CLAIMS:

1. A method for producing; (a) a cyclic peptide; (b) a peptide conjugate; or (c) enzymatic transpeptidation involving cleavage of an amide bond, wherein: (i) said cyclic peptide is generated by a method comprising generating a recombinant asparaginyl endopeptidase (AEP) vacuolar processing enzyme with peptide cyclization activity in a prokaryotic or eukaryotic cell and co-incubating the AEP with a linear polypeptide precursor of the cyclic peptide wherein the polypeptide precursor comprises N-terminal and/or C-terminal AEP processing site(s) for a time and under conditions sufficient to generate the cyclic peptide:(ii said peptide conjugate is generated by a method comprising co-incubating at least two peptides wherein at least one peptide comprises a C-terminal AEP recognition amino acid sequence and at least one other peptide comprises an N-terminal AEP recognition amino acid sequence with an AEP for a time and under conditions sufficient to generate a linear peptide conjugate; (iii) said enzymatic transpeptidation comprises co-incubating a polypeptide precursor with an AEP wherein the amide bond cleavage is coupled to formation of a new amide bond wherein C- and N-terminal of the polypeptide precursor are enzymatically ligated to produce a circular peptide or wherein the C- and N-terminal of at least two separate polypeptides are ligated to produce a new linear polypeptide.

2. The method of Claim 1 comprising introducing into the cell genetic material which, when expressed, generates the linear polypeptide precursor wherein the cell is incubated for a time and under conditions sufficient to generate a cyclic peptide or peptide conjugate *in vivo* and then isolating the peptide.

3. The method of Claim 1 wherein the recombinant AEP is co-incubated with a linear polypeptide precursor or a post-translationally or synthetically modified form thereof *in vitro* in a reaction vessel for a time and under conditions sufficient to generate the cyclic peptide or peptide conjugate.

4. The method of Claim 1 comprising introducing an expression vector into a prokaryotic or eukaryotic cell encoding the linear polypeptide precursor, enabling expression of the vector

to produce a recombinant linear polypeptide precursor and isolating the polypeptide from the cell and co-incubating in a reaction vessel the polypeptide precursor with the AEP for a time and under conditions sufficient to generate the cyclic peptide or peptide conjugate.

5. The method of Claim 1 wherein the polypeptide precursor is in the form of multiple repeats of the peptide to be cyclized or conjugated or is in the form of multiple different polypeptides to be cyclized or conjugated.

6. A method of Claim 1 wherein the AEP comprises an amino acid sequence having at least 80% similarity to any one or more of SEQ ID NOs:1, 2 and/or 4 after optimal alignment and the presence of 5 or more of residues or absence of residues at 139K, 161D, 186K, 192D, 247C, 248Y, 253Q, 255A, 263V, 293H, Gap, Gap, Gap, Gap, Gap (between residues 299 and 300), 314E and 316G wherein Gap means the absence of a residue.

7. The method of Claim 1 comprising introducing one or more expression vectors into a prokaryotic or eukaryotic cell encoding the AEP and the polypeptide precursor, enabling expression of the vector to produce a recombinant AEP and a recombinant linear polypeptide precursor and isolating a cyclic peptide or peptide conjugate from the appropriate compartment or expression medium of the eukaryotic or prokaryotic cell wherein the expression vector is a multi-gene expression vehicle consisting of a polynucleotide comprising from 2 or more transcription segments, each segment encoding the AEP or linear polypeptide precursor, each segment being joined to the next in a linear sequence by a linker segment encoding a linker peptide, the transcription segments all being in the same reading frame operably linked to a single promoter and terminator.

8. The method of Claim 1 wherein the cell is *E. coli or* a yeast wherein the yeast is *Pichia* spp., *Saccharomyces* spp. or *Kluyvermoyces* spp.

9. The method of Claim 1 wherein the cyclic peptide or peptide conjugate exhibits antipathogenic or therapeutic properties including for the treatment of infection or infestation by a pathogen or treatment of cancer, cardiovascular disease, immune disease and pain.

10. The method of Claim 1 wherein the C-terminal AEP processing site comprises P3 to P1 prior to the actual cleavage site and comprising P1' to P3' after the cleavage site towards the C-terminal ends wherein P3 to P1 and P1 to P3 have the amino acid sequence:

$X_2X_3X_4X_5X_6X_7$

wherein X is an amino acid residue and:

X_2 is optional or is any amino acid;

X_3 is optional or is any amino acid;

X_4 is N or D;

X_5 is G or S;

X_6 is L or A or I; and

X_7 is optional or any amino acid;

and/or wherein the N-terminal processing site may contain no specific AEP processing site or may contain a processing site defined by any one of the P1" through P3" wherein P1" to P3" is defined by:

$X_9X_{10}X_{11}$

wherein X is an amino acid residue:

X_9 is optional and any amino acid or G, Q, K, V or L;

X_{10} is optional or any amino acid or L, F or I or an hydrophobic amino acid residue;

X_{11} is optional and any amino acid.

11. The method of Claim 10 wherein X_2 through X_7 comprise the amino acid sequence:

$X_2X_3NGLX_7$

wherein X_2, X_3 and X_7 are as defined in Claim 10 above; and

wherein X_9 through X_{11} comprise the amino acid sequence:

GLX_{11}

wherein X_{11} is optional and any amino acid.

12. The method of Claim 1 wherein the AEP processing site comprises N- and C-terminal end sequences comprising the sequence:

GLX_{11} $[X_n]$ $X_2X_3NGLX_7$

wherein X_{11}, X_2, X_3, and X_7 are as defined above and $[X_n]$ is absent (n=0) or any amino acid residue in a sequence of from 1 to 2000 amino acids.

13. The method of Claim 1 wherein the cyclic peptide or peptide conjugate comprises a functional portion fused or embedded in a backbone framework of a cyclotide.

14. An agronomical composition or pharmaceutical composition comprising the cyclic peptide or peptide conjugate generated by the method of Claim 1.

15. A method for identifying an AEP with cyclizing ability, said method comprising co-incubating an AEP to be tested with an internally-quenched fluorescent (IQF) peptide and assaying for a change in fluorescent intensity over time due to fluorescence upon spatial separation of a fluorescence donor/quencher pair following enzymatic cleavage of the peptide wherein an elevation in the of fluorescent intensity is indicative of an AEP with cyclizing ability wherein fluorescence intensity is monitored over time at excitation/emission wavelengths 320/420nm wherein preferably the IQF peptide is selected from the group consisting of Abz-STRNGLPS-Y($3NO_2$) [SEQ ID NO:21] and Abz-STRNGAPS-Y($3NO_2$) [SEQ ID NO:25]; or a method for determining whether an AEP is likely to have cyclization activity, said method comprising determining the amino acid sequence of the AEP, aligning the sequence with a best fit to the amino acid sequence of $OaAEP1_b$ (SEQ ID NO:1) and screening for the presence of 5 or more of residues or absence of residues at 180K, 219D, 274K, 280D, 352C, 353Y, 359Q, 361A, 379V, 506H, 519Gap, 520Gap, 521Gap, 525Cap, 526Gap, 542E and 544G wherein gap means the absence of a residue wherein the presence of 5 or more of the listed residues or absence of residues is indicative of an AEP which is a cyclase.