 70 75 80  
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Arg Gly Pro Ser Glu Val Gly Ala Ile Leu Gly Tyr Val Trp Phe  
100 105 110  
Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120 125

<210> 849  
<211> 112  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 849  
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly  
1 5 10 15  
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser  
20 25 30  
Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser  
35 40 45  
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro  
50 55 60  
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile  
65 70 75 80  
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala  
85 90 95  
Arg Arg Ile Pro Ile Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
100 105 110

<210> 850  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 850  
Gly Tyr Thr Phe Thr Asp His Ala Ile His Trp Val  
1 5 10

<210> 851  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 851  
Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr  
1 5 10



<210> 852  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 852  
Lys Arg Ser Leu Ser Thr Pro Tyr  
1 5

<210> 853  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 853  
Gln Ser Leu Leu Asn Arg Gly Asn His Lys Asn Tyr  
1 5 10

<210> 854  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 854  
Trp Ala Ser Thr Arg Glu Ser  
1 5

<210> 855  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 855

Gln Asn Asp Tyr Thr Tyr Pro Tyr Thr  
1 5

<210> 856

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 856

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

<210> 857

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 857

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Val | Met | Thr | Gln | Ser | Pro | Asp | Ser | Leu | Ala | Val | Ser | Leu | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Arg | Ala | Thr | Ile | Asn | Cys | Lys | Ser | Ser | Gln | Ser | Leu | Leu | Asn | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Asn | His | Lys | Asn | Tyr | Leu | Thr | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Pro | Lys | Leu | Leu | Ile | Tyr | Trp | Ala | Ser | Thr | Arg | Glu | Ser | Gly | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Asp | Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ser | Ser | Leu | Gln | Ala | Glu | Asp | Val | Ala | Val | Tyr | Tyr | Cys | Gln | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Tyr | Thr | Tyr | Pro | Tyr | Thr | Phe | Gly | Gln | Gly | Thr | Lys | Val | Glu | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 858  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 858  
 Asn Tyr Asp Ile Asn  
 1 5

<210> 859  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 859  
 Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe Lys  
 1 5 10 15  
 Ala

<210> 860  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 860  
 Gly Tyr Glu Asp Ala Met Asp Tyr  
 1 5

<210> 861

<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 861  
Lys Ala Ser Gln Asp Ile Asn Ser Tyr Leu Ser  
1 5 10

<210> 862  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 862  
Arg Ala Asn Arg Leu Val Asp  
1 5

<210> 863  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 863  
Leu Gln Tyr Asp Glu Phe Pro Leu Thr  
1 5

<210> 864  
<211> 117  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 864  
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1 5 10 15  
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr



1 5

<210> 867  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 867  
Trp Ile Asn Thr Tyr Ser Gly Glu Pro Arg Tyr Ala Asp Asp Phe Lys  
1 5 10 15  
Gly

<210> 868  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 868  
Asp Tyr Gly Arg Trp Tyr Phe Asp Val  
1 5

<210> 869  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 869  
Arg Ala Ser Ser Ser Val Ser His Met His  
1 5 10

<210> 870  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 870

Ala Thr Ser Asn Leu Ala Ser  
1 5

<210> 871

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 871

Gln Gln Trp Ser Ser Thr Pro Arg Thr  
1 5

<210> 872

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 872

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

<210> 873

<211> 106

<212> PRT

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

### <213> Artificial Sequence

<223> Synthetic

Asp Tyr Tyr Ile His  
1 5

### <213> Artificial Sequence

## <223> Synthetic

Tyr Ile Asn Pro Asn Ser Gly Tyr Thr Asn Tyr Ala Gln Lys Phe Gln  
1 5 10 15  
Gly



<210> 876  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 876  
Tyr Met Trp Glu Arg Val Thr Gly Phe Phe Asp Phe  
1 5 10

<210> 877  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 877  
Leu Ala Ser Glu Asp Ile Ser Asp Asp Leu Ala  
1 5 10

<210> 878  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 878  
Thr Thr Ser Ser Leu Gln Ser  
1 5

<210> 879  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 879  
Gln Gln Thr Tyr Lys Phe Pro Pro Thr  
1 5

<210> 880  
<211> 121  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 880  
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1 5 10 15  
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr  
20 25 30  
Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile  
35 40 45  
Gly Tyr Ile Asn Pro Asn Ser Gly Tyr Thr Asn Tyr Ala Gln Lys Phe  
50 55 60  
Gln Gly Arg Ala Thr Met Thr Ala Asp Lys Ser Ile Asn Thr Ala Tyr  
65 70 75 80  
Val Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Phe Cys  
85 90 95  
Thr Arg Tyr Met Trp Glu Arg Val Thr Gly Phe Phe Asp Phe Trp Gly  
100 105 110  
Gln Gly Thr Met Val Thr Val Ser Ser  
115 120

<210> 881  
<211> 107  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 881  
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly  
1 5 10 15  
Asp Arg Val Thr Ile Thr Cys Leu Ala Ser Glu Asp Ile Ser Asp Asp  
20 25 30  
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Val  
35 40 45  
Tyr Thr Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60  
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80  
Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Thr Tyr Lys Phe Pro Pro  
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 882

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 882

Gly Phe Thr Phe Ser Asn Tyr Ala  
1 5

<210> 883

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 883

Ile Ser Gly Ser Gly Asp Tyr Thr  
1 5

<210> 884

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 884

Ala Arg Ser Pro Trp Gly Tyr Tyr Leu Asp Ser  
1 5 10

<210> 885

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 885

Gln Gly Ile Ser Ser Arg

1 5

<210> 886

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 886

Ala Ala Ser

1

<210> 887

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 887

Gln Gln Tyr Asn Ser Tyr Pro Tyr Thr

1 5

<210> 888

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 888

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr  
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Ser Ile Ser Gly Ser Gly Asp Tyr Thr Tyr Tyr Thr Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Leu | Gln | Met | Asn | Ser | Leu | Arg | Ala | Glu | Asp | Thr | Ala | Val | Tyr | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  | Cys |
| Ala | Arg | Ser | Pro | Trp | Gly | Tyr | Tyr | Leu | Asp | Ser | Trp | Gly | Gln | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 | Thr |
| Leu | Val | Thr | Val | Ser | Ser |     |     |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |

<210> 889

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 889

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