

5 BUTELASE-MEDIATED PEPTIDE LIGATION

CROSS-REFERENCE TO RELATED APPLICATION

[0001] This application makes reference to and claims the benefit of priority of a
10 Singapore Application for "Site-specific N-terminal Labelling of Peptides and Proteins using
butelase 1 and Thiodipeptide" filed on October 01, 2015, and duly assigned application
number 10201508158V. The content of said application filed on October 01, 2015, is
incorporated herein by reference for all purposes, including an incorporation of any element or
part of the description, claims or drawings not contained herein and referred to in Rule 20.5(a)
15 of the PCT, pursuant to Rule 4.18 of the PCT.

FIELD OF THE INVENTION

[0002] The present invention relates generally to a method of enzymatically ligating
20 peptides.

BACKGROUND OF THE INVENTION

[0003] Site-specific protein modifications with tags and probes offer useful tools for
25 various biochemical studies involving protein-protein interactions (J. Biotechnol. 2011, 152, 37;
Bioconjug Chem 2010, 21, 2227; J. Am. Chem. Soc: 2008, 130, 16338), structure-function
relationships (J Biomol NMR 2009, 43, 145), biomaterials (Biopolymers 2008, 90, 450; PLoS
One 2007, 2, e1164; Biotechnology letters 2008, 30, 1603; Biochemistry (Mosc.) 2010, 49,
2604; Bioconjug. Chem. 2007, 18, 469) and therapeutics (Curr Opin Chem Biol 2003, 7, 734; J
30 Org Chem 2007, 72, 3909). A common approach is by chemical means (Angew Chem Int Ed
Engl 2008, 47, 10030). Many employ N-terminal amino acid- or side chain functional group-
specific methods (Bioconjug Chem 2003, 14, 614; Science 1994, 266, 776; Angewandte
Chemie International Edition 2006, 45, 5307) which include cysteine-directed derivatization
(Science 1994, 266, 776; Curr Opin Chem Biol 2010, 14, 781; Angew Chem Int Ed Engl 2004,
35 43, 828; Angew Chem Int Ed Engl 2011, 50, 9611), conjugation of lysine side chain (Bioorg
Med Chem Lett 2009, 19, 6268; J Am Chem Soc 2009, 131, 13592; Chem Commun (Camb)
2010, 46, 7199), and Click reaction (Bioconjug Chem 2003, 14, 614; Science 1994, 266, 776;
Angewandte Chemie International Edition 2006, 45, 5307; Org Lett 2006, 8, 4505; Org Lett

2007, 9, 1; Chem Commun (Camb) 2007, 3249; J Am Chem Soc 2004, 126, 13998; Org Lett 2001, 3, 781; J Am Chem Soc 2002, 124, 10773; J Am Chem Soc 2003, 125, 4686; J Am Chem Soc 2003, 125, 3192). Despite being powerful and robust, chemical methods generally require an excess amount of a labeling reagent, and a carefully controlled reaction condition (Bioconjug Chem 2006, 17, 179). Often, site specificity becomes a challenge when multiple copies of a targeted amino acid or functional group are present in a protein substrate (Angewandte Chemie International Edition 2006, 45, 5307). Recently, enzymatic approaches using peptide ligases under mild reaction conditions provide an attractive alternative with *exquisite* site-specificity (J Org Chem 2007, 72, 3909; J Am Chem Soc 2004, 126, 2670; Nat Chem Biol 2007, 3, 707; Angew Chem Int Edit 2011, 50, 5024; Mini-Rev Org Chem 2008, 5, 47; Biotechnology Letters 2010, 32, 1; J Am Chem Soc 2008, 130, 2132; Chembiochem 2008, 9, 802; ChemBioChem 2009, 10, 787; Angew. Chem. Int. Ed. Engl. 2014, 53, 3024). Enzymatic ligation is C-terminal-amino-acid-specific and orthogonal to chemical approaches in achieving protein labeling and conjugation reactions. Currently, sortase A is the most popular ligase (Proc. Natl. Acad. Sci. U. S. A. 2000, 97, 5013; FEMS Microbiol Rev 2008, 32, 307; Microbiol Mol Biol Rev 2006, 70, 192; Science 1999, 285, 760; Mol. Microbiol. 2001, 40, 1049; Proc. Natl. Acad. Sci. U. S. A. 1999, 96, 12424), but it has low catalytic efficiency, requires a long reaction time and a high molar equivalent of enzyme (typically 0.1 to 1 molar ratio) (Angew Chem Int Ed Engl 2008, 47, 10030; J Am Chem Soc 2009, 131, 10800; J Org Chem 2014, 79, 487; Angew. Chem. Int. Ed. Engl. 2012, 51, 9377; Chem Commun (Camb) 2011, 47, 4742; Nat. Protoc. 2013, 8, 1800). In addition, sortase A has a stringent substrate requirement, leaving behind an additional sorting sequence LPXTG in the resulting modified proteins (Proc. Natl. Acad. Sci. U. S. A. 1999, 96, 12424). A ligase with a broad substrate specificity, efficient kinetics, and traceless ligation would be highly desirable.

[0004] Recently, as disclosed in the International Patent Publication No. WO2015163818 A1, which is hereby incorporated by reference in its entirety, the inventors of the present invention isolated an Asn/Asp(Asx)-specific ligase called butelase 1 from the medicinal plant *Clitoria ternatea* (Nat Chem Biol 2014, 10, 732). Butelase 1 is a cysteine ligase mediating the backbone cyclization in the biosynthesis of cyclotides, a family of circular plant defense peptides (J Mol Biol 1999, 294, 1327; J. Biol. Chem. 2013, 288, 3370; J. Biol. Chem. 2012, 287, 17598; J. Biol. Chem. 2007, 282, 29721). Butelase 1 has three attractive features: (1) it is the fastest known ligase with high catalytic efficiencies of up to $542,000 \text{ M}^{-1} \text{ s}^{-1}$ (Nat Chem Biol 2014, 10, 732; J. Biol. Chem. 2013, 288, 12500; J Am Chem Soc 2009, 131, 2122), (2) it is C-terminal specific for Asx with a sorting signal not more than two amino acids after Asx, and

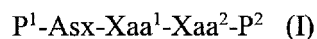
(3) it displays a very broad specificity for the acceptor nucleophilic amino acids (all natural amino acids except Pro) to form a new Asx-Xaa peptide bond. These features make butelase 1 an attractive new tool for protein engineering. However, while the butelase-mediated intramolecular ligation proceeds with high efficiency and is irreversible, the intermolecular peptide ligation is reversible and requires an excess amount of substrate to drive the reaction to completion (Nat Chem Biol 2014, 10, 732), a condition also found in sortase A (J Am Chem Soc 2004, 126, 2670; Nat Chem Biol 2007, 3, 707; Angew Chem Int Edit 2011, 50, 5024; Mini-Rev Org Chem 2008, 5, 47; Biotechnology Letters 2010, 32, 1).

[0005] Therefore, there is still need in the art for alternative methods that overcome the drawbacks of existing techniques.

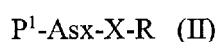
SUMMARY OF THE INVENTION

[0006] The present invention satisfies the aforementioned need in the art by providing the presently disclosed method.

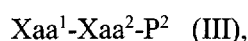
[0007] In a first aspect, the present invention provides a method of forming a peptide of Formula (I)



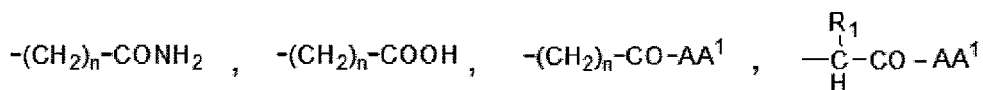
by ligating a first peptide of Formula (II)



to a second peptide of Formula (III)



wherein P^1 and P^2 are each independently any peptide, modified or unmodified; Asx is Asp or Asn, preferably Asn; X is O or S, preferably S; R is a substituted or unsubstituted alkyl, preferably selected from the group consisting of



wherein n is an integer of 1 to 10, R₁ is H, or any other side chain of a naturally occurring amino acid, and AA¹ is any amino acid or is absent; Xaa¹ is any naturally occurring amino acid with the exception of Pro; Xaa² is any naturally occurring amino acid, but preferably is a hydrophobic amino acid or Cys, more preferably Val, Ile, Leu, or Cys,

by enzymatically cleaving the bond between “Asx” and “X” in the first peptide of Formula (II) and ligating the fragment P¹-Asx of the first peptide to the second peptide of Formula (III) to form a ligated peptide of Formula (I), wherein the enzymatic cleavage and ligation reaction is catalyzed by a polypeptide having the activity of butelase 1 (SEQ ID NO:1) under conditions allowing said ligation.

[0008] In various embodiments, Asx is Asn, X is S, R is -CH(R₁)-CO-AA¹, R₁ is H, and AA¹ is any amino acid or absent.

[0009] In various embodiments, Asx is Asn, X is S, R is -CH(R₁)-CO-AA¹, R₁ is H, and AA¹ is Val.

[00010] In various embodiments, the polypeptide having the ligase activity of butelase 1 (SEQ ID NO:1) comprises or consists of:

- (a) the amino acid sequence as set forth in SEQ ID NO:1 (butelase 1);
- (b) an amino acid sequence that shares at least 60, preferably at least 70, even more preferably at least 80, most preferably at least 90 % sequence identity with the amino acid sequence as set forth in SEQ ID NO:1; or
- (c) an amino acid sequence that shares at least 80, preferably at least 90, more preferably at least 95 % sequence homology with the amino acid sequence as set forth in SEQ ID NO:1; or
- (d) a fragment of any one of (a)-(c).

[00011] In various embodiments, the polypeptide having the ligase activity of butelase 1 (SEQ ID NO:1) comprises or consists of the amino acid sequence as set forth in SEQ ID NO:2.

[00012] In various embodiments, the polypeptide having the ligase activity of butelase 1 (SEQ ID NO:1) comprises

- 5 (a) the amino acid residue Asn at the position corresponding to position 19 of SEQ ID NO:1; and/or
- (b) the amino acid residue His at the position corresponding to position 124 of SEQ ID NO:1; and/or
- (c) the amino acid residue Cys at the position corresponding to position 166 of SEQ ID NO:1.
- 10 **[00013]** In various embodiments, the polypeptide having the ligase activity of butelase 1 (SEQ ID NO:1) is the polypeptide as described above or comprises or consists of
- (a) any one of the amino acid sequences as set forth in SEQ ID Nos:3-109;
- (b) an amino acid sequence that shares at least 60, preferably at least 70, more preferably at least 80, most preferably at least 90 % sequence identity with any one of the amino acid sequences of (a) over its entire length;
- 15 (c) an amino acid sequence that shares at least 80, preferably at least 90, more preferably at least 95 % sequence homology with any one of the amino acid sequences of (a) over its entire length; or
- 20 (d) a fragment of any one of (a)-(c).
- [00014]** In various embodiments, P¹ or P² is modified by an affinity tag, a detectable label, a solid support material, or a scaffold molecule.
- [00015]** In various embodiments, P¹ or P² is modified by a biotin, a fluorescent marker, a polymer resin, or a dendrimer.
- 25 **[00016]** In various embodiments, P¹ or P² is modified by a dendrimer.
- [00017]** In various embodiments, each dendrimer is conjugated to 2 or more copies of the second peptide via P², such that the ligation of the first peptide and the second peptide results in a dendrimeric peptide assembly comprising 2 or more copies of the ligated peptide P¹-Asx-Xaa¹-Xaa²-P².
- 30 **[00018]** In various embodiments, the dendrimer is a lysyl dendrimer.
- [00019]** In various embodiments, the first peptide is P¹-Asn-thioglc-Val, and P¹ is an antimicrobial peptide.
- [00020]** In various embodiments, P¹ is an antimicrobial peptide comprising a BHBB tetrapeptide motif.
- 35 **[00021]** In various embodiments, P¹ is an antimicrobial peptide comprising an Arg-Leu-Tyr-Arg (SEQ ID NO:121) tetrapeptide.
- [00022]** In various embodiments, the first peptide is Ac-Arg-Leu-Tyr-Arg-Asn-thioglc-Val (SEQ ID NO:120).

5 [00023] In various embodiments, the second peptide is Arg-Ile-βAla conjugated to a lysyl dendrimer via βAla.

[00024] In various embodiments, the first peptide is Ac-Arg-Leu-Tyr-Arg-Asn-thioglc-Val (SEQ ID NO:120), and each lysyl dendrimer is conjugated to 2 or more copies of the second peptide Arg-Ile-βAla via βAla, such that the ligation of the first peptide and the second
10 peptide results in a dendrimeric peptide assembly comprising 2 or more copies of Ac-Arg-Leu-Tyr-Arg-Asn-Arg-Ile-βAla (SEQ ID NO:131).

[00025] In a second aspect, the invention provides peptides prepared using the presently disclosed method.

[00026] In a third aspect, the invention provides dendrimeric peptide assembly prepared
15 using the presently disclosed method.

[00027] In various embodiments, the presently disclosed dendrimeric peptide assembly comprises 2 or more copies of Ac-Arg-Leu-Tyr-Arg-Asn-Arg-Ile-βAla (SEQ ID NO:131).

[00028] In a fourth aspect, the invention provides use of the presently disclosed dendrimeric peptide assembly as a vaccine, medicament, or diagnostic agent.

20 [00029] In a final aspect, the invention provides use of the presently disclosed dendrimeric peptide assembly as an antimicrobial agent.

BRIEF DESCRIPTION OF THE DRAWINGS

25 [00030] The invention will be better understood with reference to the detailed description when considered in conjunction with the non-limiting examples and the accompanying drawings.

[00031] Figure 1. Butelase 1 ligation using a) natural peptide and b) thiodepsipeptide.

[00032] Figure 2. Synthetic strategy for a) thiodepsipeptide 1 and b) depsipeptide 2.

30 [00033] Figure 3. Time-course of butelase-mediated ligation of peptides 1-4 with peptide 5. The reaction was monitored by HPLC. Reaction conditions: 50 nM butelase 1, 100 μM peptide 5, corresponding ratios of peptide 1-4, 20 mM phosphate buffer, 1 mM EDTA, pH 6.5, 42 °C.

[00034] Figure 4. a) Schematic illustration of the butelase-mediated N-terminal
35 modification of ubiquitin by the use of thiodepsipeptide 1. b) Time-course analysis of ubiquitin labeling reaction. c) ESI spectra of unmodified and modified ubiquitin. d) Deconvoluted ESI spectra of unmodified and modified ubiquitin.

[00035] Figure 5. a) Schematic illustration of the butelase-mediated N-terminal ligation

of ubiquitin modified with a short linker peptide by the use of thiodipeptide 1. A quantitative ligation yield was obtained as shown by the deconvoluted ESI spectra. b) Schematic illustration of the butelase-mediated N-terminal modification of ubiquitin by the use of thiodipeptide 8 which carries a biotin tag. A quantitative ligation yield was obtained with four equivalent of peptide 8 and 0.001 molar equivalent of butelase 1.

[00036] Figure 6. Irreversible butelase-mediated ligation: A novel approach to render the ligation irreversible by using a thiodipeptide substrate. A ligation yield of >95% was achieved with a minimal excess of substrate and a low catalytic amount of butelase 1 (0.0005 to 0.001 molar equivalent). This method has been successfully applied to introduce a functional tag to ubiquitin and green fluorescent protein with high yields.

[00037] Figure 7. Butelase-mediated ligation with glycerol. Incubation of a model peptide WRLYRGRLYRRNHV (SEQ ID NO:132) (100 μ M) with butelase 1 in the presence of 20% glycerol for 2 hours led to formation of three major products: a hydrolyzed product (WRLYRGRLYRRN) (SEQ ID NO:133), a cyclized product (WRLYRGRLYRRN) (SEQ ID NO:134), and a ligated product with glycerol (WRLYRGRLYRRN-OCH₂(OH)CH₂OH) (SEQ ID NO:135).

[00038] Figure 8. Butelase-mediated ligation with (O)GVYKV peptide (SEQ ID NO:115). A model peptide ERLYRGRLYRRNHV (SEQ ID NO:116) (50 μ M) was incubated with butelase 1 (50 nM) and (O)GVYKV (SEQ ID NO:115) (5 mM) in 20 mM sodium phosphate buffer, pH 6.0 at 37 °C for 2 h. Analysis by mass spectrometry showed the formation of the ligated product with about 25% yield.

[00039] Figure 9. Degradation time course for thiodipeptide 1 and dipipeptide 2. Each peptide (100 μ M) was incubated in the absence or presence of butelase 1 (50 nM) at 42 °C. The peptide stability was monitored by HPLC every 15 min.

[00040] Figure 10. a) Schematic illustration of the butelase-mediated N-terminal modification of GFP by the use of thiodipeptide 1. b, c) Deconvoluted ESI spectra of GFP before (b) and after (c) the ligation reaction. Unmodified and modified GFP have observed masses of 29406.5 and 29813.7 Da, respectively.

[00041] Figure 11. a) Schematic illustration of the butelase-mediated N-terminal modification of GFP by the use of thiodipeptide 8 which carries a biotin tag. b, c) Deconvoluted ESI spectra of GFP before (b) and after (c) the ligation reaction. Unmodified and modified GFP have observed masses of 29406.5 and 30142.6 Da, respectively.

- 5 [00042] Figure 12. SDS-PAGE analysis of butelase 1. The gel was visualized by silver staining. The left lane is the purified butelase 1 and the right lane is the protein ladder with molecular weight labeled in kDa.
- [00043] Figure 13. Mass spectrum of Peptide 1 YKN-thioglc-V (SEQ ID NO:110). ESI-MS (positive) 595.71 (observed, M+H) 596.21 (calculated, M).
- 10 [00044] Figure 14. Mass spectrum of Peptide 2 YKN-glc-V (SEQ ID NO:111). ESI-MS (positive) 580.22 (observed, M+H) 602.37 (observed, M+Na) 618.11 (observed, M+K) 579.30 (calculated, M).
- [00045] Figure 15. Mass spectrum of Peptide 4 YKNGV (SEQ ID NO:113). ESI-MS (positive) 579.16 (observed, M+H) 578.66 (calculated, M).
- 15 [00046] Figure 16. Mass spectrum of Peptide 3 YKNHV (SEQ ID NO:112). ESI-MS (positive) 659.27 (observed, M+H) 681.41 (observed, M+Na) 659.36 (calculated, M).
- [00047] Figure 17. Mass spectrum of Peptide 5 GIGGIR (SEQ ID NO:114). ESI-MS (positive) 571.30 (observed, M+H) 570.69 (calculated, M).
- [00048] Figure 18. Mass spectrum of Peptide 8 biotin-TYKN-thioglc-V (SEQ ID NO:117). ESI-MS (positive) 923.34 (observed, M+H) 945.42 (observed, M+Na) 922.40 (calculated, M).
- 20 [00049] Figure 19. Butelase-mediated peptide dendrimer synthesis (bivalent format as example), using A) native peptides and B) thiopeptides as acyl donor substrates.
- [00050] Figure 20. Schematic presentation of selected peptide dendrimer structures assembled by butelase-mediated bioconjugation. A) bivalent peptide dendrimer (Ac-RYRLNRI β A)₂KY; B) tetravalent peptide dendrimer (Ac-RYRLNRI β A)₄K₂KY; C) octavalent peptide dendrimer (Ac-RYRLNRI β A)₈K₄K₂KY.
- 25 [00051] Figure 21. Analytical HPLC monitoring of butelase-mediated peptide dendrimer bioconjugation using A) thiopeptide – peak a: peptide Ac-RYRLN-thioglc-V (SEQ ID NO:118); peak b: desired bivalent product (Ac-RYRLNRI β A)₂KY with an observed mass of 2478.5 (calc. 2478.4 Da) or B) normal peptide – peak a': peptide RYRLNHV (SEQ ID NO:119); peak b': dendron core (RI β A)₂KY; peak c': the monovalent product; peak d': the desired bivalent product (RYRLNRI β A)₂KY.
- 30 [00052] Figure 22. Analytical HPLC monitoring of butelase-mediated preparation of (A) tetravalent dendrimer – peak a: linear peptide Ac-RYRLN-thioglc-V (SEQ ID NO:118); peak b: the desired tetravalent product (Ac-RYRLNRI β A)₄K₂KY with an observed mass of 4903.5 Da (calc. 4903.8 Da) and (B) octavalent dendrimer – peak a: linear peptide Ac-RYRLN-
- 35

thioglc-V (SEQ ID NO:118); peak b': the desired octavalent product (Ac-RYRLNRI β A)₈K₄K₂KY with an observed mass of 9753.4 Da (calc. 9754.7 Da).

[00053] Figure 23. HPLC profile of the ligation between the thiodipeptide RYRLN(S)GV (SEQ ID NO: 142) and the bivalent dendron core (RI)₂KY in the presence of butelase 1 (100 nM) and TCEP (1 mM) in pH 6.5 20 mM phosphate buffer, 42 °C. Peak a refers to the dendron core, peak b refers to thiodipeptide, peak c refers to the monovalent product, peak d refers to bivalent product, peak e refers to byproduct caused by self-ligation (inset: MALDI mass spec of desired bivalent product).

[00054] Figure 24. SDS-PAGE (silver staining) of isolated butelase 1 (left lane) and protein markers (right lane).

[00055] Figure 25. Mass spectrum of RYRLN(S)GV-NH₂ (SEQ ID NO: 136). ESI-MS (positive) 893.45 (observed, M+H) 893.5 (calculated, M+H).

[00056] Figure 26. Mass spectrum of Ac-RYRLN(S)GV-NH₂ (SEQ ID NO:137). MALDI-MS 935.5 (observed, M+H) 935.5 (calculated, M+H).

[00057] Figure 27. Mass spectrum of Ac-RLYRN(S)GV-NH₂ (SEQ ID NO:138). ESI-MS (positive) 935.50 (observed, M+H) 1048.82 (observed, M+TFA) 935.5 (calculated, M+H).

[00058] Figure 28. Mass spectrum of RLRY-NH₂ (SEQ ID NO:139). ESI-MS (positive) 606.52 (observed, M+H) 719.83 (observed, M+TFA) 606.4 (calculated, M+H).

[00059] Figure 29. Mass spectrum of RYRLNHV-NH₂ (SEQ ID NO:140). ESI-MS (positive) 956.68 (observed, M+H) 1069.94 (observed, M + Na) 956.5 (calculated, M).

[00060] Figure 30. Mass spectrum of (RI β A)₂KY-NH₂ ESI-MS (positive) 989.76 (observed, M+H) 1103.00 (observed, M+TFA) 989.6 (calculated, M+H).

[00061] Figure 31. Mass spectrum of (RI β A)₄K₂KY-NH₂. MALDI-MS 1926.1 (observed, M+H) 1926.3 (calculated, M).

[00062] Figure 32. Mass spectrum of (RI β A)₈K₄K₂KY-NH₂. MALDI-MS 3799.6 (observed, M+H) 3799.5 (calculated, M+H).

[00063] Figure 33. Mass spectrum of (Ac-RLYRNRI β A)₂KY-NH₂. MALDI-MS 2478.5 (observed, M+H) 2478.4 (calculated, M+H).

[00064] Figure 34. Mass spectrum of (Ac-RLYRNRI β A)₄K₂KY-NH₂. MALDI-MS 4905.2 (observed, M+H) 4903.8 (calculated, M+H).

[00065] It should be noted that a significant percentage of peptide being hydrolyzed or reacting with glycerol instead of intramolecular cyclization as the model peptide contains an Arg at the second position which is not preferred by butelase 1 for cyclization.

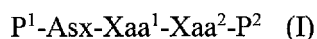
5 DETAILED DESCRIPTION OF THE INVENTION

[00066] The following detailed description refers to, by way of illustration, specific details and embodiments in which the invention may be practiced. These embodiments are described in sufficient detail to enable those skilled in the art to practice the invention. Other
10 embodiments may be utilized and structural, and logical changes may be made without departing from the scope of the invention. The various embodiments are not necessarily mutually exclusive, as some embodiments can be combined with one or more other embodiments to form new embodiments.

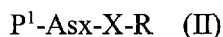
[00067] Unless otherwise defined, all technical and scientific terms used herein have the
15 same meaning as commonly understood by one of ordinary skill in the art. The singular terms "a," "an," and "the" include plural referents unless context clearly indicates otherwise. Similarly, the word "or" is intended to include "and" unless the context clearly indicates otherwise. The term "comprises" means "includes." In case of conflict, the present specification, including explanations of terms, will control.

[00068] The object of the present invention is to provide a technique for ligating
20 peptides, taking advantage of the superior site specificity and catalytic efficiency of butelase 1-like Asx-specific protein ligases.

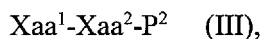
[00030] To this end, provided in a first aspect of the present disclosure is a method of forming a peptide of Formula (I)
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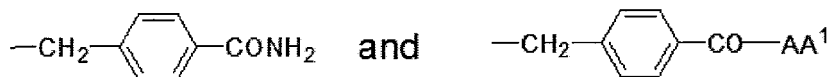
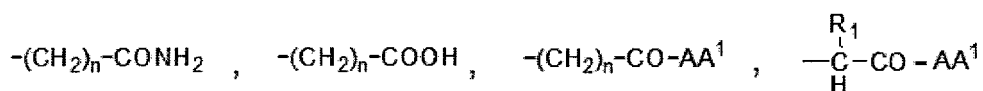
by ligating a first peptide of Formula (II)



to a second peptide of Formula (III)



35 wherein P^1 and P^2 are each independently any peptide, modified or unmodified; Asx is Asp or Asn, preferably Asn; X is O or S, preferably S; R is a substituted or unsubstituted alkyl, preferably selected from the group consisting of



wherein n is an integer of 1 to 10, R_1 is H, or any other side chain of a naturally occurring amino acid, and AA^1 is any amino acid or is absent; Xaa^1 is any naturally occurring amino acid with the exception of Pro; Xaa^2 is any naturally occurring amino acid, but preferably is a hydrophobic amino acid or Cys, more preferably Val, Ile, Leu, or Cys,

by enzymatically cleaving the bond between "Asx" and "X" in the first peptide of Formula (II) and ligating the fragment P^1 -Asx of the first peptide to the second peptide of Formula (III) to form a ligated peptide of Formula (I), wherein the enzymatic cleavage and ligation reaction is catalyzed by a polypeptide having the activity of butelase 1 (SEQ ID NO:1) under conditions allowing said ligation.

[00069] It is also envisaged that, when the first peptide and the second peptide are the same peptide, the presently disclosed method cyclizes said peptide.

[00070] In the whole context of the present application, the terms "polypeptide", "peptide" and "protein" are used interchangeably to refer to polymers of amino acids of any length connected by peptide bonds. The polymer may comprise modified amino acids, it may be linear or branched, and it may be interrupted by non-amino acids. The terms also encompass an amino acid polymer that has been modified naturally or by intervention; for example, disulfide bond formation, glycosylation, lipidation, acetylation, phosphorylation, or any other manipulation, such as conjugation to a labeling component.

[00071] The term "amino acid" refers to natural and/or unnatural or synthetic amino acids, including both the D and L optical isomers, amino acid analogs (for example norleucine is an analog of leucine) and peptidomimetics. The term "naturally occurring amino acid", as used herein, relates to the 20 naturally occurring L-amino acids, namely Gly, Ala, Val, Leu, Ile, Phe, Cys, Met, Pro, Thr, Ser, Glu, Gln, Asp, Asn, His, Lys, Arg, Tyr, and Trp. The term "peptide bond" refers to a covalent amide linkage formed by loss of a molecule of water between the carboxyl group of one amino acid and the amino group of a second amino acid. For example, the "-" between P^1 and Asx in Formula (II), as well as all "-" in Formulae (I) and (III) represent peptide bonds. The "-" between X and R in Formula (II) represents a covalent bond. In addition, the "-" between C(O) and AA^1 in $-(\text{CH}_2)-\text{CO}-\text{AA}^1$, $-\text{CH}(\text{R}_1)-\text{CO}-\text{AA}^1$, and $-\text{CH}_2-\text{C}_6\text{H}_4-\text{CO}-\text{AA}^1$

- 5 represents a covalent bond between the carbonyl group and the amino group of AA¹, i.e. the carbonyl group shown and the amino group of AA¹ also form a peptide bond. Generally, in all formulae depicted herein, the peptides are shown in the N- to C-terminal orientation.
- [00072] The term "hydrophobic amino acid", as used herein, refers to an amino acid selected from the group consisting of Ala, Gly, Ile, Leu, Met, Phe, Pro, Trp, and Val.
- 10 [00073] The term "amino acid side chain" as used herein refers to a moiety attached to the α -carbon in an amino acid, preferably a naturally occurring amino acid. For example, the amino acid side chain may be methyl, isopropyl, 1-methylpropyl, 2-methylpropyl, benzyl, methyl(4-hydroxyphenyl), hydroxymethyl, 1-hydroxy-ethyl, carboxymethyl, 2-carboxyethyl, etc.
- 15 [00074] The term "alkyl", as used herein, refers to a linear, branched, or cyclic saturated hydrocarbon group. The term "unsubstituted" means that the specified group bears no substituents but the respective positions are occupied by hydrogen atoms only. By "substituted" as in "substituted alkyl" is meant that in the alkyl at least one hydrogen atom bound to a carbon (or other) atom is replaced with one or more non-hydrogen substituents. Examples of such
- 20 substituents include, without limitation: functional groups such as halo, hydroxyl, sulfhydryl, C₁-C₂₄ alkoxy, C₂-C₂₄ alkenyloxy, C₂-C₂₄ alkynyloxy, C₅-C₂₀ aryloxy, acyl (including C₂-C₂₄ alkylcarbonyl (-CO-alkyl) and C₆-C₂₀ arylcarbonyl (-CO-aryl), acyloxy (-O-acyl), C₂-C₂₄ alkoxycarbonyl (-(CO)-O-alkyl), C₆-C₂₀ aryloxycarbonyl (-(CO)-O-aryl), halocarbonyl (-(CO)-X where X is halo), C₂-C₂₄ alkylcarbonato (-O-(CO)-O-alkyl), C₆-C₂₀ arylcarbonato (-O-(CO)-O-aryl), carboxy (-COOH), carboxylato (-COO⁻), carbamoyl (-(CO)-NH₂), mono-(C₁-C₂₄ alkyl)-substituted carbamoyl (-(CO)-NH(C₁-C₂₄ alkyl)), di-(C₁-C₂₄ alkyl)-substituted carbamoyl (-(CO)-N(C₁-C₂₄ alkyl)₂), mono-substituted arylcarbamoyl (-(CO)-NH-aryl), thiocarbamoyl (-(CS)-NH₂), carbamido (-NH-(CO)-NH₂), cyano (-C $\equiv$ N), isocyano (-N⁺ $\equiv$ C⁻), cyanato (-O-C $\equiv$ N), isocyanato (-O-N⁺ $\equiv$ C⁻), isothiocyanato (-S-C $\equiv$ N), azido (-N=N⁺=N⁻), formyl (-(CO)-H),
- 30 thioformyl (-(CS)-H), amino (-NH₂), mono- and di-(C₁-C₂₄ alkyl)-substituted amino, mono- and di-(C₅-C₂₀ aryl)-substituted amino, C₂-C₂₄ alkylamido (-NH-(CO)-alkyl), C₆-C₂₀ arylamido (-NH-(CO)-aryl), imino (-CR=NH where R = hydrogen, C₁-C₂₄ alkyl, C₅-C₂₀ aryl, C₆-C₂₄ alkaryl, C₆-C₂₄ aralkyl, etc.), alkylimino (-CR=N(alkyl), where R = hydrogen, alkyl, aryl, alkaryl, etc.), arylimino (-CR=N(aryl), where R = hydrogen, alkyl, aryl, alkaryl, etc.), nitro (-NO₂), nitroso (-NO), sulfo (-SO₂-OH), sulfonate (-SO₂-O⁻), C₁-C₂₄ alkylsulfanyl (-S-alkyl; also termed "alkylthio"), arylsulfanyl (-S-aryl; also termed "arylthio"), C₁-C₂₄ alkylsulfanyl (-(SO)-alkyl), C₅-C₂₀ arylsulfanyl (-(SO)-aryl), C₁-C₂₄ alkylsulfonyl (-SO₂-alkyl), C₅-C₂₀ arylsulfonyl (-SO₂-aryl), phosphono (-P(O)(OH)₂), phosphonato(-P(O)(O⁻)₂), phosphinato (-P(O)(O⁻)), phospho (-
- 35

PO₂), and phosphino (-PH₂); and the hydrocarbyl moieties C₁-C₂₄ alkyl (preferably C₁-C₁₈ alkyl, more preferably C₁-C₁₂ alkyl, most preferably C₁-C₆ alkyl), C₂-C₂₄ alkenyl (preferably C₂-C₁₈ alkenyl, more preferably C₂-C₁₂ alkenyl, most preferably C₂-C₆ alkenyl), C₂-C₂₄ alkynyl (preferably C₂-C₁₈ alkynyl, more preferably C₂-C₁₂ alkynyl, most preferably C₂-C₆ alkynyl), C₅-C₂₀ aryl (preferably C₅-C₁₄ aryl), C₆-C₂₄ alkaryl (preferably C₆-C₁₈ alkaryl), and C₆-C₂₄ aralkyl (preferably C₆-C₁₈ aralkyl). In addition, the aforementioned functional groups may, if a particular group permits, be further substituted with one or more additional functional groups. By "(C_x-C_y)" (x and y being two different integers) is meant that the group contains x to y carbon atoms.

[00075] Without wishing to be bound to any particular theory, applicant believes that, the sorting signal HX-R, e.g. HXC(HR₁)C(O)-AA¹, cleaved off from the first peptide is a non-substrate of the polypeptide having the ligase activity of butelase 1 (SEQ ID NO:1), consequently rendering the ligation process essentially irreversible.

[00076] In various embodiments, Asx is Asp or Asn, X is O or S, R is -CH(R₁)-CO-AA¹, R₁ is H, or any other side chain of a naturally occurring amino acid, and AA¹ is any amino acid or is absent. Accordingly, the sorting signal HX-R (i.e. HX-C(HR₁)-C(O)-AA¹) is a modified peptide wherein the amino group of the first amino acid is substituted by -O- or -S-. When AA¹ is absent, the sorting signal HX-C(HR₁)C(O)-AA¹ is HXC(HR₁)C(O)OH.

[00077] In preferred embodiments, Asx is Asn, X is S, R is -CH(R₁)-CO-AA¹, R₁ is H, and AA¹ is any amino acid or absent. In this case, the sorting signal is HS-CH₂C(O)-AA¹, which is a thiodepsipeptide.

[00078] In particularly preferred embodiments, Asx is Asn, X is S, R is -CH(R₁)-CO-AA¹, R₁ is H, and AA¹ is Val. In this case, the sorting signal is H-S-CH₂C(O)-Val, herein denoted as H-thioglc-Val. Accordingly, "thioglc", as used herein, represents the structure -S-CH₂C(O)-.

[00079] A polypeptide according to the present invention possesses the ligase activity of butelase 1 (SEQ ID NO:1) as described in International Patent Publication No. WO2015163818 A1, which is hereby incorporated by reference in its entirety.

[00080] The polypeptide is utilizable for enzymatic coupling and has an ability to site-specifically break a peptide bond and then reform a new bond with an incoming nucleophile. It is "Asx-specific" in that the amino acid C-terminal to which ligation occurs, i.e. the C-terminal end of the peptide that is ligated, is either Asn or Asp, preferably Asn. As set forth above, it recognizes the motif Asx-X-R, at the C-terminus of the first peptide of Formula (II), and mediates peptide ligation by cleaving off the sorting signal HX-R and ligating P¹-Asx to the N-

5 terminal residue of the second peptide Xaa¹-Xaa²-P² to form a ligated peptide P¹-Asx-Xaa¹-Xaa²-P².

[00081] In various embodiments, the polypeptide comprises or consists of the amino acid sequence as set forth in SEQ ID NO:1 (butelase 1).

10 [00082] In various embodiments, the polypeptide comprises or consists of an amino acid sequence that is at least 60%, 65%, 70%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 90.5%, 91%, 91.5%, 92%, 92.5%, 93%, 93.5%, 94%, 94.5%, 95%, 95.5%, 96%, 96.5%, 97%, 97.5%, 98%, 98.5%, 99%, 99.25%, or 99.5% identical or homologous to the amino acid sequence set forth in SEQ ID NO:1 over its entire length. In some embodiments, it has an amino acid sequence that shares at least 60, preferably at least 70,
15 more preferably at least 80, most preferably at least 90 % sequence identity with the amino acid sequence set forth in SEQ ID NO:1 over its entire length or has an amino acid sequence that shares at least 80, preferably at least 90, more preferably at least 95 % sequence homology with the amino acid sequence set forth in SEQ ID NO:1 over its entire length.

[00083] In various embodiments, the polypeptide may be a precursor of the mature
20 enzyme. In such embodiments, it may comprise or consist of the amino acid sequence set forth in SEQ ID NO:2. Also encompassed are polypeptides having an amino acid sequence that is at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 90.5%, 91%, 91.5%, 92%, 92.5%, 93%, 93.5%, 94%, 94.5%, 95%, 95.5%, 96%, 96.5%, 97%, 97.5%, 98%, 98.5%, 99%, 99.25%, or 99.5% identical or homologous to the amino acid
25 sequence set forth in SEQ ID NO:2 over its entire length.

[00084] The identity of nucleic acid sequences or amino acid sequences is generally determined by means of a sequence comparison. This sequence comparison is based on the BLAST algorithm that is established in the existing art and commonly used (cf. for example Altschul et al. (1990) "Basic local alignment search tool", J. Mol. Biol. 215:403-410, and
30 Altschul et al. (1997): "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs"; Nucleic Acids Res., 25, p. 3389-3402) and is effected in principle by mutually associating similar successions of nucleotides or amino acids in the nucleic acid sequences and amino acid sequences, respectively. A tabular association of the relevant positions is referred to as an "alignment." Sequence comparisons (alignments), in particular
35 multiple sequence comparisons, are commonly prepared using computer programs which are available and known to those skilled in the art.

[00085] A comparison of this kind also allows a statement as to the similarity to one another of the sequences that are being compared. This is usually indicated as a percentage

identity, i.e. the proportion of identical nucleotides or amino acid residues at the same positions or at positions corresponding to one another in an alignment. The more broadly construed term "homology", in the context of amino acid sequences, also incorporates consideration of the conserved amino acid exchanges, i.e. amino acids having a similar chemical activity, since these usually perform similar chemical activities within the protein. The similarity of the compared sequences can therefore also be indicated as a "percentage homology" or "percentage similarity." Indications of identity and/or homology can be encountered over entire polypeptides or genes, or only over individual regions. Homologous and identical regions of various nucleic acid sequences or amino acid sequences are therefore defined by way of matches in the sequences. Such regions often exhibit identical functions. They can be small, and can encompass only a few nucleotides or amino acids. Small regions of this kind often perform functions that are essential to the overall activity of the protein. It may therefore be useful to refer sequence matches only to individual, and optionally small, regions. Unless otherwise indicated, however, indications of identity and homology herein refer to the full length of the respectively indicated nucleic acid sequence or amino acid sequence.

[00086] In various embodiments, the polypeptide described herein comprises the amino acid residue Asn at the position corresponding to position 19 of SEQ ID NO:1; and/or the amino acid residue His at the position corresponding to position 124 of SEQ ID NO:1; and/or the amino acid residue Cys at the position corresponding to position 166 of SEQ ID NO:1. It has been found that these amino acid residues putatively play a role in the catalytic activity of the polypeptide. In preferred embodiments, the polypeptides thus comprise at least two, more preferably all three of the above indicated residues at the given or corresponding positions.

[00087] While it is recognized that various polypeptides as described above may be suitable for the practice of the present invention, it is preferable to use one with potent protein ligase activity. In various embodiments, this means that it can ligate a given peptide with an efficiency of at least 50 %, more preferably at least 70 %, most preferably at least 90 %. The protein ligation reaction is preferably comparably fast, i.e. said polypeptide can ligate two given peptides with a K_m of 500 μM or less, preferably 250 μM or less; and/or a k_{cat} of at least $0.05 s^{-1}$, preferably at least $0.5 s^{-1}$, more preferably at least $1.0 s^{-1}$, most preferably at least $1.5 s^{-1}$. Preferred polypeptides satisfy both requirements, i.e. the K_m and k_{cat} requirement. Methods to determine such Michaelis-Menten kinetics are well known in the art and can be routinely applied by those skilled in the art. It is preferred that the polypeptides of the invention have at least 50 %, more preferably at least 70 %, most preferably at least 90 % of the protein ligase activity of the enzyme having the amino acid sequence of SEQ ID NO:1.

5 [00088] Polypeptides according to the present application can comprise amino acid modifications, in particular amino acid substitutions, insertions, or deletions. Such polypeptides are, for example, further developed by targeted genetic modification, i.e. by way of mutagenesis methods, and optimized for specific purposes or with regard to special properties (for example, with regard to their catalytic activity, stability, etc.). The objective may be to introduce targeted
10 mutations, such as substitutions, insertions, or deletions, into the known molecules in order, for example, to alter substrate specificity and/or improve the catalytic activity. For this purpose, in particular, the surface charges and/or isoelectric point of the molecules, and thereby their interactions with the substrate, can be modified. Alternatively or additionally, the stability of the polypeptide can be enhanced by way of one or more corresponding mutations, and its catalytic
15 performance thereby improved. Advantageous properties of individual mutations, e.g. individual substitutions, can supplement one another.

[00089] In various embodiments, the polypeptide may be characterized in that it is obtainable from a polypeptide as described above as an initial molecule by single or multiple conservative amino acid substitution. The term "conservative amino acid substitution" means
20 the exchange (substitution) of one amino acid residue for another amino acid residue, where such exchange does not lead to a change in the polarity or charge at the position of the exchanged amino acid, e.g. the exchange of a nonpolar amino acid residue for another nonpolar amino acid residue. Conservative amino acid substitutions in the context of the invention encompass, for example, G=A=S, I=V=L=M, D=E, N=Q, K=R, Y=F, and S=T.

25 [00090] Alternatively or additionally, the polypeptide may be characterized in that it is obtainable from a polypeptide contemplated herein as an initial molecule by fragmentation or by deletion, insertion, or substitution mutagenesis, and encompasses an amino acid sequence that matches the initial molecule over a length of at least 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 325, 330, 331, 332, 333, 334, 335, 336, 337,
30 338, 339, 340, 341, or 342 continuously connected amino acids. It is preferred that in such embodiments, the amino acids Asn19, His124 and Cys166 contained in the initial molecule are still present.

[00091] In various embodiments, the present invention thus also relates to fragments of the polypeptides described herein, with said fragments retaining enzymatic activity. It is
35 preferred that they have at least 50 %, more preferably at least 70, most preferably at least 90 % of the protein ligase and/or cyclase activity of the initial molecule, preferably of the polypeptide having the amino acid sequence of SEQ ID NO:1. The fragments are preferably at least 150 amino acids in length, more preferably at least 200 or 250, most preferably at least 300. It is

5 further preferred that these fragments comprise the amino acids Asn, His and Cys at positions corresponding to positions 19, 124 and 166 of SEQ ID NO:1. Preferred fragments therefore comprise amino acids 19-166, more preferably 10-200, most preferably 1-277 of the amino acid sequence set forth in SEQ ID NO:1.

[00092] As set forth above, the peptides to be ligated in accordance with the present
10 application may be modified by, for example, conjugation to a labeling component, either covalently or non-covalently. A labeling component may be any molecules such as, without limitation, an affinity tag, detectable label, solid support material, or scaffold molecule. The modified peptides may be prepared using standard techniques known to those skilled in the art of synthetic organic chemistry, or may be deduced by reference to the pertinent literature.

15 [00093] In various embodiments, P¹ or P² is modified by an affinity tag, a detectable label, a solid support material, a scaffold molecule.

[00094] In various embodiments, P¹ or P² is modified by a biotin, a fluorescent marker, a polymer resin, or a dendrimer.

[00095] In various embodiments, P¹ or P² is modified by a dendrimer.

20 [00096] In various embodiments, each dendrimer is conjugated to 2 or more copies of the second peptide via P², such that the ligation of the first peptide and the second peptide results in a dendrimeric peptide assembly comprising 2 or more copies of the ligated peptide P¹-Asx-Xaa¹-Xaa²-P².

[00097] The term “affinity tag” as used herein refers to a moiety such as biotin that can
25 be used to separate a molecule to which the affinity tag is attached from other molecules that do not contain the affinity tag.

[00098] The term “detectable label” is intended to mean at least one label capable of
directly or indirectly generating a detectable signal. In non-limiting examples, a detectable label can be an enzyme producing a detectable signal, for example by colorimetry, fluorescence or
30 luminescence; a chromophore, such as a fluorescent, luminescent or dye compound, e.g. GFP; a group with an electron density detectable by electron microscopy or by virtue of their electrical property, such as conductivity, amperometry, voltammetry or impedance; detectable group, for example the molecules of which are sufficiently large to induce detectable modifications of their physical and/or chemical characteristics (this detection can be carried out by optical methods
35 such as diffraction, surface plasmon resonance, surface variation or contact angle variation, or physical methods such as atomic force spectroscopy or the tunnel effect; or a radioactive molecule such as ³²P, ³⁵S or ¹²⁵I.

5 [00099] The term “solid support material” as used herein refers to conventional solid supports for the synthesis of peptides, which are well known for the skilled in the art. The nature of the solid support is not particularly restricted and may be an inorganic substance or an organic substance such as a cross-linked polymer.

10 [000100] The term “scaffold molecule” as used herein refers to a compound to which other moieties are attached (e.g., conjugated). Various scaffold molecules, e.g. dendrimers, are well known in the art.

[000101] The term “dendrimer” refers to polymers having a regular branched structure of a fractal nature. Dendrimers are well known in the art. For the purpose of this application, dendrimers include, without limitation, hyperbranched polymers, dendrigraft polymers, tecto-
15 dendrimers, core-shell (tecto)dendrimers, hybrid linear-dendritic copolymers, dendronized polymers, dendrimer-based supramolecular assemblies, and dendrimer-functionalized solid particles, which are within the purview of one of skill in the art.

[000102] Dendrimers have a core from which the inner branches emanate. Further branches may emanate from the inner branches and so forth. Distal from the core are the
20 terminal branches, i.e., branches from which no further branches emanate. The periphery is defined as that portion of the dendrimeric polymer attached to the distal branches from which no further branches emanate. The periphery consists of the collection of terminal chains, i.e., that portion of the dendrimeric polymer distal from the terminal branches and ending with the chain ends. As an inherent consequence of their fractal nature, dendrimers may have a large number
25 of functional groups at their chain ends. It is the chain ends that interact with the environment of the dendrimer and impart the properties of the dendrimer. The terms “chain end” and “functional group” are somewhat synonymous. However, the term “chain end” emphasizes the physical location of a section of the dendrimer; and the term “functional group” emphasizes the physical properties imparted by the “chain end”. The “functional group” may be any chemical
30 moiety compatible for use as “chain end”.

[000103] Dendrimers possess many advantages including well-defined structure, mono-dispersity, multi-valency and ease of surface functionalization and provide a flexible polymeric scaffold to incorporate one or more types of peptides for enzymatic conjugation thereto.

[000104] In preferred embodiments, the dendrimer is a lysyl dendrimer.

35 [000105] Lysyl dendrimers according to the present invention are, as well known in the art, molecules with a tree-like structure whereby the branching is formed of repetitive lysine units. However, lysyl dendrimers may not exclusively consist of lysine units only, but may also

5 involve other units as linkers such as 1,6-hexandiamine or dithioacetylhexan diamine between two lysine branches.

[000106] In accordance with the present application, every terminal lysine of a lysyl dendrimer provides two amino groups that may be used for coupling of a second peptide of the present application, to which a first peptide carrying a C-terminal Asx motif of Formula (II) may be ligated as mediated by a polypeptide having the ligase activity of butelase 1 (SEQ ID NO:1) to generate a bi- or multi-valent peptide-dendrimer conjugate. Alternatively, the lysyl dendrimer may comprise a first peptide having a C-terminal Asx motif, while the peptide for conjugation to said dendrimer may bear a N-terminal acceptor sequence as described above.

[000107] In addition, one skilled in the art would readily appreciate that, using the presently disclosed method, a dendrimer may be conjugated to 2 or more different types of peptides.

[000108] In various embodiments, the first peptide is P¹-Asn-thioglc-Val, and P¹ is an antimicrobial peptide.

[000109] The term “antimicrobial peptide” as used herein refers to any peptide with antimicrobial activity. The term “antimicrobial activity” refers to the ability of a peptide of the present invention to modify a function or metabolic process of a target microorganism, for example so as to at least partially affect replication, vegetative growth, toxin production, survival, viability in a quiescent state, or other attribute. In an embodiment, the term relates to inhibition of growth of a microorganism. In a particular embodiment, antimicrobial activity relates to the ability of a peptide to kill at least one bacterial species. Non-limiting examples of antimicrobial peptides include all those available in the APD (<http://aps.unmc.edu/AP/main.php>) and LAMP (<http://biotechlab.fudan.edu.cn/database/lamp/>) databases, which are hereby incorporated by reference in their entirety.

[000110] In various embodiments, P¹ is an antimicrobial peptide comprising a BHHB (each B represents a basic amino acid; each H represents a hydrophobic amino acid) tetrapeptide motif.

[000111] In various embodiments, P¹ is an antimicrobial peptide comprising an Arg-Leu-Tyr-Arg (SEQ ID NO:121) tetrapeptide.

[000112] In various embodiments, the first peptide is Ac-Arg-Leu-Tyr-Arg-Asn-thioglc-Val (SEQ ID NO:120). By “Ac-Arg” is meant acetyl Arginine.

[000113] In various embodiments, the second peptide is Arg-Ile-βAla conjugated to a lysyl dendrimer via βAla.

- 5 [000114] In various embodiments, the first peptide is Ac-Arg-Leu-Tyr-Arg-Asn-thioglyc-Val (SEQ ID NO:120), and each lysyl dendrimer is conjugated to 2 or more copies of the second peptide Arg-Ile- β Ala via β Ala, such that the ligation of the first peptide and the second peptide results in a dendrimeric peptide assembly comprising 2 or more copies of Ac-Arg-Leu-Tyr-Arg-Asn-Arg-Ile- β Ala (SEQ ID NO:112).
- 10 [000115] In a second aspect, the invention provides peptides prepared using the presently disclosed method.
- [000116] In a third aspect, the invention provides dendrimeric peptide assembly prepared using the presently disclosed method.
- 15 [000117] In a fourth aspect, the invention provides use of the presently disclosed dendrimeric peptide assembly as a vaccine, medicament, or diagnostic agent. For administration, the composition may be dispersed in a pharmaceutically acceptable adjuvant or carrier.
- [000118] In a final aspect, the invention provides use of the presently disclosed dendrimeric peptide assembly as an antimicrobial agent.
- 20 [000119] The present invention is further illustrated by the following examples. However, it should be understood, that the invention is not limited to the exemplified embodiments.

EXAMPLES

- 25 *Example 1: Site-specific N-terminal Labeling of Peptides and Proteins using butelase 1 and Thiodepsipeptide*

A. Materials and Reagents

- 30 [000120] Amino acids, coupling reagents and resins were obtained from Chemimpex, Novabiochem and GL Biochem. All other chemical reagents were of analytical grade, and were obtained from Sigma Aldrich, Alfa Aesar and Acros Organics. All solvents and chemicals were used as received without purification unless otherwise indicated. Mouse anti-ubiquitin antibody was obtained from Santa Cruz biotechnology, anti-mouse secondary antibody was purchased from Dako, and anti-biotin, HRP-linked antibody was from Cell Signaling Technology.

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B. High Performance Liquid Chromatography (HPLC)

- [000121] Analytical RP-HPLC was run on a Nexera LC-30AD instrument (Shimadzu) with an analytical column (Aeris peptide XB-C18, 4.6 x 250 mm). Semi-preparative HPLC was

- 5 performed on a Shimadzu system using a Jupiter C18 column (5 micron, 10 x 250 mm). All HPLC runs were done using the mixture of two solutions, A (0.045% TFA in water) and B (0.045% TFA in acetonitrile). UV detection was carried out at 220 nm wave length.

C. Mass spectrometry

- 10 [000122] Electrospray ionisation mass spectrometry (ESI-MS) was performed on a Thermo Finnigan LCQ DECA XP MAX or a Q Exactive hybrid quadrupole-Orbitrap (Thermo Fisher). The deconvoluted data were obtained using the software of MegTran 1.03 and ESIProt 1.0.

15 D. Cloning and expression of recombinant proteins

[000123] *Ubiquitin (Met-Gly-Ile-Ubiquitin-His₆) (SEQ ID NO:122):*

[000124] MGIMQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGK
QLEDGRTLSDYNIQKESTLHLVLRRLRGHHHHHH

[000125] *Green fluorescent protein (Met-Ile-His₆-GFP): (SEQ ID NO:123):*

- 20 [000126] MIIHHHHHSGVDLGTEENLYFQSMKGEELFTGVVPILVELDGDVNGHK
FSVSGEGEGDATYGKLTALKFICTTGKLPVPWPTLVTTLTYGVCFSRYPDHMKQHDFE
KSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEY
NYNSHNIVYMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYL
STQSALS KDPNEKRDHMLLEFVTAAGITLGMDELYK

- 25 [000127] *Ubiquitin (Met-GISGSGS-Ubiquitin-His₆) (SEQ ID NO:124):*

[000128] MGISGSGSQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIF
AGKQLEDGRTLSDYNIQKESTLHLVLRRLRGHHHHHH

- [000129] Ubiquitin with two residues Gly-Ile added after the start codon (SEQ ID NO:122) was cloned into the pET3b vector (inserted residues were underlined). Green fluorescent protein with an additional Ile residue inserted after the start codon (SEQ ID NO:123) was cloned into the pNIC28-Bsa4 vector. The constructed plasmids were transformed into *E. coli* BL21 (DE3) competent cells for expression. Single colony was inoculated into 10 ml LB medium supplemented with ampicillin (for pET3b vector) or kanamycin (for pNIC28-Bsa4 vector) at 37 °C overnight. The cultures were transferred into 1 l of LB medium containing antibiotics until the OD₆₀₀ reached ~0.6. IPTG was then added to a final concentration of 0.3 mM to induce the expression of the recombinant proteins at 18 °C overnight. Cells were harvested and lysed in PBS buffer (10 mM sodium phosphate, 150 mM NaCl, pH 7.4) by
- 30
- 35

5 sonication. The lysates were filtered and loaded into the Ni-NTA column (Qiagen) for affinity purification.

E. Isolation and purification of butelase 1

[000130] The entire purification process of butelase 1 was conducted at 4°C to minimize
10 protein degradation. About 500 gram pods of *Clitoria ternatea* was blended with one liter of extraction buffer (20mM sodium phosphate, 1 mM EDTA, 1 mM PMSF, and 5 mM mercaptoethanol (β -ME), pH 6.0). The homogenate was centrifuged at 9000 rpm for 15 minutes by using Beckman coulter Avanti™ J-25 centrifuge, with JA-10 rotor. The supernatant was then filtered and ammonium sulfate was added to reach 15% saturation. The supernatant was then
15 centrifuged and the precipitated proteins were discarded. Ammonium sulfate was further added to reach the final concentration of 85%. The solution was then centrifuged and the precipitated proteins were redissolved in 500 ml of extraction buffer. The dissolved solution was dialyzed against extraction buffer using Snakeskin dialysis tubing with a 10 kDa molecular weight cut-off (MWCO). The dialyzed extract was filtered and loaded to the flash chromatography column
20 with Q Sepharose Fast Flow anion exchange resin (GE Healthcare). The column was washed with one litre of wash buffer (10 mM sodium phosphate, 1 mM EDTA and 5 mM β -ME, pH 6.0) and eluted with 500 ml elution buffer (0.5 M NaCl, 10 mM sodium phosphate, 1 mM EDTA and 5 mM β -ME, pH 6.0). The eluent was dialyzed against wash buffer and subject to fractionation by HPLC using a preparative anion exchange column (PolyWAX LP, PolyLC).
25 Fractions contain ligase activity were pooled and concentrated to a final volume of 3 ml using Amicon Ultra centrifugal filter (Millipore Ireland Ltd) of 10 kDa MWCO. The concentrated solution was subjected to size exclusion chromatography using a Biosuite HPLC column (21.5 × 300 mm) and further purified by anion exchange chromatography using analytical PolyWax HPLC column (Poly LC, 4.6 x 250 mm). The purity of the isolated butelase 1 was determined
30 by SDS-PAGE and silver staining (Figure 12). Approximately 0.5 mg butelase 1 can be obtained from 500 gram plant materials.

F. Synthesis of trityl-protected thioglycolic acid

[000131] Triphenylmethanol (805 mg, 3 mmol) was mixed with thioglycolic acid (208.4
35 μ l, 3 mmol) in the presence of neat trifluoroacetic acid (TFA, 4 mL). The reaction was stirred at room temperature for 30 min. After removal of TFA in vacuo, toluene was added to removal the residual water. After complete removal of solution in the reaction mixture, desired product was

- 5 obtained as white powder in quantitative yield and it was used in the following SPPS without further purification.

G. Peptide synthesis

[000132] All native peptides 3, 4, 5 were synthesized using standard Fmoc chemistry on
10 rink-amide-MBHA resin (0.7 mmol/g). Before the synthesis, the resin was pre-swelled in dichloromethane (DCM) for 10 min. Fmoc group removal was done using 20% piperidine in dimethylformamide (DMF) for 2 min and another 20 min. After deprotection, the resin was washed with DMF, DCM, and DMF alternatively. For the coupling reaction, 4 eq. of Fmoc-AA-OH, 4 eq. of PyBOP were first dissolved in DMF/DCM mixture and added to the resin. 8 eq. of
15 DIEA was then added in. Coupling reaction was carried out for about 60-90 min. Coupling efficiency could be monitored by using Kaiser test. After the whole sequence was assembled, the peptide was cleaved from the solid support using a cleavage solution of 95% TFA, 2.5% water and 2.5% TIS for 1 h. Precipitated by cold ether, the crude peptides were purified by HPLC. The desired products were identified using ESI-MS. After lyophilization, peptides were obtained
20 in powder form, which could be used freshly or stored at -20 °C for further use.

[000133] The depsipeptide 2 and 6 were also synthesized using standard Fmoc chemistry on rink amide MBHA resin. Building block used were Fmoc-Tyr(tBu)-OH, Fmoc-Lys(Boc)-OH, Fmoc-Asn(Trt)-OH, glycolic acid, Fmoc-Val-OH. The difference of this synthesis from the above native peptide synthesis was the coupling of glycolic acid and the subsequent Fmoc-
25 Asn(Trt)-OH. As for glycolic acid coupling, 4 eq. of glycolic acid and 4 eq. of PyBOP dissolved in DMF/DCM were first added to the resin. 8 eq. of DIEA was subsequently added in. After coupling for 2 h, a 30 min treatment of 10% hydrazine/DMF was used for removal of the over-coupled glycolic acid. To couple the next amino acid Fmoc-Asn(Trt)-OH, instead of PyBOP, a stronger coupling condition DIC/HOBT was employed. The resin was first suspended in
30 DCM/DMF mixture (9:1 v/v). 5 eq. of Fmoc-Asn(Trt)-OH and 5 eq. of HOBT were dissolved in a minimum amount of DMF facilitated by vortex and sonication. After adding the solution to the resin, 5 eq. of DIC was added followed by 0.1 eq. of DMAP. The reaction was shaken for overnight. 5% acetic anhydride in pyridine was used to cap the uncoupled hydroxyl groups for 30 min.

35 [000134] Both thiodepsipeptides 1 and 8 were synthesized using standard Boc chemistry on MBHA resin (1.03 mmol/g). The Boc chemistry differs from Fmoc chemistry in the way of deprotection and final cleavage. For Boc deprotection, 30% TFA in DCM was used to remove Boc protecting group for 2 min and 20 min. For trityl removal, besides 30% TFA in DCM, TIS

5 was also used. For substrate 1, the building blocks used were Boc-Tyr(2-Br-Z)-OH, Boc-Lys(2-Cl-Z)-OH, Boc-Asn(Trt)-OH, Trityl-protected thioglycolic acid, Boc-Val-OH. For substrate 6, building blocks used were biotin, Boc-Thr(Bzl)-OH, Boc-Tyr(2-Br-Z)-OH, Boc-Lys(2-Cl-Z)-OH, Boc-Asn(Trt)-OH, Trityl-protected thioglycolic acid, Boc-Val-OH. For cleavage (scale of 250 mg resin), first add 750 µl thioanisole/ethanedithiol mixture (2:1) on the ice, then add 5 ml
10 TFA followed by 500 µl TFMSA. The cleavage was allowed to proceed for 1 h at room temperature.

[000135] Fmoc chemistry has also been applied for the synthesis of the thiodepsipeptide 1. Since the thioester moiety is susceptible towards the nucleophilic piperidine, inventors used the modified Fmoc deprotection cocktail containing 25% 1-methylpyrrolidine, 2%
15 hexamethyleneimine, 2% HOBT in NMP/DMSO (1:1) mixture as described previously (Tetrahedron Lett. 1998, 39, 8669).

H. Butelase-mediated ligation and kinetic characterization

[000136] Ligation assays were performed in 50-µl mixtures containing reaction buffer (1
20 mM EDTA, 20 mM phosphate buffer, pH 6.5), 0.1 µM butelase 1, 1 mM GIGGIR (SEQ ID NO:114) and varying concentrations of peptides 1-4 (25 to 400 µM). The reactions were performed in triplicate at 42 °C and quenched by adding 5 µl of 1 M HCl solution. The peptides were separated by using a reversed-phase C18 analytical column (150 x 2.1 mm, Vydac) with a linear gradient from 5% to 40% acetonitrile over 15 min on a Nexera UHPLC system
25 (Shimadzu). The ligation velocities were calculated by converting the HPLC-peak areas of remained linear precursors or the ligated products into concentrations. The identity of each HPLC peak was analyzed by MALDI-TOF MS (ABI 4800 MALDI TOF/TOF). The kinetic parameters (k_{cat} and K_m) for each peptide were obtained by the Lineweaver–Burk plot.

I. Proteins labeling with thiodepsipeptides 1 and 8

[000137] The labeling of proteins were performed in reaction buffer (1 mM EDTA, 20
mM phosphate buffer, pH 6.5) containing 100 µM protein and 0.1 µM butelase 1. One equivalent of thiodepsipeptide substrate was added every 30 min. For ubiquitin, 5 equivalents of thiodepsipeptide were added in total, as for GFP, 4 equivalents were added. The labeling
35 reactions were monitored by HPLC and ESI-MS.

[000138] Here inventors report the use of thiodepsipeptide as an acceptable sorting signal but a poor competing nucleophile after its release to render the butelase-mediated intermolecular

ligation irreversible (Figure 1). Inventors obtained quantitative ligation yields of >95% for a model peptide at 0.0005 molar equivalent of butelase 1 and two molar equivalents of the thiodepsipeptide. Inventors also successfully applied the proposed method to label ubiquitin and GFP with high yields. This method is based on inventors' previous work that incubation of butelase 1 with a model peptide KALVINHV (SEQ ID NO:125) with the dipeptide HV as a leaving group in the presence of various alkyl and aryl thiols did not lead to any detectable amount of peptide thioester (Nat Chem Biol 2014, 10, 732). This result suggested that thiol groups are poor competing nucleophiles than the HV dipeptide sorting signal. Thus, inventors hypothesized that intermolecular ligation reactions would be irreversible if the scissile asparaginyl amide bond is replaced by a thioester linkage. For comparison, inventors also synthesized a depsipeptide because it has been demonstrated that ligation yields were improved for sortase A using a depsipeptide substrate (Angew. Chem. Int. Ed. Engl. 2012, 51, 9377). However, the applications of depsipeptide for N-terminal protein labeling required 0.1-0.2 molar equivalents of sortase A and a time-consuming solution-phase synthesis of a depsipeptide precursor.

[000139] To support this hypothesis, inventors prepared four different peptide substrates sharing a common sequence YKNXV (SEQ ID NO:126) 1-4 with a XV as a sorting signal (X= thio- or glycolic acid, His and Gly, respectively). Thiodepsipeptide 1 and depsipeptide 2 contain a *S*- and *O*-ester bond as a (*S*)GV and (*O*)GV analog, respectively, at the scissile bond compared with an amide bond in the two control peptides 3 (HV) and 4 (GV). Thiodepsipeptide 1 was prepared by a standard solid-phase synthesis (Figure 2a). First, a mixture of an equal equivalent of thioglycolic acid and triphenylmethanol in the presence of neat trifluoroacetic acid yielded trityl-protected thioglycolic acid after solvent removal. This compound was used without further purification. Thiodepsipeptides were synthesized on MBHA resin with Boc-protected amino acids and the pre-made building block by Boc chemistry. Alternatively, the thiodepsipeptide 1 can also be prepared by Fmoc chemistry. Since the thioester moiety is susceptible towards piperidine, inventors used the modified Fmoc deprotection cocktail containing 25% 1-methylpyrrolidine, 2% hexamethyleneimine, 2% HOBt in NMP/DMSO (1:1) mixture (Tetrahedron Lett. 1998, 39, 8669). For depsipeptide 2, unlike previously reported method that required a carefully controlled solution-phase synthesis (Angew. Chem. Int. Ed. Engl. 2012, 51, 9377), inventors developed a fully solid-phase compatible and straightforward approach (Figure 2b). The depsipeptides were synthesized on Rink amide MBHA resin with Fmoc amino acids and glycolic acid.

[000140] Hydrazinolysis of the glycolic acid-coupled product removed all side products

- 5 of oligomers because of their susceptibility to hydrazine, leaving only one glycolic acid attached to the preceding residue as a stable amide bond. Inventors' synthesis scheme provides a new convenient method for preparing depsipeptides.

[000141] Table 1. List of peptide substrates and their corresponding molecular weight

Peptide	SEQ ID NO:	Sequence	MW (MH ⁺)	
			Calc.	Obs.
1	110	YKN(S)GV	596.28	596.28
2	111	YKN(O)GV	580.30	580.19
3	112	YKNHV	659.36	659.27
4	113	YKNGV	579.32	579.16
5	114	GIGGIR	571.36	571.3
6	115	(O)GVYKV	565.33	565.28
7	116	ERLYRGRLYRRNHV	1888.05	1888.2
8	117	biotin-TYKN-thioglc-V	923.4	923.31

- 10 [000142] Inventors evaluated the ligation efficiency of each peptide substrate to a model peptide GIGGIR (SEQ ID NO:114) 5 to form the ligated product YKNGIGGIR (SEQ ID NO:127) by HPLC. The reactions were performed in the presence of 100 μ M GIGGIR (SEQ ID NO:114), one or two molar equivalents of each peptide substrate, and 50 nM of butelase 1 (0.0005 molar equivalent). Time-course analysis showed that thiodepsipeptide 1 was the most efficient substrate followed by depsipeptide 2. Peptide 3 and peptide 4 were the least efficient. All ligation reactions reached equilibrium after 60 min with marginal yield improvement after 90 min. At two molar equivalents of 1, >95% of peptide 5 was converted into the ligation product within 1 h (Figure 3). In contrast, the ligation yields only reached 31%, 59% and 68%, respectively, for peptide 4, 3 and 2 under similar conditions.

- 20 [000143] Even at one molar equivalent of thiodepsipeptide 1, the ligation yield still reached 73%, confirming thiodepsipeptide is the best of the four substrates. Table 2 shows a kinetic study to quantify the difference among peptides 1-4. The result was in agreement with the time-course experiments with thiodepsipeptide 1 having the highest catalytic efficiency (k_{cat}/K_m) and peptide 4 being the lowest.

- 25 [000144] Table 2 Kinetic parameters of butelase 1 for peptides 1-4

Peptide	SEQ ID NO:	Sequence	k_{cat} (s ⁻¹)	K_m (mM)	k_{cat}/K_m (M ⁻¹ s ⁻¹)
1	110	YKN-thioglc-V	56.5 $\pm$ 7.5	2.76 $\pm$ 0.3	20,480

2	111	YKN-glc-V	12.4 ± 0.32	0.74 ± 0.01	16,840
3	112	YKNHV	4.1 ± 0.65	0.3 ± 0.01	13,490
4	113	YKNGV	7.9 ± 0.72	0.88 ± 0.08	8,900

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[000145] Next inventors sought to determine what shifts the equilibrium to a higher yield for thiodepsipeptide 1 as compared to depsipeptide 2, because their leaving groups are a thiol or an alcohol, both of which are poor nucleophiles in a butelase-mediated ligation. It was found that the model peptide accepts glycerol as a nucleophile to give about 20% of the ligated product (Figure 7). This observation suggests that butelase 1 can recognize an alcohol as an acceptor nucleophile. To demonstrate that butelase 1 indeed accepts an alcohol group, inventors synthesized peptide 6, (O)GVYKV (SEQ ID NO:115), with glycolic acid as the N-terminal residue. Ligation of peptide 6 with peptide 7 (ERLYRGRLYRRNHV; SEQ ID NO:116) led to a ligated product ERLYRGRLYRRN(O)GVYKV (SEQ ID NO:117) with about 25% yield (Figure 8). No detectable ligation product was formed when ligated 7 with a (S)GV peptide under the same condition. These results indicate that the butelase-mediated ligation is reversible for depsipeptide and irreversible for thiodepsipeptide, which could explain for the higher yields of thiodepsipeptide 1 at equilibrium as compared to depsipeptide 2.

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[000146] To apply butelase 1 for N-terminal labeling of proteins, inventors used ubiquitin and green fluorescent protein (GFP) as examples (Figure 4). Since butelase 1 prefers a hydrophobic amino acid (Ile/Leu/Val) or Cys at the P2" position of an acceptor nucleophile, inventors prepared a recombinant ubiquitin protein (SEQ ID NO:122) with Gly-Ile at the N-terminus and His-tag at the C-terminus. It was also examined whether this method would work if His-tag was located at the N-terminus. Inventors thus prepared a recombinant GFP (SEQ ID NO:123) with an additional Ile inserted between the start codon and the N-terminal His-tag. Both proteins were labeled with the model thiodepsipeptide 1 in the presence of 0.001 molar equivalent of butelase 1. The labeling of proteins was slower as compared to the labeling of peptide 5, probably due to large differences in size between the model peptide and proteins. Furthermore, the N-terminal amino group of proteins may have a lower accessibility to butelase 1 as compared to peptides. Additionally, it was also found that the half-life of the thiodepsipeptide labeling reagent was relatively short mainly due to hydrolysis and aspartimide formation which was associated with the nature of the asparagine residue. The half-life of

- thiodepsipeptide 1 in inventors' reaction buffer is about 75 min in the absence of butelase 1 and 40 min in the presence of 0.0005 molar equivalent of butelase 1 (Figure 9). For depsipeptide 2, the half-life is 45 min and 37 min in the absence and presence of butelase 1, respectively. This feature poses a problem when the ligation proceeds slowly, and a moderate yield (~60%) was obtained after five equivalents of thiodepsipeptide 1 being completely consumed in the reaction.
- Due to the instability of the thiodepsipeptide, one molar equivalent of the labeling reagent was added to the reaction every thirty minutes instead of adding them all at once. This strategy improved the ubiquitin labeling to 82% yield with five molar peptide equivalents after 2.5 h (Figure 4). Comparatively, <10% ligation product observed when ligating ubiquitin with LPETGG peptide (SEQ ID NO:128) when using sortase A. This result suggests that the N-terminal of ubiquitin may be buried and less accessible for ligation than small peptides, a finding in agreement with a previous study that sortase A is unable to modify myoglobin and fly pumilio RNA binding domain (Angew. Chem. Int. Ed. Engl. 2012, 51, 9377). Using the same strategy, 70% of GFP was labelled with four molar peptide equivalents (Figure 9). This is also first example to explore the application of butelase 1 for protein labeling.
- [000147] To improve the ligation yield by introducing an additional linker to the N-terminal of proteins, another recombinant ubiquitin (SEQ ID NO:124) with a short liker peptide GISGSGS (SEQ ID NO:129) was expressed. Inventors obtained quantitative labeling for ubiquitin (~95%) with four equivalents of the thiodepsipeptide 1 in the presence of 0.001 molar equivalent of butelase 1 in 100 min (Figure 5a). The ligation yield also reached >90% yield for sortase A after introducing the linker peptide (GGSGSGS) (SEQ ID NO: 130), a result consistent with a literature precedent (Angew. Chem. Int. Ed. Engl. 2012, 51, 9377; Nat. Protoc. 2013, 8, 1800). However, sortase A required 0.1 molar equivalent of enzyme to catalyze the ligation as compared to 0.001 molar equivalent of butelase 1.
- [000148] With the success on the model thiodepsipeptide, conjugation with biological functional groups was also investigated. A thiodepsipeptide 8 carrying a biotin functional group at its N-terminus was synthesized. Successful labeling was achieved on both ubiquitin and GFP with the biotinylated thiodepsipeptide 8 (Figures 5b, 11), demonstrating the applicability of the presently disclosed method to introduce a functional tag into peptides and proteins. The labeling yields are comparable between thiodepsipeptides 1 and 8, which indicates that the biotin group does not affect the labeling efficiency.
- [000149] In conclusion, inventors have developed a novel method for butelase-mediated ligation using thiodepsipeptides as substrates. The ligation yield of >95% could be achieved for the model peptide and ubiquitin with a small excess of substrate. The developed method is also

5 applicable for introducing a functional group such as biotin into proteins. The ligation efficiency was greatly improved as the (S)GV byproduct is a poor recognizing substrate in the reverse direction. Furthermore, the preparation of the labeling reagent and the use of this method are simple and straight forward. Inventors anticipate a broad application of this method for N-terminal modification of peptides and proteins.

10 *Example 2: Bioconjugation: Efficient butelase-mediated synthesis of peptide dendrimers and their application as antimicrobials*

A. Materials and Reagents

15 [000150] For peptide synthesis, all the amino acids, coupling reagents and resins were obtained from chemimpex and GL biochem. All other chemical reagents were of analytical grade, obtained from Sigma Aldrich, alfa aesar and Acros Organics. All solvents and chemicals were used as received without purification unless otherwise indicated.

[000151] The materials for radial diffusion assay were prepared as following:

20 [000152] Trypticase soy broth (TSB): Full-strength broth contains 30 grams of TSB powder per liter of deionized water. It was autoclaved at 120 °C for 20 min and stored at room temperature.

[000153] Underlay gel: 50 mL of 100 mM sodium phosphate buffer, 5 ml full-strength TSB and 5 g agarose were mixed in a beaker followed by addition of deionized water to 500 mL. The medium was autoclaved at 120 °C for 20 min. Before use, it was maintained at 42 °C to prevent from solidifying.

[000154] Overlay gel: One liter of overlay gel contains 60 g of TSB powder and 10 g of agarose. The medium was autoclaved at 120 °C for 20 min. To prevent from solidifying, it was maintained at 42 °C before use.

30 *B. High Performance Liquid Chromatography (HPLC)*

[000155] The analytical HPLC analyses were carried out on a SHIMADZU NexraX₂ LC-30AD system with an analytical column (Aeris peptide XB-C18, 4.6 x 250 mm for peptide analysis. The peptide purifications were performed using Shimadzu HPLC equipped with a semi-preparative HPLC column (Jupiter C18, 5 μM, 10 x 250 mm). All the HPLC runs were done using the mixture of two solutions, A (0.045% TFA in water) and B (0.039% TFA in acetonitrile/water (9/1) mixture). Flow rate was 0.8 ml/min for analysis and 2.5 ml/min for purification. UV detection was carried out at 220 nm.

5 *C. Mass spectrometry*

[000156] Peptides ESI mass spectra data were obtained on both ESI (Thermo Finnigan LCQ DECA XP MAX) and MALDI TOF MS (ABI 4800 MALDI TOF/TOF system).

D. Peptide synthesis

10 [000157] The peptides RYRLNHV-NH₂ (SEQ ID NO:140), RLYR-NH₂ (SEQ ID NO:139), (RIβA)₂KY-NH₂, (RIβA)₄K₂KY-NH₂ and (RIβA)₈K₄K₂KY-NH₂ were prepared by standard Fmoc chemistry using Rink Amide MBHA resin. Prior to use, resin was swelled with DCM for 5 min. Before coupling the first residue, an Fmoc deprotection was performed using 20% piperidine in dimethylformamide (DMF) for 2 min, followed by another 20 min treatment.

15 For standard coupling reactions, 4 eq. of Fmoc-AA-OH, 4 eq. of PyBOP were first mixed in DCM/DMF mixture and added to the resins. 8 eq. of DIEA was added subsequently. Coupling reaction mixtures were shaken on the belly dancer for 60 to 90 min, efficiency monitored by Kaiser test. Between couplings and deprotections, resins were washed with DMF and DCM alternatively. For efficient synthesis of the dendrons, it is recommended to perform acetic anhydride capping (0.5 eq to the coupling capacity) after the deprotection of the first residue.

20 The building blocks used for the peptides mentioned above were Fmoc-Tyr(tbu)-OH, Fmoc-Arg(Pbf)-OH, Fmoc-Leu-OH, Fmoc-Asn(Trt)-OH, Fmoc-His(Trt)-OH, Fmoc-Val-OH, Fmoc-Ile-OH, Fmoc-βAla-OH, Fmoc-Lys(Fmoc)-OH. Upon completion of peptide assembling, peptides were cleaved from the resin using a mixture containing 95% TFA, 2.5 % TIS and 2.5% water. Peptides were precipitated from the cleavage reaction using cold ether.

[000158] Thiodipeptides RYRLN-thioglc-V (SEQ ID NO:142), Ac-RYRLN-thioglc-V-NH₂ (SEQ ID NO:137) and Ac-RLYRN-thioglc-V-NH₂ (SEQ ID NO:138) were prepared by Boc chemistry using MBHA resin. Coupling procedures were the same as Fmoc. For Boc deprotection, 30% TFA in DCM was used. The building blocks used were Boc-Arg(Mts)-OH, Boc-Leu-OH.H₂O, Boc-Asn(Trt)-OH, Boc-Tyr(2-Br-Z)-OH, trityl-protected thioglycolic acid, Boc-Val-OH. Acetic anhydride was used to introduce an acetyl group at the N-terminus. For the final cleavage (scale of 100 mg resin), 450 μl mixture of thioanisole/ethanethiol was first added to the resin, 3 ml of TFA was subsequently added to the reaction chilled on ice. After 10 min, 300 μl of TFMSA was added dropwise and the reaction was stirred at room temperature for 1 h.

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E. Butelase 1 preparation

[000159] A four-step chromatographic procedure was used to extract butelase 1 from the plant *Clitoria ternatea*. 1 kg of freshly collected *Clitoria ternatea* pods were homogenized with

1 l of extraction buffer EB1 (20 mM sodium phosphate, 2 ml of 0.5 M EDTA, 174 mg of PMSF, 0.35 ml of β -ME, pH 6.0). After removing the plant debris by filtration, ammonium sulfate solid was added to 15% saturation. The undesired large proteins were precipitated and removed by centrifuge. Ammonium sulfate was further added to 85% saturation and the precipitated proteins were collected after centrifuge. The extraction buffer EB1 was added to redissolve the proteins. The protein solution was dialyzed for overnight against extraction buffer EB2 (20 mM sodium phosphate, 1 mM EDTA and 5 mM β -ME, pH 6.0).

[000160] On the second day, the dialyzed protein solution was subjected to the flash chromatography column containing 300 ml slurry of Q Sepharose Fast Flow anion exchange resin (GE Healthcare). The column was first washed with EB2 and then eluted with 500 ml of elution buffer (EB2 + 200 mM NaCl). The eluent was dialyzed against EB2 for 4 h and fractionated using preparative PolyWax anion-exchange column (PolyLC, 21 x 250 mm). Fractions containing ligase activity were determined by testing on a cyclizable linear peptide substrate (GRCTKISPPICFPNHV, SEQ ID NO:141). All the fractions containing ligase activity were combined and concentrated using centrifugal filter with a MWCO of 10 kDa. The concentrated samples were first purified by a size-exclusion chromatography with Biosuite HPLC column and further purified by analytical anion-exchange chromatography using 4.6 x 200 mm PolyWax column. The purity of the isolated butelase 1 was determined by SBS-PAGE and silver staining, the enzyme showing a band at 37 kDa in SDS-gel. The concentration of butelase 1 was determined by OD280 based on the modeling. Around 5 mg of enzyme was obtained from the starting 1 kg of pods. Figure 24 shows the SDS-PAGE (silver staining) of isolated butelase 1 (left lane) and protein markers (right lane).

F. Ligation protocol

[000161] For all analytical reactions, a total system of 100 μ l was used. Before the reaction, the stocks of thiodipeptides and butelase 1 were placed on the ice. The order of addition was: pH 6.5 phosphate buffer (20 mM), TCEP (1 mM), dendron core (50 μ M), thiodipeptide (1.5 eq. per branch), butelase 1 (0.001 eq. per branch). After all reagents were added, the reaction was heated at 42 °C in a heating bath. A volume of 20 μ l was taken out for HPLC analysis.

G. Radial diffusion assay

[000162] The following protocol was applied to the radial diffusion assay.

- 5 [000163] 1. A single colony was picked and transferred into a 5 ml tube containing 2.5 ml TSB. The culture was shaken at 37 °C for 18 h.
- [000164] 2. 50 µl of the stationary phase culture was diluted to 2.5 mL of autoclaved TSB (1:50 dilution) and shaken at 37 °C for another 3 h.
- 10 [000165] 3. This subculture was centrifuged at 5000 rpm for 5 min and the supernatant was discarded. The residual cells were washed with cold sterile 10 mM phosphate buffer, pH 7.4 and the buffer was discarded after centrifuge. 5 ml of the same buffer was added to resuspend the cells and its bacteria concentration was determined by measuring its optical density at 620 nm.
- 15 [000166] 4. 10 ml of autoclaved, molten underlay gel agar was transferred to a 15-ml eppendorf tube and mixed with 4×10^6 CFU of bacteria by vortexing. The mixture was then poured into a petri dish and gelled in less than 3 min. Wells were punched against the gel using a Pasteur pipette.
- [000167] 5. Peptides to be tested were serially diluted and 3.5 µl of each sample was added to the well. The plates were incubated at 37 °C for 3 h with gel-side up.
- 20 [000168] 6. Next, each underlay gel was covered with 10 ml of overlay gel. After the gel solidified, the plates were turned gel-side up and incubated at 37 °C for overnight.
- [000169] 7. The following morning, all the plates were taken out and the zone diameters were measured with ruler. All the samples were tested in duplicates and the results were averaged. The final minimum inhibition concentration (MIC) was determined using excel.
- 25 [000170] Conjugation methods are enabling tools for biochemical studies. Their applications include labeling proteins with a biophysical probe or a bioactive cargo to enable structural studies, drug development as well as preparing biomaterials and immobilizing peptides and proteins on solid supports (Bioconjug Chem. 2014, 25, 825-839; Curr Org Chem. 30 2010, 14, 138-147).
- [000171] Chemical strategies for a site-selective protein conjugation often utilize classic acylation or alkylation chemistries, taking advantages of the side-chain functionalities of Lys, Asp/Glu, and Cys residues (Chem Rev. 2015, 115, 2174-2195). A limitation of these methods is that they are not site-specific because proteins often carry multiple copies of these "selective" 35 residues. Consequently, they lead to heterogeneous products. Recent advances have addressed this limitation including the use of recombinant methods to incorporate unnatural amino acids with unique chemical activities to allow both site-selective and site-specific conjugation on proteins in the presence of other natural amino acids to render a modified protein product

5 homogenous (Nat Rev Mol Cell Biol. 2006, 7, 775-782).

[000172] Ligases, peptide-bond forming enzymes, provide an exciting complementary strategy through a ligase-mediated bioconjugation to the existing chemical conjugation methods. Bioconjugation, because of the inherent chemoselectivity of a ligase, produces exquisite site-selectivity and site-specificity (Bioconjug Chem. 2013, 24, 1277-1294). Current
10 peptide ligases include sortase A (Chemistry. 2014, 20, 8516-8529) and subtiligase (Proc Natl Acad Sci U S A. 1994, 91, 12544-12548). Recently, a new peptide ligase, namely butelase 1, was isolated from a cyclotide-producing plant *Clitoria ternatea* (Nat Chem Biol. 2014 10, 732-738). butelase 1 is the enzyme responsible for the macrocyclization of cliotides, cyclotides from *C. ternatea*, during their biosynthesis and recognizes a linear precursor with a C-terminal
15 tripeptide motif Asn/Asp(Asx)-His-Val. It cleaves the bond between Asx and His to accept an N-terminal residue Xaa, resulting in a new Asx-Xaa bond in the cyclized peptide. butelase 1 exhibits not only the highest catalytic kinetics among all the peptide ligases found so far, but also a broad substrate specificity for the N-terminal amino acid, Xaa which can be any amino acid except Pro, making it an attractive tool for bioconjugation and peptide ligation (Chem
20 Commun (Camb). 2015, 51, 17289-17292; Angew Chem Int Ed Engl. 2015, 54, 15694-15698; J Am Chem Soc. 2015, 137, 15398-15401).

[000173] Multiple antigen peptide system (MAP), a strategy to present multiple functional peptides in a clustered dendrimeric format, was first developed by Tam to amplify the immunogenicity of small antigenic peptides (J Biol Chem. 1988, 263, 1719-1725; Proc Natl
25 Acad Sci U S A. 1988, 85, 5409-5413). This chemical platform has also found wide applications in peptide-based therapeutics and biomaterials (J Biotechnol. 2002, 90, 195-229). A common MAP design contains a scaffold, a branching oligolysine dendron core, to which various copies of a functional peptide are attached. Often, stepwise solid phase peptide synthesis (SPPS) or a convergent synthetic strategy is used to prepare such peptide dendrimers (Mol Immunol. 1991,
30 28, 623-630). For many applications, stepwise SPPS suffices; however, as the size of a MAP increases, the likelihood of synthetic errors such as residue deletion also increases, making purification a challenge to arrive at a homogeneous product from a synthetic mixture. Although this problem could be partially mitigated by an optimized SPPS methodology, increased attentions have been focused on employing a convergent strategy in which the dendron core and
35 the antigenic peptides are separately synthesized and purified to homogeneity and then brought together using chemoselective conjugation reactions. Conjugation chemistries developed thus far include disulfide (Int J Pept Protein Res. 1991, 37, 27-32), thioether (Int J Pept Protein Res. 1992, 40, 214-221), thiazolidine (J Am Chem Soc. 1994, 116, 6975-6976), oxime (Mol

Immunol. 1995, 32, 1031-1037), hydrazine (Int J Pept Prot Res. 1995, 45, 78-85), maleimide (Bioconjug Chem. 2013, 24, 578-585) and native chemical ligation (Biopolymers. 2008, 90, 624-632). Compared with the stepwise SPPS method, the convergent strategy often gives higher yield and greater purity of the final MAP products.

[000174] Inventors envisioned that, with its exquisite site-specificity and site selectivity, butelase 1 would be useful for peptide dendrimer synthesis whereby a peptide as an acyl donor could be bioconjugated to a lysyl dendron core containing appropriate N-terminal acceptor amino acids to form a multi-valent dendrimeric product (Figures 19 and 20). An enzymatic synthesis of a highly clustered peptide dendrimer (such as the octavalent one) would present a stringent test of a butelase-mediated ligation (BML) and help to advance the development of peptide-based vaccines and therapeutics.

[000175] In a trial reaction in which a conventional peptide substrate containing the C-terminal -NHV motif (peptide 4, Table 3) was used to bioconjugate to a bivalent lysyl dendron core (entry 2, Table 3), a sluggish reaction even with an excess of the monomeric peptide 4 and in a prolonged period was observed. Inventors attributed this poor outcome to the reversibility of the BML reaction because the released dipeptide His-Val acts as a competing nucleophile (Figure 19A). Prompted by this observation, inventors sought to use thiodepsipeptides as acyl donors for peptide dendrimer synthesis to overcome the reversibility issue. It has been previously shown that thiodepsipeptides are superior substrates for butelase-mediated N-terminal labeling of proteins (Angew Chem Int Ed Engl. 2015, 54, 15694-15698). The use of thiodepsipeptide has two advantages. First, it contains a thioester linkage as the scissile bond which is more susceptible to enzymatic cleavage compared to its amide bond counterpart. Second, after the reaction, it releases a thiol byproduct which, unlike its native dipeptide counterpart, is a poor acyl-acceptor substrate of butelase 1, essentially rendering the BML reaction irreversible (Figure 19B).

[000176] Table 3. Sequences of the used peptides.

Number	SEQ ID NO:	Sequence
1	118	Ac-RYRLN-thioglc-V
2		(RI β A) ₂ KY
3		(Ac-RYRLNRI β A) ₂ KY
4	119	RYRLNHV
5		(RYRLNRI β A) ₂ KY
6		(RI β A) ₄ K ₂ KY

7		(RI β A) ₈ K ₄ K ₂ KY
8		(Ac-RYRLNRI β A) ₄ K ₂ KY
9		(Ac-RYRLNRI β A) ₈ K ₄ K ₂ KY
10	120	Ac-RLYRN-thioglc-V
11	121	RLYR
12		(Ac-RLYRNRI β A) ₂ KY
13		(Ac-RLYRNRI β A) ₄ K ₂ KY

5

[000177] To test this hypothesis, inventors first conducted a bioconjugation between an N-acetylated thiodepsipeptide 1 (Table 3) and the bivalent lysyl scaffold 2. The N-terminus of the thiodepsipeptide was acetylated because inventors found self-ligation of N-terminus-free thiodepsipeptide as a minor side reaction (Figure 23) possibly due to high reactivity of the thioester. Thiodepsipeptide 1 was conveniently prepared by Boc chemistry as previously reported (Angew Chem Int Ed Engl. 2015, 54, 15694-15698). Using HPLC, the ligation reaction of 1 with 2 in forming the bivalent product 3 was evaluated (Figure 20A). The reaction was performed in the presence of 50 μ M scaffold 2, 150 μ M thiodepsipeptide 1 (1.5 equiv. per branch), 100 nM butelase 1 (0.001 equiv. per branch), 1 mM TCEP, pH 6.5 phosphate buffer at 42 $^{\circ}$ C. The dendron core was consumed in 30 min and the desired product 3 was formed in > 95% yield based on HPLC analysis (Figure 21A). This is in strong contrast to the sluggish ligation between the native peptide 4 which contains the -NHV motif and the scaffold 2. Under similar conditions, >50% of the starting materials were not consumed after 2h (Figure 21B). HPLC analysis showed that the monovalent product was the major product (peak c' in Figure 2B) whereas the desired bivalent product was a minor product (peak d' in Figure 21B). Side reactions due to self-ligation of the unacetylated peptide 4 were not observed.

[000178] To further test enzymatic multimerization of peptides at a higher density level, tetra- and octavalent lysly dendron cores 6 and 7 with four and eight branches, respectively, were then prepared by SPPS using a low-loading resin. Under similar reaction conditions, clean and efficient ligations of thiodepsipeptide 1 with these two dendron cores were observed in HPLC profiles and dendron cores 6 and 7 were consumed after 45 min and 180 min (Figure 22), respectively, to give the corresponding tetra- and octavalent products 8 and 9 (peak b and b' in Figure 22A and B) in excellent yields (> 85%). It should be noted that upon completion of the reaction, few intermediate low-order ligation products were found, a desirable scenario for purification purpose to achieve high product homogeneity. The synthesis of these MAPs with four and eight peptide branches showed the powerful nature of the butelase-mediated ligation

5 reaction. To the best of inventors' knowledge, this is the first time that a peptide ligase has been used for the synthesis of an octabranched dendrimeric peptide. Moreover, the presently disclosed bioconjugation method forms native peptide bonds between the monomeric peptides and lysyl dendron cores, as opposed to most chemical conjugation methods which form non-peptidic linkages.

10 [000179] There is a growing interest to develop peptide-based antibiotics (Annu Rev Immunol. 1995, 13, 61-92; J Intern Med. 2003, 254, 197-215; Cent Eur J Biol 2007, 2, 1-33; Int J Pept Res Ther. 2010, 16, 199-213) because, compared with conventional antibiotics, they are less likely to develop drug resistance and have fewer side effects (J Med Chem. 2015, 58, 6533-6548; Biochemistry-US. 2000, 39, 7159-7169; Eur J Biochem. 2000, 267, 3289-3300; Nucleic
15 Acids Res. 2012, 40, W199-204). To apply the presently disclosed enzymatic method in preparing dendrimeric antimicrobials, inventors synthesized two antimicrobials 12 (bivalent) and 13 (tetravalent) (MS shown in supporting information) which harbored a tetrapeptide RLYR (SEQ ID NO:121) as the antibacterial sequence (Eur J Biochem. 2002, 269, 923-932) by ligating N-acetylated thiodipeptide 10 Ac-RLYRN-thioglc-V (SEQ ID NO:120) with
20 dendron core 2 and 6 respectively. The RLYR (SEQ ID NO:121) tetrapeptide contains a BHHB motif (*B* = basic, *H* = hydrophobic) which is commonly found in certain potent and broad-spectrum β -stranded antimicrobial peptides (BioDrugs. 2013, 27, 479-493) such as PG (protegrins) (Febs Lett. 1993, 327, 231-236) and RTD-1 (rhesus monkey theta defensin) (Science. 1999, 286, 498-502). This consensus motif with positive charged and hydrophobic
25 residues was successfully used as a dendrimeric antimicrobial in 2002 (Eur J Biochem. 2002, 269, 923-932). Such short peptide-based dendrimeric antimicrobials are broad-spectrum antibiotics and kill bacterial cells through electrostatic and hydrophobic interactions with the negatively charged microbial cytoplasmic membranes (Biochemistry-US. 2009, 48, 5642-5657). Using a radial diffusion assay, inventors tested the antimicrobial activities against *E. coli* and *S.*
30 *aureus* of these two dendrimeric peptides together with prototypical monomer 11 RLYR (SEQ ID NO:121), mono-, tri-lysine dendron core 2 and 6 for comparison. All assays were performed under a high-salt condition (100 mM NaCl) to simulate physiological conditions. The monomeric peptide 11 showed no appreciable activity against either *E. coli* or *S. aureus* (Table 4). However, significant antimicrobial activities were observed with the bivalent product 12
35 which had a MIC of 18.3 μ M against *E. coli* and 3.4 μ M against *S. aureus*. The tetravalent dendrimeric structure 13 had further improved antimicrobial activities with MICs < 3 μ M against both strains. When testing 13 against several drug-resistant strains under high-salt condition, the tetramer construct was broadly active against all six tested strains with MICs

5 ranging from 0.87 to 4.8 μM . The results suggest that MAP-based dendrimeric peptides, which can be easily prepared using BML, are an effective platform for the design of antimicrobial agents. A possible reason for this success is that the dendrimeric structure increases the effective molarity of the functional monomeric units and reduces the entropy cost associated with peptide self-assembly on bacterial plasma membranes (Eur J Biochem. 2002, 269, 923-932).

10 [000180] Table 4. Antimicrobial activity of different peptides against *E. coli* and *S. aureus*.

Peptide	MIC (μM)	
	<i>E. coli</i>	<i>S. aureus</i>
Monomer 11	> 300	> 300
Bivalent dendron core 2	> 150	> 150
Tetravalent dendron core 6	> 150	> 150
Dimer 12	18.3	3.4
Tetramer 13	2.4	1.4

[000181] Table 5. Antimicrobial activity of tetramer 13 against different drug-resistant strains.

Organism	MIC (μM)
<i>E. cloacae</i> DM 09800	0.9
<i>K. species</i> DR 13779	1.5
<i>E. coli</i> DM 04604	4.5
<i>S. aureus</i> DB 14329	4.8
<i>P. aeruginosa</i> DM 14158	2.3
<i>E. coli</i> DU 09777	2.2

15 [000182] In conclusion, inventors have developed a novel method to prepare peptide dendrimers using butelase 1 as the catalyst for bioconjugation of thiodipeptides with a lysyl dendron core. Using a small excessive of a monomeric peptide substrate (1.5 equiv. per branch to the dendron core) and a low catalytic amount of the enzyme butelase 1 (0.001 equiv.),
 20 inventors obtained very efficient synthesis of the bi-, tetra- and octavalent dendrimers. No other peptide ligases have been used for the synthesis of such dendrimeric peptides. Inventors further used this bioconjugation method to evaluate the polyvalent feature of peptide dendrimers as antimicrobials. Inventors found that a tetravalent dendrimer containing a tetrapeptide sequence with the *BHHB* motif is a potent broad-spectrum antimicrobial (MICs < 5 μM), including

5 several drug-resistant bacterial strains. The presently disclosed butelase-mediated bioconjugation method works under mild conditions and is user-friendly as it requires no complicated chemistry operations. Inventors anticipate this method to be a useful tool in preparing peptide dendrimers.

[000183] The invention has been described broadly and generically herein. Each of the
10 narrower species and subgeneric groupings falling within the generic disclosure also form part of the invention. This includes the generic description of the invention with a proviso or negative limitation removing any subject matter from the genus, regardless of whether or not the excised material is specifically recited herein. Other embodiments are within the following claims. In addition, where features or aspects of the invention are described in terms of Markush
15 groups, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group.

[000184] One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. Further, it will be readily apparent to one skilled in the art that varying
20 substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention. The compositions, methods, procedures, treatments, molecules and specific compounds described herein are presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art which are
25 encompassed within the spirit of the invention are defined by the scope of the claims. The listing or discussion of a previously published document in this specification should not necessarily be taken as an acknowledgement that the document is part of the state of the art or is common general knowledge.

[000185] The invention illustratively described herein may suitably be practiced in the
30 absence of any element or elements, limitation or limitations, not specifically disclosed herein. Thus, for example, the terms "comprising", "including," containing", etc. shall be read expansively and without limitation. The word "comprise" or variations such as "comprises" or "comprising" will accordingly be understood to imply the inclusion of a stated integer or groups of integers but not the exclusion of any other integer or group of integers. Additionally,
35 the terms and expressions employed herein have been used as terms of description and not of limitation, and there is no intention in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be

5 understood that although the present invention has been specifically disclosed by exemplary
embodiments and optional features, modification and variation of the inventions embodied
therein herein disclosed may be resorted to by those skilled in the art, and that such
modifications and variations are considered to be within the scope of this invention.

[000186] The content of all documents and patent documents cited herein is incorporated
10 by reference in their entirety.

SEQUENCE LISTING

<110> Nanyang Technological University
 <120> BUTELASE-MEDIATED PEPTIDE LIGATION
 <130> P111075
 <150> Singapore Patent Application No. 10201508158V
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Leu Asn Ile Tyr Ala Thr Thr Ala Ser Asn Ala Glu Glu Ser Ser Trp
225 230 235 240

Gly Thr Tyr Cys Pro Gly Glu Tyr Pro Ser Pro Pro Ser Glu Tyr Glu
245 250 255

Thr Cys Leu Gly Asp Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Glu
260 265 270

Val His Asn Leu Arg Ser Glu Thr Leu Lys Gln Gln Tyr His Leu Val
275 280 285

Lys Thr Arg Thr Ser Asn Gly Asn Ser Ala Tyr Gly Ser His Val Met
290 295 300

Gln Tyr Gly Asp Leu Lys Leu Ser Val Asp Asn Leu Phe Leu Tyr Met
305 310 315 320

Gly Thr Asn Pro Ala Asn Asp Asn Tyr Thr Phe Val Asp Asp Asn Ala
325 330 335

Leu Arg Pro Ser Ser Lys Ala Ile Asn Gln Arg Asp Ala Asp Leu Val
340 345 350

His Phe Trp Asp Lys Phe Arg Lys Ala Pro Glu Gly Ser Leu Arg Lys
355 360 365

Glu Glu Ala Ala Lys Gln Val Phe Glu Ala Met Ser His Arg Met His
370 375 380

Ile Asp Ser Ser Ile Lys Leu Val Gly Lys Leu Leu Phe Gly Ile Glu
385 390 395 400

Arg Gly Ser Glu Ile Leu Asn Ala Val Arg Pro Ala Gly Gln Pro Leu
405 410 415

Ala Asp Asp Trp Ala Cys Leu Lys Ser Leu Val Arg Thr Phe Glu Thr
420 425 430

His Cys Gly Ser Leu Ser Gln Tyr Gly Met Lys His Met Arg Thr Val
435 440 445

Ala Asn Ile Cys Asn Ala Gly Ile Thr Lys Glu Gln Met Ala Glu Ala
450 455 460

Ala Ala Gln Ala Cys Val Ser Val Pro Ser Asn Pro Trp Ser Ser Leu
465 470 475 480

Ser Gly Gly Phe Ser Ala
485

<210> 10
<211> 483
<212> PRT
<213> Phaseolus vulgaris

<400> 10

Met Asp Gly Phe Pro Ile Leu Phe Leu Leu Ala Thr Leu Ile Thr Leu
1 5 10 15

Val Ser Gly Gly Arg Asp Glu Ile Leu Arg Leu Pro Ser Glu Ala Ser
20 25 30

Arg Phe Phe Gln Ala Pro Ala Ala Asp Gln Asn Gln Glu Gly Thr Arg
35 40 45

Trp Ala Leu Leu Ile Ala Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His
50 55 60

Gln Ser Asp Val Cys His Ala Tyr Gln Leu Leu Arg Lys Gly Gly Leu
65 70 75 80

Lys Glu Glu Asn Ile Val Val Phe Met Tyr Asp Asp Ile Ala Phe Asn
85 90 95

Glu Glu Asn Pro Arg Pro Gly Val Ile Ile Asn Ser Pro His Gly Asn
100 105 110

Asp Val Tyr Lys Gly Val Pro Lys Asp Tyr Val Gly Glu Asp Val Thr
115 120 125

Val Asn Asn Phe Phe Ala Ala Ile Leu Gly Asn Lys Ser Ala Leu Thr
130 135 140

Gly Gly Ser Gly Lys Val Ile Asp Ser Gly Pro Asn Asp His Ile Phe
145 150 155 160

Ile Tyr Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Met Pro Thr
165 170 175

Ser Pro Tyr Met Tyr Ala Ser Asp Leu Ile Glu Val Leu Lys Lys Lys

180

185

190

His Ala Ser Glu Thr Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys
 195 200 205

Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Glu Gly Met Asn Ile
 210 215 220

Tyr Ala Thr Thr Ala Ala Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr
 225 230 235 240

Cys Pro Gly Glu Tyr Pro Ser Pro Pro Pro Glu Tyr Glu Thr Cys Leu
 245 250 255

Gly Asp Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Ile His Asn
 260 265 270

Leu Gln Thr Glu Thr Leu His Gln Gln Phe Glu Leu Val Lys Gln Arg
 275 280 285

Thr Ile Asn Gly Asn Ser Ala Tyr Gly Ser His Val Met Gln Tyr Gly
 290 295 300

Asp Ile Gly Leu Ser Lys Asn Asn Leu Ser Leu Tyr Leu Gly Thr Asn
 305 310 315 320

Pro Ala Asn Asp Asn Phe Ala Phe Arg Glu Lys Asn Ser Leu Val Pro
 325 330 335

Pro Ser Lys Ala Val Asn Gln Arg Asp Ala Asp Leu Val His Leu Trp
 340 345 350

Asp Lys Tyr Arg Lys Ala Pro Val Gly Ser Ser Arg Lys Ser Val Ala
 355 360 365

Gln Lys Gln Ile Leu Glu Ala Met Ser His Arg Met His Ile Asp Asp
 370 375 380

Ser Met Lys Leu Ile Gly Lys Leu Leu Phe Gly Ile Glu Glu Gly Pro
 385 390 395 400

Lys Leu Leu Asn Ser Val Arg Pro Ala Gly Gln Pro Leu Val Asp Asp
405 410 415

Trp Asp Cys Leu Lys Thr Leu Val Arg Thr Phe Glu Thr His Cys Gly
420 425 430

Ser Leu Ser Gln Tyr Gly Met Lys His Met Arg Ser Phe Ala Asn Phe
435 440 445

Cys Asn Ala Gly Ile Gly Lys Glu Gln Met Ala Glu Ala Ser Ala Gln
450 455 460

Ala Cys Val Ser Ile Pro Ala Thr Pro Trp Ser Ser Leu Arg Ser Gly
465 470 475 480

Phe Ser Ala

<210> 11
<211> 484
<212> PRT
<213> Glycine max

<400> 11

Met Asp Arg Phe Pro Ile Leu Phe Leu Val Ala Thr Leu Ile Thr Leu
1 5 10 15

Ala Ser Gly Ala Arg His Asp Ile Leu Arg Leu Pro Ser Glu Ala Ser
20 25 30

Arg Phe Phe Lys Ala Pro Ala Asn Ala Asp Gln Asn Asp Glu Gly Thr
35 40 45

Arg Trp Ala Val Leu Val Ala Gly Ser Asn Gly Tyr Trp Asn Tyr Arg
50 55 60

His Gln Ser Asp Val Cys His Ala Tyr Gln Leu Leu Arg Lys Gly Gly
65 70 75 80

Val Lys Glu Glu Asn Ile Val Val Phe Met Tyr Asp Asp Ile Ala Phe
85 90 95

Asn Glu Glu Asn Pro Arg Pro Gly Val Ile Ile Asn Ser Pro His Gly
100 105 110

Asn Asp Val Tyr Lys Gly Val Pro Lys Asp Tyr Val Gly Glu Asp Val
115 120 125

Thr Val Asp Asn Phe Phe Ala Ala Ile Leu Gly Asn Lys Ser Ala Leu
130 135 140

Thr Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro Asn Asp His Ile
145 150 155 160

Phe Ile Tyr Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Met Pro
165 170 175

Thr Asn Pro Tyr Met Tyr Ala Ser Asp Leu Ile Glu Val Leu Lys Lys
180 185 190

Lys His Ala Ser Gly Thr Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala
195 200 205

Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Glu Gly Leu Asn
210 215 220

Ile Tyr Ala Thr Thr Ala Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr
225 230 235 240

Tyr Cys Pro Gly Glu Tyr Pro Ser Pro Pro Pro Glu Tyr Glu Thr Cys
245 250 255

Leu Gly Asp Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Ile His
260 265 270

Asn Leu Arg Thr Glu Thr Leu His Gln Gln Tyr Asp Leu Val Lys Glu
275 280 285

Arg Thr Met Asn Gly Asn Ser Ile Tyr Gly Ser His Val Met Gln Tyr
290 295 300

Gly Asp Ile Gly Leu Ser Lys Asn Asn Leu Val Leu Tyr Leu Gly Thr
305 310 315 320

Asn Pro Ala Asn Asp Asn Phe Thr Phe Val His Lys Asn Ser Leu Val
325 330 335

Pro Pro Ser Lys Ala Val Asn Gln Arg Asp Ala Asp Leu Ile His Phe
340 345 350

Trp Asp Lys Phe Arg Lys Ala Pro Val Gly Ser Ser Arg Lys Ala Ala
355 360 365

Ala Glu Lys Glu Ile Leu Glu Ala Met Ser His Arg Met His Ile Asp
370 375 380

Asp Asn Met Lys Leu Ile Gly Lys Leu Leu Phe Gly Ile Glu Lys Gly
385 390 395 400

Pro Glu Leu Leu Ser Ser Val Arg Pro Ala Gly Gln Pro Leu Val Asp
405 410 415

Asp Trp Asp Cys Leu Lys Thr Leu Val Arg Thr Phe Glu Thr His Cys
420 425 430

Gly Ser Leu Ser Gln Tyr Gly Met Lys His Met Arg Ser Phe Ala Asn
435 440 445

Phe Cys Asn Ala Gly Ile Arg Lys Glu Gln Met Ala Glu Ala Ser Ala
450 455 460

Gln Ala Cys Val Ser Ile Pro Ala Ser Ser Trp Ser Ser Leu His Arg
465 470 475 480

Gly Phe Ser Ala

<210> 12

<211> 483

<212> PRT

<213> Homo sapiens

<400> 12

Met Asp Arg Phe Pro Ile Leu Phe Leu Leu Ala Thr Leu Ile Thr Leu
1 5 10 15

Ala Ser Gly Ala Arg His Asp Ile Leu Arg Leu Pro Ser Glu Ala Ser
20 25 30

Thr Phe Phe Lys Ala Pro Gly Gly Asp Gln Asn Asp Glu Gly Thr Arg
35 40 45

Trp Ala Val Leu Ile Ala Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His
50 55 60

Gln Ser Asp Val Cys His Ala Tyr Gln Leu Leu Arg Lys Gly Gly Leu
65 70 75 80

Lys Glu Glu Asn Ile Val Val Phe Met Tyr Asp Asp Ile Ala Phe Asn
85 90 95

Glu Glu Asn Pro Arg Pro Gly Val Ile Ile Asn Ser Pro His Gly Asn
100 105 110

Asp Val Tyr Lys Gly Val Pro Lys Asp Tyr Ile Gly Glu Asp Val Thr
115 120 125

Val Gly Asn Phe Phe Ala Ala Ile Leu Gly Asn Lys Ser Ala Leu Thr
130 135 140

Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro Asn Asp His Ile Phe
145 150 155 160

Ile Tyr Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Met Pro Thr
165 170 175

Asn Pro Tyr Val Tyr Ala Ser Asp Leu Ile Glu Val Leu Lys Lys Lys
180 185 190

His Ala Ser Gly Ser Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys
195 200 205

Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Glu Gly Leu Asn Ile

210

215

220

Tyr Ala Thr Thr Ala Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr
 225 230 235 240

Cys Pro Gly Glu Tyr Pro Ser Pro Pro Ser Glu Tyr Glu Thr Cys Leu
 245 250 255

Gly Asp Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Ile His Asn
 260 265 270

Leu Gln Thr Glu Thr Leu His Gln Gln Tyr Glu Leu Val Lys Gln Arg
 275 280 285

Thr Met Asn Gly Asn Ser Ile Tyr Gly Ser His Val Met Gln Tyr Gly
 290 295 300

Asp Ile Gly Leu Ser Glu Asn Asn Leu Val Leu Tyr Leu Gly Thr Asn
 305 310 315 320

Pro Ala Asn Asp Asn Phe Thr Phe Val Leu Lys Asn Ser Leu Val Pro
 325 330 335

Pro Ser Lys Ala Val Asn Gln Arg Asp Ala Asp Leu Ile His Phe Trp
 340 345 350

Asp Lys Phe Arg Lys Ala Pro Val Gly Ser Ser Arg Lys Ala Ala Ala
 355 360 365

Glu Lys Gln Ile Leu Glu Ala Met Ser His Arg Met His Ile Asp Asp
 370 375 380

Ser Met Lys Arg Ile Gly Lys Leu Phe Phe Gly Ile Glu Lys Gly Pro
 385 390 395 400

Glu Leu Leu Ser Ser Val Arg Pro Ala Gly Gln Pro Leu Val Asp Asp
 405 410 415

Trp Asp Cys Leu Lys Thr Leu Val Arg Thr Phe Glu Thr His Cys Gly
 420 425 430

Ser Leu Ser Gln Tyr Gly Met Lys His Met Arg Ser Phe Ala Asn Phe
435 440 445

Cys Asn Ala Gly Ile Arg Lys Glu Gln Met Ala Glu Ala Ser Ala Gln
450 455 460

Ala Cys Val Asn Ile Pro Ala Ser Ser Trp Ser Ser Met His Arg Gly
465 470 475 480

Phe Ser Ala

<210> 13
<211> 483
<212> PRT
<213> Vigna mungo

<400> 13

Met Asn Arg Phe Pro Ile Ile Phe Val Val Ala Asn Leu Ile Thr Leu
1 5 10 15

Val Ser Gly Gly Arg Asp Glu Ile Leu Arg Met Pro Ser Glu Ala Ser
20 25 30

Arg Phe Phe Gln Ala Pro Ala Thr Asp Glu Asn Asp Glu Gly Thr Arg
35 40 45

Trp Ala Val Leu Ile Ala Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His
50 55 60

Gln Ser Asp Val Cys His Ala Tyr Gln Leu Leu Thr Lys Gly Gly Leu
65 70 75 80

Lys Glu Glu Asn Ile Val Val Phe Met Tyr Asp Asp Ile Ala Phe Asn
85 90 95

Glu Glu Asn Pro Arg Pro Gly Val Ile Ile Asn Ser Pro His Gly Asn
100 105 110

Asp Val Tyr Lys Gly Val Pro Lys Asp Tyr Val Gly Glu Asp Val Thr
115 120 125

Val Asn Asn Phe Phe Ala Ala Ile Leu Gly Asn Lys Ser Ala Leu Thr
130 135 140

Gly Gly Ser Gly Lys Val Val Asn Ser Gly Pro Asn Asp His Ile Phe
145 150 155 160

Ile Tyr Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Met Pro Thr
165 170 175

Ser Pro Tyr Met Tyr Ala Ser Asp Leu Ile Glu Val Leu Lys Lys Lys
180 185 190

His Ala Ser Gly Thr Tyr Lys Ser Leu Ala Phe Tyr Leu Glu Gly Cys
195 200 205

Glu Ser Gly Ser Ile Phe Gly Gly Leu Leu Pro Glu Gly Leu Asn Ile
210 215 220

Tyr Ala Thr Thr Ala Ala Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr
225 230 235 240

Cys Pro Gly Asp Asn Pro Ser Pro Pro Pro Glu Tyr Glu Thr Cys Leu
245 250 255

Gly Asp Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Ile His Asn
260 265 270

Leu Arg Thr Glu Thr Leu His Gln Gln Phe Glu Leu Val Lys Gln Arg
275 280 285

Thr Met Asn Gly Asn Ser Ala Tyr Gly Ser His Val Met Gln Tyr Gly
290 295 300

Asp Val Gly Leu Ser Lys Asn Asn Val Ser Leu Tyr Leu Gly Thr Asn
305 310 315 320

Pro Ala Asn Asp Asn Phe Pro Phe Arg Glu Lys Asn Ser Leu Val Pro
325 330 335

Pro Ser Lys Ala Val Asn Gln Arg Asp Ala Asp Leu Val His Phe Trp
340 345 350

Asp Lys Phe Pro Lys Ala Pro Leu Gly Ser Ser Arg Lys Ser Val Ala
355 360 365

Gln Lys Gln Ile Leu Glu Ala Met Ser His Arg Met His Ile Asp Asp
370 375 380

Ser Val Thr Leu Ile Gly Lys Leu Leu Phe Gly Ile Glu Glu Gly Pro
385 390 395 400

Glu Leu Leu Ser Ser Val Arg Pro Ala Gly Gln Pro Leu Val Asp Asp
405 410 415

Trp Asp Cys Leu Lys Thr Leu Val Arg Thr Phe Glu Thr His Cys Gly
420 425 430

Ser Leu Ser Gln Tyr Gly Met Lys His Met Arg Ser Phe Ala Asn Leu
435 440 445

Cys Asn Ala Gly Ile Arg Lys Glu Gln Met Ala Glu Ala Ser Ala Gln
450 455 460

Ala Cys Val Ser Ile Pro Ala Thr Pro Trp Ser Ser Leu Ser Ser Gly
465 470 475 480

Phe Ser Ala

<210> 14

<211> 488

<212> PRT

<213> Cicer arietinum

<400> 14

Met Tyr Arg Phe Pro Thr Pro Thr Leu Leu Phe Leu Ile Val Thr Leu
1 5 10 15

Ile Ala Leu Val Ser Ser Asn Pro Glu Asp Phe Leu Arg Leu Pro Ser
20 25 30

Glu Ser Ser Arg Phe Phe His Ser Pro Ser Ala Asp Asp Lys Glu Asn
35 40 45

Asn Glu Gly Thr Arg Trp Ala Ile Leu Ile Ala Gly Ser Asn Gly Tyr
50 55 60

Trp Asn Tyr Arg His Gln Ser Asp Val Cys His Ala Tyr Gln Val Leu
65 70 75 80

Arg Lys Gly Gly Leu Lys Glu Glu Asn Ile Val Val Phe Met Tyr Asp
85 90 95

Asp Ile Ala Phe Asn Glu Glu Asn Pro Arg Pro Gly Val Ile Ile Asn
100 105 110

Ser Pro His Gly Asp Asp Val Tyr Lys Gly Val Pro Lys Asp Tyr Thr
115 120 125

Gly Glu Asp Val Asn Val Asp Asn Phe Phe Ala Ala Leu Leu Gly Asn
130 135 140

Lys Ser Ala Leu Thr Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro
145 150 155 160

Asn Asp His Ile Phe Ile Tyr Tyr Ser Asp His Gly Gly Pro Gly Val
165 170 175

Leu Gly Met Pro Thr Ser Pro Tyr Met Tyr Ala Ser Asp Leu Ile Glu
180 185 190

Val Leu Lys Lys Lys His Ala Ser Gly Thr Tyr Lys Ser Leu Val Phe
195 200 205

Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro
210 215 220

Glu Gly Leu Asn Ile Tyr Ala Thr Thr Ala Ala Asn Ala Asp Glu Ser
225 230 235 240

Ser Trp Gly Thr Tyr Cys Pro Gly Glu Phe Pro Ser Pro Pro Pro Glu

245

250

255

Tyr Glu Thr Cys Leu Gly Asp Leu Tyr Ser Val Ala Trp Met Glu Asp
 260 265 270

Ser Asp Met His Asn Leu Gln Ser Glu Thr Leu His Gln Gln Tyr Glu
 275 280 285

Leu Val Lys Glu Arg Thr Lys Asn Gly Asn Thr Leu Tyr Gly Ser His
 290 295 300

Val Met Gln Tyr Gly Asp Ile Gly Leu Ser Glu Asn Ser Leu Phe Leu
 305 310 315 320

Tyr Leu Gly Thr Asn Pro Ala Asn Glu Asn Phe Thr Phe Val Gly Arg
 325 330 335

Asn Ser Leu Val Pro Pro Ser Lys Ala Val Asn Gln Arg Asp Ala Asp
 340 345 350

Leu Val His Phe Trp Asp Lys Phe Arg Lys Ala Pro Gln Gly Ser Pro
 355 360 365

Arg Lys Ala Ala Ala Glu Lys Gln Val Leu Glu Ala Met Ser His Arg
 370 375 380

Met His Ile Asp Asp Ser Ile Lys Leu Val Gly Lys Leu Leu Phe Gly
 385 390 395 400

Met Glu Lys Gly Pro Glu Val Leu Thr Ser Val Arg Pro Ala Gly Gln
 405 410 415

Pro Leu Ala Asp Asp Trp Asn Cys Leu Lys Thr Leu Val Arg Thr Phe
 420 425 430

Glu Thr Tyr Cys Gly Ser Leu Ser Gln Tyr Gly Met Lys His Met Arg
 435 440 445

Ser Phe Ala Asn Phe Cys Asn Ala Gly Ile His Lys Glu Gln Met Ala
 450 455 460

Glu Ala Ser Ala Gln Ala Cys Val Asn Val Pro Ala Asn Pro Trp Ser
465 470 475 480

Ser Leu Arg Ser Gly Phe Ser Ala
485

<210> 15
<211> 492
<212> PRT
<213> Ricinus communis

<400> 15

Met Thr Ile Arg Leu Ser Thr Gly Ile Ile Leu Ile Leu Leu Thr Leu
1 5 10 15

Cys Gly Val Val Ser Ser Ser Arg Asp Ile Val Gly Asp Val Ile Arg
20 25 30

Leu Pro Ser Glu Ala Ser Arg Phe Phe Arg Pro Ala Asp Gly Lys Asn
35 40 45

Gly Asp Asp Asp Ser Ala Gly Thr Arg Trp Ala Ile Leu Ile Ala Gly
50 55 60

Ser Asn Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp Val Cys His Ala
65 70 75 80

Tyr Gln Leu Leu Arg Lys Gly Gly Leu Lys Glu Glu Asn Ile Ile Val
85 90 95

Phe Met Tyr Asp Asp Ile Ala Tyr Asn Glu Glu Asn Pro Arg Gln Gly
100 105 110

Ile Ile Ile Asn Asn Pro His Gly Glu Asp Val Tyr Lys Gly Val Pro
115 120 125

Lys Asp Tyr Thr Gly Glu Asn Val Thr Val Gly Asn Phe Phe Ala Ala
130 135 140

Ile Leu Gly Asn Arg Thr Ala Leu Thr Gly Gly Arg Gly Lys Val Val
145 150 155 160

Asp Ser Gly Pro Asn Asp His Ile Phe Val Tyr Tyr Thr Asp His Gly
165 170 175

Gly Pro Gly Val Leu Gly Met Pro Thr Asn Pro Tyr Leu Tyr Ala Asn
180 185 190

Asp Leu Ile Asp Val Leu Lys Lys Lys His Ala Ser Gly Thr Tyr Lys
195 200 205

Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu
210 215 220

Gly Leu Leu Pro Glu Gly Leu Asn Ile Tyr Ala Thr Thr Ala Ser Asn
225 230 235 240

Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Tyr Pro Ser
245 250 255

Pro Pro Pro Glu Tyr Glu Thr Cys Leu Gly Asp Leu Tyr Ser Ile Ala
260 265 270

Trp Met Glu Asp Ser Asp Val His Asn Leu Gln Thr Glu Thr Leu His
275 280 285

Gln Gln Tyr Glu Leu Val Lys Arg Arg Thr Ser Asn Gly Asn Ser Ala
290 295 300

Tyr Gly Ser His Val Met Gln Tyr Gly Asp Val Gly Leu Ser Arg Glu
305 310 315 320

Asn Leu Phe Leu Tyr Met Gly Thr Asn Pro Ala Asn Asp Asn Tyr Thr
325 330 335

Phe Val Asp Glu Asn Ser Leu Thr Pro Pro Ser Lys Ala Val Asn Gln
340 345 350

Arg Asp Ala Asp Leu Val His Phe Trp Asp Lys Tyr Arg Lys Ala Pro
355 360 365

Asp Gly Ser Ala Arg Lys Asp Gln Ala Gln Lys Gln Phe Val Glu Ala
370 375 380

Met Ser His Arg Met His Ile Asp His Ser Val Lys Leu Ile Gly Lys
385 390 395 400

Leu Leu Phe Gly Leu Glu Lys Ala Ser Glu Val Leu Ser Thr Val Arg
405 410 415

Pro Ala Gly Gln Pro Leu Val Asp Asp Trp Asp Cys Leu Lys Lys Leu
420 425 430

Val Arg Thr Phe Glu Thr His Cys Gly Ser Ile Ser Gln Tyr Gly Met
435 440 445

Lys His Met Arg Ser Leu Ala Asn Leu Cys Asn Ala Gly Ile Arg Glu
450 455 460

Glu Gln Met Ala Glu Ala Ser Ala Gln Ala Cys Ile Thr Phe Pro Ser
465 470 475 480

Gly Pro Trp Ser Ser Leu His Lys Gly Phe Ser Ala
485 490

<210> 16

<211> 487

<212> PRT

<213> Theobroma cacao

<400> 16

Met Thr Arg Leu Val Ser Gly Val Ile Leu Leu Leu Leu Ser Leu Thr
1 5 10 15

Gly Ile Val Ser Ala Gly Arg Asp Ile Thr Gly Asp Val Leu Arg Leu
20 25 30

Pro Ser Glu Ala Ser Lys Phe Phe Arg Gly Ser Asn Asp Asp Glu Val
35 40 45

Glu Gly Thr Arg Trp Ala Val Leu Ile Ala Gly Ser Asn Gly Tyr Trp
50 55 60

Asn Tyr Arg His Gln Ala Asp Val Cys His Ala Tyr Gln Leu Leu Lys
65 70 75 80

Lys Gly Gly Leu Lys Asp Glu Asn Ile Ile Val Phe Met Tyr Asp Asp
85 90 95

Ile Ala Phe Asn Glu Glu Asn Pro Arg Pro Gly Ile Ile Ile Asn Ser
100 105 110

Pro His Gly Asp Asp Val Tyr Glu Gly Val Pro Lys Asp Tyr Thr Gly
115 120 125

Glu Asp Val Thr Val Asn Asn Leu Leu Ala Ala Ile Leu Gly Asn Lys
130 135 140

Thr Ala Leu Thr Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro Asn
145 150 155 160

Asp His Ile Phe Ile Tyr Tyr Thr Asp His Gly Gly Pro Gly Val Leu
165 170 175

Gly Met Pro Thr Phe Pro Tyr Leu Tyr Ala Asp Asp Leu Ile Glu Val
180 185 190

Leu Lys Lys Lys His Ala Ser Gly Thr Tyr Lys Ser Leu Val Phe Tyr
195 200 205

Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Glu
210 215 220

Gly Leu Asn Ile Tyr Ala Thr Thr Ala Ser Asn Ala Glu Glu Ser Ser
225 230 235 240

Trp Gly Thr Tyr Cys Pro Gly Glu Tyr Pro Ser Pro Pro Pro Glu Tyr
245 250 255

Glu Thr Cys Leu Gly Asp Leu Tyr Ser Val Ala Trp Met Glu Asp Ser
260 265 270

Asp Ile His Asn Leu Gln Thr Glu Thr Leu His Gln Gln Tyr Glu Leu

275

280

285

Val Lys Arg Arg Thr Ile Asn Gly Asn Ser Ala Tyr Gly Ser His Val
 290 295 300

Met Gln Tyr Gly Asp Ile Gly Leu Ser Lys Asp Ile Val Phe Val Tyr
 305 310 315 320

Leu Gly Thr Asn Pro Ala Asn Asp Asn Phe Thr Phe Val Asp Glu Asn
 325 330 335

Ser Leu Gln Pro Pro Thr Lys Ala Val Asn Gln Arg Asp Ala Asp Leu
 340 345 350

Val His Phe Trp Asp Lys Tyr Arg Lys Ala Pro Asp Gly Ser Val Arg
 355 360 365

Lys Leu Glu Ala Gln Lys Gln Phe Val Glu Ala Met Ser His Arg Met
 370 375 380

His Ile Asp Asn Ser Met Lys Leu Ile Gly Lys Leu Leu Phe Gly Ile
 385 390 395 400

Glu Lys Gly Pro Glu Val Met Lys Thr Val Arg Pro Ala Gly Gln Pro
 405 410 415

Leu Val Asp Asp Trp Lys Cys Leu Lys Lys Met Val Arg Thr Phe Glu
 420 425 430

Thr His Cys Gly Ser Leu Ala Gln Tyr Gly Met Lys His Met Arg Ser
 435 440 445

Leu Ala Asn Ile Cys Asn Ala Gly Ile Gln Thr Glu Gln Met Ala Glu
 450 455 460

Ala Ser Ala Gln Ala Cys Val Ser Ile Pro Ser Gly His Trp Ser Ser
 465 470 475 480

Val Gln Lys Gly Phe Ser Ala
 485

<210> 17
<211> 484
<212> PRT
<213> *Medicago truncatula*

<400> 17

Met Ala Arg Phe Leu Phe Leu Ile Ile Ala Thr Leu Ile Pro Ile Phe
1 5 10 15

Ser Ala Ala Thr Ala Thr Ala Gly Asp Asp Phe Leu Arg Leu Pro Ser
20 25 30

Gln Ala Ser Arg Phe Phe Gln Ser Asp Asp Asp Asn Asn Glu Gly Thr
35 40 45

Lys Trp Ala Ile Leu Ile Ala Gly Ser Asn Gly Tyr Trp Asn Tyr Arg
50 55 60

His Gln Ser Asp Val Cys His Ala Tyr Gln Val Leu Arg Lys Gly Gly
65 70 75 80

Leu Lys Glu Glu Asn Ile Ile Val Phe Met Tyr Asp Asp Ile Ala Asp
85 90 95

Asn Gln Glu Asn Pro Arg Pro Gly Val Ile Ile Asn Ser Pro His Gly
100 105 110

Asp Asp Val Tyr Lys Gly Val Pro Lys Asp Tyr Thr Gly Asp Asp Val
115 120 125

Asn Val Asn Asn Phe Phe Ala Ala Leu Leu Gly Asn Lys Ser Ala Leu
130 135 140

Thr Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro Asn Asp His Ile
145 150 155 160

Phe Ile Tyr Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Met Pro
165 170 175

Thr Gly Pro Phe Met Tyr Ala Thr Asp Leu Ile Glu Val Leu Lys Lys
180 185 190

Lys His Ala Ser Glu Thr Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala
195 200 205

Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Glu Gly Leu Asn
210 215 220

Ile Tyr Ala Thr Thr Ala Ala Asn Ala Glu Glu Ser Ser Trp Gly Thr
225 230 235 240

Tyr Cys Pro Gly Glu Asn Pro Ser Pro Pro Pro Glu Tyr Glu Thr Cys
245 250 255

Leu Gly Asp Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Ile His
260 265 270

Asn Leu Gln Thr Glu Thr Leu His Gln Gln Tyr Glu Leu Val Lys Glu
275 280 285

Arg Thr Ser Asn Gly Asn Ser Ile Tyr Gly Ser His Val Met Gln Phe
290 295 300

Gly Asp Ile Gly Leu Ser Arg Asp Ser Leu Phe Leu Tyr Leu Gly Ser
305 310 315 320

Asn Pro Ala Asn Glu Asn Phe Thr Phe Met Gly Arg Asn Ser Leu Val
325 330 335

Pro Pro Ser Lys Thr Val Asn Gln Arg Asp Ala Asp Leu Ile His Phe
340 345 350

Trp Asp Lys Phe Arg Lys Ala Pro Gln Gly Ser Pro Arg Lys Val Ala
355 360 365

Ala Gln Lys Gln Val Leu Glu Ala Met Ser His Arg Met His Ile Asp
370 375 380

Glu Ser Ile Lys Leu Val Gly Lys Leu Leu Phe Gly Met Lys Lys Gly
385 390 395 400

Pro Glu Val Leu Ala Ser Val Arg Pro Ala Gly Gln Pro Val Val Asp
405 410 415

Asp Trp Asp Cys Leu Lys Ser Leu Val Arg Thr Phe Glu Thr Tyr Cys
420 425 430

Gly Ser Leu Ser Gln Tyr Gly Met Lys His Met Arg Ser Phe Ala Asn
435 440 445

Phe Cys Asn Ala Gly Ile His Ser Glu Gln Met Ala Glu Ala Ser Ala
450 455 460

Gln Ala Cys Ile Asn Ile Pro Ala Asn Pro Trp Ser Ser Leu His Gly
465 470 475 480

Gly Phe Ser Ala

<210> 18
<211> 493
<212> PRT
<213> Populus tomentosa

<400> 18

Met Thr Arg Leu Ile Ala Gly Val Ile Phe Leu Leu Ile Ala Phe Cys
1 5 10 15

Gly Ile Ala Val Gly Val Arg Asp Ile Val Gly Asp Val Leu Arg Leu
20 25 30

Pro Ser Glu Ala Ser Arg Phe Phe Arg Ser Gly Lys Phe Asn Asp Asp
35 40 45

Asn Ser Asp Asp Asp Ser Ser Gly Thr Arg Trp Ala Ile Leu Leu Ala
50 55 60

Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp Val Cys His
65 70 75 80

Ala Tyr Gln Leu Leu Arg Lys Gly Gly Leu Lys Glu Glu Asn Ile Ile
85 90 95

Val Phe Met Tyr Asp Asp Ile Ala Asp Asn Pro Glu Asn Pro Arg Pro
100 105 110

Gly Val Ile Ile Asn Asn Pro Gln Gly Glu Asp Val Tyr Glu Gly Val
115 120 125

Pro Lys Asp Tyr Thr Gly Gln Asp Val Thr Val Gly Asn Phe Phe Ala
130 135 140

Ala Ile Leu Gly Asn Lys Thr Ala Leu Thr Gly Gly Ser Gly Lys Val
145 150 155 160

Val Asp Ser Gly Pro Asn Asp His Ile Phe Ile Tyr Tyr Thr Asp His
165 170 175

Gly Gly Pro Gly Val Leu Gly Met Pro Thr Asn Pro Tyr Leu Tyr Ala
180 185 190

Asp Asp Leu Ile Asp Val Leu Lys Lys Lys His Ala Ser Gly Thr Tyr
195 200 205

Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe
210 215 220

Glu Gly Leu Leu Pro Gln Gly Leu Asn Ile Tyr Ala Thr Thr Ala Ser
225 230 235 240

Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Tyr Pro
245 250 255

Ser Pro Pro Pro Glu Tyr Glu Thr Cys Leu Gly Asp Leu Tyr Ser Val
260 265 270

Ala Trp Met Glu Asp Ser Asp Ile His Asn Leu Arg Thr Glu Thr Leu
275 280 285

His Gln Gln Tyr Glu Leu Val Lys Arg Arg Thr Ser Asp Glu Asn Ser
290 295 300

Ala Tyr Gly Ser His Val Met Gln Tyr Gly Asp Val Gly Leu Ser Lys

305		310		315		320									
Glu	Asp	Leu	Phe	Gln	Tyr	Met	Gly	Thr	Asn	Pro	Ala	Asn	Asp	Asn	Phe
				325					330					335	
Thr	Phe	Leu	Glu	Asp	Asn	Ser	Leu	Arg	Pro	Pro	Ser	Lys	Ala	Val	Asn
			340					345					350		
Gln	Arg	Asp	Ala	Asp	Leu	Val	His	Phe	Trp	Ala	Lys	Tyr	Arg	Lys	Ala
		355					360					365			
Pro	Glu	Gly	Ser	Ser	Arg	Lys	Val	Glu	Ala	Gln	Lys	Gln	Phe	Val	Glu
	370					375					380				
Ala	Met	Ser	His	Arg	Met	His	Ile	Asp	His	Ser	Ile	Lys	Leu	Ile	Gly
385					390					395					400
Lys	Leu	Leu	Phe	Gly	Ile	Glu	Lys	Ala	Ser	Glu	Val	Leu	Asn	Asn	Val
				405					410					415	
Arg	Pro	Ala	Gly	Gln	Pro	Leu	Val	Asp	Asp	Trp	Val	Cys	Leu	Lys	Thr
			420					425					430		
Leu	Val	Arg	Thr	Phe	Glu	Thr	His	Cys	Gly	Ser	Ile	Ser	Gln	Tyr	Gly
		435					440					445			
Met	Lys	His	Met	Arg	Ser	Leu	Ala	Asn	Leu	Cys	Asn	Ala	Gly	Ile	Val
	450					455					460				
Lys	Glu	Gln	Met	Ala	Glu	Ala	Ser	Ala	Gln	Ala	Cys	Val	Ser	Ile	Pro
465					470				475						480
Ser	Gly	Ser	Trp	Ser	Ser	Leu	His	Lys	Gly	Phe	Ser	Ala			
				485					490						

<210> 19
 <211> 489
 <212> PRT
 <213> Populus trichocarpa
 <400> 19

Met Thr Gly Leu Ala Thr Gly Ala Ile Phe Leu Leu Ile Ser Leu Cys
1 5 10 15

Gly Ile Ala Ala Ala Gly Arg Asp Thr Val Gly Asp Val Leu Arg Leu
20 25 30

Pro Ser Glu Ala Ser Arg Phe Phe His Asn Asp Asp Asn Ser Asp Asp
35 40 45

Asp Ser Thr Gly Thr Arg Trp Ala Ile Leu Leu Ala Gly Ser Asn Gly
50 55 60

Tyr Trp Asn Tyr Arg His Gln Ala Asp Val Cys His Ala Tyr Gln Leu
65 70 75 80

Leu Arg Lys Gly Gly Leu Lys Glu Glu Asn Ile Ile Val Phe Met Tyr
85 90 95

Asp Asp Ile Ala Tyr Asn Ser Glu Asn Pro Arg Arg Gly Val Ile Ile
100 105 110

Asn Ser Pro Gln Gly Glu Asp Val Tyr Lys Gly Val Pro Lys Asp Tyr
115 120 125

Thr Gly Glu Asp Val Thr Val Gly Asn Phe Phe Ala Ala Ile Leu Gly
130 135 140

Asn Lys Thr Ala Leu Thr Gly Gly Ser Gly Lys Val Val Asp Ser Gly
145 150 155 160

Pro Asn Asp His Ile Phe Ile Tyr Tyr Thr Asp His Gly Gly Pro Gly
165 170 175

Val Leu Gly Met Pro Thr Asn Pro Tyr Leu Tyr Ala Asp Asp Leu Ile
180 185 190

Asp Val Leu Lys Lys Lys His Ala Ser Gly Thr Tyr Lys Ser Leu Val
195 200 205

Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu
210 215 220

Pro Gln Gly Leu Asn Ile Tyr Ala Thr Thr Ala Ser Asn Ala Glu Glu
225 230 235 240

Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Asn Pro Ser Pro Pro Pro
245 250 255

Glu Tyr Glu Thr Cys Leu Gly Asp Leu Tyr Ser Val Ala Trp Met Glu
260 265 270

Asp Ser Asp Ile His Asn Leu Gln Thr Glu Thr Leu His Gln Gln Tyr
275 280 285

Glu Leu Val Lys Arg Arg Thr Ser Asn Asp Asn Ser Pro Tyr Gly Ser
290 295 300

His Val Met Gln Tyr Gly Asp Val Gly Leu Ser Lys Asp Asn Ile Phe
305 310 315 320

Leu Tyr Met Gly Thr Asn Pro Ala Asn Asp Asn Phe Thr Phe Met Asp
325 330 335

Glu Asn Leu Leu Arg Pro Arg Ser Lys Ala Val Asn Gln Arg Asp Ala
340 345 350

Asp Leu Val His Phe Trp Asp Lys Tyr Arg Lys Ala Pro Glu Gly Ser
355 360 365

Ser Arg Lys Val Glu Ala Gln Lys Gln Phe Val Glu Ala Met Ser His
370 375 380

Arg Met His Ile Asp His Ser Ile Lys Leu Ile Gly Lys Leu Leu Phe
385 390 395 400

Gly Ile Glu Lys Ala Ser Glu Val Leu Asn Ala Ile Arg Pro Ala Gly
405 410 415

Gln Pro Leu Val Asp Asp Trp Asp Cys Leu Lys Thr Leu Val Arg Thr
420 425 430

Phe Glu Thr His Cys Gly Ser Val Ser Gln Tyr Gly Met Lys His Met
435 440 445

Arg Ser Leu Ala Asn Leu Cys Asn Ala Gly Ile Gly Lys Glu Gln Met
450 455 460

Ala Glu Ala Ser Ala Gln Ala Cys Val Ser Phe Pro Ser Gly Pro Trp
465 470 475 480

Ser Thr Leu His Lys Gly Phe Ser Ala
485

<210> 20
<211> 494
<212> PRT
<213> Malus hupehensis var. mengshanensis

<220>
<221> MISC_FEATURE
<222> (264)..(264)
<223> Xaa can be any naturally occurring amino acid

<400> 20

Met Thr Arg Leu Ala Ser Ala Val Val Leu Leu Phe Leu Ala Ser Val
1 5 10 15

Leu Ala Ser Ala Ala Gly Ser Arg Asp Leu Ile Gly Asp Val Leu Arg
20 25 30

Leu Pro Ser Glu Ala Ser Arg Phe Phe Gly Arg Gly Asp Asp Ala Pro
35 40 45

Asp Gln Gln Asp Asp Gly Thr Val Gly Thr Arg Trp Ala Val Leu Ile
50 55 60

Ala Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp Ile Cys
65 70 75 80

His Ala Tyr Gln Leu Leu Lys Lys Gly Gly Leu Lys Asp Glu Asn Ile
85 90 95

Val Val Phe Met Tyr Asp Asp Ile Ala Tyr Asn Glu Glu Asn Pro Arg

100

105

110

Gln Gly Val Ile Ile Asn Ser Pro His Gly Ser Asp Val Tyr Glu Gly
 115 120 125

Val Pro Lys Asp Tyr Thr Gly Glu Asp Val Thr Val Asn Asn Phe Phe
 130 135 140

Ala Ala Ile Leu Gly Asn Lys Thr Ala Leu Thr Gly Gly Ser Gly Lys
 145 150 155 160

Val Val Asp Ser Gly Pro Asn Asp His Ile Phe Ile Tyr Tyr Thr Asp
 165 170 175

His Gly Gly Pro Gly Ile Leu Gly Met Pro Thr Ser Pro Tyr Ile Tyr
 180 185 190

Ala Asn Asp Leu Ile Glu Val Leu Lys Lys Lys His Ala Ala Gly Thr
 195 200 205

Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile
 210 215 220

Phe Glu Gly Leu Leu Pro Glu Gly Leu Asn Ile Phe Ala Thr Thr Ala
 225 230 235 240

Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Tyr
 245 250 255

Pro Ser Pro Pro Pro Glu Tyr Xaa Thr Cys Leu Gly Asp Leu Tyr Ser
 260 265 270

Val Val Trp Met Glu Asp Ser Asp Val His Asn Leu Arg Ser Glu Thr
 275 280 285

Leu His Gln Gln Tyr Glu Leu Val Lys Met Arg Thr Ala Asn Asp Asn
 290 295 300

Ser Gly Phe Gly Ser His Val Met Gln Tyr Gly Asp Val Gly Leu Ser
 305 310 315 320

Lys Asn Asn Leu Phe Val Tyr Met Gly Thr Asn Pro Ala Asn Asp Asn
325 330 335

Tyr Thr Phe Leu Gly Glu Asn Ser Leu Arg Pro Ser Ser Lys Ala Val
340 345 350

Asn Gln Arg Asp Ala Asp Leu Leu Arg Phe Trp His Lys Tyr Arg Lys
355 360 365

Ala Pro Glu Gly Ser Ala Arg Lys Ile Gln Ala Gln Lys Asp Phe Val
370 375 380

Glu Ala Met Ser His Arg Met His Ile Asp Gln Thr Met Lys Leu Ile
385 390 395 400

Gly Lys Leu Leu Phe Gly Ile Glu Lys Gly Pro Gln Val Leu Asn Ala
405 410 415

Val Arg Pro Ala Gly Gln Pro Leu Val Asp Asp Trp Asp Cys Leu Lys
420 425 430

Thr Met Val Arg Ser Phe Glu Thr His Cys Gly Ser Leu Ser Gln Tyr
435 440 445

Gly Met Lys His Met Arg Ser Leu Ala Asn Ile Cys Asn Ala Gly Met
450 455 460

Thr Gln Glu Gln Met Ala Glu Ala Ser Ala Gln Ala Cys Val Ser Ala
465 470 475 480

Pro Ser Gly Arg Trp Ser Ser Leu His Arg Gly Phe Ser Ala
485 490

<210> 21
<211> 480
<212> PRT
<213> Glycine max

<400> 21

Met Pro Thr Phe Phe Leu Pro Thr Leu Leu Leu Leu Ile Ala Phe
1 5 10 15

Ala Thr Ser Val Ser Gly Arg Arg Asp Leu Val Gly Asp Phe Leu Arg
20 25 30

Leu Pro Ser Glu Thr Asp Asn Asp Asp Asn Phe Lys Gly Thr Arg Trp
35 40 45

Ala Val Leu Leu Ala Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His Gln
50 55 60

Ala Asp Val Cys His Ala Tyr Gln Ile Leu Arg Lys Gly Gly Leu Lys
65 70 75 80

Glu Glu Asn Ile Ile Val Phe Met Tyr Asp Asp Ile Ala Phe Asn Gly
85 90 95

Glu Asn Pro Arg Pro Gly Val Ile Ile Asn Lys Pro Asp Gly Gly Asp
100 105 110

Val Tyr Lys Gly Val Pro Lys Asp Tyr Thr Gly Glu Asp Val Thr Val
115 120 125

Asp Asn Phe Phe Ala Ala Leu Leu Gly Asn Lys Ser Ala Leu Thr Gly
130 135 140

Gly Ser Gly Lys Val Val Asp Ser Gly Pro Asp Asp His Ile Phe Val
145 150 155 160

Tyr Tyr Thr Asp His Gly Gly Pro Gly Val Leu Gly Met Pro Ala Gly
165 170 175

Pro Tyr Leu Tyr Ala Asp Asp Leu Ile Glu Val Leu Lys Lys Lys His
180 185 190

Ala Ser Gly Thr Tyr Lys Asn Leu Val Phe Tyr Leu Glu Ala Cys Glu
195 200 205

Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Glu Asp Ile Asn Ile Tyr
210 215 220

Ala Thr Thr Ala Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys
225 230 235 240

Pro Gly Glu Tyr Pro Ser Pro Pro Pro Glu Tyr Thr Thr Cys Leu Gly
245 250 255

Asp Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Arg His Asn Leu
260 265 270

Arg Thr Glu Thr Leu His Gln Gln Tyr Lys Leu Val Lys Glu Arg Thr
275 280 285

Ile Ser Gly Asp Ser Tyr Tyr Gly Ser His Val Met Gln Tyr Gly Asp
290 295 300

Val Gly Leu Ser Arg Asp Val Leu Phe His Tyr Leu Gly Thr Asp Pro
305 310 315 320

Ala Asn Asp Asn Phe Thr Phe Val Asp Glu Asn Ser Leu Trp Ser Pro
325 330 335

Ser Lys Pro Val Asn Gln Arg Asp Ala Asp Leu Ile His Phe Trp Asp
340 345 350

Lys Phe Arg Lys Ala Pro Glu Gly Ser Leu Arg Lys Asn Thr Ala Gln
355 360 365

Lys Gln Val Leu Glu Ala Met Ser His Arg Met His Val Asp Asn Ser
370 375 380

Val Lys Leu Ile Gly Lys Leu Leu Phe Gly Ile Glu Lys Gly Pro Glu
385 390 395 400

Val Leu Asn Ala Val Arg Pro Ala Gly Ser Ala Leu Val Asp Asp Trp
405 410 415

His Cys Leu Lys Thr Met Val Arg Thr Phe Glu Thr His Cys Gly Ser
420 425 430

Leu Ser Gln Tyr Gly Met Lys His Met Arg Ser Phe Ala Asn Ile Cys
435 440 445

Asn Val Gly Ile Lys Asn Glu Gln Met Ala Glu Ala Ser Ala Gln Ala
450 455 460

Cys Val Ser Ile Pro Ser Asn Pro Trp Ser Ser Leu Gln Arg Gly Phe
465 470 475 480

<210> 22
<211> 481
<212> PRT
<213> Glycine max

<400> 22

Met Ala Thr Leu Leu Leu Pro Thr Leu Leu Leu Leu Ile Pro Phe Ala
1 5 10 15

Thr Leu Val Ser Ala Arg Pro His Leu Ala Gly Asp Phe Leu Arg Leu
20 25 30

Pro Ser Glu Thr Asp Asn Asp Asp Asn Val Gln Gly Thr Arg Trp Ala
35 40 45

Val Leu Leu Ala Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His Gln Ala
50 55 60

Asp Val Cys His Ala Tyr Gln Ile Leu Arg Lys Gly Gly Leu Lys Glu
65 70 75 80

Glu Asn Ile Ile Val Phe Met Tyr Asp Asp Ile Ala Phe Asn Gly Glu
85 90 95

Asn Pro Arg Pro Gly Val Ile Ile Asn Lys Pro Asp Gly Gly Asp Val
100 105 110

Tyr Glu Gly Val Pro Lys Asp Tyr Thr Gly Glu Asp Val Thr Val Gly
115 120 125

Asn Phe Phe Ala Ala Leu Leu Gly Asn Lys Ser Ala Leu Thr Gly Gly
130 135 140

Ser Gly Lys Val Val Asp Ser Gly Pro Asp Asp His Ile Phe Val Tyr

145		150		155		160									
Tyr	Thr	Asp	His	Gly	Gly	Pro	Gly	Val	Leu	Gly	Met	Pro	Ala	Gly	Pro
				165					170					175	
Tyr	Leu	Tyr	Ala	Asp	Asp	Leu	Ile	Glu	Val	Leu	Lys	Lys	Lys	His	Ala
			180					185					190		
Ser	Gly	Thr	Tyr	Lys	Asn	Leu	Val	Phe	Tyr	Leu	Glu	Ala	Cys	Glu	Ser
		195					200					205			
Gly	Ser	Ile	Phe	Glu	Gly	Leu	Leu	Pro	Glu	Asp	Ile	Asn	Ile	Tyr	Ala
	210					215					220				
Thr	Thr	Ala	Ser	Asn	Ala	Glu	Glu	Ser	Ser	Trp	Gly	Thr	Tyr	Cys	Pro
225					230					235					240
Gly	Glu	Tyr	Pro	Ser	Pro	Pro	Pro	Glu	Tyr	Ser	Thr	Cys	Leu	Gly	Asp
				245					250					255	
Leu	Tyr	Ser	Val	Ala	Trp	Met	Glu	Asp	Ser	Asp	Arg	His	Asn	Leu	Arg
			260					265					270		
Thr	Glu	Thr	Leu	His	Gln	Gln	Tyr	Lys	Leu	Val	Lys	Glu	Arg	Thr	Ile
		275					280					285			
Ser	Gly	Asp	Ser	Tyr	Tyr	Gly	Ser	His	Val	Met	Gln	Tyr	Gly	Asp	Val
	290					295					300				
Arg	Leu	Ser	Ser	Asp	Val	Leu	Phe	His	Tyr	Leu	Gly	Thr	Asp	Pro	Ala
305					310					315					320
Asn	Asp	Asn	Phe	Thr	Phe	Val	Asp	Glu	Asn	Ser	Leu	Trp	Ser	Pro	Ser
				325					330					335	
Lys	Pro	Val	Asn	Gln	Arg	Asp	Ala	Asp	Leu	Ile	His	Phe	Trp	Asp	Lys
			340					345					350		
Phe	Arg	Lys	Ala	Pro	Glu	Gly	Ser	Leu	Arg	Lys	Asn	Ala	Ala	Gln	Lys
		355					360					365			

Gln Val Leu Glu Ala Met Ser His Arg Met His Val Asp Asn Ser Val
370 375 380

Lys Leu Ile Gly Lys Leu Leu Phe Gly Ile Glu Lys Gly Pro Glu Val
385 390 395 400

Leu Asn Ala Val Arg Pro Ala Gly Ser Ala Leu Val Asp Asp Trp His
405 410 415

Cys Leu Lys Thr Met Val Arg Thr Phe Glu Thr His Cys Gly Ser Leu
420 425 430

Ser Gln Tyr Gly Met Lys His Met Arg Ser Phe Ala Asn Ile Cys Asn
435 440 445

Val Gly Ile Lys Asn Glu Gln Met Ala Glu Ala Ser Ala Gln Ala Cys
450 455 460

Val Ser Ile Pro Ser Asn Pro Trp Ser Ser Leu Gln Arg Gly Phe Ser
465 470 475 480

Ala

<210> 23
<211> 494
<212> PRT
<213> Prunus persica

<400> 23

Met Thr Arg Leu Ala Ser Ala Val Val Leu Leu Phe Leu Val Ser Leu
1 5 10 15

Ser Ser Phe Ala Ala Gly Ser Arg Asp Leu Ile Gly Asp Val Leu Arg
20 25 30

Leu Pro Ser Glu Ala Ser Arg Phe Phe Gly Arg Gly Asp Asp Gly Pro
35 40 45

Asp Glu Gln Asp Asp Gly Thr Val Gly Thr Arg Trp Ala Val Leu Ile
50 55 60

Ala Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp Ile Cys
65 70 75 80

His Ala Tyr Gln Leu Leu Lys Lys Gly Gly Leu Lys Asp Glu Asn Ile
85 90 95

Val Val Phe Met Tyr Asp Asp Ile Ala Tyr Asn Glu Glu Asn Pro Arg
100 105 110

Pro Gly Val Ile Ile Asn Ser Pro His Gly Asp Asp Val Tyr Lys Gly
115 120 125

Val Pro Lys Asp Tyr Thr Gly Asp Asp Val Thr Val Asn Asn Phe Phe
130 135 140

Ala Ala Ile Leu Gly Asn Lys Thr Ala Leu Thr Gly Gly Thr Gly Lys
145 150 155 160

Val Val Asp Ser Gly Pro Asn Asp His Ile Phe Ile Tyr Tyr Ser Asp
165 170 175

His Gly Gly Pro Gly Val Leu Gly Met Pro Thr Ser Pro Tyr Ile Tyr
180 185 190

Ala Asn Asp Leu Ile Glu Val Leu Lys Lys Lys His Ala Ala Gly Thr
195 200 205

Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile
210 215 220

Phe Glu Gly Leu Leu Pro Glu Gly Leu Asn Ile Phe Ala Thr Thr Ala
225 230 235 240

Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Tyr
245 250 255

Pro Ser Pro Pro Pro Glu Tyr Glu Thr Cys Leu Gly Asp Leu Tyr Ser
260 265 270

Val Ala Trp Met Glu Asp Ser Asp Ile His Asn Leu Arg Ser Glu Thr
275 280 285

Leu His Gln Gln Tyr Glu Leu Val Lys Thr Arg Thr Ala Asn Asp Asn
290 295 300

Ser Gly Phe Gly Ser His Val Met Gln Tyr Gly Asp Val Gly Leu Ser
305 310 315 320

Lys Glu Asn Leu Phe Val Tyr Met Gly Thr Asn Pro Ala Asn Asp Asn
325 330 335

Tyr Thr Phe Leu Gly Glu Asn Ser Leu Arg Pro Ser Thr Lys Ala Val
340 345 350

Asn Gln Arg Asp Ala Asp Leu Val His Phe Trp His Lys Tyr Arg Lys
355 360 365

Ala Pro Glu Gly Ser Pro Arg Lys Ile Gln Ala Gln Lys Asp Phe Val
370 375 380

Glu Ala Met Ser His Arg Met His Met Asp Gln Thr Met Lys Leu Ile
385 390 395 400

Gly Lys Leu Leu Phe Gly Ile Lys Lys Gly Pro Glu Val Leu Asn Thr
405 410 415

Val Arg Pro Ala Gly Gln Pro Leu Val Asp Asp Trp Asp Cys Leu Lys
420 425 430

Thr Met Val Arg Ser Phe Glu Thr Tyr Cys Gly Ser Leu Ser Gln Tyr
435 440 445

Gly Met Lys His Met Arg Ser Leu Ala Asn Ile Cys Asn Ala Gly Met
450 455 460

Thr Lys Glu Gln Met Thr Glu Ala Ser Ala Gln Ala Cys Thr Ser Val
465 470 475 480

Pro Ser Ser Arg Trp Ser Ser Leu His Arg Gly Phe Ser Ala
485 490

<210> 24
<211> 487
<212> PRT
<213> Arachis diogoi

<400> 24

Met Glu Ser Leu Leu Arg Ile Thr Leu Leu Phe Phe Ala Phe Thr Thr
1 5 10 15

Phe Val Ala Ser Ala Ser Gly Arg Arg Asp Ile Val Gly Gly Thr Leu
20 25 30

Arg Leu Pro Ser Glu Ala Ile Ser Arg Phe Phe His Glu Pro Glu Asn
35 40 45

Glu Gly Thr Lys Trp Ala Val Leu Leu Ala Gly Ser Asn Gly Tyr Trp
50 55 60

Asn Tyr Arg His Gln Ala Asp Ile Cys His Ala Tyr Gln Leu Leu Arg
65 70 75 80

Ser Gly Gly Val Lys Glu Glu Asn Ile Ile Val Phe Met Phe Asp Asp
85 90 95

Ile Ala Tyr Ser Glu Glu Asn Pro Arg Pro Gly Val Ile Ile Asn Lys
100 105 110

Pro Asp Gly Gly Asp Val Tyr Lys Gly Val Pro Lys Asp Tyr Thr Gly
115 120 125

Lys Asp Val Asn Val Asn Asn Phe Phe Ala Ala Leu Leu Gly Asn Lys
130 135 140

Ser Ala Leu Thr Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro Asn
145 150 155 160

Asp His Ile Phe Val Phe Tyr Ser Asp His Gly Gly Pro Gly Ile Leu
165 170 175

Gly Met Pro Val Gly Pro Tyr Leu Tyr Ala Asn Asp Leu Asn Glu Val

180

185

190

Leu Lys Lys Lys His Ala Ser Gly Gly Tyr Lys Ser Leu Val Phe Tyr
 195 200 205

Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Glu
 210 215 220

Asp Ile Asn Ile Tyr Ala Thr Thr Ala Ser Asn Ala Val Glu Ser Ser
 225 230 235 240

Trp Gly Thr Tyr Cys Pro Gly Glu Asp Pro Ser Pro Pro Pro Glu Tyr
 245 250 255

Ser Thr Cys Leu Gly Asp Leu Tyr Ser Ile Ser Trp Met Glu Asp Ser
 260 265 270

Asp Thr His Asn Leu Arg Thr Glu Thr Leu His Gln Gln Tyr Lys Leu
 275 280 285

Val Lys Asp Arg Thr Leu Asn Gly Asn Ala Tyr Tyr Gly Ser His Ala
 290 295 300

Met Gln Tyr Gly Asp Val Gly Ile Ser Glu Asn Leu Leu Phe Gln Tyr
 305 310 315 320

Leu Gly Thr Asn Pro Ala Asn Asp Asn Tyr Thr Phe Val Asp Glu Asn
 325 330 335

Ser Leu Arg Thr Pro Ser Lys Ala Val Asn Gln Arg Asp Ala Asp Leu
 340 345 350

Ile His Phe Trp Glu Lys Phe Arg Lys Ala Pro Glu Gly Ser Ser Ser
 355 360 365

Lys Ile Thr Ala Gln Lys Gln Val Val Glu Val Met Ser His Arg Met
 370 375 380

His Ile Asp Asn Ser Val Lys Leu Ile Gly Asn Leu Leu Phe Gly Thr
 385 390 395 400

Glu Lys Gly Pro Glu Leu Leu Ser Ala Val Arg Pro Ala Gly Lys Pro
405 410 415

Leu Val Asp Asp Trp Asp Cys Leu Lys Asn Met Val Arg Thr Phe Glu
420 425 430

Thr His Cys Gly Ser Leu Ser Gln Tyr Gly Met Lys His Met Arg Thr
435 440 445

Phe Ala Asn Ile Cys Asn Ala Gly Ile His Lys Asp Gln Met Asp Glu
450 455 460

Ala Thr Ala Gln Ala Cys Val Ser Ile Pro Ser Asn Pro Trp Ser Ser
465 470 475 480

Leu Glu Arg Gly Phe Ser Ala
485

<210> 25
<211> 493
<212> PRT
<213> Populus trichocarpa

<400> 25

Met Thr Arg Leu Ile Ala Gly Val Ile Phe Leu Leu Ile Ser Phe Cys
1 5 10 15

Gly Ile Ala Val Gly Val Arg Asp Ile Val Gly Asp Val Leu Arg Leu
20 25 30

Pro Ser Glu Ala Ser Arg Phe Phe Arg Pro Gly Lys Phe Asn Asp Asp
35 40 45

Asn Ser Asp Asp Asp Ser Ser Gly Thr Arg Trp Ala Ile Leu Leu Ala
50 55 60

Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp Val Cys His
65 70 75 80

Ala Tyr Gln Leu Leu Arg Gln Gly Gly Leu Lys Glu Glu Asn Ile Ile
85 90 95

Val Phe Met Tyr Asp Asp Ile Ala Asp Asn Pro Glu Asn Pro Arg Pro
100 105 110

Gly Val Ile Ile Asn Asn Pro Gln Gly Glu Asp Val Tyr Lys Gly Val
115 120 125

Pro Lys Asp Tyr Thr Gly Pro Asp Val Thr Val Gly Asn Phe Phe Ala
130 135 140

Ala Ile Leu Gly Asn Lys Thr Ala Leu Thr Gly Gly Ser Gly Lys Val
145 150 155 160

Ile Asp Ser Gly Pro Asn Asp His Ile Phe Ile Tyr Tyr Thr Asp His
165 170 175

Gly Gly Pro Gly Val Leu Gly Met Pro Thr Asn Pro Tyr Leu Tyr Ala
180 185 190

Asp Asp Leu Ile Asp Val Leu Lys Lys Lys His Ala Ser Gly Thr Tyr
195 200 205

Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe
210 215 220

Glu Gly Leu Leu Pro Gln Gly Leu Asn Ile Tyr Ala Thr Thr Ala Ser
225 230 235 240

Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Tyr Pro
245 250 255

Ser Pro Pro Pro Glu Tyr Glu Thr Cys Leu Gly Asp Leu Tyr Ser Val
260 265 270

Ala Trp Met Glu Asp Ser Asp Ile His Asn Leu Arg Thr Glu Thr Leu
275 280 285

His Gln Gln Tyr Glu Leu Val Lys Arg Arg Thr Ser Tyr Asp Asn Ser
290 295 300

Pro Tyr Gly Ser His Val Met Gln Tyr Gly Asp Val Gly Leu Ser Lys
305 310 315 320

Asp Asp Leu Phe Gln Tyr Met Gly Thr Asn Pro Ala Asn Asp Asn Tyr
325 330 335

Thr Phe Val Glu Glu Asn Ser Leu Arg Pro His Ser Lys Val Val Asn
340 345 350

Gln Arg Asp Ala Asp Leu Val His Phe Trp Thr Lys Tyr Arg Lys Ala
355 360 365

Pro Glu Gly Ser Ser Arg Lys Val Glu Ala Gln Lys Gln Phe Val Glu
370 375 380

Ala Met Ser His Arg Met His Ile Asp His Ser Ile Lys Leu Ile Gly
385 390 395 400

Lys Leu Leu Phe Gly Ile Glu Lys Ala Ser Glu Ala Leu Asn Thr Val
405 410 415

Arg Pro Ala Gly Gln Pro Leu Val Asp Asp Trp Val Cys Leu Lys Thr
420 425 430

Leu Val Arg Thr Phe Glu Thr His Cys Gly Ser Ile Ser Gln Tyr Gly
435 440 445

Met Lys His Met Arg Ser Leu Ala Asn Leu Cys Asn Ala Gly Ile Val
450 455 460

Lys Glu Gln Met Ala Glu Ala Ser Ala Gln Ala Cys Val Ser Phe Pro
465 470 475 480

Ser Gly Ser Trp Ser Ser Leu His Lys Gly Phe Ser Ala
485 490

<210> 26

<211> 492

<212> PRT

<213> Cicer arietinum

<400> 26

Met Asp Arg Ser Lys Ile Ser Thr Leu Leu Phe Leu Ile Val Ala Leu
1 5 10 15

Thr Phe Leu Ala Ala Val Ser Ala Val Arg Asp Leu Pro Gly Asp Tyr
20 25 30

Leu Arg Leu Pro Ser Asp Ala Ser Arg Phe Phe His Glu Pro Glu Asn
35 40 45

Asp Asp Asn Val Gln Gly Thr Arg Trp Ala Ile Leu Leu Ala Gly Ser
50 55 60

Asn Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp Val Cys His Ala Tyr
65 70 75 80

Gln Ile Leu Arg Lys Gly Gly Leu Lys Glu Glu Asn Ile Ile Val Phe
85 90 95

Met Tyr Asp Asp Ile Ala Phe Asp Ile Glu Asn Pro Arg Pro Gly Val
100 105 110

Ile Ile Asn Lys Pro Asp Gly Gly Asp Val Tyr Ala Gly Val Pro Lys
115 120 125

Asp Tyr Thr Gly Asp Asp Val Asn Val Asp Asn Phe Tyr Ala Ala Leu
130 135 140

Leu Gly Asn Lys Ser Ala Leu Thr Gly Gly Ser Gly Lys Val Val Asp
145 150 155 160

Ser Gly Pro Asn Asp His Ile Phe Val Tyr Tyr Thr Asp His Gly Gly
165 170 175

Pro Gly Val Leu Gly Met Pro Val Gly Pro Tyr Leu Tyr Ala Ser Asp
180 185 190

Leu Asn Glu Val Leu Lys Lys Lys His Ala Ser Gly Ser Tyr Lys Ser
195 200 205

Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly

210

215

220

Leu Leu Pro Glu Asn Ile Asn Ile Tyr Ala Thr Thr Ala Ser Asn Ala
 225 230 235 240

Asp Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Tyr Pro Pro Pro
 245 250 255

Pro Pro Glu Tyr Ser Thr Cys Leu Gly Asp Leu Tyr Ser Val Ala Trp
 260 265 270

Met Glu Asp Ser Asp Ile His Asn Leu Arg Thr Glu Ser Leu His Gln
 275 280 285

Gln Tyr Lys Val Val Lys Asp Arg Thr Ile Asn Gly Val Tyr Tyr Gly
 290 295 300

Ser His Val Met Glu Tyr Gly Asp Val Gly Leu Ser Asn Asn His Leu
 305 310 315 320

Phe Ile Tyr Leu Gly Thr Asn Pro Ala Asn Asp Asn Ile Ser Phe Val
 325 330 335

Asp Glu Ser Ser Leu Thr Leu Arg Ser Pro Ser Ala Ala Val Asn Gln
 340 345 350

Arg Asp Ala Asp Leu Ile His Phe Trp Asp Lys Phe Arg Lys Ala Pro
 355 360 365

Glu Gly Ser Ala Arg Lys Asn Glu Ala Glu Lys Gln Val Leu Glu Ala
 370 375 380

Met Ser His Arg Lys His Val Asp Asn Ser Val Glu Leu Ile Gly Lys
 385 390 395 400

Leu Leu Phe Gly Ile Glu Lys Gly Pro Glu Leu Phe Asn Thr Val Arg
 405 410 415

Pro Ala Gly Leu Pro Leu Val Asp Asn Trp Asp Cys Leu Lys Thr Met
 420 425 430

Val Arg Thr Phe Glu Thr His Cys Gly Ser Leu Ser Gln Tyr Gly Met
435 440 445

Lys His Met Arg Ser Phe Ala Asn Ile Cys Asn Ala Gly Ile Gln Asn
450 455 460

Glu Gln Met Ala Glu Ala Ser Ala Gln Ala Cys Ser Asn Ile Pro Ala
465 470 475 480

Asn Pro Trp Ser Ser Leu His Arg Gly Phe Ser Ala
485 490

<210> 27
<211> 493
<212> PRT
<213> Vitis vinifera

<400> 27

Met Thr Ile Phe Pro Ala Ala Val Ala Ala Phe Leu Ala Leu Ser Thr
1 5 10 15

Leu Val Ala Gly Gly Arg His Phe Ala Gly Asp Asn Gly Leu Leu Leu
20 25 30

Pro Ser Glu Ala Ser Arg Phe Phe Arg Pro Gly Gly Ala Ala Asp Asp
35 40 45

Asp Thr Gly Ala Glu Ser Ala Gly Thr Arg Trp Ala Val Leu Ile Ala
50 55 60

Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp Ile Cys His
65 70 75 80

Ala Tyr Gln Leu Leu Lys Lys Gly Gly Leu Lys Asp Glu Asn Ile Ile
85 90 95

Val Phe Met Tyr Asp Asp Ile Ser Phe Asn Glu Glu Asn Pro Arg Pro
100 105 110

Gly Ile Ile Ile Asn Ser Pro His Gly Glu Asp Val Tyr Glu Gly Val
115 120 125

Pro Lys Asp Tyr Thr Gly Glu Asp Val Thr Val Asp Asn Phe Phe Ala
130 135 140

Val Ile Leu Gly Asn Lys Thr Ala Leu Ser Gly Gly Ser Gly Lys Val
145 150 155 160

Leu Asp Ser Gly Pro Asn Asp His Ile Phe Ile Tyr Tyr Ser Asp His
165 170 175

Gly Gly Pro Gly Val Leu Gly Met Pro Thr Ser Pro Tyr Leu Tyr Ala
180 185 190

Asn Asp Leu Ile Glu Val Leu Lys Lys Lys His Ala Ser Gly Thr Tyr
195 200 205

Asn Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe
210 215 220

Glu Gly Leu Leu Pro Glu Gly Leu Asn Ile Tyr Ala Thr Thr Ala Ala
225 230 235 240

Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Asp Pro
245 250 255

Ser Pro Pro Pro Glu Tyr Glu Thr Cys Leu Gly Asp Leu Tyr Ser Val
260 265 270

Ala Trp Met Glu Asp Ser Asp Val His Asn Leu Arg Thr Glu Thr Leu
275 280 285

Arg Gln Gln Tyr Glu Leu Val Lys Lys Arg Thr Ala Asn Asp Asn Ser
290 295 300

Val Tyr Gly Ser His Val Met Gln Tyr Gly Asp Leu Gly Leu Asn Lys
305 310 315 320

Glu Asp Leu Val Leu Tyr Met Gly Thr Asn Pro Ala Asn Asp Asn Tyr
325 330 335

Thr Phe Val Asp Asn Asn Ser Leu Arg Leu Pro Ser Lys Ala Val Asn
340 345 350

Gln Arg Asp Ala Asp Leu Val His Phe Trp Asp Lys Phe Arg Lys Ala
355 360 365

Pro Glu Gly Ser Pro Arg Lys Ala Glu Ala Gln Lys Gln Phe Leu Glu
370 375 380

Ala Met Ser His Arg Thr His Ile Asp His Ala Ile Lys Leu Val Gly
385 390 395 400

Arg Leu Leu Phe Gly Met Lys Lys Gly Ser Glu Val Leu Lys Thr Val
405 410 415

Arg Pro Ala Gly Gln Pro Leu Val Asp Asp Trp His Cys Leu Lys Thr
420 425 430

Leu Val Arg Thr Phe Glu Ala His Cys Gly Ser Leu Ser Gln Tyr Gly
435 440 445

Met Lys His Met Arg Ser Ile Ala Asn Ile Cys Asn Ala Gly Ile Glu
450 455 460

Lys Glu Gln Met Ala Glu Ala Ser Ala Gln Ala Cys Val Thr Ile Pro
465 470 475 480

Pro Gly Pro Trp Ser Ser Leu Asp Lys Gly Phe Ser Ala
485 490

<210> 28

<211> 484

<212> PRT

<213> Phaseolus vulgaris

<400> 28

Met Ala Thr Thr Thr Ala Thr Thr Ser Leu Leu Ala Leu Leu Leu Leu
1 5 10 15

Phe Leu Val Ala Leu Val Ser Ala Gly Arg Asp Leu Val Gly Asp Phe
20 25 30

Leu Arg Leu Pro Ser Asp Ser Gly Asn Gly Asp Asn Val His Gly Thr
35 40 45

Arg Trp Ala Ile Leu Phe Ala Gly Ser Ser Gly Tyr Trp Asn Tyr Arg
50 55 60

His Gln Ala Asp Ile Cys His Ala Tyr Gln Leu Leu Arg Lys Gly Gly
65 70 75 80

Leu Lys Asp Glu Asn Ile Ile Val Phe Met Tyr Asp Asp Ile Ala Phe
85 90 95

Asn Ser Glu Asn Pro Arg Arg Gly Val Ile Ile Asn Ser Pro Asn Gly
100 105 110

Asp Asp Val Tyr Lys Gly Val Pro Lys Asp Tyr Thr Gly Glu Asp Val
115 120 125

Thr Ala His Asn Phe Tyr Ala Ala Leu Leu Gly Asp Lys Ser Lys Leu
130 135 140

Thr Gly Gly Ser Gly Lys Val Val Asn Ser Gly Pro Asn Asp His Ile
145 150 155 160

Phe Ile Phe Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Ser Pro
165 170 175

Ala Gly Pro Tyr Ile Tyr Ala Ser Asp Leu Asn Glu Val Leu Lys Lys
180 185 190

Lys His Ala Ser Gly Thr Tyr Lys Asn Leu Val Phe Tyr Leu Glu Ala
195 200 205

Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Glu Asp Ile Asn
210 215 220

Val Tyr Ala Thr Thr Ala Ser Asn Ala Asp Glu Ser Ser Trp Gly Thr
225 230 235 240

Tyr Cys Pro Gly Glu Asp Pro Ser Pro Pro Pro Glu Tyr Ser Thr Cys

245

250

255

Leu Gly Asp Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Arg His
 260 265 270

Asn Leu Arg Thr Glu Thr Leu His Gln Gln Tyr Lys Leu Val Lys Glu
 275 280 285

Arg Thr Ile Ser Gly Gly Leu Tyr Tyr Gly Ser His Val Met Gln Tyr
 290 295 300

Gly Asp Val Gly Leu Ser Lys Asp Ile Leu Phe His Tyr Leu Gly Thr
 305 310 315 320

Asp Pro Ala Asn Glu Asn Leu Thr Phe Val Asp Glu Asn Ser Leu Trp
 325 330 335

Ser Ser Ser Lys Ala Val Asn Gln Arg Asp Ala Asp Leu Val His Phe
 340 345 350

Trp Asp Lys Phe Arg Lys Ala Pro Glu Gly Ser Pro Lys Lys Asn Glu
 355 360 365

Ala Arg Lys Gln Val Leu Glu Val Met Ser His Arg Met His Ile Asp
 370 375 380

Asp Ser Val Glu Leu Val Gly Lys Leu Leu Phe Gly Ile Glu Lys Ala
 385 390 395 400

Pro Glu Leu Leu Asn Ala Val Arg Pro Ala Gly Ser Ala Leu Val Asp
 405 410 415

Asp Trp Asp Cys Leu Lys Thr Met Val Arg Thr Phe Glu Thr His Cys
 420 425 430

Gly Ser Leu Ser Gln Tyr Gly Met Lys His Met Arg Ser Phe Ala Asn
 435 440 445

Met Cys Asn Val Gly Ile Lys Lys Glu Gln Met Arg Glu Ala Ser Ala
 450 455 460

Gln	Ala	Cys	Val	Thr	Ile	Pro	Ala	Asn	Pro	Trp	Ser	Ser	Leu	Gln	Arg
465					470					475					480

Gly Phe Ser Ala

<210> 29
 <211> 484
 <212> PRT
 <213> Phaseolus vulgaris

<400> 29

Met	Ala	Thr	Thr	Thr	Ala	Thr	Thr	Ser	Leu	Leu	Ala	Leu	Leu	Leu	Leu
1				5					10					15	

Phe	Leu	Val	Ala	Leu	Val	Ser	Ala	Gly	Arg	Asp	Leu	Val	Gly	Asp	Phe
			20					25					30		

Leu	Arg	Leu	Pro	Ser	Asp	Ser	Gly	Asn	Gly	Asp	Asn	Val	His	Gly	Thr
		35					40					45			

Arg	Trp	Ala	Ile	Leu	Phe	Ala	Gly	Ser	Ser	Gly	Tyr	Trp	Asn	Tyr	Arg
	50					55					60				

His	Gln	Ala	Asp	Ile	Cys	His	Ala	Tyr	Gln	Leu	Leu	Arg	Lys	Gly	Gly
65					70					75					80

Leu	Lys	Asp	Glu	Asn	Ile	Ile	Val	Phe	Met	Tyr	Asp	Asp	Ile	Ala	Phe
				85					90					95	

Asn	Ser	Glu	Asn	Pro	Arg	Arg	Gly	Val	Ile	Ile	Asn	Ser	Pro	Asn	Gly
			100					105					110		

Asp	Glu	Val	Tyr	Lys	Gly	Val	Pro	Lys	Asp	Tyr	Thr	Gly	Glu	Asp	Val
		115					120					125			

Thr	Ala	His	Asn	Phe	Tyr	Ala	Ala	Leu	Leu	Gly	Asp	Lys	Ser	Lys	Leu
	130					135					140				

Thr	Gly	Gly	Ser	Gly	Lys	Val	Val	Asn	Ser	Gly	Pro	Asn	Asp	His	Ile
145					150					155					160

Phe Ile Phe Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Ser Pro
165 170 175

Ala Gly Pro Tyr Ile Tyr Ala Ser Asp Leu Asn Glu Val Leu Lys Lys
180 185 190

Lys His Ala Ser Gly Thr Tyr Lys Asn Leu Val Phe Tyr Leu Glu Ala
195 200 205

Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Glu Asp Ile Asn
210 215 220

Val Tyr Ala Thr Thr Ala Ser Asn Ala Asp Glu Ser Ser Trp Gly Thr
225 230 235 240

Tyr Cys Pro Gly Glu Asp Pro Ser Pro Pro Pro Glu Tyr Ser Thr Cys
245 250 255

Leu Gly Asp Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Arg His
260 265 270

Asn Leu Arg Thr Glu Thr Leu His Gln Gln Tyr Lys Leu Val Lys Glu
275 280 285

Arg Thr Ile Ser Gly Gly Leu Tyr Tyr Gly Ser His Val Met Gln Tyr
290 295 300

Gly Asp Val Gly Leu Ser Lys Asp Ile Leu Phe His Tyr Leu Gly Thr
305 310 315 320

Asp Pro Ala Asn Glu Asn Leu Thr Phe Val Asp Glu Asn Ser Leu Trp
325 330 335

Ser Ser Ser Lys Ala Val Asn Gln Arg Asp Ala Asp Leu Val His Phe
340 345 350

Trp Asp Lys Phe Arg Lys Ala Pro Glu Gly Ser Pro Lys Lys Asn Glu
355 360 365

Ala Arg Lys Gln Val Leu Glu Val Met Ser His Arg Met His Ile Asp
370 375 380

Asp Ser Val Glu Leu Val Gly Lys Leu Leu Phe Gly Ile Glu Lys Ala
385 390 395 400

Pro Glu Leu Leu Asn Ala Val Arg Pro Ala Gly Ser Ala Leu Val Asp
405 410 415

Asp Trp Asp Cys Leu Lys Thr Met Val Arg Thr Phe Glu Thr His Cys
420 425 430

Gly Ser Leu Ser Gln Tyr Gly Met Lys His Met Arg Ser Phe Ala Asn
435 440 445

Met Cys Asn Val Gly Ile Lys Lys Glu Gln Met Arg Glu Ala Ser Ala
450 455 460

Gln Ala Cys Val Thr Ile Pro Ala Asn Pro Trp Ser Ser Leu Gln Arg
465 470 475 480

Gly Phe Ser Ala

<210> 30
<211> 493
<212> PRT
<213> Vitis vinifera

<400> 30

Met Thr Ile Phe Pro Ala Ala Val Ala Ala Leu Leu Ala Leu Ser Thr
1 5 10 15

Leu Val Ala Gly Gly Arg His Phe Ala Gly Asp Asn Gly Leu Leu Leu
20 25 30

Pro Ser Glu Ala Ser Arg Phe Phe Arg Pro Gly Gly Ala Ala Asp Asp
35 40 45

Asp Thr Gly Gly Glu Ser Ala Gly Thr Arg Trp Ala Val Leu Ile Ala
50 55 60

Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp Ile Cys His
65 70 75 80

Ala Tyr Gln Leu Leu Lys Lys Gly Gly Leu Lys Asp Glu Asn Ile Ile
85 90 95

Val Phe Met Tyr Asp Asp Ile Ser Phe Asn Glu Glu Asn Pro Arg Pro
100 105 110

Gly Ile Ile Ile Asn Ser Pro His Gly Glu Asp Val Tyr Glu Gly Val
115 120 125

Pro Lys Asp Tyr Thr Gly Glu Asp Val Thr Val Asp Asn Phe Phe Ala
130 135 140

Val Ile Leu Gly Asn Lys Thr Ala Leu Ser Gly Gly Ser Gly Lys Val
145 150 155 160

Leu Asp Ser Gly Pro Asn Asp His Ile Phe Ile Tyr Tyr Ser Asp His
165 170 175

Gly Gly Pro Gly Val Leu Gly Met Pro Thr Ser Pro Tyr Leu Tyr Ala
180 185 190

Asn Asp Leu Ile Glu Val Leu Lys Lys Lys His Ala Ser Gly Thr Tyr
195 200 205

Asn Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe
210 215 220

Glu Gly Leu Leu Pro Glu Gly Leu Asn Ile Tyr Ala Thr Thr Ala Ala
225 230 235 240

Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Asp Pro
245 250 255

Ser Pro Pro Pro Glu Tyr Glu Thr Cys Leu Gly Asp Leu Tyr Ser Val
260 265 270

Ala Trp Met Glu Asp Ser Asp Val His Asn Leu Arg Thr Glu Thr Leu

275

280

285

Arg Gln Gln Tyr Glu Leu Val Lys Lys Arg Thr Ala Asn Asp Asn Ser
 290 295 300

Val Tyr Gly Ser His Val Met Gln Tyr Gly Asp Leu Gly Leu Asn Lys
 305 310 315 320

Glu Asp Leu Val Leu Tyr Met Gly Thr Asn Pro Ala Asn Asp Asn Tyr
 325 330 335

Thr Phe Val Asp Asn Asn Ser Leu Arg Leu Pro Ser Lys Ala Val Asn
 340 345 350

Gln Arg Asp Ala Asp Leu Val His Phe Trp Asp Lys Phe Arg Lys Ala
 355 360 365

Pro Glu Gly Ser Pro Arg Lys Ala Glu Ala Gln Lys Gln Phe Leu Glu
 370 375 380

Ala Met Ser His Arg Thr His Ile Asp His Ala Ile Lys Leu Val Gly
 385 390 395 400

Arg Leu Leu Phe Gly Met Lys Lys Gly Ser Glu Val Leu Lys Thr Val
 405 410 415

Arg Pro Ala Gly Gln Pro Leu Val Asp Asp Trp His Cys Leu Lys Thr
 420 425 430

Leu Val Arg Thr Phe Glu Ala His Cys Gly Ser Leu Ser Gln Tyr Gly
 435 440 445

Met Lys His Met Arg Ser Ile Ala Asn Ile Cys Asn Ala Gly Ile Glu
 450 455 460

Lys Glu Gln Met Ala Glu Ala Ser Ala Gln Ala Cys Val Thr Ile Pro
 465 470 475 480

Pro Gly Pro Trp Ser Ser Leu Asp Lys Gly Phe Ser Ala
 485 490

<210> 31
<211> 493
<212> PRT
<213> Cucumis sativus

<400> 31

Met Ala Arg Ile Pro Thr Gly Val Leu Leu Ser Leu Leu Phe Leu Ala
1 5 10 15

Val Ile Gly Leu Pro Ala Gly Ala Arg Asp Leu Pro Gly Asp Phe Leu
20 25 30

Arg Leu Pro Ser Glu Ala Leu Lys Phe Phe Arg Gly Gly Ala Ser Asp
35 40 45

Ala Ser Asp Glu Asp Ser Val Gly Thr Arg Trp Ala Val Leu Ile Ala
50 55 60

Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp Ile Cys His
65 70 75 80

Ala Tyr Gln Leu Leu Arg Lys Asn Gly Leu Lys Asp Glu Asn Ile Ile
85 90 95

Val Phe Met Tyr Asp Asp Ile Ala Phe Asn Pro Glu Asn Pro Arg Pro
100 105 110

Gly Val Ile Ile Asn His Pro Lys Gly Ser Asp Val Tyr His Gly Val
115 120 125

Pro Lys Asp Tyr Thr Gly Glu Asp Val Thr Val Asn Asn Phe Phe Ala
130 135 140

Ala Ile Leu Gly Asn Lys Thr Ala Leu Thr Gly Gly Ser Gly Lys Val
145 150 155 160

Val Asp Ser Gly Pro Asn Asp His Ile Phe Ile Tyr Tyr Ser Asp His
165 170 175

Gly Gly Pro Gly Val Leu Gly Met Pro Thr Tyr Pro Tyr Met Tyr Ala
180 185 190

Asp Asp Leu Asn Lys Val Leu Lys Lys Lys His Ala Ala Gly Ser Tyr
195 200 205

Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe
210 215 220

Glu Gly Leu Leu Pro Glu Gly Leu Asn Ile Tyr Thr Thr Thr Ala Ser
225 230 235 240

Asn Ala Tyr Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Asp Tyr Pro
245 250 255

Ser Pro Pro Pro Glu Tyr Asp Thr Cys Leu Gly Asp Leu Tyr Ser Val
260 265 270

Ala Trp Leu Glu Asp Ser Asp Asn His Asn Leu Lys Thr Glu Ser Leu
275 280 285

Arg Gln Gln Tyr Glu Leu Val Lys Lys Arg Thr Ile Ser Gly Gln Tyr
290 295 300

Ala Tyr Gly Ser His Val Met Gln Tyr Gly Asp Leu Met Leu Asn Lys
305 310 315 320

Asn Ala Leu Phe Ser Tyr Leu Gly Thr Asp Pro Ala Asn Glu Asn Asn
325 330 335

Thr Phe Val Glu Glu Asn Ser Leu Arg Pro Ala Thr Lys Phe Thr Asn
340 345 350

Gln Arg Asp Ala Asp Leu Val His Phe Trp Glu Lys Phe Arg Lys Ala
355 360 365

Pro Glu Gly Ser Leu Thr Lys Val Glu Ala Gln Lys Lys Phe Val Glu
370 375 380

Ala Met Ser His Arg Ala His Ile Asp Asn Ser Val Lys Leu Val Gly
385 390 395 400

Lys Leu Leu Phe Gly Ile Lys Glu Gly Pro Glu Val Leu Glu Ala Ile
405 410 415

Arg Pro Ala Gly Arg Pro Leu Val Asp Asp Trp Asn Cys Leu Arg Asn
420 425 430

Met Val Arg Ser Phe Glu Ala Arg Cys Gly Ser Leu Ser Gln Tyr Gly
435 440 445

Met Lys His Met Arg Ser Phe Ala Asn Leu Cys Asn Ala Gly Ile Ser
450 455 460

Lys Glu Gln Met Ala Glu Ala Ser Ala Gln Ala Cys Met Ser Val Pro
465 470 475 480

Pro Gly Pro Trp Ser Ser Leu Leu Lys Gly Phe Thr Ala
485 490

<210> 32
<211> 493
<212> PRT
<213> Cucumis sativus

<400> 32

Met Ala Arg Ile Pro Thr Gly Val Leu Leu Ser Leu Leu Phe Leu Ala
1 5 10 15

Val Ile Gly Leu Pro Ala Gly Ala Arg Asp Leu Pro Gly Asp Phe Leu
20 25 30

Arg Leu Pro Ser Glu Ala Leu Lys Phe Phe Arg Gly Gly Ala Ser Asp
35 40 45

Ala Ser Asp Glu Asp Ser Val Gly Thr Arg Trp Ala Val Leu Ile Ala
50 55 60

Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp Ile Cys His
65 70 75 80

Ala Tyr Gln Leu Leu Arg Lys Asn Gly Leu Lys Asp Glu Asn Ile Ile
85 90 95

Val Phe Met Tyr Asp Asp Ile Ala Phe Asn Pro Glu Asn Pro Arg Pro
100 105 110

Gly Val Ile Ile Asn His Pro Lys Gly Ser Asp Val Tyr His Gly Val
115 120 125

Pro Lys Asp Tyr Thr Gly Glu Asp Val Thr Val Asn Asn Phe Phe Ala
130 135 140

Ala Ile Leu Gly Asn Lys Thr Ala Leu Thr Gly Gly Ser Gly Lys Val
145 150 155 160

Val Asp Ser Gly Pro Asn Asp His Ile Phe Ile Tyr Tyr Ser Asp His
165 170 175

Gly Gly Pro Gly Val Leu Gly Met Pro Thr Tyr Pro Tyr Met Tyr Ala
180 185 190

Asp Asp Leu Asn Lys Val Leu Lys Lys Lys His Ala Ala Gly Ser Tyr
195 200 205

Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe
210 215 220

Glu Gly Leu Leu Pro Glu Gly Leu Asn Ile Tyr Thr Thr Thr Ala Ser
225 230 235 240

Asn Ala Tyr Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Asp Tyr Pro
245 250 255

Ser Pro Pro Pro Glu Tyr Asp Thr Cys Leu Gly Asp Leu Tyr Ser Val
260 265 270

Ala Trp Leu Glu Asp Ser Asp Asn His Asn Leu Lys Thr Glu Ser Leu
275 280 285

Arg Gln Gln Tyr Glu Leu Val Lys Lys Arg Thr Leu Ser Gly Gln Tyr
290 295 300

Ala Tyr Gly Ser His Val Met Gln Tyr Gly Asp Leu Met Leu Asn Lys

305		310		315		320									
Asn	Ala	Leu	Phe	Ser	Tyr	Leu	Gly	Thr	Asp	Pro	Ala	Asn	Glu	Asn	Asn
				325					330					335	
Thr	Phe	Val	Glu	Glu	Asn	Ser	Leu	Arg	Pro	Ala	Thr	Lys	Phe	Thr	Asn
			340					345					350		
Gln	Arg	Asp	Ala	Asp	Leu	Val	His	Phe	Trp	Glu	Lys	Phe	Arg	Lys	Ala
		355					360					365			
Pro	Glu	Gly	Ser	Leu	Thr	Lys	Val	Glu	Ala	Gln	Lys	Lys	Phe	Val	Glu
	370					375					380				
Ala	Met	Ser	His	Arg	Ala	His	Ile	Asp	Asn	Ser	Val	Lys	Leu	Val	Gly
385					390				395						400
Lys	Leu	Leu	Phe	Gly	Ile	Lys	Glu	Gly	Pro	Glu	Val	Leu	Glu	Ala	Ile
				405					410					415	
Arg	Pro	Ala	Gly	Arg	Pro	Leu	Val	Asp	Asp	Trp	Asn	Cys	Leu	Arg	Asn
			420					425					430		
Met	Val	Arg	Ser	Phe	Glu	Ala	Arg	Cys	Gly	Ser	Leu	Ser	Gln	Tyr	Gly
		435					440					445			
Met	Lys	His	Met	Arg	Ser	Phe	Ala	Asn	Leu	Cys	Asn	Ala	Gly	Ile	Ser
	450					455					460				
Lys	Glu	Gln	Met	Ala	Glu	Ala	Ser	Ala	Gln	Ala	Cys	Met	Ser	Val	Pro
465					470				475					480	
Pro	Gly	Pro	Trp	Ser	Ser	Leu	Leu	Lys	Gly	Phe	Thr	Ala			
				485					490						

<210> 33
 <211> 493
 <212> PRT
 <213> Vicia sativa

 <400> 33

Met Gly Ser Ser Gln Leu Ser Thr Leu Leu Phe Phe Thr Ile Val Val
1 5 10 15

Thr Phe Leu Thr Val Val Ser Ser Gly Arg Asp Leu Pro Gly Asp Tyr
20 25 30

Leu Arg Leu Pro Ser Glu Thr Ser Arg Phe Phe Arg Glu Pro Lys Asn
35 40 45

Asp Asp Asp Phe Glu Gly Thr Arg Trp Ala Ile Leu Leu Ala Gly Ser
50 55 60

Asn Gly Tyr Trp Asn Tyr Arg His Gln Ser Asp Val Cys His Ala Tyr
65 70 75 80

Gln Leu Leu Arg Lys Gly Gly Ser Lys Glu Glu Asn Ile Ile Val Phe
85 90 95

Met Tyr Asp Asp Ile Ala Ser Asn Glu Glu Asn Pro Arg Pro Gly Val
100 105 110

Ile Ile Asn Lys Pro Asp Gly Asp Asp Val Tyr Ala Gly Val Pro Lys
115 120 125

Asp Tyr Thr Gly Ala Glu Val His Ala Asp Asn Phe Tyr Ala Ala Leu
130 135 140

Leu Gly Asn Lys Ser Ala Leu Thr Gly Gly Ser Gly Lys Val Val Asp
145 150 155 160

Ser Gly Pro Asn Asp His Ile Phe Val Tyr Tyr Thr Asp His Gly Gly
165 170 175

Pro Gly Val Leu Gly Met Pro Val Gly Pro Tyr Leu Tyr Ala Ser Asp
180 185 190

Leu Asn Glu Val Leu Lys Lys Lys His Ala Ser Gly Thr Tyr Lys Ser
195 200 205

Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly
210 215 220

Leu Leu Pro Asp Asp Leu Asn Ile Tyr Ala Thr Thr Ala Ser Asn Ala
225 230 235 240

Glu Glu Ser Ser Trp Gly Tyr Tyr Cys Pro Gly Asp Lys Pro Pro Pro
245 250 255

Pro Pro Glu Tyr Ser Thr Cys Leu Gly Asp Leu Tyr Ser Ile Ala Trp
260 265 270

Met Glu Asp Ser Glu Val His Asn Leu Gln Thr Glu Ser Leu Gln Gln
275 280 285

Gln Tyr Lys Leu Val Lys Asn Arg Thr Ile Ser Glu Pro Tyr Gly Ser
290 295 300

His Val Met Glu Tyr Gly Asp Ile Gly Leu Ser Lys Asn Asp Leu Tyr
305 310 315 320

Gln Tyr Leu Gly Thr Asn Pro Ala Asn Asp Asn Asn Ser Phe Val Asp
325 330 335

Glu Thr Glu Asn Ser Leu Lys Leu Arg Thr Pro Ser Ala Ala Val Asn
340 345 350

Gln Arg Asp Ala Asp Leu Ile His Phe Trp Glu Lys Phe Arg Lys Ala
355 360 365

Pro Glu Gly Ser Ser Gln Lys Asn Glu Ala Glu Lys Gln Val Leu Glu
370 375 380

Ala Met Ser His Arg Lys His Ile Asp Asn Ser Val Lys Leu Ile Gly
385 390 395 400

Gln Leu Leu Phe Gly Ile Glu Lys Gly Thr Glu Leu Leu Asp Val Val
405 410 415

Arg Pro Ala Gly Ser Pro Leu Val Asp Asn Trp Asp Cys Leu Lys Thr
420 425 430

Met Val Lys Thr Phe Glu Thr His Cys Gly Ser Leu Ser Gln Tyr Gly
435 440 445

Met Lys His Met Arg Ser Phe Ala Asn Ile Cys Asn Ala Gly Ile Pro
450 455 460

Asn Glu Pro Met Ala Glu Ala Ser Ala Gln Ala Cys Ala Ser Ile Pro
465 470 475 480

Ala Asn Pro Trp Ser Ser Leu Gln Gly Gly Phe Ser Ala
485 490

<210> 34

<211> 493

<212> PRT

<213> Medicago truncatula

<400> 34

Met Asp Phe Ser Gln Phe Ser Thr Ile Leu Phe Leu Thr Val Ile Leu
1 5 10 15

Thr Ile Phe Ala Ala Val Ser Gly Ser Arg Asp Leu Pro Gly Asp Tyr
20 25 30

Ile Arg Leu Pro Ser Gln Ser Gln Ala Ser Arg Phe Phe His Glu Pro
35 40 45

Glu Asn Asp Asp Asn Asp Gln Gly Thr Arg Trp Ala Ile Leu Leu Ala
50 55 60

Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp Val Cys His
65 70 75 80

Ala Tyr Gln Leu Leu Arg Lys Gly Gly Leu Lys Glu Glu Asn Ile Ile
85 90 95

Val Phe Met Tyr Asp Asp Ile Ala Ser Asn Val Glu Asn Pro Arg Pro
100 105 110

Gly Val Ile Ile Asn Lys Pro Asp Gly Gly Asp Val Tyr Glu Gly Val
115 120 125

Pro Lys Asp Tyr Thr Gly Ala Glu Val His Ala Asp Asn Phe Tyr Ala
130 135 140

Ala Leu Leu Gly Asn Lys Ser Ala Leu Thr Gly Gly Ser Gly Lys Val
145 150 155 160

Val Asp Ser Gly Pro Asn Asp His Ile Phe Val Tyr Tyr Thr Asp His
165 170 175

Gly Gly Pro Gly Val Leu Gly Met Pro Val Gly Pro Tyr Leu Tyr Ala
180 185 190

Ser Asp Leu Asn Glu Val Leu Lys Lys Lys His Ala Ser Gly Ser Tyr
195 200 205

Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe
210 215 220

Glu Gly Leu Leu Pro Glu Asp Ile Asn Ile Tyr Ala Thr Thr Ala Ser
225 230 235 240

Asn Ala Val Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Tyr Pro
245 250 255

Pro Pro Pro Pro Glu Tyr Ser Thr Cys Leu Gly Asp Leu Tyr Ser Ile
260 265 270

Ala Trp Met Glu Asp Ser Asp Ile His Asn Leu Arg Thr Glu Ser Leu
275 280 285

His Gln Gln Tyr Lys Leu Val Lys Asp Arg Thr Ile Asn Gly Tyr Tyr
290 295 300

Gly Ser His Val Met Glu Tyr Gly Asp Val Gly Leu Ser Asn Asn His
305 310 315 320

Leu Phe Leu Tyr Leu Gly Thr Asn Pro Ala Asn Asp Asn Ile Ser Phe
325 330 335

Val Asp Glu Ser Ser Leu Lys Leu Arg Ser Pro Ser Thr Ala Val Asn

340

345

350

Gln Arg Asp Ala Asp Leu Ile His Phe Trp Asp Lys Phe Arg Lys Ala
 355 360 365

Pro Glu Gly Ser Leu Arg Lys Asn Glu Ala Gln Lys Glu Val Leu Glu
 370 375 380

Ala Met Ser His Arg Met His Val Asp Asn Ser Ala Lys Leu Ile Gly
 385 390 395 400

Lys Leu Leu Phe Gly Ile Glu Lys Gly Thr Glu Leu Leu Gly Asn Val
 405 410 415

Arg Pro Ala Gly Ser Pro Leu Val Asp Asn Trp Asp Cys Leu Lys Thr
 420 425 430

Met Val Lys Thr Phe Glu Thr His Cys Gly Ser Leu Ser Gln Tyr Gly
 435 440 445

Met Lys His Met Arg Ser Phe Ala Asn Ile Cys Asn Ala Gly Ile Gln
 450 455 460

Thr Glu Gln Met Ala Glu Ala Ser Ala Gln Ala Cys Ala Ser Ile Pro
 465 470 475 480

Ala Asn Pro Trp Ser Ser Leu Gln Arg Gly Phe Ser Ala
 485 490

<210> 35

<211> 494

<212> PRT

<213> *Fragaria vesca* subsp. *vesca*

<400> 35

Met Thr Arg Leu Ala Ala Val Val Ala Val Val Leu Phe Phe Leu Val
 1 5 10 15

Ser Leu Phe Ser Ser Ser Thr Ser Ala Arg Asp Leu Pro Gly Asp Val
 20 25 30

Leu Arg Leu Pro Ser Glu Thr Ser Arg Phe Phe Arg Ala Gly Asp Asp
35 40 45

Gln Gln Asp Asp Gly Thr Val Gly Thr Arg Trp Ala Val Leu Ile Ala
50 55 60

Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp Ile Cys His
65 70 75 80

Ala Tyr Gln Leu Leu Lys Lys Gly Gly Leu Lys Asp Glu Asn Ile Val
85 90 95

Val Phe Met Tyr Asp Asp Ile Ala Tyr Asn Glu Glu Asn Pro Arg Gln
100 105 110

Gly Val Ile Ile Asn Ser Pro His Gly Asp Asp Val Tyr Lys Gly Val
115 120 125

Pro Lys Asp Tyr Thr Gly Glu Asp Val Thr Val Gly Asn Phe Phe Ala
130 135 140

Ala Ile Leu Gly Asn Lys Thr Ala Ile Ser Gly Gly Ser Gly Lys Val
145 150 155 160

Val Asp Ser Gly Pro Asn Asp His Ile Phe Ile Tyr Tyr Ser Asp His
165 170 175

Gly Gly Pro Gly Val Leu Gly Met Pro Thr Ser Pro Tyr Ile Tyr Ala
180 185 190

Asp Arg Leu Ile Glu Val Leu Lys Lys Lys His Ala Ala Gly Thr Tyr
195 200 205

Glu Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe
210 215 220

Glu Gly Leu Leu Pro Glu Gly Leu Asn Ile Phe Ala Thr Thr Ala Ser
225 230 235 240

Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Tyr Pro
245 250 255

Ser Pro Pro Pro Glu Tyr Glu Thr Cys Leu Gly Asp Leu Tyr Ser Val
260 265 270

Ala Trp Met Glu Asp Ser Asp Ile His Asn Leu Arg Ser Glu Thr Leu
275 280 285

His Gln Gln Tyr Glu Leu Val Lys Ser Arg Thr Ala Ser Asp Asn Ser
290 295 300

Pro Tyr Gly Ser His Val Met Gln Tyr Gly Asp Ile Pro Leu Ser Lys
305 310 315 320

Asn Asn Leu Phe Met Tyr Met Gly Thr Asn Pro Ala Asn Asp Asn Tyr
325 330 335

Thr Phe Met Pro Gln Asn Phe Leu Arg Pro Ser Ser Ser Lys Ala Val
340 345 350

Asn Gln Arg Asp Ala Asp Leu Val His Phe Trp His Lys Tyr Arg Lys
355 360 365

Ala Pro Glu Gly Ser Ala Arg Lys Ala Gln Ala Gln Lys Glu Phe Leu
370 375 380

Glu Ala Met Ser His Arg Met His Ile Asp Glu Ser Val Lys Leu Ile
385 390 395 400

Gly Lys Leu Leu Phe Gly Ile Lys Lys Gly Pro Glu Val Leu Ser Ala
405 410 415

Val Arg Pro Ala Gly Gln Pro Leu Val Asp Asp Trp Asp Cys Leu Lys
420 425 430

Thr Met Val Arg Ser Phe Glu Thr Tyr Cys Gly Ser Leu Ser Gln Tyr
435 440 445

Gly Met Lys His Met Arg Ser Leu Ala Asn Ile Cys Asn Ala Gly Met
450 455 460

Thr Lys Glu Gln Met Ala Glu Ala Ser Ala Gln Ala Cys Val Asn Val
465 470 475 480

Pro Ser Gly Arg Trp Ser Ser Leu His Arg Gly Phe Ser Ala
485 490

<210> 36
<211> 482
<212> PRT
<213> Solanum tuberosum

<400> 36

Met Asn Arg Ser Ile Ala Gly Val Leu Phe Leu Ile Ala Leu Ser Leu
1 5 10 15

Asn Val Ser Val Ser Glu Ser Arg Asn Phe Leu Lys Leu Pro Ser Glu
20 25 30

Gly Ser Arg Phe Phe Asp Ala Asp Glu Asn Asp Ser Val Gly Thr Arg
35 40 45

Trp Ala Ile Leu Leu Ala Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His
50 55 60

Gln Ala Asp Ile Cys His Ala Tyr Gln Leu Leu Lys Lys Gly Gly Leu
65 70 75 80

Lys Asp Glu Asn Ile Val Val Phe Met Tyr Asp Asp Ile Ala Asn Asn
85 90 95

Glu Glu Asn Pro Arg Gln Gly Val Ile Ile Asn Ser Pro His Gly Glu
100 105 110

Asp Val Tyr Lys Gly Val Pro Lys Asp Tyr Thr Gly Asp Asp Val Thr
115 120 125

Val Asn Asn Phe Leu Ala Ala Leu Leu Gly Asn Lys Thr Ala Ile Thr
130 135 140

Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro Asn Asp His Ile Phe
145 150 155 160

Ile Phe Tyr Ser Asp His Gly Gly Ala Gly Val Ile Gly Met Pro Thr
165 170 175

Asp Pro Tyr Leu Tyr Ala Asn Asp Leu Ile Asp Ala Leu Lys Lys Lys
180 185 190

His Ala Ser Gly Thr Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys
195 200 205

Glu Ser Gly Ser Met Phe Glu Gly Leu Leu Pro Glu Gly Leu Asn Ile
210 215 220

Tyr Ala Thr Thr Ala Ser Asn Ala Asp Glu Ser Ser Trp Gly Thr Tyr
225 230 235 240

Cys Pro Gly Glu Phe Pro Ser Pro Pro Ile Glu Tyr Gly Thr Cys Leu
245 250 255

Gly Asp Leu Tyr Ser Ile Ser Trp Met Glu Asp Ser Glu Arg His Asn
260 265 270

Leu Arg Thr Glu Thr Leu Lys Gln Gln Tyr His Leu Val Lys Glu Arg
275 280 285

Thr Ala Ser Gly Asn Pro Ala Tyr Gly Ser His Val Met Gln Tyr Gly
290 295 300

Asp Val His Leu Ser Lys Asp Val Leu Phe Leu Tyr Met Gly Thr Asp
305 310 315 320

Pro Ala Asn Asp Asn Ser Thr Phe Met Asp Asp Asn Ser Met Arg Val
325 330 335

Ser Lys Ala Val Asn Gln Arg Asp Ala Asp Leu Val His Phe Trp Tyr
340 345 350

Lys Phe His Lys Ala Pro Glu Gly Ser Val Arg Lys Thr Glu Ala Gln
355 360 365

Lys Gln Leu Asn Glu Ala Ile Ser His Arg Met His Leu Asp Asn Ser

370

375

380

Ile Ala Leu Val Gly Lys Leu Leu Phe Gly Ile Lys Lys Gly Pro Glu
 385 390 395 400

Val Leu Thr Ser Val Arg Pro Ala Gly Gln Pro Leu Val Asp Asp Trp
 405 410 415

Asp Cys Leu Lys Ser Tyr Val Arg Thr Phe Glu Thr His Cys Gly Ser
 420 425 430

Leu Ser Gln Tyr Gly Met Lys His Met Arg Ser Val Ala Asn Ile Cys
 435 440 445

Asn Ala Gly Ile Lys Met Glu Gln Met Val Glu Ala Ser Ala Gln Ala
 450 455 460

Cys Pro Ser Val Pro Ser Asn Thr Trp Ser Ser Leu Gln Arg Gly Phe
 465 470 475 480

Ser Ala

<210> 37

<211> 482

<212> PRT

<213> Solanum tuberosum

<400> 37

Met Asn Arg Ser Ile Ala Gly Val Leu Phe Leu Ile Ala Leu Ser Leu
 1 5 10 15

Asn Val Ser Val Ser Glu Ser Arg Asn Phe Leu Lys Leu Pro Ser Glu
 20 25 30

Gly Ser Arg Phe Phe Asp Ala Asp Glu Asn Asp Ser Val Gly Thr Arg
 35 40 45

Trp Ala Ile Leu Leu Ala Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His
 50 55 60

Gln Ala Asp Ile Cys His Ala Tyr Gln Leu Leu Lys Lys Gly Gly Leu
65 70 75 80

Lys Asp Glu Asn Ile Val Val Phe Met Tyr Asp Asp Ile Ala Asn Asn
85 90 95

Glu Glu Asn Pro Arg Gln Gly Val Ile Ile Asn Ser Pro His Gly Glu
100 105 110

Asp Val Tyr Lys Gly Val Pro Lys Asp Tyr Thr Gly Asp Asp Val Thr
115 120 125

Val Asn Asn Phe Leu Ala Ala Leu Leu Gly Asn Lys Thr Ala Ile Thr
130 135 140

Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro Asn Asp His Ile Phe
145 150 155 160

Ile Phe Tyr Ser Asp His Gly Gly Ala Gly Val Ile Gly Met Pro Thr
165 170 175

Asp Pro Tyr Leu Tyr Ala Asn Asp Leu Ile Asp Ala Leu Lys Lys Lys
180 185 190

His Ala Ser Gly Thr Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys
195 200 205

Glu Ser Gly Ser Met Phe Glu Gly Leu Leu Pro Glu Gly Leu Asn Ile
210 215 220

Tyr Ala Thr Thr Ala Ser Asn Ala Asp Glu Ser Ser Trp Gly Thr Tyr
225 230 235 240

Cys Pro Gly Glu Phe Pro Ser Pro Pro Ile Glu Tyr Gly Thr Cys Leu
245 250 255

Gly Asp Leu Tyr Ser Ile Ser Trp Met Glu Asp Ser Gly Arg His Asn
260 265 270

Leu Arg Thr Glu Thr Leu Lys Gln Gln Tyr His Leu Val Lys Glu Arg
275 280 285

Thr Ala Ser Gly Asn Pro Ala Tyr Gly Ser His Val Met Gln Tyr Gly
290 295 300

Asp Val His Leu Ser Lys Asp Val Leu Phe Leu Tyr Met Gly Thr Asp
305 310 315 320

Pro Ala Asn Asp Asn Ser Thr Phe Met Asp Asp Asn Ser Met Arg Val
325 330 335

Ser Lys Ala Val Asn Gln Arg Asp Ala Asp Leu Val His Phe Trp Tyr
340 345 350

Lys Phe His Lys Ala Pro Glu Gly Ser Val Arg Lys Thr Glu Ala Gln
355 360 365

Lys Gln Leu Asn Glu Ala Ile Ser His Arg Met His Leu Asp Asn Ser
370 375 380

Ile Ala Leu Val Gly Lys Leu Leu Phe Gly Ile Lys Lys Gly Pro Glu
385 390 395 400

Val Leu Thr Ser Val Arg Pro Ala Gly Gln Pro Leu Val Asp Asp Trp
405 410 415

Asp Cys Leu Lys Ser Tyr Val Arg Thr Phe Glu Thr His Cys Gly Ser
420 425 430

Leu Ser Gln Tyr Gly Met Lys His Met Arg Ser Val Ala Asn Ile Cys
435 440 445

Asn Ala Gly Ile Lys Met Glu Gln Met Val Glu Ala Ser Ala Gln Ala
450 455 460

Cys Pro Ser Val Pro Ser Asn Thr Trp Ser Ser Leu Gln Arg Gly Phe
465 470 475 480

Ser Ala

<210> 38
<211> 454
<212> PRT
<213> Glycine max

<400> 38

Met Asp Arg Phe Pro Ile Leu Phe Leu Leu Ala Thr Leu Ile Thr Leu
1 5 10 15

Ala Ser Gly Ala Arg His Asp Ile Leu Arg Leu Pro Ser Glu Ala Ser
20 25 30

Thr Phe Phe Lys Ala Pro Gly Gly Asp Gln Asn Asp Glu Gly Thr Arg
35 40 45

Trp Ala Val Leu Ile Ala Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His
50 55 60

Gln Ser Asp Val Cys His Ala Tyr Gln Leu Leu Arg Lys Gly Gly Leu
65 70 75 80

Lys Glu Glu Asn Ile Val Val Phe Met Tyr Asp Asp Ile Ala Phe Asn
85 90 95

Glu Glu Asn Pro Arg Pro Gly Val Ile Ile Asn Ser Pro His Gly Asn
100 105 110

Asp Val Tyr Lys Gly Val Pro Lys Asp Tyr Ile Gly Glu Asp Val Thr
115 120 125

Val Gly Asn Phe Phe Ala Ala Ile Leu Gly Asn Lys Ser Ala Leu Thr
130 135 140

Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro Asn Asp His Ile Phe
145 150 155 160

Ile Tyr Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Met Pro Thr
165 170 175

Asn Pro Tyr Met Tyr Ala Ser Asp Leu Ile Glu Val Leu Lys Lys Lys
180 185 190

His Ala Ser Gly Ser Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys
195 200 205

Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Glu Gly Leu Asn Ile
210 215 220

Tyr Ala Thr Thr Ala Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr
225 230 235 240

Cys Pro Gly Glu Tyr Pro Ser Pro Pro Ser Glu Tyr Glu Thr Cys Leu
245 250 255

Gly Asp Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Ile His Asn
260 265 270

Leu Gln Thr Glu Thr Leu His Gln Gln Tyr Glu Leu Val Lys Gln Arg
275 280 285

Thr Met Asn Gly Asn Ser Ile Tyr Gly Ser His Val Met Gln Tyr Gly
290 295 300

Asp Ile Gly Leu Ser Glu Asn Asn Leu Val Leu Tyr Leu Asp Leu Ile
305 310 315 320

His Phe Trp Asp Lys Phe Arg Lys Ala Pro Val Gly Ser Ser Arg Lys
325 330 335

Ala Ala Ala Glu Lys Gln Ile Leu Glu Ala Met Ser His Arg Met His
340 345 350

Ile Asp Asp Ser Met Lys Arg Ile Gly Lys Leu Phe Phe Gly Ile Glu
355 360 365

Lys Gly Pro Glu Leu Leu Ser Ser Val Arg Pro Ala Gly Gln Pro Leu
370 375 380

Val Asp Asp Trp Asp Cys Leu Lys Thr Leu Val Arg Thr Phe Glu Thr
385 390 395 400

His Cys Gly Ser Leu Ser Gln Tyr Gly Met Lys His Met Arg Ser Phe

405

410

415

Ala Asn Phe Cys Asn Ala Gly Ile Arg Lys Glu Gln Met Ala Glu Ala
 420 425 430

Ser Ala Gln Ala Cys Val Asn Ile Pro Ala Ser Ser Trp Ser Ser Met
 435 440 445

His Arg Gly Phe Ser Ala
 450

<210> 39

<211> 490

<212> PRT

<213> Papaver rhoeas

<400> 39

Met Val Lys Phe Leu Phe Ser Val Ile Ile Leu Phe Phe Leu Leu Ser
 1 5 10 15

Ala Val Gly Ser Ser Ala Arg Asn Ile Glu Glu Asp Gly Val Ile Arg
 20 25 30

Leu Pro Ser Glu Val Lys Asp Phe Ile Asn Gly Lys Asn Ile Asp Asp
 35 40 45

Asp Ser Val Gly Gly Thr Arg Trp Ala Val Leu Ile Ala Gly Ser Ser
 50 55 60

Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp Val Cys His Ala Tyr Gln
 65 70 75 80

Val Leu Lys Arg Gly Gly Val Lys Asp Glu Asn Ile Val Val Phe Met
 85 90 95

Tyr Asp Asp Ile Ala Leu Asn Glu Glu Asn Pro Arg Pro Gly Val Ile
 100 105 110

Ile Asn His Pro Lys Gly Glu Asp Val Tyr Ala Gly Val Pro Lys Asp
 115 120 125

Tyr Thr Gly Arg Asp Val Thr Ala His Asn Phe Tyr Ser Val Leu Leu
130 135 140

Gly Asn Lys Thr Ala Val Lys Gly Gly Ser Gly Lys Val Ile Asp Ser
145 150 155 160

Gly Pro Asn Asp His Ile Phe Ile Tyr Tyr Ser Asp His Gly Gly Pro
165 170 175

Gly Val Leu Gly Met Pro Thr Tyr Pro Tyr Leu Tyr Ala Asp Asp Leu
180 185 190

Val Asn Val Leu Lys Gln Lys His Ala Leu Gly Ala Tyr Lys Ser Leu
195 200 205

Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Ile
210 215 220

Leu Pro Lys Gly Leu Asn Ile Tyr Ala Thr Thr Ala Ser Asn Ala Glu
225 230 235 240

Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Phe Pro Ser Pro Pro
245 250 255

Ser Glu Tyr Glu Thr Cys Leu Gly Asp Leu Tyr Ser Val Ala Trp Met
260 265 270

Glu Asp Ser Asp Val His Asn Leu Arg Ser Glu Thr Leu Lys Gln Gln
275 280 285

Tyr His Leu Val Lys Glu Arg Thr Gln Asn Ala Asn Ser Ala Tyr Gly
290 295 300

Ser His Val Met Gln Tyr Gly Asp Leu Glu Val Ser Lys Glu Asp Leu
305 310 315 320

Phe Leu Tyr Met Gly Thr Asn Pro Ala Asn Asp Asn Asn Lys Phe Ile
325 330 335

Glu Gln Asn Ser Leu Pro Ser Leu Ser Gly Ser Val Asn Gln Arg Glu
340 345 350

Ala Asp Leu Ile His Phe Trp Gln Lys Tyr Arg Lys Ala Pro Glu Gly
355 360 365

Ser Gln Arg Lys Ala Asp Ala Gln Lys Gln Phe Val Glu Val Met Ala
370 375 380

His Arg Met His Val Asp His Ser Ile Lys Leu Ile Gly Lys Leu Leu
385 390 395 400

Phe Gly Phe Glu Lys Gly Pro Gln Val Leu Glu Ala Val Arg Pro Ala
405 410 415

Gly Gln Pro Leu Val Asp Asp Trp Asp Cys Leu Lys Thr Met Val Arg
420 425 430

Thr Phe Glu Ala Gln Cys Gly Ser Leu Ser Gln Tyr Gly Met Lys His
435 440 445

Met Arg Ser Val Ala Asn Ile Cys Asn Ala Gly Ile Lys Lys Glu Gln
450 455 460

Met Ala Glu Ala Ala Ser Gln Ala Cys Val Thr Ile Pro Asn Gly Ser
465 470 475 480

Trp Ser Ser Thr His Gln Gly Phe Ser Ala
485 490

<210> 40
<211> 483
<212> PRT
<213> Vigna radiata

<400> 40

Met Ala Thr Thr Thr Thr Ser Leu Ser Thr Leu Phe Leu Leu Phe Leu
1 5 10 15

Ala Thr Val Ala Leu Val Ala Ala Gly Arg Asp Leu Val Gly Asp Phe
20 25 30

Leu Arg Leu Pro Ser Asp Ser Gly Asn Asp Asp Asn Val Lys Gly Thr

35

40

45

Arg Trp Ala Ile Leu Phe Ala Gly Ser Asn Gly Tyr Trp Asn Tyr Arg
 50 55 60

His Gln Ala Asp Ile Cys His Ala Tyr Gln Ile Leu Arg Lys Gly Gly
 65 70 75 80

Leu Lys Glu Glu Asn Ile Ile Val Phe Met Tyr Asp Asp Ile Ala Phe
 85 90 95

Asn Trp Asp Asn Pro Arg Pro Gly Val Ile Ile Asn Lys Pro Asp Gly
 100 105 110

Asp Asp Val Tyr Glu Gly Val Pro Lys Asp Tyr Thr Gly Glu Asp Ala
 115 120 125

Thr Ala His Asn Phe Tyr Ser Ala Leu Leu Gly Asp Lys Ser Ala Leu
 130 135 140

Thr Gly Gly Ser Gly Lys Val Val Asn Ser Gly Pro Asp Asp Arg Ile
 145 150 155 160

Phe Ile Phe Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Thr Pro
 165 170 175

Ala Gly Pro Tyr Ile Tyr Ala Ser Asp Leu Val Glu Val Leu Lys Lys
 180 185 190

Lys His Ala Ser Gly Thr Tyr Lys Asn Leu Val Phe Tyr Leu Glu Ala
 195 200 205

Cys Glu Ala Gly Ser Ile Phe Glu Gly Leu Leu Pro Glu Asp Ile Asn
 210 215 220

Ile Tyr Ala Thr Thr Ala Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr
 225 230 235 240

Tyr Cys Pro Gly Glu Tyr Pro Ser Pro Pro Pro Glu Tyr Ser Thr Cys
 245 250 255

Leu Gly Asp Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Arg His
260 265 270

Asn Leu Arg Thr Glu Ser Leu His Gln Gln Tyr Lys Val Val Lys Asp
275 280 285

Arg Thr Leu Ser Gly Gly Trp Tyr Gly Ser His Val Met Gln Tyr Gly
290 295 300

Asp Val Glu Phe Ser Lys Asp Thr Leu Phe Leu Tyr Leu Gly Thr Asp
305 310 315 320

Pro Ala Asn Asp Asn Leu Thr Phe Val Asp Glu Asn Ser Leu Trp Ser
325 330 335

Ser Ser Thr Ala Val Asn Gln Arg Asp Ala Asp Leu Val His Phe Trp
340 345 350

His Lys Phe Arg Lys Ala Pro Glu Gly Ser Pro Lys Lys Asn Glu Ala
355 360 365

Arg Lys Gln Val Leu Glu Val Met Ser His Arg Met His Ile Asp Asp
370 375 380

Ser Val Lys Leu Val Gly Lys Leu Leu Phe Gly Phe Glu Lys Ala Pro
385 390 395 400

Glu Val Leu Asn Ala Val Arg Pro Ala Gly Ser Ala Leu Val Asp Asp
405 410 415

Trp Ala Cys Leu Lys Thr Met Val Arg Thr Phe Glu Thr His Cys Gly
420 425 430

Ser Leu Ser Gln Tyr Gly Met Lys His Met Arg Ser Phe Ala Asn Ile
435 440 445

Cys Asn Val Gly Ile Lys Lys Glu Gln Met Ala Glu Ala Ser Ala Gln
450 455 460

Ala Cys Val Thr Val Pro Ala Ser Ser Trp Ser Ser Leu Gln Arg Gly

465

470

475

480

Phe Ser Ala

<210> 41

<211> 489

<212> PRT

<213> Nicotiana tabacum

<400> 41

Met Ile Arg Tyr Val Ala Gly Thr Leu Phe Leu Ile Gly Leu Ala Leu
 1 5 10 15

Asn Val Ala Val Ser Glu Ser Arg Asn Val Leu Lys Leu Pro Ser Glu
 20 25 30

Val Ser Arg Phe Phe Gly Ala Asp Glu Ser Asn Ala Gly Asp His Asp
 35 40 45

Asp Asp Ser Val Gly Thr Arg Trp Ala Ile Leu Leu Ala Gly Ser Asn
 50 55 60

Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp Ile Cys His Ala Tyr Gln
 65 70 75 80

Leu Leu Lys Lys Gly Gly Leu Lys Asp Glu Asn Ile Val Val Phe Met
 85 90 95

Tyr Asp Asp Ile Ala Asn Asn Glu Glu Asn Pro Arg Arg Gly Val Ile
 100 105 110

Ile Asn Ser Pro His Gly Glu Asp Val Tyr Lys Gly Val Pro Lys Asp
 115 120 125

Tyr Thr Gly Asp Asp Val Thr Val Asp Asn Phe Phe Ala Val Ile Leu
 130 135 140

Gly Asn Lys Thr Ala Leu Ser Gly Gly Ser Gly Lys Val Val Asn Ser
 145 150 155 160

Gly Pro Asn Asp His Ile Phe Ile Phe Tyr Ser Asp His Gly Gly Pro
165 170 175

Gly Val Leu Gly Met Pro Thr Asp Pro Tyr Leu Tyr Ala Asn Asp Leu
180 185 190

Ile Asp Val Leu Lys Lys Lys His Ala Ser Gly Thr Tyr Lys Ser Leu
195 200 205

Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu
210 215 220

Leu Pro Glu Gly Leu Asn Ile Tyr Ala Thr Thr Ala Ser Asn Ala Glu
225 230 235 240

Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Tyr Pro Ser Pro Pro
245 250 255

Ile Glu Tyr Met Thr Cys Leu Gly Asp Leu Tyr Ser Ile Ser Trp Met
260 265 270

Glu Asp Ser Glu Leu His Asn Leu Arg Thr Glu Ser Leu Lys Gln Gln
275 280 285

Tyr His Leu Val Lys Glu Arg Thr Ala Thr Gly Asn Pro Val Tyr Gly
290 295 300

Ser His Val Met Gln Tyr Gly Asp Leu His Leu Ser Lys Asp Ala Leu
305 310 315 320

Tyr Leu Tyr Met Gly Thr Asn Pro Ala Asn Asp Asn Tyr Thr Phe Met
325 330 335

Asp Asp Asn Ser Leu Arg Val Ser Lys Ala Val Asn Gln Arg Asp Ala
340 345 350

Asp Leu Leu His Phe Trp His Lys Phe Arg Thr Ala Pro Glu Gly Ser
355 360 365

Val Arg Lys Ile Glu Ala Gln Lys Gln Leu Asn Glu Ala Ile Ser His
370 375 380

Arg Val His Leu Asp Asn Ser Val Ala Leu Val Gly Lys Leu Leu Phe
385 390 395 400

Gly Ile Glu Lys Gly Pro Glu Val Leu Ser Gly Val Arg Pro Ala Gly
405 410 415

Gln Pro Leu Val Asp Asp Trp Asp Cys Leu Lys Ser Phe Val Arg Thr
420 425 430

Phe Glu Thr His Cys Gly Ser Leu Ser Gln Tyr Gly Met Lys His Met
435 440 445

Arg Ser Ile Ala Asn Ile Cys Asn Ala Gly Ile Lys Lys Glu Gln Met
450 455 460

Val Glu Ala Ser Ala Gln Ala Cys Pro Ser Val Pro Ser Asn Thr Trp
465 470 475 480

Ser Ser Leu His Arg Gly Phe Ser Ala
485

<210> 42
<211> 482
<212> PRT
<213> Solanum lycopersicum

<400> 42

Met Asn Arg Ser Val Ala Gly Val Leu Phe Leu Ile Ala Leu Ser Leu
1 5 10 15

Asn Val Ser Val Ser Glu Ser Arg Asn Phe Leu Lys Leu Pro Ser Glu
20 25 30

Gly Ser Arg Phe Phe Asp Ala Asp Glu Ile Asp Ser Val Gly Thr Arg
35 40 45

Trp Ala Ile Leu Leu Ala Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His
50 55 60

Gln Ala Asp Ile Cys His Ala Tyr Gln Leu Leu Lys Lys Gly Gly Leu

80

95

110

125

140

160

Pro

190

205

220

240

CvS

270

285

Thr Ala Ser Gly Asn Pro Ala Tyr Gly Ser His Val Met Gln Tyr Gly
290 295 300

Asp Val His Leu Ser Lys Asp Ala Val Phe Leu Tyr Met Gly Thr Asp
305 310 315 320

Pro Ala Asn Asp Asn Ser Thr Phe Met Asp Asp Asn Ser Leu Arg Val
325 330 335

Ser Lys Ala Val Asn Gln Arg Asp Ala Asp Leu Val His Phe Trp Tyr
340 345 350

Lys Phe His Lys Ala Pro Glu Gly Ser Val Ser Lys Thr Glu Ala Gln
355 360 365

Lys Arg Leu Asn Glu Ala Ile Ser His Arg Met His Leu Asp Asn Ser
370 375 380

Ile Ala Leu Val Gly Lys Leu Leu Phe Gly Ile Lys Lys Gly Pro Glu
385 390 395 400

Val Leu Thr Ser Val Arg Pro Ala Gly Gln Pro Leu Val Asp Asn Trp
405 410 415

Asp Cys Leu Lys Ser Tyr Val Arg Thr Phe Glu Thr His Cys Gly Ser
420 425 430

Leu Ser Gln Tyr Gly Met Lys His Met Arg Ser Val Ala Asn Ile Cys
435 440 445

Asn Ala Gly Ile Lys Met Glu Gln Met Val Glu Ala Ser Ala Gln Ala
450 455 460

Cys Pro Ser Val Pro Ser Tyr Thr Trp Ser Ser Leu His Arg Gly Phe
465 470 475 480

Ser Ala

<211> 494
<212> PRT
<213> Citrus clementina

<400> 43

Met Thr Arg Leu Ala Ser Gly Val Leu Ile Thr Leu Leu Val Ala Leu
1 5 10 15

Ala Gly Ile Ala Asp Gly Ser Arg Asp Ile Ala Gly Asp Ile Leu Lys
20 25 30

Leu Pro Ser Glu Ala Tyr Arg Phe Phe His Asn Gly Gly Gly Gly Ala
35 40 45

Lys Val Asn Asp Asp Asp Ser Val Gly Thr Arg Trp Ala Val Leu
50 55 60

Leu Ala Gly Ser Asn Gly Phe Trp Asn Tyr Arg His Gln Ala Asp Ile
65 70 75 80

Cys His Ala Tyr Gln Leu Leu Arg Lys Gly Gly Leu Lys Asp Glu Asn
85 90 95

Ile Ile Val Phe Met Tyr Asp Asp Ile Ala Phe Asn Glu Glu Asn Pro
100 105 110

Arg Pro Gly Val Ile Ile Asn His Pro His Gly Asp Asp Val Tyr Lys
115 120 125

Gly Val Pro Lys Asp Tyr Thr Gly Glu Asp Val Thr Val Glu Asn Phe
130 135 140

Phe Ala Val Ile Leu Gly Asn Lys Thr Ala Leu Thr Gly Gly Ser Gly
145 150 155 160

Lys Val Val Asp Ser Gly Pro Asn Asp His Ile Phe Ile Phe Tyr Ser
165 170 175

Asp His Gly Gly Pro Gly Val Leu Gly Met Pro Thr Ser Arg Tyr Ile
180 185 190

Tyr Ala Asp Glu Leu Ile Asp Val Leu Lys Lys Lys His Ala Ser Gly
195 200 205

Asn Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser
210 215 220

Ile Phe Glu Gly Leu Leu Pro Glu Gly Leu Asn Ile Tyr Ala Thr Thr
225 230 235 240

Ala Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu
245 250 255

Ile Pro Gly Pro Pro Pro Glu Tyr Ser Thr Cys Leu Gly Asp Leu Tyr
260 265 270

Ser Ile Ala Trp Met Glu Asp Ser Asp Ile His Asn Leu Arg Thr Glu
275 280 285

Thr Leu His Gln Gln Tyr Glu Leu Val Lys Thr Arg Thr Ala Ser Tyr
290 295 300

Asn Ser Tyr Gly Ser His Val Met Gln Tyr Gly Asp Ile Gly Leu Ser
305 310 315 320

Lys Asn Asn Leu Phe Thr Tyr Leu Gly Thr Asn Pro Ala Asn Asp Asn
325 330 335

Tyr Thr Phe Val Asp Glu Asn Ser Leu Arg Pro Ala Ser Lys Ala Val
340 345 350

Asn Gln Arg Asp Ala Asp Leu Leu His Phe Trp Asp Lys Tyr Arg Lys
355 360 365

Ala Pro Glu Gly Thr Pro Arg Lys Ala Glu Ala Gln Lys Gln Phe Phe
370 375 380

Glu Ala Met Ser His Arg Met His Val Asp His Ser Ile Lys Leu Ile
385 390 395 400

Gly Lys Leu Leu Phe Gly Ile Glu Lys Gly Pro Glu Ile Leu Asn Thr
405 410 415

Val Arg Pro Ala Gly Gln Pro Leu Val Asp Asp Trp Gly Cys Leu Lys
420 425 430

Ser Leu Val Arg Thr Phe Glu Ser His Cys Gly Ala Leu Ser Gln Tyr
435 440 445

Gly Met Lys His Met Arg Ser Leu Ala Asn Ile Cys Asn Thr Gly Ile
450 455 460

Gly Lys Glu Lys Met Ala Glu Ala Ser Ala Gln Ala Cys Glu Asn Ile
465 470 475 480

Pro Ser Gly Pro Trp Ser Ser Leu Asp Lys Gly Phe Ser Ala
485 490

<210> 44
<211> 481
<212> PRT
<213> Nicotiana tabacum

<400> 44

Met Ile Ser Tyr Ala Ala Gly Ile Phe Phe Leu Val Gly Phe Ser Ile
1 5 10 15

Ala Ala Ala Ala Asp Gly Arg Asn Val Leu Lys Leu Pro Ser Glu Ala
20 25 30

Ser Arg Phe Phe Asp Glu Ala Asp Asp Ser Val Gly Thr Arg Trp Ala
35 40 45

Val Leu Leu Ala Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His Gln Ala
50 55 60

Asp Val Cys His Ala Tyr Gln Leu Leu Arg Lys Gly Gly Leu Lys Asp
65 70 75 80

Glu Asn Ile Ile Met Phe Met Tyr Asp Asp Ile Ala Tyr Asn Glu Glu
85 90 95

Asn Pro Arg Gln Gly Val Ile Ile Asn Ser Pro Ala Gly Glu Asp Val

100

105

110

Tyr Lys Gly Val Pro Lys Asp Tyr Thr Gly Asp Asp Val Asn Val Asp
 115 120 125

Asn Phe Leu Ala Val Leu Leu Gly Asn Lys Thr Ala Leu Thr Gly Gly
 130 135 140

Ser Gly Lys Val Val Asp Ser Gly Pro Asn Asp His Ile Phe Ile Phe
 145 150 155 160

Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Met Pro Thr Asn Pro
 165 170 175

Tyr Leu Tyr Ala Ser Asp Leu Ile Asp Val Leu Lys Lys Lys His Ala
 180 185 190

Ser Gly Thr Tyr Lys Ser Leu Val Leu Tyr Ile Glu Ala Cys Glu Ser
 195 200 205

Gly Ser Ile Phe Glu Gly Leu Leu Pro Lys Gly Leu Asn Ile Tyr Ala
 210 215 220

Thr Thr Ala Ser Asn Ala Val Glu Ser Ser Trp Gly Thr Tyr Cys Pro
 225 230 235 240

Gly Asp Tyr Pro Ser Leu Pro Pro Gly Tyr Glu Thr Cys Leu Gly Asp
 245 250 255

Leu Tyr Ala Val Ser Trp Met Glu Asp Ser Glu Met His Asn Leu Arg
 260 265 270

Thr Glu Asn Leu Arg Gln Gln Tyr His Leu Val Lys Glu Arg Thr Ala
 275 280 285

Asn Gly Asn Ser Ala Tyr Gly Ser His Val Leu Gln Phe Gly Asp Leu
 290 295 300

Gln Leu Gly Met Asp Ser Leu Phe Met Tyr Met Gly Thr Asn Pro Ala
 305 310 315 320

Asn Asp Asn Tyr Thr Tyr Val Asp Asp Asn Ser Leu Arg Ala Ser Ser
325 330 335

Lys Ala Val Asn Gln Arg Asp Ala Asp Leu Leu His Phe Trp Asp Lys
340 345 350

Phe Arg Lys Ala Pro Glu Gly Ser Ala Arg Lys Val Glu Ala Gln Lys
355 360 365

Gln Phe Thr Glu Ala Met Ser His Arg Met His Leu Asp Asn Ser Met
370 375 380

Ala Leu Val Gly Lys Leu Leu Phe Gly Ile Gln Lys Gly Pro Glu Val
385 390 395 400

Leu Lys Arg Val Arg Pro Val Gly Gln Pro Leu Val Asp Asp Trp Thr
405 410 415

Cys Leu Lys Tyr Phe Val Arg Thr Phe Glu Thr His Cys Gly Ser Leu
420 425 430

Ser Gln Tyr Gly Met Lys His Met Arg Ser Ile Ala Asn Ile Cys Asn
435 440 445

Ala Gly Ile Lys Met Glu Gln Met Val Glu Ala Ser Thr Gln Ala Cys
450 455 460

Pro Ser Val Pro Thr Asn Ile Trp Ser Ser Leu His Arg Gly Phe Ser
465 470 475 480

Ala

<210> 45
<211> 481
<212> PRT
<213> Capsella rubella

<400> 45

Met Thr Arg Ile Val Ala Val Ile Val Val Val Leu Phe Leu Ser Leu
1 5 10 15

Val Ala Ala Ala Ser Asp Asn Phe Ile Arg Leu Pro Ser Glu Ala Ser
20 25 30

Lys Phe Phe Arg Pro Asn Asn Glu Asn Asp Asp Ser Thr Arg Trp Ala
35 40 45

Val Leu Val Ala Gly Ser Ser Gly Tyr Trp Asn Tyr Arg His Gln Ala
50 55 60

Asp Val Cys His Ala Tyr Gln Leu Leu Lys Lys Gly Gly Val Lys Glu
65 70 75 80

Glu Asn Ile Val Val Phe Met Tyr Asp Asp Ile Ala Asn Asn Glu Glu
85 90 95

Asn Pro Arg Pro Gly Val Ile Ile Asn Ser Pro Asn Gly Glu Asp Val
100 105 110

Tyr Asn Gly Val Pro Lys Asp Tyr Thr Gly Asp Glu Val Asn Val Asn
115 120 125

Asn Phe Phe Ala Val Leu Leu Gly Asn Lys Thr Ala Leu Lys Gly Gly
130 135 140

Ser Gly Lys Val Val Asn Ser Gly Pro Asn Asp His Ile Phe Ile Tyr
145 150 155 160

Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Met Pro Thr Ser Pro
165 170 175

Tyr Leu Tyr Ala Lys Asp Leu Asn Asp Val Leu Lys Lys Lys His Ala
180 185 190

Ser Gly Thr Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser
195 200 205

Gly Ser Ile Phe Glu Gly Leu Leu Pro Glu Gly Leu Asn Ile Tyr Ala
210 215 220

Thr Thr Ala Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro
225 230 235 240

Gly Glu Asp Pro Ser Pro Pro Ser Glu Tyr Glu Thr Cys Leu Gly Asp
245 250 255

Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Lys His Asn Leu Gln
260 265 270

Thr Glu Ser Leu His Gln Gln Tyr Glu Leu Val Lys Lys Arg Thr Ala
275 280 285

Gly Thr Gly Ser Ser Tyr Gly Ser His Val Leu Glu Phe Gly Asp Ile
290 295 300

Gly Leu Ser Lys Glu Lys Leu Val Leu Tyr Met Gly Thr Asn Pro Ala
305 310 315 320

Asn Glu Asn Phe Thr Phe Val Asp Glu Asn Ser Ser Leu Arg Leu Pro
325 330 335

Ser Arg Val Thr Asn Gln Arg Asp Ala Asp Leu Val His Phe Trp Asp
340 345 350

Lys Tyr Arg Lys Ala Pro Glu Gly Ser Ala Arg Lys Val Glu Ala Gln
355 360 365

Lys Gln Val Leu Glu Ala Met Ser His Arg Leu His Val Asp Asn Ser
370 375 380

Val Leu Leu Ile Gly Lys Leu Leu Phe Gly Leu Glu Gly Pro Ala Val
385 390 395 400

Leu Asn Lys Val Arg Pro Ser Gly Arg Pro Leu Val Asp Asp Trp Asp
405 410 415

Cys Leu Lys Ser Met Val Arg Ala Phe Glu Arg His Cys Gly Ser Leu
420 425 430

Ser Gln Tyr Gly Ile Lys His Met Arg Ser Ile Ala Asn Ile Cys Asn
435 440 445

Ala Gly Ile Gln Met Gly Leu Met Glu Glu Ala Ala Lys Gln Ala Cys
450 455 460

Pro Ser Ile Pro Ala Gly Pro Trp Ser Ser Leu His Arg Gly Phe Ser
465 470 475 480

Ala

<210> 46
<211> 479
<212> PRT
<213> Arabidopsis lyrata subsp. lyrata

<400> 46

Met Thr Thr Val Ala Val Thr Phe Leu Ala Leu Phe Leu Tyr Leu Val
1 5 10 15

Ala Ala Val Ser Gly Asp Val Ile Lys Leu Pro Ser Gln Ala Ser Lys
20 25 30

Phe Phe His Pro Thr Glu Asn Asp Asp Asp Ser Thr Arg Trp Ala Val
35 40 45

Leu Val Ala Gly Ser Ser Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp
50 55 60

Val Cys His Ala Tyr Gln Leu Leu Lys Lys Gly Gly Val Lys Glu Glu
65 70 75 80

Asn Ile Val Val Phe Met Tyr Asp Asp Ile Ala Lys Asn Glu Glu Asn
85 90 95

Pro Arg Pro Gly Val Ile Ile Asn Ser Pro Asn Gly Glu Asp Val Tyr
100 105 110

Asn Gly Val Pro Lys Asp Tyr Thr Gly Asp Asp Val Asn Val Asp Asn
115 120 125

Leu Leu Ala Val Ile Leu Gly Asn Lys Thr Ala Val Lys Gly Gly Ser

130

135

140

Gly Lys Val Val Asp Ser Gly Pro Asn Asp His Ile Phe Ile Tyr Tyr
 145 150 155 160

Ser Asp His Gly Gly Pro Gly Val Leu Gly Met Pro Thr Ser Pro Tyr
 165 170 175

Leu Tyr Ala Asn Asp Leu Asn Asp Val Leu Lys Lys Lys His Ala Ser
 180 185 190

Gly Thr Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly
 195 200 205

Ser Ile Phe Glu Gly Leu Leu Pro Glu Gly Leu Asn Ile Tyr Ala Thr
 210 215 220

Thr Ala Ser Asn Ala Val Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly
 225 230 235 240

Glu Asp Pro Ser Pro Pro Ser Glu Tyr Glu Thr Cys Leu Gly Asp Leu
 245 250 255

Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Ile His Asn Leu Gln Thr
 260 265 270

Glu Thr Leu His Gln Gln Tyr Glu Leu Val Lys Lys Arg Thr Ala Gly
 275 280 285

Ser Gly Lys Ser Phe Gly Ser His Val Met Glu Phe Gly Asp Ile Gly
 290 295 300

Leu Ser Lys Glu Lys Leu Val Leu Tyr Met Gly Thr Asn Pro Ala Asn
 305 310 315 320

Glu Asn Phe Thr Phe Val Asn Glu Asn Ser Leu Arg Pro Pro Ser Arg
 325 330 335

Val Thr Asn Gln Arg Asp Ala Asp Leu Val His Phe Trp Asp Lys Tyr
 340 345 350

Arg Lys Ala Pro Glu Gly Ser Ala Arg Lys Val Glu Ala Gln Lys Gln
355 360 365

Val Leu Glu Ala Met Ser His Arg Leu His Val Asp Asn Ser Ile Leu
370 375 380

Leu Ile Gly Lys Leu Leu Phe Gly Leu Asp Ser Pro Ala Val Leu Asn
385 390 395 400

Asn Val Arg Pro Ser Gly Thr Pro Leu Val Asp Asp Trp Asp Cys Leu
405 410 415

Lys Ser Leu Val Arg Val Phe Glu Met His Cys Gly Ser Leu Ser Gln
420 425 430

Tyr Gly Ile Lys His Met Arg Ser Ile Ala Asn Ile Cys Asn Ala Gly
435 440 445

Ile Gln Met Gly Gln Met Glu Glu Ala Ala Met Gln Ala Cys Pro Thr
450 455 460

Ile Pro Ala Ser Pro Trp Ser Ser Leu Glu Arg Gly Phe Ser Ala
465 470 475

<210> 47
<211> 482
<212> PRT
<213> Capsella rubella

<400> 47

Met Thr Arg Leu Thr Val Gly Val Leu Phe Leu Ser Leu Ile Ala Leu
1 5 10 15

Ser Ala Ala Arg Asn Gly Pro Asp Asp Val Ile Lys Leu Pro Ser Gln
20 25 30

Ala Ser Arg Phe Phe Arg Pro Pro Glu Asn Asp Ala Gly Thr Arg Trp
35 40 45

Ala Val Leu Val Ala Gly Ser Ser Gly Tyr Gly Asn Tyr Arg His Gln
50 55 60

Ala Asp Ile Cys His Ala Tyr Gln Leu Leu Arg Lys Gly Gly Leu Lys
65 70 75 80

Glu Glu Asn Ile Val Val Phe Met Tyr Asp Asp Ile Ala Asn Asn Tyr
85 90 95

Glu Asn Pro Arg Pro Gly Thr Ile Ile Asn Ser Pro His Gly Lys Asp
100 105 110

Val Tyr Gln Gly Val Pro Lys Asp Tyr Thr Gly Asp Asp Val Thr Val
115 120 125

Asp Asn Leu Phe Ala Val Ile Leu Gly Asp Lys Thr Ala Ile Lys Gly
130 135 140

Gly Ser Gly Lys Val Val Asp Ser Gly Pro Asn Asp His Ile Phe Ile
145 150 155 160

Phe Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Met Pro Thr Phe
165 170 175

Pro Tyr Ile Tyr Ala Asn Asp Leu Asn Asp Val Leu Lys Lys Lys His
180 185 190

Ala Leu Gly Thr Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu
195 200 205

Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Glu Gly Leu Asn Ile Tyr
210 215 220

Ala Thr Thr Ala Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys
225 230 235 240

Pro Gly Glu Glu Pro Ser Pro Pro Pro Glu Tyr Asp Thr Cys Leu Gly
245 250 255

Asp Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Gly Ile His Asn Leu
260 265 270

Gln Thr Glu Thr Leu Gln Gln Gln Tyr Glu Leu Val Lys Lys Arg Thr
275 280 285

Ala Leu Asp Gly Tyr Tyr Tyr Gly Ser His Val Met Gln Tyr Gly Asp
290 295 300

Val Gly Leu Ser Lys Asp Lys Leu Glu Ile Tyr Met Gly Thr Asn Pro
305 310 315 320

Ala Asn Glu Asn Ser Thr Phe Val Asp Ser Asn Ser Leu Lys Leu Pro
325 330 335

Ser Arg Val Thr Asn Gln Arg Asp Ala Asp Leu Val His Phe Trp Glu
340 345 350

Lys Tyr Arg Lys Ala Pro Glu Gly Ser Ser Arg Lys Ala Glu Ala Gln
355 360 365

Lys Gln Val Leu Glu Val Met Ser His Arg Leu His Val Asp Asn Ser
370 375 380

Val Ile Leu Val Gly Lys Ile Leu Phe Gly Ile Ser Lys Gly Pro Gln
385 390 395 400

Val Leu Asn Glu Val Arg Ser Ala Gly Gln Pro Leu Val Asp Asp Trp
405 410 415

Asn Cys Leu Lys Asn Met Val Arg Ala Phe Glu Arg His Cys Gly Ser
420 425 430

Leu Ser Gln Tyr Gly Ile Lys His Met Arg Ser Phe Ala Asn Phe Cys
435 440 445

Asn Ser Gly Ile Gln Met Glu Gln Met Glu Glu Ala Ala Ser Gln Ala
450 455 460

Cys Thr Thr Ile Pro Pro Gly Pro Trp Ser Ser Leu His Arg Gly Phe
465 470 475 480

Ser Ala

<210> 48
<211> 482
<212> PRT
<213> Vigna mungo

<400> 48

Met Ala Thr Thr Thr Ser Leu Ser Thr Leu Phe Leu Leu Phe Leu Ala
1 5 10 15

Thr Val Ala Leu Val Ala Ala Arg Arg Asp His Val Gly Asp Phe Leu
20 25 30

Arg Leu Pro Ser Asp Ser Gly Asn Asp Asp Asn Val Gln Gly Thr Arg
35 40 45

Trp Ala Ile Leu Phe Ala Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His
50 55 60

Gln Ala Asp Ile Cys His Ala Tyr Gln Ile Leu Arg Lys Gly Gly Leu
65 70 75 80

Lys Glu Glu Asn Ile Ile Val Phe Met Tyr Asp Asp Ile Ala Phe Asn
85 90 95

Trp Asp Asn Pro Arg Pro Gly Val Ile Ile Asn Lys Pro Asp Gly Asp
100 105 110

Asp Val Tyr Glu Gly Val Pro Lys Asp Tyr Thr Gly Glu Asp Ala Thr
115 120 125

Ala His Asn Phe Tyr Ser Ala Leu Leu Gly Asp Lys Ser Ala Leu Thr
130 135 140

Gly Gly Ser Gly Lys Val Val Ser Ser Gly Pro Asp Asp Arg Ile Phe
145 150 155 160

Ile Phe Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Thr Pro Ala
165 170 175

Gly Pro Tyr Ile Tyr Ala Ser Asp Leu Val Glu Val Leu Lys Lys Lys

180

185

190

His Ala Ser Gly Thr Tyr Lys Asn Leu Val Phe Tyr Leu Glu Ala Cys
 195 200 205

Glu Ala Gly Ser Ile Phe Glu Gly Leu Leu Pro Glu Asp Ile Asn Ile
 210 215 220

Tyr Ala Thr Thr Ala Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr
 225 230 235 240

Cys Pro Gly Glu Tyr Pro Ser Pro Pro Pro Glu Tyr Ser Thr Cys Leu
 245 250 255

Gly Asp Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Arg His Asn
 260 265 270

Leu Arg Thr Glu Ser Leu His Gln Gln Tyr Lys Val Val Lys Asp Arg
 275 280 285

Thr Leu Ser Gly Gly Trp Tyr Gly Ser His Val Met Gln Tyr Gly Asp
 290 295 300

Val Glu Phe Ser Lys Asp Ala Leu Phe Leu Tyr Leu Gly Thr Asp Pro
 305 310 315 320

Ala Asn Asp Asn Leu Thr Phe Val Asp Glu Asn Ser Leu Trp Ser Ser
 325 330 335

Ser Thr Ala Val Asn Gln Arg Asp Ala Asp Leu Val His Phe Trp His
 340 345 350

Lys Phe Arg Lys Ala Pro Glu Gly Ser Pro Lys Lys Asn Glu Ala Arg
 355 360 365

Lys Gln Val Leu Glu Val Met Ser His Arg Met His Ile Asp Asp Ser
 370 375 380

Val Lys Leu Val Gly Lys Leu Leu Phe Gly Phe Glu Lys Ala Pro Glu
 385 390 395 400

Val Leu Asn Ala Val Arg Pro Ala Gly Ser Ala Leu Val Asp Asp Trp
405 410 415

Ala Cys Leu Lys Thr Met Val Arg Thr Phe Glu Thr His Cys Gly Ser
420 425 430

Leu Ser Gln Tyr Gly Met Lys His Met Ser Pro Phe Ala Asn Ile Cys
435 440 445

Asn Val Gly Ile Lys Lys Glu Gln Met Ala Glu Ala Ser Ala Gln Ala
450 455 460

Cys Val Thr Val Pro Ala Ser Ser Trp Ser Ser Leu Gln Arg Gly Phe
465 470 475 480

Ser Ala

<210> 49

<211> 488

<212> PRT

<213> Eutrema salsugineum

<400> 49

Met Thr Ser Val Ala Val Pro Leu Leu Val Leu Leu Leu Ser Leu Ile
1 5 10 15

Ala Val Ser Ala Ala Arg Gln Gly Pro Asp Asp Ile Ile Lys Leu Pro
20 25 30

Ser Gln Ala Ser Met Phe Phe Arg Pro Ala Asp Asp Asp Asn Asp Ser
35 40 45

Ser Ala Gly Thr Arg Trp Ala Val Leu Val Ala Gly Ser Asn Gly Tyr
50 55 60

Trp Asn Tyr Arg His Gln Ala Asp Ile Cys His Ala Tyr Gln Leu Leu
65 70 75 80

Arg Lys Gly Gly Val Lys Glu Asp Asn Ile Val Val Phe Met Tyr Asp
85 90 95

Asp Ile Ala Asn Asn Glu Glu Asn Pro Arg Arg Gly Ile Ile Ile Asn
100 105 110

Ser Pro His Gly Lys Asp Val Tyr Gln Gly Val Pro Lys Asp Tyr Thr
115 120 125

Gly Asp Asp Val Thr Val Asp Asn Leu Phe Ala Val Ile Leu Gly Asn
130 135 140

Lys Thr Ala Thr Lys Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro
145 150 155 160

Asn Asp His Ile Phe Ile Phe Tyr Ser Asp His Gly Gly Pro Gly Val
165 170 175

Leu Gly Met Pro Thr Ser Pro Tyr Leu Tyr Ala Asn Asp Leu Asn Asp
180 185 190

Val Leu Lys Lys Lys His Ala Ser Gly Thr Tyr Lys Ser Leu Val Phe
195 200 205

Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Glu
210 215 220

Glu Gly Leu Asn Ile Tyr Ala Thr Thr Ala Ser Asn Ala Val Glu Ser
225 230 235 240

Ser Trp Gly Thr Tyr Cys Pro Gly Glu Asp Pro Ser Leu Pro Pro Glu
245 250 255

Tyr Glu Thr Cys Leu Gly Asp Leu Tyr Ser Val Ser Trp Met Glu Asp
260 265 270

Ser Gly Met His Asn Leu Gln Thr Glu Thr Leu Arg Gln Gln Tyr Glu
275 280 285

Leu Val Lys Arg Arg Thr Ala Gly Val Gly Ser Ala Tyr Gly Ser His
290 295 300

Val Met Gln Tyr Gly Asp Val Gly Leu Ser Lys Asp Lys Leu Asp Leu
305 310 315 320

Tyr Met Gly Thr Asn Pro Ala Asn Asp Asn Phe Thr Phe Val Asp Glu
325 330 335

Asn Ser Leu Thr Pro Pro Ser Arg Val Thr Asn Gln Arg Asp Ala Asp
340 345 350

Leu Val His Phe Trp Asp Lys Tyr Arg Lys Ala Pro Glu Gly Ser Thr
355 360 365

Arg Lys Thr Glu Ala Gln Lys Gln Val Leu Glu Ala Met Ser His Arg
370 375 380

Leu His Val Asp Asn Ser Val Lys Leu Val Gly Lys Leu Leu Phe Gly
385 390 395 400

Ile Ser Glu Gly Pro Glu Val Leu Asn Lys Val Arg Ser Ala Gly Gln
405 410 415

Pro Leu Val Asp Asp Trp Asn Cys Leu Lys Asn Leu Val Arg Ala Phe
420 425 430

Glu Arg His Cys Gly Ser Leu Ser Gln Tyr Gly Ile Lys His Met Arg
435 440 445

Ser Phe Ala Asn Ile Cys Asn Ala Gly Ile Gln Met Glu Gln Met Glu
450 455 460

Glu Ala Ser Ser Gln Ala Cys Thr Thr Ile Pro Pro Gly Pro Trp Ser
465 470 475 480

Ser Leu His Arg Gly Phe Ser Ala
485

<210> 50

<211> 494

<212> PRT

<213> Citrus sinensis

<400> 50

Met Thr Arg Leu Ala Ser Gly Val Leu Ile Thr Leu Leu Val Ala Leu
1 5 10 15

Ala Gly Ile Ala Asp Gly Ser Arg Asp Ile Ala Gly Asp Ile Leu Lys
20 25 30

Leu Pro Ser Glu Ala Tyr Arg Phe Phe His Asn Gly Gly Gly Gly Ala
35 40 45

Lys Val Asn Asp Asp Asp Asp Ser Val Gly Thr Arg Trp Ala Val Leu
50 55 60

Leu Ala Gly Ser Asn Gly Phe Trp Asn Tyr Arg His Gln Ala Asp Ile
65 70 75 80

Cys His Ala Tyr Gln Leu Leu Arg Lys Gly Gly Leu Lys Asp Glu Asn
85 90 95

Ile Ile Val Phe Met Tyr Asp Asp Ile Ala Phe Asn Glu Glu Asn Pro
100 105 110

Arg Pro Gly Val Ile Ile Asn His Pro His Gly Asp Asp Val Tyr Lys
115 120 125

Gly Val Pro Lys Asp Tyr Thr Gly Glu Asp Val Thr Val Glu Lys Phe
130 135 140

Phe Ala Val Val Leu Gly Asn Lys Thr Ala Leu Thr Gly Gly Ser Gly
145 150 155 160

Lys Val Val Asp Ser Gly Pro Asn Asp His Ile Phe Ile Phe Tyr Ser
165 170 175

Asp His Gly Gly Pro Gly Val Leu Gly Met Pro Thr Ser Arg Tyr Ile
180 185 190

Tyr Ala Asp Glu Leu Ile Asp Val Leu Lys Lys Lys His Ala Ser Gly
195 200 205

Asn Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser

210

215

220

Ile Phe Glu Gly Leu Leu Leu Glu Gly Leu Asn Ile Tyr Ala Thr Thr
 225 230 235 240

Ala Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu
 245 250 255

Ile Pro Gly Pro Pro Pro Glu Tyr Ser Thr Cys Leu Gly Asp Leu Tyr
 260 265 270

Ser Ile Ala Trp Met Glu Asp Ser Asp Ile His Asn Leu Arg Thr Glu
 275 280 285

Thr Leu His Gln Gln Tyr Glu Leu Val Lys Thr Arg Thr Ala Ser Tyr
 290 295 300

Asn Ser Tyr Gly Ser His Val Met Gln Tyr Gly Asp Ile Gly Leu Ser
 305 310 315 320

Lys Asn Asn Leu Phe Thr Tyr Leu Gly Thr Asn Pro Ala Asn Asp Asn
 325 330 335

Tyr Thr Phe Val Asp Glu Asn Ser Leu Arg Pro Ala Ser Lys Ala Val
 340 345 350

Asn Gln Arg Asp Ala Asp Leu Leu His Phe Trp Asp Lys Tyr Arg Lys
 355 360 365

Ala Pro Glu Gly Thr Pro Arg Lys Ala Glu Ala Gln Lys Gln Phe Phe
 370 375 380

Glu Ala Met Ser His Arg Met His Val Asp His Ser Ile Lys Leu Ile
 385 390 395 400

Gly Lys Leu Leu Phe Gly Ile Glu Lys Gly Pro Glu Ile Leu Asn Thr
 405 410 415

Val Arg Pro Ala Gly Gln Pro Leu Val Asp Asp Trp Gly Cys Leu Lys
 420 425 430

Ser Leu Val Arg Thr Phe Glu Ser His Cys Gly Ala Leu Ser Gln Tyr
435 440 445

Gly Met Lys His Met Arg Ser Leu Ala Asn Ile Cys Asn Thr Gly Ile
450 455 460

Gly Lys Glu Lys Met Ala Glu Ala Ser Ala Gln Ala Cys Glu Asn Ile
465 470 475 480

Pro Ser Gly Pro Trp Ser Ser Leu Asp Lys Gly Phe Ser Ala
485 490

<210> 51
<211> 484
<212> PRT
<213> Capsicum annuum

<400> 51

Met Asn Tyr Gln Val Ala Gly Ile Leu Phe Ile Val Gly Leu Ser Val
1 5 10 15

Ala Ile Ala Val Thr Ala Val Asp Gly Arg Asn Val Leu Lys Leu Pro
20 25 30

Thr Glu Ala Ser Arg Phe Phe Asp His Ala Asp Asp Asp Ser Val Gly
35 40 45

Thr Arg Trp Ala Val Leu Leu Ala Gly Ser Asn Gly Tyr Trp Asn Tyr
50 55 60

Arg His Gln Ala Asp Val Cys His Ala Tyr Gln Leu Leu Arg Lys Gly
65 70 75 80

Gly Leu Lys Asp Glu Asn Ile Ile Val Phe Met Tyr Asp Asp Ile Ala
85 90 95

Tyr Asn Glu Glu Asn Pro Arg Pro Gly Val Ile Ile Asn Asn Pro Ala
100 105 110

Ala Glu Asp Val Tyr Glu Gly Val Pro Lys Asp Tyr Thr Arg Asp Glu
115 120 125

Val Asn Val His Asn Phe Leu Ala Val Leu Leu Gly Asn Lys Thr Ala
130 135 140

Leu Thr Gly Gly Ser Gly Lys Val Val Asn Ser Gly Pro Asn Asp His
145 150 155 160

Ile Phe Ile Phe Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Met
165 170 175

Pro Thr Asn Pro Tyr Leu Tyr Ala Ser Asp Leu Ile Asn Ala Leu Lys
180 185 190

Lys Lys His Ala Ala Gly Ala Tyr Lys Ser Leu Val Leu Tyr Ile Glu
195 200 205

Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Thr Gly Leu
210 215 220

Asn Ile Tyr Ala Thr Thr Ala Ser Asn Ala Val Glu Ser Ser Trp Gly
225 230 235 240

Thr Tyr Cys Pro Gly Glu Tyr Pro Ser Pro Pro Pro Glu Tyr Glu Thr
245 250 255

Cys Leu Gly Asp Leu Tyr Ala Val Ser Trp Met Glu Asp Ser Glu Met
260 265 270

His Asn Leu Arg Thr Glu Asn Leu Arg Gln Gln Tyr His Leu Val Lys
275 280 285

Arg Arg Thr Ala Asn Gly Asn Thr Cys Gly Ser His Val Met Gln Phe
290 295 300

Gly Asp Leu Gln Leu Ser Met Glu Ser Leu Phe Ser Phe Met Gly Thr
305 310 315 320

Asn Pro Ala Asn Asp Asn Tyr Thr Tyr Val Asp Asp Asn Ser Leu Trp
325 330 335

Ala Ser Ser Arg Ala Val Asn Gln Arg Asp Ala Asp Leu Leu His Phe
340 345 350

Trp Asp Lys Phe Arg Lys Ala Pro Glu Gly Ser Ala Arg Lys Val Glu
355 360 365

Ala Gln Lys Gln Phe Thr Glu Ala Met Ser His Arg Met His Leu Asp
370 375 380

Asn Ser Ile Ala Leu Val Gly Lys Leu Leu Phe Gly Ile Gln Lys Gly
385 390 395 400

Pro Glu Val Leu Lys Arg Val Arg Ser Ala Gly Gln Pro Leu Val Asp
405 410 415

Asp Trp Ala Cys Leu Lys Ser Phe Val Arg Thr Phe Glu Thr His Cys
420 425 430

Gly Ser Leu Ser Gln Tyr Gly Met Lys His Met Arg Ser Ile Ala Asn
435 440 445

Ile Cys Asn Ala Gly Ile His Thr Glu Gln Met Val Glu Ala Ser Ala
450 455 460

Gln Ala Cys Pro Ser Ile Pro Ala Asn Thr Trp Ser Ser Leu His Arg
465 470 475 480

Gly Phe Ser Ala

<210> 52

<211> 480

<212> PRT

<213> Solanum lycopersicum

<400> 52

Met Val His Val Ala Gly Val Phe Ile Leu Val Gly Ile Ala Val Leu
1 5 10 15

Ala Ala Val Glu Gly Arg Asn Val Leu Lys Leu Pro Ser Glu Ala Ser
20 25 30

Arg Phe Phe Asp Asp Ala Asp Asp Ser Val Gly Thr Arg Trp Ala Val
35 40 45

Leu Leu Ala Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp
50 55 60

Val Cys His Ala Tyr Gln Leu Leu Arg Lys Gly Gly Leu Lys Asp Glu
65 70 75 80

Asn Ile Ile Val Phe Met Tyr Asp Asp Ile Ala His His Glu Glu Asn
85 90 95

Pro Arg Pro Gly Val Ile Ile Asn Ser Pro Ala Gly Glu Asp Val Tyr
100 105 110

Glu Gly Val Pro Lys Asp Tyr Thr Gly Asp Asp Val Asn Val His Asn
115 120 125

Phe Leu Ala Val Leu Leu Gly Asn Lys Thr Ala Leu Thr Gly Gly Ser
130 135 140

Gly Lys Val Val Asn Ser Gly Pro Asn Asp His Ile Phe Ile Phe Tyr
145 150 155 160

Ser Asp His Gly Gly Pro Gly Val Leu Gly Met Pro Thr Asn Pro Tyr
165 170 175

Leu Tyr Ala Asp Asp Leu Ile Ala Val Leu Lys Lys Lys His Ala Ala
180 185 190

Gly Thr Tyr Lys Ser Leu Val Leu Tyr Ile Glu Ala Cys Glu Ser Gly
195 200 205

Ser Ile Phe Glu Gly Leu Leu Pro Asn Gly Leu Asn Ile Tyr Ala Thr
210 215 220

Thr Ala Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly
225 230 235 240

Glu Tyr Pro Ser Pro Pro Pro Glu Tyr Glu Thr Cys Leu Gly Asp Leu

245

250

255

Tyr Ala Val Ser Trp Met Glu Asp Ser Glu Met His Asn Leu Arg Thr
 260 265 270

Glu Asn Leu Arg Gln Gln Tyr His Leu Val Lys Lys Arg Thr Ala Asn
 275 280 285

Gly Asn Thr Ala Tyr Gly Ser His Val Met Gln Phe Gly Asp Leu Gln
 290 295 300

Leu Ser Met Glu Ser Leu Phe Arg Phe Met Gly Thr Asn Pro Ala Asn
 305 310 315 320

Asp Asn Tyr Thr Tyr Val Asp Asp Asn Ser Leu Leu Ala Ser Ser Lys
 325 330 335

Ala Val Asn Gln Arg Asp Ala Asp Leu Leu His Phe Trp Asp Lys Phe
 340 345 350

Arg Lys Ala Pro Glu Gly Ser Ala Arg Lys Val Glu Ala Gln Lys Gln
 355 360 365

Phe Thr Glu Ala Met Ser His Arg Met His Leu Asp Glu Arg Ile Ala
 370 375 380

Leu Val Gly Lys Leu Leu Phe Gly Ile Gln Lys Gly Pro Glu Val Leu
 385 390 395 400

Lys His Val Arg Ser Ala Gly Gln Pro Leu Val Asp Asp Trp Ala Cys
 405 410 415

Leu Lys Ser Phe Val Arg Thr Phe Glu Ser His Cys Gly Ser Leu Ser
 420 425 430

Gln Tyr Gly Met Lys His Met Arg Ser Ile Ala Asn Ile Cys Asn Ala
 435 440 445

Gly Ile Gln Met Glu Gln Met Val Glu Ala Ser Ala Gln Ala Cys Pro
 450 455 460

Ser Ile Pro Ser Asn Ile Trp Ser Ser Leu His Arg Gly Phe Ser Ala
465 470 475 480

<210> 53
<211> 480
<212> PRT
<213> Solanum tuberosum

<400> 53

Met Ile His Val Ala Gly Val Phe Ile Leu Val Gly Val Ala Val Leu
1 5 10 15

Ala Ala Val Glu Gly Arg Asn Val Leu Lys Leu Pro Ser Glu Ala Ser
20 25 30

Arg Phe Phe Asp Val Ala Asp Asp Ser Val Gly Thr Arg Trp Ala Val
35 40 45

Leu Leu Ala Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp
50 55 60

Val Cys His Ala Tyr Gln Leu Leu Arg Lys Gly Gly Leu Lys Asp Glu
65 70 75 80

Asn Ile Ile Val Phe Met Tyr Asp Asp Ile Ala His His Glu Glu Asn
85 90 95

Pro Arg Pro Gly Val Ile Ile Asn Ser Pro Ala Gly Glu Asp Val Tyr
100 105 110

Glu Gly Val Pro Lys Asp Tyr Thr Gly Asp Asp Val Asn Val His Asn
115 120 125

Phe Leu Thr Val Leu Leu Gly Asn Lys Thr Ala Leu Thr Gly Gly Ser
130 135 140

Gly Lys Val Val Asn Ser Gly Pro Asn Asp His Ile Phe Ile Phe Tyr
145 150 155 160

Ser Asp His Gly Gly Pro Gly Val Leu Gly Met Pro Thr Asn Pro Tyr
165 170 175

Leu Tyr Ala Asn Asp Leu Ile Ala Val Leu Lys Lys Lys His Ala Ala
180 185 190

Gly Thr Tyr Lys Ser Leu Val Leu Tyr Ile Glu Ala Cys Glu Ser Gly
195 200 205

Ser Ile Phe Glu Gly Leu Leu Pro Lys Gly Leu Asn Ile Tyr Ala Thr
210 215 220

Thr Ala Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly
225 230 235 240

Glu Tyr Pro Ser Pro Pro Pro Glu Tyr Glu Thr Cys Leu Gly Asp Leu
245 250 255

Tyr Ala Val Ser Trp Met Glu Asp Ser Glu Met His Asn Leu Arg Thr
260 265 270

Glu Asn Leu Arg Gln Gln Tyr His Leu Val Lys Lys Arg Thr Ala Asn
275 280 285

Gly Asn Thr Ala Tyr Gly Ser His Val Met Gln Phe Gly Asp Leu Gln
290 295 300

Leu Ser Met Glu Ser Leu Phe Arg Phe Met Gly Thr Asn Pro Ala Asn
305 310 315 320

Asp Asn Tyr Thr Tyr Val Asp Asp Asn Ser Leu Trp Ala Ser Ser Lys
325 330 335

Ala Val Asn Gln Arg Asp Ala Asp Leu Leu His Phe Trp Asp Lys Phe
340 345 350

Arg Lys Ala Pro Glu Gly Ser Ala Arg Lys Val Glu Ala Gln Lys Gln
355 360 365

Phe Thr Glu Ala Met Ser His Arg Met His Leu Asp Glu Arg Ile Ala
370 375 380

Leu Val Gly Lys Leu Leu Phe Gly Ile Gln Lys Gly Pro Glu Val Leu
385 390 395 400

Lys His Val Arg Ser Ala Gly Gln Pro Leu Val Asp Asp Trp Ala Cys
405 410 415

Leu Lys Ser Phe Val Arg Thr Phe Glu Ser His Cys Gly Ser Leu Ser
420 425 430

Gln Tyr Gly Met Lys His Met Arg Ser Ile Ala Asn Ile Cys Asn Ala
435 440 445

Gly Val Gln Met Glu Gln Met Val Glu Ala Ser Val Gln Ala Cys Pro
450 455 460

Ser Ile Pro Ser Asn Thr Trp Ser Ser Leu His Arg Gly Phe Ser Ala
465 470 475 480

<210> 54
<211> 480
<212> PRT
<213> Solanum lycopersicum

<400> 54

Met Val His Val Ala Gly Val Phe Ile Leu Val Gly Ile Ala Val Leu
1 5 10 15

Ala Ala Val Glu Gly Arg Asn Val Leu Lys Leu Pro Ser Glu Ala Ser
20 25 30

Arg Phe Phe Asp Asp Ala Asp Asp Ser Val Gly Thr Arg Trp Ala Val
35 40 45

Leu Leu Ala Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp
50 55 60

Val Cys His Ala Tyr Gln Leu Leu Arg Lys Gly Gly Leu Lys Asp Glu
65 70 75 80

Asn Ile Ile Val Phe Met Tyr Asp Asp Ile Ala His His Glu Glu Asn
85 90 95

Pro Arg Pro Gly Val Ile Ile Asn Ser Pro Ala Gly Glu Asp Val Tyr
100 105 110

Glu Gly Val Pro Lys Asp Tyr Thr Gly Asp Asp Val Asn Val His Asn
115 120 125

Phe Leu Ala Val Leu Leu Gly Asn Lys Thr Ala Leu Thr Gly Gly Ser
130 135 140

Gly Lys Val Val Asn Ser Gly Pro Asn Asp His Ile Phe Ile Phe Tyr
145 150 155 160

Ser Asp His Gly Gly Pro Gly Val Leu Gly Met Pro Thr Asn Pro Tyr
165 170 175

Leu Tyr Ala Asp Asp Leu Ile Ala Val Leu Lys Lys Lys His Ala Pro
180 185 190

Gly Thr Tyr Lys Ser Leu Val Leu Tyr Ile Glu Ala Cys Glu Ser Gly
195 200 205

Ser Ile Phe Glu Gly Leu Leu Pro Asn Gly Leu Asn Ile Tyr Ala Thr
210 215 220

Thr Ala Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly
225 230 235 240

Glu Tyr Pro Ser Pro Pro Pro Glu Tyr Glu Thr Cys Leu Gly Asp Leu
245 250 255

Tyr Ala Val Ser Trp Met Glu Asp Ser Glu Met His Asn Leu Arg Thr
260 265 270

Glu Asn Leu Arg Gln Gln Tyr His Leu Val Lys Lys Arg Thr Ala Asn
275 280 285

Gly Asn Thr Ala Tyr Gly Ser His Val Met Gln Phe Gly Asp Leu Gln
290 295 300

Leu Ser Met Glu Ser Leu Phe Arg Phe Met Gly Thr Asn Pro Ala Asn

305		310		315		320									
Asp	Asn	Tyr	Thr	Tyr	Val	Asp	Asp	Asn	Ser	Leu	Leu	Ala	Ser	Ser	Lys
				325					330					335	
Ala	Val	Asn	Gln	Arg	Asp	Ala	Asp	Leu	Leu	His	Phe	Trp	Asp	Lys	Phe
			340					345					350		
Arg	Lys	Ala	Pro	Glu	Gly	Ser	Ala	Arg	Lys	Val	Glu	Ala	Gln	Lys	Gln
		355					360					365			
Phe	Thr	Glu	Ala	Met	Ser	His	Arg	Met	His	Leu	Asp	Glu	Arg	Ile	Ala
	370					375					380				
Leu	Val	Gly	Lys	Leu	Leu	Phe	Gly	Ile	Gln	Lys	Gly	Pro	Glu	Val	Leu
385					390					395					400
Lys	His	Val	Arg	Ser	Ala	Gly	Gln	Pro	Leu	Val	Asp	Asp	Trp	Ala	Cys
				405					410					415	
Leu	Lys	Ser	Phe	Val	Arg	Thr	Phe	Glu	Ser	His	Cys	Gly	Ser	Leu	Ser
			420					425					430		
Gln	Tyr	Gly	Met	Lys	His	Met	Arg	Ser	Ile	Ala	Asn	Ile	Cys	Asn	Ala
		435					440					445			
Gly	Ile	Gln	Met	Glu	Gln	Met	Val	Glu	Ala	Ser	Ala	Gln	Ala	Cys	Pro
	450					455					460				
Ser	Ile	Pro	Ser	Asn	Ile	Trp	Ser	Ser	Leu	His	Arg	Gly	Phe	Ser	Ala
465					470					475					480
<210> 55															
<211> 490															
<212> PRT															
<213> Eutrema salsugineum															
<400> 55															
Met	Ser	Arg	Val	Ser	Val	Thr	Val	Thr	Val	Ala	Val	Ser	Phe	Leu	Ala
1				5					10					15	

Leu Phe Ile Ser Leu Val Thr Val Ser Cys Asp Val Ile Lys Leu Pro
20 25 30

Ser Gln Ala Ser Lys Phe Phe Arg Thr Thr Lys His Asn Asp Asp Gly
35 40 45

Asp Ser Ser Ala Gly Thr Lys Trp Ala Val Leu Val Ala Gly Ser Ser
50 55 60

Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp Val Cys His Ala Tyr Gln
65 70 75 80

Leu Leu Arg Lys Gly Gly Leu Lys Glu Glu Asn Ile Ile Val Phe Met
85 90 95

Tyr Asp Asp Ile Ala Lys Asn Lys Glu Asn Pro Arg Pro Gly Ile Ile
100 105 110

Ile Asn Ser Pro Asn Gly Asn Asp Val Tyr Asn Gly Val Pro Lys Asp
115 120 125

Tyr Thr Gly Asp Asp Val Asn Val Asp Asn Leu Phe Ala Val Ile Leu
130 135 140

Ala Asn Lys Thr Ala Leu Lys Gly Gly Ser Gly Lys Val Val Asp Ser
145 150 155 160

Gly Pro Asp Asp His Ile Phe Ile Tyr Tyr Ser Asp His Gly Gly Pro
165 170 175

Gly Val Leu Gly Met Pro Thr Ser Pro His Leu Tyr Ala Asn Asp Leu
180 185 190

Ile Asp Ile Leu Lys Lys Lys His Ala Ser Gly Thr Tyr Lys Ser Leu
195 200 205

Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu
210 215 220

Leu Pro Glu Gly Leu Asn Ile Tyr Ala Thr Thr Ala Ser Asn Ala Glu
225 230 235 240

Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Asp Asp Ser Ser Pro Pro
245 250 255

Lys Glu Tyr Glu Thr Cys Leu Gly Asp Leu Tyr Ser Val Ser Trp Met
260 265 270

Glu Asp Ser Asp Gln His Asn Leu Gln Thr Glu Ser Leu His Gln Gln
275 280 285

Tyr Glu Leu Val Lys Lys Arg Thr Ala Gly Ser Asn Thr Ser Tyr Gly
290 295 300

Ser His Val Met Glu Phe Gly Asp Ile Gly Leu Ser Lys Glu Met Leu
305 310 315 320

Val Leu Tyr Met Gly Thr Asn Pro Asp Asn Glu Asn Tyr Thr Phe Val
325 330 335

Asp Lys Asn Ser Leu Arg Pro Pro Ser Arg Val Thr Asn Gln Arg Asp
340 345 350

Ala Asp Leu Val His Phe Trp Asp Lys Tyr Gln Lys Ala Pro Glu Gly
355 360 365

Ser Ala Arg Lys Ala Glu Ala Gln Lys Gln Val Leu Glu Ala Met Ser
370 375 380

His Arg Leu His Ile Asp Asn Ser Phe Leu Met Ile Gly Lys Leu Leu
385 390 395 400

Phe Gly Ile Ser Glu Gly Pro Leu Val Leu Asn Lys Val Arg Pro Ser
405 410 415

Gly Lys Pro Leu Val Asp Asp Trp Asp Cys Leu Lys Thr Leu Val Arg
420 425 430

Ala Tyr Glu Arg His Cys Gly Ser Leu Ser Gln Tyr Gly Ile Lys His
435 440 445

Met Arg Ser Ile Ala Asn Ile Cys Asn Ala Gly Ile Gln Val Glu Gln
450 455 460

Met Glu Glu Ala Ala Met Gln Ala Cys Pro Thr Ile Pro Ala Gly Pro
465 470 475 480

Trp Ser Ser Leu His Arg Gly Phe Ser Ala
485 490

<210> 56

<211> 492

<212> PRT

<213> Ipomoea batatas

<400> 56

Met Ile Arg Ser Val Val Ala Ser Leu Leu Leu Leu Thr Val Ser Ile
1 5 10 15

Val Ala Val Ala Asp Gly Arg Gly Phe Leu Lys Leu Pro Ser Glu Ala
20 25 30

Arg Arg Phe Phe Arg Pro Ala Glu Glu Glu Asn Arg Glu Ala Asp Gly
35 40 45

Asp Asp Ser Val Gly Thr Arg Trp Ala Val Leu Ile Ala Gly Ser Asn
50 55 60

Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp Ile Cys His Ala Tyr Gln
65 70 75 80

Ile Leu Lys Ala Gly Gly Leu Lys Asp Glu Asn Ile Val Val Phe Met
85 90 95

Tyr Asp Asp Ile Ala Tyr Asn Glu Glu Asn Pro Arg Lys Gly Ile Ile
100 105 110

Ile Asn Ser Pro His Gly Glu Asp Val Tyr His Gly Val Pro Lys Asp
115 120 125

Tyr Thr Gly Asp Asp Val Thr Ala Asn Asn Leu Leu Ala Val Ile Leu
130 135 140

Gly Asp Lys Ser Ala Val Lys Gly Gly Ser Gly Lys Val Val Asp Ser
145 150 155 160

Gly Pro Asn Asp His Ile Phe Ile Tyr Tyr Ser Asp His Gly Gly Pro
165 170 175

Gly Val Leu Gly Met Pro Thr Ser Pro Tyr Leu Tyr Ala Asp Glu Leu
180 185 190

Asn Ala Ala Leu Lys Lys Lys His Ala Ala Gly Ala Tyr Lys Ser Leu
195 200 205

Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Ile
210 215 220

Leu Pro Lys Asp Ile Asn Ile Tyr Ala Thr Thr Ala Ser Asn Ala Ile
225 230 235 240

Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Tyr Pro Ser Pro Pro
245 250 255

Pro Glu Tyr Glu Thr Cys Leu Gly Asp Leu Tyr Ser Ile Ala Trp Met
260 265 270

Glu Asp Ser Asp Ile His Asn Leu Arg Thr Glu Ser Leu Lys Gln Gln
275 280 285

Tyr Asn Leu Val Lys Asp Arg Thr Leu Asn Gly Asn Thr Ala Tyr Gly
290 295 300

Ser His Val Met Gln Tyr Gly Asp Leu Glu Leu Asn Ala Asp Ser Leu
305 310 315 320

Phe Met Tyr Met Gly Thr Asn Pro Ala Asn Glu Asn Phe Thr Phe Val
325 330 335

Asp Glu Lys Ser Leu Lys Leu Ser Ala Pro Arg Arg Ala Val Asn Gln
340 345 350

Arg Asp Ala Asp Leu Leu His Phe Trp Asp Lys Phe Arg Asn Ala Pro

355

360

365

Glu Gly Ser Ala Arg Lys Ser Glu Ala Gln Lys Gln Phe Thr Glu Ala
 370 375 380

Ile Thr His Arg Thr His Leu Asp Asn Ser Ile Ala Leu Val Gly Lys
 385 390 395 400

Leu Leu Phe Gly Met Glu Lys Gly Pro Glu Val Leu Ser Ser Val Arg
 405 410 415

Ala Thr Gly Leu Pro Leu Val Asp Asp Trp Ser Cys Leu Lys Ser Tyr
 420 425 430

Val Arg Ala Phe Glu Thr His Cys Gly Ser Leu Ser Gln Tyr Gly Met
 435 440 445

Lys His Met Arg Ser Ile Ala Asn Ile Cys Asn Ala Gly Ile Ser Glu
 450 455 460

Glu Arg Met Ala Glu Ala Ser Ala Gln Ala Cys Pro Thr Phe Pro Ser
 465 470 475 480

Tyr Ser Trp Ser Ser Leu Arg Gly Gly Phe Ser Ala
 485 490

<210> 57

<211> 490

<212> PRT

<213> Nicotiana tabacum

<400> 57

Met Ile Arg His Ile Ala Gly Thr Leu Phe Ile Ile Gly Leu Ala Leu
 1 5 10 15

Asn Val Ala Val Ser Glu Ser Arg Asn Val Leu Lys Leu Pro Ser Glu
 20 25 30

Val Ser Arg Phe Phe Gly Ala Asp Lys Ser Asn Val Gly Asp Asp His
 35 40 45

Asp Asp Asp Ser Val Gly Thr Arg Trp Ala Ile Leu Leu Ala Gly Ser
50 55 60

Asn Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp Ile Cys His Ala Tyr
65 70 75 80

Gln Leu Leu Lys Lys Gly Gly Leu Lys Asp Glu Asn Ile Val Val Phe
85 90 95

Met Tyr Asp Asp Ile Ala Asn Asn Glu Glu Asn Pro Arg Pro Gly Val
100 105 110

Ile Ile Asn Ser Pro His Gly Glu Asp Val Tyr Lys Gly Val Pro Lys
115 120 125

Asp Tyr Thr Gly Asp Asp Val Thr Val Asn Asn Phe Phe Ala Ala Leu
130 135 140

Leu Gly Asn Lys Thr Ala Leu Ser Gly Gly Ser Gly Lys Val Val Asn
145 150 155 160

Ser Gly Pro Asn Asp His Ile Leu Ile Phe Tyr Ser Asp His Gly Gly
165 170 175

Pro Gly Val Leu Gly Met Pro Thr Asp Pro Tyr Leu Tyr Ala Asn Asp
180 185 190

Leu Ile Asp Val Leu Lys Lys Lys His Ala Ser Gly Thr Tyr Lys Ser
195 200 205

Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly
210 215 220

Leu Leu Pro Glu Gly Leu Asn Ile Tyr Ala Thr Thr Ala Ser Asn Ala
225 230 235 240

Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Tyr Pro Ser Pro
245 250 255

Pro Ile Glu Tyr Glu Thr Cys Leu Gly Asp Leu Tyr Ser Ile Ser Trp
260 265 270

Met Glu Asp Ser Glu Leu His Asn Leu Arg Thr Glu Ser Leu Lys Gln
275 280 285

Gln Tyr His Leu Val Arg Glu Arg Thr Ala Thr Gly Asn Pro Val Tyr
290 295 300

Gly Ser His Val Met Gln Tyr Gly Asp Leu His Leu Ser Lys Asp Ala
305 310 315 320

Leu Tyr Leu Tyr Met Gly Thr Asn Pro Ala Asn Asp Asn Tyr Thr Phe
325 330 335

Met Asp Asp Asn Ser Leu Arg Val Ser Lys Ala Val Asn Gln Arg Asp
340 345 350

Ala Asp Leu Leu His Phe Trp Tyr Lys Phe Arg Lys Ala Pro Glu Gly
355 360 365

Ser Val Arg Lys Ile Glu Ala Gln Lys Gln Leu Asn Glu Ala Ile Ser
370 375 380

His Arg Val His Leu Asp Asn Ser Ile Ala Leu Val Gly Lys Leu Leu
385 390 395 400

Phe Gly Ile Lys Lys Gly Pro Glu Val Leu Ser Ser Val Arg Pro Ala
405 410 415

Gly Gln Pro Leu Val Asp Asp Trp Asp Cys Leu Lys Ser Phe Val Arg
420 425 430

Thr Phe Glu Thr His Cys Gly Ser Leu Ser Gln Tyr Gly Met Lys His
435 440 445

Met Arg Ser Ile Ala Asn Ile Cys Asn Val Gly Ile Lys Met Ala Gln
450 455 460

Met Val Glu Ala Ser Ala Gln Ala Cys Pro Ser Phe Ala Ser Asn Thr
465 470 475 480

Trp Ser Ser Leu Gln Arg Gly Phe Ser Ala
485 490

<210> 58

<211> 494

<212> PRT

<213> Arabidopsis lyrata subsp. lyrata

<400> 58

Met Ala Thr Thr Met Thr Arg Val Pro Val Gly Ala Phe Leu Leu Val
1 5 10 15

Leu Leu Val Ser Leu Val Ala Val Ser Thr Ala Arg Ser Gly Pro Asp
20 25 30

Asp Val Ile Lys Leu Pro Ser Gln Ala Ser Arg Phe Phe Arg Pro Ala
35 40 45

Gln Asp Asp Asp Asp Ser Asn Ala Gly Thr Arg Trp Ala Val Leu Val
50 55 60

Ala Gly Ser Ser Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp Ile Cys
65 70 75 80

His Ala Tyr Gln Leu Leu Arg Lys Gly Gly Leu Lys Glu Glu Asn Ile
85 90 95

Val Val Phe Met Tyr Asp Asp Ile Ala Asn Asn Tyr Glu Asn Pro Arg
100 105 110

Pro Gly Thr Leu Ile Asn Ser Pro His Gly Lys Asp Val Tyr Gln Gly
115 120 125

Val Pro Lys Asp Tyr Thr Gly Asp Asp Val Asn Val Asp Asn Leu Phe
130 135 140

Ala Val Ile Leu Gly Asp Lys Thr Ala Val Lys Gly Gly Ser Gly Lys
145 150 155 160

Val Val Asp Ser Gly Pro Asn Asp His Ile Phe Ile Phe Tyr Ser Asp
165 170 175

His Gly Gly Pro Gly Val Leu Gly Met Pro Thr Ser Pro Tyr Leu Tyr
180 185 190

Ala Asn Asp Leu Asn Asp Val Leu Lys Lys Lys His Ala Ser Gly Thr
195 200 205

Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile
210 215 220

Phe Glu Gly Leu Leu Pro Glu Gly Leu Asn Ile Tyr Ala Thr Thr Ala
225 230 235 240

Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Glu
245 250 255

Pro Ser Pro Pro Pro Glu Tyr Glu Thr Cys Leu Gly Asp Leu Tyr Ser
260 265 270

Val Ala Trp Met Glu Asp Ser Gly Met His Asn Leu Gln Thr Glu Thr
275 280 285

Leu His Gln Gln Tyr Glu Leu Val Lys Arg Arg Thr Ala Pro Val Gly
290 295 300

Tyr Ser Tyr Gly Ser His Val Met Gln Tyr Gly Asp Val Gly Leu Ser
305 310 315 320

Lys Asp Asn Leu Asp Leu Tyr Met Gly Thr Asn Pro Ala Asn Asp Asn
325 330 335

Phe Thr Phe Ala Asp Ala Asn Ser Leu Lys Pro Pro Ser Arg Val Thr
340 345 350

Asn Gln Arg Asp Ala Asp Leu Val His Phe Trp Glu Lys Tyr Arg Lys
355 360 365

Ala Pro Glu Gly Ser Ala Arg Lys Thr Glu Ala Gln Lys Gln Val Leu
370 375 380

Glu Ala Met Ser His Arg Leu His Val Asp Asn Ser Val Ile Leu Val

385 390 395 400
 Gly Lys Ile Leu Phe Gly Ile Ser Glu Gly Pro Glu Val Leu Asn Lys
 405 410 415
 Val Arg Ser Ala Gly Gln Pro Leu Val Asp Asp Trp Asn Cys Leu Lys
 420 425 430
 Asn Leu Val Arg Ala Phe Glu Arg His Cys Gly Ser Leu Ser Gln Tyr
 435 440 445
 Gly Ile Lys His Met Arg Ser Phe Ala Asn Ile Cys Asn Ala Gly Ile
 450 455 460
 Arg Thr Glu Gln Met Glu Glu Ala Ala Ser Gln Ala Cys Thr Ser Ile
 465 470 475 480
 Pro Pro Gly Pro Trp Ser Ser Leu His Arg Gly Phe Ser Ala
 485 490

 <210> 59
 <211> 478
 <212> PRT
 <213> Thellungiella halophila

 <400> 59

 Met Thr Ser Val Ala Val Pro Leu Leu Val Leu Leu Leu Ser Leu Ile
 1 5 10 15

 Ala Val Ser Ala Ala Arg Gln Gly Pro Asp Asp Ile Ile Lys Leu Pro
 20 25 30

 Ser Gln Ala Ser Met Phe Phe Arg Pro Ala Asp Asp Asp Asn Asp Ser
 35 40 45

 Ser Ala Gly Thr Arg Trp Ala Val Leu Val Ala Gly Ser Asn Gly Tyr
 50 55 60

 Trp Asn Tyr Arg His Gln Ala Asp Ile Cys His Ala Tyr Gln Leu Leu
 65 70 75 80

Arg Lys Gly Gly Val Lys Glu Asp Asn Ile Val Val Phe Met Tyr Asp
85 90 95

Asp Ile Ala Asn Asn Glu Glu Asn Pro Arg Arg Gly Ile Ile Ile Asn
100 105 110

Ser Pro His Gly Lys Asp Val Tyr Gln Gly Val Pro Lys Asp Tyr Thr
115 120 125

Gly Asp Asp Val Thr Val Asp Asn Leu Phe Ala Val Ile Leu Gly Asn
130 135 140

Lys Thr Ala Thr Lys Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro
145 150 155 160

Asn Asp His Ile Phe Ile Phe Tyr Ser Asp His Gly Gly Pro Gly Val
165 170 175

Leu Gly Met Pro Thr Ser Pro Tyr Leu Tyr Ala Asn Asp Leu Asn Asp
180 185 190

Val Leu Lys Lys Lys His Ala Ser Gly Thr Tyr Lys Ser Leu Val Phe
195 200 205

Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Glu
210 215 220

Glu Gly Leu Asn Ile Tyr Ala Thr Thr Ala Ser Asn Ala Val Glu Ser
225 230 235 240

Ser Trp Gly Thr Tyr Cys Pro Gly Glu Asp Pro Ser Leu Pro Pro Glu
245 250 255

Tyr Glu Thr Cys Leu Gly Asp Leu Tyr Ser Val Ser Trp Met Glu Asp
260 265 270

Ser Gly Met His Asn Leu Gln Thr Glu Thr Leu Arg Gln Gln Tyr Glu
275 280 285

Leu Val Lys Arg Arg Thr Ala Gly Val Gly Ser Ala Tyr Gly Ser His
290 295 300

Val Met Gln Tyr Gly Asp Val Gly Leu Ser Lys Asp Lys Leu Asp Leu
305 310 315 320

Tyr Met Gly Thr Asn Pro Ala Asn Asp Asn Phe Thr Phe Val Asp Glu
325 330 335

Asn Ser Leu Thr Pro Pro Ser Arg Val Thr Asn Gln Arg Asp Ala Asp
340 345 350

Leu Val His Phe Trp Asp Lys Tyr Arg Lys Ala Pro Glu Gly Ser Thr
355 360 365

Arg Lys Thr Glu Ala Gln Lys Gln Val Leu Glu Ala Met Ser His Arg
370 375 380

Leu His Val Asp Asn Ser Val Lys Leu Val Gly Lys Leu Leu Phe Gly
385 390 395 400

Ile Ser Glu Gly Pro Glu Val Leu Asn Lys Val Arg Ser Ala Gly Gln
405 410 415

Pro Leu Val Asp Asp Trp Asn Cys Leu Lys Asn Leu Val Arg Ala Phe
420 425 430

Glu Arg His Cys Gly Ser Leu Ser Gln Tyr Gly Ile Lys His Met Arg
435 440 445

Ser Phe Ala Asn Ile Cys Asn Ala Gly Ile Gln Met Glu Gln Met Glu
450 455 460

Glu Ala Ser Ser Gln Ala Cys Thr Thr Ile Pro Pro Gly Pro
465 470 475

<210> 60

<211> 486

<212> PRT

<213> Beta vulgaris

<400> 60

Met Met Ile Arg Tyr Thr Ser Gly Val Leu Ile Val Leu Cys Val Leu

1					5					10					15				
Met	Ser	Ser	Val	Val	Asp	Ser	Arg	Leu	Met	Val	Asp	Asn	Leu	Ile	Arg				
			20					25					30						
Trp	Pro	Ser	Asp	His	Pro	Ser	Ile	Phe	Glu	Ser	Asp	Asp	Asp	Ser	Val				
		35					40					45							
Gly	Thr	Arg	Trp	Ala	Val	Leu	Ile	Ala	Gly	Ser	Ser	Gly	Tyr	Trp	Asn				
	50					55					60								
Tyr	Arg	His	Gln	Ala	Asp	Val	Cys	His	Ala	Tyr	Gln	Val	Leu	Lys	Lys				
65					70					75					80				
Gly	Gly	Leu	Lys	Asp	Glu	Asn	Ile	Ile	Val	Phe	Met	Tyr	Asp	Asp	Ile				
				85					90					95					
Ala	Tyr	Asp	Glu	Glu	Asn	Pro	Arg	Pro	Gly	Val	Leu	Ile	Asn	Ser	Pro				
			100					105					110						
Tyr	Gly	His	Asp	Val	Tyr	Ala	Gly	Val	Pro	Lys	Asp	Tyr	Thr	Gly	Glu				
		115					120					125							
Asp	Val	Thr	Val	Asn	Asn	Phe	Phe	Ala	Ala	Ile	Leu	Gly	Asn	Lys	Asp				
	130					135					140								
Ala	Ile	Thr	Gly	Gly	Ser	Gly	Lys	Val	Val	Asn	Ser	Gly	Pro	Asn	Asp				
145					150					155					160				
His	Ile	Phe	Ile	Phe	Tyr	Ser	Asp	His	Gly	Gly	Ala	Gly	Val	Leu	Gly				
				165					170					175					
Met	Pro	Thr	Tyr	Pro	Tyr	Leu	Tyr	Ala	Asp	Glu	Leu	Ile	Glu	Thr	Leu				
			180					185					190						
Lys	Glu	Lys	His	Ala	Ser	Gly	Thr	Tyr	Lys	Ser	Leu	Val	Val	Tyr	Ile				
		195					200					205							
Glu	Ala	Cys	Glu	Ser	Gly	Ser	Ile	Phe	Glu	Gly	Ile	Leu	Pro	Glu	Gly				
	210					215					220								

Leu Asn Ile Tyr Ala Thr Thr Ala Ser Asn Ala Val Glu Ser Ser Trp
225 230 235 240

Gly Thr Tyr Cys Pro Gly Gln Asp Pro Asn Val Pro Pro Glu Tyr Asp
245 250 255

Thr Cys Leu Gly Asp Leu Tyr Ser Val Ser Trp Ile Glu Asp Ser Glu
260 265 270

Arg His Asn Leu His Thr Glu Ser Leu Lys Gln Gln Tyr Glu Val Val
275 280 285

Lys Thr Lys Thr Ala Glu Lys Pro Phe Tyr Gly Ser His Val Met Gln
290 295 300

Tyr Gly Asp Lys Glu Leu Thr Gln Asp Met Leu Tyr Leu Tyr Met Gly
305 310 315 320

Thr Asn Pro Asn Asn Glu Asn Tyr Thr Tyr Val Asp Asp Asn Ser Leu
325 330 335

His Pro Thr Ser Ser Asn Ala Val Asn Gln Arg Asp Ala Asp Leu Ile
340 345 350

His Phe Trp Asn Lys Phe Arg Lys Ala Ser Glu Gly Ser Gln Arg Lys
355 360 365

Ile Asn Ala Gln Lys Gln Phe Met Glu Val Met Ser His Arg Val His
370 375 380

Leu Asp Asp Ser Ile Lys Leu Ile Gly Lys Leu Leu Phe Gly Ile Glu
385 390 395 400

Lys Gly Leu Gly Val Leu Gln Thr Val Arg Pro Thr Gly Gln Pro Leu
405 410 415

Val Asp Asp Trp Asn Cys Leu Lys Thr Leu Val Arg Thr Phe Glu Lys
420 425 430

His Cys Gly Ser Leu Ser Gln Tyr Gly Met Lys His Met Arg Ser Ile

435

440

445

Ala Asn Ile Cys Asn Ala Gly Ile Thr Thr Asn Gln Met Ala Glu Ala
 450 455 460

Ser Ala Gln Ala Cys Pro Ser Phe Pro Ser Gly Pro Trp Ser Ser Leu
 465 470 475 480

His Arg Gly Phe Ser Ala
 485

<210> 61

<211> 494

<212> PRT

<213> Arabidopsis thaliana

<400> 61

Met Ala Thr Thr Met Thr Arg Val Ser Val Gly Val Val Leu Phe Val
 1 5 10 15

Leu Leu Val Ser Leu Val Ala Val Ser Ala Ala Arg Ser Gly Pro Asp
 20 25 30

Asp Val Ile Lys Leu Pro Ser Gln Ala Ser Arg Phe Phe Arg Pro Ala
 35 40 45

Glu Asn Asp Asp Asp Ser Asn Ser Gly Thr Arg Trp Ala Val Leu Val
 50 55 60

Ala Gly Ser Ser Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp Ile Cys
 65 70 75 80

His Ala Tyr Gln Leu Leu Arg Lys Gly Gly Leu Lys Glu Glu Asn Ile
 85 90 95

Val Val Phe Met Tyr Asp Asp Ile Ala Asn Asn Tyr Glu Asn Pro Arg
 100 105 110

Pro Gly Thr Ile Ile Asn Ser Pro His Gly Lys Asp Val Tyr Gln Gly
 115 120 125

Val Pro Lys Asp Tyr Thr Gly Asp Asp Val Asn Val Asp Asn Leu Phe
130 135 140

Ala Val Ile Leu Gly Asp Lys Thr Ala Val Lys Gly Gly Ser Gly Lys
145 150 155 160

Val Val Asp Ser Gly Pro Asn Asp His Ile Phe Ile Phe Tyr Ser Asp
165 170 175

His Gly Gly Pro Gly Val Leu Gly Met Pro Thr Ser Pro Tyr Leu Tyr
180 185 190

Ala Asn Asp Leu Asn Asp Val Leu Lys Lys Lys His Ala Leu Gly Thr
195 200 205

Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile
210 215 220

Phe Glu Gly Leu Leu Pro Glu Gly Leu Asn Ile Tyr Ala Thr Thr Ala
225 230 235 240

Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Glu
245 250 255

Pro Ser Pro Pro Pro Glu Tyr Glu Thr Cys Leu Gly Asp Leu Tyr Ser
260 265 270

Val Ala Trp Met Glu Asp Ser Gly Met His Asn Leu Gln Thr Glu Thr
275 280 285

Leu His Gln Gln Tyr Glu Leu Val Lys Arg Arg Thr Ala Pro Val Gly
290 295 300

Tyr Ser Tyr Gly Ser His Val Met Gln Tyr Gly Asp Val Gly Ile Ser
305 310 315 320

Lys Asp Asn Leu Asp Leu Tyr Met Gly Thr Asn Pro Ala Asn Asp Asn
325 330 335

Phe Thr Phe Ala Asp Ala Asn Ser Leu Lys Pro Pro Ser Arg Val Thr
340 345 350

Asn Gln Arg Asp Ala Asp Leu Val His Phe Trp Glu Lys Tyr Arg Lys
355 360 365

Ala Pro Glu Gly Ser Ala Arg Lys Thr Glu Ala Gln Lys Gln Val Leu
370 375 380

Glu Ala Met Ser His Arg Leu His Ile Asp Asn Ser Val Ile Leu Val
385 390 395 400

Gly Lys Ile Leu Phe Gly Ile Ser Arg Gly Pro Glu Val Leu Asn Lys
405 410 415

Val Arg Ser Ala Gly Gln Pro Leu Val Asp Asp Trp Asn Cys Leu Lys
420 425 430

Asn Gln Val Arg Ala Phe Glu Arg His Cys Gly Ser Leu Ser Gln Tyr
435 440 445

Gly Ile Lys His Met Arg Ser Phe Ala Asn Ile Cys Asn Ala Gly Ile
450 455 460

Gln Met Glu Gln Met Glu Glu Ala Ala Ser Gln Ala Cys Thr Thr Leu
465 470 475 480

Pro Thr Gly Pro Trp Ser Ser Leu Asn Arg Gly Phe Ser Ala
485 490

<210> 62
<211> 490
<212> PRT
<213> Arabidopsis thaliana

<400> 62

Met Thr Arg Val Ser Val Gly Val Val Leu Phe Val Leu Leu Val Ser
1 5 10 15

Leu Val Ala Val Ser Ala Ala Arg Ser Gly Pro Asp Asp Val Ile Lys
20 25 30

Leu Pro Ser Gln Ala Ser Arg Phe Phe Arg Pro Ala Glu Asn Asp Asp

35

40

45

Asp Ser Asn Ser Gly Thr Arg Trp Ala Val Leu Val Ala Gly Ser Ser
 50 55 60

Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp Ile Cys His Ala Tyr Gln
 65 70 75 80

Leu Leu Arg Lys Gly Gly Leu Lys Glu Glu Asn Ile Val Val Phe Met
 85 90 95

Tyr Asp Asp Ile Ala Asn Asn Tyr Glu Asn Pro Arg Pro Gly Thr Ile
 100 105 110

Ile Asn Ser Pro His Gly Lys Asp Val Tyr Gln Gly Val Pro Lys Asp
 115 120 125

Tyr Thr Gly Asp Asp Val Asn Val Asp Asn Leu Phe Ala Val Ile Leu
 130 135 140

Gly Asp Lys Thr Ala Val Lys Gly Gly Ser Gly Lys Val Val Asp Ser
 145 150 155 160

Gly Pro Asn Asp His Ile Phe Ile Phe Tyr Ser Asp His Gly Gly Pro
 165 170 175

Gly Val Leu Gly Met Pro Thr Ser Pro Tyr Leu Tyr Ala Asn Asp Leu
 180 185 190

Asn Asp Val Leu Lys Lys Lys His Ala Leu Gly Thr Tyr Lys Ser Leu
 195 200 205

Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu
 210 215 220

Leu Pro Glu Gly Leu Asn Ile Tyr Ala Thr Thr Ala Ser Asn Ala Glu
 225 230 235 240

Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Glu Pro Ser Pro Pro
 245 250 255

Pro Glu Tyr Glu Thr Cys Leu Gly Asp Leu Tyr Ser Val Ala Trp Met
260 265 270

Glu Asp Ser Gly Met His Asn Leu Gln Thr Glu Thr Leu His Gln Gln
275 280 285

Tyr Glu Leu Val Lys Arg Arg Thr Ala Pro Val Gly Tyr Ser Tyr Gly
290 295 300

Ser His Val Met Gln Tyr Gly Asp Val Gly Ile Ser Lys Asp Asn Leu
305 310 315 320

Asp Leu Tyr Met Gly Thr Asn Pro Ala Asn Asp Asn Phe Thr Phe Ala
325 330 335

Asp Ala Asn Ser Leu Lys Pro Pro Ser Arg Val Thr Asn Gln Arg Asp
340 345 350

Ala Asp Leu Val His Phe Trp Glu Lys Tyr Arg Lys Ala Pro Glu Gly
355 360 365

Ser Ala Arg Lys Thr Glu Ala Gln Lys Gln Val Leu Glu Ala Met Ser
370 375 380

His Arg Leu His Ile Asp Asn Ser Val Ile Leu Val Gly Lys Ile Leu
385 390 395 400

Phe Gly Ile Ser Arg Gly Pro Glu Val Leu Asn Lys Val Arg Ser Ala
405 410 415

Gly Gln Pro Leu Val Asp Asp Trp Asn Cys Leu Lys Asn Gln Val Arg
420 425 430

Ala Phe Glu Arg His Cys Gly Ser Leu Ser Gln Tyr Gly Ile Lys His
435 440 445

Met Arg Ser Phe Ala Asn Ile Cys Asn Ala Gly Ile Gln Met Glu Gln
450 455 460

Met Glu Glu Ala Ala Ser Gln Ala Cys Thr Thr Leu Pro Thr Gly Pro

465 470 475 480

Trp Ser Ser Leu Asn Arg Gly Phe Ser Ala
 485 490

<210> 63
<211> 484
<212> PRT
<213> Nicotiana tabacum

<400> 63

Met Ile Val Arg Tyr Val Val Ser Ala Ile Leu Ile Ile Gly Leu Ser
1 5 10 15

Val Val Ala Ala Val Asp Gly Arg Asp Val Leu Lys Leu Pro Ser Glu
 20 25 30

Ala Ser Thr Phe Phe Ser Gly Asn Tyr Asp Asp Asp Ser Ile Gly Thr
 35 40 45

Lys Trp Ala Val Leu Val Ala Gly Ser Arg Gly Tyr Trp Asn Tyr Arg
50 55 60

His Gln Ala Asp Val Cys His Ala Tyr Gln Leu Leu Lys Lys Gly Gly
65 70 75 80

Leu Lys Asp Glu Asn Ile Ile Val Phe Met Tyr Asp Asp Ile Ala His
 85 90 95

Asn Phe Glu Asn Pro Arg Pro Gly Val Ile Ile Asn Ser Pro Asn Gly
 100 105 110

Asp Asp Val Tyr Lys Gly Val Pro Lys Asp Tyr Thr Gly His His Val
115 120 125

Thr Ala Asn Asn Phe Leu Ala Val Ile Leu Gly Asn Lys Ala Ala Leu
130 135 140

Ser Gly Gly Ser Gly Lys Val Val Glu Ser Gly Pro Asn Asp His Ile
145 150 155 160

Phe Ile Phe Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Met Pro
165 170 175

Ser Gly Pro Tyr Leu Tyr Ala Asp Asp Leu Ile Asp Val Leu Lys Arg
180 185 190

Lys His Ala Ser Gly Thr Tyr Lys Ser Leu Val Phe Tyr Ile Glu Ala
195 200 205

Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Glu Gly Leu Asn
210 215 220

Ile Tyr Ala Thr Thr Ala Ser Asn Ala Glu Glu Asp Ser Trp Gly Thr
225 230 235 240

Tyr Cys Pro Gly Asp Tyr Pro Gly Pro Pro Pro Glu Tyr Gln Thr Cys
245 250 255

Leu Gly Asp Leu Tyr Ala Val Ser Trp Met Glu Asp Ser Glu Lys His
260 265 270

Asn Leu Arg Arg Glu Thr Leu Gly Met Gln Tyr Glu Leu Val Lys Arg
275 280 285

Arg Thr Ala Asn Ser Phe Pro Tyr Ala Ser Ser His Val Met Gln Tyr
290 295 300

Gly Asp Leu Lys Leu Met Asp Asp Pro Leu Ser Leu Tyr Met Gly Thr
305 310 315 320

Asn Pro Ala Asn Asp Asn Tyr Thr Phe Leu Asp Glu Asn Ser Ser Leu
325 330 335

Leu Ser Ala Lys Pro Val Asn Gln Arg Asp Ala Asp Leu Leu His Phe
340 345 350

Trp Asp Lys Phe Leu Lys Ala Pro Gln Gly Ser Val Arg Lys Val Glu
355 360 365

Ala Gln Lys Gln Leu Ser Glu Ala Met Ser His Arg Met His Ile Asp
370 375 380

Asp Ser Ile Ala Leu Val Gly Arg Leu Leu Phe Gly Ile Glu Lys Gly
385 390 395 400

Pro Asp Val Leu Ile Arg Val Arg Pro Thr Gly Glu Pro Leu Val Asp
405 410 415

Asp Trp Asn Cys Leu Lys Ser Phe Val Arg Thr Phe Glu Thr Arg Cys
420 425 430

Gly Ser Leu Ser Gln Tyr Gly Met Lys His Met Arg Ala Val Ala Asn
435 440 445

Ile Cys Asn Ser Cys Ile Thr Met Glu Gln Ile Ala Lys Ala Ser Ala
450 455 460

Gln Ala Cys Val Ser Ile Pro Ser Asn Ser Trp Ser Ser Leu Asp Glu
465 470 475 480

Gly Phe Ser Ala

<210> 64
<211> 478
<212> PRT
<213> Arabidopsis thaliana

<400> 64

Met Thr Thr Val Val Ser Phe Leu Ala Leu Phe Leu Phe Leu Val Ala
1 5 10 15

Ala Val Ser Gly Asp Val Ile Lys Leu Pro Ser Leu Ala Ser Lys Phe
20 25 30

Phe Arg Pro Thr Glu Asn Asp Asp Asp Ser Thr Lys Trp Ala Val Leu
35 40 45

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

Cys His Ala Tyr Gln Leu Leu Lys Lys Gly Gly Val Lys Glu Glu Asn

65

70

75

80

Ile Val Val Phe Met Tyr Asp Asp Ile Ala Lys Asn Glu Glu Asn Pro
85 90 95

Arg Pro Gly Val Ile Ile Asn Ser Pro Asn Gly Glu Asp Val Tyr Asn
100 105 110

Gly Val Pro Lys Asp Tyr Thr Gly Asp Glu Val Asn Val Asp Asn Leu
115 120 125

Leu Ala Val Ile Leu Gly Asn Lys Thr Ala Leu Lys Gly Gly Ser Gly
130 135 140

Lys Val Val Asp Ser Gly Pro Asn Asp His Ile Phe Ile Tyr Tyr Ser
145 150 155 160

Asp His Gly Gly Pro Gly Val Leu Gly Met Pro Thr Ser Pro Asn Leu
165 170 175

Tyr Ala Asn Asp Leu Asn Asp Val Leu Lys Lys Lys Tyr Ala Ser Gly
180 185 190

Thr Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser
195 200 205

Ile Phe Glu Gly Leu Leu Pro Glu Gly Leu Asn Ile Tyr Ala Thr Thr
210 215 220

Ala Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu
225 230 235 240

Asp Pro Ser Pro Pro Ser Glu Tyr Glu Thr Cys Leu Gly Asp Leu Tyr
245 250 255

Ser Val Ala Trp Ile Glu Asp Ser Glu Lys His Asn Leu Gln Thr Glu
260 265 270

Thr Leu His Glu Gln Tyr Glu Leu Val Lys Lys Arg Thr Ala Gly Ser
275 280 285

Gly Lys Ser Tyr Gly Ser His Val Met Glu Phe Gly Asp Ile Gly Leu
290 295 300

Ser Lys Glu Lys Leu Val Leu Phe Met Gly Thr Asn Pro Ala Asp Glu
305 310 315 320

Asn Phe Thr Phe Val Asn Glu Asn Ser Ile Arg Pro Pro Ser Arg Val
325 330 335

Thr Asn Gln Arg Asp Ala Asp Leu Val His Phe Trp His Lys Tyr Gln
340 345 350

Lys Ala Pro Glu Gly Ser Ala Arg Lys Val Glu Ala Gln Lys Gln Val
355 360 365

Leu Glu Ala Met Ser His Arg Leu His Val Asp Asn Ser Ile Leu Leu
370 375 380

Ile Gly Ile Leu Leu Phe Gly Leu Glu Gly His Ala Val Leu Asn Lys
385 390 395 400

Val Arg Pro Ser Gly Glu Pro Leu Val Asp Asp Trp Asp Cys Leu Lys
405 410 415

Ser Leu Val Arg Ala Phe Glu Arg His Cys Gly Ser Leu Ser Gln Tyr
420 425 430

Gly Ile Lys His Met Arg Ser Ile Ala Asn Met Cys Asn Ala Gly Ile
435 440 445

Gln Met Arg Gln Met Glu Glu Ala Ala Met Gln Ala Cys Pro Thr Ile
450 455 460

Pro Thr Ser Pro Trp Ser Ser Leu Asp Arg Gly Phe Ser Ala
465 470 475

<210> 65

<211> 478

<212> PRT

<213> Genlisea aurea

<400> 65

Ile Val Leu Leu Leu Leu Ser Val Ser Ile Leu Thr Ser Asp Cys Arg
1 5 10 15

Asn Gln Phe Ile Lys Leu Pro Ser Glu Val Phe Ser Tyr Gly Gly Glu
20 25 30

Ser Glu Asp Asp Ser Val Gly Thr Arg Trp Ala Val Leu Val Ala Gly
35 40 45

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

Tyr Gln Ile Leu Lys Arg Gly Gly Leu Lys Asp Glu Asn Ile Ile Val
65 70 75 80

Phe Met Tyr Asp Asp Ile Ala Gln Asn Leu Glu Asn Pro Arg Pro Gly
85 90 95

Ile Val Ile Asn Asn Pro His Gly Glu Asp Val Tyr His Gly Val Pro
100 105 110

Lys Asp Tyr Val Gly Arg Gln Val Thr Ala His Asn Phe Tyr Ser Val
115 120 125

Leu Leu Gly Asp Lys Ala Gly Leu Thr Gly Gly Ser Gly Lys Val Ile
130 135 140

Glu Ser Gly Pro Asn Asp His Ile Phe Ile Tyr Tyr Thr Asp His Gly
145 150 155 160

Gly Pro Gly Val Leu Gly Met Pro Ser Gly Pro Tyr Ile Tyr Ala Asp
165 170 175

Asp Leu Asn Asp Val Leu Lys Lys Lys His Ala Ser Gly Thr Tyr Lys
180 185 190

Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu
195 200 205

Gly Ile Leu Pro Asp Asn Leu Asn Ile Tyr Ala Thr Thr Ala Ser Asn
210 215 220

Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Asp Ile Ile Ala
225 230 235 240

Pro Pro Leu Glu Tyr Asp Thr Cys Leu Gly Asp Leu Tyr Ser Ile Ala
245 250 255

Trp Met Glu Asp Ser Asp Ile His Asn Leu Arg Thr Glu Ser Leu Glu
260 265 270

Gln Gln Tyr Gln Val Val Lys Lys Arg Thr Ala Asn Gly Asp Ser Tyr
275 280 285

Tyr Gly Ser His Val Met Gln Tyr Gly Glu Leu Lys Leu Asp Leu Glu
290 295 300

Asn Leu Phe Leu Tyr Leu Gly Thr Asp Pro Ala Asn Asp Asn Tyr Thr
305 310 315 320

Phe Val Glu Gly Asn Ser Leu Ser Thr Ser Pro Ser Gly Arg Val Asn
325 330 335

Gln Arg Asp Ala Asp Leu Leu His Phe Trp His Lys Phe Trp Lys Ala
340 345 350

Pro Glu Arg Ser Ser Glu Lys Asp Glu Ala Gln Arg Arg Leu Ala Glu
355 360 365

Val Val Ser His Arg Ser His Ile Asp Asp Ser Ile Glu Leu Ile Gly
370 375 380

Asp Leu Leu Phe Gly Ser Thr Glu Gly Thr Arg Val Leu Lys His Val
385 390 395 400

Arg Pro Ser Gly Arg Pro Val Val Asp Asp Trp Asp Cys Leu Arg Ser
405 410 415

Leu Val Arg Thr Phe Glu Thr Tyr Cys Gly Ser Leu Ser Gln Tyr Gly
420 425 430

Met Lys His Met Arg Ser Phe Ala Asn Ile Cys Asn Ser Gly Val Lys
435 440 445

Ala Glu Lys Met Gly Glu Ala Thr Gln Gln Val Cys Thr Ala Phe Pro
450 455 460

Ser His Asn Pro Trp Ser Ser Leu His Arg Gly Phe Ser Ala
465 470 475

<210> 66
<211> 486
<212> PRT
<213> Zea mays

<400> 66

Met Val Ala Ala Arg Leu Arg Leu Ala Leu Leu Leu Ser Val Cys Leu
1 5 10 15

Cys Ser Ala Trp Ala Arg Pro Arg Leu Glu Thr Ala Ile Arg Leu Pro
20 25 30

Ser Gln Arg Ala Ala Ala Ala Asp Glu Thr Asp Asp Gly Ala Val Gly
35 40 45

Thr Arg Trp Ala Val Leu Ile Ala Gly Ser Ser Gly Tyr Tyr Asn Tyr
50 55 60

Arg His Gln Ala Asp Ile Cys His Ala Tyr Gln Ile Met Lys Lys Gly
65 70 75 80

Gly Leu Lys Asp Glu Asn Ile Ile Val Phe Met Tyr Asp Asp Ile Ala
85 90 95

His Ser Pro Glu Asn Pro Arg Pro Gly Val Ile Ile Asn His Pro Gln
100 105 110

Gly Gly Asp Val Tyr Ala Gly Val Pro Lys Asp Tyr Thr Gly Arg Asp
115 120 125

Val Asn Val Asp Asn Phe Phe Ala Val Leu Leu Gly Asn Lys Thr Ala

130

135

140

Leu Arg Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro Asp Asp His
 145 150 155 160

Ile Phe Val Phe Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Met
 165 170 175

Pro Thr Tyr Pro Tyr Leu Tyr Gly Asp Asp Leu Val Asp Val Leu Lys
 180 185 190

Lys Lys His Ala Ala Gly Thr Tyr Lys Ser Leu Val Phe Tyr Leu Glu
 195 200 205

Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Asn Asp Ile
 210 215 220

Asn Val Tyr Ala Thr Thr Ala Ser Asn Ala Glu Glu Ser Ser Trp Gly
 225 230 235 240

Thr Tyr Cys Pro Gly Glu Phe Pro Ser Pro Pro Pro Glu Tyr Asp Thr
 245 250 255

Cys Leu Gly Asp Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Phe
 260 265 270

His Asn Leu Arg Thr Glu Ser Leu Lys Gln Gln Tyr Lys Leu Val Lys
 275 280 285

Asp Arg Thr Ala Val His Asp Thr Phe Ser Tyr Gly Ser His Val Met
 290 295 300

Gln Tyr Gly Ala Leu Glu Leu Asn Val Gln Arg Leu Phe Ser Tyr Ile
 305 310 315 320

Gly Thr Asp Pro Ala Asn Asp Gly Asn Thr Phe Ile Glu Asp Asn Ser
 325 330 335

Leu Pro Ser Phe Ser Lys Ala Val Asn Gln Arg Asp Ala Asp Leu Val
 340 345 350

Tyr Phe Trp Gln Lys Tyr Arg Lys Leu Ala Asp Ser Ser Pro Pro Lys
355 360 365

Ser Glu Ala Arg Lys Glu Leu Leu Glu Val Met Ala His Arg Ser His
370 375 380

Val Asp Ser Ser Val Glu Leu Ile Gly Ser Leu Leu Phe Gly Ser Glu
385 390 395 400

Asp Gly Pro Arg Val Leu Lys Ala Val Arg Ala Pro Gly Glu Pro Leu
405 410 415

Val Asp Asp Trp Ser Cys Leu Lys Ser Ile Val Arg Thr Phe Glu Ala
420 425 430

Arg Cys Gly Ser Leu Ala Gln Tyr Gly Met Lys His Met Arg Ser Phe
435 440 445

Ala Asn Met Cys Asn Ala Gly Ile Leu Pro Glu Ala Val Ser Lys Val
450 455 460

Thr Ala Gln Ala Cys Ser Ser Ile Pro Ser Asn Pro Trp Ser Ser Ile
465 470 475 480

His Lys Gly Phe Ser Ala
485

<210> 67
<211> 486
<212> PRT
<213> Zea mays

<400> 67

Met Val Ala Ala Arg Leu Arg Leu Ser Leu Leu Leu Ser Val Cys Leu
1 5 10 15

Ser Ser Ala Trp Ala Arg Pro Arg Leu Glu Pro Ala Ile Arg Leu Pro
20 25 30

Ser Gln Arg Ala Ala Ala Ala Asp Glu Thr Asp Asp Gly Asp Val Gly
35 40 45

Thr Arg Trp Ala Val Leu Ile Ala Gly Ser Ser Gly Tyr Tyr Asn Tyr
50 55 60

Arg His Gln Ala Asp Ile Cys His Ala Tyr Gln Ile Met Lys Lys Gly
65 70 75 80

Gly Leu Lys Asp Glu Asn Ile Ile Val Phe Met Tyr Asp Asp Ile Ala
85 90 95

His Ser Pro Glu Asn Pro Arg Pro Gly Val Ile Ile Asn His Pro Gln
100 105 110

Gly Gly Asp Val Tyr Ala Gly Val Pro Lys Asp Tyr Thr Gly Arg Asp
115 120 125

Val Asn Val Asp Asn Phe Phe Ala Val Leu Leu Gly Asn Lys Thr Ala
130 135 140

Leu Arg Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro Asn Asp His
145 150 155 160

Ile Phe Val Phe Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Met
165 170 175

Pro Thr Tyr Pro Tyr Leu Tyr Gly Asp Asp Leu Val Asp Val Leu Lys
180 185 190

Lys Lys His Ala Ala Gly Thr Tyr Lys Ser Leu Val Phe Tyr Leu Glu
195 200 205

Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Asn Asp Ile
210 215 220

Asn Val Tyr Ala Thr Thr Ala Ser Asn Ala Asp Glu Ser Ser Trp Gly
225 230 235 240

Thr Tyr Cys Pro Gly Glu Phe Pro Ser Pro Pro Pro Glu Tyr Asp Thr
245 250 255

Cys Leu Gly Asp Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Phe
260 265 270

His Asn Leu Arg Thr Glu Ser Leu Lys Gln Gln Tyr Lys Leu Val Lys
275 280 285

Asp Arg Thr Ala Val His Asp Thr Phe Ser Tyr Gly Ser His Val Met
290 295 300

Gln Tyr Gly Ala Leu Glu Leu Asn Val Gln Arg Leu Phe Ser Tyr Ile
305 310 315 320

Gly Thr Asp Pro Ala Asn Asp Gly Asn Thr Phe Ile Glu Asp Asn Ser
325 330 335

Leu Pro Ser Phe Ser Lys Ala Val Asn Gln Arg Asp Ala Asp Leu Val
340 345 350

Tyr Phe Trp Gln Lys Tyr Arg Lys Leu Ala Asp Ser Ser His Ala Lys
355 360 365

Asn Glu Ala Arg Lys Glu Leu Leu Glu Val Met Ala His Arg Ser His
370 375 380

Val Asp Ser Ser Val Glu Leu Ile Gly Ser Leu Leu Phe Gly Ser Glu
385 390 395 400

Asp Gly Pro Arg Val Leu Lys Ala Val Arg Ala Pro Gly Glu Pro Leu
405 410 415

Val Asp Asp Trp Ser Cys Leu Lys Ser Ile Val Arg Thr Phe Glu Ala
420 425 430

Arg Cys Gly Ser Leu Ala Gln Tyr Gly Met Lys His Met Arg Ser Phe
435 440 445

Ala Asn Met Cys Asn Ala Gly Ile Leu Pro Glu Ala Val Ser Lys Val
450 455 460

Ala Ala Gln Ala Cys Ser Ser Ile Pro Ser Asn Pro Trp Ser Ser Ile
465 470 475 480

His Lys Gly Phe Ser Ala
485

<210> 68
<211> 488
<212> PRT
<213> Saccharum officinarum

<400> 68

Met Val Thr Ala Arg Leu Arg Leu Ala Leu Leu Leu Leu Ser Val Phe
1 5 10 15

Leu Cys Ser Ala Trp Ala Arg Pro Arg Leu Glu Pro Thr Ile Arg Leu
20 25 30

Pro Ser Glu Arg Ala Ala Ala Ala Ala Gly Asp Glu Thr Asp Asp Ala
35 40 45

Val Gly Thr Arg Trp Ala Val Leu Val Ala Gly Ser Ser Gly Tyr Tyr
50 55 60

Asn Tyr Arg His Gln Ala Asp Ile Cys His Ala Tyr Gln Ile Met Lys
65 70 75 80

Lys Gly Gly Leu Lys Asp Glu Asn Ile Ile Val Phe Met Tyr Asp Asp
85 90 95

Ile Ala His Ser Ala Glu Asn Pro Arg Pro Gly Val Val Ile Asn His
100 105 110

Pro Gln Gly Gly Asp Val Tyr Ala Gly Val Pro Lys Asp Tyr Thr Gly
115 120 125

Arg Gln Val Ser Val Asn Asn Phe Phe Ala Val Leu Leu Gly Asn Lys
130 135 140

Thr Ala Leu Thr Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro Asn
145 150 155 160

Asp His Ile Phe Val Phe Tyr Ser Asp His Gly Gly Pro Gly Val Leu

165

170

175

Gly Met Pro Thr Tyr Pro Tyr Leu Tyr Gly Asp Asp Leu Val Asp Val
 180 185 190

Leu Lys Lys Lys His Ala Ala Gly Ser Tyr Lys Ser Leu Val Phe Tyr
 195 200 205

Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Asp
 210 215 220

Asp Ile Asn Val Tyr Ala Thr Thr Ala Ser Asn Ala Glu Glu Ser Ser
 225 230 235 240

Trp Gly Thr Tyr Cys Pro Gly Glu Phe Pro Ser Pro Pro Pro Glu Tyr
 245 250 255

Asp Thr Cys Leu Gly Asp Leu Tyr Ser Val Ser Trp Met Glu Asp Ser
 260 265 270

Asp Phe His Asn Leu Arg Thr Glu Ser Leu Lys Gln Gln Tyr Lys Leu
 275 280 285

Val Lys Asp Arg Thr Ala Ala Gln Asp Thr Phe Ser Tyr Gly Ser His
 290 295 300

Val Met Gln Tyr Gly Ser Leu Glu Leu Asn Val Gln Lys Leu Phe Ser
 305 310 315 320

Tyr Ile Gly Thr Asn Pro Ala Asn Asp Gly Asn Thr Phe Val Glu Asp
 325 330 335

Asn Ser Leu Pro Ser Phe Ser Lys Ala Val Asn Gln Arg Asp Ala Asp
 340 345 350

Leu Val Tyr Phe Trp Gln Lys Tyr Arg Lys Leu Ala Asp Gly Ser Ser
 355 360 365

Lys Lys Asn Glu Ala Arg Lys Glu Leu Leu Glu Val Met Ser His Arg
 370 375 380

Ser His Val Asp Asn Ser Val Glu Leu Ile Gly Ser Leu Leu Phe Gly
385 390 395 400

Ser Glu Asp Gly Pro Arg Val Leu Lys Ala Val Arg Ala Ala Gly Glu
405 410 415

Pro Leu Val Asp Asp Trp Ser Cys Leu Lys Ser Met Val Arg Thr Phe
420 425 430

Glu Ala Gln Cys Gly Ser Leu Ala Gln Tyr Gly Met Lys His Met Arg
435 440 445

Thr Phe Ala Asn Ile Cys Asn Ala Gly Ile Leu Pro Glu Ala Val Ser
450 455 460

Lys Val Ala Ala Gln Ala Cys Thr Ser Ile Pro Ser Asn Pro Trp Ser
465 470 475 480

Ser Ile Asp Lys Gly Phe Ser Ala
485

<210> 69
<211> 486
<212> PRT
<213> Zea mays

<400> 69

Met Val Ala Ala Arg Leu Arg Leu Ala Leu Leu Leu Ser Val Cys Leu
1 5 10 15

Cys Ser Ala Trp Ala Arg Pro Arg Leu Glu Thr Ala Ile Arg Leu Pro
20 25 30

Ser Gln Arg Ala Ala Ala Ala Asp Glu Thr Asp Asp Gly Ala Val Gly
35 40 45

Thr Arg Trp Ala Val Leu Ile Ala Gly Ser Ser Gly Tyr Tyr Asn Tyr
50 55 60

Arg His Gln Ala Asp Ile Cys His Ala Tyr Gln Ile Met Lys Lys Gly
65 70 75 80

Gly Leu Lys Asp Glu Asn Ile Ile Val Phe Met Tyr Asp Asp Ile Ala
85 90 95

His Ser Pro Glu Asn Pro Arg Pro Gly Val Ile Ile Asn His Pro Gln
100 105 110

Gly Gly Asp Val Tyr Ala Gly Val Pro Lys Asp Tyr Thr Gly Arg Asp
115 120 125

Val Asn Val Asp Asn Phe Phe Ala Val Leu Leu Gly Asn Lys Thr Ala
130 135 140

Leu Arg Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro Asp Asp His
145 150 155 160

Ile Phe Val Phe Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Met
165 170 175

Pro Thr Tyr Pro Tyr Leu Tyr Gly Asp Asp Leu Val Asp Val Leu Lys
180 185 190

Lys Lys His Ala Ala Gly Thr Tyr Lys Ser Leu Val Phe Tyr Leu Glu
195 200 205

Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Asn Asp Ile
210 215 220

Asn Val Tyr Ala Thr Thr Ala Ser Asn Ala Glu Glu Ser Ser Trp Gly
225 230 235 240

Thr Tyr Cys Pro Gly Glu Phe Pro Ser Pro Pro Pro Glu Tyr Asp Thr
245 250 255

Cys Leu Gly Asp Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Phe
260 265 270

His Asn Leu Arg Thr Glu Ser Leu Lys Gln Gln Tyr Lys Leu Val Lys
275 280 285

Asp Arg Thr Ala Val His Asp Thr Phe Ser Tyr Gly Ser His Val Met
290 295 300

Gln Tyr Gly Ala Leu Glu Leu Asn Val Gln His Leu Phe Ser Tyr Ile
305 310 315 320

Gly Thr Asp Pro Ala Asn Asp Gly Asn Thr Phe Ile Glu Asp Asn Ser
325 330 335

Leu Pro Ser Phe Ser Lys Ala Val Asn Gln Arg Asp Ala Asp Leu Val
340 345 350

Tyr Phe Trp Gln Lys Tyr Arg Lys Phe Ala Asp Ser Pro Pro Ala Lys
355 360 365

Ser Glu Ala Arg Lys Glu Leu Leu Glu Val Met Ala His Arg Ser His
370 375 380

Val Asp Ser Ser Val Glu Leu Ile Gly Ser Leu Leu Phe Gly Ser Glu
385 390 395 400

Asp Gly Pro Arg Val Leu Lys Ala Val Arg Ala Pro Gly Glu Pro Leu
405 410 415

Val Asp Asp Trp Ser Cys Leu Lys Ser Ile Val Arg Thr Phe Glu Ala
420 425 430

Arg Cys Gly Ser Leu Ala Gln Tyr Gly Met Lys His Met Arg Ser Phe
435 440 445

Ala Asn Met Cys Asn Ala Gly Ile Leu Pro Glu Ala Val Ser Lys Val
450 455 460

Ala Ala Gln Ala Cys Ser Ser Ile Pro Ser Asn Pro Trp Ser Ser Ile
465 470 475 480

His Lys Gly Phe Ser Ala
485

<210> 70
<211> 481

<212> PRT

<213> Sorghum bicolor

<400> 70

Met Val Ala Ala Arg Leu Arg Leu Ala Leu Leu Leu Leu Leu Pro Val
1 5 10 15

Phe Leu Cys Ser Ala Trp Ala Arg Pro Arg Leu Glu Pro Thr Ile Arg
20 25 30

Leu Pro Ser Asp Arg Ala Asp Asp Ala Val Gly Thr Arg Trp Ala Val
35 40 45

Leu Val Ala Gly Ser Asn Gly Tyr Tyr Asn Tyr Arg His Gln Ala Asp
50 55 60

Ile Cys His Ala Tyr Gln Ile Met Lys Lys Gly Gly Leu Lys Asp Glu
65 70 75 80

Asn Ile Ile Val Phe Met Tyr Asp Asp Ile Ala His Ser Pro Glu Asn
85 90 95

Pro Arg Pro Gly Val Leu Ile Asn His Pro Gln Gly Gly Asp Val Tyr
100 105 110

Ala Gly Val Pro Lys Asp Tyr Thr Gly Arg Glu Val Ser Val Asn Asn
115 120 125

Phe Phe Ala Val Leu Leu Gly Asn Lys Thr Ala Leu Lys Gly Gly Ser
130 135 140

Gly Lys Val Val Asp Ser Gly Pro Asn Asp His Ile Phe Val Phe Tyr
145 150 155 160

Ser Asp His Gly Gly Pro Gly Val Leu Gly Met Pro Thr Tyr Pro Tyr
165 170 175

Leu Tyr Gly Asp Asp Leu Val Asp Val Leu Lys Lys Lys His Ala Ala
180 185 190

Gly Thr Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly

195

200

205

Ser Ile Phe Glu Gly Leu Leu Pro Asp Asp Ile Asn Val Tyr Ala Thr
 210 215 220

Thr Ala Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly
 225 230 235 240

Glu Phe Pro Ser Pro Pro Pro Glu Tyr Asp Thr Cys Leu Gly Asp Leu
 245 250 255

Tyr Ser Val Ser Trp Met Glu Asp Ser Asp Phe His Asn Leu Arg Thr
 260 265 270

Glu Ser Leu Lys Gln Gln Tyr Lys Leu Val Lys Asp Arg Thr Ala Val
 275 280 285

Gln Asp Thr Phe Ser Tyr Gly Ser His Val Met Gln Tyr Gly Ser Leu
 290 295 300

Glu Leu Asn Val Gln Lys Leu Phe Ser Tyr Ile Gly Thr Asn Pro Ala
 305 310 315 320

Asn Asp Gly Asn Thr Phe Val Glu Asp Asn Ser Leu Pro Ser Phe Ser
 325 330 335

Lys Ala Val Asn Gln Arg Asp Ala Asp Leu Val Tyr Phe Trp Gln Lys
 340 345 350

Tyr Arg Lys Leu Ala Asp Asp Ser Ser Lys Lys Asn Glu Ala Arg Lys
 355 360 365

Glu Leu Leu Glu Val Met Ala His Arg Ser His Val Asp Asn Ser Val
 370 375 380

Glu Leu Ile Gly Ser Leu Leu Phe Gly Ser Glu Asp Gly Pro Arg Val
 385 390 395 400

Leu Lys Ala Val Arg Ala Ala Gly Glu Pro Leu Val Asp Asp Trp Ser
 405 410 415

Cys Leu Lys Ser Met Val Arg Thr Phe Glu Ala Gln Cys Gly Ser Leu
420 425 430

Ala Gln Tyr Gly Met Lys His Met Arg Ser Phe Ala Asn Ile Cys Asn
435 440 445

Ala Gly Ile Leu Pro Glu Ala Val Ser Lys Val Ala Ala Gln Ala Cys
450 455 460

Thr Ser Ile Pro Ser Asn Pro Trp Ser Ser Ile Asp Lys Gly Phe Ser
465 470 475 480

Ala

<210> 71
<211> 488
<212> PRT
<213> Saccharum hybrid cultivar SP80-3280

<400> 71

Met Val Ala Ala Arg Leu Arg Leu Ala Leu Leu Leu Leu Ser Val Cys
1 5 10 15

Leu Cys Ser Ala Trp Ala Arg Pro Arg Leu Glu Pro Thr Ile Arg Leu
20 25 30

Pro Ser Glu Arg Ala Ala Ala Ala Gly Asp Glu Thr Asp Asp Ala
35 40 45

Val Gly Thr Arg Trp Ala Val Leu Val Ala Gly Ser Ser Gly Tyr Tyr
50 55 60

Asn Tyr Arg His Gln Ala Asp Ile Cys His Ala Tyr Gln Ile Met Lys
65 70 75 80

Lys Gly Gly Leu Lys Asp Glu Asn Ile Ile Val Phe Met Tyr Asp Asp
85 90 95

Ile Ala His Ser Ala Glu Asn Pro Arg Pro Gly Val Val Ile Asn His
100 105 110

Pro Gln Gly Gly Asp Val Tyr Ala Gly Val Pro Lys Asp Tyr Thr Gly
115 120 125

Arg Gln Val Ser Val Asn Asn Phe Phe Ala Val Leu Leu Gly Asn Lys
130 135 140

Thr Ala Leu Thr Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro Asn
145 150 155 160

Asp His Ile Phe Val Phe Tyr Ser Asp His Gly Gly Pro Gly Val Leu
165 170 175

Gly Met Pro Thr Tyr Pro Tyr Leu Tyr Gly Asp Asp Leu Val Asp Val
180 185 190

Leu Lys Lys Lys His Ala Ala Gly Thr Tyr Lys Ser Leu Val Phe Tyr
195 200 205

Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Asp
210 215 220

Asp Ile Asn Val Tyr Ala Thr Thr Ala Ser Asn Ala Glu Glu Ser Ser
225 230 235 240

Trp Gly Thr Tyr Cys Pro Gly Glu Phe Pro Ser Pro Pro Glu Tyr
245 250 255

Asp Thr Cys Leu Gly Asp Leu Tyr Ser Val Ser Trp Met Glu Asp Ser
260 265 270

Asp Phe His Asn Leu Arg Thr Glu Ser Leu Lys Gln Gln Tyr Lys Leu
275 280 285

Val Lys Asp Arg Thr Ala Ala Gln Asp Thr Phe Ser Tyr Gly Ser His
290 295 300

Val Met Gln Tyr Gly Ser Leu Glu Leu Asn Val Gln Lys Leu Phe Ser
305 310 315 320

Tyr Ile Gly Thr Asn Pro Ala Asn Asp Gly Asn Thr Phe Val Glu Asp
325 330 335

Asn Ser Leu Pro Ser Phe Phe Lys Ser Cys Asn Gln Arg Asp Ala Asp
340 345 350

Leu Val Tyr Phe Trp Gln Lys Tyr Arg Lys Leu Ala Asp Gly Ser Ser
355 360 365

Lys Lys Asn Glu Ala Arg Lys Glu Leu Leu Glu Val Met Ser His Arg
370 375 380

Ser His Val Asp Asn Ser Val Glu Leu Ile Gly Ser Leu Leu Phe Gly
385 390 395 400

Ser Glu Asp Gly Pro Arg Val Leu Lys Ala Val Arg Ala Ala Gly Glu
405 410 415

Pro Leu Val Asp Asp Trp Ser Cys Leu Lys Ser Met Val Arg Thr Phe
420 425 430

Glu Ala Gln Cys Gly Ser Leu Ala Gln Tyr Gly Met Lys His Met Arg
435 440 445

Thr Phe Ala Asn Ile Cys Asn Ala Gly Ile Leu Pro Glu Ala Val Ser
450 455 460

Lys Val Ala Ala Gln Ala Cys Thr Ser Ile Pro Ser Asn Pro Trp Ser
465 470 475 480

Ser Ile Asp Lys Gly Phe Ser Ala
485

<210> 72
<211> 503
<212> PRT
<213> Oryza sativa Japonica Group

<400> 72

Met Ala Ala Arg Ala Ser Ala Phe Arg Leu Val Leu Pro Pro Ala Arg
1 5 10 15

Gly Ala Ala Pro Ser Phe Ala His Leu Ala Ala Val Ala Val Ala Arg
20 25 30

Pro Arg Trp Glu Glu Glu Gly Ser Asn Leu Arg Leu Pro Ser Glu Arg
35 40 45

Ala Val Ala Ala Gly Ala Ala Ala Asp Asp Ala Ala Glu Ala Ala Glu
50 55 60

Gly Thr Arg Trp Ala Val Leu Ile Ala Gly Ser Asn Gly Tyr Tyr Asn
65 70 75 80

Tyr Arg His Gln Ala Asp Val Cys His Ala Tyr Gln Ile Met Lys Arg
85 90 95

Gly Gly Leu Lys Asp Glu Asn Ile Ile Val Phe Met Tyr Asp Asp Ile
100 105 110

Ala His Asn Pro Glu Asn Pro Arg Pro Gly Val Ile Ile Asn His Pro
115 120 125

Gln Gly Gly Asp Val Tyr Ala Gly Val Pro Lys Asp Tyr Thr Gly Lys
130 135 140

Glu Val Asn Val Lys Asn Leu Phe Ala Val Leu Leu Gly Asn Lys Thr
145 150 155 160

Ala Val Lys Gly Gly Ser Gly Lys Val Leu Asp Ser Gly Pro Asn Asp
165 170 175

His Ile Phe Ile Phe Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly
180 185 190

Met Pro Thr Tyr Pro Tyr Leu Tyr Gly Asp Asp Leu Val Asp Val Leu
195 200 205

Lys Lys Lys His Ala Ala Gly Thr Tyr Lys Ser Leu Val Phe Tyr Leu
210 215 220

Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Asn Gly

225		230		235		240									
Ile	Asn	Val	Tyr	Ala	Thr	Thr	Ala	Ser	Asn	Ala	Asp	Glu	Ser	Ser	Trp
				245					250					255	
Gly	Thr	Tyr	Cys	Pro	Gly	Glu	Tyr	Pro	Ser	Pro	Pro	Pro	Glu	Tyr	Asp
			260					265					270		
Thr	Cys	Leu	Gly	Asp	Leu	Tyr	Ser	Val	Ala	Trp	Met	Glu	Asp	Ser	Asp
		275					280					285			
Val	His	Asn	Leu	Arg	Thr	Glu	Ser	Leu	Lys	Gln	Gln	Tyr	Asn	Leu	Val
	290					295					300				
Lys	Glu	Arg	Thr	Ser	Val	Gln	His	Thr	Tyr	Tyr	Ser	Gly	Ser	His	Val
305					310					315					320
Met	Glu	Tyr	Gly	Ser	Leu	Glu	Leu	Asn	Ala	His	His	Val	Phe	Met	Tyr
				325					330					335	
Met	Gly	Ser	Asn	Pro	Ala	Asn	Asp	Asn	Ala	Thr	Phe	Val	Glu	Asp	Asn
			340					345					350		
Ser	Leu	Pro	Ser	Phe	Ser	Arg	Ala	Val	Asn	Gln	Arg	Asp	Ala	Asp	Leu
		355					360					365			
Val	Tyr	Phe	Trp	Gln	Lys	Tyr	Arg	Lys	Leu	Pro	Glu	Ser	Ser	Pro	Glu
	370					375					380				
Lys	Asn	Glu	Ala	Arg	Lys	Gln	Leu	Leu	Glu	Met	Met	Ala	His	Arg	Ser
385					390					395					400
His	Val	Asp	Asn	Ser	Val	Glu	Leu	Ile	Gly	Asn	Leu	Leu	Phe	Gly	Ser
				405					410					415	
Glu	Glu	Gly	Pro	Arg	Val	Leu	Lys	Ala	Val	Arg	Ala	Thr	Gly	Glu	Pro
			420					425					430		
Leu	Val	Asp	Asp	Trp	Ser	Cys	Leu	Lys	Ser	Met	Val	Arg	Thr	Phe	Glu
		435					440					445			

Ala Gln Cys Gly Ser Leu Ala Gln Tyr Gly Met Lys His Met Arg Ser
450 455 460

Phe Ala Asn Ile Cys Asn Ala Gly Ile Ser Ala Glu Ala Met Ala Lys
465 470 475 480

Val Ala Ala Gln Ala Cys Thr Ser Ile Pro Ser Asn Pro Trp Ser Ser
485 490 495

Thr His Arg Gly Phe Ser Ala
500

<210> 73
<211> 481
<212> PRT
<213> Zea mays

<400> 73

Met Val Ala Asp Arg Leu Arg Leu Ala Leu Leu Leu Ser Ala Cys Leu
1 5 10 15

Cys Ser Ala Trp Ala Arg Pro Arg Leu Glu Pro Thr Ile Arg Leu Pro
20 25 30

Ser Glu Arg Ala Ala Ala Asp Asp Ala Val Gly Thr Arg Trp Ala Val
35 40 45

Leu Ile Ala Gly Ser Asn Gly Tyr Tyr Asn Tyr Arg His Gln Ala Asp
50 55 60

Ile Cys His Ala Tyr Gln Ile Met Lys Lys Gly Gly Leu Lys Asp Glu
65 70 75 80

Asn Ile Val Val Phe Met Tyr Asp Asp Ile Ala His Ser Pro Glu Asn
85 90 95

Pro Arg Pro Gly Val Ile Ile Asn His Pro Gln Gly Gly Asp Val Tyr
100 105 110

Ala Gly Val Pro Lys Asp Tyr Thr Gly Arg Glu Val Asn Val Asp Asn
115 120 125

Phe Phe Ala Val Leu Leu Gly Asn Lys Thr Ala Leu Arg Gly Gly Ser
130 135 140

Gly Lys Val Val Asp Ser Gly Pro Asn Asp His Ile Phe Val Phe Tyr
145 150 155 160

Ser Asp His Gly Gly Pro Gly Val Leu Gly Met Pro Thr Tyr Pro Tyr
165 170 175

Leu Tyr Gly Asp Asp Leu Val Asp Val Leu Lys Lys Lys His Ala Ala
180 185 190

Gly Thr Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly
195 200 205

Ser Ile Phe Glu Gly Leu Leu Pro Asn Asp Ile Asn Val Tyr Ala Thr
210 215 220

Thr Ala Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly
225 230 235 240

Glu Phe Pro Ser Pro Pro Pro Glu Tyr Asp Thr Cys Leu Gly Asp Leu
245 250 255

Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Phe His Asn Leu Arg Thr
260 265 270

Glu Ser Leu Lys Gln Gln Tyr Asn Leu Val Lys Asp Arg Thr Ala Val
275 280 285

Gln Asp Thr Phe Ser Tyr Gly Ser His Val Met Gln Tyr Gly Ser Leu
290 295 300

Glu Leu Asn Val Lys His Leu Phe Ser Tyr Ile Gly Thr Asn Pro Ala
305 310 315 320

Asn Asp Asp Asn Thr Phe Ile Glu Asp Asn Ser Leu Pro Ser Phe Ser
325 330 335

Lys Ala Val Asn Gln Arg Asp Ala Asp Leu Val Tyr Phe Trp Gln Lys
340 345 350

Tyr Arg Lys Leu Ala Asp Ser Ser Pro Glu Lys Asn Glu Ala Arg Lys
355 360 365

Glu Leu Leu Glu Val Met Ala His Arg Ser His Val Asp Ser Ser Val
370 375 380

Glu Leu Ile Gly Ser Leu Leu Phe Gly Ser Glu Asp Gly Pro Arg Val
385 390 395 400

Leu Lys Ala Val Arg Ala Ala Gly Glu Pro Leu Val Asp Asp Trp Ser
405 410 415

Cys Leu Lys Ser Thr Val Arg Thr Phe Glu Ala Gln Cys Gly Ser Leu
420 425 430

Ala Gln Tyr Gly Met Lys His Met Arg Ser Phe Ala Asn Ile Cys Asn
435 440 445

Ala Gly Ile Leu Pro Glu Ala Val Ser Lys Val Ala Ala Gln Ala Cys
450 455 460

Thr Ser Ile Pro Ser Asn Pro Trp Ser Ser Ile His Lys Gly Phe Ser
465 470 475 480

Ala

<210> 74
<211> 481
<212> PRT
<213> Zea mays

<400> 74

Met Val Ala Asp Arg Leu Arg Leu Ala Leu Leu Leu Ser Ala Cys Leu
1 5 10 15

Cys Ser Ala Trp Ala Arg Pro Arg Leu Glu Pro Thr Ile Arg Leu Pro
20 25 30

Ser Asp Arg Ala Ala Ala Asp Asp Ala Val Gly Thr Arg Trp Ala Val
35 40 45

Leu Ile Ala Gly Ser Asn Gly Tyr Tyr Asn Tyr Arg His Gln Ala Asp
50 55 60

Ile Cys His Ala Tyr Gln Ile Met Lys Lys Gly Gly Leu Lys Asp Glu
65 70 75 80

Asn Ile Val Val Phe Met Tyr Asp Asp Ile Ala His Ser Pro Glu Asn
85 90 95

Pro Arg Pro Gly Val Ile Ile Asn His Pro Gln Gly Gly Asp Val Tyr
100 105 110

Ala Gly Val Pro Lys Asp Tyr Thr Gly Arg Asp Val Asn Val Asp Asn
115 120 125

Phe Phe Ala Val Leu Leu Gly Asn Lys Thr Ala Leu Arg Gly Gly Ser
130 135 140

Gly Lys Val Val Asp Ser Gly Pro Asn Asp His Ile Ser Val Phe Tyr
145 150 155 160

Ser Asp His Gly Gly Pro Gly Val Leu Gly Met Pro Thr Tyr Pro Tyr
165 170 175

Leu Tyr Gly Asp Asp Leu Val Asp Val Leu Lys Lys Lys His Ala Ala
180 185 190

Gly Thr Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly
195 200 205

Ser Ile Phe Glu Gly Leu Leu Pro Asn Asp Ile Asn Val Tyr Ala Thr
210 215 220

Thr Ala Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly
225 230 235 240

Glu Phe Pro Ser Pro Pro Pro Glu Tyr Asp Thr Cys Leu Gly Asp Leu

245

250

255

Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Phe His Asn Leu Arg Thr
 260 265 270

Glu Ser Leu Lys Gln Gln Tyr Asn Leu Val Lys Asp Arg Thr Ala Val
 275 280 285

Gln Asp Thr Phe Ser Tyr Gly Ser His Val Met Gln Tyr Gly Ser Leu
 290 295 300

Gly Leu Asn Val Lys His Leu Phe Ser Tyr Ile Gly Thr Asn Pro Ala
 305 310 315 320

Asn Asp Asp Asn Thr Phe Ile Glu Asp Asn Ser Leu Pro Ser Phe Ser
 325 330 335

Lys Ala Val Asn Gln Arg Asp Ala Asp Leu Val Tyr Phe Trp Gln Lys
 340 345 350

Tyr Arg Lys Leu Ala Asp Ser Ser Pro Glu Lys Asn Glu Ala Arg Arg
 355 360 365

Glu Leu Leu Glu Val Met Ala His Arg Ser His Val Asp Ser Ser Val
 370 375 380

Glu Leu Ile Gly Ser Leu Leu Phe Gly Ser Glu Asp Gly Pro Arg Val
 385 390 395 400

Leu Lys Ala Val Arg Ala Ala Gly Glu Pro Leu Val Asp Asp Trp Ser
 405 410 415

Cys Leu Lys Ser Thr Val Arg Thr Phe Glu Ala Gln Cys Gly Ser Leu
 420 425 430

Ala Gln Tyr Gly Met Lys His Met Arg Ser Phe Ala Asn Ile Cys Asn
 435 440 445

Ala Gly Ile Leu Pro Glu Ala Val Ser Lys Val Ala Ala Gln Ala Cys
 450 455 460

Thr Ser Ile Pro Ser Asn Pro Trp Ser Ser Ile His Lys Gly Phe Ser
465 470 475 480

Ala

<210> 75
<211> 501
<212> PRT
<213> Oryza sativa Japonica Group

<400> 75

Met Ala Ala Arg Ala Arg Leu Arg Leu Val Leu Pro Pro Leu Ala Ala
1 5 10 15

Leu Leu Leu Phe Ala His Leu Ala Ala Val Ala Val Ala Arg Pro Arg
20 25 30

Trp Glu Glu Glu Gly Ser Asn Leu Arg Leu Pro Ser Glu Arg Ala Val
35 40 45

Ala Ala Gly Ala Ala Ala Asp Asp Ala Ala Glu Ala Ala Glu Gly Thr
50 55 60

Arg Trp Ala Val Leu Ile Ala Gly Ser Asn Gly Tyr Tyr Asn Tyr Arg
65 70 75 80

His Gln Ala Asp Val Cys His Ala Tyr Gln Ile Met Lys Arg Gly Gly
85 90 95

Leu Lys Asp Glu Asn Ile Ile Val Phe Met Tyr Asp Asp Ile Ala His
100 105 110

Asn Pro Glu Asn Pro Arg Pro Gly Val Ile Ile Asn His Pro Gln Gly
115 120 125

Gly Asp Val Tyr Ala Gly Val Pro Lys Asp Tyr Thr Gly Lys Glu Val
130 135 140

Asn Val Lys Asn Leu Phe Ala Val Leu Leu Gly Asn Lys Thr Ala Val
145 150 155 160

Lys Gly Gly Ser Gly Lys Val Leu Asp Ser Gly Pro Asn Asp His Ile
165 170 175

Phe Ile Phe Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Met Pro
180 185 190

Thr Tyr Pro Tyr Leu Tyr Gly Asp Asp Leu Val Asp Val Leu Lys Lys
195 200 205

Lys His Ala Ala Gly Thr Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala
210 215 220

Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Asn Gly Ile Asn
225 230 235 240

Val Tyr Ala Thr Thr Ala Ser Asn Ala Asp Glu Ser Ser Trp Gly Thr
245 250 255

Tyr Cys Pro Gly Glu Tyr Pro Ser Pro Pro Pro Glu Tyr Asp Thr Cys
260 265 270

Leu Gly Asp Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Val His
275 280 285

Asn Leu Arg Thr Glu Ser Leu Lys Gln Gln Tyr Asn Leu Val Lys Glu
290 295 300

Arg Thr Ser Val Gln His Thr Tyr Tyr Ser Gly Ser His Val Met Glu
305 310 315 320

Tyr Gly Ser Leu Glu Leu Asn Ala His His Val Phe Met Tyr Met Gly
325 330 335

Ser Asn Pro Ala Asn Asp Asn Ala Thr Phe Val Glu Asp Asn Ser Leu
340 345 350

Pro Ser Phe Ser Arg Ala Val Asn Gln Arg Asp Ala Asp Leu Val Tyr
355 360 365

Phe Trp Gln Lys Tyr Arg Lys Leu Pro Glu Ser Ser Pro Glu Lys Asn
370 375 380

Glu Ala Arg Lys Gln Leu Leu Glu Met Met Ala His Arg Ser His Val
385 390 395 400

Asp Asn Ser Val Glu Leu Ile Gly Asn Leu Leu Phe Gly Ser Glu Glu
405 410 415

Gly Pro Arg Val Leu Lys Ala Val Arg Ala Thr Gly Glu Pro Leu Val
420 425 430

Asp Asp Trp Ser Cys Leu Lys Ser Met Val Arg Thr Phe Glu Ala Gln
435 440 445

Cys Gly Ser Leu Ala Gln Tyr Gly Met Lys His Met Arg Ser Phe Ala
450 455 460

Asn Ile Cys Asn Ala Gly Ile Ser Ala Glu Ala Met Ala Lys Val Ala
465 470 475 480

Ala Gln Ala Cys Thr Ser Ile Pro Ser Asn Pro Trp Ser Ser Thr His
485 490 495

Arg Gly Phe Ser Ala
500

<210> 76
<211> 485
<212> PRT
<213> Zea mays

<400> 76

Met Val Ala Asp Arg Leu Arg Leu Ala Leu Leu Leu Ser Ala Cys Leu
1 5 10 15

Cys Ser Ala Trp Ala Arg Pro Arg Leu Glu Pro Thr Ile Arg Leu Pro
20 25 30

Ser Glu Arg Ala Ala Ala Asp Glu Thr Asp Asp Asp Ala Val Gly Thr
35 40 45

Arg Trp Ala Val Leu Ile Ala Gly Ser Asn Gly Tyr Tyr Asn Tyr Arg
50 55 60

His Gln Ala Asp Ile Cys His Ala Tyr Gln Ile Met Lys Lys Gly Gly
65 70 75 80

Leu Lys Asp Glu Asn Ile Val Val Phe Met Tyr Asp Asp Ile Ala His
85 90 95

Ser Pro Glu Asn Pro Arg Pro Gly Val Ile Ile Asn His Pro Gln Gly
100 105 110

Gly Asp Val Tyr Ala Gly Val Pro Lys Asp Tyr Thr Gly Arg Asp Val
115 120 125

Asn Val Asp Asn Phe Phe Ala Val Leu Leu Gly Asn Lys Thr Ala Leu
130 135 140

Arg Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro Asn Asp His Ile
145 150 155 160

Phe Val Phe Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Met Pro
165 170 175

Thr Tyr Pro Tyr Leu Tyr Gly Asp Asp Leu Val Asp Val Leu Lys Lys
180 185 190

Lys His Ala Ala Gly Thr Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala
195 200 205

Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Asn Asp Ile Asn
210 215 220

Val Tyr Ala Thr Thr Ala Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr
225 230 235 240

Tyr Cys Pro Gly Glu Phe Pro Ser Pro Pro Glu Tyr Asp Thr Cys
245 250 255

Leu Gly Asp Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Phe His

260

265

270

Asn Leu Arg Thr Glu Ser Leu Lys Gln Gln Tyr Asn Leu Val Lys Asp
 275 280 285

Arg Thr Ala Val Gln Asp Thr Phe Ser Tyr Gly Ser His Val Met Gln
 290 295 300

Tyr Gly Ser Leu Glu Leu Asn Val Lys His Leu Phe Ser Tyr Ile Gly
 305 310 315 320

Thr Asn Pro Ala Asn Asp Asp Asn Thr Phe Ile Glu Asp Asn Ser Leu
 325 330 335

Pro Ser Leu Ser Lys Ala Val Asn Gln Arg Asp Ala Asp Leu Val Tyr
 340 345 350

Phe Trp Gln Lys Tyr Arg Lys Leu Ala Asp Ser Ser Pro Glu Lys Asn
 355 360 365

Glu Ala Arg Arg Glu Leu Leu Glu Val Met Ala His Arg Ser His Val
 370 375 380

Asp Ser Ser Val Glu Leu Ile Gly Ser Leu Leu Phe Gly Ser Glu Asp
 385 390 395 400

Gly Pro Arg Val Leu Lys Ala Val Arg Ala Ala Gly Glu Pro Leu Val
 405 410 415

Asp Asp Trp Ser Cys Leu Lys Ser Thr Val Arg Thr Phe Glu Ala Gln
 420 425 430

Cys Gly Ser Leu Ala Gln Tyr Gly Met Lys His Met Arg Ser Phe Ala
 435 440 445

Asn Ile Cys Asn Ala Gly Ile Leu Pro Glu Ala Val Ser Lys Val Ala
 450 455 460

Ala Gln Ala Cys Thr Ser Ile Pro Ser Asn Pro Trp Ser Ser Ile His
 465 470 475 480

Lys Gly Phe Ser Ala
485

<210> 77

<211> 488

<212> PRT

<213> Brachypodium distachyon

<400> 77

Met Ala Ser Phe Arg Leu Leu Pro Leu Ala Leu Leu Leu Cys Ala Cys
1 5 10 15

Leu Ser Ala His Ala Arg Thr Ser Leu Leu Glu Gln Thr Ile Arg Leu
20 25 30

Pro Ser Gln Arg Gly Ala Ala Gly Gln Gln Glu Val Asp Asp Asp Ser
35 40 45

Val Gly Thr Arg Trp Ala Val Leu Ile Ala Gly Ser Asn Gly Tyr Tyr
50 55 60

Asn Tyr Arg His Gln Ala Asp Ile Cys His Ala Tyr Gln Ile Met Lys
65 70 75 80

Lys Gly Gly Leu Lys Asp Glu Asn Ile Ile Val Phe Met Tyr Asp Asp
85 90 95

Ile Ala His Asn Pro Glu Asn Pro Arg Pro Gly Val Ile Ile Asn His
100 105 110

Pro Gln Gly Gly Asp Val Tyr Ala Gly Val Pro Lys Asp Tyr Thr Gly
115 120 125

Lys Glu Val Asn Val Lys Asn Phe Phe Ala Val Leu Leu Gly Asn Lys
130 135 140

Ala Ala Val Ser Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro Asn
145 150 155 160

Asp His Ile Phe Val Phe Tyr Ser Asp His Gly Gly Pro Gly Val Leu
165 170 175

Gly Met Pro Thr Tyr Pro Tyr Leu Tyr Gly Asp Asp Leu Val Asp Val
180 185 190

Leu Lys Lys Lys His Ala Ala Gly Thr Tyr Lys Ser Leu Val Phe Tyr
195 200 205

Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Asn
210 215 220

Asp Ile Gly Ile Tyr Ala Thr Thr Ala Ser Asn Ala Glu Glu Ser Ser
225 230 235 240

Trp Gly Thr Tyr Cys Pro Gly Glu Tyr Pro Ser Pro Pro Pro Glu Tyr
245 250 255

Asp Thr Cys Leu Gly Asp Leu Tyr Ser Ile Ala Trp Met Glu Asp Ser
260 265 270

Asp Val His Asn Leu Arg Thr Glu Ser Leu Lys Gln Gln Tyr Asp Leu
275 280 285

Val Lys Lys Arg Thr Ala Pro Glu Asn Ser Tyr Ser Tyr Gly Ser His
290 295 300

Val Met Gln Tyr Gly Ser Leu Asp Leu Asn Ala Glu His Leu Phe Leu
305 310 315 320

Tyr Ile Gly Ser Asn Pro Ala Asn Asp Asn Thr Thr Phe Val Glu Gly
325 330 335

Asn Ser Leu Pro Ser Phe Ser Arg Ala Val Asn Gln Arg Asp Ala Asp
340 345 350

Leu Val Tyr Phe Trp Gln Lys Tyr Arg Lys Leu Ala Glu Ser Ser Pro
355 360 365

Ala Lys Asn Asp Ala Arg Lys Glu Leu Leu Glu Met Met Ala His Arg
370 375 380

Ser His Val Asp Asn Ser Val Glu Leu Thr Gly Asn Leu Leu Phe Gly
385 390 395 400

Ser Glu Asp Gly Pro Met Val Leu Lys Thr Val Arg Thr Ala Gly Glu
405 410 415

Pro Leu Val Asp Asp Trp Gly Cys Leu Lys Ser Thr Val Arg Ala Phe
420 425 430

Glu Ser Gln Cys Gly Ser Leu Ala Gln Tyr Gly Met Lys His Met Arg
435 440 445

Ser Phe Ala Asn Ile Cys Asn Ala Gly Ile Leu Pro Glu Ala Thr Ala
450 455 460

Lys Val Ala Ala Gln Ala Cys Pro Ser Ile Pro Ala Asn Pro Trp Ser
465 470 475 480

Ala Thr His Lys Gly Phe Ser Ala
485

<210> 78
<211> 484
<212> PRT
<213> Hordeum vulgare subsp. vulgare

<400> 78

Met Ala Met Ala Ser Phe Arg Leu Leu Pro Leu Ala Leu Leu Leu Ser
1 5 10 15

Val Ala His Ala Arg Thr Pro Arg Leu Glu Pro Thr Ile Arg Leu Pro
20 25 30

Ser Gln Arg Ala Ala Gly Gln Glu Asp Asp Asp Ser Val Gly Thr Arg
35 40 45

Trp Ala Val Leu Ile Ala Gly Ser Asn Gly Tyr Tyr Asn Tyr Arg His
50 55 60

Gln Ala Asp Ile Cys His Ala Tyr Gln Ile Met Lys Lys Gly Gly Leu
65 70 75 80

Lys Asp Glu Asn Ile Ile Val Phe Met Tyr Asp Asp Ile Ala Arg Asn
85 90 95

Pro Glu Asn Pro Arg Pro Gly Val Ile Ile Asn His Pro Gln Gly Gly
100 105 110

Asp Val Tyr Ala Gly Val Pro Lys Asp Tyr Thr Gly Lys Glu Val Asn
115 120 125

Val Lys Asn Phe Phe Ala Val Leu Leu Gly Asn Lys Thr Ala Val Asn
130 135 140

Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro Asn Asp His Ile Phe
145 150 155 160

Val Phe Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Met Pro Thr
165 170 175

Tyr Pro Tyr Leu Tyr Gly Asp Asp Leu Val Asp Val Leu Lys Lys Lys
180 185 190

His Ala Ala Gly Thr Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys
195 200 205

Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Asn Asp Ile Gly Val
210 215 220

Tyr Ala Thr Thr Ala Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr
225 230 235 240

Cys Pro Gly Glu Tyr Pro Ser Pro Pro Pro Glu Tyr Asp Thr Cys Leu
245 250 255

Gly Asp Leu Tyr Ser Ile Ser Trp Met Glu Asp Ser Asp Val His Asn
260 265 270

Leu Arg Thr Glu Ser Leu Lys Gln Gln Tyr Asn Leu Val Lys Lys Arg
275 280 285

Thr Ala Ala Gln Asp Ser Tyr Ser Tyr Gly Ser His Val Met Gln Tyr

290

295

300

Gly Ser Leu Asp Leu Asn Ala Glu His Leu Phe Ser Tyr Ile Gly Ser
 305 310 315 320

Asn Pro Ala Asn Glu Asn Thr Thr Phe Val Glu Asp Asn Ala Leu Pro
 325 330 335

Ser Leu Ser Arg Ala Val Asn Gln Arg Asp Ala Asp Leu Val Tyr Phe
 340 345 350

Trp Gln Lys Tyr Arg Lys Leu Ala Glu Ser Ser Pro Ala Lys Asn Asn
 355 360 365

Ala Arg Lys Gln Leu Leu Glu Met Met Gly His Arg Ser His Ile Asp
 370 375 380

Ser Ser Val Glu Leu Ile Gly Asn Leu Leu Phe Gly Ser Ala Gly Gly
 385 390 395 400

Pro Met Val Leu Lys Thr Val Arg Pro Ala Gly Glu Pro Leu Val Asp
 405 410 415

Asp Trp Ser Cys Leu Lys Ser Thr Val Arg Thr Phe Glu Ser Gln Cys
 420 425 430

Gly Ser Leu Ala Gln Tyr Gly Met Lys His Met Arg Ser Phe Ala Asn
 435 440 445

Met Cys Asn Ala Gly Ile Val Pro Glu Ala Met Ala Lys Val Ala Ala
 450 455 460

Gln Ala Cys Thr Ser Phe Pro Thr Asn Pro Trp Ser Ala Thr His Lys
 465 470 475 480

Gly Phe Ser Ala

<210> 79

<211> 493

<212> PRT

<213> Aegilops tauschii

<400> 79

Met Ala Met Ala Ser Phe Arg Pro Leu Pro Leu Ala Leu Leu Leu Ala
1 5 10 15

Ala Cys Leu Ser Ala Phe Val Leu Ala Val Ala His Ala Arg Thr Pro
20 25 30

Arg Leu Glu Pro Thr Ile Arg Leu Pro Ser Gln Arg Ala Ala Gly Gln
35 40 45

Glu Asp Asp Asp Ser Val Gly Thr Arg Trp Ala Val Leu Ile Ala Gly
50 55 60

Ser Asn Gly Tyr Tyr Asn Tyr Arg His Gln Ala Asp Ile Cys His Ala
65 70 75 80

Tyr Gln Ile Met Lys Lys Gly Gly Leu Lys Asp Glu Asn Ile Ile Val
85 90 95

Phe Met Tyr Asp Asp Ile Ala His Asn Pro Glu Asn Pro Arg Pro Gly
100 105 110

Val Ile Ile Asn His Pro Gln Gly Gly Asp Val Tyr Ala Gly Val Pro
115 120 125

Lys Asp Tyr Thr Gly Lys Glu Val Asn Val Lys Asn Phe Phe Ala Val
130 135 140

Leu Leu Gly Asn Lys Thr Ala Val Ser Gly Gly Ser Gly Lys Val Val
145 150 155 160

Asp Ser Gly Pro Asn Asp His Ile Phe Val Phe Tyr Ser Asp His Gly
165 170 175

Gly Pro Gly Val Leu Gly Met Pro Thr Tyr Pro Tyr Leu Tyr Gly Asp
180 185 190

Asp Leu Val Asp Val Leu Lys Lys Lys His Ala Ala Gly Thr Tyr Lys
195 200 205

Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu
210 215 220

Gly Leu Leu Pro Asn Asp Ile Gly Val Tyr Ala Thr Thr Ala Ser Asn
225 230 235 240

Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Tyr Pro Ser
245 250 255

Pro Pro Pro Glu Tyr Asp Thr Cys Leu Gly Asp Leu Tyr Ser Ile Ser
260 265 270

Trp Met Glu Asp Ser Asp Val His Asn Leu Arg Thr Glu Ser Leu Lys
275 280 285

Gln Gln Tyr Asn Leu Val Lys Lys Arg Thr Ala Ala Gln Asp Ser Tyr
290 295 300

Ser Tyr Gly Ser His Val Met Gln Tyr Gly Ser Leu Asp Leu Asn Ala
305 310 315 320

Glu His Leu Phe Ser Tyr Ile Gly Ser Asn Pro Ala Asn Glu Asn Thr
325 330 335

Thr Phe Val Glu Asp Asn Ala Leu Pro Ser Phe Ser Arg Ala Val Asn
340 345 350

Gln Arg Asp Ala Asp Leu Val Tyr Phe Trp Gln Lys Tyr Arg Lys Leu
355 360 365

Ala Glu Ser Ser Pro Glu Lys Asn Asp Ala Arg Lys Gln Leu Leu Glu
370 375 380

Met Met Gly His Arg Ser His Ile Asp Asn Ser Val Glu Pro Ile Gly
385 390 395 400

Asn Leu Leu Phe Gly Ser Ala Gly Gly Pro Met Val Leu Lys Ala Val
405 410 415

Arg Pro Ala Gly Glu Pro Leu Val Asp Asp Trp Ser Cys Leu Lys Ser
420 425 430

Thr Val Arg Thr Phe Glu Ser Gln Cys Gly Ser Leu Ala Gln Tyr Gly
435 440 445

Met Lys His Met Arg Ser Phe Ala Asn Ile Cys Asn Ala Gly Ile Val
450 455 460

Pro Glu Ala Met Ala Lys Val Ala Ala Gln Ala Arg Thr Ser Ile Pro
465 470 475 480

Thr Asn Pro Trp Ser Ala Thr His Lys Gly Phe Ser Ala
485 490

<210> 80
<211> 493
<212> PRT
<213> Triticum monococcum

<400> 80

Met Ala Met Ala Ser Phe Arg Pro Leu Pro Leu Ala Leu Leu Leu Ala
1 5 10 15

Ala Cys Leu Ser Ala Leu Val Leu Ala Val Ala His Ala Arg Ser Pro
20 25 30

Arg Leu Glu Pro Thr Ile Arg Leu Pro Ser Gln Arg Ala Ala Gly Gln
35 40 45

Glu Asp Asp Asp Ser Val Gly Thr Arg Trp Ala Val Leu Ile Ala Gly
50 55 60

Ser Asn Gly Tyr Tyr Asn Tyr Arg His Gln Ala Asp Ile Cys His Ala
65 70 75 80

Tyr Gln Ile Met Lys Lys Gly Gly Leu Lys Asp Glu Asn Ile Ile Val
85 90 95

Phe Met Tyr Asp Asp Ile Ala His Asn Leu Glu Asn Pro Gly Pro Gly
100 105 110

Val Ile Ile Asn His Pro Gln Gly Gly Asp Val Tyr Ala Gly Val Pro
115 120 125

Lys Asp Tyr Thr Gly Lys Glu Val Asn Val Lys Asn Leu Phe Ala Val
130 135 140

Leu Leu Gly Asn Lys Thr Ala Val Ser Gly Gly Ser Gly Lys Val Val
145 150 155 160

Asp Ser Gly Pro Asn Asp His Ile Phe Val Phe Tyr Ser Asp His Gly
165 170 175

Gly Pro Gly Val Leu Gly Met Pro Thr Tyr Pro Tyr Leu Tyr Gly Asp
180 185 190

Asp Leu Val Asp Val Leu Lys Lys Lys His Ala Ala Gly Thr Tyr Lys
195 200 205

Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu
210 215 220

Gly Leu Leu Pro Asn Asp Ile Gly Val Tyr Ala Thr Thr Ala Ser Asn
225 230 235 240

Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Tyr Pro Ser
245 250 255

Pro Pro Pro Glu Tyr Asp Thr Cys Leu Gly Asp Leu Tyr Ser Ile Ser
260 265 270

Trp Met Glu Asp Ser Asp Val His Asn Leu Arg Thr Glu Ser Leu Lys
275 280 285

Gln Gln Tyr Asn Leu Val Lys Lys Arg Thr Ala Ala Gln Asp Ser Tyr
290 295 300

Ser Tyr Gly Ser His Val Met Gln Tyr Gly Ser Leu Asp Leu Asn Ala
305 310 315 320

Glu His Leu Phe Ser Tyr Ile Gly Ser Asn Pro Ala Asn Glu Asn Thr

325

330

335

Thr Phe Val Glu Asp Asn Ala Leu Pro Ser Phe Ser Arg Ala Val Asn
 340 345 350

Gln Arg Asp Ala Asp Leu Val Tyr Phe Trp Gln Lys Tyr Arg Lys Leu
 355 360 365

Ala Glu Ser Ser Pro Glu Lys Asn Asp Ala Arg Lys Gln Leu Leu Glu
 370 375 380

Met Met Gly His Arg Ser His Ile Asp Asn Ser Val Glu Leu Ile Gly
 385 390 395 400

Asn Leu Leu Phe Gly Ser Ala Gly Gly Pro Met Val Leu Lys Ala Val
 405 410 415

Arg Pro Ala Gly Glu Pro Leu Val Asp Asp Trp Ser Cys Leu Lys Ser
 420 425 430

Thr Val Arg Thr Phe Glu Ser Gln Cys Gly Ser Leu Ala Gln Tyr Gly
 435 440 445

Met Lys His Met Arg Ser Phe Ala Asn Ile Cys Asn Ala Gly Ile Val
 450 455 460

Pro Glu Ala Thr Ala Lys Val Ala Ala Gln Ala Cys Thr Ser Ile Pro
 465 470 475 480

Thr Asn Pro Trp Ser Ala Thr His Lys Gly Phe Ser Ala
 485 490

<210> 81

<211> 493

<212> PRT

<213> Aegilops speltoides

<400> 81

Met Ala Met Ala Ser Phe Arg Pro Leu Pro Leu Ala Leu Leu Leu Ala
 1 5 10 15

Ala Cys Leu Ser Glu Leu Val Leu Ala Val Ala His Ala Arg Thr Pro
20 25 30

Arg Leu Glu Pro Thr Ile Arg Leu Pro Ser Gln Arg Ala Ala Gly Gln
35 40 45

Glu Asp Asp Asp Ser Val Gly Thr Arg Trp Ala Val Leu Ile Ala Gly
50 55 60

Ser Asn Gly Tyr Tyr Asn Tyr Arg His Gln Ala Asp Ile Cys His Ala
65 70 75 80

Tyr Gln Ile Met Lys Lys Gly Gly Leu Lys Asp Glu Asn Ile Ile Ile
85 90 95

Phe Met Tyr Asp Asp Ile Ala His Asn Pro Glu Asn Pro Arg Pro Gly
100 105 110

Val Ile Ile Asn His Pro Gln Gly Gly Asp Val Tyr Ala Gly Val Pro
115 120 125

Lys Asp Tyr Thr Gly Lys Glu Val Asn Val Lys Asn Phe Phe Ala Val
130 135 140

Leu Leu Gly Asn Arg Thr Ala Val Ser Gly Gly Ser Gly Lys Val Val
145 150 155 160

Asp Ser Gly Pro Asn Asp His Ile Phe Val Phe Tyr Ser Asp His Gly
165 170 175

Gly Pro Gly Val Leu Gly Met Pro Thr Tyr Pro Tyr Leu Tyr Gly Asp
180 185 190

Asp Leu Val Asp Val Leu Lys Lys Lys His Ala Ala Gly Thr Tyr Lys
195 200 205

Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu
210 215 220

Gly Leu Leu Pro Asn Asp Ile Gly Val Tyr Ala Thr Thr Ala Ser Asn
225 230 235 240

Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Tyr Pro Ser
245 250 255

Pro Pro Pro Glu Tyr Asp Thr Cys Leu Gly Asp Leu Tyr Ser Ile Ser
260 265 270

Trp Met Glu Asp Ser Asp Val His Asn Leu Arg Thr Glu Ser Leu Lys
275 280 285

Gln Gln Tyr Asn Leu Val Lys Lys Arg Thr Ala Ala Gln Asp Ser Tyr
290 295 300

Ser Tyr Gly Ser His Val Met Gln Tyr Gly Ser Leu Asp Leu Asn Ala
305 310 315 320

Glu His Leu Phe Ser Tyr Ile Gly Ser Asn Pro Ala Asn Glu Asn Thr
325 330 335

Thr Phe Val Glu Asp Asn Ala Leu Pro Ser Phe Ser Gly Ala Val Asn
340 345 350

Gln Arg Asp Ala Asp Leu Val Tyr Phe Trp Gln Lys Tyr Arg Lys Leu
355 360 365

Ala Glu Ser Ser Pro Glu Lys Asn Asp Ala Arg Lys Gln Leu Leu Glu
370 375 380

Met Met Gly His Arg Ser His Ile Asp Asn Ser Val Glu Leu Ile Gly
385 390 395 400

Asn Leu Leu Phe Gly Ser Ala Gly Gly Pro Met Val Leu Lys Ala Val
405 410 415

Arg Pro Ala Gly Glu Pro Leu Val Asp Asp Trp Ser Cys Leu Lys Ser
420 425 430

Thr Val Arg Thr Phe Glu Ser Gln Cys Gly Ser Leu Ala Gln Tyr Gly
435 440 445

Met Lys His Met Arg Ser Phe Ala Asn Ile Cys Asn Val Gly Ile Val
450 455 460

Pro Glu Ala Met Ala Lys Val Ala Ala Gln Ala Cys Thr Asn Ile Pro
465 470 475 480

Thr Asn Pro Trp Ser Ala Thr His Lys Gly Phe Ser Ala
485 490

<210> 82
<211> 469
<212> PRT
<213> Amborella trichopoda

<400> 82

Met Ala Phe Ser Gly Lys Ser Val Leu Phe Leu Ala Val Phe Met Ala
1 5 10 15

Phe Ser Gly Val Tyr Gly Arg Tyr Ser Thr Trp Ser Asp Phe Leu Arg
20 25 30

Met Pro Gln Thr Glu Asp Ser Val Gly Thr Arg Trp Ala Val Leu Val
35 40 45

Ala Gly Ser Ser Gly Tyr Gly Asn Tyr Arg His Gln Ala Asp Ile Cys
50 55 60

His Ala Tyr Gln Thr Met Ile Arg Gly Gly Leu Lys Glu Lys Asn Ile
65 70 75 80

Val Val Phe Met Tyr Asp Asp Ile Ala Tyr Asn Glu Glu Asn Pro Arg
85 90 95

Pro Gly Val Ile Ile Asn Arg Pro His Gly Glu Asp Val Tyr Ala Gly
100 105 110

Val Pro Lys Asp Tyr Val Gly Asp Asp Val Asn Val Asp Asn Leu Phe
115 120 125

Ala Val Ile Leu Gly Asn Lys Ser Ala Leu Thr Gly Gly Ser Gly Lys
130 135 140

Val Val Asp Ser Gly Pro Asp Asp His Ile Phe Ile Phe Tyr Ser Asp
145 150 155 160

His Gly Gly Ala Gly Val Leu Gly Met Pro Thr Tyr Pro Tyr Leu Tyr
165 170 175

Ala Asp Asp Leu Val Asn Val Leu Lys Lys Lys His Val Ser Gly Thr
180 185 190

Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile
195 200 205

Phe Glu Gly Leu Leu Pro Glu Gly Leu Asn Ile Tyr Ala Thr Thr Ala
210 215 220

Ser Asn Ala Val Glu Ser Ser Trp Gly Thr Tyr Cys Pro Asp Asp Ser
225 230 235 240

Pro Asp Phe Pro Gln Glu Tyr Asp Thr Cys Leu Gly Asp Leu Tyr Ser
245 250 255

Val Ser Trp Met Glu Asp Ser Asp Ile His Asn Leu Gln Phe Glu Thr
260 265 270

Leu Lys Gln Gln Tyr Glu Leu Val Lys Met Arg Thr Ser Asn Phe Glu
275 280 285

Thr Tyr Met Phe Gly Ser His Val Met Gln Tyr Gly Asp Ser Gly Leu
290 295 300

Gly Lys Glu Gln Leu Val Leu Tyr Met Gly Ser Asn Pro Ala Asn Asp
305 310 315 320

Asn Ser Thr Phe Ile Ser Arg Asn Glu Leu Pro Ser Phe Ser Lys Ala
325 330 335

Val Asn Gln Arg Asp Ala Asp Leu Val Tyr Phe Trp Asn Lys Tyr Arg
340 345 350

Lys Ser Pro Val Gly Ser Ile Lys Lys Arg Asn Ala Gln Lys Glu Leu

355

360

365

Phe Asp Val Met Ala His Arg Leu His Leu Asp Asn Ser Ile Glu Leu
 370 375 380

Ile Gly Lys Leu Leu Phe Gly Ser Glu Lys Gly Pro Glu Ile Leu Lys
 385 390 395 400

Thr Val Arg Thr Thr Gly Leu Pro Leu Val Asp Asp Trp Asp Cys Leu
 405 410 415

Lys Ala Met Val Arg Thr Phe Glu Thr Lys Cys Gly Ser Ile Ser Gln
 420 425 430

Tyr Gly Met Lys His Met Arg Ser Met Ala Asn Ile Cys Asn Ala Gly
 435 440 445

Ile Ser Lys Glu Val Met Ala Glu Ala Ser Ala Glu Ala Cys Thr Arg
 450 455 460

Ile Pro Thr Thr Ser
 465

<210> 83
 <211> 489
 <212> PRT
 <213> Hordeum vulgare subsp. vulgare

<400> 83

Met Ala Met Ala Ser Phe His Leu Leu Pro Leu Ser Leu Leu Leu Leu
 1 5 10 15

Leu Leu Val Val Ala Asn Ala Gly Thr Pro Pro Leu Glu Pro Gly Leu
 20 25 30

Arg Leu Pro Ser Gln Arg Ala Ala Ala Gly Arg Gln Glu Asn Asp Gly
 35 40 45

Ser Val Gly Thr Lys Trp Ala Val Leu Val Ala Gly Ser Asn Gly Tyr
 50 55 60

Gln Asn Tyr Arg His Gln Ala Asp Val Cys His Ala Tyr Gln Ile Ile
65 70 75 80

Lys Lys Gly Gly Leu Lys Asp Glu Asn Ile Ile Val Phe Met Tyr Asp
85 90 95

Asp Ile Ala His Asn Pro Glu Asn Pro Arg Pro Gly Val Ile Ile Asn
100 105 110

His Pro Gln Gly Gly Asp Val Tyr Ala Gly Val Pro Lys Asp Tyr Thr
115 120 125

Gly Lys Glu Val Asn Ala Lys Asn Leu Phe Ala Val Leu Leu Gly Asn
130 135 140

Lys Thr Ala Val Ser Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro
145 150 155 160

Asn Asp His Ile Phe Val Phe Tyr Ser Asp His Gly Gly Pro Gly Val
165 170 175

Ile Gly Met Pro Thr Tyr Pro Tyr Ile Tyr Gly Asp Asp Leu Val Asp
180 185 190

Val Leu Lys Lys Lys His Ala Ala Gly Thr Tyr Lys Ser Leu Val Phe
195 200 205

Tyr Leu Glu Ala Cys Glu Ala Gly Ser Val Phe Glu Gly Leu Leu Pro
210 215 220

Asn Asp Ile Gly Val Tyr Ala Thr Thr Ala Ser Asn Ala Glu Glu Ser
225 230 235 240

Ser Trp Gly Ala Tyr Cys Pro Gly Glu Tyr Pro Ser Pro Pro Pro Glu
245 250 255

Tyr Asp Thr Cys Leu Gly Asp Leu Tyr Ser Ile Ser Trp Met Glu Asp
260 265 270

Ser Asp Val His Asn Leu Arg Thr Glu Ser Leu Lys Glu Gln Tyr Asn
275 280 285

Leu Val Lys Lys Arg Thr Ala Ala Gln Asp Ser Tyr Ser Tyr Gly Ser
290 295 300

His Val Met Gln Tyr Gly Ser Leu Asp Leu Asn Ala Gln His Leu Phe
305 310 315 320

Leu Tyr Ile Gly Ser Asn Pro Ala Asn Asp Asn Ala Thr Phe Val Glu
325 330 335

Glu Asn Ser Leu Pro Ser Phe Ser Arg Ala Val Asn Gln Arg Asp Ala
340 345 350

Asp Leu Val Tyr Phe Trp His Lys Tyr Arg Lys Leu Ala Glu Ser Ser
355 360 365

Pro Glu Lys Asn Asn Ala Arg Lys Gln Leu Leu Glu Met Met Gly His
370 375 380

Arg Ser His Val Asp Asn Ser Val Glu Leu Ile Gly Asn Leu Leu Phe
385 390 395 400

Gly Ser Ala Asp Gly Pro Met Val Leu Lys Ser Val Arg Pro Ala Gly
405 410 415

Glu Pro Leu Val Asp Asp Trp Asn Cys Leu Lys Ser Thr Val His Thr
420 425 430

Phe Glu Ser Gln Cys Gly Ser Leu Ala Gln Tyr Gly Met Lys His Met
435 440 445

Arg Ser Phe Ala Asn Ile Cys Asn Ala Gly Ile Leu Pro Glu Thr Met
450 455 460

Val Lys Val Ala Ala Gln Ala Cys Thr Ser Ile Pro Thr Asn Pro Trp
465 470 475 480

Ser Gly Thr His Lys Gly Phe Ser Ala
485

<210> 84
<211> 485
<212> PRT
<213> Zea mays

<400> 84

Met Val Ala Asp Arg Leu Arg Leu Ala Leu Leu Leu Ser Ala Cys Leu
1 5 10 15

Cys Ser Ala Trp Ala Arg Pro Arg Leu Glu Pro Thr Ile Arg Leu Pro
20 25 30

Ser Glu Arg Ala Ala Ala Asp Glu Thr Asp Asp Asp Ala Val Gly Thr
35 40 45

Arg Trp Ala Val Leu Ile Ala Gly Ser Asn Gly Tyr Tyr Asn Tyr Arg
50 55 60

His Gln Ala Asp Ile Cys His Ala Tyr Gln Ile Met Lys Lys Gly Gly
65 70 75 80

Leu Lys Asp Glu Asn Ile Val Val Phe Met Tyr Asp Asp Ile Ala His
85 90 95

Ser Pro Glu Asn Pro Arg Pro Gly Val Ile Ile Asn His Pro Gln Gly
100 105 110

Gly Asp Val Tyr Ala Gly Val Pro Lys Asp Tyr Thr Gly Arg Glu Val
115 120 125

Asn Val Asp Asn Phe Phe Ala Val Leu Leu Gly Asn Lys Thr Ala Leu
130 135 140

Arg Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro Asn Asp His Ile
145 150 155 160

Phe Val Phe Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Met Pro
165 170 175

Thr Tyr Pro Tyr Leu Tyr Gly Asp Asp Leu Val Asp Val Leu Lys Lys
180 185 190

Lys His Ala Ala Gly Thr Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala
195 200 205

Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Asn Asp Ile Asn
210 215 220

Val Tyr Ala Thr Thr Ala Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr
225 230 235 240

Tyr Cys Pro Gly Glu Phe Pro Ser Pro Pro Pro Glu Tyr Asp Thr Cys
245 250 255

Leu Gly Asp Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Phe His
260 265 270

Asn Leu Arg Thr Glu Ser Leu Lys Gln Gln Tyr Asn Leu Val Lys Asp
275 280 285

Arg Thr Ala Val Gln Asp Thr Phe Ser Tyr Gly Ser His Val Met Gln
290 295 300

Tyr Gly Ser Leu Glu Leu Asn Val Lys His Leu Phe Ser Tyr Ile Gly
305 310 315 320

Thr Asn Pro Ala Asn Asp Asp Asn Thr Ser Ile Glu Asp Asn Ser Leu
325 330 335

Pro Ser Phe Ser Lys Ala Val Asn Gln Arg Asp Ala Asp Leu Val Tyr
340 345 350

Phe Trp Gln Lys Tyr Arg Lys Leu Ala Asp Ser Ser His Glu Lys Asn
355 360 365

Glu Ala Arg Arg Glu Leu Leu Glu Val Met Ala His Arg Ser His Val
370 375 380

Asp Ser Ser Val Glu Leu Ile Gly Ser Leu Leu Phe Gly Ser Glu Asp
385 390 395 400

Gly Pro Arg Val Leu Lys Ala Val Arg Ala Ala Gly Glu Pro Leu Val

405

410

415

Asp Asp Trp Ser Cys Leu Lys Ser Thr Val Arg Thr Phe Glu Ala Gln
 420 425 430

Cys Gly Ser Leu Ala His Tyr Gly Met Lys His Met Arg Ser Phe Pro
 435 440 445

Asn Ile Cys Asn Ala Gly Ile Leu Pro Glu Ala Val Ser Lys Val Ala
 450 455 460

Ala Gln Ala Cys Thr Ser Ile Pro Ser Asn Pro Trp Ser Ser Ile His
 465 470 475 480

Lys Gly Phe Ser Ala
 485

<210> 85

<211> 487

<212> PRT

<213> *Setaria italica*

<400> 85

Met Met Ala Ala Ala Arg Leu Arg Leu Ala Leu Leu Leu Tyr Val Phe
 1 5 10 15

Met Cys Ala Ala Trp Ala Arg Pro Gly Leu Glu Pro Ala Ile Arg Leu
 20 25 30

Pro Ser Glu Arg Ala Ala Ala Ala Gly Glu Gly Thr Asp Asp Ala Val
 35 40 45

Gly Thr Arg Trp Ala Val Leu Ile Ala Gly Ser Asn Gly Tyr Tyr Asn
 50 55 60

Tyr Arg His Gln Ala Asp Ile Cys His Ala Tyr Gln Ile Leu Lys Lys
 65 70 75 80

Gly Gly Leu Lys Asp Glu Asn Ile Ile Val Phe Met Tyr Asp Asp Ile
 85 90 95

Ala His Ser Pro Glu Asn Pro Arg Pro Gly Val Ile Ile Asn His Pro
100 105 110

Gln Gly Gly Asp Val Tyr Ala Gly Val Pro Lys Asp Tyr Thr Gly Arg
115 120 125

Glu Val Asn Val Asn Asn Phe Phe Ala Val Leu Leu Gly Asn Lys Thr
130 135 140

Ala Val Ser Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro Asn Asp
145 150 155 160

His Ile Phe Val Phe Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly
165 170 175

Met Pro Thr Tyr Pro Tyr Leu Tyr Gly Asp Asp Leu Val Asn Val Leu
180 185 190

Lys Lys Lys His Ala Ala Gly Thr Tyr Lys Ser Leu Val Phe Tyr Leu
195 200 205

Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Asn Asp
210 215 220

Ile Asn Val Tyr Ala Thr Thr Ala Ser Asn Ala Asp Glu Ser Ser Trp
225 230 235 240

Gly Thr Tyr Cys Pro Gly Glu Ser Pro Ser Pro Pro Pro Glu Tyr Asp
245 250 255

Thr Cys Leu Gly Asp Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Asp
260 265 270

Phe His Asn Leu Arg Thr Glu Ser Leu Lys Gln Gln Tyr Asn Leu Val
275 280 285

Lys Asp Arg Thr Ser Val His Asn Thr Phe Thr Tyr Gly Ser His Val
290 295 300

Met Gln Tyr Gly Ser Leu Asn Leu Asn Val Gln His Leu Phe Ser Tyr
305 310 315 320

Ile Gly Thr Asn Pro Ala Asn Asp Asp Asn Lys Phe Val Glu Gly Asn
325 330 335

Ser Leu Pro Ser Phe Thr Arg Ala Val Asn Gln Arg Asp Ala Asp Leu
340 345 350

Val Tyr Phe Trp Gln Lys Tyr Arg Lys Val Ala Glu Gly Ser Pro Gly
355 360 365

Lys Asn Asp Ala Arg Lys Glu Leu Leu Glu Val Met Ala His Arg Ser
370 375 380

His Val Asp Asn Ser Val Glu Leu Ile Gly Ser Leu Leu Phe Gly Ser
385 390 395 400

Glu Asp Gly Pro Arg Val Leu Lys Ala Val Arg Ala Ala Gly Glu Pro
405 410 415

Leu Val Asp Asp Trp Ser Cys Leu Lys Ser Met Val Arg Ala Phe Glu
420 425 430

Ala Gln Cys Gly Ser Leu Ser Gln Tyr Gly Met Lys His Met Arg Ser
435 440 445

Phe Ala Asn Ile Cys Asn Ala Gly Ile Leu Pro Asp Ala Val Ser Lys
450 455 460

Val Ala Ala Gln Ala Cys Thr Ser Ile Pro Ser Asn Pro Trp Ser Ser
465 470 475 480

Ile His Met Gly Phe Ser Ala
485

<210> 86

<211> 460

<212> PRT

<213> Medicago truncatula

<400> 86

Met Asp Phe Ser Gln Phe Ser Thr Ile Leu Phe Leu Thr Val Ile Leu

1	5	10	15
Thr	Ile Phe	Ala Ala Val Ser Gly	Ser Arg Asp Leu Pro Gly Asp Tyr
	20	25	30
Ile	Arg Leu Pro Ser Gln Ser	Gln Ala Ser Arg Phe Phe His Glu Pro	
	35	40	45
Glu	Asn Asp Asp Asn Asp	Gln Gly Thr Arg Trp Ala Ile Leu Leu Ala	
	50	55	60
Gly	Ser Asn Gly Tyr Trp Asn Tyr Arg His	Gln Ala Asp Val Cys His	
65	70	75	80
Ala	Tyr Gln Leu Leu Arg Lys Gly Gly	Leu Lys Glu Glu Asn Ile Ile	
	85	90	95
Val	Phe Met Tyr Asp Asp Ile Ala Ser	Asn Val Glu Asn Pro Arg Pro	
	100	105	110
Gly	Val Ile Ile Asn Lys Pro Asp Gly Gly	Asp Val Tyr Glu Gly Val	
	115	120	125
Pro	Lys Asp Tyr Thr Gly Ala Glu Val His	Ala Asp Asn Phe Tyr Ala	
	130	135	140
Ala	Leu Leu Gly Asn Lys Ser Ala Leu Thr	Gly Gly Ser Gly Lys Val	
145	150	155	160
Val	Asp Ser Gly Pro Asn Asp His Ile Phe	Val Tyr Tyr Thr Asp His	
	165	170	175
Gly	Gly Pro Gly Val Leu Gly Met Pro Val	Gly Pro Tyr Leu Tyr Ala	
	180	185	190
Ser	Asp Leu Asn Glu Val Leu Lys Lys Lys	His Ala Ser Gly Ser Tyr	
	195	200	205
Lys	Ser Leu Val Phe Tyr Leu Glu Lys Ile	Ser Ile Ser Met Arg Gln	
	210	215	220

Thr Ala Ser Asn Ala Val Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly
225 230 235 240

Glu Tyr Pro Pro Pro Pro Pro Glu Tyr Ser Thr Cys Leu Gly Asp Leu
245 250 255

Tyr Ser Ile Ala Trp Met Glu Asp Ser Asp Ile His Asn Leu Arg Thr
260 265 270

Glu Ser Leu His Gln Gln Tyr Lys Leu Val Lys Asp Arg Thr Ile Asn
275 280 285

Gly Tyr Tyr Gly Ser His Val Met Glu Tyr Gly Asp Val Gly Leu Ser
290 295 300

Asn Asn His Leu Phe Leu Tyr Leu Gly Thr Asn Pro Ala Asn Asp Asn
305 310 315 320

Ile Ser Phe Val Asp Glu Ser Ser Leu Lys Leu Arg Ser Pro Ser Thr
325 330 335

Ala Val Asn Gln Arg Asp Ala Asp Leu Ile His Phe Trp Asp Lys Phe
340 345 350

Arg Lys Ala Pro Glu Gly Ser Leu Arg Lys Asn Glu Ala Gln Lys Glu
355 360 365

Val Leu Glu Ala Met Ser His Arg Met His Val Asp Asn Ser Val Lys
370 375 380

Leu Ile Gly Lys Leu Leu Phe Gly Ile Glu Lys Gly Thr Glu Leu Leu
385 390 395 400

Asp Asn Val Arg Pro Ala Gly Ser Pro Leu Val Asp Asn Trp Asp Cys
405 410 415

Leu Lys Thr Met Val Lys Thr Phe Glu Thr His Cys Gly Ser Leu Ser
420 425 430

Gln Tyr Gly Met Lys His Met Arg Ser Phe Ala Asn Ile Cys Asn Ala

435

440

445

Gly Ile Gln Thr Glu Gln Met Ala Glu Ala Ser Ala
 450 455 460

<210> 87

<211> 478

<212> PRT

<213> Populus trichocarpa

<400> 87

Met Thr Gly Leu Ala Thr Gly Ala Ile Phe Leu Leu Ile Ser Leu Cys
 1 5 10 15

Gly Ile Ala Ala Ala Gly Arg Asp Thr Val Gly Asp Val Leu Arg Leu
 20 25 30

Pro Ser Glu Ala Ser Arg Phe Phe His Asn Asp Asp Asn Ser Asp Asp
 35 40 45

Asp Ser Thr Gly Thr Arg Trp Ala Ile Leu Leu Ala Gly Ser Asn Gly
 50 55 60

Tyr Trp Asn Tyr Arg His Gln Ala Asp Val Cys His Ala Tyr Gln Leu
 65 70 75 80

Leu Arg Lys Gly Gly Leu Lys Glu Glu Asn Ile Ile Val Phe Met Tyr
 85 90 95

Asp Asp Ile Ala Tyr Asn Ser Glu Asn Pro Arg Arg Gly Val Ile Ile
 100 105 110

Asn Ser Pro Gln Gly Glu Asp Val Tyr Lys Gly Val Pro Lys Asp Tyr
 115 120 125

Thr Gly Glu Asp Val Thr Val Gly Asn Phe Phe Ala Ala Ile Leu Gly
 130 135 140

Asn Lys Thr Ala Leu Thr Gly Gly Ser Gly Lys Val Val Asp Ser Gly
 145 150 155 160

Pro Asn Asp His Ile Phe Ile Tyr Tyr Thr Asp His Gly Gly Pro Gly
165 170 175

Val Leu Gly Met Pro Thr Asn Pro Tyr Leu Tyr Ala Asp Asp Leu Ile
180 185 190

Asp Val Leu Lys Lys Lys His Ala Ser Gly Thr Tyr Lys Ser Leu Val
195 200 205

Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu
210 215 220

Pro Gln Gly Leu Asn Ile Tyr Ala Thr Thr Ala Ser Asn Ala Glu Glu
225 230 235 240

Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Asn Pro Ser Pro Pro Pro
245 250 255

Glu Tyr Glu Thr Cys Leu Gly Asp Leu Tyr Ser Val Ala Trp Met Glu
260 265 270

Asp Ser Asp Ile His Asn Leu Gln Thr Glu Thr Leu His Gln Gln Tyr
275 280 285

Glu Leu Val Lys Arg Arg Thr Ser Asn Asp Asn Ser Pro Tyr Gly Ser
290 295 300

His Val Met Gln Tyr Gly Asp Val Gly Leu Ser Lys Asp Asn Ile Phe
305 310 315 320

Leu Tyr Met Gly Thr Asn Pro Ala Asn Asp Asn Phe Thr Phe Met Asp
325 330 335

Glu Asn Leu Leu Arg Pro Arg Ser Lys Ala Val Asn Gln Arg Asp Ala
340 345 350

Asp Leu Val His Phe Trp Asp Lys Tyr Arg Lys Ala Pro Glu Gly Ser
355 360 365

Ser Arg Lys Val Glu Ala Gln Lys Gln Phe Val Glu Ala Met Ser His
370 375 380

Arg Met His Ile Asp His Ser Ile Lys Leu Ile Gly Lys Leu Leu Phe
385 390 395 400

Gly Ile Glu Lys Ala Ser Glu Val Leu Asn Ala Ile Arg Pro Ala Gly
405 410 415

Gln Pro Leu Val Asp Asp Trp Asp Cys Leu Lys Thr Leu Val Lys Phe
420 425 430

Tyr Gly Ser Gln Pro Leu Leu Tyr His Arg Leu Thr Cys Leu Phe Ser
435 440 445

Leu Ile Ala Ser Pro Ala Gly Asp Thr Ser Lys Asp Ser Phe Pro Phe
450 455 460

Leu Arg Lys Cys Leu Leu Phe Phe Tyr Ala Gly Glu Asp Phe
465 470 475

<210> 88
<211> 431
<212> PRT
<213> Genlisea aurea

<400> 88

Asp Asp Asp Ile Val Gly Thr Arg Trp Ala Val Leu Val Ala Gly Ser
1 5 10 15

Asn Gly Tyr Trp Asn Tyr Arg His Gln Ala Asp Val Cys His Ala Tyr
20 25 30

Gln Thr Leu Lys Lys Gly Gly Leu Lys Asp Glu Asn Ile Ile Val Phe
35 40 45

Met Tyr Asp Asp Ile Ala Tyr Asn Asp Glu Asn Pro Arg Pro Gly Val
50 55 60

Ile Ile Asn His Pro His Gly Glu Asn Val Tyr Asp Gly Val Pro Lys
65 70 75 80

Asp Tyr Val Gly Asp Asp Val Thr Val Asp Asn Phe Phe Ala Val Leu

85

90

95

Leu Gly Asn Lys Thr Ala Leu Ser Gly Gly Ser Gly Lys Val Val Asp
 100 105 110

Ser Gly Pro Asn Asp His Ile Phe Val Tyr Tyr Ser Asp His Gly Gly
 115 120 125

Pro Gly Val Leu Gly Met Pro Thr Asp Pro Tyr Leu Tyr Ala Asn Asp
 130 135 140

Leu Ile Asp Val Leu Lys Arg Lys His Ala Ser Gly Thr Tyr Lys Ser
 145 150 155 160

Leu Val Phe Tyr Val Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly
 165 170 175

Leu Leu Pro Glu Gly Leu Asn Ile Phe Ala Thr Thr Ala Ser Asn Ala
 180 185 190

Glu Glu Asn Ser Trp Gly Thr Tyr Cys Pro Gly Asp Asp Ile Gly Pro
 195 200 205

Pro Pro Glu Tyr Glu Thr Cys Leu Gly Asp Met Tyr Ser Val Ser Trp
 210 215 220

Met Glu Asp Ser Asp Gln His Asn Leu Arg Thr Glu Thr Leu Arg Gln
 225 230 235 240

Gln Tyr His Val Val Arg Glu Arg Thr Ala Arg Asp Asn Ser His Arg
 245 250 255

Tyr Gly Ser His Val Met Gln Tyr Gly Asp Leu Lys Leu Ser Val Asp
 260 265 270

Lys Leu Phe Leu Tyr Met Gly Ser Asn Pro Ser Asn Asp Asn Ser Thr
 275 280 285

Phe Gly Gly Ser Val His Leu Ser Gly Asn Ser Ser Trp Pro Ser Ser
 290 295 300

Met Ala Val Ser Gln Arg Asp Ala Asp Val Leu His Phe Trp Asp Lys
305 310 315 320

Phe Arg Lys Ala Pro Glu Gly Ser Ser Arg Lys Ala Glu Ala Gln Lys
325 330 335

Gln Leu Ala Glu Val Met Val Arg Arg Ser Arg Val Asp Ile Ser Val
340 345 350

Val Ser Ile Gly Lys Leu Leu Phe Gly Ser Ser Glu Ile Met Asn Ala
355 360 365

Ile Arg Pro Ser Gly Lys Ser Leu Val Asp Asp Trp Asp Cys Leu Lys
370 375 380

Ser Leu Val Arg Ile Phe Glu Thr Tyr Cys Ser Ser Leu Ser Gly Tyr
385 390 395 400

Gly Met Lys His Met Arg Ser Ile Ala Asn Met Cys Asn Ala Gly Val
405 410 415

Ser Glu Glu Gln Met Ser Glu Ala Ser Ser Gln Val Cys Ser Ser
420 425 430

<210> 89

<211> 422

<212> PRT

<213> Triticum urartu

<400> 89

Met Ser Arg Ala Asp Ile Cys His Ala Tyr Gln Ile Leu Lys Lys Gly
1 5 10 15

Gly Leu Lys Asp Glu Asn Ile Ile Val Phe Met Tyr Asp Asp Ile Ala
20 25 30

His Asn Leu Glu Asn Pro Arg Pro Gly Val Ile Ile Asn His Pro Gln
35 40 45

Gly Gly Asp Val Tyr Ala Gly Val Pro Lys Asp Tyr Thr Gly Lys Glu
50 55 60

Val Asn Val Lys Asn Leu Phe Ala Val Leu Leu Gly Asn Lys Thr Ala
65 70 75 80

Val Asn Gly Gly Ser Gly Lys Val Leu Asp Ser Gly Pro Asn Asp His
85 90 95

Ile Phe Val Phe Tyr Ser Asp His Gly Gly Pro Gly Val Ile Gly Met
100 105 110

Pro Thr Asn Pro Tyr Val Tyr Gly Asp Asp Leu Val Asp Val Leu Lys
115 120 125

Lys Lys His Ala Ala Gly Ser Tyr Lys Ser Leu Val Phe Tyr Leu Glu
130 135 140

Ala Cys Glu Ala Gly Ser Val Phe Glu Gly Leu Leu Pro Asn Asp Ile
145 150 155 160

Gly Val Tyr Ala Thr Thr Ala Ser Asp Ala Glu Glu Ser Ser Trp Gly
165 170 175

Thr Tyr Cys Pro Gly Glu Tyr Pro Ser Pro Pro Pro Glu Tyr Asp Thr
180 185 190

Cys Leu Gly Asp Leu Tyr Ser Ile Ser Trp Met Glu Asp Ser Asp Val
195 200 205

His Asn Leu Arg Thr Glu Ser Leu Lys Gln Gln Tyr Asp Leu Val Lys
210 215 220

Lys Arg Thr Ala Ala Gln Asp Ser Tyr Ser Tyr Gly Ser His Val Met
225 230 235 240

Gln Tyr Gly Ser Leu Asp Leu Asn Ala Gln Gln Leu Phe Leu Tyr Ile
245 250 255

Gly Ser Asn Pro Ala Asn Asn Asn Thr Thr Phe Val Glu Asp Asn Ser
260 265 270

Leu Pro Ser Phe Ser Arg Ala Val Asn Gln Arg Asp Ala Asp Leu Val
275 280 285

Tyr Phe Trp His Lys Tyr Arg Lys Leu Ala Glu Ser Ser Pro Glu Lys
290 295 300

Asn Asp Ala Arg Lys Gln Leu Leu Glu Met Thr Ser His Arg Ser His
305 310 315 320

Ile Asp Asn Ser Val Glu Leu Ile Gly Asn Leu Leu Phe Gly Phe Ala
325 330 335

Asp Gly Pro Met Val Leu Lys Thr Val Arg Pro Ala Gly Glu Pro Leu
340 345 350

Val Asp Asp Trp Ser Cys Leu Lys Ser Thr Val Arg Ala Phe Glu Ser
355 360 365

Gln Cys Gly Ser Leu Ala Gln Tyr Gly Met Lys His Met Arg Ser Phe
370 375 380

Ala Asn Ile Cys Asn Ala Gly Val Leu Pro Glu Ala Met Val Lys Val
385 390 395 400

Ala Ala Gln Ala Cys Lys Ser Ile Pro Thr Asn Pro Trp Ser Ala Thr
405 410 415

His Lys Gly Phe Ser Ala
420

<210> 90

<211> 474

<212> PRT

<213> Hordeum vulgare subsp. vulgare

<400> 90

Met Ala Arg Leu Pro Cys Ser Pro Leu Leu Leu Leu Val Leu Ser
1 5 10 15

Ser Gln Leu Ala Leu Leu Val Ala Gly Glu Phe Leu Arg Leu Pro Ser
20 25 30

Glu Lys Asp Val Val Gly Thr Arg Trp Ala Val Leu Ile Ala Gly Ser
35 40 45

Asn Gly Tyr Tyr Asn Tyr Arg His Gln Ala Asp Val Cys His Ala Tyr
50 55 60

Gln Ile Met Lys Lys Gly Gly Leu Lys Asp Glu Asn Ile Ile Val Phe
65 70 75 80

Met Tyr Asp Asp Ile Ala Asn Asn Arg Asp Asn Pro Arg Pro Gly Val
85 90 95

Ile Ile Asn His Pro Lys Gly Gly Asp Val Tyr Ala Gly Val Pro Lys
100 105 110

Asp Tyr Thr Gly Ala Asp Val Asn Thr Asn Asn Phe Leu Ala Ala Leu
115 120 125

Leu Gly Asp Lys Ser Lys Leu Thr Gly Ser Gly Ser Gly Lys Val Val
130 135 140

Ser Ser Gly Pro Asp Asp His Ile Phe Val Tyr Tyr Ala Asp His Gly
145 150 155 160

Gly Pro Gly Ile Leu Gly Met Pro Glu Asp Glu Glu Tyr Leu Tyr Ala
165 170 175

Asn Asp Leu Val Arg Thr Leu Glu Lys Lys His Ala Gly Gly Ala Gly
180 185 190

Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile
195 200 205

Phe Glu Gly Leu Leu Pro Gly Asn Ile Ser Val Tyr Ala Thr Thr Ala
210 215 220

Ala Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Asp Asp
225 230 235 240

Glu Gly Ala Pro Pro Pro Glu Tyr Asp Thr Cys Leu Gly Asp Leu Tyr

245

250

255

Ser Val Ala Trp Met Glu Asp Ser Asp Ala His Asn Leu Asn Ala Glu
 260 265 270

Ser Leu Lys Gln Gln Tyr Glu Arg Val Arg Asn Arg Thr Ser Ala Asp
 275 280 285

Gly Thr Tyr Ser Leu Gly Ser His Val Met Gln Tyr Gly Asp Leu Gly
 290 295 300

Leu Asn Asp Gln Ser Leu Phe Gln Tyr Ile Gly Thr Asn Pro Ala Asn
 305 310 315 320

Asp Asn Ala Thr Phe Val Gln Ser Ser Ser Ser Arg Gln Leu Pro
 325 330 335

Gly Ala Arg Val Asn Gln Arg Asp Ala Asp Leu Val His Phe Trp His
 340 345 350

Lys Tyr Arg Arg Ser Ala Glu Gly Ser Ala Glu Lys Val Glu Ala Arg
 355 360 365

Arg Arg Leu Val Glu Thr Met Ala Arg Arg Ser Arg Val Asp Ser Ser
 370 375 380

Val Glu Leu Ile Gly Gly Leu Leu Phe Gly Ser Glu Glu Gly Ala Lys
 385 390 395 400

Val Leu Gly Thr Val Arg Pro Ala Gly Gln Pro Val Val Asp Asp Trp
 405 410 415

Gly Cys Leu Lys Ser Val Val Arg Arg Phe Glu Glu Arg Cys Gly Pro
 420 425 430

Leu Thr Gln Tyr Gly Met Lys His Met Arg Ser Leu Ala Asn Ile Cys
 435 440 445

Asn Ala Gly Val Arg Glu Glu Val Met Asp Lys Ala Ala Ser Gln Ala
 450 455 460

Cys Ala Ala Ser Pro Ser Ser Leu Ile Ile
465 470

<210> 91
<211> 424
<212> PRT
<213> Aegilops tauschii

<400> 91

Met Ser Gln Val Arg Ala Asp Ile Cys His Ala Tyr Gln Ile Leu Lys
1 5 10 15

Thr Gly Gly Leu Lys Asp Glu Asn Ile Ile Val Phe Met Tyr Asp Asp
20 25 30

Ile Ala His Asn Leu Glu Asn Pro Arg Pro Gly Val Ile Ile Asn His
35 40 45

Pro Gln Gly Gly Asp Val Tyr Ala Gly Val Pro Lys Asp Tyr Thr Gly
50 55 60

Lys Glu Val Asn Val Lys Asn Leu Phe Ala Val Leu Leu Gly Asn Lys
65 70 75 80

Thr Ala Val Ser Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro Asn
85 90 95

Asp His Ile Phe Val Phe Tyr Ser Asp His Gly Gly Pro Gly Val Ile
100 105 110

Gly Met Pro Thr Tyr Pro Tyr Val Tyr Gly Asp Asp Leu Val Asp Val
115 120 125

Leu Lys Lys Lys His Ala Ala Gly Thr Tyr Lys Ser Leu Val Phe Tyr
130 135 140

Leu Glu Ala Cys Glu Ala Gly Ser Val Phe Glu Gly Leu Leu Pro Asn
145 150 155 160

Asp Ile Gly Val Tyr Ala Thr Thr Ala Ser Asn Ala Glu Glu Ser Ser
165 170 175

Trp Gly Thr Tyr Cys Pro Gly Glu Tyr Pro Ser Pro Pro Ser Glu Tyr
180 185 190

Asp Thr Cys Leu Gly Asp Leu Tyr Ser Ile Ser Trp Met Glu Asp Ser
195 200 205

Asp Val His Asn Leu Arg Thr Glu Ser Leu Lys Gln Gln Tyr Asp Leu
210 215 220

Val Lys Lys Arg Thr Ala Ala Gln Asp Ser Tyr Ser Tyr Gly Ser His
225 230 235 240

Val Met Gln Tyr Gly Ser Leu Asp Leu Asn Asp Gln His Leu Phe Leu
245 250 255

Tyr Ile Gly Ser Asn Pro Ala Asn Asp Asn Thr Thr Phe Val Glu Asp
260 265 270

Asn Ser Leu Pro Ser Phe Ser Arg Ala Val Asn Gln Arg Asp Ala Asp
275 280 285

Leu Val Tyr Phe Trp Arg Lys Tyr Gln Lys Leu Ala Glu Ser Ser Thr
290 295 300

Glu Lys Asn Asp Ala Arg Lys Gln Leu Leu Glu Met Met Gly His Arg
305 310 315 320

Ser His Ile Asp Asn Ser Val Glu Leu Ile Gly Asn Leu Leu Phe Gly
325 330 335

Phe Ala Asp Gly Pro Met Val Leu Lys Thr Val Arg Pro Ala Gly Glu
340 345 350

Pro Leu Ala Asp Asp Trp Ser Cys Leu Lys Ser Met Val Arg Ala Phe
355 360 365

Glu Ser Gln Cys Gly Ser Leu Ala Gln Tyr Gly Met Lys His Met Arg
370 375 380

Ser Phe Ala Asn Ile Cys Asn Ala Gly Ile Leu Pro Glu Ala Met Val
385 390 395 400

Lys Met Ala Ala Gln Ala Cys Thr Ser Ile Pro Thr Asn Pro Trp Ser
405 410 415

Ala Thr His Asn Gly Phe Ser Ala
420

<210> 92
<211> 461
<212> PRT
<213> Solanum tuberosum

<400> 92

Met Asn Arg Ser Ile Ala Gly Val Leu Phe Leu Ile Ala Leu Ser Leu
1 5 10 15

Asn Val Ser Val Ser Glu Ser Arg Asn Phe Leu Lys Leu Pro Ser Glu
20 25 30

Gly Ser Arg Phe Phe Asp Ala Asp Glu Ser Asp Ser Val Gly Thr Arg
35 40 45

Trp Ala Ile Leu Leu Ala Gly Ser Asn Gly Tyr Trp Asn Tyr Arg His
50 55 60

Gln Ala Asp Ile Cys His Ala Tyr Gln Leu Leu Lys Lys Gly Gly Leu
65 70 75 80

Lys Asp Glu Asn Ile Val Val Phe Met Tyr Asp Asp Ile Ala Asn Asn
85 90 95

Glu Glu Asn Pro Arg Gln Gly Val Ile Ile Asn Ser Pro His Gly Glu
100 105 110

Asp Val Tyr Lys Gly Val Pro Lys Asp Tyr Thr Gly Asp Asp Val Thr
115 120 125

Val Asn Asn Phe Leu Ala Ala Leu Leu Gly Asn Lys Thr Ala Leu Thr
130 135 140

Gly Gly Ser Gly Lys Val Val Asp Ser Gly Pro Asn Asp His Ile Phe
145 150 155 160

Ile Phe Cys Ser Asp His Gly Gly Ala Gly Val Ile Gly Met Pro Thr
165 170 175

Asp Pro Tyr Leu Tyr Ala Asn Asp Leu Ile Asp Ala Leu Lys Lys Lys
180 185 190

His Ala Ser Gly Thr Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys
195 200 205

Glu Ser Gly Ser Met Ser Glu Gly Leu Leu Pro Glu Gly Leu Asn Val
210 215 220

Tyr Ala Thr Thr Ala Ser Asn Ala Asp Glu Ser Ser Trp Gly Thr Tyr
225 230 235 240

Cys Pro Gly Glu Tyr Pro Ser Pro Pro Ile Glu Tyr Gly Thr Cys Leu
245 250 255

Gly Asp Leu Tyr Ser Ile Ser Trp Met Glu Asp Ser Asp Arg His Asn
260 265 270

Leu Arg Thr Glu Thr Leu Lys Gln Gln Tyr His Leu Val Lys Glu Arg
275 280 285

Thr Ala Ser Gly Asn Pro Ala Tyr Gly Ser His Val Met Gln Tyr Gly
290 295 300

Asp Val His Leu Ser Lys Asp Ala Leu Phe Leu Tyr Met Gly Thr Asp
305 310 315 320

Pro Ala Asn Asp Asn Tyr Thr Phe Val Asp Asp Asn Ser Leu Arg Val
325 330 335

Ser Lys Ala Val Asn Gln Arg Asp Ala Asp Leu Val His Phe Trp Tyr
340 345 350

Lys Phe His Lys Ala Pro Glu Gly Ser Val Arg Lys Thr Glu Ala Gln

355

360

365

Lys Gln Leu Asn Glu Ala Ile Ser His Arg Met His Leu Asp Asn Ser
 370 375 380

Ile Ala Leu Val Gly Lys Leu Leu Phe Gly Ile Lys Lys Gly Pro Glu
 385 390 395 400

Val Leu Thr Ser Val Arg Pro Ala Gly Gln Pro Leu Val Asp Asp Trp
 405 410 415

Asp Cys Leu Lys Ser Tyr Val Ser Thr Pro Thr Pro Phe Ser Ser Ile
 420 425 430

Ser Phe Glu Phe Ser Gln Ile Tyr Ser Cys Ile Ser Leu Tyr Gly Gly
 435 440 445

Met Arg Leu Arg Ser Leu Val Leu Asp Ile Leu Leu Val
 450 455 460

<210> 93

<211> 441

<212> PRT

<213> Triticum urartu

<400> 93

Met Ala Met Ala Ser Phe Arg Pro Pro Pro Leu Ala Leu Leu Leu Ala
 1 5 10 15

Ala Cys Leu Ser Ala Leu Ala Asp Ile Cys His Ala Tyr Gln Ile Met
 20 25 30

Lys Lys Gly Gly Leu Lys Asp Glu Asn Ile Ile Val Phe Met Tyr Asp
 35 40 45

Asp Ile Ala His Asn Pro Glu Asn Pro Arg Pro Gly Val Ile Ile Asn
 50 55 60

His Pro Gln Gly Gly Asp Val Tyr Ala Gly Val Pro Lys Asp Tyr Thr
 65 70 75 80

Gly Lys Glu Val Asn Val Lys Asn Phe Phe Ala Val Leu Leu Gly Asn
85 90 95

Lys Thr Ala Val Ser Gly Gly Asn Gly Lys Val Val Asp Ser Gly Pro
100 105 110

Asn Asp His Ile Phe Val Phe Tyr Ser Asp His Gly Gly Pro Gly Val
115 120 125

Leu Gly Met Pro Thr Tyr Pro Tyr Leu Tyr Gly Asp Asp Leu Val Asp
130 135 140

Val Leu Lys Lys Lys His Ala Ala Gly Thr Tyr Lys Ser Leu Val Phe
145 150 155 160

Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro
165 170 175

Asn Asp Ile Gly Val Tyr Ala Thr Thr Ala Ser Asn Ala Glu Glu Ser
180 185 190

Ser Trp Gly Thr Tyr Cys Pro Gly Glu Tyr Pro Ser Pro Pro Pro Glu
195 200 205

Tyr Asp Thr Cys Leu Gly Asp Leu Tyr Ser Ile Ser Trp Met Glu Asp
210 215 220

Ser Asp Val His Asn Leu Arg Thr Glu Ser Leu Lys Gln Gln Tyr Asn
225 230 235 240

Leu Val Lys Lys Arg Thr Ala Ala Gln Asp Ser Tyr Ser Tyr Gly Ser
245 250 255

His Val Met Gln Tyr Gly Ser Leu Asp Leu Asn Ala Glu His Leu Phe
260 265 270

Ser Tyr Ile Gly Ser Asn Pro Ala Asn Glu Asn Thr Thr Phe Val Glu
275 280 285

Asp Asn Ala Leu Pro Ser Phe Ser Arg Ala Val Asn Gln Arg Asp Ala
290 295 300

Asp Leu Val Tyr Phe Trp Gln Lys Tyr Arg Lys Leu Ala Glu Ser Ser
305 310 315 320

Pro Glu Lys Asn Asp Ala Arg Lys Gln Leu Leu Glu Met Met Gly His
325 330 335

Arg Ser His Ile Asp Asn Ser Ile Glu Leu Ile Gly Asn Leu Leu Phe
340 345 350

Gly Ser Ala Gly Gly Pro Met Val Leu Lys Ala Val Arg Pro Ala Gly
355 360 365

Glu Pro Leu Val Asp Asp Trp Ser Cys Leu Lys Ser Thr Val Arg Thr
370 375 380

Phe Glu Ser Gln Cys Gly Ser Leu Ala Gln Tyr Gly Met Lys His Met
385 390 395 400

Arg Ser Phe Ala Asn Ile Cys Asn Ala Gly Ile Val Pro Glu Ala Thr
405 410 415

Ala Lys Val Ala Ala Gln Ala Cys Thr Ser Ile Pro Thr Asn Pro Trp
420 425 430

Ser Ala Thr His Lys Gly Phe Ser Ala
435 440

<210> 94
<211> 394
<212> PRT
<213> Citrus clementina

<400> 94

Met Tyr Asp Asp Ile Ala Phe Asn Glu Glu Asn Pro Arg Pro Gly Val
1 5 10 15

Ile Ile Asn His Pro His Gly Asp Asp Val Tyr Lys Gly Val Pro Lys
20 25 30

Asp Tyr Thr Gly Glu Asp Val Thr Val Glu Asn Phe Phe Ala Val Ile

35

40

45

Leu Gly Asn Lys Thr Ala Leu Thr Gly Gly Ser Gly Lys Val Val Asp
 50 55 60

Ser Gly Pro Asn Asp His Ile Phe Ile Phe Tyr Ser Asp His Gly Gly
 65 70 75 80

Pro Gly Val Leu Gly Met Pro Thr Ser Arg Tyr Ile Tyr Ala Asp Glu
 85 90 95

Leu Ile Asp Val Leu Lys Lys Lys His Ala Ser Gly Asn Tyr Lys Ser
 100 105 110

Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly
 115 120 125

Leu Leu Pro Glu Gly Leu Asn Ile Tyr Ala Thr Thr Ala Ser Asn Ala
 130 135 140

Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Ile Pro Gly Pro
 145 150 155 160

Pro Pro Glu Tyr Ser Thr Cys Leu Gly Asp Leu Tyr Ser Ile Ala Trp
 165 170 175

Met Glu Asp Ser Asp Ile His Asn Leu Arg Thr Glu Thr Leu His Gln
 180 185 190

Gln Tyr Glu Leu Val Lys Thr Arg Thr Ala Ser Tyr Asn Ser Tyr Gly
 195 200 205

Ser His Val Met Gln Tyr Gly Asp Ile Gly Leu Ser Lys Asn Asn Leu
 210 215 220

Phe Thr Tyr Leu Gly Thr Asn Pro Ala Asn Asp Asn Tyr Thr Phe Val
 225 230 235 240

Asp Glu Asn Ser Leu Arg Pro Ala Ser Lys Ala Val Asn Gln Arg Asp
 245 250 255

Ala Asp Leu Leu His Phe Trp Asp Lys Tyr Arg Lys Ala Pro Glu Gly
260 265 270

Thr Pro Arg Lys Ala Glu Ala Gln Lys Gln Phe Phe Glu Ala Met Ser
275 280 285

His Arg Met His Val Asp His Ser Ile Lys Leu Ile Gly Lys Leu Leu
290 295 300

Phe Gly Ile Glu Lys Gly Pro Glu Ile Leu Asn Thr Val Arg Pro Ala
305 310 315 320

Gly Gln Pro Leu Val Asp Asp Trp Gly Cys Leu Lys Ser Leu Val Arg
325 330 335

Thr Phe Glu Ser His Cys Gly Ala Leu Ser Gln Tyr Gly Met Lys His
340 345 350

Met Arg Ser Leu Ala Asn Ile Cys Asn Thr Gly Ile Gly Lys Glu Lys
355 360 365

Met Ala Glu Ala Ser Ala Gln Ala Cys Glu Asn Ile Pro Ser Gly Pro
370 375 380

Trp Ser Ser Leu Asp Lys Gly Phe Ser Ala
385 390

<210> 95
<211> 473
<212> PRT
<213> *Setaria italica*

<400> 95

Met Ala Thr Ala Thr Thr Arg Leu Arg Cys Leu Leu Leu Leu Phe Leu
1 5 10 15

Val Gln Leu Leu Leu Leu Leu Ser Ala Ala Ala Gly Ala Arg Trp Gln
20 25 30

Asp Phe Leu Arg Leu Pro Ser Glu Gly Gly Asp Ala Ala Ala Gly Thr
35 40 45

Arg Trp Ala Val Leu Ile Ala Gly Ser Asn Gly Tyr Tyr Asn Tyr Arg
50 55 60

His Gln Ala Asp Val Cys His Ala Tyr Gln Ile Met Lys Lys Gly Gly
65 70 75 80

Leu Lys Asp Glu Asn Ile Ile Val Phe Met Tyr Asp Asp Ile Ala Ser
85 90 95

Ser Pro Asp Asn Pro Arg Pro Gly Val Ile Ile Asn His Pro Ser Gly
100 105 110

Gly Asp Val Tyr Ala Gly Val Pro Lys Asp Tyr Thr Gly Glu Asp Val
115 120 125

Thr Val Asn Asn Phe Leu Ala Val Leu Leu Gly Asn Arg Ser Ala Val
130 135 140

Ser Gly Gly Ser Gly Lys Val Val Ala Ser Gly Pro Gly Asp His Val
145 150 155 160

Phe Val Tyr Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Met Pro
165 170 175

Ser Gly Asp Tyr Leu Tyr Ala Lys Asp Leu Val Gly Ala Leu Glu Arg
180 185 190

Lys His Asp Ala Gly Gly Tyr Arg Ser Leu Val Phe Tyr Leu Glu Ala
195 200 205

Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu Pro Glu Gly Ile Asn
210 215 220

Val Tyr Ala Thr Thr Ala Ala Asn Ala Glu Glu Ser Ser Trp Gly Thr
225 230 235 240

Tyr Cys Pro Gly Asp Asp Gln Gly Pro Pro Pro Glu Phe Asp Thr Cys
245 250 255

Leu Gly Asp Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Val His
260 265 270

Asn Leu Arg Thr Glu Ser Leu Lys Gln Gln Tyr Glu Val Val Lys Asp
275 280 285

Arg Thr Ser Ala His Gly Thr Tyr Ser Leu Gly Ser His Val Met Gln
290 295 300

Tyr Gly Asp Gln Ser Leu Asn Gly Gln Ser Leu Tyr Gln Phe Ile Gly
305 310 315 320

Thr Asp Pro Ala Asn Asp Asn Ala Thr Phe Gly Arg Asp Asn Ser Leu
325 330 335

Arg Arg Arg Ser Ser Gly Thr Val Asn Gln Arg Asp Ala Asp Leu Val
340 345 350

Tyr Phe Trp Gln Lys Tyr Lys Lys Ser Ala Glu Gly Thr Pro Glu Lys
355 360 365

Ala Glu Ala Arg Lys Arg Leu Leu Gln Val Met Ser Arg Arg Ser Arg
370 375 380

Val Asp Ser Ser Met Glu Leu Ile Gly Ser Leu Leu Phe Gly Ser Asp
385 390 395 400

Glu Gly Pro Lys Val Leu Gly Ala Val Arg Pro Ala Gly Gln Pro Leu
405 410 415

Ala Asp Asp Trp Asp Cys Leu Lys Ala Met Val His Ala Tyr Glu Ala
420 425 430

Gln Cys Gly Pro Leu Lys Gln Tyr Gly Met Lys His Met Arg Ser Phe
435 440 445

Ala Asn Ile Cys Asn Ala Gly Val Gly Glu Asp Ala Met Ala Lys Val
450 455 460

Ala Ser Gln Ala Cys Ala Ala Ala Arg
465 470

<210> 96
<211> 543
<212> PRT
<213> Aegilops tauschii

<400> 96

Met Ala Ser Asn Arg Leu Leu Pro Leu Ala Leu Leu Leu Leu Leu Leu
1 5 10 15

Ala Met Ala His Ala Asp Thr Pro Arg Leu Glu Pro Thr Val Arg Leu
20 25 30

Pro Ser Gln Arg Met Ala Ala Gly Gln Gly Asp Asp Gly Ser Val Gly
35 40 45

Thr Arg Trp Ala Ala Leu Val Ala Gly Ser Asn Gly Tyr Gln Asn Tyr
50 55 60

Arg His Gln Gly Arg Thr Leu Tyr His Gly Phe Tyr Ser Leu Leu Val
65 70 75 80

Gly Val Ser Ser Arg Asp Pro Pro Thr Phe Phe Phe Leu Ser Val Lys
85 90 95

Ser Ile Pro Ser Trp Glu Ile Arg Trp Val Asp Asp Asn Glu Val Leu
100 105 110

Cys Leu Ile Cys Gly Ala Lys Leu Cys Thr Val Gln Ala Asp Ile Cys
115 120 125

His Ala Tyr Gln Ile Leu Lys Lys Gly Gly Leu Lys Asp Glu Asn Ile
130 135 140

Ile Val Phe Met Tyr Asp Asp Ile Ala His Asn Leu Glu Asn Pro Arg
145 150 155 160

Pro Gly Val Ile Ile Asn His Pro Gln Gly Gly Asp Val Tyr Ser Gly
165 170 175

Val Pro Met Asp Tyr Thr Gly Lys Glu Val Asn Val Lys Asn Leu Phe

180

185

190

Ala Val Leu Leu Gly Asn Lys Thr Ala Val Ser Gly Gly Ser Gly Lys
 195 200 205

Val Leu Asp Ser Gly Pro Asn Asp His Ile Phe Val Phe Tyr Ser Asp
 210 215 220

His Gly Gly Pro Gly Val Ile Gly Met Pro Thr Asn Pro Tyr Val Tyr
 225 230 235 240

Gly Asp Asp Leu Val Asp Val Leu Lys Lys Lys His Ala Ala Gly Thr
 245 250 255

Tyr Arg Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ala Gly Ser Val
 260 265 270

Phe Glu Gly Leu Leu Pro Asn Asp Ile Ser Val Tyr Thr Thr Thr Ala
 275 280 285

Ser Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Glu Tyr
 290 295 300

Pro Ser Pro Pro Pro Glu Tyr Asp Thr Cys Leu Gly Asp Leu Tyr Ser
 305 310 315 320

Ile Ser Trp Met Glu Asp Ser Asp Val His Asn Leu Arg Thr Glu Ser
 325 330 335

Leu Lys Gln Gln Tyr Asp Leu Val Lys Lys Arg Thr Ala Ala Gln Asp
 340 345 350

Ser Tyr Asn Tyr Gly Ser His Val Met Gln Tyr Gly Ser Leu Asp Leu
 355 360 365

Asn Ala Gln Gln Leu Phe Leu Tyr Ile Gly Ser Asn Pro Ala Asn Asn
 370 375 380

Lys Thr Thr Phe Val Glu Asp Asn Ser Leu Pro Ser Phe Ser Arg Val
 385 390 395 400

Val Asn Gln Arg Asp Ala Asp Leu Val Tyr Phe Trp His Lys Tyr Arg
405 410 415

Lys Leu Ala Glu Ser Ser Pro Glu Lys Asn Asp Ala Arg Lys Gln Leu
420 425 430

Leu Glu Met Met Ser His Arg Ser His Ile Asp Asn Ser Val Glu Leu
435 440 445

Ile Gly Asn Leu Leu Phe Gly Ser Ala Asp Gly Pro Met Val Leu Lys
450 455 460

Thr Val Arg Pro Ala Gly Glu Pro Leu Val Asp Asp Trp Ser Cys Leu
465 470 475 480

Lys Ser Thr Val Arg Ala Phe Glu Ser Gln Cys Gly Ser Leu Ala Gln
485 490 495

Tyr Gly Met Lys His Met Arg Ser Phe Ala Asn Ile Cys Asn Ala Gly
500 505 510

Val Leu Pro Glu Ala Thr Val Lys Val Ala Ala Gln Ala Cys Lys Ser
515 520 525

Ile Pro Thr Asn Pro Trp Ser Ala Thr His Lys Gly Phe Ser Ala
530 535 540

<210> 97
<211> 493
<212> PRT
<213> Picea sitchensis

<400> 97

Met Gly Ser Ser Lys Gly Phe Gln Leu Gly Leu Leu Cys Tyr Phe Leu
1 5 10 15

Leu Leu Ser Leu Asp Ser Ser Lys Val Ala Asp Gly Ala Arg Arg Asp
20 25 30

Trp Asn Ser Leu Leu Lys Leu Pro Thr Asn His Val Asp Ala Asp Ser
35 40 45

Asp Arg Ile Gly Thr Glu Trp Ala Val Leu Leu Ala Gly Ser Ser Gly
50 55 60

Tyr Trp Asn Tyr Arg His Gln Ala Asp Val Cys His Ala Tyr Gln Ile
65 70 75 80

Leu Arg Arg Gly Gly Leu Lys Glu Glu Asn Ile Val Val Phe Met Tyr
85 90 95

Asp Asp Ile Ala Tyr Asp Glu Glu Asn Pro His Pro Gly Thr Ile Ile
100 105 110

Asn His Pro Gln Gly Ser Asp Val Tyr Ala Gly Val Pro Lys Asp Tyr
115 120 125

Thr Gly Glu Asp Val Thr Val Asn Asn Phe Phe Ala Ala Ile Leu Gly
130 135 140

Asn Lys Ser Leu Val Thr Gly Gly Ser Gly Lys Val Val Glu Ser Gly
145 150 155 160

Pro Asn Asp Arg Ile Phe Ile Tyr Tyr Ser Asp His Gly Gly Pro Gly
165 170 175

Val Leu Gly Met Pro Leu Pro Pro Tyr Leu Tyr Ala Asn Asp Phe Val
180 185 190

Gln Val Leu Lys Lys Lys His Asp Ala Gly Ser Tyr Arg Glu Met Val
195 200 205

Ile Tyr Val Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu Leu
210 215 220

Pro Thr Asp Leu Asn Ile Tyr Val Thr Thr Ala Ser Asn Ala Glu Glu
225 230 235 240

Asn Ser Trp Gly Thr Tyr Cys Pro Gly Met Asp Pro Pro Pro Pro Pro
245 250 255

Glu Tyr Asp Thr Cys Leu Gly Asp Leu Tyr Ser Val Ala Trp Met Glu
260 265 270

Asp Ser Glu Ile Asn Asn Leu Lys Glu Glu Thr Leu Leu Gln Gln Tyr
275 280 285

Asp Leu Val Lys Leu Arg Thr Ser Asn His Asn Thr Tyr Met Ser Gly
290 295 300

Ser His Val Met Gln Tyr Gly Asn Ile Thr Ile Ser Gln Glu Glu Leu
305 310 315 320

Tyr Leu Tyr Met Gly Phe Asp Ser Ala Asn Ser Asn Ala Ser Leu Val
325 330 335

Leu Glu Asn Ser Pro Leu Leu Glu Lys Thr Glu Ala Lys Ala Ile Asn
340 345 350

Gln Arg Asp Ala Asp Leu Leu Tyr Met Trp Gln Lys Tyr Lys Lys Ser
355 360 365

Lys Glu Asp Ser Pro Glu Arg Leu Thr Ala Gln Thr Gln Leu Leu Glu
370 375 380

Phe Met Ala His Arg Met His Val Asp Lys Ser Val Lys Leu Val Gly
385 390 395 400

Asn Leu Leu Phe Gly Pro Glu Lys Gly Pro Ala Val Phe Asn Ala Val
405 410 415

Arg Pro Gln Gly Glu Pro Leu Val Asp Asp Trp Asp Cys Leu Lys Lys
420 425 430

Met Val Arg Thr Phe Glu Gly His Cys Gly Ser Leu Ala Gln Tyr Gly
435 440 445

Met Lys His Met Arg Ala Leu Ala Asn Ile Cys Asn Glu Gly Ile Ser
450 455 460

Met Asp Thr Met Ala Thr Val Ser Ala Glu Ala Cys Thr Gln Phe Pro
465 470 475 480

Ala Gly Ser Trp Ser Ser Leu Gln Arg Gly Phe Ser Ala
485 490

<210> 98
<211> 380
<212> PRT
<213> *Vicia narbonensis*

<400> 98

Asp Val Cys His Ala Tyr Gln Leu Leu Arg Lys Gly Gly Leu Lys Glu
1 5 10 15

Glu Asn Ile Ile Val Phe Met Tyr Asp Asp Ile Ala Tyr Ser Glu Glu
20 25 30

Asn Pro Arg Pro Gly Val Ile Ile Asn Ser Pro His Gly Glu Asn Val
35 40 45

Tyr Glu Gly Val Pro Lys Asp Tyr Thr Gly Glu Asp Val Thr Val Gly
50 55 60

Asn Phe Phe Ala Ala Leu Leu Gly Asn Lys Ser Ala Leu Ser Gly Gly
65 70 75 80

Ser Gly Lys Val Val Asp Ser Gly Pro Asn Asp Arg Ile Phe Val Phe
85 90 95

Tyr Ser Asp His Gly Gly Pro Gly Val Leu Gly Met Pro Thr Ser Pro
100 105 110

Tyr Met Tyr Ala Ser Asp Leu Val Glu Val Leu Lys Ile Lys His Ala
115 120 125

Ala Gly Thr Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser
130 135 140

Gly Ser Ile Phe Glu Gly Leu Leu Pro Glu Gly Leu Asn Ile Tyr Ala
145 150 155 160

Thr Thr Ala Ala Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro

165

170

175

Gly Glu Asn Pro Ser Pro Pro Pro Glu Tyr Glu Thr Cys Leu Ala Asp
 180 185 190

Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Ile His Asn Leu Gln
 195 200 205

Thr Glu Thr Leu His Gln Gln Tyr Glu Leu Val Lys Glu Arg Thr Ser
 210 215 220

Asn Gly Asn Ser Asn Tyr Gly Ser His Val Met Gln Tyr Gly Asp Ile
 225 230 235 240

Glu Leu Ser Lys Asp Ser Leu Phe Leu Tyr Leu Gly Ser Asn Pro Ser
 245 250 255

Asn Glu Asn Phe Thr Phe Val Gly Arg Asn Ser Leu Val Pro Pro Ser
 260 265 270

Lys Ala Ile Asn Gln Arg Asp Ala Asp Leu Ile His Phe Trp Asp Lys
 275 280 285

Phe Arg Lys Ala Pro Gln Gly Ser Pro Arg Lys Ala Ala Ala Gln Lys
 290 295 300

Glu Val Leu Glu Ala Met Ser His Arg Met His Ile Asp Asp Ser Ile
 305 310 315 320

Lys Leu Val Gly Lys Leu Leu Phe Gly Met Lys Lys Gly Pro Glu Val
 325 330 335

Leu Thr Ser Val Arg Pro Ala Gly Gln Pro Leu Val Asp Asp Trp Asp
 340 345 350

Cys Leu Lys Thr Leu Val Arg Thr Phe Glu Thr Tyr Cys Gly Ser Leu
 355 360 365

Ser Gln Tyr Gly Met Lys His Met Arg Ser Phe Ala
 370 375 380

<210> 99
<211> 455
<212> PRT
<213> Nicotiana tabacum

<400> 99

Met Ile Arg Lys Asn Gly Val Val Pro Phe Leu Val Ala Leu Phe Val
1 5 10 15

Leu Val Cys Thr Ala Glu Gly Arg Asn Leu Leu Glu Ser Ile Val Glu
20 25 30

Asp Asp Asn Pro Thr Gly Thr Lys Trp Ala Val Leu Val Ala Gly Ser
35 40 45

Asn Glu Trp Asp Asn Tyr Arg His Gln Ala Asp Val Cys His Ala Tyr
50 55 60

Gln Leu Leu Lys Lys Gly Gly Leu Lys Asp Glu Asn Ile Ile Val Phe
65 70 75 80

Met Tyr Asp Asp Ile Ala Tyr Asn Lys Asn Asn Pro Arg Pro Gly Ile
85 90 95

Ile Ile Asn Ser Pro His Gly His Asp Val Tyr Lys Gly Val Pro Lys
100 105 110

Asp Tyr Thr Gly Lys Asp Cys Asn Ala Asp Asn Phe Phe Ala Val Ile
115 120 125

Leu Gly Asn Lys Ser Ala Leu Thr Gly Gly Ser Gly Lys Val Val Glu
130 135 140

Asn Gly Pro Asn Asp Tyr Ile Phe Ile Tyr Tyr Ala Asp His Gly Ala
145 150 155 160

Pro Gly Leu Ile Gly Met Pro Ser Gly Asp Val Val Tyr Ala Asp Asp
165 170 175

Leu Asn Arg Val Leu Ile Lys Lys His Thr Phe Gly Thr Tyr Ser Lys
180 185 190

Leu Val Phe Tyr Met Glu Ala Cys Glu Ser Gly Ser Met Phe Asp Gly
195 200 205

Leu Leu Pro Lys Gly Leu Asn Ile Tyr Val Thr Ala Ala Ser Lys Pro
210 215 220

Asp Glu Ser Ser Trp Ala Thr Tyr Cys Ile Arg Leu Gly Asp Glu Asp
225 230 235 240

Gln Cys Leu Gly Asp Leu Tyr Ser Val Ser Trp Leu Glu Asp Ser Asp
245 250 255

Leu His Asp Arg Gln Val Glu Thr Leu Glu Lys Gln Tyr Gln Leu Val
260 265 270

Arg Lys Arg Thr Leu Asn Asn Gly Thr Glu Glu Gly Ser His Val Met
275 280 285

Gln Tyr Gly Asp Leu His Ile Ser Glu Asp Pro Leu Phe Arg Tyr Met
290 295 300

Gly Ser Asn Ser Ala Lys Asn Ser Tyr Asn Thr Ser Asn Asn Asp Glu
305 310 315 320

Ser Trp Leu Pro Ser Arg Thr Val Asn Gln Arg Asp Val His Leu Met
325 330 335

His Leu Trp Ser Lys Phe Arg Ser Ala Pro Glu Gly Ser Ala Arg Lys
340 345 350

Ala Glu Ala His Arg Gln Leu Ser Glu Ala Leu Ser Gln Arg Glu Asp
355 360 365

Val Asp Asn Ser Val Arg His Ile Gly Glu Val Leu Phe Gly Val Glu
370 375 380

Lys Ser His Lys Leu Leu Asn Thr Val Arg Pro Ala Gly Gln Pro Leu
385 390 395 400

Val Asp Asp Trp Asp Cys Leu Lys Ser Phe Val Lys Ile Phe Glu Ser
405 410 415

Gln Cys Gly Thr Leu Thr Pro Tyr Gly Arg Lys His Val Arg Gly Phe
420 425 430

Ala Asn Leu Cys Asn Ala Gly Ile Arg Arg Glu Gln Met Ala Ala Ala
435 440 445

Ala Lys Gln Ala Cys Pro Pro
450 455

<210> 100
<211> 492
<212> PRT
<213> Aegilops tauschii

<400> 100

Met Ala Arg Leu Ser Cys Ser Pro Leu Leu Leu Leu Phe Leu Ser
1 5 10 15

Ser Gln Leu Ala Leu Leu Val Ala Gly Glu Phe Leu Arg Leu Pro Ser
20 25 30

Glu Lys Asp Val Val Gly Thr Arg Trp Ala Val Leu Ile Ala Gly Ser
35 40 45

Asn Gly Tyr Tyr Asn Tyr Arg His Gln Ala Gly Thr Lys Phe Pro Ile
50 55 60

Lys Tyr Ser Ser Leu Ile Thr Leu Met Glu Asn Ala Asp Val Cys His
65 70 75 80

Ala Tyr Gln Ile Met Lys Lys Gly Gly Leu Lys Asp Glu Asn Ile Ile
85 90 95

Val Phe Met Tyr Asp Asp Ile Ala Gly Asn Arg Asp Asn Pro Arg Pro
100 105 110

Gly Val Ile Ile Asn His Pro Lys Gly Gly Asp Val Tyr Ala Gly Val
115 120 125

Pro Lys Asp Tyr Thr Gly Ala Asp Val Asn Ala Asn Asn Phe Leu Ala
130 135 140

Ala Leu Leu Gly Asp Lys Ser Lys Leu Thr Gly Ser Gly Ser Gly Lys
145 150 155 160

Val Val Ser Ser Gly Ser Asp Asp His Ile Phe Val Tyr Tyr Ala Asp
165 170 175

His Gly Gly Pro Gly Ile Leu Gly Met Pro Gly Asp Glu Glu Tyr Leu
180 185 190

Tyr Ala Asn Asp Leu Val Arg Thr Leu Glu Lys Lys His Ala Gly Gly
195 200 205

Ala Gly Tyr Lys Ser Leu Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly
210 215 220

Ser Ile Phe Glu Gly Leu Leu Pro Gly Asn Ile Gly Val Tyr Ala Thr
225 230 235 240

Thr Ala Ala Asn Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly
245 250 255

Asp Asp Glu Gly Ala Pro Pro Pro Glu Tyr Asp Thr Cys Leu Gly Asp
260 265 270

Leu Tyr Ser Val Ala Trp Met Glu Asp Ser Asp Ala His Asn Leu Asn
275 280 285

Ala Glu Ser Leu Lys Gln Gln Tyr Glu Arg Val Arg Asp Arg Thr Ser
290 295 300

Ala Ala Gly Thr Tyr Ser Leu Gly Ser His Val Met Gln Tyr Gly Asp
305 310 315 320

Leu Asp Leu Asn Asp Gln Ser Leu Phe Leu Tyr Ile Gly Thr Asn Pro
325 330 335

Ala Asn Asp Asn Ala Ser Phe Val Gln Gly Ser Ser Ser Thr Ser Arg

340

345

350

Gln Leu Pro Gly Gly Arg Val Asn Gln Arg Asp Ala Asp Leu Val His
 355 360 365

Phe Trp His Lys Tyr Arg Arg Ser Ala Glu Gly Ser Ala Lys Lys Gly
 370 375 380

Glu Ala Arg Arg Arg Leu Val Glu Thr Met Ala Arg Arg Ser Arg Val
 385 390 395 400

Asp Ser Ser Val Glu Leu Ile Gly Gly Leu Leu Phe Gly Ser Glu Gln
 405 410 415

Gly Ala Lys Val Leu Gly Ala Val Arg Pro Ala Gly Gln Pro Val Val
 420 425 430

Ala Asp Trp Asp Cys Leu Lys Ser Val Val Arg Arg Phe Gln Glu Arg
 435 440 445

Cys Gly Pro Leu Thr Gln Tyr Gly Met Lys His Met Arg Ser Leu Ala
 450 455 460

Asn Leu Cys Asn Ala Gly Val Arg Glu Glu Ala Met Asp Lys Ala Ala
 465 470 475 480

Ala Gln Ala Cys Ala Ala Asn Pro Ser Ser Leu Phe
 485 490

<210> 101

<211> 467

<212> PRT

<213> Brachypodium distachyon

<400> 101

Met Ala Arg Leu Ser Cys Phe Leu Leu Leu Leu Gln Ala Gln Leu Phe
 1 5 10 15

Leu Leu Val Ala Gly Glu Phe Leu Arg Leu Pro Ser Glu Gln Asp Val
 20 25 30

Ala Gly Thr Arg Trp Ala Val Leu Ile Ala Gly Ser Asn Asp Tyr Tyr
35 40 45

Asn Tyr Arg His Gln Ala Asp Val Cys His Ala Tyr Gln Ile Met Lys
50 55 60

Lys Gly Gly Leu Lys Asp Glu Asn Ile Ile Val Phe Met Tyr Asp Asp
65 70 75 80

Ile Ala Asn Asn Pro Asp Asn Pro Arg Pro Gly Val Ile Ile Asn His
85 90 95

Pro Thr Gly Gly Asp Val Tyr Ala Gly Val Pro Lys Asp Tyr Thr Gly
100 105 110

Lys Asp Val Asn Ala Asn Asn Phe Leu Ala Ala Leu Leu Gly Asp Lys
115 120 125

Ser Lys Leu Thr Gly Ser Gly Ser Gly Lys Val Val Ser Ser Gly Pro
130 135 140

Asn Asp His Ile Phe Val Tyr Tyr Ala Asp His Gly Gly Pro Gly Val
145 150 155 160

Leu Gly Met Pro Glu Asp Glu Ser Tyr Leu Tyr Ala Asn Asp Leu Val
165 170 175

Arg Ala Leu Glu Lys Lys His Ala Gly Gly Ala Gly Tyr Lys Ser Leu
180 185 190

Val Phe Tyr Leu Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu
195 200 205

Leu Pro Gly Asn Ile Ser Val Tyr Ala Thr Thr Ala Ser Asn Ala Glu
210 215 220

Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Asp Val Asp Gly Ala Pro
225 230 235 240

Pro Ala Glu Phe Asp Thr Cys Leu Gly Asp Leu Tyr Ser Val Ala Trp
245 250 255

Met Glu Asp Ser Asp Ala His Asn Leu Lys Ala Glu Ser Leu Lys Gln
260 265 270

Gln Tyr Asp Arg Val Arg Asp Arg Thr Ser Ala His Glu Thr Tyr Asn
275 280 285

Leu Gly Ser His Val Met Gln Tyr Gly Asp Leu Gly Ile Asn Ala Gln
290 295 300

Ser Leu Asp Ile Phe Ile Gly Ser Asn Pro Ala Asn Asp Lys Ser Asn
305 310 315 320

Ser Ser Val Ser Ser Leu Leu Arg Asn Ala Arg Ala Gly Val Val His
325 330 335

Gln Arg Asp Ala Asp Leu Leu His Phe Trp His Lys Tyr Lys Arg Ser
340 345 350

Ala Glu Gly Ser Ala Arg Lys His Glu Ala Arg Arg Arg Leu Val Glu
355 360 365

Met Met Ala Arg Arg Ala Arg Val Asp Gly Ser Val Glu Leu Leu Gly
370 375 380

Gly Leu Leu Phe Gly Ser Glu Glu Gly Ala Lys Val Met Asn Ala Val
385 390 395 400

Arg Pro Ala Gly Gln Ala Leu Val Asp Asp Trp Asp Cys Leu Lys Asp
405 410 415

Val Val Arg Arg Phe Glu Ala Arg Cys Gly Pro Leu Thr Gln Tyr Gly
420 425 430

Met Lys His Met Arg Ala Leu Ala Asn Val Cys Asn Ala Gly Val Gly
435 440 445

Val Glu Ala Val Asp Arg Ala Ala Ser Gln Ala Cys Ala Val His Pro
450 455 460

Ser Val Phe
465

<210> 102
<211> 493
<212> PRT
<213> Sorghum bicolor

<400> 102

Met Ala Ala Ala Ala Trp Leu Cys Gly Leu Leu Trp Leu Leu Ala His
1 5 10 15

Ala Ala Ala Val Ala Ser Ala Ala Asp Gly Ala Asp Gly Gly Trp Glu
20 25 30

Pro Leu Ile Arg Met Pro Thr Gly Lys Gly Gly Asp Ala Ala Ala Arg
35 40 45

Ala Val Glu Glu Asp Asp Glu Val Gly Thr Arg Trp Ala Val Leu Val
50 55 60

Ala Gly Ser Ser Gly Tyr Gly Asn Tyr Arg His Gln Ala Asp Val Cys
65 70 75 80

His Ala Tyr Gln Ile Leu Arg Lys Gly Gly Val Lys Glu Glu Asn Ile
85 90 95

Val Val Phe Met Tyr Asp Asp Ile Ala His Asn Ile Leu Asn Pro Arg
100 105 110

Pro Gly Val Ile Ile Asn His Pro Lys Gly Glu Asn Val Tyr Asn Gly
115 120 125

Val Pro Lys Asp Tyr Thr Gly Asp Gln Val Thr Thr Glu Asn Phe Phe
130 135 140

Ala Val Leu Leu Gly Asn Lys Ser Ala Ile Thr Gly Gly Ser Lys Lys
145 150 155 160

Val Ile Asp Ser Lys Pro Asn Asp His Ile Phe Ile Tyr Tyr Ser Asp
165 170 175

His Gly Gly Pro Gly Val Leu Gly Met Pro Asn Leu Pro Tyr Leu Tyr
180 185 190

Ala Gly Asp Phe Ile Lys Val Leu Lys Lys Lys His Ala Cys Asn Ser
195 200 205

Tyr Ser Lys Met Val Ile Tyr Val Glu Ala Cys Glu Ser Gly Ser Ile
210 215 220

Phe Glu Gly Leu Met Pro Glu Asp Leu Asn Ile Tyr Val Thr Thr Ala
225 230 235 240

Ser Asn Pro Val Glu Asn Ser Trp Gly Thr Tyr Cys Pro Gly Met Glu
245 250 255

Pro Ser Pro Pro Pro Glu Tyr Ile Thr Cys Leu Gly Asp Leu Tyr Ser
260 265 270

Val Ser Trp Met Glu Asp Ser Gln Thr His Asn Leu Lys Lys Glu Thr
275 280 285

Ile Lys Asp Gln Tyr Glu Val Val Lys Thr Arg Thr Ser Asn Ser Asn
290 295 300

Lys Tyr Lys Glu Gly Ser His Val Met Glu Tyr Gly Asp Lys Thr Phe
305 310 315 320

Lys Asp Glu Lys Leu Phe Leu Tyr Gln Gly Phe Asp Pro Ala Asn Ala
325 330 335

Asn Ile Ala Asn Met Leu Leu Trp Pro Gly Pro Lys Gly Ala Val Asn
340 345 350

Gln Arg Asp Ala Asp Leu Leu Phe Met Trp Lys Arg Tyr Glu Gln Leu
355 360 365

Asn Gly Glu Ser Val Glu Lys Leu Arg Ala Leu Ile Glu Ile Lys Glu
370 375 380

Thr Val Gln His Arg Lys His Leu Asp Ser Ser Ile Asp Phe Ile Gly

385 390 395 400

Arg Leu Leu Phe Gly Phe Glu Lys Gly Pro Ser Met Leu Glu Ala Val
405 410 415

Arg Ala Ser Gly Leu Pro Leu Val Asp Asp Trp Asp Cys Leu Lys Arg
420 425 430

Met Val Arg Ile Phe Glu Ser Gln Cys Gly Ser Leu Thr Gln Tyr Gly
435 440 445

Met Lys Tyr Met Arg Ala Phe Ala Asn Ile Cys Asn Ser Gly Ile Ser
450 455 460

Glu Met Lys Met Arg Glu Ser Ser Ile Ser Ala Cys Ser Ser Tyr Asn
465 470 475 480

Ser Ala Arg Trp Ser Pro Met Ala Gln Gly His Ser Ala
485 490

<210> 103

<211> 491

<212> PRT

<213> Triticum monococcum

<400> 103

Met Ala Pro Arg Trp Cys Phe Ala Leu Leu Leu Leu Cys Ala Ala
1 5 10 15

Ala Arg Pro Gly Ala Asp Ala Ser Lys Gly Lys Trp Asp Pro Val Ile
20 25 30

Arg Met Pro Gly Glu Glu Glu Pro Ala Thr Gly Asp Glu Ser Ser Glu
35 40 45

Glu Gly Glu Asp Gly Val Gly Thr Arg Trp Ala Val Leu Val Ala Gly
50 55 60

Ser Ser Gly Tyr Gly Asn Tyr Arg His Gln Ala Asp Ile Cys His Ala
65 70 75 80

Tyr Gln Ile Leu Arg Lys Gly Gly Val Lys Glu Glu Asn Ile Val Val
85 90 95

Phe Met Tyr Asp Asp Ile Ala Asn Asn Pro Leu Asn Pro Arg Pro Gly
100 105 110

Val Ile Ile Asn His Pro Glu Gly Glu Asp Val Tyr Ala Gly Val Pro
115 120 125

Lys Asp Tyr Thr Gly Glu Glu Val Thr Ala Lys Asn Phe Tyr Ala Val
130 135 140

Leu Leu Gly Asn Lys Thr Ala Val Thr Gly Gly Ser Lys Lys Val Ile
145 150 155 160

Asp Ser Lys Pro Asn Asp His Ile Phe Ile Tyr Tyr Ser Asp His Gly
165 170 175

Gly Pro Gly Val Leu Gly Met Pro Asn Leu Pro Tyr Leu Tyr Ala Ala
180 185 190

Asp Phe Ile Lys Val Leu Gln Glu Lys His Ala Ser Asn Thr Tyr Ala
195 200 205

Lys Met Val Ile Tyr Val Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu
210 215 220

Gly Leu Met Pro Ala Asp Leu Asn Ile Tyr Val Thr Thr Ala Ser Asn
225 230 235 240

Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Met Glu Pro Ser
245 250 255

Pro Pro Ser Glu Tyr Ile Thr Cys Leu Gly Asp Leu Tyr Ser Ile Ser
260 265 270

Trp Met Glu Asp Ser Glu Thr Asn Asn Leu Lys Glu Glu Thr Ile Lys
275 280 285

Lys Gln Tyr Glu Val Val Lys Lys Arg Thr Ser Asp Met Asn Ser Tyr
290 295 300

Ser Ala Gly Ser His Val Met Glu Tyr Gly Asp Lys Thr Phe Lys Asp
305 310 315 320

Glu Lys Leu Tyr Leu Tyr Gln Gly Phe Asn Pro Ala Asn Thr Asn Ile
325 330 335

Thr Asn Met Leu Leu Leu Gln Ala Pro Lys Ala Ala Ile Asn Gln Arg
340 345 350

Asp Ala Asp Leu Leu Phe Leu Trp Arg Arg Tyr Glu Leu Leu His Glu
355 360 365

Lys Ser Lys Glu Lys Gly Asn Val Leu Arg Glu Ile Ser Glu Thr Val
370 375 380

Thr His Arg Lys His Leu Asp Ser Ser Ile Asp Phe Ile Gly Lys Leu
385 390 395 400

Leu Phe Gly Phe Glu Asn Gly Pro Ser Val Leu Gln Ala Val Arg Pro
405 410 415

Ser Gly Lys Pro Leu Val Asp Asp Trp Asp Cys Leu Lys Arg Met Val
420 425 430

Arg Ile Phe Glu Ser His Cys Gly Ser Leu Thr Gln Tyr Gly Met Lys
435 440 445

His Met Arg Ala Phe Ala Asn Ile Cys Asn Asn Gly Ile Ser Gly Thr
450 455 460

Thr Met Lys Glu Ala Ser Ile Gly Ala Cys Gly Val Gln Asn Ser Ala
465 470 475 480

Arg Trp Ser Ser Leu Ile Gln Gly Tyr Ser Ala
485 490

<210> 104
<211> 491
<212> PRT
<213> Aegilops speltoides

<400> 104

Met Ala Pro Arg Trp Cys Phe Ala Leu Leu Leu Leu Cys Ala Ala
1 5 10 15

Ala Gly Ala Gly Ala Asp Ala Ser Lys Gly Lys Trp Asp Pro Val Ile
20 25 30

Arg Met Pro Gly Glu Glu Glu Pro Ala Thr Gly Asp Glu Ser Ser Glu
35 40 45

Glu Gly Glu Asp Gly Val Gly Thr Arg Trp Ala Val Leu Val Ala Gly
50 55 60

Ser Ser Gly Tyr Gly Asn Tyr Arg His Gln Ala Asp Ile Cys His Ala
65 70 75 80

Tyr Gln Ile Leu Arg Lys Gly Gly Val Lys Glu Glu Asn Ile Val Val
85 90 95

Phe Met Tyr Asp Asp Ile Ala Asn Asn Pro Leu Asn Pro Arg Pro Gly
100 105 110

Val Ile Ile Asn His Pro Glu Gly Glu Asp Val Tyr Ala Gly Val Pro
115 120 125

Lys Asp Tyr Thr Gly Glu Ala Val Thr Ala Lys Asn Phe Tyr Ala Val
130 135 140

Leu Leu Gly Asn Asn Thr Ala Val Thr Gly Gly Ser Lys Lys Val Ile
145 150 155 160

Asp Ser Lys Pro Asn Asp His Ile Phe Ile Tyr Tyr Ser Asp His Gly
165 170 175

Gly Pro Gly Val Leu Gly Met Pro Asn Leu Pro Tyr Leu Tyr Ala Ala
180 185 190

Asp Phe Ile Lys Val Leu Gln Glu Lys His Ala Ser Asn Thr Tyr Ala
195 200 205

Lys Met Val Ile Tyr Val Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu
210 215 220

Gly Leu Met Pro Ala Asp Leu Asn Ile Tyr Val Thr Thr Ala Ser Asn
225 230 235 240

Ala Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Met Glu Pro Ser
245 250 255

Pro Pro Ser Glu Tyr Ile Thr Cys Leu Gly Asp Leu Tyr Ser Ile Ser
260 265 270

Trp Met Glu Asp Ser Glu Thr Asn Asn Leu Lys Glu Glu Thr Ile Lys
275 280 285

Lys Gln Tyr Glu Val Val Lys Lys Arg Thr Ser Asp Met Asn Ser Tyr
290 295 300

Ser Ala Gly Ser His Val Met Glu Tyr Gly Asp Lys Thr Phe Lys Asp
305 310 315 320

Glu Lys Leu Tyr Leu Tyr Gln Gly Phe Asn Pro Ala Asn Thr Asn Ile
325 330 335

Thr Asn Lys Leu Phe Leu Gln Ala Pro Lys Ala Ala Ile Asn Gln Arg
340 345 350

Asp Ala Asp Leu Leu Phe Leu Trp Arg Arg Tyr Glu Leu Leu His Glu
355 360 365

Lys Ser Lys Glu Lys Ala Asn Val Leu Arg Glu Ile Ser Glu Thr Val
370 375 380

Ala His Arg Lys His Leu Asp Ser Ser Ile Asp Phe Ile Gly Lys Leu
385 390 395 400

Leu Phe Gly Phe Glu Asn Gly Pro Trp Glu Leu Gln Ala Val Arg Pro
405 410 415

Ser Gly Lys Pro Leu Val Asp Asp Trp Asp Cys Leu Lys Arg Met Val

420

425

430

Arg Ile Phe Glu Ser His Cys Gly Ser Leu Thr Gln Tyr Gly Met Lys
 435 440 445

His Met Arg Ala Phe Ala Asn Ile Cys Asn Asn Gly Val Ser Gly Thr
 450 455 460

Thr Met Asn Glu Ala Ser Ile Gly Ala Cys Gly Val Gln Asn Ser Ala
 465 470 475 480

Arg Trp Ser Thr Leu Ile Gln Gly Tyr Ser Ala
 485 490

<210> 105

<211> 489

<212> PRT

<213> Aegilops tauschii

<400> 105

Met Ala Pro Arg Trp Cys Phe Ala Leu Leu Leu Leu Cys Ala Ala
 1 5 10 15

Ala Gly Ala Asp Ala Ser Lys Gly Lys Trp Asp Pro Val Ile Arg Met
 20 25 30

Pro Gly Glu Glu Glu Pro Ala Thr Gly Asp Asp Ser Ser Glu Glu Gly
 35 40 45

Glu Asp Gly Val Gly Thr Arg Trp Ala Val Leu Val Ala Gly Ser Ser
 50 55 60

Gly Tyr Gly Asn Tyr Arg His Gln Ala Asp Ile Cys His Ala Tyr Gln
 65 70 75 80

Ile Leu Arg Lys Gly Gly Val Lys Glu Glu Asn Ile Val Val Phe Met
 85 90 95

Tyr Asp Asp Ile Ala Asn Asn Pro Leu Asn Pro Arg Pro Gly Val Ile
 100 105 110

Ile Asn His Pro Glu Gly Glu Asp Val Tyr Ala Gly Val Pro Lys Asp
115 120 125

Tyr Thr Gly Glu Ala Val Thr Ala Lys Asn Phe Tyr Ala Val Leu Leu
130 135 140

Gly Asn Lys Thr Ala Val Thr Gly Gly Ser Lys Lys Val Ile Asp Ser
145 150 155 160

Lys Pro Asn Asp His Ile Phe Ile Tyr Tyr Ser Asp His Gly Gly Pro
165 170 175

Gly Val Leu Gly Met Pro Asn Leu Pro Tyr Leu Tyr Ala Ala Asp Phe
180 185 190

Ile Lys Val Leu Gln Glu Lys His Ala Ser Asn Thr Tyr Ala Lys Met
195 200 205

Val Ile Tyr Val Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly Leu
210 215 220

Met Pro Ala Asp Leu Asn Ile Tyr Val Thr Thr Ala Ser Asn Ala Glu
225 230 235 240

Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Met Glu Pro Ser Pro Pro
245 250 255

Ser Glu Tyr Ile Thr Cys Leu Gly Asp Leu Tyr Ser Ile Ser Trp Met
260 265 270

Glu Asp Ser Glu Thr Asn Asn Leu Lys Glu Glu Thr Ile Lys Lys Gln
275 280 285

Tyr Glu Val Val Lys Lys Arg Thr Ser Asp Met Asn Ser Tyr Ser Ala
290 295 300

Gly Ser His Val Met Glu Tyr Gly Asp Met Thr Phe Lys Asp Glu Lys
305 310 315 320

Leu Tyr Leu Tyr Gln Gly Phe Asn Pro Ala Asn Thr Asn Ile Thr Asn
325 330 335

Lys Leu Phe Leu Gln Ala Pro Lys Ala Ala Ile Asn Gln Arg Asp Ala
340 345 350

Asp Leu Leu Phe Leu Trp Arg Arg Tyr Glu Leu Leu His Gly Lys Ser
355 360 365

Lys Glu Lys Ala Asn Val Leu Thr Glu Ile Gly Glu Thr Val Ala His
370 375 380

Arg Lys His Leu Asp Asn Ser Ile Asp Phe Ile Gly Lys Leu Leu Phe
385 390 395 400

Gly Phe Glu Asn Gly Pro Ser Glu Leu Gln Ala Val Arg Pro Ser Gly
405 410 415

Lys Pro Leu Val Asp Asp Trp Asp Cys Leu Lys Arg Met Val Arg Ile
420 425 430

Phe Glu Ser His Cys Gly Ser Leu Thr Gln Tyr Gly Met Lys His Met
435 440 445

Arg Ala Phe Ala Asn Ile Cys Asn Asn Gly Val Ser Gly Thr Thr Met
450 455 460

Lys Glu Ala Ser Ile Asn Thr Cys Gly Gly His Asn Ser Ala Arg Leu
465 470 475 480

Ser Thr Leu Ile Gln Gly Tyr Ser Ala
485

<210> 106
<211> 460
<212> PRT
<213> Solanum tuberosum

<400> 106

Met Ile Phe Lys Tyr Asn Val Phe Val Ala Leu Val Val Val Leu Ser
1 5 10 15

Ile Trp Asp Asn Ile Glu Gly Arg Ser Val Ser Lys Phe Leu Thr Glu

20

25

30

Glu Thr Val Gly Thr Lys Trp Ala Val Leu Val Ala Gly Ser Asn Gly
 35 40 45

Trp Phe Asn Tyr Arg His Gln Ala Asp Val Cys His Ala Tyr Gln Ile
 50 55 60

Leu Lys Lys Gly Gly Leu Lys Asp Glu Asn Ile Ile Val Phe Met Tyr
 65 70 75 80

Asp Asp Ile Ala Asn Asn Thr Met Asn Pro Arg Pro Gly Val Ile Ile
 85 90 95

Asn Asn Pro His Gly Gln Asp Val Tyr Lys Gly Val Pro Lys Asp Tyr
 100 105 110

Val Gly Glu Asp Val Asn Ala Glu Asn Phe Phe Asn Val Ile Leu Ala
 115 120 125

Asn Lys Ser Gly Ile Thr Gly Gly Ser Gly Lys Val Leu Asn Ser Gly
 130 135 140

Pro Asn Asp His Ile Phe Ile Tyr Tyr Thr Asp His Gly Gly Pro Gly
 145 150 155 160

Ile Ile Ser Met Pro Thr Gly Leu Val Tyr Ala Asn Asp Leu Ile Asn
 165 170 175

Val Leu Lys Lys Lys His Ala Ser Gly Thr Tyr Ser Lys Leu Val Phe
 180 185 190

Tyr Leu Glu Ala Cys Glu Ser Gly Ser Met Phe Asp Gly Leu Leu Pro
 195 200 205

Glu Gly Leu Asn Ile Tyr Val Thr Thr Ala Ser Asn Pro Asn Glu Ser
 210 215 220

Ser Trp Gly Thr Tyr Cys Gln Met Gly Ala Gly Gly Pro Cys Leu Val
 225 230 235 240

Glu Cys Pro Pro Pro Glu Phe Gln Gly Val Cys Leu Gly Asp Leu Tyr
245 250 255

Ser Val Ala Trp Met Glu Asp Ser Glu Ala Glu Asp Arg Gln Thr Glu
260 265 270

Thr Leu Asn Asp Gln Tyr Asn Thr Val Ala Asn Arg Thr Ala Ala Asn
275 280 285

Leu Thr Tyr Gly Ser His Val Met Gln Tyr Gly Asp Thr Val Leu Ser
290 295 300

Val Asp Val Leu Phe Gln Tyr Met Gly Ala Ala Ser Val Asn His Ser
305 310 315 320

His Val Ser Met Asn Ser Glu Ser Ser Ser Gln Asn Val Asp Gln Arg
325 330 335

Asp Val Glu Leu Phe Tyr Leu Thr Ser Lys Tyr Gln Asp Ala Pro Glu
340 345 350

Gly Ser Asp Glu His Phe Glu Thr Arg Val Lys Leu Ile Lys Thr Ile
355 360 365

Ala Glu Arg Ser Gln Val Asp Asn Ser Val Lys His Ile Gly Asp Leu
370 375 380

Leu Phe Gly Val Glu Lys Gly Ser Glu Val Leu Gln His Val Arg Pro
385 390 395 400

Ala Gly Gln Pro Leu Val Asp Asn Trp Asp Cys Leu Lys Ser Tyr Ile
405 410 415

Glu Thr Phe Glu Val His Cys Gly Lys Leu Ser Ser Tyr Gly Lys Lys
420 425 430

His Ile Arg Gly Ile Ala Asn Ile Cys Asn Ala Gly Ile Lys Ser Glu
435 440 445

Gln Met Ala Ser Ala Thr Ala Gln Ala Cys Ser Ser

450

455

460

<210> 107

<211> 490

<212> PRT

<213> Brachypodium distachyon

<400> 107

Met Ala Ala Trp Trp Cys Phe Ala Leu Leu Leu Val Leu Cys Ala Pro
 1 5 10 15

Ala Gly Ala Asp Val Ser Lys Gly Lys Trp Glu Pro Leu Ile Arg Met
 20 25 30

Pro Gly Glu Lys Glu Pro Ala Thr Ala Arg Gly Phe Glu Gly Pro Glu
 35 40 45

Glu Glu Asp Gly Val Gly Thr Arg Trp Ala Val Leu Ile Ala Gly Ser
 50 55 60

Ser Gly Tyr Gly Asn Tyr Arg His Gln Ala Asp Ile Cys His Ala Tyr
 65 70 75 80

Gln Val Leu Arg Lys Gly Gly Leu Lys Glu Glu Asn Ile Val Val Phe
 85 90 95

Met Tyr Asp Asp Ile Ala Asn Ser Ala Leu Asn Pro Arg Pro Gly Val
 100 105 110

Ile Ile Asn His Pro Gln Gly Glu Asp Val Tyr Ala Gly Val Pro Lys
 115 120 125

Asp Tyr Thr Gly Glu Gln Val Thr Ala Lys Asn Leu Tyr Ala Val Leu
 130 135 140

Leu Gly Asn Lys Thr Ala Val Thr Gly Gly Ser Lys Lys Val Ile Asp
 145 150 155 160

Ser Gln Pro Lys Asp His Ile Phe Ile Tyr Tyr Ser Asp His Gly Gly
 165 170 175

Pro Gly Val Leu Gly Met Pro Asn Leu Pro Tyr Leu Tyr Ala Gly Asp
180 185 190

Phe Ile Lys Ile Leu Gln Gln Lys His Ala Ser Asn Thr Tyr Ala Lys
195 200 205

Met Val Ile Tyr Val Glu Ala Cys Glu Ser Gly Ser Ile Phe Glu Gly
210 215 220

Leu Met Pro Ala Asp Leu Asn Ile Tyr Val Thr Thr Ala Ser Asn Ala
225 230 235 240

Glu Glu Ser Ser Trp Gly Thr Tyr Cys Pro Gly Met Glu Pro Ser Pro
245 250 255

Pro Ser Glu Tyr Ile Thr Cys Leu Gly Asp Leu Tyr Ser Val Ser Trp
260 265 270

Met Glu Asp Ser Glu Asn His Asn Leu Lys Glu Glu Thr Ile Lys Lys
275 280 285

Gln Tyr Glu Val Val Lys Arg Arg Thr Ser Asp Leu Asn Ser Tyr Ser
290 295 300

Ala Gly Ser His Val Met Glu Tyr Gly Asp Lys Thr Phe Lys Asp Glu
305 310 315 320

Lys Leu Tyr Leu Tyr Gln Gly Phe Asn Pro Ala Asn Ala Asn Ile Thr
325 330 335

Asn Lys Leu Phe Trp Gln Ala Pro Arg Ala Ala Ile Asn Gln Arg Asp
340 345 350

Ala Asp Leu Leu Phe Leu Trp Arg Arg Tyr Glu Met Leu His Glu Lys
355 360 365

Ser Lys Glu Lys Val Lys Val Leu Arg Glu Ile Ser Glu Thr Val Met
370 375 380

His Arg Lys His Leu Asp Asn Ser Val Asp Leu Ile Gly Gln Leu Leu
385 390 395 400

Phe Gly Phe Glu Asn Gly Pro Ser Val Leu Gln Ala Val Arg Pro Ser
405 410 415

Gly Lys Pro Leu Val Asp Asp Trp Asp Cys Leu Lys Arg Met Val Arg
420 425 430

Ile Phe Glu Ser His Cys Gly Pro Leu Thr Gln Tyr Gly Met Lys His
435 440 445

Met Arg Ala Phe Ala Asn Ile Cys Asn Asn Gly Ile Pro Gly Ser Thr
450 455 460

Met Lys Glu Gly Ser Ile Ser Ala Cys Gly Ser Arg Asn Ile Ala Arg
465 470 475 480

Trp Ser Pro Leu Ile Gln Gly Tyr Ser Ala
485 490

<210> 108
<211> 493
<212> PRT
<213> Zea mays

<400> 108

Met Met Ala Ala Ala Ala Trp Leu Cys Gly Leu Leu Ser Leu Leu Ala
1 5 10 15

Leu Ala Gly Ala Ala Ser Ala Ala Asp Gly Ala Glu Gly Glu Trp Glu
20 25 30

Pro Leu Ile Arg Met Pro Thr Ala Lys Gly Ser Asp Ala Ala Ser Ala
35 40 45

Pro Ala Ala Glu Asp Asp Glu Val Gly Thr Arg Trp Ala Val Leu Val
50 55 60

Ala Gly Ser Phe Gly Tyr Gly Asn Tyr Arg His Gln Ala Asp Val Cys
65 70 75 80

His Ala Tyr Gln Ile Leu Gln Lys Gly Gly Val Lys Lys Glu Asn Ile

85

90

95

Val Val Phe Met Tyr Asp Asp Ile Ala His Asn Ile Leu Asn Pro Arg
 100 105 110

Pro Gly Val Ile Ile Asn His Pro Lys Gly Ala Asn Val Tyr Asp Gly
 115 120 125

Val Pro Lys Asp Tyr Thr Gly Asp Gln Val Thr Thr Glu Asn Phe Phe
 130 135 140

Ala Val Leu Leu Gly Asn Arg Ser Ala Thr Thr Gly Gly Ser Lys Lys
 145 150 155 160

Val Ile Asp Ser Lys Pro Asn Asp His Ile Phe Ile Tyr Tyr Ser Asp
 165 170 175

His Gly Gly Pro Gly Val Leu Gly Met Pro Asn Leu Pro Tyr Leu Tyr
 180 185 190

Ala Gly Asp Phe Ile Lys Val Leu Lys Lys Lys His Ala Ser Asn Ser
 195 200 205

Tyr Ser Lys Met Val Ile Tyr Val Glu Ala Cys Glu Ser Gly Ser Ile
 210 215 220

Phe Glu Gly Leu Met Pro Glu Asp Leu Asn Ile Tyr Val Thr Thr Ala
 225 230 235 240

Ser Asn Pro Val Glu Asn Ser Trp Gly Thr Tyr Cys Pro Gly Met Glu
 245 250 255

Pro Ser Pro Pro Pro Glu Tyr Ile Thr Cys Leu Gly Asp Leu Tyr Ser
 260 265 270

Val Ser Trp Met Glu Asp Ser Glu Thr His Asn Leu Lys Lys Glu Thr
 275 280 285

Ile Lys Asp Gln Tyr Glu Val Val Lys Thr Arg Thr Ser Asn Ser Asn
 290 295 300

Lys Tyr Lys Glu Gly Ser His Val Met Glu Tyr Gly Asp Lys Thr Phe
305 310 315 320

Lys Asp Glu Lys Leu Ser Phe Tyr Gln Gly Phe Asp Pro Ala Asn Ala
325 330 335

Asn Ile Ala Asn Met Leu Leu Trp Pro Gly Pro Lys Gly Ala Val Asn
340 345 350

Gln Arg Asp Ala Asp Leu Leu Phe Met Trp Lys Arg Tyr Glu Gln Leu
355 360 365

Asn Gly Gly Thr Glu Glu Lys Leu Arg Ala Leu Ile Glu Ile Lys Glu
370 375 380

Thr Val Gln His Arg Lys His Leu Asp Ser Ser Ile Asp Phe Val Gly
385 390 395 400

Arg Leu Val Phe Gly Phe Glu Lys Gly Pro Ser Met Leu Glu Ala Val
405 410 415

Arg Thr Ser Gly Gln Pro Leu Val Asp Asp Trp Asp Cys Leu Lys Arg
420 425 430

Met Val Arg Ile Phe Glu Ser Gln Cys Gly Ser Leu Thr Gln Tyr Gly
435 440 445

Met Lys Tyr Met Arg Ala Phe Ala Asn Ile Cys Asn Ser Gly Ile Ser
450 455 460

Glu Met Lys Met Arg Glu Ser Ser Ile Ser Ala Cys Ser Ser Tyr Asn
465 470 475 480

Ser Ala Arg Trp Ser Pro Met Ala Arg Gly His Ser Ala
485 490

<210> 109
<211> 492
<212> PRT
<213> *Setaria italica*

<400> 109

Met Ala Ala Ala Ala Trp Leu Cys Gly Leu Leu Ser Leu Leu Ala Val
1 5 10 15

Ala Ala Ala Ala Ser Val Asp Gly Ala Glu Glu Glu Trp Glu Pro Leu
20 25 30

Ile Arg Met Pro Thr Glu Lys Gly Gly Asn Ala Ala Ala Ala Pro
35 40 45

Ala Ala Glu Glu Asp Glu Val Gly Thr Arg Trp Ala Val Leu Val Ala
50 55 60

Gly Ser Ser Gly Tyr Gly Asn Tyr Arg His Gln Ala Asp Val Cys His
65 70 75 80

Ala Tyr Gln Ile Leu Leu Lys Gly Gly Val Lys Glu Glu Asn Ile Val
85 90 95

Val Phe Met Tyr Asp Asp Ile Ala His Asn Ile Leu Asn Pro Arg Pro
100 105 110

Gly Val Ile Ile Asn His Pro Lys Gly Glu Asn Val Tyr Pro Gly Val
115 120 125

Pro Lys Asp Tyr Thr Gly Asp Gln Val Thr Thr Glu Asn Phe Phe Ala
130 135 140

Val Leu Leu Gly Asn Arg Ser Ala Ile Thr Gly Gly Ser Lys Lys Val
145 150 155 160

Ile Asp Ser Lys Pro Asn Asp His Ile Phe Ile Tyr Tyr Ser Asp His
165 170 175

Gly Gly Pro Gly Val Leu Gly Met Pro Asn Leu Pro Tyr Leu Tyr Ala
180 185 190

Gly Asp Phe Ile Lys Val Leu Lys Lys Lys His Ala Ser Asn Ser Tyr
195 200 205

Ser Lys Met Val Ile Tyr Val Glu Ala Cys Glu Ser Gly Ser Ile Phe
210 215 220

Glu Gly Leu Met Pro Gln Asp Leu Asn Ile Tyr Val Thr Thr Ala Ser
225 230 235 240

Asn Pro Val Glu Asn Ser Trp Gly Thr Tyr Cys Pro Gly Met Asp Pro
245 250 255

Ser Pro Pro Pro Glu Tyr Ile Thr Cys Leu Gly Asp Leu Tyr Ser Val
260 265 270

Ser Trp Met Glu Asp Ser Gln Thr His Asn Leu Met Lys Glu Thr Ile
275 280 285

Lys Asp Gln Tyr Glu Val Val Lys Thr Arg Thr Ser Asn Leu Lys Lys
290 295 300

Tyr Lys Glu Gly Ser His Val Met Glu Tyr Gly Asp Lys Thr Phe Thr
305 310 315 320

Asn Glu Lys Leu Phe Leu Tyr Gln Gly Phe Asp Pro Ala Asn Ala Asn
325 330 335

Ala Ala Asn Thr Leu Leu Trp Pro Gly Pro Lys Gly Ala Val Asn Gln
340 345 350

Arg Asp Ala Asp Leu Leu Phe Met Trp Lys Arg Tyr Glu Gln Leu Asp
355 360 365

Gly Gly Ser Glu Glu Lys Leu Arg Ala Leu Arg Glu Ile Lys Glu Thr
370 375 380

Val Gln His Arg Lys His Leu Asp Ser Ser Ile Asp Phe Ile Gly Arg
385 390 395 400

Leu Val Phe Gly Phe Glu Asn Gly Pro Lys Met Leu Glu Ala Val Arg
405 410 415

Ala Ser Gly Gln Pro Leu Val Asp Asp Trp Asp Cys Leu Lys Arg Met
420 425 430

Val Arg Ile Phe Glu Ala Gln Cys Gly Ser Leu Thr Gln Tyr Gly Met
435 440 445

Lys Tyr Met Arg Ala Phe Ala Asn Ile Cys Asn Ser Gly Ile Ser Glu
450 455 460

Ala Lys Met Arg Glu Ser Ser Ile Ser Ala Cys Gly Gly Tyr Asn Ser
465 470 475 480

Ala Arg Trp Ser Pro Met Ala Gln Gly His Ser Ala
485 490

<210> 110
<211> 5
<212> PRT
<213> artificial construct

<220>
<223> synthesized peptide

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa is Gly with -NH- being replaced by -S-.

<400> 110

Tyr Lys Asn Xaa Val
1 5

<210> 111
<211> 5
<212> PRT
<213> artificial construct

<220>
<223> synthesized peptide

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa is Gly with -NH- being replaced by -O-.

<400> 111

Tyr Lys Asn Xaa Val
1 5

<210> 112
<211> 5
<212> PRT
<213> artificial construct

<220>
<223> synthesized peptide

<400> 112

Tyr Lys Asn His Val
1 5

<210> 113
<211> 5
<212> PRT
<213> artificial construct

<220>
<223> synthetic peptide

<400> 113

Tyr Lys Asn Gly Val
1 5

<210> 114
<211> 6
<212> PRT
<213> artificial construct

<220>
<223> synthesized peptide

<400> 114

Gly Ile Gly Gly Ile Arg
1 5

<210> 115
<211> 5
<212> PRT
<213> artificial construct

<220>
<223> synthesized peptide

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is Gly with -NH2 being replaced by -OH

<400> 115

Xaa Val Tyr Lys Val
1 5

<210> 116
<211> 14
<212> PRT
<213> artificial construct

<220>
<223> synthetic peptide

<400> 116

Glu Arg Leu Tyr Arg Gly Arg Leu Tyr Arg Arg Asn His Val
1 5 10

<210> 117
<211> 6
<212> PRT
<213> artificial construct

<220>
<223> synthetic peptide

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is Thr conjugated to biotin.

<220>
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<222> (5)..(5)
<223> Xaa is Gly with -NH- being replaced by -O-.

<400> 117

Xaa Tyr Lys Asn Xaa Val
1 5

<210> 118
<211> 7
<212> PRT

<213> artificial construct

<220>

<223> synthetic peptide

<220>

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<222> (1)..(1)

<223> Xaa ia acetyl Arg.

<220>

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<222> (6)..(6)

<223> Xaa ia Gly with -NH- being replaced by -S-.

<400> 118

Xaa Tyr Arg Leu Asn Xaa Val
1 5

<210> 119

<211> 7

<212> PRT

<213> artificial construct

<220>

<223> synthetic peptide

<400> 119

Arg Tyr Arg Leu Asn His Val
1 5

<210> 120

<211> 7

<212> PRT

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<220>

<223> synthetic peptide

<220>

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<222> (1)..(1)

<223> Xaa is acetyl Arg.

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> Xaa is Gly with -NH- being replaced by -S-.

<400> 120

Xaa Leu Tyr Arg Asn Xaa Val
1 5

<210> 121

<211> 4

<212> PRT

<213> artificial construct

<220>

<223> synthetic peptide

<400> 121

Arg Leu Tyr Arg
1

<210> 122

<211> 85

<212> PRT

<213> artificial construct

<220>

<223> artificial construct

<400> 122

Met Gly Ile Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile
1 5 10 15

Thr Leu Glu Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys
20 25 30

Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe
35 40 45

Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile
50 55 60

Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly His
65 70 75 80

His His His His His
85

<210> 123
<211> 260
<212> PRT
<213> artificial construct

<220>
<223> artificial construct

<400> 123

Met Ile His His His His His Ser Gly Val Asp Leu Gly Thr Glu
1 5 10 15

Asn Leu Tyr Phe Gln Ser Met Ser Lys Gly Glu Glu Leu Phe Thr Gly
20 25 30

Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys
35 40 45

Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu
50 55 60

Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro
65 70 75 80

Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr
85 90 95

Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu
100 105 110

Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr
115 120 125

Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg
130 135 140

Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly
145 150 155 160

His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala
165 170 175

Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn
180 185 190

Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr
195 200 205

Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser
210 215 220

Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met
225 230 235 240

Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp
245 250 255

Glu Leu Tyr Lys
260

<210> 124
<211> 89
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<213> artificial construct

<220>
<223> artificial construct

<400> 124

Met Gly Ile Ser Gly Ser Gly Ser Gln Ile Phe Val Lys Thr Leu Thr
1 5 10 15

Gly Lys Thr Ile Thr Leu Glu Val Glu Pro Ser Asp Thr Ile Glu Asn
20 25 30

Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln
35 40 45

Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ser
50 55 60

Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu
65 70 75 80

Arg Gly Gly His His His His His His
85

<210> 125
<211> 8
<212> PRT
<213> artificial construct

<220>
<223> synthetic peptide

<400> 125

Lys Ala Leu Val Ile Asn His Val
1 5

<210> 126
<211> 5
<212> PRT
<213> artificial construct

<220>
<223> synthesized peptide

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa is thio- or glycolic acid, His and Gly, respectively.

<400> 126

Tyr Lys Asn Xaa Val
1 5

<210> 127
<211> 9
<212> PRT
<213> artificial construct

<220>
<223> synthesized peptide

<400> 127

Tyr Lys Asn Gly Ile Gly Gly Ile Arg
1 5

<210> 128

<211> 6
<212> PRT
<213> artificial construct

<220>
<223> synthesized peptide

<400> 128

Leu Pro Glu Thr Gly Gly
1 5

<210> 129
<211> 7
<212> PRT
<213> artificial construct

<220>
<223> synthesized peptide

<400> 129

Gly Ile Ser Gly Ser Gly Ser
1 5

<210> 130
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<400> 130

Gly Gly Ser Gly Ser Gly Ser
1 5

<210> 131
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<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is Acetyl Arg

<220>
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<222> (8)..(8)
<223> Xaa is beta-Ala

<400> 131

Xaa Leu Tyr Arg Asn Arg Ile Xaa
1 5

<210> 132
<211> 14
<212> PRT
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<220>
<223> synthesized peptide

<400> 132

Trp Arg Leu Tyr Arg Gly Arg Leu Tyr Arg Arg Asn His Val
1 5 10

<210> 133
<211> 12
<212> PRT
<213> artificial construct

<220>
<223> synthesized peptide

<400> 133

Trp Arg Leu Tyr Arg Gly Arg Leu Tyr Arg Arg Asn
1 5 10

<210> 134
<211> 12
<212> PRT
<213> artificial construct

<220>
<223> synthesized peptide

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is W which also forms a peptide bond with N at position 12

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Xaa is N which also forms a peptide bond with W at position 1

<400> 134

Xaa Arg Leu Tyr Arg Gly Arg Leu Tyr Arg Arg Xaa
1 5 10

<210> 135
<211> 12
<212> PRT
<213> artificial construct

<220>
<223> synthesized peptide

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Xaa is ASN-OCH₂(OH)CH₂OH

<400> 135

Trp Arg Leu Tyr Arg Gly Arg Leu Tyr Arg Arg Xaa
1 5 10

<210> 136
<211> 7
<212> PRT
<213> artificial construct

<220>
<223> synthesized peptide

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa ia Gly with -NH- being replaced by -S-.

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is amidated Val.

<400> 136

Arg Tyr Arg Leu Asn Xaa Xaa
1 5

<210> 137
<211> 7
<212> PRT
<213> artificial construct

<220>
<223> synthesized peptide

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is acetyl Arg.

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is Gly with -NH- being replaced by -S-.

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is amidated Val.

<400> 137

Xaa Tyr Arg Leu Asn Xaa Xaa
1 5

<210> 138
<211> 7
<212> PRT
<213> artificial construct

<220>
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<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is acetyl Arg.

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is Gly with its -NH- being replaced with -S-.

<220>
<221> MISC_FEATURE
<222> (7)..(7)

<223> Xaa is amidated Val.

<400> 138

Xaa Leu Tyr Arg Asn Xaa Xaa
1 5

<210> 139

<211> 4

<212> PRT

<213> artificial construct

<220>

<223> synthesized peptide

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Xaa is amidated Arg.

<400> 139

Arg Leu Tyr Xaa
1

<210> 140

<211> 7

<212> PRT

<213> artificial construct

<220>

<223> synthesized peptide

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> Xaa is amidated Val.

<400> 140

Arg Tyr Arg Leu Asn His Xaa
1 5

<210> 141

<211> 16

<212> PRT

<213> artificial construct

<220>

<223> synthesized peptide

<400> 141

Gly	Arg	Cys	Thr	Lys	Ile	Ser	Pro	Pro	Ile	Cys	Phe	Pro	Asn	His	Val
1				5					10					15	

<210> 142

<211> 7

<212> PRT

<213> artificial construct

<220>

<223> synthesized peptide

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> Xaa is Gly with its -NH- being replaced by -S-.

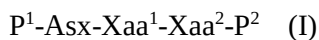
<400> 142

Arg	Tyr	Arg	Leu	Asn	Xaa	Val
1				5		

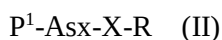
5 CLAIMS

What is claimed is:

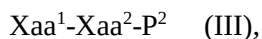
1. Method of forming a peptide of Formula (I)



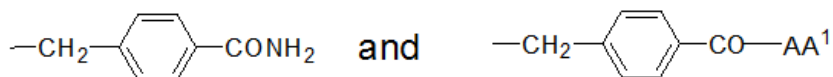
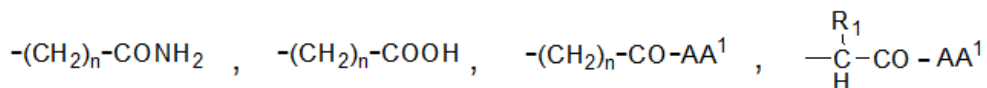
by ligating a first peptide of Formula (II)



to a second peptide of Formula (III)



wherein P^1 and P^2 are each independently any peptide, modified or unmodified; Asx is Asp or Asn, preferably Asn; X is O or S, preferably S; R is a substituted or unsubstituted alkyl, preferably selected from the group consisting of



wherein n is an integer of 1 to 10, R_1 is H, or any other side chain of a naturally occurring amino acid, and AA^1 is any amino acid or is absent; Xaa^1 is any naturally occurring amino acid with the exception of Pro; Xaa^2 is any naturally occurring amino acid, but preferably is a hydrophobic amino acid or Cys, more preferably Val, Ile, Leu, or Cys,

by enzymatically cleaving the bond between “Asx” and “X” in the first peptide of Formula (II) and ligating the fragment $P^1\text{-Asx}$ of the first peptide to the second peptide of Formula (III) to form a ligated peptide of Formula (I), wherein the enzymatic cleavage and ligation reaction is catalyzed by a polypeptide having the activity of butelase 1 (SEQ ID NO:1) under conditions allowing said ligation.

- 5 2. The method according to claim 1, wherein Asx is Asn, X is S, R is -CH(R₁)-CO-AA¹,
R₁ is H, and AA¹ is any amino acid or absent.
3. The method according to claim 1 or 2, wherein Asx is Asn, X is S, R is -CH(R₁)-CO-
AA¹, R₁ is H, and AA¹ is Val.
- 10 4. The method according to any one of claims 1-3, wherein the polypeptide having the
ligase activity of butelase 1 (SEQ ID NO:1) comprises or consists of:
(a) the amino acid sequence as set forth in SEQ ID NO:1 (butelase 1);
(b) an amino acid sequence that shares at least 60, preferably at least 70, even more
15 preferably at least 80, most preferably at least 90 % sequence identity with the
amino acid sequence as set forth in SEQ ID NO:1; or
(c) an amino acid sequence that shares at least 80, preferably at least 90, more
preferably at least 95 % sequence homology with the amino acid sequence as set
forth in SEQ ID NO:1; or
20 (d) a fragment of any one of (a)-(c).
5. The method according to any one of claims 1-4, wherein the polypeptide having the
ligase activity of butelase 1 (SEQ ID NO:1) comprises or consists of the amino acid
sequence as set forth in SEQ ID NO:2.
- 25 6. The method according to any one of claims 1-5, wherein the polypeptide having the
ligase activity of butelase 1 (SEQ ID NO:1) comprises
(a) the amino acid residue Asn at the position corresponding to position 19 of SEQ ID
NO:1; and/or
30 (b) the amino acid residue His at the position corresponding to position 124 of SEQ ID
NO:1; and/or
(c) the amino acid residue Cys at the position corresponding to position 166 of SEQ ID
NO:1.
- 35 7. The method according to any one of claims 1-6, wherein the polypeptide having the
ligase activity of butelase 1 (SEQ ID NO:1) is the polypeptide of any one of claims 4-6
or comprises or consists of

- 5 (a) any one of the amino acid sequences as set forth in SEQ ID Nos:3-109;
(b) an amino acid sequence that shares at least 60, preferably at least 70, more preferably at least 80, most preferably at least 90 % sequence identity with any one of the amino acid sequences of (a) over its entire length;
(c) an amino acid sequence that shares at least 80, preferably at least 90, more
10 preferably at least 95 % sequence homology with any one of the amino acid sequences of (a) over its entire length; or
(d) a fragment of any one of (a)-(c).
8. The method according to any one of claims 1-7, wherein P¹ or P² is modified by an
15 affinity tag, a detectable label, a solid support material, or a scaffold molecule.
9. The method according to any one of claims 1-8, wherein P¹ or P² is modified by a biotin, a fluorescent marker, a polymer resin, or a dendrimer.
- 20 10. The method according to any one of claims 1-9, wherein P¹ or P² is modified by a dendrimer.
11. The method according to claim 10, wherein each dendrimer is conjugated to 2 or more copies of the second peptide via P², such that the ligation of the first peptide and the
25 second peptide results in a dendrimeric peptide assembly comprising 2 or more copies of the ligated peptide P¹-Asx-Xaa¹-Xaa²-P².
12. The method according to any one of claims 9-11, wherein the dendrimer is a lysyl dendrimer.
- 30 13. The method according to any one of claims 1-12, wherein the first peptide is P¹-Asn-thioglc-Val, and P¹ is an antimicrobial peptide.
14. The method according to claim 13, wherein P¹ is an antimicrobial peptide comprising a
35 BHHB tetrapeptide motif.
15. The method according to claim 14, wherein P¹ is an antimicrobial peptide comprising an Arg-Leu-Tyr-Arg (SEQ ID NO:121) tetrapeptide.

- 5 16. The method according to claim 15, wherein the first peptide is Ac-Arg-Leu-Tyr-Arg-Asn-thioglc-Val (SEQ ID NO:120).
17. The method according to any one of claims 1-16, wherein the second peptide is Arg-Ile-βAla conjugated to a lysyl dendrimer via βAla.
- 10 18. The method according to any one of claims 12-17, wherein the first peptide is Ac-Arg-Leu-Tyr-Arg-Asn-thioglc-Val (SEQ ID NO:120), and each lysyl dendrimer is conjugated to 2 or more copies of the second peptide Arg-Ile-βAla via βAla, such that the ligation of the first peptide and the second peptide results in a dendrimeric peptide assembly comprising 2 or more copies of Ac-Arg-Leu-Tyr-Arg-Asn-Arg-Ile-βAla (SEQ ID NO:131).
- 15